A THEORY OF CONCEPTUAL ADVANCE: EXPLAINING CONCEPTUAL CHANGE IN EVOLUTIONARY, MOLECULAR, AND EVOLUTIONARY DEVELOPMENTAL BIOLOGY

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Abstract

The theory of concepts advanced in the dissertation aims at accounting for a) how a concept makes successful practice possible, and b) how a scientific concept can be subject to rational change in the course of history. Traditional accounts in the philosophy of science have usually studied concepts in terms only of their reference; their concern is to establish a stability of reference in order to address the incommensurability problem. My discussion, in contrast, suggests that each scientific concept consists of three components of content: 1) reference, 2) inferential role, and 3) the epistemic goal pursued with the concept's use. I argue that in the course of history a concept can change in any of these three components, and that change in one component — including change of reference — can be accounted for as being *rational* relative to other components, in particular a concept's epistemic goal.

This semantic framework is applied to two cases from the history of biology: the *homology concept* as used in 19$^{\text{th}}$ and 20$^{\text{th}}$ century biology, and the *gene concept* as used in different parts of the 20$^{\text{th}}$ century. The homology case study argues that the advent of Darwinian evolutionary theory, despite introducing a new definition of homology, did not bring about a new homology concept (distinct from the pre-Darwinian concept) in the 19th century. Nowadays, however, distinct homology concepts are used in systematics/evolutionary biology, in evolutionary developmental biology, and in molecular biology. The emergence of these different homology concepts is explained as occurring in a rational fashion. The gene case study argues that conceptual progress occurred

with the transition from the classical to the molecular gene concept, despite a change in reference. In the last two decades, change occurred internal to the molecular gene concept, so that nowadays this concept's usage and reference varies from context to context. I argue that this situation emerged rationally and that the current variation in usage and reference is conducive to biological practice.

The dissertation uses ideas and methodological tools from the philosophy of mind and language, the philosophy of science, the history of science, and the psychology of concepts.

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PREFACE

This dissertation grew out of my graduate studies at the University of Pittsburgh, where the Department of History and Philosophy of Science and the Department of Philosophy provided a wonderfully stimulating environment and many opportunities for philosophical discussion. During my years in Pittsburgh, the Department of History and Philosophy of Science has been my intellectual home, and I am grateful to the whole faculty for their outstanding intellectual and financial support, to Rita Levine and Joann McIntyre for administrative support, and to the HPS graduate students for the exchange of ideas and emotional encouragement.

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My greatest debt is to my dissertation advisors Paul Griffiths and Anil Gupta. Anil helped me in getting clear about what my philosophical project is most fundamentally after, and he provided crucial advice on how to understand epistemic and semantic issues arising in science using ideas from the philosophy of mind and language. I have worked with and received intellectual guidance from Paul since the beginning of my studies at Pittsburgh. He was patient with me at all stages of my graduate career, and among other things showed me how to use various methodological tools and combine ideas from different philosophical and non-philosophical disciplines for a fruitful philosophical study of biology. Paul's work and ideas influenced the whole dissertation.

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1.0 INTRODUCTION

One central object of study for philosophy is the human intellect. Philosophy attempts to understand rationality and objectivity as a characteristic of different forms of theoretical and practical reasoning. This is a study in philosophy of science, and thereby concerns a particular manifestation of the human intellect — science. From this perspective, philosophy of science is metascience in that one of its central aims is *the study of scientific rationality*, which is to a large extent an epistemological concern. The particular topic of the dissertation is conceptual change in science, more specifically, *conceptual change in biology*. The task of a discussion of conceptual change is the study of historical episodes in science so as to offer a philosophical account of how and why scientific concepts, scientific language use, and scientists' epistemic practices changed. A fundamental assumption of the present discussion is that *conceptual change is rational* (for the most part), so that a central task for a study of conceptual change is to offer an account of why it was rational for a scientific community to change the meaning of certain scientific terms. This can by rephrased by saying that an account of conceptual change involves two basic components: *conceptual phylogeny*, i.e., the historical study of concepts and their change; and *conceptual ecology*, an account of the intellectual and epistemic factors associated with concept use, which may bring about conceptual change and account for the rationality of semantic change.

Philosophy of science, as branch of philosophy, obviously uses philosophical tools and ideas from philosophy. As it studies science and scientific rationality, philosophy of science necessarily has to pay close attention to how science works and the philosopher of science must have a good grasp not only of basic scientific theories, but of scientific practice as well. Apart from the methods of philosophy and science, a third crucial domain the philosopher has to know about is the history of science. There is a simple argument for why the study of the history of science is relevant for the present discussion. My concern is conceptual change in science, which necessarily involves historical changes in science. But there is also a reason why the history of science is important for any study

in philosophy of science. History of science is relevant for philosophy of science similar to the way in which history of philosophy is important for contemporary philosophical issues. Philosophy of science often addresses conceptual problems and theoretical debates in contemporary science. However, a full understanding of such current issues makes it necessary to know about the history of science. For conceptual problems have certain presuppositions which can be made explicit and understood only by studying the history of this problem (Lennox 2001a, 2001b). Contemporary debates and theoretical issues may have certain parallels to past debates and ideas that scientists have forgotten in the meantime, so that an understanding of historical episodes in science may yield clues as to how to successfully address contemporary issues. In these pages I will not offer a defense of the general relevance of the history of science for the philosophy of science, as it is uncontroversial that for my particular purpose — the study of conceptual change — a consideration of the history of science is important. (Some aspects of my cases studies hint at the import of history for current science, though.) In sum, an account of conceptual change presupposes knowledge about the theories and methods from philosophy, science, and history of science.

The dissertation proceeds according to the following strategy. First, I shall lay out a basic *framework of concepts and conceptual change*, which is intended as a methodological tool to study concrete instances of conceptual change in biology. Then this framework will be used to understand two cases from the history of biology: the *homology concept* and the *gene concept*. I shall offer detailed philosophical discussion of the history of each concept, applying my semantic framework to these historical episodes. The central tenet is that the framework developed and used is fruitful as it offers philosophical insights about these instances of conceptual change. An account of conceptual change presupposes an account of concepts. The notion of concepts is a crucial notion from the philosophy of mind and language, and philosophers have offered different semantic theories and accounts of concepts. My study in the philosophy of science is sensitive to semantic considerations and demands on theories of concepts, as they arise in the philosophy of mind and language. Overall, the dissertation uses ideas and methodological tools from *the philosophy of mind and language, the philosophy of science, the history of science, and the psychology of concepts*.

The first main chapter (Chapter 2) addresses the topic of conceptual change from the point of view of the philosophy of science. It criticizes standard approaches to concepts in the philosophy of science, so as to motivate my alternative framework (to be developed in the subsequent chapter). Traditional studies of conceptual change have focused on rebutting the *incommensurability* threat and therefore emphasized *referential stability*, while being reluctant to admit differences in meaning

or change in meaning, so that the very notion of meaning was avoided. However, an exclusive focus on reference is unwarranted. For the incommensurability problem is ultimately about the possibility of rational theory choice, and thus an epistemic issue that cannot be solved by purely semantic notions such as reference. In contrast to traditional approaches in the philosophy of science, my discussion explicitly acknowledges that scientific terms may *change in the meaning*, assuming that substantial meaning change and the emergence of novel concepts is part of and constitutive of scientific progress. In some cases even the reference of a scientific term may change, and this has to be philosophically accounted for as well. Thus, the central task is to work toward an account of concepts that underwrites the idea that *semantic change in science such as meaning and reference change is rational*. Three *desiderata for a theory of conceptual change* emerge from this discussion. An account of conceptual change should include: a) an account of concept individuation that permits the philosopher to track meaning change and to detect the emergence of novel concepts; b) an intellectual explanation of why conceptual change rationally occurred; c) an evaluation of whether or not conceptual change was progressive. A prominent and sophisticated account of conceptual change, Philip Kitcher's theory of conceptual progress is discussed and criticized in detail. Kitcher views a scientific concept as a 'reference potential' (a set of modes of reference associated with a term). Apart from unsolved semantic issues in his account, the main criticism is that Kitcher's account of concepts fails to meet my above three desiderata. In particular, his account leaves out important features of concepts that rationally bring about conceptual change, and that constitute conceptual progress. This is the way in which concepts are used for the purposes of inference and explanation. A crucial aspect of conceptual progress is that novel concepts permit scientists to justify new hypotheses, explain novel phenomena, or conduct practical discovery in a more effective way. While Kitcher — in line with the tradition in philosophy of science — views concept possession as the *ability to refer to categories in the world*, I emphasize that concept possession also entails crucial epistemic abilities, such as the *ability to justify hypotheses and explain phenomena*.

Chapter 3 approaches the issue of concepts and conceptual change from the perspective of the philosophy of mind and language. On my account, the very rationale for introducing semantic notions such as 'concept' and 'meaning' is to address *Two Constraints on Any Theory of Scientific Concepts*. Such a theory has to account for A) *how a concept makes successful practice possible* (including how it figures in communication and rational reasoning and action), and B) *how a concept can be subject to rational change* in the course of history. I argue that adequately addressing these constraints makes it necessary to acknowledge several semantic properties. More specifically, I

suggest that *there are three components of content*, in that each scientific concept has to be studied in terms of *1) the concept's reference, 2) the concept's inferential role, and 3) the epistemic goal pursued by the concept's use*. These are different components of content or different dimensions of meaning as in the course of history a term's meaning can change along any of these dimensions. All three are to be acknowledged as genuine semantic aspects of a scientific concept as change in one component can be philosophically accounted for with reference to the other components.

Most of the various semantic doctrines found in the philosophy of mind and language acknowledge reference as a property of a concept. While the notion of reference does in some cases bear on accounting for how a concept makes successful practice possible (Constraint A), I suggest that often an adequate account has to make use of a more fine-grained semantic property, such as a concept's inferential role (also called conceptual role), which is the inferences and explanations supported by a concept as shared by a language community. Apart from the doctrine of semantic atomism — which views reference as the only component of content — most other traditional semantic theories acknowledge the notion of inferential role or similar semantic notions such as term's intension, which in one way or another represent certain beliefs individuals have about a term's referent (e.g., analytic statements as meaning-constitutive statements about the referent). While semantic theories in the philosophy of mind and language have more or less directly paid attention to the question of how a concept underwrites successful communication, reasoning, and action (Constraint A), my account stresses the additional question of accounting for the rationality of a scientific concept's change (Constraint B). To this end, my semantic theory introduces a third and novel component of meaning: the *epistemic goal* pursued by a term's use. The idea is that scientists have certain reasons for introducing or continuing to use a particular concept. Scientists use concepts for particular epistemic purposes, e.g., a concept is supposed to be able to confirm certain kinds of hypothesis, to explain certain phenomena, or to support effective discovery. While it is not surprising that a scientific field has certain epistemic and theoretical goals, my point is that an individual scientific concept may be used by a scientific community to pursue certain epistemic goals. I view epistemic goal as a genuine component of a concept's content as this philosophical notion is vital for accounting for the *rationality of conceptual change* (Constraint B). In a nutshell, the particular epistemic goal pursued by a concept's use sets the standards for which changes in the other components — inferential role or reference — count as rational. Given an epistemic goal, a concept is intended to deliver a particular epistemic product (certain kinds of inferences and explanations), and changing a concept's inferential role is rational if the new inferential role (the

inferences and explanations supported by the concept at this later point) meets the epistemic goal to a higher extent than the old version of the concept.

For the most part, the semantic notions of *inferential role* and *epistemic goal* account for how A) a concept underwrites successful practice and B) can be subject to rational change; and these two notions form the basis for evaluating conceptual progress. Whereas traditional accounts in the philosophy of science have stressed the notion of *reference*, the dissertation shows that the historical change in reference is in need of explanation, rather than the notion of reference having explanatory significance in accounts of conceptual change. Overall, traditional semantic accounts in philosophy in general have construed concepts in terms of reference and/or assumed that a concept consists in certain *beliefs about the referent*. The novelty of my semantic theory is to introduce the idea of an epistemic goal being pursued by a concept's use, and to view this feature as an independent component of a concept's content. In a nutshell, in addition to studying a concept in terms of certain beliefs scientists have, the novel idea is that another relevant question is *what scientists are trying to achieve by having those beliefs* (as it accounts for the rationality of semantic change).

While Chapter 2 among other things motivates the idea that concepts are closely related to inference and explanation from the point of view of the philosophy of science, Chapter 3 proposes a semantic account that does justice to this idea (without discussing other possible semantic theories that could account for the connection of concepts and inference). My semantic approach aligns in two ways with *inferential role semantics* as a traditional account of meaning and conceptual content endorsed by some philosophers of mind and language. First, I acknowledge inferential role as a genuine component of content. Second, I endorse inferential role semantics as an account of philosophical semantics *sensu* Brandom (1994), i.e., as an account of those features in virtue of which a person counts as possessing a concept. I assume that a term obtains its semantic properties (reference, inferential role, epistemic goal) in virtue of its overall use, which I call *total inferential role*. On my approach, meaning is not identical to total inferential role (as inferential role semantics is sometimes misconstrued), rather meaning is determined by total inferential role. I endorse a *moderate holism* about meaning determination, by assuming that each of a term's three semantic properties need not be reducible to particular beliefs or causal relations between the individual and the world. For instance, a concept being used to pursue a certain epistemic goal is not even determined by the beliefs and actions of a single scientist, but is an emergent feature of this concept's use within a whole scientific community. Given the significance of the notion of inference for my semantic approach, Chapter 3 offers a detailed explication of the notions of

inference and inferential role. I also adduce several motivations for inferential role semantics; and given prominent criticism of this approach, I address some of its challenges: the compositionality of concepts (as put forward by Fodor), the relation between inferential roles and reference, and the sharing of concepts between individuals. Appendix A points to some parallels between my semantic account (in particular the notion of inferential role) and recent developments in the psychology of concepts.[1]

The semantic account in Chapter 3 is spelled out in sufficient detail to support the idea that inferential role semantics is a viable account of meaning. However, the account of concepts developed in the dissertation is not defended as the right metaphysical account of the nature of concepts (or as a theory of intentionality). Rather it is laid out to be used as a *methodological tool* for studying conceptual change in science, to be evaluated in terms of its fruitfulness for this task. My philosophical aim is not so much to give a metaphysical analysis (such as a naturalistic reduction) of the semantic properties of reference, inferential role, and a concept's epistemic goal. My primary aim is to show that these semantic properties can be ascribed to certain scientific terms as actually used, that the historical change of these semantic features can be studied in actual cases, and that this yields semantic and epistemological insights about scientific practice, in particular that the historical change in these three components of concepts can be accounted for as rational.

A relevant topic for my semantic account is the individuation of scientific concepts. For my biological case studies will make claims about how many and which homology and gene concepts have been used at a particular point in time or across history. Given that on my account terms may change and differ in several semantic properties (reference, inferential role, epistemic goal), dissimilarity with respect to several or simply one of these features could be philosophically relevant and thus the basis for postulating different concepts being in use. As a result, there need not be unique criteria of concept individuation, and the labeling of two scientists' term use as expressing the same or a different concept may not be fruitful as such. Most contemporary philosophers of mind and language — unless they reject the very notion of meaning — endorse a meaning monism, by assuming (at least implicitly) that concepts have unique and determinate meanings and that a concept can be individuated in a unique and clearly delineated way. I criticize some such proposals as to how to individuate concepts, in order to motivate an alternative approach — *meaning pluralism*. This is the idea that some scientific concepts can be individuated in more than one way. My

[1] While my notion of the epistemic goal of a concept's use goes beyond inferential role semantics, it broadly aligns with this approach in that a concept's epistemic goal is not the demand that a concept refer to certain entities, but the demand that a concept support certain inferences and explanations, i.e., that it has an intended inferential role.

suggestion is that each instance of concept ascription is based on particular philosophical purposes, which may vary from case to case. Since the same concept can by approached in different studies with different philosophical aims in mind, different studies may individuate this concept in a different way. My case studies will base their individuation decisions on two basic considerations. First, as regards inferential role I do not assume that for two persons to share a concept it is necessary that they endorse the same set of inferences. For while concept possession presupposes having certain epistemic abilities (such as carrying out inferences), in the case of a scientific concept these epistemic abilities may be spread out over a whole community, so that the successful communal use of a concept may be dependent on some scientists making different inferences. Therefore, I do not endorse the traditional picture according to which two persons share a concept if they have grasped the same definition or accept the same analytic statements. Instead, concept possessions consist in having a minimal set of inferential dispositions and epistemic abilities so as to be able to meaningfully communicate with other scientists and to conduct scientific research. Second, in my context the epistemic goal of concept use will be the most significant semantic property for concept individuation. The idea is that scientists count as investigating the same phenomenon and pursuing the same scientific problem not if they merely happen to refer to the same entity with a term, but if they use this term for the same epistemic purpose. Different scientists will react to novel empirical findings and challenges in similar ways and be able to communicate with each other to the extent to which they use a term to pursue the same epistemic goal, so that this semantic property is significant for concept individuation.

This basic framework of concepts and conceptual change will in turn be applied to two concrete cases from the history of biology: the *homology concept* as used in different branches of comparative biology in the 19$^{\text{th}}$ and 20$^{\text{th}}$ century, and the *gene concept* as used in 20$^{\text{th}}$ century genetics and molecular biology. Both concepts are central biological concepts: Homology individuates biological characters by breaking down an organism into its natural units (each of which can evolve relatively independently of the others). The homology concept achieves this by viewing the corresponding token-units in different organisms as type-identical, calling one structure in an individual 'homologous to' a structure in another organism. For instance, two structures in different species are homologous in case they are derived from the same structure in the common ancestor. The homology concept is the core notion of comparative and evolutionary biology, in that it is conceptually presupposed by any biological practice that studies different species and the evolution of biological characters. Given that homology individuates biological characters, it can be viewed as

the fundamental notion of all of biology. The gene concept has likewise proven to be an important concept, at least for recent biology. While it is a notion from molecular genetics, genes are studied by and knowledge about genetic mechanisms is used by many other biological disciplines. As a consequence, the gene concept is used in a variety of contemporary biological subdisciplines: biochemistry, molecular biology, developmental biology, and evolutionary biology, among others. Apart from being important biological concepts, the homology concept and the gene concept are suitable for a study of conceptual change as both have a rich history and underwent semantic change while being used in different historical periods and in different biological fields. Despite its biological importance and novel developments in recent years, the homology concept has been subject to only sparse philosophical discussion.[2] For this reason, apart from the semantic questions and the semantic framework pursued in my later chapters, I am convinced that my thorough discussion of the homology concept offers novel historical and philosophical perspectives on this concept. The gene concept, in contrast, has been widely discussed in the philosophical literature (at least in the context of the relation between classical and molecular genetics). This gives me the opportunity to compare my account with former studies, showing that my framework of concepts and conceptual change can offer a few new insights.

Whereas the homology concept has important implications for the study of evolution, it was introduced in pre-Darwinian comparative biology. Chapter 4 discusses the history of the homology concept until 1950. The conventional wisdom — an implicit or at least undefended assumption — among historians of biology, biologists, and philosophers of biology is that the advent of evolutionary theory brought about a novel homology concept: a Darwinian ('phylogenetic') homology concept, which is viewed as distinct from the pre-Darwinian ('idealistic') homology concept.[3] This is motivated by the fact that after Darwin, biologists defined homology in terms of common ancestry — unlike pre-Darwinian biologists. Based on a detailed study, I challenge this conventional wisdom by arguing that *Darwinism did not bring about a new homology concept in the 19^{th} century.* Motivated by my account of concepts and concept individuation, I focus on those aspects of the homology concept that were (and still are) the basis of its successful use in biological practice. It turns out that regards these features of the concept's use there is substantial continuity through-

[2]The studies published in philosophical journals during the last two decades of which I am aware are Amundson and Lauder (1994), Griffiths (1994, 1996b), Matthen (1998, 2000), Brandon (1999), and Brigandt (2002). Many of these do not offer a discussion of all aspects of homology. Brandon (1999) and Brigandt (2002) are the only ones addressing the important developmental approaches to homology that emerged in the 1980s.

[3]A corresponding assumption exists about a pre-Darwinian as opposed to a Darwinian species concept, but this question has been explicitly debated by historians and philosophers of biology.

out the 19th century, whereas particular definitions of homology (which may or may not appeal to common ancestry) are largely peripheral to the content of the homology concept. The practice embodied by the homology concept — for the most part developed prior to Darwin — yielded crucial support for evolutionary theory and the idea of common ancestry, as the homology concept as used before Darwin was able to provide a good deal of the evidence for the construction of phylogenetic trees. Furthermore, the advent of evolutionary theory did not change what biologists were trying to achieve when using the homology concept. Thus, my account emphasizes the conceptual continuity regards the homology concept in the 19th century, and highlights the potential of the (pre-Darwinian) homology concept to underwrite later phylogenetic research.

While denying that 19th century evolutionary theory introduced a novel homology concept, I do think that new homology concepts emerged in the course of history. This happened, however, in the second half of the 20th century as a result of the increasing disciplinary specialization in biology. Once the original homology concept entered newly developed biological subbranches and came to be used in them, conceptual change and diversification took place. Chapter 5 argues that currently three distinct homology concepts are used in systematics/evolutionary biology, in evolutionary developmental biology, and in molecular biology — which I call *the phylogenetic, the developmental, and the molecular homology concept*, respectively. These are different concepts as they support different types of inferences and explanations, and are used for different epistemic purposes. Not only do different biological branches have different theoretical goals, but each of these fields uses its homology concept to pursue its particular theoretical goals. In fact, my study explains the *rational* emergence of distinct homology concepts by the fact that the original homology concept — having entered new biological fields — came to be used by different fields for different *epistemic goals*. The resulting conceptual diversification and the fact that nowadays the term 'homology' corresponds to distinct concepts is conducive to biological practice as each of these concepts is a specialized conceptual tool effectively fulfilling some scientific functions. Thus, the study illustrates how a scientific field changes and shapes a concept, until the concept is designed to meet the epistemic goal pursued with its usage in an adequate fashion.

A large part of this second homology chapter is concerned with the developmental homology concept and the field in which it is used — *evolutionary developmental biology* (evo-devo). As an independent discipline, evo-devo is a quite recent approach to evolution that emerged in the last two decades. While traditional neo-Darwinian evolutionary theory maintains that the study of development has no bearing on understanding the mechanisms of evolutionary change, evolution-

ary developmental biologists argue that knowledge about developmental mechanisms is the key to explaining several crucial evolutionary phenomena, such as evolvability and the origin of evolutionary novelties and body plans. Evo-devo thereby has a broader understanding of the causal factors in evolution and makes use of a richer explanatory framework. A central task for this field is to work towards a developmental homology concept, which bears on accounting for morphological evolvability (how organismal organization makes phenotypic variation possible on which natural selection can subsequently act, thereby providing the basis for flexible and functionally integrated morphological evolution). An interesting feature is that evolutionary developmental biology as a progressive contemporary approach to evolution in general, and the developmental homology concept in particular, revive ideas from 19$^{\text{th}}$ century biology, including pre-Darwinian ideas about homology. One such parallel between 19$^{\text{th}}$ century morphology and evo-devo is the idea that homologous structures are governed by the same developmental principles. As a consequence, evo-devo approaches view common ancestry as a sufficient, but not as a necessary condition for two structures being homologous — in contrast to the phylogenetic homology concept nowadays used in mainstream evolutionary biology, which identifies homology and the common ancestry of traits. While Section 5.2 focuses on the developmental homology concept and how it bears on the scientific goals of evo-devo, Appendix B provides a more detailed discussion of this new field.[4]

The semantic account of the phylogenetic and the developmental homology concept forms the basis of a *critique of the causal theory of reference for natural kind terms*. I argue that the causal theory offers an inadequate account of the factors that determine the reference of these homology concepts, even though they are natural kind concepts. Traditional descriptive theories of reference — focusing on descriptions of the referent — are also found to leave out relevant factors that determine reference. My suggestion is that some additional features that influence reference determination are the pragmatic and epistemic features associated with concept use, such as the epistemic goals that scientists pursue with using a particular concept.

Chapter 6 turns to the historical change of the gene concept. The first section addresses the gene concept in classical genetics until the emergence of a molecular gene concept in the late 1950s. I give a brief overview of the very origin of the classical gene concept, the practical methods that were

[4]This is one example that clearly shows that the history of science crucially bears on the philosophy of science. Understanding even remote history (19$^{\text{th}}$ century morphology, including pre-Darwinian morphology) can contribute to understanding contemporary biology in a better fashion. Some contemporary conceptual problems and theoretical debates about some aspects of evolution had partial historical antecedent, though they occurred in a seemingly different context (such as pre-Darwinian biology). This shows that modern conceptual problems and theoretical debates are not just about what we usually take them to be, so that a consideration of the history is vital for our current situation — for getting a better idea about potential ways to address conceptual and methodological problems.

used to find out about the properties of genes, and the changing conceptions and disputes about the nature of classical genes. The main aim is to explicate what I view as the classical gene concept, based on how it was used in experimental practice and in theoretical explanations. A fundamental feature is that while the classical gene concept supports the prediction of Mendelian patterns of inheritance, it underwrites explanations only in the sense of explaining phenotypic *differences* in terms of genotypic *differences*. The chapter briefly discusses how this concept is used in population genetics, showing that the classical gene concept is actually used in some contemporary branches of biology. This way of individuating the classical gene concept highlights the contrast with the molecular gene concept (discussed in the remainder of the chapter), so as to exhibit conceptual progress. Yet in line with my meaning pluralism, I offer an additional way to individuate the gene concept as used by classical genetics. I distinguish different classical gene concepts so as be in a position to explain how classical genetics developed and gave rise to molecular genetics.

Then the discussion proceeds with the molecular gene concept as used in the 1960s and 70s, the so-called *classical molecular gene concept*. I contrast the classical (Mendelian) gene concept with the molecular gene concept. They are distinct concepts as they differ in the type of explanations they support and the epistemic goals pursued by their use. In the 70s and 80s, philosophers of biology prominently debated whether the theory of classical genetics can be reduced to the theory of molecular biology. I follow the majority by assuming that classical genetics cannot be reduced to molecular biology, and emphasize that the classical gene concept is still important for certain tasks, even within molecular biology. One motivation for the reduction debate was the idea that a historically later theory reducing a precursor theory is a clear-cut type of progress. Likewise, debates about scientific progress in general philosophy of science — surrounding issues such as realism, incommensurability, and the pessimistic meta-induction — have assumed that conceptual progress necessarily requires that the reference of a term remains stable, so that scientists' conception of *this* referent can improve. However, neither stability of reference nor reduction apply to the transition from the classical to the molecular gene concept. *Despite the fact that the classical gene concept cannot fully be replaced by or reduced to the molecular gene concept, and despite the reference of the term 'gene' changing from classical to molecular genetics, there is still a clear sense in which substantial conceptual progress occurred with the advent of the molecular gene concept.* The molecular gene concept is theoretically more powerful than the classical gene concept as it supports causal-mechanistic explanations of molecular, cellular, and developmental phenomena that cannot be delivered by the classical gene concept. Given that different epistemic goals are pursued with

the classical and the molecular gene concept, even what biologists were trying to achieve by using the term 'gene' changed in the history of genetics. Yet I show how this substantial semantic change can be conceived of as occurring in a rational fashion. On my account, the change of reference that occurred (largely unbeknownst to geneticists) with the advent of the molecular gene concept was a mere by-product of rational and progressive meaning change.

The final part of Chapter 6 addresses conceptual changes that occurred in the last two decades — leading to the *contemporary gene concept*. More recent findings rejected the assumption of the 60s and 70s that genes are structurally defined and clearly delineated genetic units. Nowadays, genes are viewed as forming a very heterogeneous category. Different biologists may disagree as to whether or not a certain genetic element is actually a gene and how to tell whether something is a gene. A consequence of this recent development is that the usage of the contemporary gene concept varies substantially — even the reference of the term 'gene' may vary from context to context. On my account, the contemporary gene concept can be viewed as a single concept, but it is a fragmented concept, which exhibits substantial variation across the various fields in which it is used. I consider the context-sensitivity and flexibility of the molecular gene concept an epistemically significant feature, and explain how this instance of *context-dependent variation in usage and reference promotes successful biological practice*. The discussion suggests that in an important sense, the *contemporary molecular* gene concept is still the same concept as the *classical molecular* gene concept (as both are used to pursue the same epistemic goal). At the same time, genuine change occurred internal to this concept during the last three decades, and I explain that this change can be accounted for as *rational* based on the concept's epistemic goal (and novel empirical findings). Finally, in particular the recent history of the gene concept shows that the reference of the term 'gene' changed across time, and changes even from context to context. I use this fact to argue for a *moderate holism about reference determination*, pointing out that semantic accounts of indexicals cannot easily capture this case of context-sensitive reference.

The concluding chapter (Chapter 7) briefly restates my framework of concepts and evaluates its merits and fruitfulness for the study of conceptual change in science. This proceeds by a summary of the main results of the two case studies from the history of biology, highlighting the semantic and epistemological insights that the application of my framework to these cases yielded. Some of the facts about the biological case and the semantic point made have implications for any theory of conceptual change, so that I conclude with laying out some of the constraints for theories of concepts and conceptual change that emerge from the two biological concepts discussed.

2.0 CONCEPTUAL CHANGE AS A PHILOSOPHICAL PROBLEM

This first main chapter lays out the ways in which philosophers of science have addressed the issue of conceptual change in the last few decades. Typically, accounts of conceptual change in science have tried to deal with the problem of semantic incommensurability, as stemming from the work of Kuhn and Feyerabend. Since the main reply to the incommensurability threat was to focus on the reference of scientific terms, in the first section I shall review and discuss how theories of reference were employed in the philosophy of science. An account of reference alone, however, cannot solve every issue a theory of conceptual change should address. For this reason, my second section will present the theory of conceptual progress advanced by Philip Kitcher. Kitcher's theory is a very sophisticated account of conceptual change that goes beyond the mere study of reference. My critical discussion of Kitcher will reveal that his account does not address certain aspects of conceptual change that I view as crucial. The reason is that Kitcher's approach like most former accounts in the philosophy of science are still primarily attempts to solve the incommensurability problem and consequently neglect other important aspects of conceptual change. I shall make explicit what I view instead as some crucial questions a good theory of conceptual change should address. Thus this chapter will lay out my constraints on a theory of conceptual change, which my own approach to concepts and conceptual advance in science — presented in the subsequent chapter — is intended to meet. In sum, the goal of this introductory discussion is to point out the limitations of former approaches that were used to analyze and explain change of scientific concepts, and to motivate my alternative framework.

2.1 REFERENTIAL APPROACHES TO CONCEPTS AND CONCEPTUAL CHANGE

During most of the second half of the 20$^{\text{th}}$ century, conceptual change was not just seen as a fact that needs to be studied and explained. The very idea of conceptual change became a genuine philosophical problem. This situation is primarily due to the work of Norwood Russell Hanson, Thomas Kuhn, and Paul Feyerabend. Some of their ideas — most prominently the notion of incommensurability of theories — challenged the view that scientific change is progressive and that scientists have good reasons to prefer one theory over another. Hanson (1958) made popular the idea that scientific observations are theory-laden, and the subsequent discussion of Kuhn and Feyerabend used this idea to claim that researchers endorsing substantially different theories sometimes cannot agree on their observations and perceptual evidence. This potential challenge to scientific rationality may be called the incommensurability of perceptions. Apart from this, Kuhn argued for the incommensurability of standards. The idea is that different paradigms embody different standards as to what scientific phenomena have to be explained, what counts as an adequate explanation, and what counts as evidence for a hypothesis, so that the arguments advanced by scientists from one paradigm inevitably beg the question against the evidential and methodological standards of another paradigm. The third type of incommensurability is the incommensurability of meaning or the *incommensurability of concepts*. Semantic incommensurability has been viewed as the main threat to the picture that science is objective and progressive. As a result this type of incommensurability has received most of the attention among philosophers of science — in attempts to show that there is no semantic incommensurability at all or at least no problematic incommensurability. Consequently, my following discussion will deal with the incommensurability of concepts only.

Positivist philosophy of science was committed to a theory-independent observation language that serves as an epistemic basis for different theories. In addition, models of theory reduction assumed that precursor theories can be logically deduced from more mature theories. Feyerabend (1962, 1965a, 1965b) claimed that both assumptions relied on the idea that observational as well as theoretical terms occurred with the *same meaning in different theories* — otherwise observational statements cannot apply to several theories and the content of one theory cannot be deduced from another theory. Against this, he argued that the meaning of a term is given by the theoretical context in which it occurs (more precisely, the fundamental principles of a theory), so that there are meaning differences between theories that use different basic principles. Since corresponding state-

ments actually differ in meaning, Feyerabend suggested that theories containing incommensurable concepts do not make predictions that can be compared (1962, p. 94). In fact, the content of such theories cannot be compared due to meaning incommensurability (1970, p. 90). Kuhn (1962) came to similar conclusions, making fundamental use of the notion of a paradigm. His original discussion implicitly assumed that the meaning of scientific terms is given by the theoretical framework of a particular paradigm, so that different scientific theories or paradigms may have a certain term in common, but associate a completely different meaning with it. A term occurring in different theories with a different meaning was viewed by Kuhn as having different physical referents (1962, p. 100). One of his controversial claims was that due to these meaning differences, scientist from rival paradigms fail to communicate properly and tend to talk past each other (pp. 108, 131). Kuhn's and Feyerabend's claims about semantic incommensurability proved to be fundamental challenges for the standard picture of science and its history. Since seemingly contradictory statement can be true at the same time given that the terms appearing in them have a different meaning (Kuhn 1962, pp. 148), it appears to be impossible that two theories contradict each other. The notion of semantic incommensurability challenges the idea that we can effectively compare diverging claims or theories. If we cannot say that certain claims involving a term are true while others are false, an account of scientific progress becomes impossible.

Philosophers were quick to point out problems with Kuhn's and Feyerabend's position. First, even though their arguments about incommensurability essentially depend on semantic notions such as the meaning of terms, in particular Kuhn did not provide an explicit account of concepts and their meaning. In fact, Feyerabend's and Kuhn's claims appear to be based on incoherent or implausible semantic views (Achinstein 1964; Shapere 1966; Scheffler 1967; Achinstein 1968; Kordig 1971). Their assumption was that scientific theories provide implicit definitions of their terms, so that a change of theoretical postulates implies a change in the meaning of a term. But in the meantime this came to be often viewed as a problematic and inadequate theory of the meaning of terms. Second and more important, even if this account of meaning is adequate and concepts from different theories are not intertranslatable, it does not follow that these concepts are not about the same thing. The main reply to the challenge of semantic incommensurability was to focus on the *reference* of scientific terms, and to point out that scientists may very well refer to the same entity despite the fact that they have different theories or different beliefs about this referent. Once common reference across different theories is secured, the claims of these theories can be semantically evaluated and compared. Thus Kuhn's and Feyerabend's tenet that meaning incommensurability prevents

the comparison of different theories turns out to be problematic once the distinction between meaning and reference is kept in mind. Israel Scheffler (1967) was only the first to argue against incommensurability based on a referential approach, as many other philosophers of science have stressed the importance of the notion of reference for an account of conceptual change and progress. Philip Kitcher puts this standard reply to the incommensurability threat succinctly as follows: "The remedy is to begin with the notion of reference" (Kitcher 1978, p. 522). In fact, as long as philosophers of science did not just address the change of theories in general, most studies of scientific *concepts* and their change in the last decades have been referential approaches to scientific concepts (Scheffler 1967; Putnam 1973a; Martin 1971; Fine 1975; Devitt 1979; Leplin 1979; Levin 1979; Newton-Smith 1981; Kitcher 1978; Hacking 1983; Burian 1985; Miller 1987; Papineau 1987; Sankey 1994, 1997a; Psillos 1999; Andersen 2001; Boyd 2002).

The crucial aspect of a theory of the reference of scientific terms is to explain how scientists with different theories and beliefs about the referent can still refer to the same entity. A solution to this question was offered by the emerging *causal theory of reference*, which was first proposed for names and singular terms by Keith Donnellan (1966, 1972) and Saul Kripke (1972). But soon this account was extended by Hilary Putnam to the reference of natural kind terms as well (Putnam 1970, 1973b, 1975; Kripke 1980). Former, so-called *descriptive accounts of reference* assumed that the referent of a term is that object that satisfies a defining description that a speaker associates with the term. The problem with this approach is that scientists often introduce concepts when they are still ignorant about the scientifically relevant features of the kind denoted. According to the causal theory of reference, we introduce a new term by picking out a certain sample of the natural kind that falls under this term. (The sample can be picked out by means of ostension or by description.) The extension of the term is the set of objects that belong to the same kind as the objects from the original sample. Nowadays natural kinds are often viewed as having an essence, which embodies the defining properties of the kind. Thus the picture is that nature does its share in the determination of reference. We can introduce concepts by picking out samples from a kind and the reference is determined according to the objective structure of the world even though we are still ignorant about the actual extension of the natural kind referred to.

Note that even though one may use a description to pick out a sample of the kind, this description does not define kind membership (Putnam 1970; Kripke 1980). For example, we may introduce the term 'swan' in Australia by picking out some Australian swans by a description that includes the fact that they have black feathers. Our term introduced will refer to all swans — the actual

natural kind — even though swans around the globe have for the most part white feathers. Thus, we can possess a concept without knowing about the properties of the kind denoted. This points to a solution to our original problem — even though scientists may have quite different beliefs about the nature of the kind, they still can refer to exactly the same kind. Another aspect of the causal theory of reference is the assumption that after the introduction of a term other people can inherit the reference of this term across generations. Thus a person may be ignorant or wrong about the features of kind, but she still refers to the same kind as others because the reference of the term as used by her is parasitic on prior established reference. The picture is that reference is stable, while scientists find out about the referent and thus their beliefs about the referent change.[1]

Some kinds as we find them in physics or chemistry are not observable, so that we cannot pick them out by ostension or description of their observable appearance. But the causal effects of these kinds can be observed, so that the referent of an introduced term is that kind that is causally responsible for the observed effects (Newton-Smith 1981; Sterelny 1983). Originally, the causal theory of reference was not developed for theoretical terms in general, but more specifically for natural kind terms (apart from singular terms). Its proponents, though, take many important scientific concepts to be natural kind concepts (Sterelny 1983; Stanford and Kitcher 2000; Fodor 1998a even assumes that all scientific concepts are natural kinds concepts). No matter whether most theoretical terms are best viewed as natural kind terms referring to kinds that have an essence, we can still use the insights of the causal theory, which explains how one can refer to entities in the absence of detailed knowledge about these entities in virtue of the structure of the world.

The causal theory of reference was in need of refinement and revision. In fact, while it was introduced in opposition to descriptive theories of reference, current theories include descriptive factors of reference fixing as well. This is due to several reasons. Michael Devitt made plain that a sample used to introduce a natural kind term is often a member of several natural kinds. A particular tiger, for instance, is a member of its species, its genus, a vertebrate, an animal, etc. So in order to obtain a valid account of the reference of natural kind terms in the first place, we have to take into account that at the introduction of the kind term the sample is viewed *qua* belonging to a certain type of natural kind. Thus certain descriptive information about the sample ('This is a new species') is a determinant of reference as well (Devitt 1981; Devitt and

[1] Another philosophically important aspect of the causal theory of reference concerns the modal dimensions of natural kind concepts, such as Kripke's notion of rigid designation. However, philosophers of science have not paid much attention to these issues because they are hardly relevant for their purposes. Philosophers of science extensively invoked the causal theory of reference precisely because it promises a solution to semantic incommensurability.

Sterelny 1999). This description necessarily applies to the members of the kind, as in the case of descriptive theories of reference but in contrast to purely causal theories. In addition, according to the purely causal picture, reference is established independent of information about the referent and inherited over generations in a stable fashion. Philosophers pointed out, however, that there are several cases from the history of science where scientific terms did not refer to anything (Fine 1975; Enç 1976; Zemach 1976; Nola 1980; Kroon 1985). The natural kind terms 'phlogiston' or 'ether' are such examples. Reference failure is due to the fact that certain descriptions were the reference-determining features of a concept (e.g., 'phlogiston is the substance that is emitted in combustion'), but there is actually no entity that has these properties. A purely causal approach, however, cannot account for reference failure (it may have to conclude that the term 'phlogiston' refers to oxygen, because oxygen is causally responsible for the reactions described by phlogiston chemists). In addition, scientific terms change their reference. But the assumption that reference is originally grounded and then simply inherited cannot account for this fact. Instead, descriptive factors such as scientist's beliefs may imply that former reference-grounding conditions are not effective any longer. If new beliefs about the referent become relevant for reference determination the reference may change. Nowadays theories of reference — including the reference of scientific and natural kind terms — combine both causal and descriptive factors of reference-fixing (Sankey 1994; Devitt and Sterelny 1999; Psillos 1999; Stanford and Kitcher 2000).[2]

2.1.1 Limitations of Referential Accounts in the Philosophy of Science

After this review of theories of reference, I want to address an unsolved issue. My claim is that current accounts are not sufficiently elaborated yet and do not offer a complete account of the reference of a term. This is due to the fact that nowadays two distinct components of reference-fixing are acknowledged — causal factors as well as descriptive factors — but it is not clear how these two components combine. In some cases, the reference of a term is fixed by a description. If a scientist makes a statement containing the term, then this term refers to those objects to which

[2]It is quite common to tell the history of theories of reference as used in the philosophy of science as I have done in the last few pages: see Sankey (1994), Chapter 2, and Weber (2005), Chapter 7.

Apart from the inclusion of descriptive considerations, causal theories offer further refinements. Devitt (1981) argued that the reference of a term is usually multiply grounded by different reference fixing events or several causal chains. This idea can account for continuous change of reference in the course of history. Kitcher's (1978) idea that different utterances of the same term may refer to different referents will be discussed below in Section 2.2. Field (1973) introduced the idea that a term can partially refer to several different extensions at the same time. If scientists originally conflated two distinct natural kinds, then the statements of these scientists partially refer to both kinds.

the property expressed by the statement applies. In other cases, however, the reference is fixed in a causal fashion. In such a case an uttered statement in which the term under consideration occurs is a claim about the referent, where the referent need not satisfy the description as reference is established causally. Thus the statement can be a false statement about the referent. The problem is that theories of reference have not offered yet an account that enables us to tell which of these two options obtains in a particular case.[3] This unsolved issue is particularly pressing as most causal approaches to reference are realist and naturalistic approaches, which assume that reference is a physical or at least objective relation between terms and objects. If there is a matter of fact to which objects a term refers, then we need an account in virtue of which objective features (causal or descriptive ones) the extension of a term is determined. From the point of view of the study of conceptual change, resolving how descriptive and causal factors precisely combine is important as *the two factors are invoked for different and conflicting reasons.* As an example take the discussion of incommensurability by Howard Sankey (1994). He starts out with a critique of descriptive theories of reference, pointing out that they lead to problematic incommensurability in the sense that different scientific theories cannot refer to the same object. As a solution he cheers the causal theory of reference.[4] When Sankey subsequently addresses issues such as reference failure and reference change, he simply states we can make use of descriptive factors of reference fixing — without addressing the issue that his discussion so far assumed that descriptive factors are the source of referential incommensurability.[5] Sankey like some others is not fully aware of the tension between the causal and descriptive component — a theory of reference that invokes both causal and descriptive factors could in principle inherit the problems of the purely causal theory in addition to the problems of the purely descriptive theory of reference. A combined theory of reference that shows how the two components actually integrate is likely to solve these potential problems — but such a theory is yet to be given.[6]

[3] As a third option, one could assume that both causal and descriptive factors combine to pick out the referent of a particular term. In this case, the question is what determines which descriptions and causal features pick out the referent and how causal and descriptive factors combine to pick out the referent.

[4] "Scheffler [criticizing Kuhn] himself worked with a classic description theory of reference ... However, such a theory of reference has acute difficulties in dealing with conceptual change: e.g. it implies excessive discontinuity of reference in the evolution of particular concepts and between rival concepts. Indeed, the description theory of reference even lends support to the incommensurability thesis: for theories with incompatible descriptive content would have no common reference and hence fail to enter logical conflict. The approach was extended by Putnam, who embraced referential comparison within a causal theory of reference. ... Hence theories may diverge conceptually even to the point of incompatible descriptive content, yet still have common reference." (Sankey 1994, pp. 36–37)

[5] "In this section I will discuss two problems which require extension of the causal theory of reference to include a greater role for descriptions in reference determination. These two problems are the so-called 'qua problem' and the problem of the reference of theoretical terms." (Sankey 1994, pp. 61)

Causal theories of reference are still quite popular in the context of natural kind terms (Devitt and Sterelny 1999; Stanford and Kitcher 2000). However, in Section 5.2.4 I shall argue against this assumption. The phylogenetic and the developmental homology concepts are two distinct natural kind concepts that differ in their extension. Thus, an adequate theory of reference has to account at least for this difference in extension. I shall argue that standard causal theories of reference cannot account for this. Moreover, nowadays even causal theories make use of descriptive factors of reference determination. But my claim will be that descriptions and other theoretical statements about the referent are also insufficient to mark this difference in reference. I shall suggest that in addition to causal factors and descriptions of the referent, there are other factors that have a crucial influence on reference determination. These are pragmatic aspects of how concepts are scientifically used and for what epistemic purposes they are used. As this argument is based on my discussion of the two homology concepts, I will present it in this later section of my dissertation. Apart from this case-based argument, Chapter 3 will present my own theory of concepts, with Section 3.2.2 offering some remarks on the nature of reference. But now I proceed with my discussion of the study of reference and conceptual change in the philosophy of science.

In the last few decades, most discussions in the philosophy of science about concepts and their change have focused on reference. As I explained, this is due to the fact that approaches to conceptual change have viewed the rebuttal of the incommensurability problem as their primary concern. A recent review by Richard Boyd puts is this way: "In the philosophy of science ... the impact of Hanson and Kuhn has been mainly to stimulate the articulation of naturalistic or causal conceptions of reference and essentialist conceptions of the definitions of scientific kinds and properties."[7] After this review of how and why theories of reference — in particular the causal theory of reference — are used in the philosophy of science, I turn to a critique of the standard motivation for the focus on reference. Even if the only goal of an account of conceptual change were to deal with the incommensurability threat, an account of reference is not sufficient for refuting incommensurability. I present two closely connected reasons for why reference alone cannot do the

[6]Another example is Stanford and Kitcher (2000), who first present a sophisticated version of a purely causal theory of reference, and then acknowledge that a causal approach has to be complemented by descriptive ways of reference determination. As regards the question as to how these two components combine, they only say the following: "It is worth pointing out that, on our account, no single answer to this question will apply to all cases: when a reference-grounder cannot ostend the referent of her term directly, *some* kind of description must play the role of samples and foils in the act of grounding reference, but whether this is a description of internal structure, causal role, causal mechanisms, or something else altogether will vary with the term-type and even with the term-token under consideration." (Stanford and Kitcher 2000, p. 125)

[7]Boyd 2002. Examples of philosophers working in the referentialist tradition to scientific terms are: Scheffler 1967; Putnam 1973a; Martin 1971; Fine 1975; Devitt 1979; Leplin 1979; Levin 1979; Newton-Smith 1981; Kitcher 1978; Hacking 1983; Burian 1985; Miller 1987; Papineau 1987; Sankey 1994; Psillos 1999.

job. First, an account of reference addresses *semantic* considerations, but incommensurability is ultimately an *epistemic* issue. Obviously, the above mentioned incommensurability of standards and the incommensurability of perception are epistemic challenges. No matter whether or not one buys into Kuhn's conception of paradigms, philosophy of science has to address the fact that different scientists may have different beliefs and standards and show why this need not lead to fundamental epistemic problems. This is the fundamental challenge to rationality stemming from Kuhn's work. But the same applies to semantic incommensurability. In Kuhn's work incommensurability of concepts has problematic consequences *because* scientists are claimed to not be able to rationally choose between different theories. Due to meaning incommensurability, scientists from different paradigms tend to talk past each other and are barred from understanding and appreciating the claims and arguments given by researchers from a rival paradigm. Thus a rational and objective assessment of the credentials of theories is not possible.

An account of reference by itself, however, has not much to offer on this epistemic issue. The purely semantic notion of reference allows the philosopher to verify that scientists endorsing different theories refer to the same entity, and (using a Tarski style semantics) it allows her to assign truth values to the statements made by scientists. In such a manner we can get an account of progress in the sense that we can show that false theories were replaced by true theories. However, pointing out that later theories were right where former scientists made false claims does not show that scientists had good *reasons* to abandon former beliefs. Epistemic considerations are necessary to address this issue. As my later case studies will explain in detail, the reference of a scientific term may change in the course of history in a *rational* fashion. Accounting for the rationality of reference change presupposes philosophical notions apart from reference. For similar reasons, reference alone does not explain why scientists are able to engage in successful communication. As a typical representative of the referential way to reply to the incommensurability consider again Sankey (1994). While he agrees with Kuhn that literal translation between different theories is often impossible, he is satisfied with pointing to reference as a rebuttal of the problematic consequences of incommensurability. Incommensurability is treated by Sankey primarily as a semantic challenge; and his discussion does not address the fact that this does not deal with Kuhn's epistemic challenge and that non-translatability was one reason for Kuhn to claim that scientists endorsing different theories talk past each other and cannot rationally convince others of their position.[8] Despite my

[8] "Identity of reference of sentence components is enough for the truth of one to be able to preclude the truth of the other. And such conflict between the sentences of rival theories is enough for comparison with respect to particular points of disagreement." (p. 40) "This putative connection between untranslatability and incomparability is refuted

choice of Sankey's discussion as an illustration of my critique, he is only one among many others who overestimate the merits of an account of reference.[9] Apart from reference, we need to have at least an account of when and why scientists have an implicit *understanding* of the reference (and meaning) of their concepts, as well as the concepts used by rival theorists, so as to account for successful communication. Such an account involves semantic considerations, but it is also an epistemic issue. And other epistemic considerations have to be taken into account once we realize that Kuhn invokes meaning incommensurability as an epistemic challenge. Thus, while an account reference is one ingredient in a successful discussion of scientific objectivity, it is by no means sufficient to explain how rational theory choice is possible.

There is another way to make this point that the traditional focus on reference does not solve the incommensurability problem. Kuhn's argument surrounding incommensurability is structured as follows. Kuhn starts out with the observation that scientists from different paradigms have strongly different beliefs — which is an epistemic point. His first step is to argue that this existence of different theories and paradigms implies that the same term can be used with very different meanings. The second step is the suggestion that meaning difference or meaning incommensurability brings about fundamental epistemic problems. Thus, overall Kuhn's argument starts with an epistemic point (difference in belief), and using a semantic detour (differences in meaning) he draws the epistemic conclusion that scientists cannot rationally choose between different theories. My stance on this argument is to reject that second step. Then one could even accept the first step. On a certain holistic construal of meaning, every difference in belief may amount to a difference in meaning, but then these differences in meaning do not have any radical epistemic implications — insofar as de facto differences in beliefs do not imply epistemic incommensurability. The interesting point is that the standard referentialist tradition in the philosophy of science does not reject the second part of Kuhn's argument. In fact, the idea that differences in meaning lead to incommensurability is the very motivation for invoking reference. Richard Burian (1985), for instance, states that

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by the referential approach to content comparison espoused in Chapter Two. Comparison of content requires only that expressions be related via reference, not that they have the same meaning. Without the dependence of comparison on translation, theories may be untranslatable yet comparable with respect to content by means of reference." (p. 73)

This ignores that while *de re* beliefs are relevant for truth assignment, what is relevant in the case of issues such as inference, argument, and communication are *de dicto* beliefs. Brandom (1994) and Føllesdal (1997) emphasize that successful communication presupposes the ability to relate different *de dicto* beliefs that happen to be about the same object, i.e., a person must have the ability to translate another person's *de dicto* belief into a *de re* belief.

[9]Devitt (1979) is another philosopher who tends to treat incommensurability as a purely semantic question. A similar point applies to Philip Kitcher (1978) (see footnote 13 below). Shapere (1982), on contrast, argues that since scientists need not know about the reference of theoretical term, a scientific argument for the adoption of a new theory has to involve other factors than reference. Shapere (1989) even suggest that the best rational account of continuity in scientific change is not based on stability of reference but on the continuity of scientific reasons.

philosophers have often have accepted "some form of holism about theoretical concepts," and that "holism brings radical incommensurability with it" (p. 24).[10] However, the usual position is not to deal with Kuhn's inference from difference in meaning to incommensurability by *denying* that there are meanings (or senses) and that the only semantic property of terms is reference. Instead, philosophers of science usually chose to focus on reference, and not to *talk* about meanings (or admit differences in meanings).[11] However, meanings and differences in meaning are implicitly acknowledged. After all, if conceptual change is about change in concepts and not just about change in reference, then concepts do actually change. Sankey (1994), as already mentioned, accepts that perfect and literal translation between theories is sometimes impossible. Kitcher (1993), whose position will be discussed on more detail in the next section, offers an account of reference to deal with semantic incommensurability. But his account of conceptual change also develops the notion of a 'mode of reference' as a proxy for the meaning or sense of a term, and Kitcher explicitly points out that there are different modes of reference (or senses) associated with a term. Consequently some philosophers of science are actually committed to the existence of meaning differences. In sum, the Kuhnian inference from differences in meaning to incommensurability is usually not rejected and instead is used as a motivation for the primary focus on reference instead of meaning. If this inference is accepted, however, then it is quite problematic that many philosophers of science do not or cannot reject the notion of meaning, the existence of differences in meaning, or meaning change in the course of history. Moreover, an account of *reference* does not address at all the idea that *meaning* differences entail epistemic troubles. Instead, we have to deal with the notion of meaning and show that meaning differences need not imply that scientists cannot convey their claims and arguments to their opponents. If the challenge of meaning incommensurability is understood in this way, then considerations about reference turn out to be peripheral to this problem.

I offered reasons that challenged the traditional focus on reference, arguing that considerations about reference alone are insufficient to deal with the incommensurability problem, understood as a challenge to scientific rationality. But apart from addressing Kuhnian issues, the study of conceptual change has to offer more than the study of reference anyway. A concept may change even if its reference remains stable. Thus we need a more fine-grained account of concepts. There are approaches to conceptual change that go beyond the mere study of reference; and I now turn to one prominent account from the philosophy of science.

[10] Burian now endorses a qualified and more refined position, as Burian et al. (1996) shows.

[11] Shapere (1966), in an early response to Kuhn's work, suggests that the best thing to do is to avoid the notion of meaning altogether to understand the workings of scientific concepts and theories.

2.2 BRINGING CONCEPTS BACK IN: EXPLAINING AND ASSESSING CONCEPTUAL CHANGE

In semantic discussions of the recent past, philosophers have sometimes not used the notion of 'concepts' but talked about 'terms' instead. This does not necessarily reflect a deliberate philosophical preference but is due to historical contingencies. One historical reason for this development is logical positivism with its emphasis on the formal and syntactic reconstruction of language. Another reason is the later movement of the linguistic turn, focusing on linguistic entities such as terms and definitional statements in order to shed light on knowledge or thought. Philosophers of science have taken over this talk about 'scientific terms'; and given the threat of meaning incommensurability, they could be quite happy of this opportunity to avoid discussions about 'concepts', 'meanings', 'senses', and other obscure intensional entities. I view the exclusive discussion of 'terms' as problematic and instead deliberately talk about scientific concepts and their change. In the course of history, scientific terms may change their meaning so substantially that we can say that this term corresponds to a new concept. If we want to track conceptual change in a more fine-grained way than the study of reference, then we need an account of what conceptual content is and what a change of a concept is.

2.2.1 Kitcher's Theory of Conceptual Change

There are approaches in the philosophy of science that go beyond the mere study of the reference of terms, assuming that concepts have meanings which may change in the course of history (see, e.g., Newton-Smith 1981). In what follows I discuss Philip Kitcher's account only, as he offers a theory of conceptual change that is much more general and sophisticated than any other account in the philosophy of science. Kitcher developed his account in a series of publications. His groundbreaking essay "Theories, Theorists, and Theoretical Change" (1978) lays out his basic framework. The paper "Genes" (1982) restates Kitcher's account and applies it to the history of the gene concept. *The Advancement of Science* (1993) uses the same account of conceptual change with some modifications, and goes beyond former discussions by adding an account of conceptual progress.

The basic notions and features of Kitcher's framework are as follows. Kitcher clearly belongs to the tradition in philosophy of science reacting to Kuhn's work and the threat of incommensurability. His discussion starts out with questions about truth and reference. Considering the phlogiston

chemist Priestley, Kitcher states that "Historians of science are interested in discovering what Priestley was talking about, and how much of what he said is true," but that Kuhn and Feyerabend argued that this cannot be achieved (1978, p. 519). Kitcher views the incommensurability threat as a semantic issue concerning reference: "The idea that conceptual relativism is a thesis about reference has been cogently presented by Israel Scheffler." (1978, p. 521).[12] Consequently, Kitcher starts out with an account of reference. He offers an important refinement by arguing that different tokens of a term, uttered on different occasions, may differ in their reference. For example, when Priestley talked about 'phlogiston' in certain contexts, then the description that phlogiston is the substance that is emitted in combustion was reference-determining and Priestley's utterances turned out to be non-referential. In other situations, however, for instance when Priestley described the effects of him breathing 'dephlogisticated air' he is best viewed as talking about the substance he is actually breathing, namely oxygen, even though the description 'dephlogisticated air' totally misconstrues the referent. Thus by saying that different tokens of the term 'phlogistons' had a different referent we can make sense of Priestley, because we acknowledge that his statements referred sometimes and were actually true while still maintaining that in many other contexts he did not refer due to his misguided theory. Kitcher's insight is that term-tokens or utterances in addition to term-types are an important level of philosophical analysis.

Kitcher's account goes beyond the mere study of reference. His core notion is that of the *reference potential of a term*. Kitcher identifies scientific concepts with reference potentials (1978, p. 543); thus conceptual change is change in reference potential. This account works as follows. Even though scientists endorsing different theories may refer with the same term to the same category, they still may associate a different meaning with this term. Scientists may refer to the same thing, but they refer in a different manner. Kitcher acknowledges the theory-ladenness of scientific terms by using the notion of a *mode of reference*. This is the way in which a term token refers or the way in which reference is fixed by a term token. There are many ways to pick out a certain referent, so a term type is usually associated with different modes of reference. This allows for a more fine-grained philosophical account than the mere study of reference, because we can distinguish different ways of referring to the same referent. Kitcher calls the totality of modes of reference of a term the *reference potential* of a term, and makes clear that the reference potential of a theoretical term is usually heterogeneous, as it consist of many different modes of reference.

[12]This obviously neglects the above mentioned epistemic implications of incommensurability and the fact that considerations about reference do not address other relevant semantic issues such as whether we have differences in meaning or non-translatability between theories.

Thus, conceptual change is the addition or deletion of particular modes of reference. In the course of history, the reference potential of a term may enlarge if we acquire new ways of referring to a known entity or it may contract in case former modes of reference are deemed to be problematic.[13]

Let us take a closer look at Kitcher's theory. The main example used to illustrate his ideas is the term 'phlogiston' and the difference between phlogiston and oxygen chemists. As already mentioned, Kitcher assumes that the term 'phlogiston' sometimes referred to oxygen due to a causal mode of reference, and sometimes did not refer at all due to a descriptive way of reference determination. On his earlier account, modes of reference are *events*. An utterance of a term token is the terminal event in a historical-causal sequence of events; and the first event — the so-called initiating event — is the mode of reference, which determines the referent of the term token and specifies how reference is fixed in this instance. One historical event-chain may start with an event in which a description fixes reference and end with an utterance of the term 'phlogiston'. Another chain may start with another event where a different description is used; thus we have a second descriptive mode of reference. Still other historical event chains that end with a 'phlogiston' token begin with an event which specifies the referent in a causal fashion. There is the following tension in Kitcher's 1978 discussion. On the one hand, he uses a picture that is similar to original purely causal theories of reference, assuming that there are long historical chains going back to the event in the past that marks the first time reference was determined in this way. In the case of descriptive modes of reference, Kitcher emphasizes that his account is different from traditional descriptive theories of reference because "the description which determines the referent of a speaker's token will not necessarily be a description which he would provide, but rather a description used to single out an entity in the event which initiated the production of the token." (1978, p. 543). As it seems, when a speaker utters a description that actually applies to the referent, this utterance-event is *not* the mode of reference, but instead the mode of reference is an event in the past where this description was used (possibly by another speaker) for the very first time to fix reference in

[13] A point made in Section 2.1.1 re-emerges. If Kitcher is serious about rebutting incommensurability, then it is not sufficient to study reference and reference potential. To show that communication between scientists is possible, Kitcher would need an account as to how scientists have an implicit *understanding* of the reference and reference potential of terms as used by them *and* by other scientists. My impression is that Kitcher thinks that such an account follows relatively straightforward from the definition of reference and reference potential (which is another expression of the idea that a purely semantic framework can easily solve some epistemic issues). This ambiguity can be illustrated when Kitcher (1978) states that his account of reference ensures that "the scientists in question will be able to *formulate* their disagreements" (p. 528). However, an account of reference can show that two scientists talk about the same entity and make statements with a different truth-value. But this does not entail that the scientists *know* about the fact that they actually refer to the same entity, and if they do not know that they make contradictory statements, they actually cannot formulate their disagreements. Kitcher addresses the issue of communication too briefly (1978, pp. 541–542; 1993, p. 103). This is exactly the issue that must be discussed in detail.

this manner. On the other hand, a fundamental feature of Kitcher's account is the idea that the reference potential of term is heterogeneous. There are many modes of reference, and in the course of history, new modes are acquired and old ones abandoned. However, the picture according to which we always go back in the past to the original initiating event does not tell us how speakers succeed in abandoning old causal chains and initiating events.

Kitcher's subsequent paper offers an improved account. Kitcher (1982) for the most part simply restates the original account, but a novelty is the fact the Kitcher explicitly stresses the importance of the intentions of a speaker. Kitcher's appeal to intentions can be viewed as addressing the tension just mentioned. Sometimes the primary intention of a speaker is to conform to the usage of others. In this case, she inherits reference from others and thus we have a causal chain starting with an event where former scientists fixed the reference. In other cases, a scientist intends to refer to a natural kind, with which she may be in direct or indirect causal contact. In this case, the speaker and the state of the external world around her determine reference in a causal fashion. In still further cases, a person intends to refer to what she has specified or can specify. In such a case a descriptive mode of reference obtains. Thus the speaker's intentions determines which type of mode of reference obtains, how far we go back in history, and which event in the distant or recent past qualifies as the mode of reference for her term token.

2.2.2 Unsolved Issues in Kitcher's Account

After this presentation of Kitcher's early account, I want to highlight the fact that so far modes of reference have been defined as the initiating events of a causal chain that lie in the immediate or distant past of the speaker; and the reference potential is the set of these initiating events. It is not quite clear why Kitcher does not count the total causal chain as a mode of reference. After all, the total causal chain and in particular the terminal events including the speaker's intentions determine reference. Thus, events apart from initiating events are seemingly part of a mode of reference. On Kitcher's account, modes of reference cut finer than reference. Two term tokens that have the same referent can be initiated by different modes of reference (i.e., different initiating events). But the speaker's intentions cut finer than modes of reference as well. Different intentions or contexts of utterance can pick out and refer back to one and the same initiating event. Thus, Kitcher's identification of modes of reference with initiating events only offers an intermediate fineness of grain. He does not explain why he proceeds this way, but maybe his motivation is that idea that a

mode of reference is a sort of referential strategy that can be used and re-used in various contexts.

The Advancement of Science (1993) uses basically the same framework, but Kitcher introduces a few modifications. Kitcher still focuses on sequences of events that end with a speaker's utterance and he uses the same theory of reference. But while in his earlier discussions the mode of reference was viewed as the initiating event of a causal chain only, now the mode of reference is defined as the total "complex causal chain that stands behind her [i.e., the speaker's] current vocalization;" and Kitcher is explicit about the fact that the speaker's external environment as well as her intentions are part of the mode of reference (p. 77). Kitcher does not point out why he introduces this modification (indeed, he does not state that this is a departure from his former account). But the later account still agrees with the former in that a mode of reference includes events *external* to the speaker's mind. The reason is that Kitcher makes use of the work of Hilary Putnam (1975). Restating Putnam's Twin Earth examples, Kitcher concludes: "'What is in the speaker's head' does not therefore determine reference. I shall articulate my approach to scientific language by building on the recent insights about reference." (1993, p. 76). Consequently, Kitcher defines a mode of reference as a causal chain that includes events outside the speaker's head. One page later, however, apparent contradiction arises when Kitcher views a mode of reference as being inside the head. This is no slippage, but is due to the fact that on Kitcher's account a mode of reference, like a Fregean sense, is supposed to be sensitive to "differences in cognitive content" (p. 78). Even though two distinct modes of reference may refer to the same object, the rational agent may not know this and reason differently with one mode of reference than with another. Kitcher illustrates this with Frege's example, according to which the descriptions 'evening star' and 'morning star' are different modes of reference for the same object. In some context the speaker may use 'evening star' but be unwilling to use 'morning star' because it is associated with a different sense. To play this cognitive role, a sense has to be grasped by the speaker — using Frege's terminology. Consequently, based on his naturalistic account of cognition, Kitcher states that "acquiring the reference potential of a term consists in incorporating a set of propensities into procedural memory" (p. 78). One page after stating that a reference potential consist of causal chains *external* to the speaker, suddenly the reference potential is a set of propensities *inside* the head.

Kitcher has to find a way to resolve this tension. This is not straightforward. For the lesson of Putnam's Twin Earth stories was precisely that Frege's ideal of a sense as something that determines reference *and* something that can make a cognitive difference (once being grasped by the thinker) cannot be fulfilled. Putnam's argument has widely been accepted. In the philosophy

of mind and language it brought about the distinction between narrow content (inside the head) and wide content (sensitive to reference to the external world). Whether there is an adequate way to reunite these two aspects of Frege's notion of a sense in one thing is open to debate. Given that Kitcher is most fundamentally after rebutting the incommensurability threat, the natural recommendation for him is to focus on the reference of terms. This suggest a picture according to which meaning and concepts are outside the head, so that Kitcher can stick with his definition of mode of reference which includes initiating events and other events outside the speaker's head. A contradiction can be easily avoided if Kitcher abandons the claim that a mode of reference is also a sort of Fregean sense that is sensitive to cognitive differences. In this case, Kitcher would still have an approach to conceptual change that goes beyond the mere study of reference, because modes of reference cut finer than extension. This strategy of resolving the tension in Kitcher's account has the drawback that we may wonder why one needs the more fine-grained approach in the first place. The traditional motivation is that we ascribe different concepts (meanings, senses, intensions) to different speakers because they reason and act differently with their concepts. The very rationale for ascribe concepts to persons is to explain thinking and rational behavior. And this is important for the study of conceptual change in science as well. Researchers prefer to conduct different experiments if they have different concepts; and contemporary scientists reason differently about certain phenomena because they have different concepts compared to scientists from the 19^{th} century. The idea that modes of reference are sensitive to cognitive differences like Fregean senses was already a motivation in Kitcher's original 1978 discussion for introducing the notion of a mode of reference.[14] Yet the above considerations show that this results in a tension in Kitcher's account — which is implicit in his 1978 discussion and leads to apparently contradictory statement in his 1993 account. As a result, Kitcher seems to be barred from using the idea that concepts (intensions) are sensitive to cognitive differences as the reason for using an approach to concepts that is more fine-grained than the extension of terms. Thus his identification of concepts with reference potentials is still in need of defense.

There is another unsolved internal issue that Kitcher's account raises and that suggest that his notion of reference potential has to be elaborated in more detail. In his earlier writings Kitcher may appear to waver between assuming that the reference potential of a term is a property of a

[14] "The reference potential is akin to the second idea of [a Fregean] sense as 'the manner in which reference is presented'. If we identify scientific concepts with reference potentials (thus explicating the ordinary, *non*-Fregean, notion of 'concept'), we can clarify the idea that theoretical concepts must absorb theoretical hypotheses and so enhance our understanding of conceptual change in science." (Kitcher 1978, p. 543)

whole scientific group (1978, p. 540), or rather of an individual (1982, p. 345). The most plausible interpretation — which fits the account in Kitcher (1993) — is to assume that reference potential is first of all a property of an individual scientist, it is the modes of reference that this person may make use of. Different researchers may potentially use different modes of reference, but there is a substantial overlap in their reference potentials, so that one still gets the idea that these persons use the same concept. Nevertheless, we should investigate whether researchers from different research communities can actually share the same concept on Kitcher's account.[15] This question is important because Kuhn's and Feyerabend's incommensurability challenge is based on the claim that researchers from different paradigms have different concepts or use the same term with a different meaning. Kitcher stresses causal modes of reference, but it is not clear that these are usually shared.[16] For example, the species concept was introduced by different naturalists in different research communities, and even in different countries. Thus there are different initiating events, i.e., modes of reference, which are used in different communities. But we still want to say that different research traditions use the same concept and can communicate with each other. This point is particularly pressing if one uses Kitcher's later account according to which a mode of reference is not only the initiating event but the total causal chain that produces the utterance of a term token. As the total causal chain will be different from context to context, and from token to token, it appears that it cannot be shared at all. One option is to come up with an appropriate notion of the 'same type' of causal chain that abstract from the peculiarities of token situations — but such an account is yet to be given. The crucial challenge is to explain when different initiating events (e.g., different baptizing events in different countries) are part of the same causal mode of reference. It is not possible to say that two (token) initiating events are of the same type whenever they pick out the same referent, for the whole point of Kitcher's fine-grained account is that there are many different modes of reference designating the same referent, including different causal modes. In sum, the causal theory of reference yields conceptual stability in the sense of referential stability — individuals with radically different background beliefs can refer to the same entity. However, it is not clear under which conditions causal modes of reference (causal chains) are shared between two persons. As Kitcher identifies concepts with modes of reference, he still has to show that concepts on this account are shared so that there is real conceptual stability (in

[15]The notion of a 'concept' was introduced in the philosophy of mind and language; and the rationale for this notion is that concepts make propositional attitudes possible by being part of propositions. Consequently, sharing propositional attitudes presupposes sharing concepts (Fodor 1994).

[16]Anil Gupta suggested this point to me.

addition to mere referential stability). Thus, Kitcher has to explain his notion of initiating event and causal chain in more detail, to ensure that reference potentials are actually shared between individuals and research communities.

The discussion so far focussed largely on causal modes of reference and Kitcher's use of the causal theory of reference. But in addition to the use of causal modes, Kitcher also acknowledges descriptive modes of reference. In fact, while Kitcher (1993) starts out with emphasizing the causal theory of reference and with the assertion that modes of reference are causal chains that include events outside the agent, his subsequent discussion and his examples shift towards a picture that focuses on descriptions, statements, and events inside the head such as beliefs and intentions. Apart from his initial explanation of the idea of a causal mode of reference, all of Kitcher's concrete examples are descriptive modes of reference. For example, he assumes that with the advent of Darwinism biologists acquired new modes of reference for the terms 'species' and 'homology', stating explicitly that new descriptions fix the reference (1993, p. 32). In his case study on the change of the gene concept, the three modes of reference that Kitcher (1982) explicitly mentions are descriptive modes as well (see p. 36 below). Descriptive modes of reference are also crucial for Kitcher's theory of conceptual progress (to be discussed below in Section 2.2.3). For while conceptual change consist in the addition of any type of modes of reference, conceptual progress on Kitcher's account is to be assessed in terms of the addition and deletion of descriptive modes of reference.[17]

Ignoring causal modes of reference for the moment and focusing on descriptive modes, note that conceptual change on Kitcher's account is not just the acquisition or abandonment of descriptions of the referent. Instead, his definition of conceptual change is explicitly about the addition and deletion of descriptive *modes of reference* — and not every statement or description is a mode of reference. Some statements fix reference descriptively and are thus modes of reference. Others, however, do not fix reference. But they still refer, because reference is parasitic on prior statements that are actually reference-determining (or causal modes of reference). The first type of statements that fix reference may be called reference-analytic — as they are modes of reference we cannot abandon them without potentially changing the reference of the term. Reference-analytic statements fix meaning

[17] As explained in Section 2.1, the causal theory of reference was introduced in opposition to views that are claimed to lead to incommensurability such as a purely descriptive theory of reference. We saw that Kitcher emphasized the very idea of causal modes of reference for this reason. The causal theory is surely of some philosophical importance. But if — as for instance in the case of Kitcher's concrete examples — the actual focus in studies of conceptual change is on descriptive modes of reference and conceptual progress is assessed in terms of descriptions of the referent, then the rejection of traditional descriptive approaches to concepts (and the cheering of the causal theory) turns out to be a tempest in a teapot. (Similarly, Burian (1985) and Weber (2005) discuss of the history gene concept, endorsing Kitcher's framework. Even though they point to the causal theory of reference as a reply to referential instability, their examples of modes of reference include descriptive modes only.)

in the sense of reference. The second type of statements that do not determine reference can be called reference-synthetic. Scientists can deny these reference-synthetic statements or disagree over them without influencing the reference of the term involved. As in this case reference is parasitic on reference-analytic statements (or causal modes of reference), it is possible to make false statements that are still about the same referent, which is philosophically important.[18] On Kitcher's account, conceptual change is not change of the totality of statements accepted or utterances made by scientists. Instead, it is about the subset of statements that are descriptive modes of reference. In my terminology, conceptual change is the acceptance or abandonment of reference-*analytic* statements. Thus in order to assess whether and what sort of conceptual change occurred we need to be able to tell apart reference-analytic from reference-synthetic statements.

Given that Kitcher's account of conceptual change includes descriptive modes of reference (and his account of conceptual progress is based on descriptive modes as discussed below), Kitcher is committed to a distinction between reference-analytic and reference-synthetic statements. His 1982 discussion actually mentions this at one point by stating that "not all community shared beliefs which use a particular term may be employed in fixing the reference of that term. ... I rely on a distinction between beliefs which are employed in reference-fixing and beliefs which are not" (p. 347). The problem is that Kitcher has not offered an account that is elaborated enough to draw a principled and clear-cut reference-analytic/synthetic distinction. This is at root the same problem as the one about how descriptive and causal factors of reference combine, as mentioned in Section 2.1.1. For in this context the question was what determines which causal factors and/or descriptive factors combine to pick out a particular referent in a specific case. In general, the question is in virtue of what do some of the many causal relations in the world and some of the various descriptions of a speaker entertains become determinants of reference. As Kitcher's theory invokes both causal and descriptive modes of reference he has to address the same issue. In particular, he needs an account the conditions under which a particular description or belief that a speaker may entertain is a descriptive mode of reference, i.e., reference-analytic.

Kitcher's later account (1982, 1993) offers a basic resource to address this question: the speaker's intentions. We saw above that Kitcher assumes that the speaker's intentions determine whether a causal mode or whether a descriptive mode of reference obtains (or whether reference is inherited

[18]Given that Kitcher identifies concepts with reference potentials and that the notion of a mode of reference is his proxy for the meaning or sense of a term, the distinction between reference-analytic and reference-synthetic statements is in fact a real analytic/synthetic distinction: it distinguishes meaning-constitutive statements from other statements, and what is meaning-constitutive is precisely what is reference-determining on Kitcher's account.

from others). To restate his main example: while traditional accounts assumed that the term 'phlogiston' as used by phlogiston chemists was non-referential (because nothing satisfies the associated description), Kitcher argues that on certain occasions tokens of this term referred as reference was fixed in a causal fashion. This was the case when Priestley and Cavendish prepared a gas that they took to be 'dephlogisticated air' and described its effect on them while breathing it. Kitcher explains why a causal mode of reference obtained in certain contexts as follows: "Their *dominant intention* is to refer to the kind of stuff that was isolated in the experiments they are reporting — to wit, oxygen" (1993, p. 102; my emphasis). In my terminology, Priestley's statement that the gas isolated is dephlogisticated air is reference-synthetic, it misconstrues the properties of the gas without determining reference in a descriptive fashion. The same idea applies to reference-analytic statements. While in some cases the speaker intends to refer to a natural kind in a causal fashion, "In other cases in the interest of ensuring that the intended reference is clearly understood, a scientist's *dominant intention* may be to refer to whatever satisfies a particular description, even though it may turn out, unluckily, that this is not a natural kind" (Kitcher 1982, p. 344; my emphasis). Thus, Kitcher apparently assumes that a description is reference-analytic if and only if it is the speaker's dominant intention that this description picks out the referent.

I agree with Kitcher that the speaker's intentions are an important determinant of reference. Still, I feel that his account is unsatisfactory as it stands. In fact, Stathis Psillos (1997) and Christina McLeish (2005) — the only two explicit discussions of Kitcher's theory of reference I am aware of — focus on and strongly criticize Kitcher's idea that the reference of a term may change from token to token due to the shifting use of causal and descriptive modes of reference (see also Bishop and Stich 1998). These critiques argue that Kitcher has not shown that different dominant intentions (or something else) determine different modes of reference on different occasions. In what follows, I do not want to restate the arguments against Kitcher made in these two discussions; instead I focus on what I view as the main problems with Kitcher's notion of dominant intentions to refer. First, given that Kitcher's account boils down to asserting that 'a statement is reference-analytic iff it is the speaker's dominant intention that this statement is reference-analytic', this sounds as if such an intention to refer is a *single* and *explicit* intention. However, it is more plausible that many of the beliefs and intentions an individual has bear on reference determination. Kitcher either has to give an account of how these intentions and beliefs combine to yield a dominant intention, or in case he think that only one of the speaker's intentions bears on reference, he has to explain what determines which intention is the dominant one. Moreover, it is clearly not the case that

reference presupposes that a scientist has an explicit intention or belief that p, where p involves semantic notions such as 'concept' and 'reference'. Scientists have intentions about their research objects and experiments, but not necessarily intentions about their mental contents and the latter's semantic properties. Scientists count as referring to objects and possessing concepts even if they do not have semantic concepts such as 'reference' and 'concept'. Thus, Kitcher's idea that scientists have a 'dominant intention to refer' is in need of philosophical clarification.

Second, I actually think that in many important cases involving theoretical concepts there is no 'dominant' intention to refer. While Kitcher apparently assumes that the speaker's intentions uniquely determine the particular mode of reference and the referent of the term token, my claim is that these intentions will often underdetermine which mode of reference obtains. For the speaker's intentions and beliefs may — unbeknownst to her — conflict with each other. For instance, in the above example Kitcher assumes that Priestley had the 'dominant' intention to refer to the gas he experimentally prepared, so that a causal rather than descriptive mode of reference obtained. Even if the idea that on such an occasion a phlogiston chemist referred to oxygen is plausible, Kitcher does not have a satisfactory semantic account of this historical interpretation. For Priestley's very *motivation* for conducting this experiment was to analyze the properties of 'dephlogisticated air'. The phlogiston theory — involving the problematic description of 'dephlogisticated air' — explained for Priestley why the experimental procedure used had to be followed to obtain 'dephlogisticated air'; and it provided evidence for Priestley that the gas he was breathing was in fact 'dephlogisticated air'. Thus, given that the phlogiston theory intentionally guided every step of his practice, Priestley had a strong intention to refer to the substance that falls under the description 'dephlogisticated air' in addition to the intention to refer to the gas he prepared — it is not the case that one intention was stronger than the other. Kitcher is actually aware of the fact that there can be conflicts between the ideals of referring to a natural kind (causal mode of reference), to what is described (descriptive mode of reference), and to what others refer (reference borrowing). But he assumes that there is a matter of fact which intention is the primary and reference determining one: "There are many situations in which these maxims conflict. When they do, the scientist 'chooses' among them—in the sense that there is a dominant intention to obey one rather than the others." (1993, p. 104). My discussion of the Priestley example, however, shows that there are cases where there may be no dominant intention — so that reference would be indeterminate if the speaker's intentions and beliefs were the only factor that determines which mode of reference obtains. I assume that such situations are quite common in science. Scientists often have strong, but erroneous and thus

empirically contradictory beliefs about the entities they refer to, and their intentions (and more generally their research practices) are built on some false beliefs. A theory of reference for scientific concepts has to acknowledge the fact that misconceptions are widespread in certain crucial episodes in science. It is important for an approach that includes causal factors of reference determination that false beliefs of the scientist need not interfere with reference.

While emphasizing that a term's reference potential consists of many modes of reference (due to the theory-ladenness of scientific concepts), Kitcher nonetheless postulates the universal existence of 'dominant intentions to refer' that unambiguously pick out a unique mode of reference for each utterance of this term. I find this assumption quite implausible, as my above discussion of the phlogiston case suggested that there can be two (or more) modes of reference operative in a particular context, even though each of these modes picks out a different referent. Note that issues arise for Kitcher's account even in cases where different modes of reference pick out the same entity. In a case where the reference potential of a concept consists of several coreferential modes of reference, no matter which mode of reference is operative in a particular context, the unique referent of the concept will be picked out and referential indeterminacy cannot arise. Still, apart from reference one may wonder whether it is always precisely determined which one of these *modes of reference* is operative in a given situation. Otherwise, there would be vagueness as to which mode of reference is used in a particular case, and as 'mode of reference' is Kitcher's proxy for the meaning of a term, the meaning of the term as used in a particular situation would be vague or indeterminate. Kitcher does not offer any explanation of why he assumes that there is always a dominant intention picking out a unique mode of reference. The above considerations cast doubt on Kitcher's tenet, suggesting that if we only take a scientist's beliefs and intentions into account there is in fact vagueness as to what the 'mode of reference' or meaning of a term token is.[19]

Kitcher's assumption that the mode of reference is picked out by a dominant intention implies in particular that reference is solely determined by the intentions and beliefs of a *single individual*. However, in Section 3.3 I will point out that an important aspect of a scientific concept is a cognitive division of labor. Even though a concept is shared by a whole scientific community, it is not the case that everyone has 'grasped' the same definition of the concept. Rather, different scientists have

[19]Papineau (1996) and Burian et al. (1996) acknowledge that there may be vagueness as to which descriptions are reference fixing. While this vagueness about meaning usually does not lead to referential vagueness or indeterminacy, in certain cases it may. In Section 3.3.2 I shall argue that a concept can be individuated in different ways depending on the explanatory purposes that underlie a particular study of conceptual change. The same applies for which factors are reference-determining and which entity is the referent — both may depend on the philosophical interests that underlie reference ascription. By taking these philosophical interests into account, I make use of more resources that determine reference ascription than Kitcher (see Schiffer 1981 for a similar idea).

different beliefs and epistemic abilities, and this communal variation and specialization in beliefs and epistemic abilities tied to the possession of a concept are significant for the successful use of a scientific concept by total community. As a result, what a concept is and what determines reference may nor be 'inside the head' of a single individual. More specifically, I will argue that an important component of the meaning of a scientific concept is the epistemic goal that is pursued by its use, and that the features that determine for which epistemic goal a concept is used are not determined by the beliefs and actions of a single scientist, but by the total communal use of a scientific concept.

In sum, while agreeing that the speaker's intentions have an impact on reference fixing, I do not think that Kitcher has made plain that there is always a dominant intention to refer and what this intention consist of. As his account of conceptual change and progress is committed to a principled and clear-cut distinction between the statements that are reference-analytic and those that are reference-synthetic in particular context, which does not appear to admit of indeterminacy, he has to offer an improved account as to what makes a statement reference-analytic (a descriptive mode of reference).

Even if one accepts my contention that Kitcher still lacks a philosophically satisfactory account of the distinction between reference-analytic and reference-synthetic statements, one might view this as a theoretical problem that concerns primarily the philosophy of language, but which is not of fundamental concern for the philosophy of science. However, Kitcher's approach to conceptual change is not only an abstract account, but his claim is that we should study episodes in the history of science based on his framework. A philosophical account of conceptual change must be applicable to the philosophical study of science. What we need at least is an account that helps us to detect and study reference potentials in concrete cases. But Kitcher does not offer precise criteria of how to pin down modes of reference and distinguish them from beliefs that do not influence reference. For this reason, it is not obvious how Kitcher's framework ought to be applied to concrete cases. Let us take a look at his essay "Genes" (1982), which is intended to study the reference potential of the gene concept from classical to molecular genetics. The brief history of the gene that Kitcher discusses picks out very interesting points. But is hardly an application of his philosophical framework. Kitcher mentions only three modes of reference: First, the description that genes are segments within which recombination cannot occur (1982, p. 351). This idea was put forward by Sturtevant in 1915. Parts of a chromosome can be transferred to another chromosome by a process called crossing over. Many classical geneticists assumed that a single gene cannot be split apart by crossing-over, this is why Sturtevant's description was viewed as holding of genes.

However, this assumption turned out to be erroneous. Second, Kitcher points to the cis-trans test (p. 352). This is an operational criterion that permits to determine whether a continuous segment of a chromosome is a unit of physiological function. In 1957, Benzer proposed that one way of explicating the notion of the gene is by assuming that genes are those entities that pass the cis-trans test. Third, Kitcher refers to the one gene–one enzyme hypothesis (p. 354). This idea, as being put forward by Beadle in 1941, suggests that each gene codes for exactly one enzyme, thereby connecting genes with biochemical molecules of the cell. As it turned out, this hypothesis is true only to a very rough approximation.

The problem which Kitcher's historical account is that while he considers these three statements to be descriptive modes of reference, he does not offer any indication of why he takes them to be reference-analytic. In fact, as these three statements do not pick out genes as nowadays understood, each of these statements could be nothing but a (false) claim about genes while the reference of the term 'gene' occurring in them was fully fixed by prior statements or in a causal fashion (so that these three statements mentioned by Kitcher are actually reference-synthetic). Surely we cannot exclude the possibility that in certain contexts individual geneticists used one of these statements as a descriptive mode of reference. But this would mean that such a person referred to a category that does not coincide with genes as understood nowadays. And since the three descriptions pick out distinct categories, throughout history the reference of the term 'gene' was changing from context to context. While these three statements may have been used as descriptive modes of reference in certain isolated cases, Kitcher's analysis is relevant only if he succeeds in pointing to some modes of reference that had widespread usage at some point in history. At any rate, Kitcher does not indicate why he takes these statements to be reference-analytic, in particular, he does not appeal to dominant intentions. As long as we do not have a prima facie idea of why we are dealing in these concrete cases with modes of reference (rather than other utterances), Kitcher's *semantic* framework is not really applied to this historical case. In addition, Kitcher's three isolated examples alone do not give us a good idea as to how the reference potential of the term 'gene' changed (and it does not give us a comparison between the classical and molecular gene concept). If the study of conceptual change is the study of reference potential (which is supposed to encompass many modes of reference), then we need a detailed account of how several new modes of reference emerged rather than three isolated examples.

In sum, while Kitcher's framework commits us to detect and study modes of reference (but not other entities), it is not clear how this account is to be applied to concrete cases; and actually,

Kitcher (1982) himself does not offer a real application of his own framework.

2.2.3 Critique of Kitcher's Referential Framework of Conceptual Change

The discussion so far has offered an internal criticism of Kitcher's account. I have discussed the extent to which his account is coherent and sufficiently elaborated. I have also addressed to what degree his account is adequate to meet the goals that Kitcher sets for his approach. In the last part of this chapter, I turn to an external critique of Kitcher in that I discuss the suitability of Kitcher's approach for philosophical aims that Kitcher does not explicitly view as aims for an account of conceptual change. Kitcher's goal is to have an approach to conceptual change that deals convincingly with the incommensurability challenge. However, there are other legitimate and important goals an account of conceptual change should pursue. In what follows, I will lay out these additional goals. Given that Kitcher does not address these issues, it is not surprising that his theory does not offer an explicit and immediate solution to these demands. But as it turns out, Kitcher's approach is not particularly promising to deal with all of these goals. My own account of conceptual change will not primarily be concerned with referential incommensurability. Instead, the aims to be laid out in the rest of this chapter are the constraints that my account of conceptual change — to be developed in the next chapter — is intended to meet. My rival approach to conceptual change will directly address these issues and is therefore in a better position than Kitcher's to adequately deal with them.

First, an account of conceptual change should be able to *track the historical development and the change of concepts*. Concepts form historical lineages just like species.[20] Sometimes in the course of history, a scientific concept may split into two concepts, and we should be able to identify such an event. The later chapters on the homology concept will argue that nowadays the term 'homology' corresponds to three different concepts. In the part on the gene concept I will claim that currently we still use the classical gene concept apart from the molecular gene concept, so that the molecular gene concept emerged by branching off from a previously existing gene concept. Similarly, even without a conceptual split, in the course of history the meaning of a term may change so substantially that one might want to consider it corresponding to a different concept. For instance, it is sometimes assumed that Darwin's evolutionary theory brought about a changed species concept, as species

[20]The next chapter will spell out this idea using the phylogenetic approach to the history and philosophy of science proposed by Jim Lennox (2001a, 2001b).

came to be defined as genealogical groups derived from common ancestors. While this philosophical claim is quite contentious, a theory of conceptual change must be in a position to answer whether or not Darwinism introduced a new species concept. Thus, a philosophical account of conceptual change needs to be able to tell whether a term corresponds to one or several concepts. Kitcher's account, as it stands, simply assumes that for each term there is exactly one reference potential (consisting of several modes of reference). Kitcher can note that the reference potential of a term such as 'homology' as currently used is highly heterogeneous. However, this ignores the fact some conceptual variation is best viewed as being due to the existence of several concepts or senses being associated with the same term. Kitcher is surely not barred from developing an account that partitions the total reference potential of a term into different concepts — but such an account that tells us which modes of reference belong to one concept is yet to be given.

Second, a theory of conceptual change should be able to *explain why conceptual change occurred in a rational fashion.* A crucial contention of my dissertation is that many semantic changes in science are rational. If the meaning of a term changes, an explanation is needed that exhibits the intellectual and epistemic factors that brought about conceptual change in a rational fashion. In some cases, a certain change may occur internal to a concept, without leading to the advent of a novel and distinct concept (such as a revised theoretical characterization of a phenomenon). In other cases, semantic change leads to the origin of a novel concept or to a split in a conceptual lineage. If one concept splits into two, we need an account of why this diversification rationally happened. This is an issue that Kitcher simply does not address as it is not a concern for him. It is not obvious how Kitcher could or would add to his reference-potential based account in order to obtain a theory that accounts for conceptual change. Nor is it obvious that Kitcher cannot offer a convincing enlarged theory that deals with the explanation of conceptual change. In any case, rationally explaining why conceptual change occurred is a legitimate constraint that a theory of conceptual change should satisfy. My own approach will introduce the notion of the 'epistemic goal' of a concept's use as part of an account of concepts that views them as tools that researchers use to meet certain scientific and explanatory goals. Concepts are shaped, re-designed and honed to meet these goals in a better fashion. Sometimes there is change in what scientists try to achieve primarily, which may lead to conceptual change. In a nutshell, my approach will account for the rationality of conceptual change with reference to the epistemic goal that is pursued with the use of a scientific concept. Overall, the explanation of conceptual change as a rational process is the main concern for my discussion — which clearly bears on some issues surrounding incommensurability and Kuhnian

ideas about conceptual change. The later case study will offer explanations of conceptual change that essentially involve semantic features in addition to reference and modes of reference, thereby casting doubt on the adequacy of any purely referential framework (such as Kitcher's) to account for conceptual change.

Third, an account of conceptual change should be able to *assess whether conceptual change was progressive*. While Kitcher's earlier essays do not address this issue, his 1993 discussion offers a prima facie account of conceptual progress. Whereas for Kitcher conceptual change consists in the addition and deletion of modes of reference, conceptual progress is restricted to changes in the *descriptive* modes of reference belonging to a reference potential. Conceptual progress occurs if new descriptive modes of reference are added to the reference potential of a term or if inadequate descriptions are eliminated from the reference potential. Conceptual change is progressive in case

> "the reference potential of e^* refines the reference potential of e, either by adding a description that picks out the pertinent kind or by abandoning a mode of reference determination belonging to the reference potential of e that failed to pick out the pertinent kind." (1993, p. 105)

However, I argue that this approach misses important aspects of conceptual progress. As an example, take the emergence of the molecular gene concept out of the classical gene concept. In my view, we should consider the molecular gene concept a different concept not only because some theoretical change took place, but in fact significant conceptual progress occurred with the origin of molecular genetics. While Kitcher counts every addition to a reference potential as progressive, I prefer to reserve the notion of progress to substantial conceptual changes that have an impact on the scientific discipline under consideration. More important is the fact that Kitcher does not fully defend his particular notion of conceptual progress. For on his account conceptual progress is *not* the acquisition of true statements and the abandonment of false statements, progress is the acquisition of true descriptive *modes of reference* and the abandonment of false descriptive *modes of reference*. What is the justification for this? On my above terminology, in contrast to reference-analytic statements (= descriptive modes of reference), reference-synthetic statements are beliefs about the referent that are not part of the reference potential. Arguably, the adoption of any novel true theoretical belief is progressive. Yet reference-synthetic statements, i.e., descriptions that are not modes of reference, are not part of the reference potential and thus *by Kitcher's definition of conceptual change* cannot contribute to conceptual progress. However, Kitcher does not offer a defense of this assumption. Why should additions of true reference-analytic statements be necessarily more progressive than additions of true reference-synthetic statements?

Moreover, adding new modes of reference and eliminating problematic modes of reference may

be all there is to progress in the change of *reference potentials*. But I think that change in reference potentials hardly exhausts conceptual progress in science. What is crucial about conceptual change is that certain changes *facilitate scientific discovery*, permit scientists to *justify new hypotheses*, and enable them to *explain new ranges of phenomena*. This is in my view the main impact of conceptual progress on science. For example, conceptual progress may occur in the case of the introduction of a completely new term, in case this concept permits us to explain new phenomena. The introduction of the concept of natural selection was important because it permitted scientists to explain phenomena that could not have been explained (at least not adequately explained) without this concept. My chapters on the gene concept will argue that the transition from the classical to the molecular gene concept is an instance of conceptual progress precisely because the molecular gene concept supports explanations that the classical gene concept does not support. To illustrate this point, take Marcel Weber's (2005) discussion of the history of the gene concept, which makes use of Kitcher's framework. Weber argues that the classical and the molecular gene concept differ somewhat in reference, and he discusses in more detail than Kitcher (1982) how the reference potential of the term 'gene' changed throughout history. In spite of his insightful discussion, Weber does not offer an account of why the new modes of reference that were introduced are scientifically significant. The importance of the emergence of the molecular gene concept is not only that nowadays biologists are able to refer to another natural kind — molecular genes — in addition to classical genes. Instead, the main impact of this instance of *conceptual* change is that the molecular gene concept supports new types of explanations. The change in reference and possibility to refer to a new kind is simply a consequence of this important case of conceptual progress. Thus, an account of conceptual progress has to take into account that new and changed concepts support novel explanations. Apart from scientific explanation, the same point applies to inference and justification. Natural kind concepts make this plain. It is widely recognized that a crucial feature of a natural kind is that it is governed by a set of laws, causal mechanisms, or other regularities. This permits the projectability of properties of the kind: if some instances of the kind have a certain property, then it is very likely that other instances have this property as well. The fact that natural kinds are governed by important regularities is the reason why philosophers of science have emphasized the importance of natural kinds for science (Boyd 2002). However, *semantic* accounts of natural kind terms have focused on natural kind term reference, in particular emphasizing the causal theory of reference. But in addition to the ability to refer to natural kinds, an important feature of natural kind concepts is that they support inductive inferences (due to the projectability

of the properties of natural kinds). When scientists get a better understanding of the properties of a natural kind and thus the natural kind concept is refined, this changed concept permits inductive inferences and scientific justifications that have a higher degree of validity compared to the old concept. In sum, improved concepts support better inferences and new explanations — a fact that a theory of conceptual progress has to take into account.

Thus I emphasize that conceptual changes and new concepts contribute to scientific discovery, justification and explanation. Kitcher (1993) actually discusses two types of scientific progress: conceptual and explanatory progress (explicating the latter based on his notion of an explanatory schema). However, Kitcher's account of conceptual progress and explanatory progress are completely unrelated. On his approach, it appears to be an accident that conceptual change, i.e., change in reference potential, often occurs together with explanatory progress. In my view, explanatory progress occurs precisely *because* concepts change in certain ways. Perhaps Kitcher could elaborate his account of reference potential such that it becomes clear how concepts contribute to explanation. While Kitcher's account so far focuses on the way in which concepts enable scientists to refer to certain categories, he would have to show that this can also yield an account of how concepts enable scientists to make certain inferences and explanations. However, I do not think that a reference-potential based framework is a particularly promising starting point. This becomes plain if we consider Kitcher's original construal of a mode of reference, according to which a mode of reference (Kitcher's equivalent for the sense of a term) is an initiating event in the past of the scientist. It is not clear how an event in the speaker's past could be part of or support an explanation given by the speaker — but concepts definitely do support explanations. More precisely, a scientist has crucial epistemic abilities in virtue of possessing scientific concepts, such as the ability to put forward explanations. In the case of the term 'natural selection', Kitcher can surely note that the introduction of this concept established reference to a biological process and that we refer by means of an initiating event. But the ability to refer to a new kind or mechanism does not immediately show how such a new concept opens new ranges of explanations. If we take seriously the idea that concepts figure in explanations, then we need a picture of concepts according to which concepts have a bearing on the way in which scientists reason. Kitcher (1993) tried to account for the cognitive content of concepts (the evening and morning star example) by assuming that reference potentials are dispositions in procedural memory. But, as we saw, this conflicts with his focus on reference and the idea that meanings are outside the head. Ultimately, Kitcher's theory of conceptual change is designed to address the incommensurability threat. This leads him to develop

a referential framework: "we can adequately describe the phenomena of conceptual change by charting the shifts in referential relations between words and the world" (1982, p. 339). However, there is more to conceptual change and progress than changes in the way scientists refer. As it stands, Kitcher's framework fails to capture the way in which concepts contribute to scientific explanation and justification. And it is not obvious how he can amend or add to his account such that this dimension of conceptual change is taken into account.

2.2.4 Summary of the Chapter

I started out discussing how conceptual change has been dealt with in the philosophy of science. For the most part, philosophers of science have focused on the study of the reference of scientific terms. This is due to the fact that traditionally accounts of conceptual change attempted to address the incommensurability threat and consequently focused on reference and referential stability. I explained why theories of reference alone are not sufficient to adequately solve the incommensurability problem understood as an epistemic issue. We saw that Kitcher's theory of conceptual change goes beyond the mere study of reference. Still, his prime motivation is to address referential incommensurability, which is the reason why he defines concepts as reference potentials and meanings as modes of reference. I mentioned some unsolved issues for Kitcher's account that show that his core notions of 'mode of reference' and 'reference potential' are not spelled out in sufficient detail. It turned out that it is unclear whether modes of reference are best viewed as being inside the head or whether they include causal chains of the external world. The discussion pointed out that it is not immediately clear whether Kitcher's account of concepts ensures that concepts are shared by different individuals or research communities. In addition, Kitcher is committed to offer an account that in virtue of which a particular mode of reference obtains in a certain context and in virtue of what a statement is reference-analytic in a particular case. He assumed to had answered this question by appealing to a speaker's dominant intention to refer in a particular way (e.g., a statement is reference-analytic just in case the speaker intends it to be reference-analytic). However, I explained why I find the notion of dominant intentions to refer wanting.

Kitcher may very well attempt to solve these open issues. Still, I am not convinced that Kitcher's idea that we can explicate the notion of 'concept' or 'sense' along the lines of his approach is a particularly promising strategy. A philosophical analysis is supposed to explicate a certain problematic concept (e.g., semantic notions such as 'concept' and 'reference') in terms of notions

that are better understood than the concept to be analyzed. It is not clear to me that we have or will get a better grasp of notions that are essential for Kitcher's account such as 'mode of reference', 'reference-analytic', and 'dominant intention to refer' than we already have of the notion of a concept. Moreover, I pointed out that because of his concern with incommensurability and reference Kitcher may have to view reference potentials as including causal chains external to the speaker's mind. If this implies that reference potentials as being outside the mind do not have cognitive significance, then it is unclear why we simply should identify concepts with reference potential as Kitcher maintains.

Apart from these unsolved issues internal to Kitcher's account, the most crucial part of my critique was that there are important philosophical goals a theory of conceptual change has to pursue but which Kitcher does not address, since he focuses on rebutting the incommensurability threat. *First*, an account of conceptual change should be able to individuate concepts, so that it is possible to track conceptual change and the emergence of novel concepts. *Second*, it is desirable to be in a position to explain why conceptual change rationally occurred, in particular when meaning change leads to a novel concept growing out of an existing one or if a concept splits into two new concepts. We saw that Kitcher's theory does not address and is not intended to address these two issues. *Third*, a theory of conceptual change should be able to evaluate whether or not an instance of conceptual change was progressive. While Kitcher's original account did not deal with this issue, Kitcher later added an account of conceptual progress. However, since his account focuses on additions and deletions of modes of reference only, this approach misses crucial aspects of conceptual change. Scientific concepts are crucially involved in discovery, confirmation, and explanation. Novel concepts permit scientists to infer and justify new theoretical claims, and concepts are actively changed and shaped to permit the explanation of new phenomena. This is an aspect of conceptual progress that a theory of conceptual change must take into account, while it is unclear whether Kitcher's theory can do so, as he focuses on new ways of referring to an entity. These three goals for an account of conceptual change will be the desiderata that my dissertation will be concerted with. It is quite possible that Kitcher's account could be elaborated so that these three desiderata are adequately dealt with. However, my strategy will not be to amend Kitcher's framework. Instead, the next chapter will lay out a theory of concepts and conceptual change that directly and solely targets these three philosophical goals, rather than focusing on referential incommensurability.

3.0 AN ACCOUNT OF CONCEPTS IN TERMS OF SEVERAL SEMANTIC COMPONENTS

The task of the present chapter is to lay out a basic theory of concepts and conceptual change, which in turn can be fruitfully applied to the subsequent case studies. The previous chapter served the purpose of motivating my account by discussing how conceptual change has been viewed in the philosophy of science. Special and critical attention was given to Philip Kitcher's sophisticated theory. Kitcher followed the tradition in the philosophy of science by viewing an argument for the *stability of reference* across theoretical change as a solution to the incommensurability problem. Due to this focus on the reference of scientific terms, Kitcher's account construes a concept as a set of modes of reference; in other words, possessing a concept is having the *ability to refer to a kind*.

My framework, in contrast, does not primarily focus on reference and stability of reference. Rather, I view as the primary task of a study of conceptual change to provide an account of how and why a scientific concept changes, including *why change in a scientific term's meaning (and potentially reference) occurred in a rational fashion*. Such an account has two basic components. The first is a *phylogenetic approach* to conceptual change. Concepts are to be viewed as historical entities that form lineages and may change over time — just like species are parts of phylogenetic lineages. This idea figures prominently in Jim Lennox's (2001a, 2001b) phylogenetic approach to the history and philosophy of science. Lennox has used it as a fruitful alternative to the more standard way of combining the history and the philosophy of science, which consists in using facts about the history of science as evidence to test normative philosophical theories about the nature and development of science (Kuhn 1962; Laudan 1977). In contrast, Lennox uses the history of science in order to understand conceptual and foundational problems by tracing the historical origin of these problems. Recent problems and their theoretical presuppositions can be understood in a deeper fashion by studying the relevant history (see also Love 2005). One ingredient in Lennox's phylogenetic approach is to view scientific concepts from a historical point of view, and tracing

conceptual change by conceiving of concepts as forming phylogenetic lineages. My framework on scientific concepts and conceptual change will use this idea of a phylogeny of concepts.

In addition to this, a second component is an account of when a conceptual lineage counts as splitting into two concepts and why novel concepts originate. This presupposes an account of concept individuation that permits the student of the history of science to assess whether a term corresponds to one or several concepts at a particular point in time or across time. Furthermore, the meaning of a scientific term may change during history — in the case of substantial change a new concept can emerge — and changes in meaning are (for the most part) rational. *Conceptual innovation and advance* is a hallmark of science; and scientists usually have good reasons for changing their concepts. As mentioned in the foregoing chapter, traditional approaches in the philosophy of science often assumed that theoretical progress presupposes that the reference of scientific terms remains unchanged during theoretical change, and avoided talking about the notions of 'meaning' and in particular 'change of meaning', suggesting that concepts and semantic properties of terms cannot change for theoretical progress to occur. In contrast, my approach assumes that conceptual innovation and advance is not only consistent with substantial change in meaning, but that changes in meaning are part and parcel of conceptual advance. Thus, the task is to make room for a view of concepts according to which it can be *rational* for science to change the meaning of terms and develop new concepts. For this reason, it is vital for a study of conceptual change to pay attention to the epistemic practices in which concepts are used and to study the intellectual factors that bring about and justify conceptual change. To stick to the biological metaphor, an account of conceptual phylogeny is to be complemented by a *conceptual ecology* (Stotz and Griffiths 2004).

My previous discussion criticized Kitcher's account of conceptual change on related grounds. The critique was that Kitcher's theory does not address or fails to successfully address three issues, which I view as fundamental desiderata for a theory of conceptual change: any such theory should include *a) an account of concept individuation that permits the philosopher to detect the emergence of novel concepts; b) an explanation of why conceptual change rationally occurred; c) an evaluation of the progressiveness of conceptual change.* In Section 2.2.3 we saw that Kitcher does not address desiderata a and b, and that his account of conceptual progress (desideratum c) is incomplete, as his focus on the addition and deletion of modes of reference fails to capture how improved and novel concepts permit scientists to justify new hypothesis and explain new phenomena. Rather than trying to amend Kitcher's theory so as to attempt to address some issues that Kitcher's present theory leaves out, I shall develop a different framework of concepts and conceptual change.

The strategy is to put forward an alternative account that directly focuses on the above three desiderata. The previous critique already suggested one feature that is missing from Kitcher's approach. He views concept possession as the ability to refer to certain categories, but we saw above that another crucial aspect of concepts is that concept possession implies the ability to justify hypotheses and explain phenomena. Concepts figure in scientific inference and explanation, and the latter are crucial features of scientific practice and theorizing. My semantic account accommodates this fact by assuming that one component of a concept's content is *inferential role*. Thereby my approach aligns with *inferential role semantics*, a doctrine from the philosophy of mind and language maintaining that the ability to make inferences is constitutive of possessing a concept.

While philosophers of science have studies concepts in terms of reference and inferential role semantics has construed concepts in terms of inferential role, my theory will introduce a further semantic notion: the idea of *epistemic goals pursued with a concept's use*. On my overall theory *a scientific concept consist of three components of content: 1) the concept's reference, 2) the concept's inferential role, and 3) the epistemic goal pursued by the concept's use.* These are different components of content or different dimensions of meaning as a concept may historically change in any of these properties (or two terms may differ in any of these semantic properties). All three semantic properties are to be acknowledged as they fulfill different important philosophical functions regards the study of scientific concepts. In particular, the change of concepts is to be studied in these terms, as the change in one component of a concept can be explained relative to other components. Whereas traditional accounts in the philosophy of science have stressed the notion of reference, my later case studies will show that the historical change in reference is in need of explanation, rather than the notion of reference having explanatory significance in accounts of conceptual change. In a nutshell, the rationality of conceptual change — including a change in reference — can be accounted for by the notion of a concept's epistemic goal (desideratum b). Conceptual progress can be assessed using the notion of inferential role (desideratum c). My account of concept individuation will make use of the properties of inferential role and epistemic goal (desideratum a).

The task of this chapter is to develop a theory of concepts that accounts for A) how a concept makes successful practice possible, and B) how a concept can be subject to rational change. To this end, I will spell out the notions of inferential role and epistemic goal, and explain how terms obtain their reference, inferential role, and epistemic goal by sketching a version of inferential role semantics. While attempting to show that inferential role semantics is a viable semantic theory, the present discussion cannot offer a fully developed theory of conceptual content and address all

semantic considerations and conditions of adequacy that arise in the philosophy of mind and language. Rather, the adequacy of my framework is ultimately to be judged based on the extent to which it provides a *fruitful tool* for the philosophical study of historical episodes in science.

Section 3.1 will give a basic outline of my semantic account and its motivations. The subsequent two sections offer clarifications by addressing some prominent challenges to inferential role semantics, namely, the compositionality of concepts, reference, and concept individuation. In particular the issue of concept individuation (Section 3.3) is significant for my two following case studies, as they will advance claims about the existence of several homology and gene concepts. Appendix A will take a look at theories of concepts in contemporary psychology. This discussion is intended to show that the psychological study of concepts is not incommensurable with a semantic theory such as the one developed here, and that some recent developments in the psychology of concepts align to some extent with inferential role semantics. Section 3.4 will summarize my account of concepts and conceptual change, so as provide a methodological tool for the subsequent application of this framework to my two case studies — the homology concept and the gene concept.

3.1 INFERENTIAL ROLE AND EPISTEMIC GOAL AS COMPONENTS OF CONTENT

The notion of a 'concept' is crucial for the philosophy of mind and language, as it is closely tied to other semantic core ideas such as propositional attitudes and the intentionality of thought. A central task is to explain how mental states such as propositional attitudes obtain their intentionality and in what the intentional content of propositional attitudes consists. A related question is how linguistic expressions obtain their meaning. In the philosophy of mind, a *concept* is understood as that constituent of the mind that makes propositional attitudes possible by being part of propositions. More precisely, a person can have propositional attitudes in virtue in virtue of possessing concepts. Thus, a central task for a theory of concepts is to offer an explication of the notion of *concept possession* so as to explain how concept possession makes propositional attitudes and intentional thought possible. What this basic idea involves and what the constraints on a theory of concept possession are can be spelled out by laying out the semantic purposes of *concept ascription* (and propositional attitude ascription). A person is viewed as possessing a concept by ascribing this

concept to her; and thus the question is what semantic purposes are pursued when philosophers ascribe concepts, mental contents, or meanings.

What I view as a central purpose of concept ascription (and propositional attitude ascription) is the intentional explanation of the verbal and non-verbal behavior of individuals. This is more commonly expressed by saying that concepts figure in reasoning and rational action. A person reasons and behaves in a certain way due to the mental contents she entertains, and differences in the verbal and non-verbal behavior that two persons exhibit can be intentionally explained by ascribing different concepts to them. Closely related to the explanation of verbal behavior is the demand that semantics offers an account of successful communication. This is more commonly expressed by saying that concepts are shared between individuals, and that concept sharing makes communication possible. These demands can be summarized by saying that a theory of concepts should account for how concepts make successful theorizing and practice possible.

The idea that concepts figure in reasoning and are shared is quite standard for discussions in the philosophy of mind and language, but an additional semantic purpose emerges from the philosophy of science. Scientific concepts change in the course of history, and thus a theory of concepts ought to underwrite the study of conceptual change. To some extent, this is related to the previous idea. Given that by ascribing a particular concept to a group of scientists one can explain scientific practice, by ascribing different concepts to scientists from different historical episodes (thereby assuming that the meaning of a term changed over time) one can make explicit historical differences in theorizing and scientific practice. But there is an issue surrounding the study of conceptual change that goes beyond the intentional explanation of behavior. This is the question of how conceptual change can be *rational*, i.e., of why the change in the meaning of a term can be rational and progressive. The use of scientific terms change over time, and these changes typically consist in a progress in scientific practice, and scientists often have good reasons to change their language use. A semantic theory has to account for the rationality of the change in concepts and language use. My discussion in the previous chapter emphasized this demand on a theory of scientific concepts, and spelled it out by breaking it down into three parts: an account of concepts and conceptual change should be able to track the emergence of new concepts, to explain why conceptual change rationally occurred, and to assess to which extent it was progressive. The philosophy of mind and language has traditionally offered accounts of meaning and concepts without paying attention to the question of why the change of meaning can be rational. Thus, the philosophy of science offers a novel and important desideratum on theories of concepts.

In sum, my discussion attempts to meet *Two Constraints on Any Theory of Scientific Concepts*:
A) *How does a concept make successful practice possible?* An account of concepts should explain how concepts figure in rational reasoning and action, and how concepts are shared among individuals and term use serves the purposes of effective communication.
B) *How it is possible for a concept to change in the course of history in a rational fashion?* A theory of concepts should account for the rationality of change in the semantic properties of terms.

My tenet is that to meet these different constraints in an adequate fashion makes it necessary to acknowledge several different semantic properties. On my theory, three semantic properties can be ascribed to a term as used by a scientific community. In other words, *a concept consists of three components of content, which are 1) the concept's reference, 2) its inferential role, and 3) the epistemic goal pursued by the concept's use.* In a nutshell, the notion of reference bears on explaining how concepts figure in successful practice, but below I will argue that it offers an incomplete account and that the notion of a concept's *inferential role* is essential to account for Constraint A. Basically, inferential role (also called conceptual role) is the set of inferences and explanations supported by a concept as shared by a language community. I introduce the novel notion of a concept's *epistemic goal*, as it is central to an account of the rationality of conceptual change (Constraint B). It is well-known that scientists or scientific communities have certain scientific goals. Not only does overall scientific activity pursue epistemic aims, the idea of a concept's epistemic goal is that some *individual concepts* are used for specific epistemic purposes. The very rationale for introducing certain scientific concepts and continuing their use is to meet certain epistemic goals. Concepts are intended to deliver a certain epistemic product, consisting in certain types of knowledge: the confirmation of some hypotheses, kinds of explanations, or experimental discoveries. Thus, the idea is that due to the epistemic goal of its use, a scientific concept is supposed to support certain inferences, explanations, or practical investigation — independently of whether at the present state the concept is actually able to yield the demanded epistemic product. This notion permits an explanation of the rationality of concept change. In brief, a concept's epistemic goal sets standards specifying which possible changes in this concept's reference or inferential role are rational. A change in a term's inferential role is epistemically warranted if the new inferences and explanations supported meet the epistemic goal to a higher degree than the previous inferential role.

By introducing the notion of a concept's epistemic goal and suggesting that a concept consist of three components — reference, inferential role, epistemic goal — I maintain that all three are genuine *semantic* properties of scientific terms. The reason for viewing *all* of them as part of a concept's

content is that they fulfill important philosophical functions by addressing the above constraints. In addition, in the course of history a scientific term may change in any of these three properties, so that they can be viewed as different dimensions of meaning. My approach endorses an inferential role semantics by assuming that a term obtains these semantic properties (reference, inferential role, epistemic goal) in virtue of what I call *total inferential role*. *Total* inferential role is the way in which a term is used by an individual, and it may vary between persons. A concept's inferential role, in contrast, is shared within a whole linguistic community (being determined together with the concept's reference and epistemic goal by the various total inferential roles used by the different members of the community). A little more will be said about the notion of epistemic goal in this chapter (in particular in Section 3.3.3), but for the most part the case studies in the subsequent chapter will illustrate this idea in concrete cases and show in detail how it permits to account for the rationality of semantic change: a change in a term's inferential role, its reference, and in special cases a change in its epistemic goal. Most of this chapter is devoted to discussing the notions of inferential role and total inferential role, and to show that in spite of criticism inferential role semantics is a viable semantic account. While explicating the notions of reference, inferential role, and epistemic goal, my primary aim in the dissertation is not to offer a metaphysical analysis of these semantic properties (such as a naturalistic reduction). Rather, the primary philosophical work to be done is to show in the later case studies how these semantic notions can be used in the case of actual concepts and that using these notions yields substantial insights into how concepts underwrite successful scientific practice and how semantic change can be rational.

3.1.1 Inferential Role Semantics

The critique of Kitcher's theory of conceptual progress motivated some issues on which a theory of conceptual change should focus, namely, the way in which scientific concepts figure in inference and explanation (Section 2.2.3). This idea that emerged from my perspective on the philosophy of science is actually related to the above idea that concept ascription serves the purposes of the intentional explanation of action, which is prominent in the philosophy of mind and language. I spell out one semantic approach which ensures a close connection between concepts and inference, namely a version of *inferential role semantics* (IRS). By assuming that the way in which a term figures in inference is constitutive for its meaning, IRS favors an inferentialist rather than representationalist order of explanation to account for intentionality (Brandom 1994). Traditional representationalist

approaches start out with an account of the representational aspect of intentionality, by offering an account of concepts that views representational features of concepts such as their reference as meaning-constitutive. Inferential aspects of intentionality, such as the question of how concepts figure in reasoning and what counts as a good inference, are addressed only in a second step. IRS reverses the order of explanation by viewing the inferential dimension of concept use as meaning-constitutive, and offering an account of what makes concepts refer to worldly categories in a second step. Inferential role semantics will not be defended in these pages as a metaphysical doctrine that offers the right account of the nature of conceptual content. Instead, IRS is used as a heuristic tool to study conceptual change in science. In this sense, inference is viewed as prior to representation not for metaphysical, but methodological reasons. Sections 2.1.1 and 2.2.3 on traditional accounts in the philosophy of science pointed to limitations in understanding conceptual change and scientific rationality in terms of reference, and the subsequent case studied will attempt to show what additional insights can be obtained by approaching conceptual change from the point of view of inference. Theories of concepts as advanced in the philosophy of mind and language have traditionally focused either on logical-mathematical or ordinary perceptual concepts, while the present account will explore the nature and behavior of scientific and theoretical terms.

Inferential role semantics, often called conceptual role semantics (or functional role semantics), is not a particular theory, rather it is a broad framework that encompasses various (sometimes very different) semantic approaches (see, e.g., Block 1986, 1987; Boghossian 1993b; Brandom 1994, 2000; Field 1977; Gupta 1999; Harman 1973, 1975, 1982; Horwich 1994, 1998; Kalderon 2001; Loar 1981, 1982; McGinn 1982, 1989; McLauglin 1993; Montminy 2005; Pagin 1997; Peacocke 1992; Rapaport 2002; Sellars 1953, 1954, 1956, 1968, 1969, 1974; Schiffer 1981; Senor 1992; Wedgwood 2001). The idea of inferential role semantics is that the content of linguistic expressions or mental representations is at least partially constituted by the cognitive or inferential role they have for a thinker or community. Concepts have a specific role in thought, perception, decision making, and action. In what follows, I will spell out a particular variant of inferential role semantics.

Different approaches differ as to whether they focus on explaining the semantic properties of linguistic expressions or rather of mental entities. A prominent strategy is to view IRS as an account of mental content, and to explain the content of mental representations in terms of their causal and cognitive role. One possible way to flesh this out is to endorse the language of thought hypothesis, which assumes that there is a language of thought ('Mentalese') consisting of mental symbols with syntactic properties analogous to a formal language (e.g., expressions combine to

form sentences). Each mental symbol has semantic properties as well, which is why such a symbol is called a mental representation. There are different ways to explain how mental symbols obtain their semantic content, but variants of inferential role semantics that at the same time endorse the language of thought hypothesis maintain that the content of such a mental symbol is given by its causal or functional connections to other symbols (Schiffer 1981). In this case, IRS is primarily an account of mental content, and the meaning of linguistic expressions is explained by the content of the corresponding mental entities. The strategy to view mental content prior to linguistic meaning is quite prominent (also among non-IRS approaches, see Fodor 2001), but the present approach will make nothing out of it. The reason is that my approach is fundamentally concerned with scientific concepts and thus with the language use of scientists and the meaning of scientific terms. For the purpose of the study of scientific language use and conceptual change, it is not necessary to endorse a particular theory of the mind. Consequently, I will not commit myself to (once) popular theories from the philosophy of mind such as the language of thought hypothesis, functionalism, or computationalism. Instead, I will focus on *linguistic expressions*, and use inferential roles semantics as an account of the *meaning of scientific terms* (even if an exclusive focus on language use does not answer questions about language and the mind that are beyond the concern of a study of science).

A basic notion of my approach is the idea of *a term's total inferential role* (or total conceptual role). As inference is a relation between sentences, the account has to define first the *total inferential role* of a sentence p, which is the total set of inferences in which p figures (either as one of the premisses or as a conclusion), where this total set is the set of inferences as endorsed by a particular person. On this preliminary account, inference is construed as a relation between sentences; as a relation purely internal language — as if semantic content had nothing to do with the world external to the mind. However, my intention is to include language-world (mind-world) relations as well, by taking into account how sentences relate to perception and action. Not only can one arrive at a statement by inferring it from other sentences (premisses), but also by observing certain circumstances in the external world. Likewise, not only do sentences inferentially lead to other sentences (conclusions), but they also lead to action. My strategy is to construe the notion of inference broadly, as including not only relations between sentences, but also how sentences relate to perception and action (thereby following Brandom 1994). Thus, *the total inferential role of a sentence does not only include intra-linguistic relations, but also language-world connections.* One reason is that each of these types of inferential dispositions — the disposition to draw inferences between statements, the ability to use observed states of the world as evidence for claims, and the

ability to use knowledge to carry out experimental investigations — is a crucial *epistemic ability* that scientists possess and that enables their theoretical and practical success. Given that my account is committed to capture how concepts make successful practice possible (Constraint A on p. 50), I have to take into account how concepts endow scientists with different epistemic abilities (involving inference between sentences, perception, and action). A second reason — significant for the issue of conceptual change and incommensurability of meaning — is that a scientific term's criteria of application can be quite stable in the face of theoretical change (Burian 1975). My account of the homology concept in Chapter 4 will argue that this concept's application (language-world relations) is an essential part of its meaning, while theoretical definitions are more peripheral to its content. Thereby my account of this concept yields conceptual stability during theoretical change.

The total inferential (conceptual) role of a term t can be defined in turn as the total set of inferences in which t figures (as being a constituent of the premisses or the conclusion, including how it relates to perception and action), as endorsed by an individual person. As a consequence, two terms t_1 and t_2 have the same total inferential role iff substituting t_1 for t_2 in some sentences never turns an inference endorsed by the person into an inference not endorsed. The basic idea of inferential role semantics is that the meaning of a term is determined by its total inferential role. Thus, if two terms have the same total inferential role, they can be freely exchanged and are thus treated as synonyms by the person endorsing this set of inferences. To say that meaning is *determined by* total inferential role is not to claim that meaning *is* total inferential role. Meaning — the content of a concept — consists on my account of three features: reference, inferential role (to be distinguished from total inferential role), and epistemic goal. While meaning and concepts are shared between persons, *total* inferential role is how a term is used by an *individual* and may vary between different persons. Inferential role semantics maintains that meaning *supervenes* on total inferential role, in that a term having its meaning (a certain reference, inferential role, and epistemic goal) is determined by the various total inferential roles of this term as used by different members of the language community. Thereby IRS is a doctrine about concept *possession*; the claim is that a person counts as possessing a concept only if she uses a term with one or the other total inferential role. Section 3.1.3 will say more about the relation between total inferential role as a property of individuals and concepts and inferential roles as operating in the level of language communities, and explain why the notion of total inferential role is relevant for my account of concepts. An immediate *heuristic impact* of this account for the study of conceptual change is the following: Given that concepts supervene on total inferential roles, two persons can use the same term with

a different meaning only insofar they use different total inferential roles. Thus, in order to detect meaning differences between different communities or a change in a concept across time one has to study total inferential roles, i.e., how individuals use terms in inference and explanation. The rest of this section will flesh out and clarify my account and in particular lay out its motivations.[1]

3.1.2 Formal Semantics and Semantic Atomism

Before developing the account further I want to clarify some issues about the approach adopted here by contrasting IRS with two other semantic approaches. The first is *formal semantics*. Formal semantics offers a formal characterization of the semantic value of simple expressions, and how the semantic value of complex expressions can be derived from the semantic values of simple expressions. The standard approach is to view truth-values as the semantic value of sentences, and the truth-value of a complex sentence can be calculated from the truth-values of its constituent sentences. Moreover, the semantic value of a simple sentence can be derived from the semantic values of subsentential expressions. Assuming that the semantic value of a singular term is an individual object, that the semantic value of a predicate is a class of objects, etc., the truth-value of a sentence can be calculated from the semantic values of the its subsentential constituents in a Tarski-style fashion. In the case of empirical rather than mathematical expressions, a sentence has a truth-condition in addition to a mere truth-value, and a predicate has an intension in addition to a mere extension. This can be formally modeled by assuming that the semantic value of a sentence is a function from possible worlds to truth-values (stating for each possible world whether the sentence is true or false in this world, thereby modeling the truth-condition of the sentence). The semantic value of a predicate is a function from possible worlds to sets of objects (giving for each possible world the extension of the predicate in this world, thereby modeling the intension of the predicate), and so on for other subsentential expressions. In this manner, the semantic values of different types of subsentential expressions can be formally specified (which implies an account of how different syntactic types of expressions differ semantically), and it is explained how the semantic values of complex expressions can be calculated from the semantic values of simple expressions.

[1] I construed the notion of inferential role as a relation between syntactic entities such as statements and terms. It is natural to start out with syntactic entities and then explain their semantic properties. A version of IRS endorsing the language of thought hypothesis may attempt at a naturalistic reduction of semantic to non-semantic notions, by appealing only to non-semantic notions such as mental symbols (structures in the brain) and their causal connections, attempting to explain semantic content in terms of the causal role of these symbols. However, the present discussion is not concerned with the question of a naturalistic semantics. For instance, it is not clear whether my (semantic) notion of 'inference' between sentences can be given an interpretation in fully non-semantic terms.

Formal semantic is in prima facie opposition with inferential role semantics, as formal semantics makes use of the traditional representational notions of truth and reference.[2] However, formal semantic and IRS are not rival doctrines. This is because there are two distinct, yet complementary projects that go by the name 'semantics'. *Formal semantics* deals with the semantic values (meanings) of particular expressions in particular languages and how they combine to form the semantic values of complex expressions. The other and project may be called — following Robert Brandom — *philosophical semantics*. Philosophical semantics is concerned with how expressions obtain their meaning and semantic value in the first place, it offers an account of in virtue of what a linguistic expression is meaningful. In other words, it attempts to explain what it is about an individual that she counts as possessing concepts and issuing contentful thoughts; it offers an account of the properties or abilities an individual has in virtue of understanding a concept. Inferential role semantics is a doctrine on the level of philosophical semantics (Brandom 1994; Block 1998). A formal semantic theory alone cannot do the job of philosophical semantics. For instance, if the semantic value of a concept is taken to be a function from possible worlds to extensions, then this does not yield an account of in virtue of what an individual counts as possessing a concept thusly construed. Formal semantics does not explain what enables a person understanding the terms of a language (Harman 1974). Inferential role semantics claims that linguistic expressions obtain their meaning in virtue of figuring in certain linguistic and epistemic practices. A sufficient condition for a person possessing a certain concept (using a term with a certain meaning) is that she is disposed to make and accept certain inferences in which the term occurs, and in case the concept plays a certain role for her in perception and action. This is the sense in which IRS maintains that meaning *supervenes* on total inferential role. It is consistent with IRS to assume that the semantic value (the 'meaning') of a sentence is its truth-value, in line with traditional theories of formal semantics. In fact, my particular variant of IRS takes reference/extensions as one aspect of a term's meaning (the other aspects being inferential role and epistemic goal). IRS claims that a term obtains this 'meaning' in virtue of being used in a certain way — thereby offering a theory of meaning in a second sense (a theory of how meaning is determined) by claiming that the semantic value ('meaning' in the first sense) supervenes on total inferential role. IRS is usually viewed as a holistic semantic theory, as on this account a concept is inferentially and thus semantically connected to many other concepts. The total inferential role of a term is a holistic entity, but this does not necessitate that

[2] It is not necessary that formal semantics uses the notions of truth and reference. Brandom's (unpubl. b) account — discussed in Section 3.2.1 — defines semantic values in terms of inferential incompatibility between sentences.

the semantic value of a term is holistic — it can be an extension in accordance with standard formal semantic theories. Given that total inferential role is the holistic supervenience base that determines meaning, IRS as a theory on the level of philosophical semantics maintains that meaning is *determined* in a holistic fashion, but it need not maintain that meaning *is* holistic.

The other semantic approach with which I want to compare inferential role semantics is Jerry Fodor's informational theory of content, an *atomistic semantics*. This is now a theory on the level of philosophical semantics. It is obviously not the only alternative to IRS, but contrasting IRS with Fodor's atomism serves the purpose of clarifying the nature of IRS and illustrating some of its motivations. Fodor's theory is an informational semantics because he views conceptual content as constituted by causal-nomological relations between symbols in Mentalese (the language of thought) and the properties to which they refer. (The meaning of linguistic expressions is in turn explained by the content of mental symbols.) The basic idea is that the concept 'cow' has its particular content because cows as the referent of the concept (or the property of cowhood) typically trigger a tokening of the mental symbol 'cow'. Due to this causal relation between cows and the symbol 'cow', a tokening of the symbol carries information about the external world; this is why the sort of theory appealing to such causal correlations is called an informational semantics. This basic account has to be refined as a mental symbol is nomologically correlated with many properties and categories in the world, only one of which can qualify as the referent. Fodor attempts to solve this issue by appeal to asymmetric dependencies between nomological relations.[3]

Above all, Fodor's theory is an atomistic theory of content. Concepts are atoms in the sense that the content of one concept is independent of other concepts. For in principle *a person could possess a single concept without possessing any other concept*, in case an informational link between this concept and its referent obtains. Inferential role semantics, in contrast, claims that possessing a certain concept is dependent on the ability to perform certain inferences, which presupposes possessing other concepts. The motivation for the present account stems from the way in which concepts figure in scientific practice. It is a hallmark of science that scientists possess various epistemic abilities, which they demonstrate in theoretical reasoning and practical investigation. Inferential role semantics assumes that this is precisely the case because scientists possess certain concepts and are part of a communal linguistic practice. A consequence of this view is that a lay person may not count as possessing a scientific concept such as the gene concept as used by biologists, since the lay person does not exhibit the epistemic capacities that go with possessing

[3]See Fodor (1987, 1994, 1998a, 2001, 2004) for his position; the most concise account is Fodor (1990b).

the scientific concept of the gene (Stich 1983). This may sound counterintuitive given that the lay person is to be viewed as referring to genes when uttering the term 'gene'. If both lay persons and biologists count as issuing thoughts about genes and making (potentially false) claims about them, why deny that the lay person possesses the gene concept? The reply is that while the expert and the lay person associate a different concept with the term 'gene', their concepts are co-referential. Reference is inherited in that the reference of the lay person's concept is parasitic on the reference of the expert's concept (in particular if the lay person is willing to appeal to experts). Given ascription of the same referent, both expert and lay person count as referring to the same category and are ascribed the same *de re* beliefs in case they make identical assertions — just like a denotational semantics such as Fodor's maintains. Still, the present proposal is fundamentally motivated by the idea that while in virtue of inheriting reference from the experts the lay person need not possess particular epistemic abilities to count as referring to genes, the same cannot apply to the term as used by experts. The reference of the term 'gene' as used by geneticists cannot be parasitic on the usage of other persons, instead, my version of IRS maintains that geneticists count as referring to genes in virtue of their epistemic abilities — the ability to justify hypothesis involving the gene concept, to explain genetic phenomena, and to experimentally investigate molecular and cellular phenomena. This does not presuppose that every geneticist possesses the very same epistemic abilities and exhibits the same linguistic and world-engaged behavior. The scientific division of labor does not require this, and to the extent that the various epistemic abilities that determine the success of scientific activity are spread out over the research community the scientific concept is to be viewed as being a property of the community rather than of isolated individuals — yielding a sense in which meaning is not inside the head on my account. A scientist need not have all the epistemic abilities that are present in the community, but she needs to have some minimal epistemic abilities so that she can successfully communicate with other scientists and engage in the communal linguistic practice of scientific theorizing and experimentation. (My account of concept individuation in Section 3.3 will say more about the conditions an individual have to meet in order to possess a communal concept.) In any case, a scientist must have certain epistemic capacities to count as possessing a concept, and the layman does not possess the concept to the extent she does not have these abilities and cannot successfully communicate with the scientist.

The atomist Fodor, in contrast, explicitly expresses the conviction that epistemic abilities and any sort of epistemic features have nothing to do with semantic issues such as concept possession.[4]

[4]Fodor (2004) does so by contrasting two "paradigms": the "pragmatist" view of concepts that "has defined the

Fodor would not deny that the epistemic, practical, and linguistic abilities of individuals — on which IRS focuses — are somehow connected with concept possession. For creatures like us would not have thoughts and concepts without having certain psychological and linguistic features. But Fodor (1998a) insists that concepts only *causally* depend on these features, but do not *metaphysically* presuppose them. It is informational relations between mental symbols and external properties that are *constitutive* of content, while epistemic abilities merely causally explain why these informational relations originated and are maintained in humans (Margolis 1998; Laurence and Margolis 2002). This disagreement about which features are concept-constitutive vs. causally supportive can be put as follows: Fodor's conceptual atomism maintains that there is a possible world (though this is not the actual world) where there is a being that possesses only one concept without having any inferential and epistemic abilities (maybe an angel being in the right informational relation), whereas inferential role semantics denies this possibility.

Given that in the actual world there are probably different features correlated with concept possession — having epistemic abilities, standing in informational relations, etc. — and if it is not quite clear which of them are really concept-constitutive, then the methodologically relevant question is which of these features are *the most important and fruitful ones to study.* It strikes me that IRS is on the right track. A similar point applies to the psychology of concepts (to be discussed in more detail in Appendix A). While IRS focuses on the rational role of concepts in reasoning and intentional action, psychology is concerned with the causal role of concepts in reasoning and action. Fodor (1998a) rejects these features and processes studied by psychology as being non-constitutive of conceptual content — though he would have to acknowledge that they causally explain concept acquisition and conceptual performances. My reply is that psychology still does the crucial intellectual work. Psychology attempts to account for how concepts are acquired, how they are maintained, and how they change during cognitive development. It studies the cognitive processes that bring about the behavioral and verbal performances characteristic for concept possession. Thus, a good deal of the explanatory force stems from the psychological theories, while it is unclear what Fodor's approach has to contribute to accounting for human conceptual abilities, including reasoning and language understanding. In analogy to this, IRS focuses on features that matter for scientific rationality, as

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mainstream of Anglophone philosophy of language/mind for decades" assuming that "concept possession is some sort of dispositional, epistemic condition"; as opposed to Fodor's "Cartesian" view of concepts "according to which having [concept] C is being able to think about Cs *as such*" (p. 29). Needless to say, this Fodor vs. "the Twentieth Century" dichotomy (p. 29) is an inadequate way to classify semantic approaches. Other, non-Fodorian semantic theories also try to account for intentionality and a speaker's ability to think about objects just like Fodor's Cartesianism (Peacocke 2004). Inferential role semantics, for instance, claims that an individual counts as referring to objects and issuing thoughts about the external world in virtue of taking part in epistemic and world-directed linguistic practices.

its notion of inferential role captures the epistemic abilities that underlie the rational theoretical and practical use of scientific concepts. A motivating assumption of the present framework on conceptual change in science is that conceptual advance is closely tied to an increasing sophistication of the epistemic abilities of scientists, including inference, explanation, and experimentation (inferential role). The heuristic value and fruitfulness of my framework will be illustrated by the subsequent case studies, while it is quite obscure to me how Fodor's informational semantics could be applied to the study of concrete concepts, and what insight about conceptual change it could yield. Keil and Wilson (2000a) criticize Fodor's atomist theory of concepts, because it does not make sense of cognitive development and scientific conceptual change. In his reply, Fodor (2000) states that arguments from conceptual change beg the question against his approach, thereby showing that he does not care whether or not his approach underwrites the study of conceptual change.

In sum, a fundamental desideratum for my approach is to account for how concepts underwrite successful scientific practice (Constraint A on p. 50). To this end, my strategy is to assume that a concept's inferential role is actually a part of the concept (rather than merely being correlated with the concept). Even if Fodor were right, then my approach — taking into account inferential role though it is not really content-constitutive — would still study features that are philosophically significant, especially for the study of conceptual change in science. Inferential role semantics is not defended here as the right metaphysical doctrine about the nature of concepts, instead it is used as a heuristic tool to study conceptual change. The claim is not that my semantic account must always be adopted as a theory of concepts; rather the subsequent case studies attempt to display the advantages of adopting it for the present purposes. For this reason, my account is to be evaluated in terms of its fruitfulness for understanding conceptual change. This approach to scientific concepts exhibits analogies to other studies in the philosophy of science, such as Sandra Mitchell's (1997, 2000, 2003) pragmatic approach to scientific laws. Rather than spelling out a definition of laws and measuring various scientific theories on this definition, Mitchell focuses on how (putative) laws figure in scientific practice and theorizing. This yields an account of the various types of generalizations that are used in scientific theories and explanations — which is a fruitful approach to the question of what laws are as it exhibits several important features of scientific rationality such as prediction, explanation, and causal investigation. Mitchell fruitfully studies a metaphysical category — laws of nature — by studying how law-like generalization and knowledge about laws is used in scientific theory and practice. In the similar vein, my strategy is to understand the category of concepts by studying how concepts are used in scientific theory and practice.

3.1.3 Motivations for Inferential Role Semantics

The considerations offered so far point at a general motivation for inferential role semantics as an account of concepts, at least as far as theoretical concepts are concerned. Many theoretical concepts are definable only in connection with other concepts. A scientific concept can usually be understood only if a person knows about the basic theory in which it figures, which is shown by the fact that learning a novel concept involves learning the background theory as well.[5] An individual learns a theoretical term by learning to use it in theoretical and practical reasoning, for instance by solving scientific problems, understanding and advancing explanations, and carrying out (experimental) investigations. This idea is closely related to the motivation that emerged in the critique of Kitcher's referential theory of conceptual change. While Kitcher views concept possession as the ability to refer to categories, I stressed that concept possession also involves the ability to justify hypotheses, explain phenomena, and discover facts.

This motivation is connected to an above mentioned desideratum on a theory of concepts, namely, that it underwrites the rational explanation of reasoning and intentional behavior (p. 49). One of the central purposes of concept ascription is to explain action, as one makes a person's behavior (including her verbal behavior) intelligible by viewing her as entertaining certain mental contents (propositional attitudes such as beliefs and desires). A consequence is that a difference in the behavior of two persons is to be explained by ascribing different contents to them. This presupposes that propositional contents are individuated more finely than truth-values and that concepts are individuated more finely than reference. Frege's ([1892] 1960) central motivation for introducing the notion of sense (Sinn) in addition to reference/denotation (Bedeutung) was that co-referential concepts may behave differently in rational reasoning, as the evening star/morning star example shows. Kripke's (1979) 'puzzle about belief' offers further examples for this. Denotational theories of content such as direct reference theory or Fodor's informational semantics individuate meaning in terms of reference: two terms referring to the same category ipso facto have the same content. For this reason, these semantic approaches typically have problems to account for the role of concept ascription for the explanation of action.[6] Inferential role semantics

[5] This is not to say that the content of biological concepts is specified by explicit definitions (as e.g. the Ramsey-Carnap-Lewis approach assumes). IRS maintains that concepts are defined by their role in theoretical reasoning rather in an explicit theory. As my study of the homology concept will show, I resist the assumption that standard 'definitions' offered by scientists yields the content of a scientific term. Chapter 4 will rely on the way in which the homology concept was used in scientific practice as a better guide to its content than typical definitions of homology.

[6] Fodor (1990a) attempts to deal with this issue by assuming that two symbols in Mentalese that have the same reference (and thus are thus *semantically* identical on his theory) but play a different role in reasoning are *syntactically* different, so that there is a difference between the two symbols that can underwrite their different cognitive roles.

is in a position to individuate concepts in a sufficiently fine-grained manner that underwrites the intentional explanation of behavior, as the starting point for concept ascription is what I call the total inferential role of a term, as used by a particular individual. The total inferential role of a term is the set of inferences in which a term figures, including relations between sentences and perception/action. It is a property of an individual in that it refers to the inferences an individual is willing to accept. IRS is commonly called a 'holistic' semantic theory, as total inferential role involves relations between all the contents a person entertains. Arguments in support of semantic holism depend in one way or another on the fact that content ascription serves the purposes of the rational explanation of reasoning and intentional behavior (Davidson 1984b; Bilgrami 1992; Block 1995a, 1995b). The idea is that any difference in total inferential role between two persons (or any difference in belief) may be relevant for some explanation of why they reason or behave differently.[7]

This does not mean that I endorse a radical holism — the view that two persons associate different meanings with a term (possess different concepts) whenever they differ in some belief, i.e., whenever they endorse different total inferential roles. My version of IRS does not identify a concept's meaning with its *total* inferential role, rather it assumes that meaning *supervenes on* total inferential role (where a concept's meaning consist in its reference, its epistemic goal, and its inferential role, to be distinguished from an individual's total inferential role). Due to this supervenience, two total inferential roles may count as corresponding to the same concept. This relates to the idea that concept ascription serves the purposes of the explanation of intentional behavior as follows. The same explanation of behavior may apply to two persons endorsing different total inferential roles — in which case it is possible to ascribe the same concept. For it may be sufficient for two persons to agree on a limited set of inferences endorsed (or to share a limited set of beliefs), which are relevant for this particular intentional explanation. For instance, a layman and

Fodor can do so by individuating syntactic entities in terms of their cognitive/inferential role. However, this is not an account that is really different from inferential role semantics, as Fodor individuates certain mental entities in terms of inferential role and just calls this a syntactic issue, while IRS views this as a semantic issue. Fodor's attempt to offer a syntactic solution to the Frege and Kripke cases is successfully criticized by Bilgrami (1998), who argues that problems that are fundamentally about rationality cannot be dealt with in a syntactic fashion.

[7] For Davidson semantics is about the intentional explanation of action in that he stresses *interpretation*. Brandom's (1994) IRS arrives at holism in a different, but partially analogous way. Brandom's starting point is to demarcate verbal responses that exhibit *understanding* of what is uttered from those that do not (such as animal behavior). He argues that a being understands statements to the extent that she views them as standing in need of justification and as a justification for other statements, so that it is its inferential articulation that makes a statement contentful. Brandom emphasizes that what a person is committed to infer from a statement endorsed (and to what claims she is entitled) depends on the all other statements endorsed by her — yielding a semantic holism. For two persons endorsing the same statement may be committed to make different conclusions from it in case they are committed to different collateral beliefs. (Brandom's contrast between humans and animals is to some extent analogous to my above contrast between scientists and laymen. In Section 3.1.2 I argued that a laymen counts as referring to a scientific entity only derivatively to the scientists who genuinely possesses a scientific concept and refer in an underived manner.)

a Drosophila geneticist have quite different conceptions of a fruit fly, i.e., they associate different total inferential roles with the term 'fruit fly'. But when we explain how they succeed in catching a fruit fly, we just need to make recourse to a few shared beliefs/inferences about flies that are sufficient to explain their behavior, such as the assumption that fruit flies fly in a certain manner. The *inferential role* of the shared concept consists of this limited set of inferences (a common subset of the total inferential roles), so that inferential role can be shared by individuals. Thus, differences between *total* inferential roles need not necessarily imply that different concepts are used. At the same time, the notion of total inferential role (and the associated holism) is important, if intentional explanations are to cover any possible case. In some contexts as the one just mentioned, the different beliefs of a layman and an expert about fruit flies are irrelevant, but in other context, they may be important and necessary to explain a difference in behavior (e.g., why experts and laymen make different claims about fruit flies or why they go about differently to find out about their biological properties). Thus, in the case of an explanation of a particular instance of behavior, the total inferential role an individual associates with a term is as such not necessary for the explanation: just a particular part of the total inferential role is necessary. But the total inferential role is an important resource for a whole range of different explanations. Any difference in individualistic total inferential role may feed into some explanation. Thus, what is holistic is not the concept ascribed. My semantic approach does not endorse a holism about meaning *individuation*. What is holistic is the total inferential role, which forms the very basis for concept ascription (the basis on which concepts supervene). My holism is a *moderate holism* about meaning *determination*.[8]

This can be rendered more systematic by distinguishing three levels of features relating to content; the former being more fine-grained than the latter: a) total inferential roles, b) inferential roles, and c) referents. A concept's inferential role supervenes on and is determined by the various total inferential roles endorsed by the members of the language community. The concept's referent is determined by the inferential role together with the world. A total inferential role of a term is a property of an individual; it is the conception this individual has of the object denoted by the term. Individuals may very well differ in their conceptions of things (their mental representations

[8] A *radical* holism about meaning determination assumes that *all* inferences (or beliefs) in which a concept figures are *necessary* to determine the meaning of this concept. A *moderate* holism, instead, acknowledges that some inferences are irrelevant for meaning determination (while other inferences are more or less relevant for meaning determination). However, a moderate holism is a holism in that it maintains that the factors that determine meaning (e.g. inferences) form an open an unbounded set. For moderate holism assumes that the degree to which a particular factor is salient is context-sensitive: in one context where a term is used by a person a statement may be salient for determining the term's meaning, in another context (e.g., as used by another person) the same statement may be less salient. This contrasts with approaches that assume that the set of factors that determine meaning can be reduced to a limited and clearly delineated set of features (such as analytic statements). More on this idea in Sections 3.2.2 and 3.3.

of objects). Concepts, in contrast, are ascribed to and shared by larger groups of persons, and thus operate on a different level. IRS as an account of philosophical (rather than formal) semantics maintains that a person possesses concepts in virtue of taking part in world-engaged inferential practices. A person possesses a particular concept (with a certain inferential role and reference) by endorsing one or the other total inferential role. The fact that two individuals use distinct total inferential roles is consistent with them possessing the same concept. Thus, holism attaches to meaning determination and the level of total inferential role, rather than to meaning individuation and the level of concepts. The notions of an individual's total inferential role, a concept's inferential role and its reference and the relation of these semantic properties will be spelled out in more detail below in my discussion of reference (Section 3.2.2) and concept individuation (Section 3.3).

A stronger motivation for inferential role semantics that has been prominent in past discussions is functionalism, which assumes that a mental state obtains its content in virtue of its functional relations to other mental states. I do not rely on this motivation for IRS, as my study of conceptual change in science does not endorse a particular theory of the mind such as functionalism (or computationalism). My semantic strategy is to focus on the public use of language, and to be agnostic about the underlying metaphysics of the mind. In particular, *I do not use the notion of narrow content*, which has been prominent in related debates about mental content. Narrow content is purely 'inside the head' as it supervenes on the person, thus assuming that the external world around an agent does not contribute to the determination of its mental contents. This yields a solipsistic and internalist view of conceptual content (Fodor 1980; Segal 2000; Rapaport 2002). While the notion of (total) inferential role has sometimes been identified with narrow content, I depart from this possibility of construing IRS in two ways. First, my semantics is externalist in that in my view concepts are ascribed based on the linguistic behavior of an agent *and* the state of the world around her, including the way in which she interacts with the world. In this sense, meaning does not supervene on the head only. This does not mean that concepts are to be viewed as objects external to the mind. My semantic externalism is an externalism about how concepts are ascribed and what determines concept *possession*. Second, I do not identify total inferential role with narrow content, because as discussed in Section 3.1.1 the notion of inferential role is broadly construed as it includes not only inferences between sentences, but also how sentences (or propositional attitudes) relate to perception and action. The (total) inferential role of a term includes mind-world in addition to mind-mind relations and thereby does not yield an internalistic view of content. In fact, an important motivation for my approach is that concepts are important

for *successful practice*, which includes interaction with other persons and finding out about the world. (Despite being part of an influential tradition, the idea of narrow content and content being inside the person is becoming increasingly unpopular in cognitive science; see Wilson 2004.)

In his essay "Meaning and Misconceptions," Anil Gupta (1999) uses the fact that concepts underwrite successful practice and that a semantic theory should account for successful practice to motivate non-representational theories of content (such as inferential role semantics). He points out that philosophers often implicitly assume that engagement with the world implies representationalism. Realists insist on scientific success and engagement with the world and thus feel compelled to endorse a representational account of language. Anti-realists reject representationalism and thus tend to deny engagement with the world. *Gupta rejects this common assumption that world-engagement entails representationalism* by favoring a non-representational approach to semantics, yet stressing that concepts and language users are fundamentally engaged with the world.[9] Gupta's discussion focuses on the phenomenon of misconceptions; and the fact that concepts involving misconceptions nonetheless underwrite successful practice is used as a challenge for representational approaches. The challenge is as follows. Gupta considers a concept whose application is governed by the use of two criteria or characterizations of the referent, which are empirically non-equivalent and thus to some extent empirically inconsistent — where this is unknown to the language community, so that they tend to *theoretically conflate* these criteria. (This is of course a typical situation for scientific concepts even in mature stages of science, as the different criteria used never perfectly match and concepts involve at least a minimal degree of misconception. A prominent example is the early gene concept; see Section 6.1.1.) Arbitrary use of and shifting between the two criteria would lead to obvious contradictions (the deductive closure of the theory that views the criteria as identical is inconsistent). However, in practice no genuine contradictions arise as one criterion is primarily used in one type of situation, while the other criterion is used in other circumstances (maybe because it is more feasible to use it in these cases) — where the language community is not aware of this *practical dissociation* of the criteria. Thus, concepts embodying misconceptions is consistent with their largely successful use and with them being good guides to action.

Representational theories of language assume that semantic analysis boils down to assigning referents to terms and thereby truth-values to sentences (or that this is the starting point for se-

[9]Section 3.1 indicated why my semantic approach takes language to be world-engaged. In contrast, a representational theory such Fodor's yields a picture of concepts that is disconnected from world-engagement, as on his account concept possession has nothing to do with epistemic abilities (Section 3.1.2). Likewise, my critique of the referential tradition in the philosophy of science argued that the (representational) notion of reference alone cannot solve the incommensurability issue as a challenge to scientific rationality and thereby an epistemic issue (Section 2.1.1).

mantics). Using a correspondence theory of truth, the classical idea for a representational approach is that true statements are good guides for action, whereas false statements lead only accidentally to successful practice (Kitcher 2002). Gupta uses the case of concepts involving misconceptions to point to limits of this approach. In the above example, two non-identical criteria are in use, each of which expresses a certain property in the world, say R and S. Gupta considers different options of assigning a referent to the term (the referent is R, or S, or $R \wedge S$, or the term refers partially to R and to S). *Each* of these options has certain drawbacks. For instance, the idea that the term partially refers to both properties entails that many statements containing the term have indeterminate truth-values and thus are neither true not false. Other options may imply that certain statements have the truth-value false, while such statements *still enable successful practice*. Thus a representational approach would have to offer an explanation of how certain sentences evaluated as false are nonetheless good guides for action, whereas their true negations are poor guides.[10]

I agree with Gupta that merely assigning referents to terms may offer unsatisfactory philosophical accounts of concepts, in particular as far as scientific concepts are concerned. The referential tradition in the philosophy of science has discussed scientific progress broadly in the following terms: 1) inadequate scientific theories contain many statements that involve a non-referential term (which can be viewed as meaningless); a more progressive situation obtains when 2) the statements of a theory are referential, but many statements are false; and a mature theory is characterized by 3) mostly true statements. This scheme of classifying a sentence into three categories or stages (non-referential, false, true) is quite rigid; and in Section 2.2.1 we saw Kitcher attempting to work towards a more flexible account. Kitcher denied that a concept or a term type always has a particular referent, arguing that different term tokens may refer differently, so that he could say that while the phlogiston concept was often non-referential (stage 1), some statements in which it occurred were referential and in fact true (stage 3). Interestingly enough, more traditional realists such as Stathis Psillos (1997) are dissatisfied with the latter idea: "the principle of humanity, coupled with Kitcher's view that tokens of expression-types may systematically refer to different things, makes conceptual progress too easy" (p. 259). Unlike Psillos, I think that Kitcher is right in attempting to revise canonical theories of reference, as from the perspective of the present discussion there is in fact a need to account for the (partial) practical success of some statements involving the

[10] A representational semantics can account for such a case only if additional considerations are adduced that show why in certain cases true statements are bad guides to action and false statements are good guides. However, in this case the successful use of language is not explained by the truth-values of statements, rather the explanatory force comes from the auxiliary considerations, which are not part of a traditional representational semantics.

highly misconceived notion of 'phlogiston'. However, I do not think that this can be achieved within the boundaries of a representational semantics alone. (Section 2.2.2 offered a critique of Kitcher's account of token reference based on a speaker's dominant intention to refer; and Gupta's essay argues against the idea that his example can be satisfactorily dealt with by assuming that a concept is context-dependent like an indexical.) My semantic strategy is not to focus exclusively on reference but to pay attention to the practical use of concepts as a guideline to their meaning. To the extent that assigning reference yields philosophical insights, it is only a secondary step of semantic analysis. The primary concern has to be how the possession of particular concepts enables successful scientific theorizing and practical investigation (including effective communication).

Gupta (1999) offers the following non-representational semantic account of concepts — based on the case of misconceptions. He distinguishes between *absolute content* and *effective content*. The former takes all the conceptual connections into account in which a term is used on some occasions. In the above example it includes the two criteria of application and the assumption that they are equivalent (though this can yield inconsistencies). Effective content is the content that takes not only conceptual connections into account, but also dissociations between concepts that occur in practice. In the example it includes the fact that the two criteria are in practice not always conflated, i.e., that an inference from one criterion to the other is often not carried out (which guarantees that no empirical contradictions arise in the actual usage of the term). Absolute content is the content one is committed to when using the term; effective content is the content in play. The idea is that *absolute* content is what is often called meaning; while it is actually the *effective* content that — together with the world — yields the truth value of an assertion. Gupta introduces the notion of a *frame* to express how to obtain the more relevant effective content from the absolute content: Absolute content (meaning) plus frame determines effective content. A frame goes beyond the rules of language (meaning) in that it specifies how the rules of language are to be applied, and in that language users are not explicitly aware of the frame. Frames contain information that accounts for effective uses of language, and this information need not be available to the language user in the sense that this information is not always necessary for using language. Gupta assumes that successful communication as such does not presuppose a frame (the meaning or absolute content is sufficient for this), while successful practice based on linguistic information requires the existence of a frame (independently of whether language users are aware of its existence). In the case of conceptual change, meaning (absolute content) and frame may change independently.

The upshot of Gupta's essay is that it is not clear that a standard representational semantic

theory as such can account for the successful use of language in practice. In fact, on his account language alone does not represent anything, it only represent in combination with a frame (for absolute content yields truth-values only given a frame). Gupta avoids some weaknesses of both semantic realism and antirealism by making room for an account according to which language does not (always) mirror the world, yet is fully engaged with the world: effective content is intended to account for how language use underwrites successful practice. Representational notions such as referents and truth-values are to be assigned in a subsequent step only, and in some cases it may even be impossible to assign a determine truth-value (or to systematically assign truth-values so as to account for the success of language use). While my account so far has emphasized the importance of inference and conceptual connections for the content of scientific concepts, a crucial insight of Gupta is that *conceptual dissociations* are significant as well (e.g., different criteria are implicitly distinguished by being treated differently in practice, though they are not kept apart in thought). The notion of a frame makes plain that language use is not a monolithic whole, but fragmented into parts. Not only conceptual connections, but also conceptual dissociations enable the world-engagement of language. In what follows, I will use these ideas, in particular Gupta's notion of a frame. When I subsequently talk about 'inferential role' or 'total inferential role', I do not just refer to a set of inferences (Gupta's absolute content), but also how these inferences are carried out in practice (Gupta's effective content as including the frame).

3.1.4 Material Inference

The discussion so far has emphasized that the notions of 'inference' and '(total) inferential role of a term' have to be understood broadly, as including not only inferential relations between concepts, but also the way in which concepts relate to perception and action. Now I want to stress that I construe inference as *material inference*, following Wilfrid Sellars (1953, 1974), Robert Brandom (1994, 2000), and Anil Gupta (1999). Traditional accounts typically view inference as a formal relation, which is particularly clear in the context of deductive inference. A deductive inference is viewed as valid purely in terms of its logical *form*, independent of the *content* involved. Induction was assimilated to the idea of formal inference by attempting to represent an inductive inference as an instance of a certain inference *scheme* and to assess the inference in these terms (W. Salmon 1963; M. Salmon 2002). In fact, logic is generally viewed as being about form, not content. Likewise, accounts of *scientific explanation* have viewed good explanations as conforming to particular

formal schemes (Hempel 1965; Salmon 1971; Kitcher 1989). Traditional accounts in the philosophy of science about the relation of different theories and scientific concepts have focused on *theory reduction*, i.e., the idea that one theory can be logically derived from other theories (Nagel 1949, 1961; Kemeny and Oppenheim 1956; Schaffner 1967b, 1993; Brigandt and Love forth.). However, in my view a formal construal of scientific reasoning is of limited value. For instance, formal accounts of analogical reasoning as a type of induction construe an inference from an object a having property P to object b having this property as justified in case objects a and b are similar in that they share properties Q_1, $Q_2, \ldots$ Such a formal account has to acknowledge that the inductive inference $Pa \vdash Pb$ is justified only insofar as the degree of similarity between objects a and b is *significant* and the properties Q_i are *relevant* for the property P to be transferred (Salmon 2002). However, what is relevant or significant crucially depends on the features of the particular case, and thus the plausibility of the inference essentially depends on empirical information, while the logical form of the inference is actually quite insignificant for the inference's validity. Marcel Weber (2005) argued based on concrete examples from experimental biology that formal schemes of scientific inference (including Bayesianism) yield an unsatisfactory account. Instead, scientists rely on empirical considerations that are specific to the particular field and case, so that scientific inference is domain-specific rather than based on general schemes. I take this to be a general fact of reasoning in biology, but will not spend time to adduce more examples to support this assumption. In a more general context, John Norton (2003) recently argued for a 'material theory of induction'. In contrast to formal theories of induction, Norton argues that there are no universal inference schemas. Inductive inferences in science are grounded in matters of fact — the 'material' of the induction — that hold only in particular domains. New scientific knowledge generates new inferential power, but not by yielding new abstract schemas of inference. Norton is a philosopher of physics, so the idea that induction is material rather than formal is not peculiar to biology, but a general feature of science. Whether a particular inference is good essentially depends on those facts that are pertinent to the matter of the particular induction, so that formal accounts of scientific inference are incomplete by leaving out an important factor that determines the quality of the inference.

I want to go a little further than Norton by stressing the notion of material inference. While on the traditional picture an inference is taken to be valid because of its form, a material inference is an inference that is taken to be good because of its content. The content of the particular premises and conclusions involved determines the acceptability of the inference, where this content involves empirical and substantial scientific knowledge. My view is that *scientific inference is material*

inference. More specifically, I assume that the *concepts* occurring in the inference determine the acceptability of the inference, as the meaning of scientific terms embodies crucial empirical knowledge.[11] For instance, one case in which an analogical inference of the form $Pa \vdash Pb$ is justified is if a and b are two instances of a natural kind and P is a projectable property of this natural kind. Whether this is the case depends on substantial prior empirical knowledge, including that scientists possess a natural kind *concept* that embodies the information that P is likely to be a projectable property for the objects under consideration. In this sense, natural kind concepts support scientific inferences. My critique of Kitcher's referential approach to concepts already pointed out that possessing a concept is not merely a person's the ability to refer to a category, but that concepts figure in scientific reasoning such as inference and explanation (Section 2.2.3). The idea that inference is material inference and thus based on semantic content clearly fits with the basic tenets of inferential role semantics. According to IRS, the very content of a sentence is determined by the inferences in which it figures. (Derivatively, the content of terms is determined by their role in inference.) On this account of semantic content, a person takes an inference to be good precisely because the premisses and the conclusion have the content they have.[12]

The assumption that scientific inference is material inference has the following advantages. First, it yields an account of inference that fits scientific practice better than formal models of inference. Philosophers of science such as Norton (2003) and Weber (2005) point out that scientific inference cannot be captured by purely formal and domain-independent schemes; rather, scientific inference is domain-specific and its inferential power derives to a large extent from substantial

[11] A formal inference is *taken to be valid* due its form but need not be valid due to its form because the inference rules may be unsound. This distinction is important in the case of material inference, as such an inference may contain concepts that are empirically flawed. Whether a material inference is actually good depends not only on its content, but also on whether the content conforms to the state of the world. If a concept turns out to be empirically inadequate, it ought to be modified, so that the novel concept supports more adequate inferences. Therefore, IRS provides an account of why it is possible to criticize empirical concepts: given that this account construed concepts as figuring in inference, a concept can be legitimately criticized to the extent that an empirical concept tends to lead to empirically problematic inferences. For instance, Griffiths (2002) argues that the concept of 'innateness' should be abandoned as it embodies various empirically illegitimate inferences. In sum, the idea of material inference is that an inference is *taken to be valid* due to the content involved. Scientists reason in a certain way because of the concepts they possess. Despite the possibility of empirically flawed concepts, given that scientific concepts are based on substantial prior experience, scientists are usually justified in inferring a conclusion based on material inference.

[12] Formal-deductive models of inference have a basic way to attempt to include empirical content as bearing on the quality of the inference. Namely, an inference that is materially good but not formally valid is viewed as being based on implicit premisses that have been omitted. A formal account has to add premisses that define the meaning of the empirical terms involved (meaning postulates) and statements that specify empirical facts about these objects referred to by these terms. If enough premisses have been added, the conclusion follows in a purely syntactic way. One problem with this proposal is that it is not clear whether the meaning of empirical terms can always be defined in this way (Sections 3.3.1, 4.4, and 6.3.2). I view formal-deductive inference as a special case where the quality of the inference depends solely on the meaning of the logical terms involved (but not on any empirical contents). See Section 2.IV of Brandom (1994) for a detailed discussion of the difference between formal and material inference.

body of empirical knowledge that underlies a specific instance of inference. The assumption that scientific inference is material inference offers a philosophical explanation of these facts about scientific practice. Moreover, it provides a model of how scientific inference can be rational if scientific inference is neither deductive inference nor conforms to certain formal schemes.

Second, the notion of material inference unifies various modes of scientific reasoning, by viewing them as different species of one genus. For instance, some material inferences are *counterfactual-supporting*, e.g., if the empirical content that supports the inference embodies knowledge about scientific laws (Sellars 1948; Brandom 1994). Standard formal models of inference are incapable of picking out statements that express laws in a purely formal and syntactic fashion; instead, they have to add that, for instance, a universal statement is a law (rather than an accidental generalization). Scientific inferences can be counterfactually robust to various degrees, and so are material inferences. Similarly, *material inference includes causal reasoning and scientific explanation.* The discussion in Section 2.2.3 stressed that concepts do not only figure in inference and justification, but also scientific explanation. Consequently, while the terms 'conceptual role semantics' and 'inferential role semantics' are usually used as synonyms, I stress that the notion of conceptual/inferential role on my account includes not only how a concept figures in scientific inference (as traditionally understood), but also how concepts figure in explanation. If 'inference' is understood as material inference, rather than as formal inference, then this broader notion of inference captures both scientific inference — in the traditional sense of justification and confirmation — and scientific explanation. The idea that both scientific inference and explanation are species of one genus (material inference) does not mean that inference and explanation are to be identified. Wesley Salmon (1970) prominently argued that explanations are not arguments (neither inductive nor deductive). On the present proposal, inference and explanation can be viewed as different types of material inference. In this sense, material inference is not a homogeneous category. But the above discussion already showed that even the material inferences involved in scientific inference and confirmation form a heterogeneous category. Inferences depend on the particular empirical knowledge that is relevant for the particular domain and inferences. Inference is local and domain-dependent and may vary from case to case. Likewise, different explanations may be of a different type. In the case of statistical explanations, concepts may pick out a class and appropriate reference classes and link them to statistical relevance relations. In causal explanations a concept picks out a set of entities that are part of similar causal processes or governed by the same causal law.[13]

[13]Apart from capturing causal-nomological reasoning by potentially being modally robust, material inferences can

The notion of material inference also bridges the gap between scientific discovery and confirmation. Many recent accounts have denied the assumption that discovery — unlike confirmation — is not a rational process and that it should not be subject to philosophical analysis (Schaffner 1974a; Hacking 1983; Darden 1991; Weber 2005). At the same time some of these accounts of discovery, focusing on experimental science, have argued that there is no logic of discovery and that discovery is not based on unchanging principles. However, this does not explain how discovery can be a rational process (Brigandt forth. b). On my account, confirmation is rational not because it fits certain formal schemes, but because it involves material inference. In the same vein, I view discovery as being based on material inference. As in the case of inference and explanation, this is not to assert that the material inferences involved in discovery are the very same ones as the inferences involved in confirmation. Certain inferences are permitted in the case of discovery that are usually prohibited in the context of confirmation. Yet, both confirmation and discovery are closely related as they are two species of one genus: rational reasoning in the form of material inference.[14]

Let me give a preliminary summary of the account so far. I do not defend inferential role semantics as a metaphysical doctrine; instead I use it as a tool to study the change of scientific concepts. IRS is understood as the idea that expressions obtain their meaning in virtue of figuring in inferential practices. Communal meaning — a concept's reference, inferential role, and epistemic goal — is determined by (supervenes on) total inferential role. The notion of inference and inferential role is broadly construed. Inference is viewed as material (rather than formal) inference, thereby encompassing various forms of reasoning, including scientific inference and justification, scientific explanation, and reasoning involved in discovery. In addition, inference is not narrowly construed as a relation between different sentences only, but also includes the way in which concepts and mental contents relate to perception and action. Thus, my version of IRS assumes that concepts obtain their content in virtue of figuring in world-engaged practices involving language use.

This basic account raises some questions and is in need of elaboration. In what follows, I develop the account further and offer some clarifications by addressing some prominent challenges to IRS.

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also capture moral reasoning. For instance, the concept of a 'person' as used in bioethics refers to an individual that has a certain moral status (such as the right to life). In addition, a particular concept of a person contains (descriptive) criteria that specify which individuals are persons (such as the ability to feel pain, or having interests). In this sense, the concept of a person supports an inference from descriptive conditions to normative status.

[14] An issue that cannot be explored here is the fact that arguments both for the underdetermination of theory by evidence and for epistemic holism (à la Quine) assume that the relation between theory and evidence is formal deduction — which can be challenged by an approach such as mine. Quine's epistemic holism is misguided as due to the particular empirical knowledge embodied in concepts and statements, a certain statement materially bears on other statements in that it confirms or disconfirms them, but it is materially independent of many other statements.

3.2 CRITICISMS OF INFERENTIAL ROLE SEMANTICS

This and the subsequent section address prominent challenges to inferential role semantics raised in the philosophical literature. I cannot give a satisfactory solution to each of these problems — this is a future task for philosophers of mind and language. But I discuss to which extent these issues are problematic and sketch ways in which these issues can be solved. A more general function of replying to criticisms is to support the idea that inferential role semantics is a potentially viable theory of conceptual content, so that it can be used for the study of scientific concepts. A more specific aim is to develop further and spell out my own version of IRS so as to obtain a basic framework on concepts that can function as a heuristic tool for the subsequent studies of conceptual change. The criticisms of IRS to be addressed in turn are the compositionality of concepts, the relation between inferential role and reference, and — in Section 3.3 — the question of how to individuate concepts. The latter issue is particularly significant as one of the tasks of my case studies is to determine whether one or several homology or gene concepts have been used in history.

3.2.1 Compositionality of Concepts

Jerry Fodor and Ernest Lepore made the compositionality of concepts the main criticism of holist theories of concepts. While discussing other challenges to inferential role semantics, Fodor and Lepore consider this novel argument the most decisive one (Fodor and Lepore 1991, 1992, 2001a, 2001b). Compositionality is not an issue peculiar to IRS alone. In fact, Fodor and Lepore use the compositionality of concepts as an argument against any non-atomistic or non-denotational semantic theory (Fodor 1998b, 2000, 2001; Fodor and Lepore 1993a, 1993b, 2002). See for instance Fodor's "Having Concepts: A Brief Refutation of the Twentieth Century" (2004). In addition to incessantly criticizing various philosophical theories of concepts, in *Concepts: Where Cognitive Science Went Wrong* (1998a) Fodor argues that most theories of concepts in cognitive science violate compositionality and are thereby false (see also Fodor and Lepore 1996a, 1996b, 1999).[15]

Depending on the particular semantic theory, the semantic value of an expression may be an extension, an intension, a category, etc. *Compositionality* is the idea that the semantic value of a complex semantic expression is a function of the semantic values of its parts (together with the syn-

[15]For some replies to Fodor and Lepore see Block 1993; Keil and Wilson 2000a; Machery 2004; McLauglin 1993; Pagin 1997; Peacocke 2004; Robbins 2002; Warfield 1993; and the contributions in Fodor and Lepore 1994.

tactic mode of composition of the parts). For instance, the meaning of the combined concept 'pet fish' ought to be a function of the meaning of 'pet' and the meaning of 'fish'. Fodor views compositionality as a constraint on any theory of concepts as it explains the productivity and systematicity of thought. *Systematicity* is the fact that there are certain symmetries of expressive power in conceptual thought. For instance, if a person can entertain the thought that John loves Mary, then she can entertain the thought that Mary loves John. *Productivity* is the fact that a person can entertain a potentially infinite number of complex concepts and propositions, and understand a potentially infinite number of expressions. A person can possess only finitely many primitive (lexical) concepts, as long-term memory is limited (e.g., 'president', 'grandmother', etc). Still, a person can form and understand arbitrarily complex concepts ('the president's grandmother who spies on dinosaurs on the moon') and an infinite number of propositions composed of concepts. If concepts are compositional, then productivity and systematicity can be explained as follows. A person possesses and thereby understands the meaning of primitive concepts. Given compositionality, the meaning of complex concepts is a function of the meaning of primitive concepts (this function is given by the rules of conceptual combination). Thus, if a person possesses the primitive concepts and the rules of conceptual combination, then she can entertain any complex concept or proposition. Similarly, if a person learns a novel word, then she can automatically understand any complex expression in which this word occurs, as she already possesses the universal rules of conceptual combination.

Compositionality is a challenge for holist theories of meaning because compositionality is violated whenever in conceptual combination there arise so-called *emergent properties*. To use one of Fodor's favorite examples, assume that a person happens to believe that brown cows are dangerous, so that from her concept 'brown cow' the concept 'dangerous' follows.[16] As the person does not infer 'dangerous' from either 'brown' or from 'cow', dangerousness is an emergent property in that it is not a part of the meaning of the simple concepts 'brown' and 'cow', yet it is a part of the meaning (inferential role) of the complex concept 'brown cow'. Any instance of an emergent property violates compositionality: in the present example the semantic value (the meaning) of 'brown cow' is not a function of the semantic values of 'brown' and 'cow'. Holist theories that construe the meaning of a term as its *total* inferential role necessarily violate compositionality of meaning:

> ... the inferential role of 'brown cow' depends not only on the inferential role of 'brown' and of the inferential role of 'cow' *but also on what you happen to believe about brown cows*. So unlike meaning, inferential role is in general not compositional. (Fodor and Lepore 1991, p. 334)

[16] As pointed out in Section 3.1.1, inference is a relation between sentences rather than terms, so that one should better say that 'x is a brown cow' implies that 'x is dangerous'. Here I ignore this issue for purposes of simplicity.

Not only radically holist theories of meaning violate compositionality. Most theories of concepts allow for emergent properties as they view some beliefs about the referent as concept-constitutive. For instance, psychological theories of concepts such as the prototype theory face the compositionality challenge (Fodor and Lepore 1996b; Fodor 1998a). The prototype theory assumes that a concept consists of a statistical description of the typical features of the concept's referent — thereby connecting a concept to other concepts by construing a concept as containing background beliefs about the referent. Fodor points out that the prototype of 'pet fish' contains features such as 'small', 'gold', 'lives in small glass bowl', however, these properties are very untypical for pets as well as for fishes, so that the prototypes for 'pet' and 'fish' does not contain these properties. Given that the prototype (the statistical feature list) of 'pet fish' cannot be calculated from the prototype of 'pet' and the prototype of 'fish' alone, compositionality is violated, which apparently argues against the identification of concepts with prototypes. In a similar vein, Fodor (1998b) argues that recognitional abilities cannot be part of the possession conditions of concepts. Even for a concept like 'red', the ability to perceive red things cannot bear on possessing this concept.[17] For recognitional abilities do not compose. (The idea is that good instances of the composed category 'being A and B' need not be good instances of either 'being A' and 'being B' so that the ability to recognize As and Bs does not guarantee the ability to recognize objects that are A and B.) In general, Fodor has used the compositionality constraint as an argument against any non-atomistic or non-denotational theory of concepts, criticizing various semantic theories that view some inferential relations between concepts or recognitional abilities as concept-constitutive.[18]

In summary, Fodor's and Lepore's (1991) basic argument against IRS proceeds as follows:[19]

1) Meanings are compositional,
2) but inferential roles are not compositional.

So, meanings can't be inferential roles.

My basic reply is to re-emphasize the distinction between formal and philosophical semantics (Section 3.1.2). The former offers a formal characterization of the semantic value of an expression, while the latter offers an account of the features that determine the semantic value in the first place (it offers an account of the conditions on concept possession). Thus, there are two questions

[17] Among many other theories of concepts, Chris Peacocke's (1992) inferential role semantics assumes that recognitional abilities are part of the possession conditions of *some* concepts (his prime example being the concept 'red').

[18] If concepts are defined by classical analyticities, then they do compose just like mathematical concepts; and in this case no emergent properties arise. Yet it is of no help for most contemporary semantic theories as they do not view empirical concepts as being defined by classical analyticities and have to allow for emergent properties.

[19] More generally including other semantic theories: "So epistemic capacities don't themselves compose. But BCP [bare bones version of Concept Pragmatism] says that there are epistemic conditions on concept possession. So BCP isn't compatible with the compositionality of concepts. So BCP isn't true." (Fodor 2004, p. 38)

that can be asked: 1) Do *semantic values* compose? 2) Do *semantic-value-makers* (concept possession conditions) compose? This distinction is significant because Fodor's own theory conforms to compositionality on the level of *formal* semantics (issue 1), while he criticizes other theories for violating compositionality on the level of *philosophical* semantics (issue 2).[20]

Fodor's atomistic theory of concepts satisfies compositionality of the semantic values (issue 1). For on his account, the semantic value of a mental symbol is a property, the referent of the symbol in the world. These features combine: if the concept 'brown' refers to brown objects (or the property of being brown) and 'cow' refers to cows (or the property of being a cow), then the complex concept 'brown cow' refers to brown cows (or the property of being a brown cow). However, Fodor's own theory of content does not conform to compositionality of semantic-value-makers (issue 2). On his account, the feature that determines the semantic value is the existence of a causal-nomological relation between a symbol in Mentalese and a property of the external world. More precisely, the causal-nomological relation must satisfy an asymmetric dependency condition (Fodor 1990b). Assume that two causal-nomological relations determine the reference of the two concepts 'brown' and 'cow'. Yet the causal-nomological relation that obtains between the complex symbol 'brown cow' and its semantic value need not be a function of the causal relations that hold of the simple concepts, as the atomists Laurence and Margolis (1999) acknowledge. This is the reason why Fodor views his asymmetric dependency account as applying only for *primitive* concepts: the content of the primitive concepts 'brown' and 'cow' is constituted by asymmetric dependency relations. Complex concepts such as 'brown cow', however, do not obtain their semantic values by means of an informational relationship, instead, the semantic value of 'brown cow' is obtained from the semantic values of 'brown' and 'cow'. But this is the above story about compositionality of the semantic values (issue 1). In sum, on Fodor's theory, semantic values compose (where the semantic values of a concept is its referent), but semantic-value-makers do not compose.

Inferential role semantics as a doctrine of philosophical semantics maintains that meaning is *determined* by total inferential role, so that total inferential roles are the semantic-value-makers. Fodor is right that total inferential roles do not compose. Thus, the semantic-value-makers postulated by IRS do not compose (issue 2). In spite of Fodor's critique that other semantic theories violate compositionality of concept possession conditions (semantic-value-makers), as regards this

[20]Rather than using the terminology of formal vs. philosophical semantics, Stalnaker (1997) distinguishes between descriptive and foundational semantics, and Block (1998) distinguishes linguistic and metaphysical semantics. Both view compositionality as a task of formal/descriptive/linguistic semantics. Thus, standard accounts assume that compositionality of semantic values ought to obtain, without requiring that semantic-value-makers ought to compose.
Edouard Machery suggested the term 'semantic-property-maker' (semantic-value-maker) to me.

issue Fodor is on a par with rival semantic approaches. Fodor's atomistic theory only conforms to the compositionality of semantic values construed as referents (issue 1). But a rival theory such as IRS can use the same strategy as Fodor's: it can assume that the reference of primitive expressions is determined by their inferential role, while the referent of complex expressions can be derived from the values of simple expressions in the standard compositional fashion. In a sense, Fodor's above argument is a fallacy of ambiguity: it trades on the different ways in which the notions of 'meaning' and 'concept' are sometimes used. If by 'meaning' we understand nothing but the semantic value of an expression, then Fodor's semantic theory conforms to compositionality in that the properties or extensions designated by syntactic entities do compose. Semantic values such as referents do compose. In this sense of 'meaning' and 'concepts', Fodor's first premiss that meanings and concepts compose is acceptable.[21] But when Fodor challenges IRS by arguing that "meanings can't be inferential roles" (the conclusion of the above argument), then he misconstrues this semantic approach. As already emphasized, IRS maintains that meaning (semantic value) is determined by (or supervenes on) total inferential role.[22] To the extent that IRS claims something along the lines of 'meaning is inferential role', 'meaning' in this context does not refer to the referent or semantic value of an expression, rather it refers those conditions that determine in the first place why an expression has its particular semantic value — the semantic-value-makers. An account of 'concepts' or 'meanings' on the level of philosophical semantics is not just an assignment of referents to concepts, instead, it is about the linguistic-cognitive features an individual must have to count as possessing a particular concept. Thus, Fodor's above argument is a fallacy of ambiguity, conflating meaning as semantic value and 'meaning' as sometimes used in the sense of semantic-value-maker.

Both IRS and Fodor's atomism acknowledge reference as a semantic property (assume referents as semantic values of expressions). And referents (extensions/truth-values) compose in the standard fashion. Thus, both IRS and atomism can account for the reference of complex concepts: no matter what theory of reference or concept possession a semantic approach may endorse, if one assumes that a person counts as referring to certain referents using simple expressions, then it follows that she counts as referring using a complex expression, and the referent of the complex expression can be calculated from the referents of the simple expressions. As it turns out, the very idea of

[21] Jackman (unpubl. b) argues that compositionality applies only to semantic values. He points out that Donald Davidson is a prominent case of combining a holist philosophical semantics (a holist account of how expressions obtain their semantic values) with an atomist formal semantics (the semantic values of sentences are taken to be truth-values, yielding a perfectly compositional semantics). Philip Robbins (2002) and Chris Peacocke (2004) view compositionality as applying primarily to the referents of expressions.

[22] Warfield (1993) and Pagin (1997) suggest that IRS is best construed as maintaining that meaning supervenes on inferential role. They use the supervenience idea to show that Fodor's argument is unsound.

compositionality of semantic values as referents does not impose a strong constraint on semantic theories; it is a merely formal constraint. To be sure, in addition to referents, my version of IRS acknowledges other types of semantic values, by maintaining that a scientific concept consists of three semantic properties: reference, inferential role, and epistemic goal. Yet I do not have a formal characterization of inferential role and epistemic goal as semantic properties of terms. So I cannot offer an account of whether and how inferential roles and epistemic goals compose. This is no problem as for the following reason semantic values other than referents need not compose.

While the compositionality of reference is a fairly trivial formal constraint, Fodor's assumption is that the compositionality issue imposes a real *psychological* constraint (Fodor and Lepore 1993b, 2001b). After all, the task is to explain how an individual is able to *understand* arbitrarily complex expressions. Thus, possessing and thereby understanding primitive concepts must bear on possessing/understanding complex concepts. So it might seem that Fodor's psychological constraint implies that concept possession conditions — i.e., semantic-value-makers — ought to compose after all. Fodor's theory, however, violates compositionality of semantic-value-makers. More importantly, it is unclear how he could possibly account for understanding expressions — including simple ones — as he takes concept possession to be independent of any cognitive ability. There is a genuine psychological constraint in the vicinity, but this is the productivity of language rather than compositionality. Fodor uses the issue of productivity to motivate the need for compositionality, however, then he goes on as if compositionality were the fundamental feature that must be met.[23] However, assuming that all concepts (or rather concept possession conditions) are compositional is only one way to explain the productivity of language, and as there may be explanations of productivity that violate general compositionality, *the task is to account for productivity, not to put forward a compositional semantics* (Montminy 2005). Productivity is a person's ability to understand arbitrarily complex expressions. If understanding is viewed as including the ability to use the concept appropriately or the ability recognize the referent in ordinary cases (or to have standard knowledge about its properties), then there is a genuine psychological constraint. However, in this case understanding of a concept involves beliefs about the referent, inferential connections between concepts, or recognitional abilities (precisely the features that Fodor wants to keep out of semantics). Then emergent properties are to be expected in conceptual combination. This is actually actively studied in current psychological research. The psychology of concepts attempts to understand the psychological features of concepts — understood as mental structures that are used by default in cognitive

[23] "So not-negotiable is compositionality that I'm not even going to tell you what it is." (Fodor 2001, p. 6)

tasks — and how simple concepts psychologically combine to yield certain cognitive performances involving complex concepts. In the literature on the psychological combination of concepts, it is well-known that emergent properties arise as background knowledge about the referent influences cognitive performances (see Murphy 2002, Chaps. 6 and 12; and my Appendix A). Psychologists attempt to identify the cognitive mechanisms that account for emergent properties in conceptual combination. But this means that conceptual combination is not fully compositional, instead, the task is to figure out which additional features (e.g., background knowledge) are involved in conceptual combination (Robbins 2002). In contrast, Fodor's atomistic semantic approach is not able to account for emergent properties; all psychological theories of concepts assume that concepts have an internal structure, and use this internal structure and the relation to other concepts to account for how conceptual combination proceeds (Keil and Wilson 2000a).

Robert Brandom's recent work also displays the importance of distinguishing between compositionality and productivity. Brandom is working towards a formal semantic theory that basically assumes inferential roles as semantic values. While being holistic and thereby non-compositional, it is a fully *recursive semantics* (Brandom unpubl. b). Unlike standard representational semantics, which uses truth values (or the set of possible worlds in which a sentence is true) as the semantic value of sentences, Brandom's semantics does not need the notion of truth. Instead, the primitive notion of his account is that of the *material incompatibility* of two statements or sets of statements, i.e., incompatibility not only in the sense of logical contradiction, but in the sense of material inference (incompatibility due to the empirical-nomological content of statements). The semantic value of a sentence p is the set of sentences $I(p)$ with which it is materially incompatible.[24] Brandom starts out by assigning for every sentence p, q, $r, \ldots$ its semantic value $I(p)$, $I(q)$, $I(r), \ldots$ Then he defines the semantic value of more complex expressions in a recursive fashion. The point is that the value of a composed expression such as $p \,\&\, q$ is not just a function of $I(p)$ and $I(q)$. Given that compositionality is the idea that the semantic value of a complex semantic expression is a function of the semantic values of its parts, compositionality is violated. Instead, on Brandom's account the semantic value of $p \,\&\, q$ is a function of the semantic values of *all* expressions that are less complex, i.e., $I(p \,\&\, q)$ is a function of $I(p)$, $I(q)$, $I(r)$, $I(s), \ldots$ For this reason complex expressions may have emergent properties as in brown-cow-dangerous example (collateral information relating to

[24]Based on the notion of material incompatibility, the notion of material inference can be introduced: p implies q iff every statement that is incompatible with q is incompatible with p. Thus, Brandom's incompatibility semantics is an inferential rather than a representational one. Construing of inferences as material, counterfactually robust inferences permits Brandom to introduce modal operators, so that his account is a modal semantics.

the sentences r, $s, \ldots$ may be imported). Despite the violation of compositionality, the semantics is fully recursive: the semantic value of a complex expression is a function of the values of less complex expressions. Thus, the notion of a recursive semantics and of a compositional semantics have to kept apart: while any compositional semantics is recursive, a recursive semantics need not be compositional. Though Brandom does not address psychological issues, what I want to point out is that a recursive semantics has the potential to offer a formal account that underwrites productivity as a psychological constraint. A genuine understanding of both simple and complex expressions requires some inferential-cognitive abilities, so that concept possession/understanding is to be construed inferentially-holistically (thereby leading to emergent features in conceptual combination). But such a holism is no obstacle to productivity (understanding complex expressions based on a prior understanding of simple expressions) if the semantics is recursive.[25]

To sum up my discussion on compositionality, Fodor's compositionality argument that he attempts to use against most non-atomistic semantic approaches lacks the intended force. Inferential role semantics conforms to the compositionality of referents as semantic values. If there is a further question about the productivity of language as a genuine psychological issue, then this is not primarily a constraint for a philosophical theory of concepts. How to account for the productivity of language is not fully solved, and conceptual combination as a psychological process is currently fruitfully studied by psychologists using their non-atomistic theories of concepts.

3.2.2 Inferential Role and Reference

One important aspect of semantic content is reference, i.e., the fact that linguistic expressions have referents as (one type of) semantic values. Terms refer to certain extensions and sentences have truth-values. Sentences need to be truth-evaluable so that the possibility of misrepresentation and error is possible: the claims individuals make and the beliefs they hold may turn out to be right or they can be wrong. In line with many versions of inferential role semantics, I conceive of inferential roles roughly as cognitive states of a person in that differences in meaning or inferential role mark cognitive differences between rational agents. As is well-known from Putnam's (1975)

[25] Apart from productivity, another psychological constraint is to account for the learning of concepts. It may appear unclear how concepts can be acquired on a holistic construal of conceptual content (Fodor and Lepore 1992; Dummett 1973, 1976). Yet Dresner (2002) presents a formal model based on Boolean and cylindrical algebras that shows that holistically individuated meanings can be partially acquired in a step-wise fashion. Psychological theories of conceptual development yield the same picture (Appendix A). The concepts of children differ from the concepts of adults. In spite of assuming that concepts have connections to other concepts, developmental psychologists need not presume that a particular child has to suddenly acquire a certain adult concept.

Twin Earth examples, cognitive state alone does not determine reference: it is possible that there are two persons that are in identical cognitive state, yet some of their concepts differ in reference. Likewise, if the world changes then a concept's extension may change (some of the objects previously falling under the concept do not exist any longer or have changed), so that reference may change without a change in a person's cognitive features. The implication is that meaning (inferential role) determines reference only together with the world, i.e., the external context of the agent. Meaning in the sense of inferential role is sometimes viewed as a sort of content (cognitive content), but a concept's reference is also viewed as content (referential or intentional content). These two types of content cannot be identified, given that cognitive content alone does not determine referential content. Another reason is that different concepts (inferential roles, intensions) may pick out the same referent, so that different cognitive contents may have the same referential content.

If cognitive and referential content have to be kept apart, the question is how these two notions of content are related. A standard solution among proponents of conceptual role semantics (inferential role semantics) is to endorse a so-called *two-factor theory* (Block 1986, 1987; Field 1977; Loar 1981, 1982; McGinn 1989; McLauglin 1993; Schiffer 1981; Senor 1992). The central idea of a two-factor theory is that there are actually two components or aspects of content: conceptual role (inferential role) and reference. Colin McGinn (1982) offers a good motivation for two-factor theories by pointing out that content ascription serves two different and equally legitimate functions. On the one hand, content ascription serves the purpose of intentional explanation of behavior. What is in this case ascribed is cognitive content, and McGinn argues that this type of content is best viewed as cognitive or conceptual role. On the other hand, content ascription serves the function of describing which information about the world is conveyed by an utterance, or which state of the world a belief assumes to obtain. (The first type of ascription, which ascribes cognitive content, corresponds to *de dicto* ascription of beliefs, the latter type, which ascribes referential content, corresponds to *de re* ascription.) Thus, both factors or aspects of content are necessary to yield full-blown content: neither is one component of content identical to the other, nor does one yield the other. While either factor is often simply called 'meaning' or 'content', one must not assume that 'meaning' in the sense of inferential role is 'meaning' in the sense of reference.

My basic picture is roughly in line with two-factor theories. More precisely, I endorse a three-factor theory by maintaining that a scientific concept consists of *three components of content*: 1) the concept's reference, 2) its inferential role, and 3) the epistemic goal pursued by the concept's use. I assume that each of these semantic properties that a term can have is determined by (supervenes

on) the term's various *total* inferential roles used by the different members of the language community. The *difference between inferential role and total inferential role* points to another difference from standard two-factor theories, which do not make this distinction and rather construe "inferential role" (conceptual role) as role of a mental symbol in an *individual's* cognition — what I call *total* inferential role. Given the distinction between total inferential role and inferential role, my particular version of IRS construes the relation between total inferential role, inferential role, and reference by assuming that one is more fine-grained than the other, and that one determines the other. In this sense there are three levels of features bearing on content: (*a*) *total inferential role* (the total set of inferences endorsed by an individual), which is very finely grained individuated as it is likely to differ between any two persons. Total inferential roles provide the holistic supervenience base on which content supervenes. The various total inferential role used within a language community, together with the world, determine what I call (*b*) *the inferential role of a concept* (the material inferences supported by a concept), which is stable and can be shared by many individuals. Two distinct inferential roles can be coreferential (as in the 'Hesperus'/'Phosphorus' example). This type of content is ascribed in de dicto ascriptions. Inferential role, together with the state of the world around the agent, determines (*c*) *reference*, i.e., extensions as a semantic value.[26] Only inferential role and reference (*b* and *c*) are properties of a concept (as shared by a language community). Genuine semantic content operates only on levels *b* and *c*, as in content ascription one ascribes features which can be shared between persons, while holistic total inferential roles are not actually ascribed to persons. Still, level *a* is the feature that determines content in the first place and therefore has to be recognized by philosophical semantics. Moreover, in the history of science a concept can change only insofar some scientists come to use modified total inferential roles. For this reason, a study of scientific concepts has to start with studying the language use of individual scientists, and a study of conceptual change has to pay attention to change in term use.

Apart from introducing the notion of a concept's epistemic goal (in addition to its reference and inferential role), and apart from distinguishing between inferential role and total inferential role, my particular account differs in other respects from traditional two-factor theories. *First*, the (total) inferential role factor has often been identified with narrow content, i.e., an internalistic or solipsistic content that supervenes on the internal state in the sense of the physical body of an agent. Narrow content is literally inside the head. As already explained in Section 3.1.1 (and in 3.1.3), I do not conceive of inferential role as narrow content. On my account, inference includes mind-world

[26]My proposal is very similar to Ned Block's (1993), who distinguishes between a) thought content (most fine-grained, differs even between persons that have the same concept), b) meaning, and c) truth-conditions.

relations by taking into account how concepts figure in perception and action. Inferential role is not just about relations between concepts, but also involves the way in which persons interact with the world and other individuals. *Second*, some proponents of two-factor theories treat the two components (cognitive and referential content) as largely independent, while I view them as closely connected. Hartry Field (1977), who introduced the very idea of a two-factor theory, models inferential roles by subjective probabilities (the conditional probability that an individuals infers one statement given other statements). Noticing that inferential roles alone do not yield truth-conditions, he suggests to add a second component — a theory of reference. Some proponents of a two-factor theory view the theory that assigns inferential role and the theory assigning reference as independent. A particularly striking example is Colin McGinn (1982): "A theory of cognitive role no more surrounds a theory of reference than a theory of desire surrounds a theory of belief in the ascription of reasons to an agent" (p. 231). McGinn appears to treat the two components of content as orthogonal, where one component does not impose constraints on the other. This is highly unsatisfactory, and it fuels the alignment problem as put forward by Fodor and Lepore:

> We have to face the nasty question, *what keeps the two notions of content stuck together*? For example, what prevents their being an expression that has the inferential role appropriate to the content that *4 is a prime number* but the truth-conditions of the content *water is wet*? (Fodor and Lepore 1992, p. 170)

My reply is to stress that I assume that the two factors — inferential role and the reference — are strongly intertwined. The inferential role imposes strong constraints on possible referents. For instance, in the case of a layman, appeal to an expert is a *bona fide* part of the inferential role of the layman's concept. Due to this appeal to experts or other members of the language community, the layman inherits the reference of the term as used by her from others, even if she does not have the knowledge to identify the referent (and which ultimately determines the reference of the term as used by experts). In the case of Putnam's Twin Earth cases, Oscar and Twin Oscar are in identical cognitive states, so that their concepts have the same inferential role, yet their concepts may differ in reference (H_2O as opposed to XYZ) as they are located in a different external context, including their past history (they live in different parts of the actual world or their histories in the actual world differed). On my account inferential role and the state of the world (relative to an agent) *determines* reference (or truth-values). Thus, inferential role imposes constraints on which referent may obtain (in a certain context or state of the world). Unlike McGinn, I assume that the theory that assigns inferential roles and the theory that assigns referents are closely related. For on my three level model, total inferential roles determine inferential role, which in turn determines

reference (together with the world). Thus, ultimately the referent is determined by the total inferential roles used within a language community — the linguistic behavior persons and the way in which they interacts with each other and the world. This means that a concept's inferential role and reference have the same supervenience base. In the overall task of interpreting an agent, one has to take a look at this supervenience base which provides the evidence both for assigning a particular inferential role and a referent. The rationale of the semantic notions of both inferential role and reference is to offer an interpretation of the linguistic behavior of agents in the world. Both notions bear on accounting for how concepts underwrite successful practice (what I called Constraint A in Section 3.1). McGinn's claim that cognitive content and referential content are ascribed for different reasons is acceptable in the sense that *de dicto* and *de re* ascription of beliefs are different types of content ascription. Yet both types of content have to be connected for *de dicto* beliefs to be translatable into *de re* beliefs (so that it is possible to relate the *de dicto* beliefs or cognitive contents of two individuals, i.e., so that it is possible to relate two conceptions of the world). Due to these considerations, there arises no alignment problem: if total inferential role (the supervenience base) is such that one ascribes to a sentence the inferential role of '4 is a prime number', then one also ought to ascribe the corresponding truth-condition in this context.

My overall semantic account assumes that a scientific concept consists of three components: its reference, its inferential role, and the epistemic goal pursued by its use. In principle, one component of a concept can change in history without any change in the other two components. At the same time, the three components have the same supervenience base, being determined by the total inferential roles used by the members of the language community. As a result, change in one component is in many cases possible only with a correlated change in other components. Above I discussed that the semantic properties of inferential role and reference are connected. But also a concept's *epistemic goal* and its *reference* are tied together. At least an appropriate assignment of a referent to a term requires taking into consideration the epistemic goal that is pursued by the term's use. The idea is that the epistemic goal influences which of the possible individual factors that may bear on reference (inferences, causal relations) actually determine reference. For instance, the epistemic goal pursued by a term's use gives a guide as to which inferences and statements in which the term figures pick out the referent. Chapter 5 will maintain that the phylogenetic homology concept and the developmental homology concept differ in reference, and my argument for this idea will be fundamentally based on the fact that both concepts are used to pursue different epistemic goals (Section 5.2.4). My account of the contemporary molecular gene concept will argue that its

reference may change from context to context, based on the idea that the molecular gene concept is used for a generic epistemic goal, which can be spelled out differently in different research contexts, so that different specific epistemic goals may lead to different referents (Section 6.3.2).

In spite of my tenet that the three components of a concept are semantically connected and that each of them supervenes on total inferential role, I do not have a metaphysical account of how the properties of reference, inferential role, and epistemic goal precisely are determined by total inferential role. In particular, I do not attempt to put forward a reductive definition of the semantic notions of reference, inferential role, or epistemic goal in terms of the notion of total inferential role. Rather than offering metaphysical analysis of these three semantic properties, my primary aim in the dissertation is to show by the later case studies that the properties of reference, inferential role, and epistemic goal can be ascribed to scientific concepts as actually used, and that such semantic ascriptions can be defended based on the fact they yield philosophical insights in the interpretation of scientific practice, in particular the rationality of conceptual change. As a result, I do not attempt to spell out a full-blown theory of reference, and my later philosophical discussion of the biological cases will explain why I view neither traditional causal nor descriptive theories of reference as adequate. Yet in the remainder of this section, I want to lay out how I conceive of reference by making some remarks on reference determination.

One reason why I view a naturalistic reduction of semantic notions as hard to achieve is because the present approach endorses a *moderate holism about meaning determination*, i.e., the features that determine which concept a person possesses. More precisely, I assume that each of a term's semantic properties (reference, inferential role, and epistemic goal) is determined by its supervenience base (total inferential role) in a moderately holist fashion. A radical holism about meaning determination would assume that all inferences (or beliefs) in which a concept figures are necessary to determine this concept's meaning. A moderate holism, instead, assumes that some inferences are irrelevant for meaning determination. (The picture is that some inferences are more salient, others less salient, and still others irrelevant for meaning determination.) However, a moderate holism is a holism in that it assumes that the factors that determine the meaning of a term (such as beliefs, inferences, causal relations) form an *open and unbounded set*. This is explained by the idea that the degree to which a particular factor is salient is *context-sensitive*: in one context where a term is used by a person a statement may be salient for determining this term's meaning, in another context (e.g., as used by another person) the same statement may be less salient. As a consequence, it is not possible to state in advance of the particular case or concept which factors are relevant for

meaning determination, leading to an unbounded set of factors that determine meaning. Moderate holism contrasts with approaches that assume that the set of factors that determine a term's meaning can be reduced to a limited and clearly delineated set of features, such as analytic statements or particular causal connections between a term and its referent. Furthermore, I do not assume that a term's semantic properties are determined by the beliefs and actions of a *single* scientist alone; rather a scientific term obtains its particular reference, inferential role, and epistemic goal in virtue of its use in an *overall scientific community*. Given this moderate holism about the determination of semantic properties, I assume that reference, inferential role, and epistemic goal are *emergent properties* of concept use. These properties, their relation, and their historical change can be fruitfully studies in actual cases, even if a naturalistic reduction of them is impossible.

Regarding the semantic property of reference, an argument for *moderate holism about reference determination* proceeds from the fact that for some scientific concepts, reference shifts from token to token. A case in point is the gene concept. Marcel Weber (2005) makes explicit that genes are not a single natural kind, instead what geneticists were tracking are several different (though overlapping) natural kinds. This and the use of various reference fixing conditions enabled what Weber calls the "*freely floating reference*" (p. 224) of the gene concept in the course of history. It is not the case that there were long phases of referential stability intermitted by revolutionary reference shifts; the reference of the term 'gene' shifted continuously, possibly from context to context unbeknownst to geneticists and without any disruption of scientific practice. Apart from historical change in reference, the reference of the contemporary gene concept may shift substantially from tokening to tokening, as will be discussed in detail in Section 6.3. The basic reason is that genes are defined as the segments of DNA that code for a molecular product, yet there are many *different types* of DNA segments that are involved in the production of genetic products. As a result, in different cases different structurally defined categories are responsible for gene expression, so that different characterizations of what a gene is are used by biologists. Furthermore, biologists may focus on a more proximate product of a gene (such as RNA) or a more distal product (such as the protein finally produced). Due to the many–many relation between genetic elements and their products, focusing on different types of products leads to different accounts of how many genes there are (and what DNA segments count as genes) for one and the same genetic region. While the contemporary molecular gene concept is used for a generic epistemic goal among different kinds of biologists, this epistemic goal may be spelled out differently by different researchers or by the same individual in different research contexts, so that the epistemic considerations that influence how genes are

characterized and to which kind the gene concept refers vary from case to case. Section 6.3.2 will offer a more detailed analysis of why the reference of the term 'gene' as used nowadays may shift from token to token, and why this is actually conducive to biological practice.

The implications of this case for reference determination are as follows. Any theory that assumes that a concept is defined by a clearly delimited set of reference determining conditions cannot account for freely floating reference in the course of history, or for reference shift from token to token — where not just the extension, but the category or kind referred to differs across term tokens. For if on each tokening the same set of reference fixing conditions obtains, then the category referred to should be the same as well. To be sure, there are well-known cases where the reference of a term is context-sensitive. This may happen if a term is ambiguous and thus actually expressing different concepts with distinct extensions on different occasions. Yet the term 'gene' is not properly construed as expressing distinct concepts. Indexicals are another type of terms where reference depends on and may vary with the context of utterance. Section 6.3.2 will argue that while for many indexicals the context of utterance can be specified in physical, non-intentional terms, the reference of the term 'gene' is essentially dependent on the epistemic, intentional context in which it is uttered. Reference depends on the various collateral beliefs and interests of a scientist using the gene concept, yielding a moderate holism about the features that determine reference.

Philip Kitcher's theory of reference, as discussed in the previous chapter, goes to some extent in the right direction. For on Kitcher's account a term type is associated with many modes of reference, while the set of modes of reference used (the reference potential of the term) changes over time. Kitcher explicitly states that different modes of reference may be operative on different tokenings of the term and as modes of reference need not be coreferential, different tokens of a term may differ in reference. However, while he is right in arguing that the set of reference determining condition of a term type is open and changing, the drawback of Kitcher's account of reference is the assumption that for each tokening a single and clearly determined mode of reference obtains. In Section 2.2.2 we saw that Kitcher does have a satisfactory account of when a certain mode of reference obtains in a certain context. A problem with Kitcher's view is that it may threaten the unity of scientific concepts. If it were really the case that on one tokening of the term exactly one mode of reference is operative while on a different tokening a distinct mode of reference obtains, then one may wonder why this does not count as switching from one concept to another. Kitcher does not have account of why a term does not correspond to as many concepts as there are distinct and clearly delimited modes of reference in the term's reference potential. Section 6.3.2 will discuss

in detail why I consider the contemporary molecular gene concept as a single concept. At the same time I view the fact that its usage and reference varies from context to context an important feature of its successful use, and my later discussion will attempt to account for this situation. My moderate holism about reference determination is consistent with the unity of scientific concepts, yet allows for change of reference from token to token. According to moderate holism, the set of conditions that determine reference of both a term type *and any of its tokens* is relatively open and unbounded. On a particular tokening of a term *many* conditions determine reference — those that are salient given the particular context. On another tokening, a different set of reference fixing conditions may be relevant, but this set may strongly overlap with the previous set. I assume that the sets of conditions that determine reference for different term token usually overlap, which guarantees a minimal degree of unity for the concept. At the same time moderate holism allows for reference shift. For the particular context determines which reference determining conditions are salient and thus relevant for which referent actually obtains. A particular reference fixing condition may be salient in one case but less salient in a different case. Thus, if in two distinct contexts two substantially different sets of reference fixing conditions are salient, which determine different referents, reference shift from token to token occurs.[27]

I already pointed out that my moderate holism is not a radical holism. The picture is not that a total set of beliefs determines a speaker's concepts and reference and that meaning or reference necessarily differs between any two speakers that differ in some beliefs. For instance, even if the conditions that determine reference for a concept are vague and unbounded, a unique referent can still obtain as long as all possibly relevant reference fixing conditions pick out the same referent (Papineau 1996). Thus, moderate holism need not lead to referential indeterminacy. The fact that vagueness about reference determining conditions is consistent with stable reference has another implication. My argument for moderate holism was based on a case where reference may strongly shift from context to context. But even if a certain concept exhibits a stable and unique referent, this does not imply that the conditions that determine reference are clearly delineated and unchanging.

[27]Shift in a concept's reference from token to token is not confined to cases from science. Henry Jackman (unpubl. a) makes the same point based on traditional thought experiments. In the case of the term 'arthritis' as used by Bert (see Burge 1979), some have argued that it refers to arthritis, while others have taken him to refer to tharthritis (a condition which includes both arthritis and rheumatoid ailments of the limbs). Jackman argues that either referent may obtain depending on the context. In some cases, Bert is best viewed as talking about arthritis (e.g., when he appeals to doctors' knowledge about 'arthritis'), in other cases, his belief that he has 'arthritis' in his thigh is more important for reference determination, so that he refers to tharthritis. Similarly, in the case of a person being unbeknownst to him moved to Twin Earth, some of his 'water' utterances refer to H_2O (e.g., when talking about his past experience), while others refer to XYZ (e.g., when directed at objects on Twin Earth). By arguing that virtually *any* belief may be reference determining in *some* special context, Jackman explicitly endorses a moderate holism.

Moderate holism may very well apply to those cases, and vagueness and shiftiness of the conditions that actually determine reference may be more common than usually assumed.

My later discussion of the homology concept will use this case to argue against the causal theory of reference and to point to limits of traditional descriptive theories of reference (Section 5.2.4). The upshot of this argument will be that the reference of the homology concept is not fixed by causal factors alone. In addition, descriptions of the referent in the sense of traditional analyticities or isolated theoretical descriptions of the referent yield an incomplete account of reference determination either. My account of the reference of the homology concept will not only rely on descriptions of the *referent* (the properties of homologues in this case), instead, features as to how the homology *concept* is used in scientific practice bear on reference determination as well. Pragmatic aspects of concept use and for what epistemic purposes and goals concepts are used are determinants of reference. These reference fixing conditions go beyond isolated beliefs or statements, as they pertain to how a concept is tied up with a whole research agenda and practice, which fits with the picture of moderate holism. In contrast to some traditional approaches that try to reduce reference to certain causal relations or descriptions, I assume that reference is an emergent semantic property that emerges from world-engaged practice and interaction of several persons.[28]

3.3 CONCEPT INDIVIDUATION

Apart from the issue of compositionality and reference, a crucial challenge against inferential role semantics is the question of meaning stability and concept individuation. Concepts are entities that have to be shareable by individuals. Different individuals have to be able to use some of their terms with the same meaning, otherwise successful communication would be impossible. A further reason why concepts have to be shared is that concepts are ascribed for explaining intentional behavior: two persons exhibit the same type of rational behavior and the same type of intentional explanation applies to both of them because both have the same propositional attitudes (Section 3.1, p. 49).

[28] I use the notion of reference as a tool to understand epistemological aspects of science such as successful practice, but this approach to reference cannot be used to support any metaphysical claim. This is not a drawback, as Bishop and Stich (1998) have argued that metaphysical claims cannot be established by a semantic detour using the notion of reference. E.g., they point out that arguments for/against the idea that *there are beliefs* claim to show that the *term* '*belief*' is referential/non-referential, while the argument offered actually begs the question, as it is without any defense based on using one among several theories of reference, which assigns another referent than a rival theory.

Fodor stressed this constraint on theories of concepts — assuming that there are genuine intentional laws — and used it against holistic theories of meaning. The challenge to inferential role semantics is that if meaning is total inferential role (i.e., meaning is constituted by all one's beliefs or the inferences one endorses), given that two individuals typically disagree on some beliefs any two persons necessarily associate a different meaning with the same sentence:

> [With atomistic theories of content] Contrast the kind of semantics that linguists call structuralist and philosophers call conceptual role theories of meaning. According to these, the content of a thought is metaphysically constituted by its role in a belief system ... My view is that all such theories are inescapably infected with holism and are therefore incompatible with the working assumption that the laws of psychology are intentional. If what you're thinking depends on all of what you believe, than nobody ever thinks the same thing twice, and no intentional laws ever get satisfied more than once; which is tantamount to saying that there aren't such laws. (Fodor 1994, p. 6)

In the context of conceptual change in science, Putnam (1987) argues that holism seems to be incompatible with the distinction between change of theory and change of meaning that occurs in the history of science. For the purposes of the study of conceptual change in science it is important to be able to decide whether a certain theoretical term has changed in meaning during history so as to correspond to a novel, distinct concept or whether a scientific term as used at a particular time in history corresponds to several distinct concepts (Section 2.2.3). Thus, a legitimate constraint on theories of meaning is that they permit for shareable concepts.

In what follows I shall address the issue of shared concepts and meaning stability. The main goal is to sketch a position on concept individuation that provides a basis for my later case studies on conceptual change. In a nutshell, I will not rely on the assumption that concepts can be individuated in a unique and clearly delineated way. Instead, in line with my assumption that meaning and conceptual content supervenes on total inferential roles I assume that it is sufficient for two persons to use *similar* (total) inferential roles to count as possessing the same concept. Instead of invoking something like similarity of meaning, the alternative approach is to endorse clearly delineated meanings by attempting to develop an analytic/synthetic distinction in one way or another. This option can be illustrated by considering Fodor and Lepore's (1992) master argument supporting conceptual atomism, which proceeds as follows. Either one assumes that no inferences in which a concepts figures are meaning-constitutive (*atomism*), or one assumes that some but not all inferences are meaning-constitutive (*localism*), or all inferences are meaning-constitutive (*holism*). Inferential role semantics, assuming that at least some inferences are meaning-constitutive, faces the following dilemma according to Fodor or Lepore. Holist versions of IRS face serious challenges such as compositionality and stability of content, so Fodor and Lepore take this option to be completely unviable. The other horn of the dilemma is to endorse a localist version of IRS. If some,

though not all inferences are meaning-constitutive for a certain concept, then two persons can in fact share it, as long as they endorse the limited set of meaning-constitutive inferences. However, as Fodor and Lepore point out, then we need an account of which inferences are meaning-constitutive and which are not, i.e., a distinction between analytic and synthetic inferences. Fodor and Lepore take it for granted that given Quine's challenges against the analytic/synthetic distinction and the abandonment of the conceptual framework of logical positivism, no one is willing to endorse or able to spell out such a distinction. Thus, given that both holist and localist versions of IRS are problematic, the remaining option favored by Fodor and Lepore is atomism.

However, some proponents of inferential role semantics have replied by endorsing localism and a determinate distinction between meaning-constitutive and non-constitutive inferences. Paul Boghossian (1993a, 1993b, 1996, 1997) and Michael Devitt (1993a, 1993b, 1994, 1996) explicitly take this approach. Given that I do not commit myself to developing an analytic/synthetic distinction, the main aim of this section is to explain why concept individuation and the study of conceptual change are possible without such a distinction. Still, I want to indicate why I take a genuine localism to be unpromising. My strategy is to take a look at some of the more prominent attempts to endorse a version of the analytic/synthetic distinction or a principled distinction between meaning-constitutive and other inferences, and offer some considerations against them.

3.3.1 Troubles With Meaning Monism

What I want to stress from the outset is that there is a difference between a semantic theory that yields clear-cut conditions of when two persons share the same concept and an account of concept identity that makes semantic sense of real concepts as actually used. For instance, Fodor's informational semantics promises the former. On his account, content is constituted by a nomological relation between a mental symbol and a property (the concept's referent). Thus, two persons share the same concept as soon as they are nomologically locked to the same property. However, as Section 6.3 on the contemporary gene concept will lay out, there are dozens of categories which can count as genes, each of which is defined by different necessary and sufficient conditions that in some research contexts are viewed as significant in biologists' decision as to what counts as a gene. As a result, the term 'gene' as used nowadays refers to a plethora of kinds, where the reference of different tokenings of this term may shift from context to context. To the extent that Fodor's theory yields determinate conditions on concept possession, his theory implies that it is a determinate

fact that biologists possess many different gene concepts, so that many biologists do not share the same concept when talking about 'genes', and even one and the same geneticist may shift from one to the other concept when using this term. (Section 6.3.2 will offer a semantic account of why the term 'gene' still expresses one concept, though its reference is context-sensitive. My account makes semantic sense of this case as it points to epistemic features that different usages of the term 'gene' have in common, and explains why the gene concept's context-sensitive reference is conducive to biological practice.) Thus, it is not sufficient to have a general proposal about conceptual content that yields a notion of analyticity or another way of specifying determinate conditions on concept individuation, if such a proposal does not fit with real concepts in that it cannot show that real concepts are actually shared so as to underwrite successful practice.

One way to draw a distinction between meaning-constitutive inferences and other inferences is to follow Michael Devitt (1993a, 1993b, 1994, 1996) in assuming that *those inferences are concept-constitutive that determine reference*. This is a very natural proposal in that it is in line with Frege's prominent assumption that sense determines reference. The same basic idea is implicit in Kitcher's theory of conceptual change. Kitcher views concepts as reference potentials — sets of mode of references, i.e., sets of features that determine reference (Section 2.2.1). In principle, I do not object to the proposal to view those inferences as meaning-constitutive that determine reference. In Section 3.2.2 I stressed that I view inferential role as determining reference (together with the world) and that the interpretative task of attributing inferential roles to expressions and of attributing referents are closely related. Thus, to the extent that a study of concepts views an inference as meaning-constitutive it is likely to view it as reference-determining and vice versa.[29] While Devitt's (1993b) reply to Fodor and Lepore (1992) puts forward the idea we get an analytic/synthetic distinction by viewing those inferences as meaning-constitutive (analytic) that are reference determining, this suggestion alone is not enough. For if there is no unique and clear-cut distinction between reference-determining and other inferences, this does not translate into a determinate distinction between analytic and synthetic inferences. In fact, my discussion in Sections 3.2.2 and 6.3.2 argues for a *moderate holism about the conditions that determine reference*. Devitt (1993a) is aware of this possibility, but he rejects it as follows: "Of course, it may be felt

[29]This agreement between my and Devitt's position is shallow as it is embedded in quite different approaches. Devitt takes a strong representationalist approach, originally endorsing a purely denotational semantics, relying on the causal theory of reference (Devitt 1981; Devitt and Sterelny 1987). In his more recent work he moved towards an inferential role semantics, while viewing the theory of reference having primacy based on the idea that reference-determining conditions yield meaning-constitutive features. For instance, he rejects the two-factor inferential role theory as non-representational due to its reliance on the inferential role factor (Devitt 1996, Sect. 4.2).

that there is no principled basis for distinguishing the [beliefs] that determine [reference] from the ones that do not. But, to repeat, this is to assume holism not to argue for it" (p. 299). However, in this case, Devitt is wrong about the burden of proof. If he postulates the existence of an analytic/synthetic distinction, then he has to offer one, so that he is committed to make plausible why there is a clear-cut distinction between reference-determining and other conditions.

Devitt's later essay *Coming to Our Senses: A Naturalistic Program for Semantic Localism* (1996) claims that we do not need a principled distinction as demanded by Fodor and Lepore, and to the extent that we need one, we have it. The clear-cut condition for a feature being meaning constitutive is as follows: "A property is a meaning if and only it plays a semantic role; that is, if and only if it is a property we ought to ascribe for semantic purposes" (p. 91). Devitt's idea that something is a meaning if and only if we ought to ascribe it as a meaning does not get us very far. His 'naturalistic methodology' proceeds from the fact that folk psychology relies on the ascription of meaning and beliefs. Given the success of these ascriptions, Devitt claims that we should ascribe them in the fashion of common sense psychology. On his account, meanings ordinarily ascribed are localist rather than holist, so that we should ascribe localist meanings. However, this confuses epistemic with ontic issues. A holist, for instance, claims that meaning ascription is holistic in that the meaning determining base is holistic, so that ultimately many conditions bear on which content obtains. Still, for a holist it is perfectly fine to acknowledge Devitt's point that in ordinary circumstances content ascriptions relies on a few salient cues that suffice to get an estimate as to which meaning obtains. While for the epistemology of meaning ascription it is sufficient to rely on a limited set of features, the holistic ontology of meaning determination insists that more features then the ones used to practically ascribe content bear on content determination — relying on a few cues gives a reliable but defeasible estimate. Thus, the ontic issue that content determination is non-holistic does not follow from the epistemic issue that content ascription in ordinary circumstances relies on a limited set of conditions. Daniel Dennett's (1987) 'intentional stance' assumes in line with Devitt that ordinary belief and desire attributions are successful in that they offer an intentional explanation of behavior, yet Dennett does not endorse determinate meanings and instead assumes that content ascription is essentially holist. Quine's (1960) arguments against analyticity and synonymy may be unsuccessful, but after his challenges to our folk conception of determinate beliefs and meanings it is naive to merely rely on the folk conception as Devitt does.[30]

[30] Another of Devitt's (1996) arguments for localism is the argument from representationalism, which claims that if meanings are entirely constituted by representational properties, then holism is false. Devitt invokes a distinction between localist and holist properties, which he never explains. His idea is that the categories to which words refer are

In my view, Devitt's arguments do not yield a genuine localism. Likewise, the previous chapter discussed Kitcher's account that construes concepts as sets of modes of reference (features that determine reference). By assuming that there is a clear-cut matter of fact as to which mode of reference obtains, Kitcher has to rely on a principled distinction between (what I called) reference-analytic and reference-synthetic statements, i.e., statements that do or do not fix reference. We saw in Section 2.2.2 that Kitcher's proposal is unsatisfactory (as it largely relies on the problematic idea that a statement is reference determining if the speaker intends it to be so). Independent of my critique of Devitt's and Kitcher's considerations that could support localism by assuming that the meaning-constitutive conditions are those that determine reference, my discussion in Sections 3.2.2 and 6.3.2 attempt to give a direct argument against this version of localism. Based on the contemporary gene concept, I argue for a moderate holism about reference determination. According to this position, there is no unique and clear-cut distinction between reference determining inferences and other inferences, and whether a particular inference determines reference may vary from context to context, so that whether or not an inference bears on reference depends on other inferences and factors that potentially influence reference. If this is the case, then the notion of reference determination does not yield a unique distinction between meaning-constituting (analytic) and other (synthetic) inferences. Moreover, even if Devitt (and Kitcher) could defend a clear-cut distinction between reference-determining and other inferences, it is implausible that this distinction aligns with how concepts are legitimately individuated. Section 3.2.2 on the moderate holism of reference determination suggested that an approach like Kitcher's may fail to underwrite the unity of scientific concepts. Kitcher acknowledges explicitly that different individuals may make use of different modes of reference of a term. If different modes of reference are viewed as different meanings or concepts, as Devitt explicitly assumes by taking reference determining conditions to be meaning-constitutive, then different scientists would often have to count as expressing different concepts with the same term. Scientists may often endorse non-identical sets of reference-determining inferences, yet philosophers should be able to view them as possessing the same concept.

Instead of relying on the relation between meaning and reference, another attempt to arrive at a principled distinction between meaning-constitutive and non-constitutive inferences is to use Wilfrid

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usually localist rather than holist. Given representationalism (which for Devitt appears to mean that mental contents mirror the categories of the world), meanings are non-holist: "if a worldly property is localistic then the meaning that represents that property must be localist also" (p. 131). Without any explanation of what a holist property or a localist property may be, this argument remains obscure. In addition, this idea conflates meaning *determination* and meaning in the sense of the semantic value ascribed (see Sections 3.1.2 and 3.2.1). As usually construed, semantic holism is a claim about how meaning is determined, while Devitt usually talks as if it refers to the idea that the meanings ascribed to expressions are holist (pp. 91, 118), whatever a 'holist' meaning/property is supposed to be.

Sellars (1948) idea that the meaning-constitutive inferences are those that support counterfactuals, where the counterfactuals corresponds to relations of nomological necessity. As with the above reference-oriented approach, one problem with this proposal is that even if it yields a clear-cut distinction between two types of inferences (counterfactually robust and other types of inferences), it is not clear that this distinction always aligns with how concepts are to be individuated. Why should there be no cases where two persons disagree about the law-like relationships in which a certain entity figures (so that these persons endorse different counterfactually robust inferences), yet they may still be viewed as possessing the same concept? For instance, two classical geneticists may disagree about which particular laws of inheritance apply to genes, though they both possess the same gene concept. Chapter 4 argues that a single homology concept was used throughout the 19^{th} century, even though different definitions of homology and theoretical accounts of the nature of homology were used. Moreover, it is not clear whether there is a unique distinction between counterfactually supporting and other inferences. Different types of nomological necessity can be legitimately viewed to exists depending on the types of laws involved (some philosophers talk about metaphysical, physical, biological, ... necessity). Some laws are more fundamental and have a larger scope than other law-like or causal relationships. Sandra Mitchell (1997, 2000, 2003) has argued against the dichotomy between nomological and other statements, and suggested a more fruitful way of thinking about laws: scientific principles form a continuum along several dimensions. On her account, there are different properties of theoretical principles each of which is important for the scientific practice in which laws are invoked (the scope of law-like statements, etc). Some of these properties may be particularly relevant for a certain scientific theoretical task, so that a statement is legitimately viewed as a law fulfilling a vital explanatory function; yet it may not conform to other hallmarks of laws that are relevant in other contexts or scientific fields.

Finally, the mere distinction between counterfactually robust and other inferences obscures the way in which conceptual change occurs and thus yields an incomplete account of concepts which may undergo rational change (Constraint B in Section 3.1). On an approach like Sellars', change in the meaning of a term occurs when the term was originally associated with one set of counterfactually robust (and thus meaning-constitutive) inferences, while at a later point this term figures in a different set of modally robust inferences, so that the term now corresponds to a new concept. Scientific concepts do and should change, so the boundary between what is viewed as nomologically necessary and contingent changes. But I take it for granted that conceptual change in science can be brought about by findings that are nomologically *contingent* (from the point of

view of the old concept or the old theory). For instance, during classical genetics the defining inferences of the gene concept could be viewed as statements about the role of genes in inheritance (a refined version of Mendel's laws): something is a gene iff it causes certain phenotypic patterns of inheritance (Section 6.1.3). From this perspective it is (nomologically) possible that genes are made of proteins, or alternatively that genes consist of DNA. As it turned out, genes are made of DNA. This empirical finding brought about conceptual change. Later in history, during the period of molecular genetics, it is arguably the case that the idea that genes are made of DNA or RNA is part of the gene concept, so that molecular biologists assume that it is (nomologically) necessary that genes are made of DNA or RNA (Section 6.2.2). The point is that this instance of conceptual change was not just causally brought about by the empirical finding that genes are made of DNA, but the empirical findings made it rational to change the gene concept. Thus beliefs that used to be about contingent matters can rationally change what is considered to be necessary, contradicting the assumption that the alleged contingent beliefs have a distinct modal status that does not affect what is necessary or counterfactually robust. If the idea that concepts are defined by what is taken to be counterfactually robust inferences is all there is to conceptual structure, then it is unclear how on this picture conceptual change can rationally occur, so that the account is incomplete.

Now I want to discuss an account of concept individuation that does not invoke the distinction between counterfactually robust and other inferences, because it is not a version of inferential role semantics. Yet this approach is closely related as it relies on the distinction between beliefs about what is necessary and what is contingent; and it deserves to be discussed due to its prominence. This is the approach of *two-dimensional semantics*. It basically maintains that concept-constitutive are those beliefs about the referent that are viewed as metaphysically necessary by a person at a certain time ("Concepts are Beliefs about Essences" in the words of Haas-Spohn and Spohn 2001). More precisely, two-dimensional semantics views a concept as a two-dimensional matrix, representing a function that maps each possible scenario (a centered possible world) and possible world to an extension. Proponents of two-dimensional semantics assume that an individual has grasped this function *a priori* in virtue of possessing the concept (for a detailed account of this framework see Braddon-Mitchell 2004, 2005; Chalmers 1996, 2002a, 2002b, 2004; Jackson 1994, 1998a, 1998b, 2004). For our purposes, only a part of this two-dimensional matrix is relevant, namely its diagonal, called the *A-intension* (Chalmers also calls it the epistemic intension). The A-intension is a function from possible scenarios (modeled by centered worlds) to extensions. Possessing a concept is having grasped this function, i.e., having the ability for any of these possible scenarios to pass a judgment

as to which objects in this possible world fall under the concept. The ability to pass these judgments is viewed as an *a priori* capacity: an individual considers a possible scenario — a way in which a world could be for all we know purely *a priori* — and using her intuitions determined by the concept grasped she figures out to which entities in this world the concept applies.

This approach yields a clear division of labor between philosophy and science: The philosopher engages in the *a priori* task of conceptual analysis, determining a concept's extension for every possible world. Yet she cannot know which of these worlds the actual world is. This is an *a posteriori* issue, the task of the scientist. Thus, once we know which of the possible worlds the actual world is, we can read off the concept's extension in our world using the *a priori* function established by conceptual analysis. Conceptual analysis does not depend on any knowledge about the actual world, as it is about applying a concept to any possible world (no matter which one is the actual one). Thereby it promises *a priori* knowledge and analyticity in the sense of conceptual truths (Jackson 1994, 1998a; Chalmers 1996; Braddon-Mitchell 2004). This framework has not just been proposed as a semantic account of concept possession. First and foremost, it is has been used as a tool to analyze philosophical concepts, arguing for particular metaphysical positions. Moreover, David Chalmers (1996) applies it to empirical concepts, arguing prominently for *a priori* limits as to what science can find out. On Chalmers' *a priori* analysis of the concept of consciousness, consciousness cannot possibly be materialistically reduced as for instance one can imagine zombies — a possible scenario in which there are beings that are physically identical to humans, yet they lack consciousness. Given that the concept of consciousness does not apply to zombies which are *a priori* possible, having our physical properties (which we share with zombies) is not enough for having consciousness, so that consciousness is not identical to material properties.

Though the framework of two-dimensional semantics promises analyticity and clearly individuated meanings, it is in my view a totally inadequate framework for empirical concepts. The general reason is that it advances a *preformationist picture of concepts*. (In developing the following critique of 2-D semantics I greatly benefited from ideas of Paul Griffiths.) Preformationism was the doctrine from 17^{th} and 18^{th} century embryology that maintained that the basic structures of the developing organism are already preformed in the sperm (or alternatively the egg). Some accounts maintained that Adam's sperm already contained all future generations (where one generation is encapsulated by the previous one). According to preformationism, the adult is no more complex than the embryo, the preformed structures simply have to unfold and grow during development. The alternative theory was epigenesis, assuming that development starts out with a relatively ho-

mogeneous mass and that during development genuinely novel structures emerge. Two-dimensional semantics endorses a preformationist picture of concepts in that all future possible scientific developments are already contained in a current concept. Once an *individual* has grasped a certain concept, *she* is able to tell to which entities the concept will apply in any possible future situation. For assume that the person imagines a possible scenario @ and that @ happens to be the actual world. The person does not know that the world @ imagined by her is in fact the actual world, as she has incomplete knowledge about the actual world's total features (while a specification of @ includes all facts about this world, the person can imagine @ like any other *a priori* possible scenario). According to 2-D semantics, the person knows *a priori* about the extension of the concept in any possible scenario, *a fortiori* she knows about the extension in @. Thus, possessing a concept involves at least knowledge about how the concept would apply to any partial specification of the actual world — relatively detailed specifications of the actual world that include facts that science has yet to reveal.

My objection is that empirical concepts do not work that way. First, 2-D semantics ignores *variation internal to a concept*, i.e., the fact that the different individuals possessing a concept have different beliefs, including differences in beliefs that bear on the concept's meaning (variation in inferential role on my approach). Variation internal to a concept (variation in a term's usage within a community) is philosophically significant as it is a determinant of conceptual change. Chapter 5 will explain the rational emergence of several distinct contemporary homology concepts based on the fact that an original, shared homology concept came to be used differently in different subfields of biology. Chapter 6 will explain the rational emergence of the contemporary gene concept based on prior conceptual variation within the molecular biology community, so that subsequently different epistemic pressures acted on different parts of molecular biology, leading to the current strong variation in the usage of the term 'gene'. How a concept changes based on novel empirical findings is not determined by the mental state of an individual scientist. It is a *communal choice* of an overall scientific field, where semantic and epistemic variation within a community influences how the *community* changes the concept and thus to which objects the concept will apply in the future. 2-D semantics goes metaphysically wrong by assuming that possessing a concept endows an *individual* with knowledge of how the concept will apply to future situations. It goes methodologically wrong by assuming that the philosopher (or anyone possessing a concept) can analyze a concept by only consulting her own intuitions. Instead, an adequate philosophical analysis of empirical concepts has to pay attention to the particular semantic variation a concept exhibits.

The second reason why 2-D semantics offers an inadequate account of empirical concepts is that no-one possessing a concept — not an individual, not even a whole language community — has the *a priori* abilities required by this approach. 2-D semantics asks us to make verdicts on possible scenarios. However, our verdict is based on our current concepts (our current conceptual schemes), which depend on present empirical knowledge. We cannot imagine any situation a description of which requires concepts that we do not currently possess. This applies even to imagining a partial specification of the *actual* world, which includes facts that have to be described by concepts that future science will develop. Science constantly introduces new concepts. Thereby new entities are postulated and new relations (new causal processes) between old and new entities are claimed to obtain. We cannot imagine these future conceptual developments, and thus using our current conceptual schemes we cannot specify future scenarios. This fact is shown by the history of science. For instance, if geneticists around 1930 (or philosophers at this time having grasped the classical gene concept) had to engage in conceptual analysis, then they would have been conceptually prevented from figuring out how the gene concept applied to situations in the actual world as we know and can describe them nowadays. For classical geneticists did not know about molecular entities such as promoters, exons, regulatory elements, spliceosomes, transfer RNA, ... , nor did they know about important molecular genetic processes such as translation, alternative splicing, RNA editing, ... The objection against 2-D semantics is not that past scientists did not *know* enough about the actual world or could not *foresee* future empirical discoveries. Instead, the objection is that past scientists did not have the *concepts* in order to *imagine* relevant possible scenarios, which is a precondition for deciding how the target concept to be analyzed applies to such a scenario. The inability to imagine possible scenarios is not just due to the fact that it is demanding to describe and scrutinize a complete possible world. Instead, it is an inability in principle — a conceptual inability — to conceive (possibly partial) specifications of *relevant* scenarios. Among the scenarios relevant for a minimal analysis of a scientific concept are those that contain a description of the actual world, including facts yet to be discovered by later science. 2-D semantics erroneously views concept possession as an *a priori* ability to anticipate any possible future conceptual development, including developments that essentially depend on future empirical findings and concepts and are therefore not simply preformed by current concepts and theories.[31]

[31] For similar ideas see Griffiths (1999b). My above example shows that the inability to imagine future scenarios is due to the present lack of collateral concepts that are distinct from the concept to be analyzed (one cannot imagine scenarios relevant to the gene concept without the concept of an exon, of alternative splicing, ...). Yet, the lack of these concepts is relevant precisely because these concepts are conceptually related to the concept to be analyzed: the introduction of the concepts of molecular biology led to a change in the gene concept.

The basic failure of two-dimensional semantics as a theory of concepts is that this approach assumes that conceptual abilities are *a priori* abilities and that it is possible to pass judgments about any "maximally specific way the world might be, for all one can know *a priori*" (Chalmers 2004, p. 177). However, empirical concepts are shaped by past experience: concepts contain empirical information; and an implication is that whether or not persons can imagine certain scenarios actually depends on and is constrained by their current conceptual scheme. 2-D semantics precisely ignores this empirically based constraint, but the constraint entails that persons cannot intuit an A-intension as required by the 2-D semantics construal of concept possession. The fact that scientific concepts embody empirical information has also a flip-side: future empirical evidence will change present concepts. Chalmers (1996) argues that consciousness cannot be materialistically reduced because we can imagine zombies. This is in fact the case, as our current conceptual scheme based on our present empirical knowledge cannot rule out this possibility. However, once new empirical findings in neuroscience will have yielded a theoretical breakthrough and a novel understanding of consciousness, it is quite likely that based on this future conceptual framework zombies cannot be imagined any longer.[32] A standard reply by the proponents of *a priori* conceptual analysis is that this simply shows that future scientists will have *changed the topic* by switching from the concept that is presently associated with the term 'consciousness' to a totally different concept that future scientists refer to by this term. (Yet the metaphysical claim that 'consciousness' is not materialistic is viewed by Chalmers as a claim about the property denoted by the current concept of consciousness.) My reply is not to deny that in such a case scientists would have changed some of their concepts and in this sense changed the topic. The real question, however, is whether changing the topic is legitimate. It is a fundamental assumption of my account that conceptual change as it occurs in science is in most cases rational and legitimate. Concepts embody experience, which gives them a basic legitimacy. At the same time, further experience makes at rational for science to change its concepts, including a change in meaning but also a change in reference. If

[32]My claim about this future possibility is supported by examples from the history of science (see Griffiths 1999b for a similar claim about the concept of consciousness, using the same example from the history of biology). E.g., the preformationist theory of embryology was consistent with a materialistic vision of life. As preformationism assumes that development is nothing but enlargement of pre-existing structures, it was plausible that this could be explained by Newtonian mechanics. 17^{th} and 18^{th} century proponents of epigenesis, in contrast, often leaned towards a non-materialist, vitalist theory of life and development. While epigenesis is the more adequate theory of development, only later conceptual development could show how epigenetic development is consistent with materialism. One fundamental step towards this was the introduction of the cell theory in the 19^{th} century. This theory introduced the concept of the cell as the idea that all tissues of organisms are made up of cells as the smallest units of development and physiological function, where the fertilized egg is a cell and development proceeds due to cell division. 17^{th} century biologists could not imagine a possible world in which epigenetic development proceeds in a purely materialistic fashion, while 20^{th} century biologists can very well do so, based on their novel conceptual scheme.

two-dimensional semantics as a theory of concepts and concept possession cannot accommodate this fact about empirical concepts, then it is an inadequate framework of concepts.[33]

3.3.2 Toward a Meaning Pluralism

So far I have discussed some semantic accounts that propose that there are determinate and clearly individuated meanings by invoking some notion of analyticity or a distinction between meaning-constitutive and non-constitutive inferences. I indicated why I find these proposals unconvincing. No matter whether my critique of alternative accounts was successful, the burden of the argument is on these approaches to show that there is actually some notion of analyticity. My own approach to conceptual individuation will not rely on the assumption that meanings can be individuated in a unique way. Rather, my task in this study is to explain how concepts can be shared by different persons and how conceptual change can be studied without this assumption.

Recall that my semantic account assumes that a scientific concept consist of three components: 1) the concept's reference, 2) its inferential role, and 3) the epistemic goal of the concept's use. Two terms may differ in any of these three semantic properties. In some philosophical contexts it may be significant that two concepts differ in reference, whereas for other philosophical purposes a difference in inferential role is relevant. For this reason, decisions for postulating that two distinct concepts are in use may be based on dissimilarity as regards simply one of these semantic features, or any combination of the three. As in the course of history a scientific concept may change

[33] Another way to arrive at determinate meanings is to appeal to normativity by viewing concepts governed by norms of application (Kripke 1982). Brandom's (1994, 2000) normative pragmatism relies on this idea: two persons may make different inferences and have different dispositions, yet they may still be committed to the same inferences given that they possess the same concept. Such an approach has to explain what constitutes the norms that govern concepts (Brandom attempts to account for this based on norms that are implicit in any practice; see also Clausen 2004). The burden is to show that the empirical concepts are in fact governed by norms that are specific enough to yield determinate meanings (and that concept possession is being committed to these norms). In contrast, Davidson (1984a, 1986) and Bilgrami (1992, 1993) reject the idea that lexical words are governed by intrinsic normativity. On their account, semantic notions such as meaning and translation are substantially about understanding communication. But they go on to argue that successful communication does not presuppose and factually occurs without determinate meanings and semantic norms. In what follows, I will not commit my self to the assumption that scientific concepts are governed by intrinsic norms. Norms do play a role in a less robust sense: individuals often have the intention to use words as other members of the language community do. These norms are rather extrinsic to language itself, as scientists may choose to use a word somewhat differently than their colleagues. Given that conceptual change in science is typically rational, scientific concepts can be governed by norms only insofar as these norms permit circumstances in which they can be violated and transformed. The change of concepts is due to experience and epistemic considerations. For this reason, I view normativity as an important element on the epistemological level, rather than on the semantic level. The assumption of conceptual norms typically implies the appeal to social and communal features of language use, in order to offer an account of the basis of these norms (as Kripke's and Brandom's accounts do in quite different ways). Even though my approach does not presuppose that scientific terms are governed by intrinsic norms, Section 3.3.3 indicates in which sense social considerations are still relevant for me.

along several dimensions of meaning (reference, inferential role, epistemic goal), the labeling of two scientists' term use as expressing the same or a different concept may not be fruitful without further explanation. Instead, I assume that any claim about concept identity has to lay out the particular individuation criteria used for this study and to explain what philosophical purposes are met by them. In what follows, I spell out this idea by suggesting that even if only one semantic property is taken into consideration, then different individuation choices may be legitimate. For the moment I focus on individuating concepts in terms of inferential role, as debates as to whether or not inferential role semantics permits shared concepts have been conducted in these terms.

My approach distinguishes between the *inferential role* of a concept as shared by a language community (which is the set of material inferences supported by a concept) and a term's *total inferential role* used by an individual. The latter is the total set of inferences (in which the term figures) that are endorsed by the individual. As two persons are likely to use different total inferential role, I do not identity concepts with total inferential roles. Rather, concepts and their inferential role supervenes on the total inferential role. Due to this supervenience, two persons can express different concepts with the same term only if they do not endorse different total inferential roles, but they may share the same concept even if they use distinct total inferential roles.

While many versions of inferential role semantics use the term 'inferential role' or 'conceptual role' to refer to what I call total inferential role (conceiving of 'conceptual role' as a mental symbol's causal role in an individual's cognition), I explicitly distinguish two levels of features that bear on conceptual content: total inferential roles operating on the level of individuals, and inferential roles (concepts) operating on the level of the language community.[34] There is a reason to reserve the notion of content only for the second level. For content is usually viewed as a semantic feature shared by persons; and *total* inferential roles are not actually ascribed to any person. When we ascribe concepts, content, or meaning to an individual — for instance in order to offer an explanation of her intentional behavior — then we do not ascribe a holistic total inferential role. Even in a *de dicto* ascription, what is ascribed is a content that can potentially be shared. The first level (total inferential role) is still significant for a theory of content as it consists of the features that ultimately determine content. Moreover, in the history of science a concept can change only insofar some scientists come to use modified total inferential roles. For this reason, a study of scientific concepts has to start with studying the language use of individual scientists. In the context of different

[34]Section 3.2.2 suggested that reference operates on a third level. Total inferential role is more fine-grained than inferential role, which is more fine-grained than reference. In each case the latter supervenes on the former (see p. 82).

homology concepts — to foreshadow my later biological example — the neo-Darwinian evolutionary biologists Ernst Mayr and the evolutionary developmental biologists Günter Wagner use the term 'homology' in quite different ways, which is due to them associating different *total* inferential roles with the term 'homology'. At the same time, differences in theorizing and practical research between Mayr and Wagner is explained *not* by ascribing certain holistic total inferential roles, but by ascribing a phylogenetic homology concept to Mayr, while ascribing a developmental homology concept to Wagner. One such homology concept is shared by a larger group of persons, e.g., the developmental homology concept is shared by most evolutionary developmental biologists.[35] The most precise way would be to refrain from calling total inferential role a sort of content or meaning (it is merely a feature bearing on content). Nothing will hinge on this terminology, and for the purposes of simplicity I will talk about two levels of content/meaning. A total inferential role can be conceived of as an *idiolect meaning* (as opposed to a genuine, communal meaning). More significant is that by distinguishing two levels, my account can make plain that it does not endorse a radical holism about *content individuation* at all. Instead, it is a holism about *content determination*: the supervenience base on which a concept's content supervenes is holistic.

As a first approximation, I view two persons as sharing a concept if their total inferential roles are sufficiently similar. The idea that meanings supervene on total inferential roles or that idiolect meaning similarity (as opposed to literal meaning identity) is sufficient for concept sharing is actually quite popular, in that various proposals of IRS or other holist semantic theories have endorsed it in more or less explicit ways (Berg 1994; Bilgrami 1992, 1998; Block 1986, 1993; Harman 1973, 1993, 1996; Jackman 1999, 2003; Khalidi 1995; Lormand 1996; Pagin 1997; Schiffer 1981; Senor 1992; Silverberg 1994; Stich 1983; Warfield 1993). In addition to philosophical approaches, many theories of concepts in cognitive science make use of the idea of conceptual similarity. To a large extent, radical holism (the idea that meaning is total inferential role or that what you mean depends on every of your beliefs) is in fact a straw man. For instance, Michael Devitt's "Critique of the Case for Semantic Holism" (1993a) turns out to argue against radical holism only. In one of his preliminary sections — succinctly entitled "A Straw Man?" — Devitt intends to make plain that the position that "all of the inferential properties of an expression token constitute its meaning" is actually endorsed so that his critique of 'holism' does not argue against a straw man (1993a,

[35]If one is interested in explaining differences between different evolutionary developmental biologists, one has to individuate in a different (probably more fine-grained manner), making use of differences in total inferential role between different evolutionary developmental biologists. This is the reason why total inferential role is semantically significant even though it is not ascribed as such: it is the basis for various possible explanations. Any difference in individual's holistic total inferential roles may feed into some explanation (see Section 3.1.3).

p. 284). Astonishingly, he explicitly refers to Gilbert Harman and Ned Block as proponents of radical holism, while Harman (1973, 1993, 1996) and Block (1986, 1993) have repeatedly stated that for two persons to share the same concept it is sufficient that they use *similar* (total) inferential roles. On my approach, the rough idea that similarity of total inferential role is sufficient for possessing the same concept is not to be understood as the idea that there is a unique similarity metric defined on the space of all total inferential roles (something like 'overall similarity' of inferential role). Rather, inferential roles can be similar with respect to certain relevant features, and similarity with respect to these features determines whether two total inferential roles are viewed as corresponding to identical or distinct concepts (more about this below).[36] Invoking similarity of idiolect meaning is also sufficient for the intentional explanation of action. It is well-known from explanations in biology (e.g., explanations of organismal development) that they apply to many organisms, usually large groups of organisms, even though each individual differs from any other individual. For biological explanations succeed in picking out certain features that many individuals share or with respect to which they are similar, and that are relevant for the particular explanation. In the context of concept ascription as part of the explanation of intentional behavior, it may be sufficient for two persons to agree on a limited set of inferences endorsed (or to share a limited set of beliefs), which are relevant for this particular intentional explanation. For instance, a layman and a Drosophila geneticist have very different conceptions of a fly (i.e., they associate different total inferential roles with the term 'fly'). But when we explain how they succeed in catching a fly, we just need to make recourse to a few shared beliefs about flies that are sufficient to explain their behavior (such as the assumption that flies can fly). Assuming that the concept's inferential role consists of these shared inferences, the concept of a fly is individuated so that it is shared by both persons.[37]

Several critics of holist theories of meaning have argued that the very idea of similarity of meaning (what I call similarity of idiolect meaning) is incoherent in that one can obtain a notion of meaning similarity only if there is a prior notion of meaning identity, while inferential role semantics cannot avail itself of the latter (and thus not of the former). Fodor (1998a, 2004) and Fodor and Lepore (1996a, 1999) have put forward this idea, as have Becker (1998) and Margolis and Laurence (1998) (who both criticize the position of Lormand 1996, which bears a certain resemblance to my approach). The supposed objection is as follows. Assume that two people

[36]Block (1986) suggests that we should replace the dichotomy between same and different meaning by an account of similarity of meaning on different dimensions, so that conceptual roles (total inferential roles) can be similar along some but not other dimensions.

[37]See Miller (1997), Senor (1992), and Silverberg (1994) for arguments against Fodor's contention that holist theories of meaning are incompatible with intentional explanation.

endorse an inference from the *concept* 'dog' to the *concept* 'animal'. Then one might think that this seeming agreement on one inference implies that there is a particular overlap in meaning between the total inferential roles endorsed by these two persons — which could be used to define a notion of similarity according to which these total inferential roles share certain features (e.g., some inferences). However, as the objection runs, there is actually no overlap in meaning whatsoever. For according to holism, these two persons have different *concepts* of an animal — the 'animal' concept is defined by the total set of inferences in which it figures, and we may safely assume that the two persons differ in one of the inferences endorsed. Thus, the two persons actually endorsed two distinct inferences: from the concept 'dog' to 'animal$_1$' or to 'animal$_2$', respectively. My reply is that this objection confuses the syntactic and the semantic level. The inferences are not to be construed on the semantic level, i.e., as inferences between concepts. Instead, the inference is between syntactic entities, i.e., written words or utterances. The inference from the word 'dog' to the word 'animal' can be shared independent of what meaning is associated with these terms by different persons. Philosophical analysis may very well proceed from this fact on the syntactic level, even if semantic analysis reveals that two persons associate a distinct meaning with the term 'animal' (e.g., because they endorse different inferences between syntactic entities).[38] IRS approaches that rely on the language of thought can offer the same solution. Two persons can have the same symbol in Mentalese in their head which enters certain causal relations with other symbols, and these causal relations can be shared — they are syntactic relations and as such independent of semantics. Meaning supervenes on these syntactic relations, as it emerges from particular overall relations between symbols. This is well-known from Quinean radical interpretation (Quine 1960). Individuals make sounds and exhibit linguistic behavior, and the task of semantics is to assign meanings to them. This issue is not at all peculiar to inferential role semantics. Any semantic theory has to assume that semantic properties supervene on non-semantic properties (independent of whether this supervenience permits a naturalistic reduction of intentionality), so it should not be surprising that IRS can explain semantic features such as sharing of concepts (or inferences between concepts) by appeal to syntactic and other non-semantic features.

To see how I conceive of concept individuation, recall the argument by Fodor and Lepore

[38] In his reply to Fodor and others, Robert Brandom (unpubl. a) likewise appeals to the idea that IRS can make use of the fact that individuals use the same expressions or make the same utterances, which is a syntactic identity that can be used to define semantic identity. The idea that certain non-semantic similarities can be used to arrive at an account of shared concepts is part and parcel of many approaches in cognitive science. Goldstone and Rogosky (2002), for instance, present an algorithm that only uses conceptual connections between the terms within one conceptual system to achieve translation between systems.

(2002) against inferential role semantics. Given that one rejects conceptual atomism and instead assumes that some inferential relations between expressions are meaning-constitutive, then the following dilemma seems to arise. On the one hand, one could endorse a *radical holism*, according to which all inferential connections are meaning-constitutive. It is well-known that this option is unattractive. On the other hand, one could endorse a *localism*, according to which some, but not all inferences are meaning-constitutive. However, then we need a principled distinction between the meaning-constitutive and non-constitutive inferences, for example, a distinction between analytic and synthetic inferences. Given Quine's arguments against analyticity and synonymy, Fodor and Lepore assume that there is no such distinction. Paul Boghossian (1993a, 1993b, 1996, 1997) replies by maintaining that there is a distinction between meaning-constitutive and non-constitutive inferences. For unlike Quine, nowadays virtually everyone is a meaning realist — including Fodor and Lepore. It is usually assumed that there are determinate facts about which expression means what, and thus it is determinate whether or not two expressions are synonymous. Thereby most contemporary participants in the debate about content are actually committed to a distinction between meaning-constitutive and non-constitutive features. Boghossian (1993b) acknowledges that no-one has a satisfactory account of what the distinction looks like; still, he assumes that there are facts about meaning and thus a distinction between meaning-constitutive and other features.

I endorse a further possible position — *moderate holism*, which does not assume localism, while avoiding to slide into radical holism. Boghossian's meaning realism is actually a *meaning monism*: he assumes that each expression has one precise and objectively given meaning (though he does not have an independent argument for this tenet apart from the fact that many contemporary philosophers make it). My rival position is to assume that some concepts can be individuated in different ways, so that one term can have more than one meaning at the same time. The idea is that a particular term may be viewed as corresponding to a single concept (which is ascribed to every person from a whole scientific field). But at the same time, we can legitimately individuate in a more fine grained manner, i.e., this term can also be considered as corresponding to two or several concepts (so that each of these concepts is attributed to a smaller group of persons only). The reason is that there are *different philosophical and explanatory interests that underlie a particular study of a scientific concept and its change*. These interests determine how a concept is to be individuated; and as the same term can be subject to different philosophical studies and interests, its content may be individuated in different ways. Thus my account disagrees with the existence of a unique and determinate relation of synonymy and consequently with Boghossian's monist version

of meaning realism. Nevertheless, this does not mean that my account is a meaning anti-realism. For given a specification of the particular interests that underlie an instance of concept ascription, the meaning ascribed is determinate and objective, as it is based on genuine features of term use that are semantically relevant. My position is best viewed as a *pluralism about meaning* (for an earlier statement of this approach see Brigandt 2004b).[39]

Individuating scientific concepts in the study of conceptual change amounts to the following question: given a scientific term (either at a particular time or across a stretch of time), does it correspond to one or several concepts, and in what manner? An account is needed that enables us to tell whether a change in a scientific term's meaning was so substantial that the term now expresses a different concept, or whether at some point in history a concepts splits into two or more concepts used by different scientists or in different scientific fields. My approach addresses this issue by assuming possibly different ways to individuate a concept. Depending on one's philosophical interests, one can view a term as corresponding to one or several concepts, i.e., ascribe a concept to larger or smaller group of persons. A fruitful analogy for this idea is *dialectology*—the field of linguistics that is concerned with the study of dialects. Our folk conception is that dialects have distinct boundaries and that together they make up the language of which they are dialects. However, linguists are well aware of the fact that there is no principled distinction between a 'mere' dialect and a 'real' language.[40] Instead, linguists start out with the idiolect of individuals and study the interpersonal variation of idiolects. Then certain collections of more or less similar idiolects are considered as dialects or languages.[41] However, this often proceeds "in an essentially ad hoc manner" (Chambers and Trudgill 1980, p. 5), as no unique notion of language (as opposed to dialect) is available. The reason is that mutual intelligibility or some other unique measure of overall similarity of idiolects is often not very useful for individuating and studying dialects.[42] Rather, the

[39] My tenet that ascription of meaning and content is guided by certain interests bears resemblance to Dennett's (1987) intentional stance. Dennett assumes that sometimes there is no unique matter of the fact as to what a person means. Quine's rejection of "the old notion of separate and distinct meanings" (Quine 1987, p. 9) and Dennett's intentional stance have often been viewed as a sheer anti-realism about meaning. I am not concerned with assessing to which extent this characterization is right. My intention is to shift the debate from the distinction between meaning realism and meaning anti-realism to the difference between meaning monism and meaning pluralism.

[40] "At some point on this graduated scale the differences become so great that linguists speak of separate but related languages, rather than dialects of the same language. Actually there is no positive and clear-cut way to establish criteria by which separate dialects can be distinguished from separate languages. ... The truth is that dialect boundaries are usually elusive to the point of non-existence." (Francis 1983, p. 1)

[41] "Yet the notion of idiolect is important, because in the last analysis a language is observable only as a collection of idiolects." (Hockett 1958, pp. 321–322)

[42] "Attempts to use criteria as mutual intelligibility in order to determine the location of the boundaries therefore founder on serious objections, both logical and factual. The distinction between dialect and language, and hence this kind of definition of dialect, cannot be sustained in any rigourous interpretation." (Newbrook 1991, p. 94)

variation and change of dialects and languages is influenced by various non-linguistic processes — including cultural, economical, and political processes.[43] For some purposes, individuation in terms of geographical distribution captures best certain features of linguistic development. In other contexts, dialects are strongly influenced by social and cultural mechanisms so that an individuation in terms of social stratification is useful. The fact that there is no pre-existing definition of what a language is and no unique way of individuating dialects and languages is often viewed as an advantage by linguists, because in each case of delineating a particular dialect one can precisely spell out the linguistic features that pick out this dialect and defend this particular choice of individuation criteria — without being committed to use these criteria in every case.[44]

I view the way in which dialectology studies linguistic features as useful analogy for the study of semantic features. At least the analogy shows how one can fruitfully study concepts and conceptual change without having to rely on a pre-existent notion of analyticity or a unique way of individuating concepts. Consequently, I do not presume that there is a unique and principled distinction between real concepts and mere variants of a concept. Starting with a term's total inferential role used by an individual (the 'idiolect' of this person), one can study the interpersonal variation in total inferential role. This variation tends to be grouped around certain poles or in certain clusters, and one can pick out one of these clusters and consider it a concept.[45] Such a choice is fruitful as long as it fits some of the philosophical interests that can underlie a particular study of conceptual change. As there are different possible explanatory interests, different ways of individuating concepts can be legitimate. As a consequence, my assumption that concepts are clusters of similar total inferential roles is not to be understood as being based on a single overall similarity metric; rather, similarity is relative to the criteria of individuation used for a particular study.[46] Just like in dialectology different non-

[43] "It seems, then, that while the criterion of mutual intelligibility may have some relevance, it is not especially useful in helping us to decide what is and is not a language. ... we have to recognize that, paradoxically enough, a 'language' is not a particularly linguistic notion at all. Linguistic features obviously come into it, but it is clear that we consider Norwegian, Swedish, Danish, and German to be single languages for reasons that are as much political, geographical, historical, sociological, and cultural as linguistic." (Chambers and Trudgill 1980, p. 5)

[44] "The relative looseness of the two terms [of language and dialect] is a merit, not a defect, for one can add as many precisely delimited technical terms as one needs, based on various criteria of similarity between idiolects." (Hockett 1958, p. 322)

[45] My account focuses on language use and thus uses the notions of idiolect and dialect. Variants of IRS that rely on the language of thought hypothesis would talk about mental representations rather than idiolect meanings. Individuals may very well differ in their mental representations (in their internal structure or how they represent, not in what they represent). In these terms, my account states that concepts are clusters of similar mental representations.

[46] This can be illustrated by Khalidi's (1995) metaphor of a person's 'mental economy'. On his account, a concept is a certain position (a functional role) or value in a mental economy, and may correspond to an analogous feature in another person's mental economy. Attributing the same concept to two persons (or translating terms from different languages) is to mark certain functional similarities or shared features of different mental economies. How much similarity is necessary for the sharing the same concept will differ for each subject interpreted and dependent on other contents possessed by her (as the functional role in an economy depends on the relations to other entities).

linguistic mechanisms shape the development of dialects, so do non-semantic mechanisms shape conceptual change. Conceptual change in science is brought about by various epistemic factors and intellectual considerations, but it is also influenced by more general features of scientific practice and organization, such as institutional and — in the case of biomedical science — economic and social factors. A particular study of conceptual change may focus on one of these factors and use it to individuate concepts and study the development of concepts thusly individuated.

Even though a particular choice can be defended and yields a notion of synonymy, this notion of synonymy is *post facto* and relative to the choice. I do not assume that there is a pre-established rule (or notion of synonymy) that prescribes in advance of the particular case how we have to individuate; this is why my approach is a moderate holism rather than a genuine localism.[47] But it is not a meaning anti-realism, because the clusters picked out as concepts are as real as the interpersonal variation itself, and a particular way of individuating is justified as long as this particular account of content yields a philosophically successful study of the change of the term under consideration. My meaning pluralism has the consequence — which I consider a virtue — of shifting the focus away from the task of developing a general philosophical notion of analyticity towards the task of reflecting on the purposes that underlie the study of conceptual change and defending how a particular way of concept individuation exhibits crucial features of scientific rationality.[48]

[47] This idea of 'post facto' analyticity/synonymy shows up — in a different disguise — in Bilgrami's (1993) rejection of the idea that lexical words are governed by intrinsic norms. Bilgrami acknowledges that logical concepts are governed by clearly specifiable rules: "With regards to violation of deductive rationality, we can say something like: *There is a norm, such that for any violation of deductive rationality, it is a violation of that norm.*" However, in the case of empirical concepts, Bilgrami reject normativity by reversing the order of the quantifiers — an analogue of what I call 'post hoc' analyticity: "*For any failure of conceptual overlap (or material inference), there is a norm, such that the failure is a violation of that norm*" (pp. 132–133).

[48] One may wonder about the implications of meaning pluralism for reference. On the one hand, even if a concept can be individuated in different ways, this does not imply that a different referent is assigned for each mode of individuation. For different meanings can have the same referent. On the other hand, an account like the present has to acknowledge that it is possible that different referents are assigned on different individuation schemes. Just like the ascription of concepts depends on the interests underlying the study of conceptual change, so does the ascription of referents. This assumption has the following advantage. In the case of indeterminacy of reference, philosophical accounts typically appeal to partial reference (e.g., if scientists conflated different natural kind, then they are viewed as partially referring to each of these kinds). Invoking partial reference alone is often unsatisfactory, however. My suggestion is that in such a case a particular interest underlying reference ascription may single out a specific referent. One possible assignment of reference makes a speaker reliable and rational about some issues, but not others, while another possible reference assignment makes her reliable and rational about other features. The interests underlying a particular study of conceptual change may fit with one particular assignment of reference much better than with others. Thus, these explanatory interests may determine a certain referent, even if reference would be indeterminate if we did not take the relevance of such interests into account. (Stephen Schiffer 1981 hinted at this issue by stating that the assignment of truth-conditions to sentences depends on the interpreter's explanatory interests.)

3.3.3 Individuating Scientific Concepts

On the present semantic account, a scientific concept consists of three components: 1) the concept's reference, 2) its inferential role, and 3) the epistemic goal pursued by the concept's use. As two terms may differ in any of these three semantic properties and a concept can undergo historical change in any of them, decisions as to how individuate a concept may be based on one or several of these semantic properties.[49] Section 3.3.2 suggested that even if only one of the three semantic properties is chosen as the basis of concept individuation, there may still be more than one way to individuate a scientific concept. Thereby I suggested a *pluralism about concept individuation*, arguing that how to individuate a concept may depend on the philosophical and explanatory interests underlying a particular study of a concept. Thus, an account of a certain concept has to make explicit the philosophical purpose pursued by the study and to defend the individuation decision by showing that this construal of the concept faithfully picks out features of the concept's actual use and that it furthers the study's philosophical purpose. In this section, I lay out different considerations and criteria about how to individuate scientific concept, which I shall use in my later case studies.

Recall that I distinguish two basic levels of features that relate to content: total inferential role (idiolect "meaning"), on which concepts and their content/meaning supervenes (this communal, genuine meaning consists of reference, inferential role, and epistemic goal). Inferential role semantics provides the fundamental account of the features on the first level. It explains how expressions obtain their semantic properties in the first place, by claiming that content is determined by the inferential and epistemic practices of term use. For this reason, IRS is an important ingredient of my account. Nonetheless, the task of concept individuation is about how to get from the first to the second level. An account of how to individuate scientific concepts in concrete cases has to make use of semantic and epistemic considerations that go beyond the basic tenets of IRS.

The two levels of features bearing on content relate to the phylogenetic study of conceptual change (Sections 2.2.3 and 3.0; Lennox 2001a) as follows. A concept is a stable feature shared across individuals and time. Yet, a particular scientific concept may gradually change over time (if its reference, inferential role, or epistemic goal changes), and in some cases it finally becomes a novel concept. On my account, change internal to a concept is due to changes in some of

[49] Alan Love's (2005) notion of a 'conceptual cluster' is partially analogous to my notion of a concept's inferential role; his notion of 'problem agenda' broadly aligns with what I call the epistemic goal pursued by a concept's use. Love studies concepts and their change in terms of conceptual clusters and problem agendas. Yet like me he does not require that concepts always must be individuated in terms of one such feature (or a specific combination thereof), acknowledging that the same concept can occur in different conceptual clusters or be tied to different problem agendas.

the total inferential roles used by the individuals possessing the concept — thus, the first level is relevant. Concepts are clusters of idiolects (total inferential roles) extended in time; and the different idiolects that are associated with a certain concept at a particular time constitute a time-slice of this concept. This idiolect variation and change internal to the concept may eventually lead to semantic change that is so substantial that the term comes to correspond to a new concept. An important task for an account of conceptual change is to explain how changes internal to a concept and the origination of new concepts can occur in a rational fashion. Given that a concept as a phylogenetic lineage is made up of idiolects (total inferential roles used by individuals) that stand in relations of historical continuity, an account of concept individuation does two things. It yields an explanation of when different idiolects are part of the same concept, explaining when different parts of a conceptual lineage correspond to one concept. At the same time, it yields an account of when different idiolects associated with a term correspond to two or several concepts, explaining for instance when a conceptual lineage splits into two concepts. In what follows, I offer some general considerations on concept individuation. The real burden of the dissertation, however, is to defend in the subsequent case studies the way in which the particular concepts studied are individuated.

My first set of remarks is about *individuating concepts in terms of inferential role*. Given that on my account a concept is a cluster of different total inferential roles, different individuals may use different total inferential roles and still count as possessing the same concept. There are two related reasons why (possessing) a concept should not be construed as (endorsing) a particular set of meaning-constitutive inferences; the first pertaining to scientific concepts and the second to successful communication in general. An account of concepts should explain how concepts make successful practice possible (Section 3.1, Constraint B); and the notion of (total) inferential role is intended to account for this. For the inferential abilities that a person has in virtue of possessing concept include various epistemic abilities, as on my construal 'inference' includes how a concept figures in perception and action, and 'inference' as material inference captures how concepts figure in justification, explanation, and discovery. Regarding scientific concepts, Section 3.3.1 criticized standard philosophical construals of concepts such as two-dimensional semantics for ignoring the semantic variation internal to a concept (which on my account is variation especially in total inferential role). For conceptual variation permits the division of scientific labor. While a scientific concept as a property of a research community embodies various epistemic abilities, some scientists possessing the concept may have some, but far from all of these epistemic abilities. The fact that the epistemic/inferential abilities constituting the concept may be spread out over the whole scientific

community may be an important feature as to how the concept underwrites successful communal practice. As a result, *not only is the situation that different scientists endorse different inferences (total inferential roles) consistent with possessing the same concept, but it can be a precondition for the overall successful scientific use of a concept.* For instance, Chapter 4 will argue that homology criteria are a central part of the content of the homology concept, yet different criteria were favored by different biologists, or different criteria were used in different research contexts. Chapter 6 will acknowledge that there are some inferences any scientists possessing the molecular gene concept must accept (such as the idea that genes are made of DNA or RNA). At the same time, I will argue that the strong variation in the usage of the contemporary molecular gene concept is epistemically significant, in that different scientists using different inferences is conducive for current biological practice. Thus, there is a difference between concept possession as a state of an individual and a concept as a property of a language community. This yields a particular sense in which concepts are not simply inside the head — inside a single head. Studies of scientific concepts must take into account their social and institutional embodiment that accounts for their successful communal use.

Robert Brandom (1994) discusses in detail why concept possession cannot be identical to endorsing a fixed set of inferences (meaning-constitutive or analytic inferences), as the latter is not sufficient for successful communication and argument. Different interlocutors may disagree about various facts, yet having different background beliefs need not forfeit communication and argument. Brandom points out that successful communication requires understanding what implications other persons' beliefs have, so that sharing a concept is not just understanding what follows from one's own premisses, but also what follows from the assumptions endorsed by others (even if oneself does not endorse these premisses). On Brandom's model, rather than assuming that a concept is a fixed set of inferences or conclusion (that one has to endorse to possess the concept), a concept is more adequately construed as a function from possible background beliefs to the conclusions that follows from each set of background beliefs (Brandom calls this a function from a person's collateral commitments to the inferential significance of this concept; 1994, pp. 510, 587, 635). For instance, while a molecular biologist draws certain inferences involving the term 'gene' (based on her particular background beliefs), successful communication and argument with other scientists requires that she understands what inferences/conclusions follow from assumptions that she does not endorse (but that other biologists endorse), or what conclusion would follow from evidence that is not yet available to her and thus not accepted by her. On Brandom's perspectival model of communication, concept possession is the ability to navigate between different doxastic perspectives (to navigate

between different possible sets of background beliefs). In what follows, I use this basic idea. Yet while construing a concept not as a single total inferential role, but as a set of total inferential roles (where each total inferential role represents which conclusion follow from which premisses), I do not assume that concept possession requires that a person is able to literally navigate between *all* these total inferential roles (or that she is able to calculate the inferential significance from *any* set of collateral beliefs). Rather, the guideline is that a person possesses a certain concept if she has minimal inferential and epistemic abilities so as to be in a position to successfully communicate with other scientists and to engage in practical research as a communal activity.[50]

One task for the study of scientific concepts is to account for their *epistemic virtues* and how they underwrite successful scientific practice. Thus, one guideline for individuation is to view those aspects of a particular concept's use as concept-constitutive that display these epistemic virtues. These could be certain types of inferences and explanations in which a concept figures at a certain time and which account for the success of the overall intellectual practice in which this concept is used, thereby yielding the concept's inferential role (conceptual role). For instance, Chapter 4 will argue that criteria of homology are more central to the homology concept's content than definitions of homology, in that they are more significant for the concept's successful use in practice. A result of this construal is that pre- and post-Darwinian biologists possessed the same homology concept despite endorsing different definitions of homology; and the account highlights the potential of the concept — as already used in pre-Darwinian times — to underwrite later phylogenetic research. An implication of the idea that the study of scientific concepts is to exhibit their epistemic virtues is that normative considerations enter. There is a matter of fact and it may be a purely descriptive issue as to which total inferential role an individual possesses and how the variation of total inferential role between various individuals is structured. But concept individuation, i.e., the step from the first to the second level of features relating to content, can involve normative considerations about scientific rationality, as it generally occurs in the philosophy of science. Individuating concepts so as to account for how they support successful practice may also allow for different ways of individuation, as there may be several distinct aspects to the successful use of a concept, or as different scientific approaches may focus on some but not others of these aspects.

[50]Brandom's model must be taken as an idealization. As new empirical evidence may bring about conceptual change, the impact of new premisses can be a change of the very concept on which the premisses bear. Inference is a process that may culminate in a change of view (Harman 1982). Thus, concept possession cannot quite be identified with the ability to calculate the inferential significance for every possible set of collateral beliefs. Brandom himself views the idea that a concept is a function from collateral beliefs to inferential significances as too strong and simply suggests that concept possession is the ability to navigate between different perspectives (Brandom 1994, pp. 477–487).

One obvious possible purpose for the philosophical study of science is an account of progress. In the context of conceptual change in science, exhibiting the epistemic virtues of concepts becomes laying out the type of progress that occurred during the semantic change that a scientific term underwent. This sort of account is likely to contrast an old concept with a new concept associated with the term and to individuate these concepts so as to highlight the novel contribution that the new concept makes. For instance, Chapter 6 will contrast the classical gene concept with the later molecular gene concept, arguing that the latter supports a range of explanations that the former does not yield. A consequence of contrasting 'the' classical with 'the' molecular gene concept is that the classical gene concept is ascribed to most geneticists who used the term 'gene' before the advent of molecular genetics. This is legitimate for the purposes of discussing scientific progress, but at the same time it may obscure other aspects of conceptual change. A *different legitimate philosophical interest* is to explain why conceptual change occurred. For instance, one may study why classical genetics developed in a certain way and how molecular genetics could grow out of it in the first place. Classical geneticists had different views about the material nature of genes. These differences explain why these biologists chose to side with different research approaches and conduct different experiments. This yielded insights into the structure and function of classical genes and provided important clues for further experimental research. 'The' classical gene concept as construed in an account of conceptual progress abstracts from all these relevant differences. Thus if one is interested in explaining theoretical change, one has to make use of a *different, more fine-grained scheme of individuation.* In this case one has to discern several classical gene concepts, each of which embodies certain relatively specific views about the structure and function of genes. My later discussion will lay out these different ways of individuating the gene concept as used in classical genetics, thereby illustrating my pluralism about concept individuation.

So far I have discussed how to individuate scientific concepts in terms of their inferential role. Now I turn to a second semantic property that is relevant for concept identity: the *epistemic goal* pursued by a concept's use. As introduced in Section 3.1, the idea behind this semantic notion is that scientific concepts are used for particular epistemic purposes in that scientists have certain reasons for introducing a term and pursue particular explanatory interests when continuing to use it. A concept is intended to deliver a certain epistemic product, which consists in certain kinds of knowledge: the confirmation of some hypotheses, kinds of explanations, or experimental discoveries. Thus, whereas a concept's inferential role is the inferences, explanations, and practical investigation supported by the concept, a concept's epistemic goal is type of inferences, explanations, or practical

investigation that the concept is *supposed to* support. My motivation for introducing the notion of epistemic goal and viewing it as a genuine component of a concept was that it permits to account for the rationality of semantic change: a concept's epistemic goal sets the standards for which changes in the concept's inferential role (or reference) count as rational. A change in inferential role is rational if the revised inferential role (the inferences and explanations supported) meets the epistemic goal (delivers the demanded inferences and explanations) to a higher extent than the old inferential role. The semantic property of a concept's epistemic goal is significant for concept identity as it bears on the possibility of communication and rational argument between scientists. Different scientists need not investigate the same phenomenon if they merely refer to the same entity with a given term. For they may ask quite different questions about this shared referent. Scientists count as jointly investigating the same phenomenon if they pursue the same epistemic goal (or at least compatible epistemic goals) with a term's use. For scientists can successfully communicate with each other using a term to the extent to which they actually pursue the same scientific problem by using this term. For instance, Chapter 5 will argue that nowadays the term 'homology' is used for a generic epistemic goal by different biologists, so that they can communicate and agree on basic matters about homology. However, the term is used for different specific epistemic goals within traditional evolutionary biology, and within evolutionary developmental biology, so that communication across these two biological subdisciplines may be hampered as regards specific issues about homology.

A shared epistemic goal ensures successful communication and scientific argument in a far-reaching sense, since a concept's epistemic goal is a rational determinant of conceptual change (which is why this semantic notion accounts for the rationality of semantic change as explained above). The epistemic goal pursued by a concept's use determines how scientists will react to novel findings and empirical challenges to previous beliefs. Thus, to the extent that different scientists or different scientific fields use a concept to pursue the same epistemic goal, they will tend to agree about the scientific relevance of new evidence and the evidence's theoretical impact (including how to change the concept's inferential role). In this sense, a term used by different scientists does not correspond to incommensurable concepts if this term is used for the same epistemic goal. As a result, individuating scientific concept's in terms of the epistemic goals of their use implies that different scientists sharing a concept thusly individuated can communicate with each other in that they are in principle in a position to resolve empirical disputes. This is the reason why my later case studies will consider this component of a concept (rather than reference or inferential role) as *the most salient semantic property for the identity of scientific concepts*, and typically individuate

concepts in these terms. An implication is that this way of concept individuation yields shared concepts across empirical disagreement and theoretical change. As my later case studies will show, in the course of history a concept's epistemic goal is often a more stable feature than its inferential role (or even its reference). A concept as used at different times in history may be intended to account for the same problem, despite changing theoretical beliefs as to how to actually account for it. Different scientists may count as addressing the same phenomenon (pursue the same epistemic goal) even if they put forward different theoretical characterizations of the phenomenon (endorse different total inferential roles). In my case studies, concept individuation in terms of the stable epistemic goal pursued by a term's use entails that any change in the term's inferential role counts as change occurring internal to the concept (not leading to a novel concept), and the change in the concept's inferential role is accounted for as being rational relative to the stable epistemic goal. (Yet is has to be acknowledged that concept individuation in terms of epistemic goal is consistent with different individuation choices, as the epistemic goal pursued by a particular concept's use can be individuated in a more or less fine-grained fashion. As indicated, the term 'homology' is used by overall biology for a generic epistemic goal, but by biological subdisciplines for different specific goals. My particular pluralism about concept individuation explains why this is not damaging.)

To be sure, also the epistemic goal pursued by a term's use can change in the course of history, leading to a novel concept growing out of an old one (assuming that concepts are individuated in terms of epistemic goal). My historical studies will explain in specific cases how a change in this semantic property (epistemic goal) can be counted as occurring in a rational fashion. Similarly, a concept may exhibit variation regards the epistemic goals pursued by its use, in that the different scientists possessing the concept at a certain point in time may use it for partially different epistemic goals.[51] Above I explained that variation within a concept in its inferential role may be philosophically significant, as it permits the division of scientific labor. In the present context, variation in a concept's epistemic goal may be an important determinant of semantic change. Chapter 5 will explain how an original homology concept with a unique, shared epistemic goal came to be used for different specific epistemic goals in different subfields of biology, leading to conceptual diversification and the rational emergence of several distinct contemporary homology concepts, which are used in different subdisciplines. Chapter 6 will explain the rational emergence of the contemporary gene concept based on the fact that different types of molecular biologists came to spell out the

[51] Variation in a concept's epistemic goal is possible as on my account the epistemic goal is not determined by how a single scientist uses a term, but how a community consisting of many scientists uses a term in potentially diverging ways, i.e., a concept's epistemic goal supervenes on the various total inferential roles accepted by the concept users.

concept's generic epistemic goal in different specific ways. This variation in the concept's epistemic goal resulted in different epistemic pressures acting on different parts of molecular biology, leading to the current strong variation in the usage that characterizes the contemporary gene concept. Thus, while reference, inferential role, and epistemic goal are properties of a concept as shared by a language community (and while concept individuation choices may be based on these properties), a concept may exhibit internal variation in each of these properties / components of conceptual content. If the particular variation that a concept's component exhibits undergoes change, then the concept changes in this semantic component. Studying the variation that one or the other component of a concept exhibits is important for understanding the reasons of semantic change.

In sum, the individuation of scientific concepts and the study of conceptual change as a rational process make it necessary to study how a concept is used in practice across a whole scientific community. One guideline for concept individuation is to individuate concepts in terms of their inferential role. Such an account may exhibit the epistemic virtues of a certain concept by focusing on those features that account for the successful use of a concept in research practice. There need not be specific inferences that an individual has to endorse to possess a communal concept. Rather, a scientist possesses a concept to the extent to which she is a position to successfully communicate with other scientists and to engage in practical research as a communal activity. Another important guideline is to individuate concepts in terms of their epistemic goals, in that different scientists share a concept to the extent that they use a term for the same epistemic purposes.

3.4 SUMMARY OF THE FRAMEWORK OF CONCEPTS

On my theory a scientific concept consist of three components of content: *1) the concept's reference, 2) the concept's inferential role, and 3) the epistemic goal pursued by the concept's use.* Reference is the set of entities denoted by the concept (the concept's extension). Inferential role (also called conceptual role) is the set of epistemic abilities that persons possessing the concept have. It may include the ability to make certain inferences, put forward certain explanations, and conduct practical investigation of a certain type. A concept's epistemic goal is the scientific purpose of the concept's use within a research community; it is the epistemic product the concept is intended to deliver (which may be the confirmation of some hypotheses, kinds of explanations, or experimental

discoveries). In a nutshell, while a concept's inferential role is the set of inferences and explanations supported by a concept, the concept's epistemic goal is the type of inferences and explanations the concept is supposed to support.

I endorsed inferential role semantics by maintaining that a term obtains each of its semantic properties (reference, inferential role, epistemic goal) due to how this term is used by the members of the language community. More precisely, a term's *total inferential role* (total conceptual role) is the total set of inferences (in which this term occurs) accepted by a particular person. I construed the notion of inference in a broader way than usual: First, it involves not only intra-linguistic relations between sentences, but also the way in which perception of states of the world leads to the assertion of sentences and how the endorsement of sentences motivates action and interaction with the world. Second, inference is not viewed as formal, but as material inference: an inference is taken to be good not in virtue of its logical form, but in virtue of the content of the premisses and the conclusion involved. Inference thereby captures reasoning involved in justification, explanation, and discovery. On my account, concepts and total inferential roles operate on different levels, as the former is a property of a language community, and the latter is a property of an individual. A term's total inferential role accepted by an individual is the conception that this individual has of the object denoted by the term; it can be conceived of as the idiolect "meaning" the person associates with the term. While two individuals usually accept different total inferential roles in which a given term figures, they may associate the same concept with this term. On my version of inferential role semantics, concepts (consisting of reference, inferential role, epistemic goal) supervene on total inferential roles, i.e., a concept's content is determined by the various total inferential roles used by the different members of the language community. Inferential role semantics maintains that a person possesses a particular concept if she uses a term with one or the other total inferential role, so that concept possession presupposes having certain epistemic-inferential abilities.

This account was put forward to meet Two Constraints on Any Theory of Scientific Concepts: A) *How does a concept make successful practice possible?* An account of concepts should explain how concepts figure in rational reasoning and action, and how concepts are shared among individuals and term use serves the purposes of effective communication. B) *How it is possible for a concept to change in the course of history in a rational fashion?* A theory of concepts should account for the rationality of change in the semantic properties of terms.

The semantic property of reference (a term's extension), acknowledged by my approach as one of the components of a concept, bears to some extent on Constraint A. Assuming an appropriate

assignment of referents to terms, an assignment of truth-values to sentences follows. Given that true statements correspond to states of the world that actually obtain, true statements are good guides to action, so that in one sense the semantic notion of reference explains how concepts underwrite successful practice. However, practical success is actually explained by a person's mental states and dispositions, which determine what the persons thinks about, i.e., to which entity the person refers (these mental features lead to a person's actions and verbal utterances, and the latter provide the evidence for an appropriate assignment of referents). The notion of inferential role precisely captures these mental/epistemic capacities, and inferential role semantics maintains that a person counts as possessing a concept (including referring with it to objects in the world) by having certain epistemic abilities. Thus, rather than a concept's extension, it is actually its inferential role that genuinely explains the success of a concept's use (Constraint A). Furthermore, in the case of concepts involving empirical misconceptions — a situation typical for scientific concepts in their early stages — no unique referent may be assignable to such a concept (it is non-referential or it partially refers to several possible properties that are conflated by scientists). As a result, statements made by scientists involving such a concept do not have a determinate truth-value (they are partially true and false at the same time), so that the partial practical success that the concept makes possible after all cannot be explained in the standard way by appeal to the truth of the statements made. The semantic property of inferential role is more fine-grained than extension, in particular it can capture and represent the misconception embodied by the concept (e.g., the inferential role specifies that the concepts conflate two non-equivalent characterizations of the putative referent). As a result, even if no referent or no determinate referent can be assigned to a concept involving misconceptions, an inferential role can, which explains why in certain situations this concept's use led to practical success, and why in other contexts it led to confusion. Even in the case of terms having unique referents, the fact that inferential role is fine-grained is philosophically relevant for a further reason. A common idea in the philosophy of mind and language is that concepts are ascribed to persons to explain their behavior, and my Constraint A accordingly includes the idea that concepts figure in reasoning and action. Differences in the way two persons reason or behave can be explained by ascribing different concepts to them. My account assumes that conceptual content supervenes on total inferential role, which is sensitive to differences between individuals. Any such cognitive or behavioral difference between two individuals corresponds to a difference in the total inferential roles they associate with a term. Even though I do not identify a concept (or its inferential role) with a total inferential role, the former supervenes on the latter, so that a

between-person difference in total inferential role can be used to delineate two distinct concepts that are ascribed to different persons so as to explain differences in (verbal) behavior.

Traditional semantic accounts have typically acknowledged reference as a semantic property, and many approaches have in addition invoked inferential role or equivalent notions that reflect some beliefs about a concept's referent (such as intensions understood as analytic statements about the referent). The novelty of my account is to introduce a further notion — the epistemic goal pursued by a concept's use — to account for how a concept can change in the course of history in a rational fashion (Constraint B). Some of the novel justified beliefs about a term's referent that scientists acquire may lead to a change of the very meaning of the term, more precisely, a change in the term's inferential role (and possible reference) on my account. A concept's epistemic goal sets the standards for which possible changes in inferential role count as rational. For the epistemic goal pursued by the concept's use is the demand that the concept deliver a certain epistemic product: justifications of certain kinds of hypotheses (the conclusion of inferences), certain types of explanations, or a certain kind of investigation and discovery. A change in a concept's inferential role and a possible correlated change in the concept's reference is rational if the new inferential role (the inferences and explanations supported by the concept at this later stage) actually meets the epistemic goal to a larger extent than the old variant of the concept. Even the epistemic goal pursued with a term's use may change, and my later case studies will explain how this type of semantic change can be accounted for as rational in special cases. In sum, while a concept's inferential role reflects some beliefs scientists have at a certain point in time, the concept's epistemic goal reflects what scientists attempt to achieve by having those beliefs. Traditional accounts have construed concepts in terms of reference and/or certain beliefs about the referent, yet my account emphasizes that a further semantic feature is what persons attempt to achieve by having those beliefs, as it accounts for the rationality of conceptual change. My account uses the notion of inferential role to meet Constraint A; the notion of epistemic goal is necessary to address Constraint B.

Concepts have to be shared between individuals for the purposes of effective communication (Constraint A). A central topic for my discussion is the individuation of scientific concepts. For my subsequent case studies will make claims about how many and which homology and gene concepts have been used at a particular point in time or across history. On my account a concept may change in history along three dimensions of meaning — reference, inferential role, epistemic goal — and a term used by two persons may differ in any of these three semantic properties. A difference in only one of these features may in some contexts be philosophically significant, so that difference in

this semantic property is the basis for postulating distinct concepts being associated with a term. In other contexts, a difference in another semantic property may be more significant, or several semantic properties can be used for individuation decisions, so that there need not be a unique set of individuation criteria. Even if only one semantic property such as inferential role is used, my discussion still questioned the meaning monism that is implicit or explicit in many contemporary accounts of meaning in the philosophy of mind and language. I challenged the assumption that there is a unique way to individuate concepts by criticizing several proposals that have been viewed as yielding an analytic/synthetic distinction or another criterion for individuating concepts in a unique and principled way. I attempted to show a way to study and individuate concepts without relying on a putative analytic/synthetic distinction, by proposing a *meaning pluralism*, i.e., the idea that some scientific concepts can be individuated in more than one way. My suggestion was that each instance of concept ascription is based on particular philosophical purposes, which may vary from case to case (e.g., explaining conceptual change, or exhibiting conceptual progress and pointing to the epistemic virtues of certain concepts). Since the same concept can by approached in different studies with different philosophical aims in mind, different studies may individuate this concept in a different way. As an analogy, I used the individuation of languages and the study of change of dialects in linguistics, suggesting that different philosophical studies can group different collections of total inferential roles (idiolect "meanings") as corresponding to a concept, so that a concept can be ascribed to a smaller or larger group of scientists — depending on and to be defended by the particular philosophical purposes served and insights yielded by such an individuation.

I suggested two guidelines for individuating scientific concepts. First, regarding individuation in terms of inferential role, one philosophical purpose is to exhibit the epistemic virtues of scientific concepts and how they underwrite successful practice. As a result, the concept's inferential role can be characterized as consisting of those inferences, explanations, and investigative abilities (supported by the concept) that exhibit some of the concept's epistemic virtues and account for its successful use in research practice. While a concept's inferential role may consist of inferences that are characteristic of the concept, there need not be particular inferences that any person possessing the concept must endorse. For the epistemic-inferential abilities that constitute a concept may be spread out over a whole scientific community, so that variation internal to a concept can underwrite its successful communal use. Moreover, persons may legitimately endorse different total inferential roles because they disagree about certain empirical premisses (such as the acceptability of putative evidence) while still sharing a concept. Successful communication and argument requires in fact

that an individual can understand the logical implications that rival beliefs and premisses have (how novel premisses lead to revised conclusions and thus to a novel total inferential role), so that communication involves the ability to relate different total inferential roles that make up a concept. My account does not assume that to count as possessing a concept a scientist has to accept specific individual inferences, rather she must have minimal inferential-epistemic abilities to be able to communicate with other scientists and conduct practical research. Second, another guideline is to individuate concepts in terms of their epistemic goal, and my subsequent case studies will view this component of content as particularly salient for individuation decision. For scientists jointly investigate a phenomenon not just if they refer to the same entity with a concept, but if the address the same scientific problem by investigating this entity (pursue the same epistemic goal with the concept). As explained above, a concept's epistemic goal is a determinant of conceptual change, in that it determines how scientists rationally react to empirical challenges by revising their concepts (the concepts' inferential roles). Thus, to the extent that different scientists or research approaches pursue the same epistemic goal by using a certain term, they react in similar ways to novel evidence. This ensures successful communication and argument across a longer period of time, so that pursuing similar epistemic goals with using a term can be a semantic criterion for individuals to count as possessing the same scientific concept.

Chapter 2 criticized Philip Kitcher's account as a prominent referential approach to conceptual change for failing to meet three desiderata. This is how my account meets these desiderata for a theory of conceptual change. a) An account of conceptual change should be able to track change in the meaning of scientific terms and to detect the emergence of novel concepts ('conceptual phylogeny'). On my approach, a concept can change and is to be studied in terms of three semantic properties: reference, inferential role, and epistemic goal. More precisely, I assume that a concept is a cluster of total inferential roles which are used by different individuals. Due to variation in term usage (total inferential role) between persons, there may be variation within a concept as a communal object regards its reference, inferential role, or epistemic goal. Change of such a variation leads to historical change in some of the concept's three semantic components. Thus, change in a communal concept is ultimately due to changes in individualistic total inferential roles; and total inferential roles (even though they are not components of communal concepts) are to be studied as they constitute the usage of a term that is the evidential basis for ascribing reference, inferential role, and epistemic goal to a term. A change in some of a term's semantic properties may lead to a novel concept growing out of an old one, or a concept may split into two or several distinct concepts.

Whether this occurs depends on the individuation criteria chosen; and above I laid out possible guidelines for individuation. Given a certain individuation criterion, say concept individuation in terms of epistemic goal, changes in the other semantic properties (inferential role and reference) count as semantic changes occurring internal to this concept, rather than as changes leading to the advent of a novel concept. b) An account of conceptual change has to be in a position to explain why conceptual change rationally occurred ('conceptual ecology'). As explained above in detail, I introduced the notion of epistemic goals being pursued by a concept's use to account for the rational change in a concept's semantic properties, in particular inferential role and reference. c) A study of conceptual change should include an evaluation of the progressiveness of conceptual change. On my account, the degree of progressiveness depends on how substantial historical change in a concept's inferential role was (relative to the concept's epistemic goal), i.e., on the degree to which the new inferences and explanations supported by the revised concept go beyond the inferences and explanations supported by the old (variant of the) concept.

While my account assumes that a concept's semantic properties (reference, inferential, epistemic goal) are determined by the total inferential roles used by the members of a language community, I did not offer a precise metaphysical analysis of how these properties supervene on total inferential role. Rather than a naturalistic reduction of these semantic properties to non-semantic features, I suggested a moderate holism about meaning determination, i.e., the idea that what determines a concept's reference, inferential role, or epistemic goal need not be reducible to a clearly delineated set of beliefs, inferences, or causal relations that determine such semantic properties. (Nor are a concept's semantic features determined by the mental state of a single individual; instead reference, inferential role, or epistemic goal are emergent features of a term's use within a whole language community.) The aim of the dissertation is not so much to offer a metaphysical characterization of the properties of reference, inferential role, and epistemic goal, rather, the aim is to show in the subsequent case studies that these semantic properties can be ascribed to concrete scientific concepts as they are actually used, and that this yields philosophical insights about scientific language use. My framework of concepts is put forward not so much as the right metaphysical account of the nature of concepts (or as a theory of intentionality), but as a *methodological tool* for studying conceptual change in science, to be evaluated in terms of its fruitfulness for this task.

Whereas traditional accounts of conceptual change have focussed on the notion of reference and argued for stability of reference, the subsequent discussion attempts to show that the historical change in reference is in need of explanation, rather than the notion of reference having explanatory

significance in accounts of semantic change. The central heuristic impact of my semantic framework is the suggestion scientific concepts are to be studied in terms of *several semantic properties*. The reason for this is that a concept may change in any of these components of content, and that change in one component of a concept can be philosophically explained based on other components. The subsequent case studies from the history of science will apply this semantic framework to two concepts: the homology concept (Chapters 4 and 5), and the gene concept (Chapter 6).

4.0 THE HOMOLOGY CONCEPT BEFORE 1950

> *The best workman uses the best tools. Terms are the tools of the teacher; and only an inferior hand persists in toiling with a clumsy instrument when a better one lies within his reach.* (Richard Owen 1866, Vol. 1, p. xiii)

The present and the subsequent chapter are devoted to the history and philosophy of the homology concept. Homology is a relation used to compare morphological structures across species. Homologous structures are the same or corresponding structures in different species. As homology individuates biological characters, it is a fundamental notion which forms the basis for all of biology. Indeed, homology refers to the units of phenotypic variation as a basis of evolution. Despite its importance for biology, the homology concept has not been prominent in philosophical discussions.

The present chapter focuses on the homology concept as used before 1950. I start out by discussing the origin of the homology concept, which emerged at the beginning of the 19$^{\text{th}}$ century in comparative anatomy. Section 4.1 will lay out the history of the homology concept before the advent of Darwinian evolutionary theory, presenting those aspects of the history that are relevant for how the homology concept was used in biological practice. The main criteria of homology were established in this pre-Darwinian phase; and the homology concept became an entrenched part of biological practice. Section 4.2 will apply my semantic framework to the homology concept as used in this historical period. I will explain what I view as the inferential role of the homology concept (the inferences that characterize the homology concept and account for its successful use in practice), and I will lay out which epistemic goals were pursued with the use of this concept.

After the advent of Darwinian evolutionary theory, it became clear that what makes two structures in different species the corresponding or homologous structures is the fact that they are derived from the common ancestor. Consequently, reference to common ancestry became part of many standard definitions of homology. The conventional wisdom among biologists, historians and also philosophers is that this new definition brought about a novel concept — a post-Darwinian 'phylogenetic' homology concept as opposed to the pre-Darwinian 'idealistic' homology concept.

However, in the second part of this chapter I shall argue that the homology concept as used in pre-Darwinian biology and the homology concept used by most biologists until the middle of the 20th century is best viewed as one and the same concept. The continuity between pre-Darwinian and post-Darwinian times — as far as the homology concept is concerned — is larger than usually granted. Section 4.3 will discuss some aspects of the history of homology after the advent of evolutionary theory that are relevant for my argument, focusing primarily on the second half of the 19thcentury. The main burden of my philosophical discussion is to show that in the decades after the advent of Darwin's evolutionary theory no novel and distinct homology concept was introduced. In Section 4.4 I shall summarize the philosophical discussion of this chapter, giving a semantic characterization of the homology concept, and explaining my reasons for maintaining that there was basically only one homology concept in comparative and evolutionary biology throughout the entire history before 1950. First, the way in which the homology concept was *used in biological practice* (how homologies were established and how this knowledge was subsequently used for morphological and taxonomic purposes) did not did not change much since the origin of this concept in pre-Darwinian comparative biology. Second, before and after Darwin the homology concept was used to pursue the *same epistemic goals* (morphological comparison of structures across species and the classification of species). My account highlights in particular the epistemic potential of the homology concept as already used before the advent of evolutionary theory: many homologies had been established by pre-Darwinian biologists and served later as genuine evidence for common ancestry. One upshot of this discussion is that a concept's content is far from exhausted by standard definitions. Moreover, while theoretical accounts of homology changed with the advent of evolutionary theory (though to a smaller extent than usually assumed), the adoption of a phylogenetic definition of homology can nonetheless be accounted for as *rational* as this novel idea yielded a more effective way of meeting the epistemic goal pursued with the use of homology concept. Thus, change in inferential role can be accounted for as rational relative to a stable epistemic goal.

The following chapter (Chapter 4) will discuss the history of the homology concept since 1950. In accordance with Jim Lennox's phylogenetic approach to the history and philosophy of science (Lennox 2001a, 2001b), the homology concept is viewed as a historical entity and its current situation is explained by tracking its development ('conceptual phylogeny') and studying the historical reasons for these changes ('conceptual ecology'). My claim will be that during its history the original homology concept split into three distinct concepts, which originated together with three newly developing, specialized biological subdisciplines. In modern evolutionary biology and systematics,

there emerged what I call the *phylogenetic homology concept*. Evolutionary developmental biology uses the *developmental homology concept*, and molecular biology possesses a *molecular homology concept*. I shall argue that the emergence of these three contemporary homology concepts was rational and that the present conceptual variation is conducive to biological practice. My argument will be based on the fact that each such homology concept is used to pursue an epistemic goal that is characteristic for the discipline in which it used. As a result, such a specialized homology concept emerged based on and is used to effectively pursue the theoretical goals of its subdiscipline.

4.0.1 Homology: The Very Idea

Before starting with my historical overview of the homology concept, let me first give a basic explanation of what this concept is. Formally speaking, homology is a binary relation, which holds of morphological structures. Two structures in different species are *homologous* if they are the same or corresponding structures. For instance, the human arm, the wing of the bat, and the flipper of the whale are homologous — they are the forelimb of mammals. In fact, as Figure 1 shows, even the individual bones that make up the forelimb in these different species neatly correspond to each other. Forelimbs across a larger taxonomic group such as mammals have a common structure or a common topology. The structures that are mutually homologous to each other are called *homologues* (homology is an equivalence relation). Homologous structures are considered the 'same' structures in different species; thus, the homology relation individuates biological characters. For this reason, homologues are usually given the same name; homologues are namesakes (see Fig. 1). Nowadays, it is clear that what makes two structures homologous is the fact that they are inherited from one and the same structure in the common ancestor. If we take a particular structure in an ancestral organism (e.g., the forelimb in the amphibian ancestor of limbed vertebrates) and consider the structures in the descendants that derive from this ancestral structure, then we have a class of homologues. But a crucial fact for my discussion is that the homology concept was introduced well before the advent of evolutionary theory. The main criteria of homology that are still used nowadays were laid out in pre-Darwinian times. Comparative anatomists were able to establish many homologies; and many of the names for structures currently used were introduced in the 19^{th} century. So far my examples focused on homology among bones. But any type of anatomical structure can be homologized: organs, muscles, nerves, blood vessels, and tissues.

As the example of the mammalian forelimb makes plain, homology is independent of the function

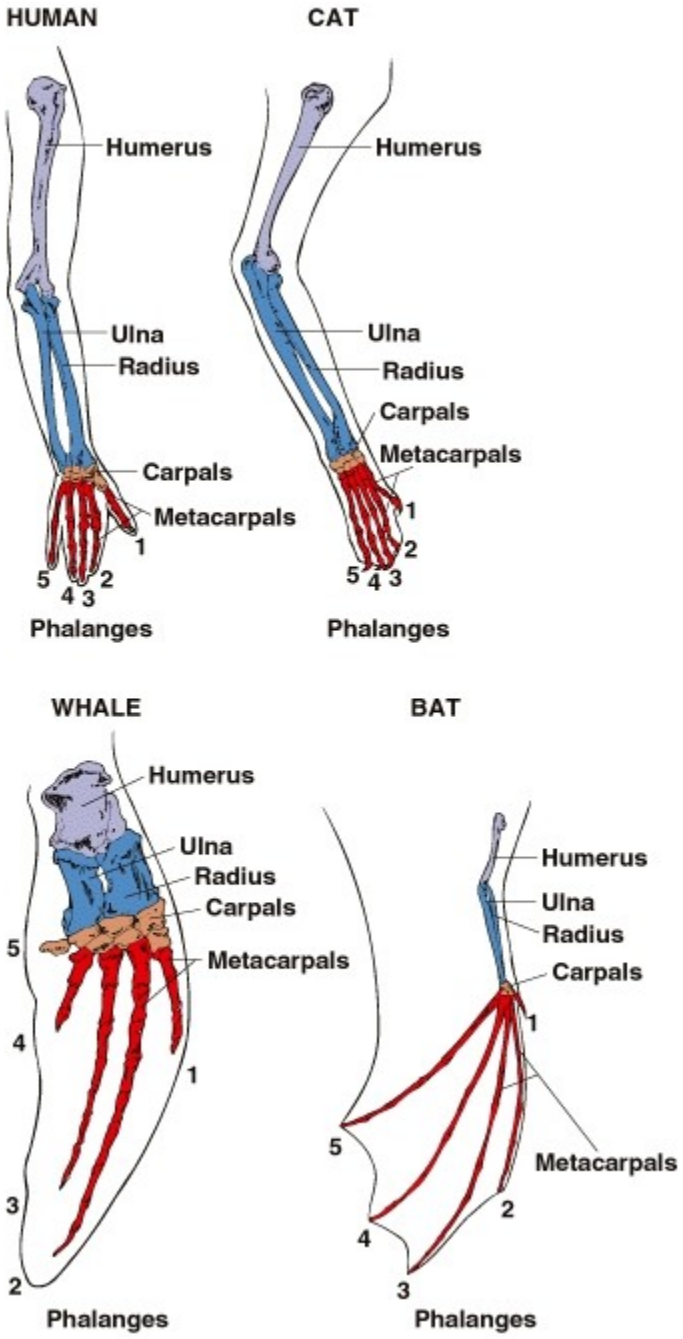

Figure 1: Homologies of the Mammalian Forelimb

of the structures involved. Forelimbs are homologous even though they serve radically different functions. The foreleg of the cat is used for running, while the wing of the bat is used for flying. The flipper of the whale is used for swimming, while the human arm is used for writing obscure German treatises on Naturphilosophie. Another, less obvious example of homology illustrates the same point. The stapes (one of the ear ossicles) as we find it in mammals is homologous to the amphibian quadrate (a part of the jaw). In the course of evolution this structure shifted and changed in shape and finally adopted a radically different function, without forfeiting homology. Homology is usually contrasted with *analogy*. Two structures are analogous if they are similar due to functional considerations. In case two unrelated organisms inhabit a similar ecological environment, they are exposed to the same selection pressure. Natural selection has the power to make individual structures quite similar, even if the structures are from unrelated organisms and thus not homologous. Even though function is nowadays often understood in terms of adaptation and the selection history of traits, the distinction between homology and analogy was made in pre-Darwinian times. The British comparative anatomist Richard Owen was the first to make this difference terminologically explicit. While in the first half of the 19$^{\text{th}}$ century different names were used for the idea of homology, Owen coined the standard terminology that we still use nowadays:

> HOMOLOGUE ... The same organ in different animals under every variety of form and function.
>
> ANALOGUE ... A part or organ in one animal which has the same function as another part or organ in a different animal. (Owen 1843, pp. 379, 374)

Owen's definition of homology makes explicit that homology is independent from function.[1]

From an evolutionary point of view, the independence of homology from function and selection can be put as follows. A homologue is the morphological entity that undergoes evolutionary change. The very possibility of evolutionary change presupposes that the same entity or morphological unit is present in different generations and species. A separate and conceptually posterior issue is how such a morphological unit (existing across individuals) changes based on functional demands and the operation of natural selection. Using the above forelimb example, the humerus in a whale looks quite different from the human humerus because of their different adaptive histories. The finger bones of bats are much longer than the fingers bones of a whale (relative to their body length) because of their different functions. (This is what Owen's homology definition refers to by "variety of form.") Thus, even though the particular shape and function of structures are subject to change in the course of evolution, still the same morphological units or building blocks reappear in subsequent species. This inheritance of structures or morphological units is what homology is

[1] Owen's definition of homology is still the favored definition of some contemporary biologists.

about — and it is independent from and conceptually prior to modification due to selection.

Evolution can be viewed as being determined by two factors: inheritance/descent, on the one hand, and natural selection (and mutation), on the other hand. Descent and inheritance account for the morphological similarity of closely related organisms, i.e., common ancestry explains why we have homologous structures. Natural selection, in contrast, explains why organisms are adapted to their environment. Appeal to both of these factors was very important for Charles Darwin's defense of his theory of evolution. By using specific cases of the taxonomic distribution of characters and the biogeographic distribution of organisms and their traits, Darwin could point to cases where morphologically similar animals lived in different ecological environments — to be explained by them being closely related by descent — and to cases where morphologically similar but taxonomically unrelated animals lived in similar environments — to be explained by natural selection.[2] Darwin's main opponents were the Oxbridge natural theologians, who basically assumed that organisms are functionally adapted to their environment due to the foresight of the creator. For this reason, the existence of homologies between different species proved to be an important argument for Darwin, as common descent could provide the only plausible and natural explanation of homology. The existence of rudimentary and vestigial organs in some species was particularly revealing. Prior to Darwin, the existence of these structures was clearly acknowledged and comparative anatomists usually agreed that in many cases a vestigial organ in one species is actually homologous to a fully developed organ in other species. Functional considerations and divine provision could hardly account for the existence of non-functional, vestigial organs. Viewing homology as being due to common ancestry could offer such an explanation (Darwin 1859, pp. 452–454; see also pp. 194–203).

Another reason why the homology concept is so important is the fact that it is a natural kind concept. Homologues — the structures that are mutually homologous to each other — form a natural kind. As each class of homologues is an equivalence class of the 'is homologous to' relation, the homology concept in fact defines a whole set of natural kinds. Homologues form a natural kind for the following reason. As homologous structures are inherited from a structure in the common ancestor, they are morphologically similar. Thus, the properties that hold of one structure are likely to hold of another homologue. This yields a projectability of properties from one homologue to another, which is a hallmark of natural kinds. I will explain this fact and the philosophical

[2] "It is generally acknowledged that all organic beings have been formed on two great laws — Unity of Type, and the Conditions of Existence. By unity of type is meant that fundamental agreement in structure, which we see in organic beings of the same class, and which is quite independent of their habits of life. On my theory, unity of type is explained by unity of descent. The expression of conditions of existence, so often insisted on by the illustrious Cuvier, is fully embraced by the principle of natural selection." (Darwin 1859, p. 206)

notion of natural kind on which it is based in more detail below (Section 4.2), for it will prove to be important for the use of the homology concept. Another characteristic feature of natural kind concepts is that they are introduced before scientists know about the 'essence' that defines the natural kind. This is clearly the case for the homology concept. This concept and the criteria for it were established before it became clear that common ancestry is the defining feature that makes two structures homologous. As we will see in the next chapter, many practitioners of evolutionary developmental biology think that common ancestry is a sufficient, but not necessary condition for homology. Thus, there still is an ongoing scientific search for the nature of homology.

Natural kinds are viewed as cutting nature at its joint. Homology does just this in a completely literal sense. For an organism is composed of different homologues. The mammalian forelimb consists of a particular set of bones, muscles, nerves, blood vessels, etc. Homology breaks an organism down into different parts. A certain spatial region of an individual is a real part or a natural unit if and only if it is a homologue. As it turns out, whether something is a natural part of an individual depends actually on whether we can identify the same part in other organisms — which is a non-obvious fact. More precisely, a structure such as the humerus is an independent part (homologue, morphological unit) because it can change in the course of evolution relatively independently from other homologues (such as the ulna or the radius). In sum, homology individuates biological characters. Owen's definition of homology expresses this fact by saying the homologues are the "same" characters in different organisms. This is the reason why this concept is so crucial for biology. Every branch of biology has to refer to biological characters and thus presupposes homology as the principle of character individuation. Biologist agree that the homology concept is of central importance for biology (Wake et al. 1991; Donoghue 1992; Raff 1996; Abouheif et al. 1997; Laubichler 2000). The zoologist David Wake puts this as follows:

> Homology is the central concept for *all* of biology. Whenever we say that a mammalian hormone is the "same" as a fish hormone, that a human gene sequence is the "same" as a sequence in a chimp or a mouse, that a HOX gene is the "same" in a mouse, a fruit fly, a frog, and a human — even when we argue that discoveries about a roundworm, a fruit fly, a frog, a mouse, or a chimp have relevance to the human condition — we have made a bold and direct statement about homology. (Wake 1994, p. 265)

4.0.2 Creationism, Teleosemantics, and Other Non-Biological Theories

Before going into the historical discussion of homology, I want to draw attention to two issues that do not directly bear on this study of conceptual change, but that relate to questions surrounding

homology which are of general interest for the philosophy of science. In my later discussion, I will only incidentally return to these issues, but it is instructive to keep them in mind throughout my historical discussion, as the history sheds some lights on these issues.

The first point is about the creationist critique of evolutionary theory. One popular creationist argument is based on the homology concept, claiming that evolutionary theory is *circular*. It is pointed out that homology is defined with reference to common ancestry: two structures are homologous in case they are inherited from a common ancestor. Thus, in order to establish homologies, biologists have to know about the phylogenetic tree of the species involved. However, phylogenetic trees are obtained in the first place by means of comparing species — more precisely, by comparing the homologous, 'corresponding' characters in these species and assessing their relative dissimilarity, which informs biologists as to how closely related these organisms are. Thus, homology presupposes phylogenetic trees and hypotheses of common ancestry, but the latter presuppose homology — we appear to be reasoning in a circle. This creationist argument is based on a misconstrual of both biological theory and practice. The goal of my dissertation is to study and explain conceptual change, so I will not disentangle the various issues raised by creationist critique in these pages. Instead, let me briefly point to two of the more obvious problems with the circularity challenge. First, phylogenetic trees and taxonomic groupings are established based on *many* characters, and well-confirmed phylogenetic hypothesis are precisely those that do not change whether we include some more characters or exclude some. Thus, if biologists have to assess whether a certain character present in several species is in fact a homology, this character is compared with a tree that was established based on many *other* characters. Thus, the phylogenetic tree was established based on information that is *independent* of the particular character itself, so that no circularity arises.[3] Second, the creationist critique ignores the distinction between the definition and the criteria of homology. The main criteria of homology do not make reference to common ancestry at all, so homology can be assessed independently of hypotheses of common ancestry, and taxonomic groupings and phylogenetic trees can be established based on this. As my subsequent discussion will explain, the homology concept and the main criteria for homology were actually well-established prior to Darwinian evolutionary theory. In the later section on homology in evolutionary theory, I will stress the continuity between pre-Darwinian and post-Darwinian times as far as the homology concept is concerned. The creationist critique is based on the erroneous assumption that common

[3]Nowadays, we are not restricted to morphological characters, but can also use molecular characters (gene sequences) to construct phylogenetic trees. Molecular characters yield an additional set of independent information.

ancestry is the sole definition and the fundamental feature of homology.[4] My later discussion will explain why I do not think that the reference to common ancestry is the most important aspect of the homology concept as it is used in biological practice, and that the new definition of homology based on common ancestry need not be viewed as amounting to a new homology concept. In fact, my main motivation for this claim is the fact that the homology concept as already used before Darwin and independently of evolutionary theory could yield the evidence for the construction of phylogenetic trees and thereby had the potential to support evolutionary research.

The second point I want to draw attention to relates to the way in which biology is usually represented by *philosophers of mind*. The prevailing view among many philosophers in general is that natural selection is the fundamental principle of all of biology. Daniel Dennett (1995) is one of the main proponents of this view — and also one of the main causes for this image of biology — by arguing that the notion of natural selection is vital to the future of philosophical theorizing. I pointed above to the two main factors of evolution: common descent and modification of traits by natural selection. The notion of *phylogeny* refers to common descent and evolutionary patterns (genealogical trees), but usually does not include evolutionary mechanisms and the way in which evolutionary change took place (e.g., adaptation due to natural selection).[5] The tendency among many philosophers is to ignore common descent in favor of adaptation. The notion of 'phylogeny' (as it may occur in discussions by biologists and philosophers of biology) is sometimes equated with 'evolution', and evolution is viewed as boiling down to adaptation by natural selection.[6] Philosophers of mind who endorse teleosemantics, such as Ruth Millikan and Karen Neander, argue that the notion of natural selection yields a notion of function that can be used to define mental content. A naturalistic account of content may try to define content in terms of the causal

[4] On page 130 above I stated that "common ancestry explains why we have homologous structures." Surely descent can causally explain homology only if descent is not viewed as being part of the very definition of homology (at least not for every usage of the term). In other words, my above usage of the term 'homology' often referred merely to a certain pattern in nature — the existence of structures that topologically correspond to each other.

[5] This difference between phylogeny and evolution is precisely the reason why Jim Lennox calls his approach to the history and philosophy of science a 'phylogenetic approach' (Lennox 2001a, 2001b). The phylogenetic approach consists in tracing the way in which a certain conceptual problem in science arose in the course of history. It is a 'phylogenetic' rather than an 'evolutionary' approach because it does not commit itself in advance to particular causal factors that influence the history of science and conceptual change, unlike Toulmin (1972), Richards (1987), and Hull (1988), who assume that scientific change takes place based on a sort of natural selection among ideas.

[6] Dennett, for instance, states that "If we gave up adaptationist reasoning, for instance, we would have to give up the best textbook argument for the very occurrence of evolution (...): the widespread existence of homologies, those suspicious similarities of design that are *not* functionally necessary." (1995, p. 238). Dennett is right that homologies and in particular rudimentary organs were one of Darwin's main arguments for evolution (as pointed out above), but homology and the idea of common descent are *not* based on adaptationism. Quite on the contrary, the natural theologians opposing Darwin rejected common descent, while endorsing adaptationism in the sense that organisms are created by God so as to be functionally adapted to their environment.

relations between the mind and the world. Teleosemantics tries to solve the problem of how to distinguish between the causal relations between the mind and the world that truly represent from those that misrepresent (proper vs. improper application of a concept to objects). The idea is that even though a diseased or otherwise non-functional heart does not carry out its function (pumping blood), by appeal to how hearts have been adaptively shaped in the past we can still say that a dysfunctional heart has the function of pumping blood — that it is 'meant' to pump blood. Such a notion of function (Millikan uses the term 'proper function' for it) can be used to make the distinction between mental representation and misrepresentation — a concept may be systematically yet erroneously applied to certain objects and visual exposure to non-instances of a concept may trigger the use of the word, but this false application is not the proper function of the concept, is not what this concept is actually 'about' or what it 'means'. Thus, the notion of natural selection promises to yield a naturalistic account of the normativity associated with intentionality.

An underlying assumption of some proposals of teleosemantics is that function, adaptation, and natural selection are the central notions of biology. For instance, Millikan's seminal book is entitled *Language, Thought, and Other Biological Categories*. Millikan's discussion and her teleosemantic account of content shows that she takes biological categories to be *functional* categories.[7] In fact, Millikan even assumes that biological characters are *individuated* based on their function. She starts her discussion by claiming "That a heart is a heart certainly has something to do with pumping blood" (1984, p. 17). The same assumption is made for kidneys: "the function that make kidneys to be kidneys" (p. 17). Karen Neander makes the same point in an explicit fashion as follows:

> For instance, "heart" cannot be defined except by reference to the function of hearts because no description purely in terms of morphological criteria could demarcate hearts from non-hearts. Biologists need a category that ranges over different species, and hearts are morphologically diverse: ... Highly significant, moreover, is that for the purposes of classifying hearts, what matters is not whether the organ in question manages to pump blood, but whether that is what it is supposed to do. (Neander 1991, p. 180)

Millikan and Neander apparently view functional classification as a Darwinian insight, because adaptation explanations — on which they models their account — could not have been given without the notion of natural selection. As my discussion already pointed out, for virtually the last two centuries, biologists have been clearly aware of the fact that biological characters are to be individuated completely independent of their function. Hearts do pump blood, but this function is not what makes it a heart; instead, structures are individuated by homology.[8] The irony is that this

[7] "My claim will be that it is the 'proper function' of a thing that puts it into a *biological* category, ... If language device tokens and mental intentional states (believing that, intending to, hoping that) are members of proper function or '*biological*' categories, ..." (Millikan 1984, p. 17; my emphasis)

[8] The above examples, making plain that the individuation of structures is independent of their function, dealt

is a pre-Darwinian insight and that Darwinism and advent of the notion of natural selection did not change this idea in any way. While function and teleology is viewed by many philosophers as the fundamental principle of biology, my following discussion will make clear that biological kinds often are not functional kinds, and that considerations about morphological structure and common descent are the more fundamental ideas.[9] A good deal of crucial knowledge and powerful practices are based on the notion of homology and quite independent of function. Millikan's and Neander's assumption that teleosemantics is a theory of mental representation that makes use of the main tool from biology is a misrepresentation of biology.

4.1 HOMOLOGY BEFORE 1859: THE EMERGENCE OF A CRUCIAL CONCEPTUAL PRACTICE

The idea of homology emerged in France and Germany independently, but from 1820 onwards French and German anatomists influenced each other as well as British zoologists. Long before the term 'homology' was introduced and the idea of homology was clearly spelled out, naturalists and comparative anatomists studied biological characters of known and newly discovered species and gave names to morphological structures, if it was deemed necessary. It was quite obvious that the same organ or structure exists in different species. But early naming practices — the idea of sameness of structures — clearly fell short of the more sophisticated practice of the 1840s and 1850s, when the homology concept in its more developed and explicit form was fully present. Naming practices were sometimes idiosyncratic in that naming and individuating decisions were based on the intuitions of the person doing the naming in absence of individuation criteria or any explicit account as to how to name structures. Not surprisingly different countries used different terms for

with bones, while Millikan's and Neander's main examples are organs such as the heart and the kidney. If some may reply in defense of the teleosemanticists that functional individuation is a more obvious approach in the case of organs with a clear-cut physiological function, a look at morphological textbooks shows that biologists think that this is clearly not the case. In his discussion of the "theory of homology", Eduard Jacobshagen's main examples are the liver and the thyroid gland (1925, pp. 87f, 92f). In an evolutionary context, de Beer states that "the most striking case of homologous organs is that of the thyroid. ... not the least remarkable feature of it is the great change in function which has taken place from an organ connected with the ciliary method of feeding [present before the origin of vertebrates] to a ductless gland regulating the metabolism of the body [in mammals]. This case is a good illustration of the fact that function is no criterion whatever in questions of homology" (de Beer 1928, p. 409).

[9] These issues have been pointed out before by some philosophers who are aware of the concept of homology, such as Amundson and Lauder 1994; Griffiths 1994, 1999a, forth.; Matthen 1998, 2000; McLaughin 2001. The interesting fact is that biologists and philosophers of biology point to the relevance of homology, while philosophers of mind assume that function and adaptation are main principles of biology.

the same structure, and even within a country different names could exist for the same organ in case two naturalists or anatomists independently studied and named this structure. Sometimes, the anatomists in the medical faculties used different names for human structures than the zoologists in the philosophical faculties used for animal structures, even though by later lights these structures in humans and animals are clearly homologous. Originally, the individuation of structures depended both on their form and function. The naming of organs was also sometimes anthropocentric in that the human body was taken as a point of reference. In case a structure in a vertebrate was similar to a structure in humans in terms of form and function, the name of the human structure was used as well; otherwise a new name was introduced for the animal structure. The emergence of the homology concept brought about a change in these naming practices, moving biology towards a more sophisticated, theoretically more explicit, and scientifically more powerful way of individuating characters. The idea that human anatomy as the point of reference was abandoned in favor of the idea that organisms are build based on a morphological plan that is common to large groups of organisms. Function became irrelevant for the individuation of structures, while considerations about topological relations of structure and the development of characters took center stage.

This section discusses the establishment of the two main criteria of homology — which are still the main criteria used nowadays. These are the positional and the embryological criteria. I explain briefly the notion of serial homology, which was of particular importance for pre-Darwinian morphology. Then a closer look is taken at a few selected parts of the work of Richard Owen, because his scientific contribution strongly advanced the use of homology in biological practice.

4.1.1 The Positional Criterion

A landmark in the establishment of the homology concept is the work of the French anatomist Etienne Geoffroy Saint-Hilaire (1772–1844). Geoffroy spelled out the criterion of homology that is often labeled the positional criterion. This criterion is probably the most important among all criteria of homology. Geoffroy's approach can be illustrated by contrasting it with the quite different functionalist anatomy of Georges Cuvier (1769–1832). The diverging approaches as to how to do anatomy led to the famous Geoffroy-Cuvier debate from 1830-32, probably the central debate in 19$^{\text{th}}$ century French biology.[10] The difference between Cuvier and Geoffroy can be viewed as centering on the question whether form or rather whether function is the prior biological principle.

[10]Toby Appel's *The Geoffroy-Cuvier Debate* (1987) is the authoritative discussion of the Cuvier–Geoffroy relation.

Cuvier assumed that function determines form, while Geoffroy argued for the view that form determines function.

Georges Cuvier was the most eminent zoologist of his time. His biological work, in particular his functionalist anatomy, influenced zoologists well beyond France. Cuvier's functionalist anatomy focused on the way in which the different parts of an organism are functionally integrated and how they fit with the environment and the ecological role of the organism. The idea is that due to functional considerations not every structure can coexist with another structure, structures have to functionally connect with other structures to yield the organisms as a functionally integrated whole. Each part of an organism is functionally contingent on other structures, and a form change in one structure necessitates changes in related structures due to functional reasons. In fact, Cuvier himself supported the legend that he could reconstruct an entire animal from a single bone or even a bone fragment (Appel 1987; Rupke 1994).[11] Cuvier divided the animal kingdom into four groups, or *embranchements*, as he called them (what we nowadays would call phyla): the vertebrates, the articulates (include segmented animals such as the insects and crustaceans), the mollusks, and the radiates (include echinoderms such as sea urchins). This grouping into basic types of animals was guided by functional considerations as well. The four *embranchements* were defined by the structure and function of the nervous system, as Cuvier assumed that the nervous system was the overarching system in animals to which other systems were functionally subordinated. Cuvier's basic division into four animal groups was accepted for large parts of the 19$^{\text{th}}$ century. While some speculative zoologists such as Jean-Baptiste Lamarck argued for evolutionary ideas, assuming that different organisms are connected by descent, Cuvier was very clear about his conviction that there are no intermediate forms between the four *embranchements*. The gaps between these four groups could not be bridged because intermediate forms were functionally impossible. The *embranchements* exhausted all possible life-styles and functional ways of being.[12]

Even though Geoffroy Saint-Hilaire initially collaborated with Cuvier, he soon came to adopt a different approach to anatomy. Geoffroy's fully developed approach, his so-called *philosophical anatomy*, stressed the morphological unity among large animal groups such as the vertebrates.

[11] Cuvier's functional anatomy was very influential among the British natural theologians, because it fitted with their program of viewing species as designed by the creator in adaptation to their ecological role. (The natural theologians modified Cuvier's very sophisticated teleological theory and integrated it into their own creationist approach, though.) "There was no place in Cuvier's thinking for useless organs or for organs created to maintain serial relationships, symmetry, or unity of plan. ... it is not surprising that Cuvier's works were enthusiastically received in Britain, where works written in the framework of natural theology were commonplace." (Appel 1987, p. 41)

[12] As mentioned, Ruth Millikan and Karen Neander assume that biological kinds are individuated by their function. The fact that Cuvier had a functional approach to anatomy does not mean that he individuated structures purely by their function. Rather, function determines structure and structures are to be studied with their function in view.

Vertebrates appear to be built on a common geometric-topological plan that consists of a certain number building block arranged in a certain topological order. This body plan exhibits striking symmetries. (Geoffroy talked usually about the 'unity of composition' rather than the 'unity of plan.') While a Cuverian *embranchement* unites the vertebrates because of a common functional organization, Geoffroy viewed the vertebrates as being unified because of an underlying topological scheme. On Cuvier's account the very existence of a particular part of an organism as well as its particular form is to be explained based on functional considerations. Geoffroy, however, explained the existence of bodily parts based on the fact that this organism is build in accordance with a shared body plan. Figure 2, depicting different vertebrate skeletons as drawn by Geoffroy, illustrates the idea of a general body plan. Another way of visualizing what the 19^{th} century proponents of the homology concept had in mind when talking about an idealized topological plan is provided by Richard Owen's so-called 'archetype' of the vertebrate skeleton (Figure 3). Owen developed the archetype a few decades after the period in which Geoffroy proposed his ideas (as will be discussed below), but Owen's drawing gives a good illustration of the notion of an abstract plan. The idea is that a vertebrate is made out of a certain set of basic skeletal elements. These may vary in particular shape and complexity, but most of the building elements exist in every vertebrate. Deviations from the general plan were often explained based on functional considerations. Even though there is clearly a variation between different vertebrates and the same building elements need not always be present in vertebrate species, there is a striking morphological and geometric unity among this group of organisms. This approach diverges so strongly from Cuvier's because Geoffroy assumed a topological plan that was ontologically prior to the modifications of it for particular purposes.

Homologous structures are the corresponding structures in different species, which can be stated by saying that two structures are homologous if they correspond to the same element in the ideal plan. Geoffroy actually used the term '*analogue*' for what we now call homologue, taking a word from ordinary French and using it in a specific morphological way. Geoffroy laid out his views in 1807, in a series of memoirs presented to the Institut de France, and published in the *Annales* of the Muséum d'Histoire Naturelle. These publications contain most of his important ideas on homology and morphology. Geoffroy attempted to show that across different vertebrates such as fish, reptiles, birds and mammals the 'same' structures were present despite the fact that these organisms live in quite different environments. Previous anatomists, including Cuvier, had assumed that many animal structures were present in only one of the four vertebrate classes (due to functional/structural similarity within such a class). Geoffroy, however, found homologies between these classes. In his

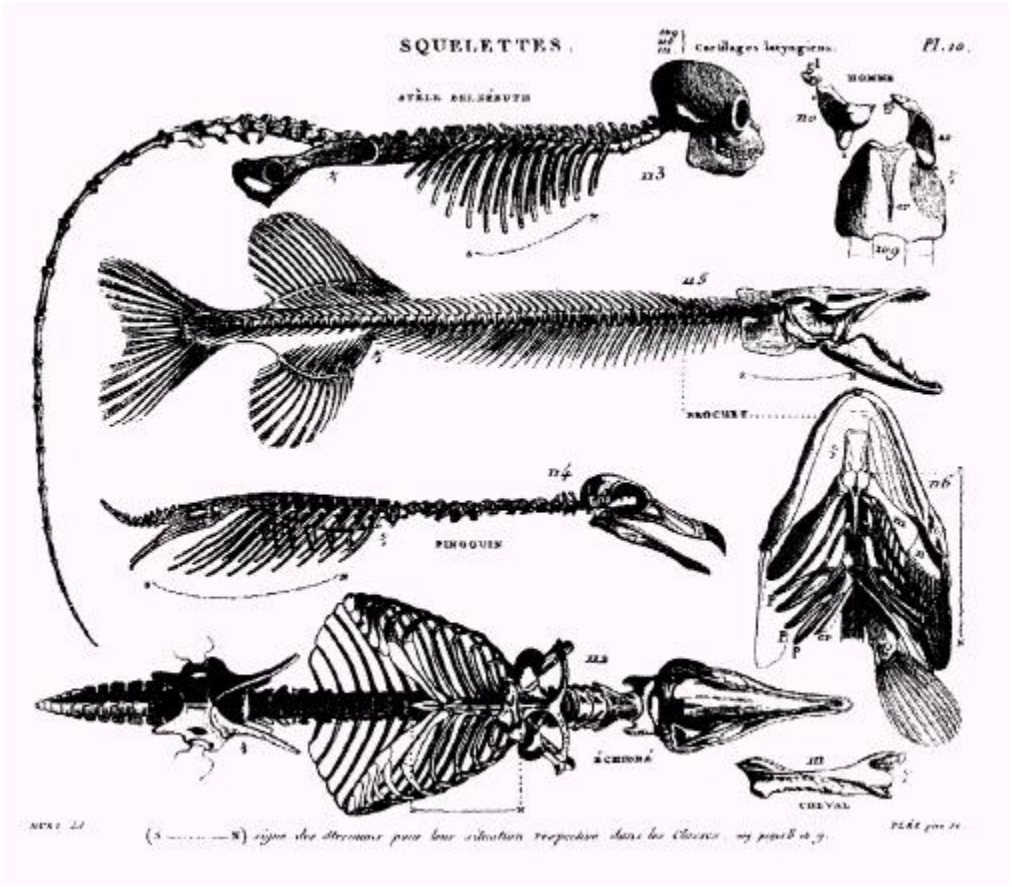

Figure 2: Table from Geoffroy Saint-Hilaire's *Philosophie anatomique* (1818)

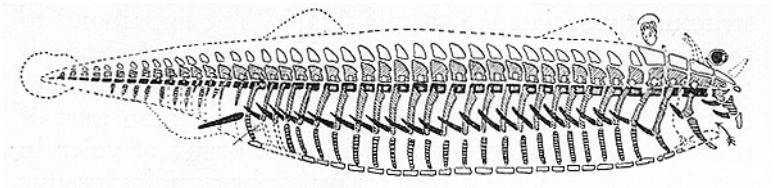

Figure 3: Richard Owen's Vertebrate Archetype (from Owen 1848)

first memoir, for instance, he showed that the furcula, the wishbone which was assumed to exist only in birds, is present in fishes as well (Geoffroy Saint-Hilaire 1807b). While the furcula in birds plays an important role for flight, it appeared to be without any function in fishes, but was still there because of nature's tendency to bring about the same structures in different species. By arguing that the function of a bone can vary from one class to another, Geoffroy made clear that homology is independent of function. A consequence for the naming of structures was that whereas previously corresponding structures from different classes had different names (because they served different functions), Geoffroy now used the same name for all structures that he deemed to be homologues (Lubosch 1931). The historian Toby Appel views Geoffroy as reacting against a traditional practice of individuating structures that used to be followed by Cuvier as well:

> Cuvier's aim was rather to exhibit the *different* structural means by which animals performed the same function. ... When bones in one class of vertebrates appeared similar and performed a similar function, Cuvier usually carried over the name from one class to the other. But when the bones in one class of vertebrates appeared sufficiently different in form and function from those in another class, Cuvier, without giving justification, used a different name. (Appel 1987, p. 86)

An elaboration and explicit defense of Geoffroy's theory was given in his masterwork, the *Philosophie anatomique* (consisting of several volumes, the first being published in 1818). Two of his basic principles are important for the present discussion. The first is the '*théorie d'analogues*', the claim that all vertebrates consist of the same number of basic building elements, i.e., homologues. Geoffroy referred to the same idea by talking about the 'unity of organic composition.'

> The forecast to which this truth leads us, that is, the presentiment that we will always find, in every family, all the organic materials that we have perceived in another: that is what I have included in my work under the designation of *Theory of Analogues*.[13]

This central idea of *philosophical anatomy* was of immense heuristic and practical value. For it motivated the search for homologies. If a zoologist studied a certain species, the 'théorie d'analogues' invited him to find structures in this species corresponding to structures in more well-known organisms, even though it was not obvious that a corresponding structure existed. Using the idea of homology made anatomists uncover a morphological unity among organisms. Geoffroy's homological research program yielded new insights about anatomical details; it permitted scientists to discover parts of organisms that had been ignored before.

> Between 1807 and 1818, philosophical anatomy with its search for homologies and symmetries threatened to displace the more traditional functional anatomy and to become the most exciting and challenging branch of comparative anatomy. Everyone, even Cuvier and his disciples, dabbled in it. (Appel 1987, p. 93)

[13]Geoffroy Saint-Hilaire, *Philosophie anatomique* (1818), Discours préliminaire. Quoted from the translation Le Guyader (2004), p. 32.

Geoffroy's other basic principle relevant for the history of the homology is the '*principe de connexions*'. It is in fact a criterion of homology, stating that what matters is the *relative position* of structures and the way in which they are topologically related to and connected with each other in an organism. Homologues in different species may vary in shape and function, but the different homologues composing a body maintain their relative position and adjacencies. In other words, different organisms that are built according to a common plan are isomorphic as regards the spatial connection of their parts. Geoffroy expresses this insight by stating that the specific shape of a structure may alter between species, or that it may be lost in some species, but the relative position will not be transposed:

> Now it is clear that the only generality to apply in the species is given by the position, the relations and the interdependence of the parts, that is to say, by what I include and designate under the name of *connections*. ... Such are the organic results, such are the physiological perspectives that can give us an idea of the law of connections and assure us against the fear of seeing its foundation sapped by exceptions: an organ is rather altered, atrophied, annihilated, than transposed.[14]

Richard Owen's later definition of homology which asserts that a homologue is the same structure in different species "under every variety of form and function" restates the idea that structures may vary in shape and function without influencing their homology. Geoffroy's homology criterion is probably the most important criterion and nowadays often referred to by the name 'positional criterion'. Figure 1 (above on p. 128) nicely illustrates the positional criterion in case of the forelimb bones in different mammals: though the shape of a homologue varies across species, its identity across species is readily discernable due to the topological relations to *other* homologues. To use another important example, muscles are virtually always connected to the same blood vessels and innervated by the same nerves — a fact that helps to re-identify these structures in other species. I mentioned above that 17th century anatomical comparisons used to take the human body as the point of reference. Geoffroy, instead, in assessing homologies and comparing species, used as a point of reference that species in which a structure was most developed, i.e., the most complex rather than vestigial instance of a homologue. This needed not be the structure in humans. For instance, in the case of the sternum, Geoffroy assumed that it was most fully developed in the tortoise, consisting of nine subparts, and he sought to trace which of these parts were present in other species and which had disappeared (Geoffroy Saint-Hilaire 1818, p. 57ff; Russell 1916, pp. 56ff). By comparing the most with the least developed instances of a structure, Geoffroy's anatomy was more aware of the variations that actually exist between different species:

[14] Geoffroy Saint-Hilaire, *Philosophie anatomique* (1818), Discours préliminaire. Quoted from the translation Le Guyader (2004), pp. 30, 32.

> Thus while comparative anatomy makes man its point of departure, and when, relying on the principle that the organs of this privileged species are more perfect, better known, and better defined, it inquires in what and how these organs are diversified, deformed, and altered in all the other animals, my new views lead me not to give preference to any anatomy in particular, but to consider the organs first where they are at the *maximum* of their development, in order then to follow them step by step to the zero of their existence.[15]

By virtue of the *principe de connexions*, Geoffroy gave a clear criterion as to how to establish homologies. His anatomical work thus contributed to establishing the idea of homology as a real concept. Geoffroy's research approach promoted further anatomical research based on this idea.[16]

The tension between George Cuvier and Geoffroy Saint-Hilaire emerged in the 1820s, when Geoffroy became increasingly bolder and speculative in his vision of the unity of animal form. His approach came to focus on the form and geometry of structures (and possibly their development), while arguing that considerations about the function of structures are as best a subordinated concern. The study of function is important for physiology, but irrelevant for anatomy. Geoffroy, together with his famous disciple E. R. A. Serres, began to study vertebrate embryology and in particular teratology — malformations in humans and animals. By attempting to homologize structures in normally developed organisms with monstrosities he treated functionally integrated and non-functional organs on a par — ignoring function at the expense of morphological unity of composition. This clearly diverged from Cuvier's functional anatomy. Previously Geoffroy had focused on vertebrate anatomy, establishing homologies between different vertebrates. In 1820, however, he began to propose homologies between the exoskeleton of insects and crustaceans and the skeleton of vertebrates. This meant no less than homologizing structures from two distinct Cuverian *embranchements* — the vertebrates and the articulates. Geoffroy's speculative vision of the unity of form made him bridge the gap between different *embranchements*, attempting to identify that which Cuvier viewed as incommensurable. This difference in scientific approach and perspective led in 1830 to the famous Geoffroy-Cuvier dispute, which was officially led in form of presentations and discussions at the Académie des Sciences until April 1830, but was also carried on unofficially in journals and the daily press. The dispute ended in 1832 with Cuvier's unexpected death.

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[15] Geoffroy Saint-Hilaire, *Philosophie anatomique* (1818), Discours préliminaire. Quoted from the translation Le Guyader (2004), p. 34.

[16] "The key to determining the ideal plan, Geoffroy showed, was to ignore the form and the function of the parts and concentrate instead on the connections between parts. Geoffroy's 'principle of connections' became, in fact, the main guide in the nineteenth century to determining homological relationships. ... Geoffroy became the chief spokesman for philosophical anatomy in France. Its key concept was that of homology. Naturalists sought homologies between the parts of different animals, homologies between the parts in a single animal, homologies between the structures in the fetus of higher animals and the adult form of lower animals, and homologies between structures in so-called monsters and those in normal animals. For the philosophical anatomists, animal organization appeared to have a constancy in the number and arrangement of parts that was independent of the form of the parts and the uses to which they were put." (Appel 1987, p. 4)

Most contemporaries took Cuvier to be the clear winner of the debate, as many of Geoffroy's fanciful speculation proved to be untenable. However, both Geoffroy and Cuvier occupied extreme positions. On the one hand, Geoffroy's claim that every organism, or at least every vertebrate, is composed out the same units was clearly wrong. Functional considerations were adduced to account for exceptions to the universal rule, but the overall idea of the unity of organic composition was too bold and unconvincing. On the other hand, Cuvier's contemporaries were aware of the existence of vestigial and rudimentary organs. In some cases it was acknowledged that a particular non-functional vestigial organ is homologous to a functional organ in a different species. Geoffroy's idea that organisms are built on a common plan offered a prima facie explanation of why vestigial organs existed, whereas Cuvier's functionalism did not provide a convincing account. As Appel (1987) points out, zoologists of the following academic generations, including many of Geoffroy's and Cuvier's disciples came to pursue an intermediate position, incorporating aspects of both approaches into their scientific practice. Despite the fact that Geoffroy's overall theory turned out to be problematic, his contributions, as already indicated, proved to be a landmark for the history of comparative biology. The homology concept and the search for homologies became part and parcel of comparative anatomy. While some historical scholarship in the past tended to contrast pre- and post-Darwinian thinking, in the last few decades some historians have pointed out the importance of pre-Darwinian anatomy for the establishment of the idea of common descent (Amundson 2005; Appel 1987; Bowler 1988; Desmond 1989; Ospovat 1981; Rupke 1994). The homological approach in anatomy led to a rejection of strict functionalism, which resonated well with the teleological-theological approach that viewed structures as being adaptation provided by the creator to supply the ecological needs of each species. Instead, homology emphasized the unity among and the natural relations between species. Later on, Darwin could build on these morphological ideas by interpreting homology as being due to common descent. Instead of assuming an abstract body plan that was modified in actual organisms due to functional considerations, Darwin could talk about the common ancestor instead of a common plan. Instead of contrasting pre- and post-Darwinian biology, it is more adequate to contrast philosophical anatomy and theological functionalism, as it points to different biological approaches and intellectual camps that co-existed and interacted in pre-Darwinian biology, and which also played a role when Darwin later used morphological evidence and the idea of common ancestry when confronting the Oxbridge natural theologians.

After the emergence of Darwinism, the homological relations between organisms were clearly viewed as being due to a natural process — genealogy. But evolutionary ideas and the notion of

descent between organisms of one taxonomic group were already present before Darwin. In pre-Darwinian comparative anatomy, homological relations between different species were viewed in different ways. Comparative anatomy before the advent of Darwinian evolution is usually called 'idealistic morphology', or 'transcendental morphology'. The current use of these labels reflects the idea that homology was viewed as an abstract geometrical relation rather than a real relation (a natural process such as descent). On an idealistic approach, a common body plan is an abstract geometric-morphological pattern, and this ideal plan is ontologically prior to any organism that actually exists. The contemporary distinction between pre-Darwinian 'idealistic' morphology and post-Darwinian evolutionary morphology is only adequate insofar as many pre-Darwinians anatomists in fact took shared body plans or archetypes to be ideas that do not actually exists in nature, but that are rather geometrical abstractions from patterns in nature (carried out by the human mind) or blueprints in the mind of the creator.[17] This appears to hold for some of the German anatomists working in the tradition of Naturphilosophie, such as Lorenz Oken. But the standard label 'idealistic' morphology has the effect of overshadowing the fact that homological relations were often viewed as real relations in nature. My discussion below will give detailed examples of non-idealistic interpretations of homology. In a nutshell, sometimes the development of animals was used as an analogy to think about natural history and the relations between different species. The early developmental stages between different species is very similar, so that development as a natural process suggested to view homology from this angle.[18] Apart from this, at least some homologies were sometimes viewed as being due to descent. The abstract body plan of a higher taxon such as a family could be viewed as the body plan of a species that actually existed in the past, and from which the extant members of this family have evolved. Thus, homologies between smaller groups of organism were viewed as being due to descent. This issue can be illustrated by Geoffroy Saint-Hilaire's later work. Geoffroy embarked on the study of embryology and malfor-

[17]The distinction between pre-Darwinian idealistic approaches and post-Darwinian evolutionary approaches was introduced before the origin of neo-Darwinism, but it played a prominent role for how neo-Darwinian biologists have reconstructed the history of biology. Ernst Mayr's (1982) dichotomy between pre-Darwinian 'typological thinking' and Darwinian 'population thinking' is an instance of this. Ron Amundson (2005) uses the label 'Synthesis Historiography' for the use of the conceptual framework of neo-Darwinism to interpret the history of biology. Synthesis Historiography originated in the late 1950s due to neo-Darwinism becoming the dominant theory of evolution, and this historiographic model was taken over by many historians of biology in the 60s and 70s. Amundson offers an account of the emergence of Synthesis Historiography and a historical critique of its adequacy.

[18]The historian Timothy Lenoir points to differences among German anatomists: "Oken's and Carus' vertebral theory of the skull are classic examples of the transcendentalist approach. This style, which led to the introduction of much mathematical mysticism in Oken's Naturphilosophie contrasts sharply with the functionalist conception employed by teleomechanists such as Kielmeyer, who stressed *forces*, interrelated *processes* and eventually developmental pattern as the basis for conceiving the type." (Lenoir 1982, p. 147)

mations. Another of his speculative ideas was to propose a teratological theory of evolution in the late 1820s. He viewed malformations as being due to external influences on the embryo and assumed that the environment was capable of directly acting on the developing fetus so that a sort of evolutionary change resulted. Consequently, Geoffroy stated that the unity of composition may at least in some cases be due to common descent. This theory of evolution was proposed for the first time in a memoir from 1825, the title of the paper indicating that the question was whether the living crocodiles "descend, by an uninterrupted route of generation, from the [fossil crocodiles] of the antediluvian ages" (Geoffroy Saint-Hilaire 1825).[19]

Ron Amundson (2005) uses the notion of 'cautious realism' to characterize the stance that many pre-Darwinian biologists took towards homological relations and the idea of archetypes and body plans. Cautious realism is the commitment to the reality of a kind of thing (a taxonomic group, a type), without pretending to understand its deeper nature. From this perspective, it is perfectly fine for a pre-Darwinian biologists to assume that homological relations are real relations ('true affinities') in nature reflecting certain laws of nature, while at the same time describing homology in geometrical terms without offering a satisfactory causal account of these laws.[20]

4.1.2 Serial Homology

So far my discussion has assumed that homology is a relation that obtains between structures of different species. However, part of the early idea of homology and the anatomy based on it was to search for morphological unity — which not only exists between species but also within an individual. The body plan of an organism has striking symmetries and it sometimes made out of the same building blocks that occur repeatedly. The body plan of many animals has a right-left symmetry so that many bodily structures exist in pairs. The right and the left arm in humans is an obvious example. Another instance of a repeated structure is the fore vs. the hind limb in tetrapods (limbed vertebrates). The human arm consists of the same bone elements as the leg, arranged in the same order. The leafs in plants and the hair in mammals are morphological structures that occur many times in an organism. Finally, in segmented animals, several segments of largely the

[19] For Geoffroy's evolutionary ideas see Appel 1987, Bourdier 1972, and Hooykaas 1963 (the latter two give a comparison with Lamarck's evolutionary theory).

[20] "The SH [Synthesis Historiography] tradition tends to label pre-Darwinian authors as anti-evolutionists (essentialists, special creationists, etc.) when they merely *fail to assert* evolution as the cause of the regularities that they studied. I will argue that many of these individuals were instead cautious realists. When we recognize cautious realism as a respectable scientific stance, we need no longer divide the nineteenth century into evolutionists and creationist-species-fixists." (Amundson 2005)

same structure occur along the anteroposterior body axis. In vertebrates, the spinal column is made of a large number vertebrae, which have largely the same structure despite difference in size and shape. The vertebrate archetype of Richard Owen (Fig. 3 on p. 139) nicely illustrates this. Owen draws vertebrae that are highly simplified and less complex than real vertebrae. His representation abstracts from variation between species, and also from the differences between the vertebrae of real organisms (compare this with Fig. 2). Thus, we get a clear sense of a vertebrate being made of the same building block — the vertebra — that occurs repeatedly along the body axis. This repeated occurrence of the same structure within one and the same individual is nowadays usually called *serial homology* (a term introduced by Owen; it is sometimes called homonomy or iterative homology as well). Thus, two structures within an organism such as the fore and the hind limb or two vertebrae of an individual are serially homologous. Anatomists in the first half of the 18$^{\text{th}}$ century usually did not have a distinct term for serial homology as opposed to homology between species. Geoffroy's term 'analogue', for instance referred to any type of homology. Due to the search for unity in nature, the idea of serial homology played a crucial role for this historical period.

Anatomists were sometimes carried away by their search for morphological unity. The notion of serial homology has such an illustrious history because it is connected with controversial attempts to homologize structures. The idea of serial homology was particularly important in the German tradition of morphology, represented for instance by Johann Wolfgang von Goethe (1749–1832), Lorenz Oken (1779–1851), and Carl Gustav Carus (1789–1869). In fact, while Geoffroy's term 'analogue' often focused on homologies between species, the German word 'Homologie' referred for the most part to serial homology. Several of the German early practitioners of anatomy were part of the Naturphilosophie movement, characterized by pantheistic ideas and the assumption of an underlying unity among the manifolds of nature. The poet-philosopher-naturalist Goethe is often credited as being the first person to come up with the very idea of homology. In 1784, Goethe discovered the intermaxillary bone (a part of skull) in humans. Despite earlier suggestions that the absence of the intermaxillary bone distinguished man from apes, Goethe assumed that vertebrates were built on an underlying plan (which he called the *Urtypus*).[21] By means of embryological studies he was able to detect the structure despite that fact that it later fuses with other bones. Goethe

[21] As mentioned, Geoffroy's work helped abandoning the practice of studying animal structures by taking human anatomy as the point of reference. Goethe made a similar contribution: "When we remember that the type to which anatomists before him had, consciously or unconsciously, referred all other structure was man himself, we see that in seeking after an abstract generalised type Goethe was reaching out to a new conception." (Russell 1916, pp. 46–47)

did not publish his ideas and only communicate them in his letters. For this reason, anatomists in France such as Geoffroy were initially not aware of these ideas. A founding document for the idea of homology, in particular serial homology, is Goethe's *Metamorphosis of Plants* (1790). Goethe's idea is that all plant structures can be morphologically reduced to a single ideal structure, the leaf. In poetic language he describes the development, metamorphosis and life-cycle of plants. He starts out with the cotyledons (the seed leafs, which are structures in the embryo of a seed plant that form a leaf after germination), which he regarded as imperfect leaves. The cotyledons were successively metamorphosed to form the sepals (that make up the calynx), the petals (forming the corolla), the stamens, and pistils under the generative influence of the ever more refined sap.[22]

The most famous, or in fact notorious, expression of the idea of serial homology was the vertebrate theory of the skull. While it is in fact the case that the skull consists of different bones that fuse during development, this theory assumed that the skull as the extension of the spinal column is in fact made up of several transformed vertebrae. Goethe proposed this idea in a letter, but it was the Naturphilosoph Lorenz Oken who first publicly announced the vertebral theory of the skull (1807). This idea was quickly picked up by others and became a hotly debated issue in France and in particular in Germany. Despite the fact that there were many proponents of this idea, individual accounts varied widely as to the number of vertebrae that were supposed to make up the skull. Oken initially proposed 3 vertebrae, but later argued for 4. Carl Gustav Carus endorsed Goethe's number: 6 (Carus 1822). Geoffroy claimed to be able to discern 7 cerebral vertebrae (Geoffroy Saint-Hilaire 1824). Lorenz Oken even viewed the idea of serial homology as applying to all main structures of the body in that he assumed that he head mirrored the whole body, i.e., the head was claimed to be structurally isomorphic to the whole animal body.

Despite the controversies and absurdities surrounding the notion of serial homology, this idea played an important role for pre-Darwinian anatomy. It was part and parcel of the study of form and the search for laws of form. As we shall see later, it continued to be relevant for some morphologists after the advent of evolutionary theory. Yet the notion of serial homology dropped out of favor in large parts of post-Darwinian evolutionary biology. The next chapter will reveal that current developmental approaches to homology take the idea of serial homology seriously again.

[22]Even though Goethe is part of the tradition usually labeled 'transcendental' morphology, that is supposed to view archetypes as mere ideas, Goethe's ideas about the metamorphosis of plants show how pervasive developmental considerations were to express the relation between homologues.

4.1.3 The Embryological Criterion

The discussion so far has focused on one main criterion of homology — the positional criterion. A peculiar and important feature of this method is that it requires the comparison of the structures of *adult* organisms only to establish homologies. The other important criterion is usually called the *embryological criterion* because it permits the assessment of homologies based on the study of the development of organisms. The comparative embryologist Karl Ernst von Baer can be viewed as having established this criterion. But before being in a position to explain this aspect of the homology concept, I first have to lay out 19$^{\text{th}}$ century ideas about the relationship between the development and the taxonomic and morphological relations of species.

Ernst Haeckel is well-known for his 'biogenetic law', that he proposed in the 1860s, being inspired by Darwin's theory. Haeckel's claim was that ontogeny recapitulates phylogeny (and that phylogeny is a mechanical cause of ontogeny).[23] Haeckel agreed with many 19$^{\text{th}}$ century evolutionists by assuming that evolution was a progressive process, leading from primitive organisms to complex species and ultimately to man. Evolution was viewed as being parallel to development, in which an undifferentiated mass of cells develops into a complex adult organism. Haeckel's theory assumed that in development an organism recapitulates its phylogenetic history in that it basically passed through the adult stages of its ancestors. Evolutionary novelties were viewed as occurring for the most part as terminal additions to a developmental sequence, i.e., ontogeny consists in a recapitulation of ancestral forms plus a final developmental event that constitutes the novel feature. In sum, this model of recapitulation assumed a parallelism between ontogeny and phylogeny, and took both to be linear processes, proceeding from the simple to the complex.

A somewhat similar model of parallelism existed some decades before the advent of evolutionary theory, though the parallel was not with phylogenetic history. Even without the idea of evolution and descent, the different groups of animals were often viewed as forming a linear sequence — from the primitive to the complex types of animals. Thus, a parallel could be viewed as holding between the development of animals and the taxonomic groups of animals, insofar as the taxonomic groups were viewed as being arranged on a complexity scale. On such a view, the development of an animal proceeds from a simple embryo to a complex adult, and the development of higher animals recapitulates the (adult) forms of the animals which are lower on the scale. One of the first to spell out the idea of recapitulation was the Naturphilosoph Lorenz Oken in his *Lehrbuch*

[23] Stephen J. Gould's *Ontogeny and Phylogeny* (1977) is the classical discussion of the idea of recapitulation.

der Naturphilosophie (1809–1811).[24] In his history of comparative anatomy, the zoologist Edward Stuart Russell (1916) called this influential idea the Meckel-Serres law, naming it after two of its most prominent proponents (and contrasting it with Haeckel's post-Darwinian model of recapitulation). Based on relatively detailed embryological observations, the German anatomist Friedrich Johann Meckel (1724–1774) defended the model in his 1811 essay "Sketch of a Portrayal of the Parallel that Obtains Between the Embryonic Condition of Higher Animals and the Permanent Condition of Lower Animals." (see also Meckel 1821–1833). In France, Etiennne Renaud Augustin Serres (1786–1868) endorsed the doctrine of recapitulation; and actually used it to defend the idea of the unity of composition of his teacher Geoffroy Saint-Hilaire. Despite Geoffroy's heroic effort to homologize the vertebrate skeleton with the exoskeleton of insects, it was relatively clear from the comparison of the adult forms of vertebrates and more primitive organisms that the idea of a body plan encompassing all animals was hard to defend. Serres, however, pointed out that comparing adult forms only may be the wrong point of reference. Instead, one has to compare the adult form of lower animals with the embryonic stage of higher organisms. Based on the idea of recapitulation, one could recover a version of the doctrine of the unity of composition that has a certain validity. Serres name for the recapitulation idea was the 'theory of arrests of development' (Serres 1824–1826, 1827). Serres and Geoffroy explained development with reference to the idea of a *nisus formativus* (formative drive), which is a force guiding the development to the final adult stage. The fact that the development of a lower animal is only an initial segment of the developmental sequence of a higher animal was explained by the claim that lower animals have less of this formative drive. Serres's theory of the arrest of development was closely tied to his study of teratology. Malformed organs were viewed as structures from an organism on a lower level of the scale of being.[25] The basic recapitulationist model was widely endorsed by pre-Darwinian naturalists.

The very idea of recapitulation along a linear scale of being was challenged by the Estonian comparative embryologist Karl Ernst von Baer (1792–1876), who worked in Königsberg. His important ideas are laid out in his work *Über Entwickelungsgeschichte der Thiere* (On the Developmental History of Animals, 1828). The first part reports von Baer's detailed observations of the chicken embryo. The second part gives his theoretical discussion on animal development, consisting of six

[24] "During its development the animal passes through all stages of the animal kingdom. The foetus is a representation of all animal classes in time." (Oken 1847, p. 45). Lenoir (1982) points out that the idea of recapitulation was present as early as 1793 in the work of Carl Friedrich Kielmeyer.

[25] A further parallel was introduced based on the succession of animals in the fossil record. Given that more complex types of organisms appear in more recent geological strata, some endorsed a threefold parallelism between embryonic development, the complexity scale of being, and natural history as represented by the fossil record (Agassiz 1859).

scholia and their colloraries. The crucial discussion takes place in Scholion V, where von Baer addresses "The dominant assumption that the embryo of higher animals goes through the permanent forms of lower animals." In a series of "doubts and objections" he offers several counterexamples to the recapitulation doctrine. Then he defends his alternative position. On his account, the early embryos of different vertebrates are hard to distinguish from each other. Later in development successive differentiation takes place in that an embryo acquires the features that characterize its order, family, and finally its species. A chick embryo can in the beginning be recognized as being a vertebrate embryo; but one cannot tell yet what kind of vertebrate it will become. A little later in development the features emerge that show that it is a bird embryo, and even later we are able to recognize that it is a chicken embryo. Thus, the picture is not that the human embryo recapitulates the forms of lower animals. Instead the human and the chick embryo have the very same development in the beginning, but then their developmental trajectories diverge. Thus, von Baer rejects a linear arrangement of different groups of animals on a complexity scale. Instead, he focuses on the hierarchical structure of taxonomy: a phylum contains several classes, each of which contains several orders, each of which contain several families, etc. Each individual has generic features that characterize it as belonging to a phylum, but also more specific features that put it in a particular family. Von Baer's claim is that the generic features develop first, while the more specific features develop subsequently. Thus, we have a parallel between development and the hierarchical organization of taxonomy. It is not the case that the embryo of a higher animal resembles the adult of a lower animal; instead, only their embryos are similar. Von Baer summarizes his position in form of four laws, which later came to be called von Baer's laws. It is a law of individual development

> 1) That the general features of a larger group of animals develop prior to the specific features in the embryo. ... 2) Out of the most general structural relations develop the less general, and so forth, until the most specific ones appear. ... 3) Every embryo of a particular type of animal — instead of going through the forms of other particular types — diverges from the others. 4) Thus, in principle the embryo of a higher type of animals never equals another type, but only its embryo. (von Baer 1828, p. 224; my translation)

From the modern point of view, von Baer's work is so important as because his divergence model of comparative development is much closer to the truth than the traditional idea of linear recapitulation, which actually became even more influential after the advent of Darwinism primarily by the work of Ernst Haeckel. A recent refinement of von Baer's ideas is the 'hourglass model' (Sander 1983; Elinson 1987; Collins 1995; Duboule 1994; Raff 1996; Sander and Schmitt-Ott 2004). This contemporary hypothesis diverges from von Baer's in that it became clear that animals of one group may differ in the very first steps of development. The hourglass model assumes that the

organisms from each phylum develop in the following way. In the very beginning of development, different organisms from a phylum are somewhat dissimilar. In the first stages of development these different embryos become more and similar, until they start to diverge during the rest of development (in accordance with von Baer's model). Apart from this, von Baer's rejection of a linear scale of being and his model of development as successive divergence reminds the contemporary biologist of the branching pattern of evolution as it is understood nowadays (in contrast to linear and progressive models of evolution popular in the 19$^{\text{th}}$ century). Von Baer's theory not only embodies a claim about the comparative development of organisms, but von Baer himself argued that his approach has implication for how to classify organisms. In the third and fourth corollary to the scholion that defends his model, von Baer argues that we need a "Classification of animals according to their mode of development." Instead of classifying animals primarily based on their adult morphology, the development yields important clues for a classification of animals into natural groups, as the developmental divergence corresponds to the taxonomic organization.

Like other comparative anatomists in his days, von Baer uses the notion of a type or a body plan that is characteristic for a larger animal taxon. He defines the *Typus* as the "relative position [Lagerungsverhältnis] of the organic elements and the organs" (1828, p. 208). He views types as hierarchically structured into main types (*Haupttypen*), such as the vertebrate type, and subordinated types (*untergeordnete Typen*), such as the bird type, proceeding from the phylum to species level. Von Baer's defense of his alternative model is actually based on the concept of a type. He states that it is not the case that the development of a higher animal passed through the main types of lower animals, instead, its main type is fixated from the early stages of development. The main type develops first, and subsequently the subordinated type develops (pp. 219ff). In his history of morphology *Form and Function* (1916), the zoologist Edward Stuart Russell appears to imply the existence of three historical phases as to how types or archetypes have been viewed. The first is the idealistic approach that defines an archetype as an abstract geometric pattern that need not actually exist in nature. The second phase emerged with the work of von Baer, who as we have seen, used the study of development to detect the type of an organism: "Von Baer set morphologists looking for the archetype in the embryo, not in the adult alone" (Russell 1916, p. 132). In addition, the relations between superordinated and subordinated types were viewed as genuine relations in nature, which occur due to the operations of the laws or principles of development. The third step was made by Darwin when he viewed the archetype as the common ancestor, where the natural relations between archetypes (ancestors) are taken to be phylogenetic relations (p. 235). To be sure,

one should not construe Russell's three phases as consecutive and separate chronological phases, but Russell is right in that he lists the possible theoretical ways in which types were viewed, though several of these viewpoints were combined by most zoologists.

So far my discussion of von Baer's works has not mentioned yet the homology concept. The digression was necessary to understand von Baer's perspective on homology. In the *Entwicklungsgeschichte*, no special term is used to refer to homology. Instead, von Baer simply talks about the 'sameness' of organs in different groups of animals. The section that deals with the individuation of characters and thus the homology concept is quite short (1828, pp. 233–237). For von Baer's position on how to determine homology immediately follows from his overall model of comparative development: it is the second corollary to Scholion V (the latter criticizing of recapitulation).

> Since every organ is what it is only through its mode of development, its true value can only be recognized from its mode of formation. At present we usually judge based on a vague intuition, instead of viewing each organ merely as a distinct product of its fundamental organ, and discerning from this viewpoint the correspondence and difference of the different types. (von Baer 1828, p. 233; my translation)

Given two species of the same phylum, their initial segments of development are identical as they belong to the same general type. Then divergence occurs and the features of the embryos differentiate to form adult structures. Von Baer's idea is that we determine whether two adult structures in two species are the homologous by tracing the development of these structures back to its embryonic precursors, up to the point where the embryos of the two species are so similar that it is obvious whether the two precursors are actually the same ones in the type represented by the embryonic stage. In short, homologous structures have the same development in that they develop *out of the same developmental precursor* in the embryo. One of von Baer's main applications of this idea is the question whether parts of the nervous system of vertebrates and segmented animals such as insects are homologous (p. 234). Vertebrates and segmented animals (articulates) belong to different Cuverian *embranchements*, thus they belong to different types and have different body plans. For this reason, von Baer denies that the ganglions on the ventral side of insects are homologous to any part of the spinal cord of vertebrates. For the spinal cord develops from the neural tube that only the vertebrate type possesses. The same situation applies to the question whether we should call the most anterior ganglion pair in insects a 'brain'. Von Baer states that such a terminological decision may depend on how we choose to use the word 'brain', but in any case these insect ganglions "are definitely not *that organ* which we call a brain in vertebrates, for the latter is the anterior end of the neural tube, which is lacking in segmented animals."[26] Furthermore, von Baer's theory implies

[26] von Baer 1828, p. 234; my translation, von Baer's emphasis.

that the individuation of characters is independent of their function. Even though the same word is commonly used for insect wings and bird wings, zoologists are well aware of the fact that the 'wings' in insects and the 'wings' in birds are different structures. What determines the identity of morphological structures is not their function, but their mode of development:

> Other bodily parts teach us in a more obvious fashion the fact that every part can only be understood based on its relation to the type and its development out of it. The tracheae of insects certainly are organs that conduct air, but they are not the organ that we call the windpipe in vertebrates, as the latter develops from the mucous membrane [Schleimhautröhre], whereas the tracheae of insects have to be formed either by histological differentiation or by invagination of the outer skin.
>
> Sometimes people have used the same word for different organs in absence of another word, acknowledging at the same time the difference. For instance, no anatomist has ever identified the insect wings with the wings in birds. (von Baer 1828, p. 236; my translation)

The idea that homologous structures develop out of the same precursors is nowadays commonly called the *embryological criterion* of homology. To some extent it was implicit in former anatomical practice in that the study of development was used as a guide to determine homologies. Geoffroy Saint-Hilaire's original success was among other things due to the fact that he was able to discover new bone segments in the skull of vertebrates. Bones are formed from characteristic centers of ossification and may later fuse into larger segments. Despite the fact that the adult skull of fish has more separate bones than the mammalian adult skull, Geoffroy was able to show that the skull in both animal groups is actually made up of the same bones by discovering additional bones in the mammalian fetus where they are still separated (Geoffroy Saint-Hilaire 1807a). While prior to von Baer the study of the development had been used as a guide for determining homologies, von Baer's specific contribution is to make explicit and defend this criterion of homology. Moreover, his divergence model of the development of different species gave a justification of why the embryological method is an appropriate guide to homology. This justification of the embryological criterion is based on an explanation of the nature of homology that appeals to natural processes: homology originates with (and is constituted by) the regular and law-governed process of development. Von Baer's embryological approach was immediately picked up by prominent anatomists and physiologists such as Heinrich Rathke (1793–1860), Johannes Müller (1801–1858), and Rudolph Wagner (1805–1846). The historian Timothy Lenoir states of this embryological school which he calls 'developmental morphology' that

> Through the distinction between 'analogous' and 'homologous' structures von Baer, Rathke, and Müller defined the valid limits of application of the embryological criterion and its importance was underscored for determining the interrelations between different groups of organisms. (Lenoir 1982, p. 54)

While I used von Baer's work to introduce the embryological criterion, its use was not necessarily

contingent on endorsing von Baer's divergence model of comparative development. Even traditional recapitulationism permitted the use of an embryological method. If the assumption is that in development a higher animal goes through the adult stages of lower forms, then we also have a correspondence between the structures of the higher animal (as present at different stages of development) and the structures of the lower animals. Thus, embryological studies could also be used as a guide to homologies by recapitulationists.

In the course of the 19$^{\text{th}}$ century, the embryological criterion became developed further based on the germ layer theory. Using modern terminology, every animal with differentiated tissue has three distinct types of embryonic tissues, the so called germ layers. The three germ layers form in early embryogenesis at a stage called gastrulation. The ectoderm is the outer covering of the embryo; the entoderm lies under the ectoderm and forms the lining of the primitive gut cavity (see Fig. 5 on p. 186). The mesoderm develops as a middle layer between the ectoderm and the entoderm.[27] The germ layers differentiate further to form the different types of tissue and the organs in the embryo. For instance, the skin and the nervous system are made of ectoderm. The epithelium of the prostate, the urinary bladder, and the urethra are derived from the entoderm. The mesoderm forms the connective tissue, teeth, and blood, among other things. Building on prior studies (such as the observations of Caspar Friedrich Wolff), the first main steps towards the germ layer theory were taken by Christian Pander, who distinguished in 1817 different types of embryonic tissues in the chicken embryo. Karl Ernst von Baer and Heinrich Rathke generalized these ideas, by distinguishing different layers in other animals and studying their development. In the 1850s Robert Remak and others refined this theory by introducing the modern terminology and the conception of the existence of exactly three distinct germ layers. Based on the germ layer theory of development, the embryological criterion implies the claim that homologous organs in different species develop from the same germ layer (a necessary criterion for homology).

4.1.4 Richard Owen: Naming and Homology

As far as the history of the biological practice based on the homology concept is concerned, its pinnacle before the advent of Darwinian evolutionary theory was the work of the British anatomist

[27] More precisely, among the animals with differentiated tissue (Eumetazoa) the sponges as the most primitive ones have only two germ layers, the ectoderm and the entoderm. All other (higher) animals have three germ layers.

Richard Owen (1804–1892).[28] Owen started his scientific career in 1828 as a lecturer in comparative anatomy at St. Bartholomew's Hospital in London. His first prestigious appointment was in 1837 as the first permanent Hunterian Professor, at the age of 32. The Hunterian Collection was an anatomical collection bought by the Crown in 1799 from John Hunter and left to the Royal College of Surgeons in London. Originally, college fellows gave anatomical lectures using the Hunterian Collection on a rotating scheme. Owen becoming a permanent Hunterian lecturer coincided with the reopening of the enlarged Hunterian Museum, so that Owen's first Hunterian lectures were attended by many members of London's intellectual and political establishment (Owen [1837] 1992). Owen was employed at the Royal College of Surgeons until 1856, and was created Knight of the Legion of Honour in this period. In the 1850s Owen became the most eminent naturalist in Great Britain. In 1856 he was appointed the first superintendent of the natural history collections at the British Museum, and in 1859 he became in addition Fullerian professor at the Royal Institution.

Originally, Owen's research approach was in to a large degree in line with Cuvier's functionalism. Owen's functionalist research secured him support by the Oxbridge naturalists such as William Buckland who were closely tied to the tradition of natural theology and emphasized the way in which the creator had equipped individual species with organs functionally adapted to the ecological role. In fact, Owen was even advertised as the 'British Cuvier'. However, from 1843 onwards, his research approach shifted towards the homological research program as previously championed by the proponents of philosophical or transcendental anatomy. Owen was influenced by French researchers such as Geoffroy Saint-Hilaire and by German anatomist such as Lorenz Oken and Carl Gustav Carus. Among other things, this shift becomes clear from the organization of Owen's lectures. Originally, his lectures tended to proceed from one organ system (whose working was explained in different animal groups) to another organ system. In the 1840s, Owen's lectures were organized taxonomically, discussing different animal groups such as invertebrates as opposed to vertebrates in turn. This way of lecturing reflects a shift from individual organ and organic function to the total organization of the animal and its body plan.[29] In his 1841 lectures, Owen had favored von Baer's model of comparative development over the standard theory of recapitulation,

[28]For a scientific biography of Owen see Nicolaas Rupke's *Richard Owen: Victorian Naturalist* (1994). See also Woods (1995), Camardi (2001), and Phillip Sloan's introductory essay to Owen) ([1837] 1992).

[29]The organization of the Hunterian collection, on which Owen had to rely for his lectures, was not completely congenial for a Cuverian approach anyway. Cuvier's *Cabinet d'Anatomie Comparée* at the Paris *Muséum d'Histoire Naturelle* reflected Cuvier's functionalism in that each particular species was displayed first in its skeletal system, and then its muscular, internal, nervous and reproductive systems was dissected out in the same display. The Hunterian collection, however, was organized according to organ systems, showing an organ system such as the nervous system for different animal groups. Thus, this collection was more congenial for a comparative approach than Cuvier's.

thus viewing development proceeding from the undifferentiated to the differentiated and from the general to the specific. Later, he applied the same idea to the succession of fossils, arguing that the progress visible in the fossil record is best viewed as a branching or radiating pattern from the more general to the more specific (Rupke 1994). In the late 1840s, the general pattern that is shared by a type of animals was no longer viewed by Owen in terms of development — as an embryo or a particular embryonic stage. Instead, he conceived of the general pattern in terms of an abstract body plan by introducing his theory of the vertebrate archetype (see Fig. 3 above on p. 139 for pictorial representation of Owen's archetype). Owen initially laid out his new idea on homology and the vertebrate skeleton in a 1846 report to the British Association for the Advancement of Science, entitled "Report on the Archetype and Homologies of the Vertebrate Skeleton." This account was later reprinted in the book *On the Archetype and Homologies of the Vertebrate Skeleton* (Owen 1848; on his notion of the archetype see Rupke 1993). Nicolaas Rupke (1994) explains the change to a new approach based on the fact that the homological approach of transcendental anatomy became popular among anatomists in London (in contrast to Oxford and Cambridge).[30]

Richard Owen was not the first to clearly distinguish between sameness of morphological structure and sameness of function, but as mentioned at the beginning of this chapter, but he was the first to use two distinct terms for these two relations: 'homology' and 'analogy'. Owen's definition quoted above (p. 129) is the first time he publicly used this terminology, it is from the glossary of his 1843 "Lectures on the Comparative Anatomy and Physiology of the Invertebrate Animals" (see also 1848, p. 7). Because of its importance I restate Owen's definition, quoting from a later work:

> A 'homologue' is a part or organ in one organism so answering to that in another as to require the same name. Prior to 1843 the term had been in use, but vaguely or wrongly. 'Analogue' and 'analogy' were more commonly current in anatomical works to signify what is now definitely meant by 'homology.' But 'analogy' strictly signifies the resemblance of two things in their relation to a third; it implies a likeness of ratios. An 'analogue' is a part or organ in one animal which has the same function as a part or organ in another animal. A 'homologue' is the same part or organ in different animals under every variety of form and function. (Owen 1866, Vol. 1, p. xii)

Owen gives the following nice illustration of the difference between homology and analogy or between structure and function, using as an example the flying lizard *Draco volans*, which has a

[30] "Owen's change of emphasis from 'function' to 'form' was never a change of heart, but reflected primarily a change of opportunity. There is no evidence of an intellectual conversion, let alone a sudden one. He knew about and was sympathetic to both positions from the start of his career. The degree to which he pursued one rather than the other approach corresponded—I believe—to the opportunities that each provided for broadening his institutional power base. By the middle 1840s, when Owen began preparing his report for the BAAS on the vertebrate archetype, he was riding a rising tide of metropolitan interest in the transcendental approach." (Rupke 1994, p. 182). This fits with Desmond's (1989) historical study, which argues that the standard focus on the debate between the Darwinians and the Oxbridge creationists distracts from the important intellectual changes among London anatomists and naturalists in the years before Darwin published his new theory.

parachute attached between its forelimbs and the body:

> In the *Draco volans* the fore-limbs are 'homologous' with the wings of the bird; the parachute is 'analogous' to them. (Owen 1866, Vol. 1, p. xii)

Apart from this very distinction, Owen emphasized the limits of a Cuvier-style functionalist anatomy. One of his examples is the skull in mammals. The skull of the human fetus consists at the time of birth of twenty-eight bones which are still separated. A traditional teleological explanation for this fact is the idea that the fetal skull should not be rigid to ensure that it can change shape when passing through the vagina. However, such an explanation can apply only to placental mammals. Other vertebrates have the same number of ossification centers from which the skull develops, but they do not need a flexible skull for birth. In this case, the homological approach and the notion of a vertebrate archetype — a refined version of Geoffroy's principle of the unity of composition — offers a better explanation for the structure of the mammalian skull. Owen summarizes the discussion of such examples by stating that "These and a hundred such facts force upon the contemplative anatomist the inadequacy of the teleological hypothesis . . . " (Owen 1848, p. 73).

> 'Homological Anatomy' seeks in the characters of an organ and part those, chiefly of relative position and connections, that guide to a conclusion manifested by applying the same name to such part or organ, so far as the determination of . . . homology has been carried out in the animal kingdom. This aim of anatomy concerns itself little, if at all, with function, and has led to generalisations of high import, beyond the reach of one who rests on final causes. (Owen 1866, Vol. 1, p. vii)

Owen actually distinguished between three particular types of homology. *Special homology* is the type of homology to which the mere term 'homology' refers most often. It is the above stated relation between two structures in different species. *General homology* is the relation between a particular structure in a species and the corresponding structure in the archetype. Finally, like the French and in particular German anatomists, Owen uses the idea of *serial homology*. The term 'serial homology' was actually coined by Owen to refer to this particular type of homology that designates the same structure within one individual. Owen defined serial homology as the repeated occurrence of essentially similar segments along the body axis.[31] The prime example is the series of individual vertebrae which are serially homologous to each other. Owen's vertebrate archetype (Fig. 3) illustrates the idea of serial homology nicely, as the different vertebrae in the pictorial representation of the archetype hardly differ. Owen assumed an 'ideal typical vertebra' (Fig. 4), a sort of structurally simplified individual vertebra, such that each vertebra in a real organism is a more complex modification of the ideal typical vertebra, where modifications are due to the

[31] Serial homology, just like special homology, was viewed as an expression of unity in nature: "The extent to which serial homologies can be determined shows the degree in which vegetative repetition prevails in the organisation of an animal." (Owen 1866, Vol. 1, p. xiii)

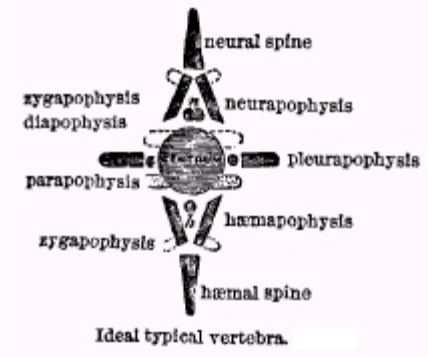

Figure 4: Owen's Ideal Typical Vertebra (from Owen 1866, Vol. 1)

different functions different vertebrae along the body axis (or in different species) fulfill.

> I have satisfactorily demonstrated that a vertebra is a natural group of bones, that it may be recognised as a primary division or segment of the endoskeleton, and that the parts of that group are definable and recognizable under all their teleological modifications, their essential relations and characters appearing through every adaptive mask.[32]

Apart from theoretical work, an important achievement of Owen was the laborious naming of the bones of the vertebrate skeleton and the unification of previously used terminology. Even though other anatomists working with the homological program had discovered new bones and traced their homologies, the naming schemes used were far from simple and unified. Anatomists from different research schools used different names for the same homologue. Sometimes long descriptive names were used that paraphrased the position of a bone relative to others. For instance, Cuvier called a particular bone of the skull 'la caisse' in crocodiles, 'os tympanique' in lizards, 'os carré' in birds, and 'caisse ou partie tympanique du termporal' in mammals. Geoffroy used the name 'énostéal' in crocodils and 'tympano-styloïd' in birds. The German anatomist Eduard Hallman used a different name for it and Friedrich Meckel and Rudolph Wagner still another. The German anatomist Thomas Samuel Soemmering called it 'lamina ossea ossis temporis a qua meatus auditorius externus oritor'. Richard Owen simply introduced the name 'tympanic' for this homologue across different vertebrates. Based on his homological theory, Owen introduced short and adequate names for each homologue, and wrote tables of synonyms that listed the different names of a bone as used by him and prior anatomists. Most of the names for bones of the vertebrate skeleton suggested by Owen are still used nowadays.

As already mentioned, at the beginning of his career Owen made use of von Baer's ideas.[33] Con-

[32] Owen 1849b, p. 41; quoted from Rupke 1994, p. 167.
[33] On Owen's use of von Baer's ideas see Bowler (1988), Ospovat (1976, 1981), and Rupke (1994).

sequently, he endorsed his embryological criterion of homology. In his first Hunterian lectures, Owen used the ideas of the developmental school in Germany (von Baer and Rathke) to argue against the speculations of the transcendental school, including Geoffroy Saint-Hilaire (Owen [1837] 1992, pp. 191f). Rupke interprets these statements as "Cuvierian window-dressing which hid from sight his real fascination with Geoffroy's ideas about the unity of type" (Rupke 1994, p. 176). In any case, even though Owen may have initially made use of the embryological criterion of homology, it was definitely not an entrenched part of his research praxis (MacLeod 1965). Owen initially conducted some embryological observations, but for the most part he relied on the material available in the Hunterian collection, which primarily contained adult specimens. Several passages show that a decade later Owen viewed the embryological as being subordinated to the positional criterion:

> There exists doubtless a close general resemblance in the mode of development of homologous parts; but this is subject to modification, like the forms, proportions, functions, and very substance of such parts, without their essential homological relationships being thereby obliterated. These relationships are mainly, if not wholly, determined by the relative position and connection of the parts, and may exist independently of form, proportions, substance, function and similarity of development. But the connections must be sought for at every period of development, and the changes of relative position, if any, during growth, must be compared with the connections which the part presents in the classes where vegetative repetition is greatest and adaptive modification least.[34]

Owen actually argued that there are cases where homologous structures develop in a different way:

> Parts are homologous, in the sense in which the term is used in this work, which are not always similarly developed: thus the 'pars occipitalis stricte dicta,' etc., of Soemmering is the special homologue of the supraoccipital bone of the cod, although it is developed out of pre-existing cartilage in the fish and out of aponeurotic membrane in the human subject. (Owen 1848, p. 5)

Whereas von Baer had claimed that development determines the identity of structure, Owen denied this and viewed instead the topological relations and connections as the defining features of homology. Once Owen had developed his theory of the vertebrate archetype his approach resembled the theory of Geoffroy. Given the archetype, homology could be read off and there was no need to study the development of different species:

> But no clue is afforded to the signification of these several centres [of ossification]: embryology is no criterion of their homologies; these are determinable on other grounds or 'ways of anatomy.' ...
>
> Embryology affords no criterion between the ossific centres that have a homological' and those that have a 'teleological' signification. A knowledge of the archetype skeleton is requisite to teach how many and which of the separate centres that appear and coalesce in the human, mammalian, or avian skeleton, represent and are to be reckoned as distinct bones, or elements of the archetype vertebra. (Owen 1866, Vol. 1, pp. xxiv–xxv)[35]

[34] Owen 1849b, p. 6; quoted from Russell 1916, pp. 107–108. Russell mentions C. G. Carus as another anatomist that viewed the embryological criterion as an aid, but subordinated to the positional criterion (p. 167).

[35] The mature Owen was prominently criticized for not taking the embryological method seriously enough. Thomas Henry Huxley, in his 1858 Croonian lecture "On the Theory of the Vertebrate Skull" rejected the vertebral theory of the skull as one of the best-known and most controversial theories of transcendental anatomy. Huxley primarily used embryological evidence for undercutting this theory, and Owen was an explicit target of this critique.

Due to the fact that Owen used the notion of an archetype, he is often put into the box labeled 'idealistic' morphology. E. S. Russell's (1916) history of morphology, for instance, proceeds by discussing Goethe, Geoffroy and the German transcendentalists. Only after the chapter "Transcendental anatomy in England – Richard Owen," does Russell begin to discuss von Baer and the embryological tradition. Richard Owen's notion of an archetype denotes an abstract body plan rather than a concrete organism; and it is sometimes assumed that Owen and other morphologists viewed types or archetypes as Platonic ideas (Haupt 1935; Desmond 1989; Kitcher 1993). This assumption is not completely unfounded in that Owen himself suggested this interpretation of the archetype. In the 1850s, Owen mentioned at a few places that the archetype exists prior to the concrete species that fall under it, and that it helps to understand the notion of a Platonic idea (Owen 1849b, 1855). Thus, the archetype appeared to be construed as a sort of Platonic idea in the mind of the creator. However, Owen's own usage of the concept of the archetype hardly fits with its reading as a Platonic idea. For a characteristic feature of a Platonic idea is that it is the highest reality; it is more perfect than any empirically existing, concrete instantiation of it. Owen's archetype is the opposite of this — the vertebrate archetype is in fact less perfect and complex than any existing vertebrate. It actually resembles a primitive vertebrate such as a fish and is not as all like man as the most perfect vertebrate (see Fig. 3 on p. 139). Owen's archetype concept assumes that we obtain the morphological structure of an existing vertebrate species by adding complexity to the archetype. For instance, the vertebrae of the archetype are very simple and resemble each other to a large extent. In a real organism, however, the vertebrae as occurring at different parts of the skeleton have different functions and thus have must have a different size and shape. The archetype denotes unity among morphological structures within an organism and between species, but functional and ecological demands require a divergence of structures so that morphological differentiation and an increase in complexity results.

Nicolaas Rupke (1993, 1994) gives a detailed discussion of this issue, offering an explanation of why Owen came to make the contradictory suggestion that the archetype is a Platonic idea. Originally, Owen actually contrasted the archetype with a Platonic idea, by arguing that an organic body develops by means of two forces (Owen 1846, 1848). The 'general and all-pervading polarizing force' accounts for the repetition of parts and the unity of organization. The archetype expressed the existence of this force. The 'adaptive or special organizing force', in contrast, produces specific modification and adaptation. This latter force was associated with Platonic ideas, as a vital force creating diversity between species. Thus it is not the case that Owen viewed the archetype and

the relation of homology as nothing but geometric and immaterial principles. Whereas the Naturphilosoph Lorenz Oken may have viewed the notion of homology as an immaterial relation (despite his developmental language), Owen himself understood Oken's account of the transformation of one form into another in an evolutionary sense (Owen 1858). The picture of the two forces has some similarity to the two principles of evolutionary theory to which I pointed at the beginning of the chapter — inheritance of structures by descent and modification by natural selection (see p. 130). Owen's all-pervading polarizing force explains what Darwin later called the 'unity of type', and the adaptive or special organizing force explains the fact that organisms are adapted to their environment, what Darwin called the 'conditions of existence'. In fact, whereas Owen is sometimes assumed to be a creationist (because of his later critique of the mechanism of natural selection), Rupke points out that "Over a period of some four decades, from the mid-1840s to the mid-1880s, Owen explicitly and repeatedly expressed — in articles, monographs, a textbook and letters — his belief in a natural origin of species." (Rupke 1994, p. 220).[36] Owen used embryological examples, in particular asexual reproduction and parthenogenesis, as a guideline to think about evolution. Aphids switch between a sexual and asexual mode of reproduction. The larva produced sexually is wingless and can reproduce asexually. After some asexual generations, females and winged males develop. The important point for Owen's evolutionary approach is the fact that a winged form suddenly develops out of a wingless form. Owen's picture was that after several generations a new species might emerge. This process of evolution is not driven by external factors (such as natural selection), but by developmental potentials and factors inside the organism (1849a). Owen clearly assumed the operation of secondary causes that accounted for the emergence of new forms, though his statements were embedded in theistic rhetoric (1849b). Rupke gives the following explanation of why Owen *later* rendered the archetype as a Platonic idea. German Naturphilosophie and transcendental anatomy were generally associated with pantheism. Owen had to ensure that his homological research approach was not viewed as promoting pantheist religion. He actually received explicit advice as to how to reinterpret the archetype in a Christian, Neoplatonic fashion: the cleric and geologists William Daniel Conybeare suggested it in a letter to Owen (Rupke 1993).[37]

[36] For Owen's evolutionism see also Bowler (1988), Camardi (2001), and Richards (1987).

[37] The discussion so far has made extensive use of the notion of a type or other terms used to refer to a body plan shared by larger groups of organisms (archetype, general type, Urtypus). Due to the emergence of the neo-Darwinian theory of evolution, the very idea of a type became suspect in the last few decades. The accusation is that pre-Darwinian biologists were under the spell of 'typology' or 'essentialism'. The most well-known form of this idea is the prominent dichotomy between 'typological thinking' and 'population thinking' coined by the neo-Darwinian biologist Ernst Mayr (Mayr 1959a, 1963, 1968, 1982). While taking pre-Darwinians as typological thinkers has been the prevailing view in the last three decades (at least among biologists and philosophers of biology), in recent years historians of biology have debunked the essentialist story (Atran 1990; Stevens 1994; McOuat 1996; Amundson 1998;

4.2 A SEMANTIC CHARACTERIZATION OF THE HOMOLOGY CONCEPT USED BEFORE 1859

Given the above review of the history of the homology concept before the advent of Darwinian evolutionary theory, I now summarize these results and offer an account of the content of this concept used in this period. In accordance with my semantic framework, I focus on 1) the homology concept's inferential role and 2) the epistemic goals pursued by the concept's use. In the subsequent sections of this chapter I shall discuss the history of the homology concept from 1859 until 1950, using the historical stability as regards these two components of content — inferential role and epistemic goal — to argue that the homology concept used by most biologists in this period is in fact the same concept as used in pre-Darwinian biology. (Due to this historical continuity, Section 4.4 will briefly restate the present characterization of the homology concept, while focusing on the argument that the homology concept used until 1950 is not different from the concept used in pre-Darwinian biology. This section will also explain why the adoption of a post-Darwinian theoretical account of homology — a change occurring internal to the concept — was indeed rational.)

We saw how the homology concept originated in comparative anatomy. When terms referring to homology (such as 'analogue' in France and 'Homologie' in Germany) were originally introduced, the homology concept was not explicitly defined based on a clear and elaborated theoretical account of this notion. Instead, the concept gained its implicit content to a large degree from how it was used in biological practice and how it was applied to certain standard instances (exemplary homologues

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Müller-Wille 1999; Camardi 2001; Winsor 2003). I mention only two problems with the neo-Darwinian critique of the notion of a type (for a detailed discussion see Amundson 2005). First, typological thinking is often equated with creationism, assuming that types were viewed as nothing but blueprints in the mind of the creator and that the structure of organisms was explained only with reference to metaphysical or religious notions. However, in the above discussion we saw that types have usually been viewed as real patterns in nature reflecting causal laws, prominently developmental principles. Second, while the idea of 'population thinking' is to stress the variation *within* a species, morphological theories were not in contradiction with this as they were not concerned with this issue. Morphology is about the relation *between* species and higher taxa, and a type represents relations between species (e.g., what different species have in common, an idea that is fundamental to contemporary phylogenetic systematics using the notion of 'synapomorphies'). Thus, typology as practiced is compatible with modern population thinking.

Even though many neo-Darwinian evolutionary biologists viewed the very idea of a type as discredited, 20$^{\text{th}}$ century morphologist and paleontologists continued using it (Davis 1949; Jacobshagen 1925; Kälin 1941; Kuhlenbeck 1967; Lubosch 1931; Løvtrup 1974; Naef 1919; Remane 1956; Riedl 1978; Schindewolf 1950; van der Hammen 1988; Voigt 1973; Waddington 1957; Zangerl 1948). Apart from the tradition in morphology, in the last decade the notion of a type became more reputable due to the emergence of evolutionary developmental biology as a new biological discipline (see Section B). One of the main goals of evolutionary developmental biology is the explanation of the origin of body plans (Arthur 1997; Wagner, Chiu, and Laubichler 2000). Consequently, notions that are related to the morphological type concept such as 'phylotype', 'zootype', 'body plan', and 'Bauplan' abound in the recent evo-devo literature (Budd 2003; Cohen 1993; Collins 1995; Collins and Valentine 2001; Duboule 1994; Fitch and Sudhaus 2002; Hall 1998; Minelli 2003; Niklas 2003; Panchen 2001; Raff 1996; Richardson 1995; Richardson, Minelli, and Coates 1999; Slack, Holland, and Graham 1993; Slack 2003; Wagner and Laubichler 2004; Wilkins 2002).

such as the vertebrae in the case of serial homology). On the level of biological practice, the idea of homology emerged implicitly by changing traditional practices as to how to name biological structures. Whereas previous practice had amounted to an individuation of structures based on structural and functional similarity, anatomists realized that the same structure could occur in larger groups of organisms despite difference in functional and overall shape of a structure. The realization of structural unity among relatively large groups of organisms led to a shift in naming practices that came to be based on topological (relative position) and embryological considerations but on not functional features. Apart from the way in which the homology concept was used in anatomical practice, it gained from early on its content in a more explicit fashion by being embedded in a basic theoretical framework. The notion of homology was often explicated based on the idea of a structural type, a body plan being shared large groups of organisms. Geoffroy argued for the idea that all organisms belonging to the same type have exactly same set of structures, and based on Owen's vertebrate archetype, homology can be characterized by the idea that two structures in different species are homologous if they correspond to the same structure or position in the archetype. Another feature that made homology a theoretical concept with a clear content was the fact that from early on explicit criteria of homology were put forward. Geoffroy made public use of the homology concept at the same time he argued for his 'principe de connexions', the positional criterion. Von Baer did not use the term 'Homologie' in his early work, but offered a clear account of how to individuate characters based on his divergence model of comparative development, yielding the embryological criterion as an explicit part of the homology concept.

My first task is to explain what I view as the *inferential role* (conceptual role) of the homology concept. Among the inferences made by biologists when using the term 'homology', those inferences have to be laid out that I conceive of as constitutive of possessing this concept. Not every inference in which the term 'homology' occurred and that was used by some biologist is meaning-constitutive. I surely have to abstract from some idiosyncratic views about homology, to ensure that most anatomists actually shared this concept. However, even though it is a legitimate philosophical demand that concepts are shared between persons, the semantic aim of delineating a homology concept by itself is not to vindicate the idea that basically one homology concept was used in comparative biology. The guideline to get at the inferences characterizing the homology concept is as follows. In Chapter 3 I suggested that one central aim of a theory of concepts is to explain how a concept makes successful practice possible, and that this consideration bears on concept individuation (Section 3.3.3). As a result, my account of what inferences characterize the homology

concept is based on those aspects of the usage of this concept that were entrenched in biological practice and that were fundamental for the biological significance of this concept. Given that the establishment of the homology concept marked crucial scientific progress, my guideline is to exhibit the epistemic virtues embodied by this new concept, i.e., to spell out those aspects of the homology concept's use that account for the novel successful biological practice based on this concept. It turns out that given this philosophical reconstruction of the homology concept, this concept was indeed shared across biologists. But the justification of the philosophical reconstruction is to lay out the powerful biological practice that emerged in virtue of the homology concept. (Section 4.4 will argue that the advent of evolutionary theory did not bring about substantial change regards the features that actually underwrote the successful use of the homology concept in biological practice.)

A relevant aspect of the homology concept is obviously the criteria for homology — how homologies are inferred. I explained that two basic criteria were in use (Sections 4.1.1 and 4.1.3). The positional criterion enables one to establish homologies by studying the anatomy of adult organisms only. On this criterion, homology is to be assessed based on the relative position of structures and their points of connection. The embryological criterion, in contrast, makes it necessary to study the development of organisms, as it assumes that homologous structures develop in the same way, i.e., out of the same precursor structure. We saw that some anatomists made extensive use of embryological studies and used the developmental criterion. Others, in contrast, preferred the positional criterion only. Owen even argued that the embryological criterion is at best a fallible guide to homology because there appear to be homologous structures that do not develop in exactly the same way. Despite these disagreements and different preferences as to how to establish homology, I view both criteria as criteria for one and the same phenomenon; and as criteria they may fail in certain cases. There is no necessary conflict between these criteria as both can be combined in practice. The embryological criterion requires the biologists to trace the development of a structure during ontogeny and how it gives rise to more differentiated structures. However, the main way to recognize a structure and track its identity during development is not by using some of its internal features (such as its texture) but by means of its position relative to other developing and changing structures. In this sense, the embryological criterion involves the positional criterion as well, albeit not restricting the positional criterion to adult structure as this use of this criterion is usually understood.[38] This is not to deny that some anatomists used only one criterion at the expense of the

[38] "But we have had to do only with a modification, not with a transformation, of the criterion of homology recognised by the anatomists. Homology is still determined by position, by connections, in the embryo as in the adult. 'Similarity of development' has become the criterion of homology in the eyes of the embryologist, but similarity of

other criterion, and that different hypothesis of homology resulted from these different preferences. But the two criteria were often used in one or another combination. The existence of two criteria does not justify the claim that two distinct homology concepts were in use — they were viewed and used as two criteria for the same phenomenon.

Anil Gupta's (1999) notion of a 'frame' offers a good semantic way to understand the interplay of the two basic criteria of homology. As discussed in Section 3.1.3, Gupta's semantic aim is to understand how concepts underwrite successful practice, including concepts involving empirical misconceptions. On his account, language does not directly mirror the world, but represents only indirectly, mediated by a frame. In addition to the rules of language (yielding 'absolute content', the content one is committed to), Gupta stresses a concept's frame, i.e., how the rules of language are to be applied (yielding 'effective content', the content in play). A concept may be associated with different criteria (inferences, rules of language) that are empirically non-equivalent, where the language users are not aware of this non-equivalence. Still, due to a frame these criteria need not be conflated in practice and each criterion is applied only in certain circumstances, accounting for the successful use of this concept. My suggestion is to make use of this semantic idea to understand the relation between the positional and embryological criterion. Even though the theoretical relation and biological adequacy of these criteria were unclear, for the most part the two criteria were kept separate in practice where necessary. Thus, even though I view the homology concept constituted by different inferences (such as the criteria used), different inferences are not conflated and a particular inference is carried out in appropriate circumstances due to the existence of a frame.

An important set of inferences in which the homology concept figured stemmed from the assumption that in case there is a genuine morphological unit in one species, then it is likely that one will find the same structure in other, even distantly related species. Geoffroy championed this assumption by his theory of the unity of organic composition (the 'théorie d'analogues', see Section 4.1.1). He was obviously quite bold in claiming that as a general rule one can find the same set of elements in modified form in all vertebrates, or even across larger animal groups. Even if later anatomists were more careful than Geoffroy, it was widely assumed that homologues exist across large taxa — homologues are shared by much larger groups of organisms than biologists would have thought before the advent of the homology concept. Von Baer's branching model of development (Section 4.1.3) also supports this idea: development starts with the emergence of the basic type of

development means, not identity of histological differentiation, but similarity of connections throughout the course of development." (Russell 1916, p. 168)

an organism, displaying the features of the phylum (Cuverian *embranchement*) to which it belongs. Thus, homologies usually exist within a type or phylum but not across phyla. In the course of ontogeny, differentiation of structures takes place in accordance with the taxonomic hierarchy — first the features of the phylum develop, than the features of the class, order, family and genus. The developmental trajectories of two embryos belonging to different species are very similar in the beginning, but at some point they diverge in accordance with their taxonomic differences. If two species are very closely related taxonomically, then divergence occurs very late in development, so that one can expect that the two animals share most structures. If, in contrast, two organisms are less closely related, then their developmental trajectories diverge relatively soon and due to divergence and further differentiation development it may happen that some adult structures do not correspond to a structure in the other species. Thus, the more closely two organisms are related taxonomically, the more homologues they share and the more likely that for a given structure there is a corresponding structure in the other species.[39]

This idea (that homologues are shared by large groups of organisms) proved to be an important *heuristic tool of discovery*. For it encouraged anatomists to search for homologues — in species that had not been studied before, and in more well-known species where a homologue had simply not been found yet. The heuristic impact of the idea of homology was a crucial factor why this concept became established. In fact, the success of transcendental anatomy was largely due to its proponents being able to establish that a structure in a species was in contrast to previous assumptions the same structure as in another species, or to uncover that was had been viewed as a structure actually consists of several independent structures. In the Geoffroy-Cuvier debate, Geoffroy emphasized that his approach would encourage search for and discover new and independent structures (a fused bone as being actually composed of several distinct elements), whereas the Cuverian functional anatomy would not yield this success (Appel 1987). In sum, the inductive inference that a homologue for a given structure is likely to exist in other species as well (depending how closely related they are) was an important tool of discovery. It enabled comparative biologists to establish new homologies and to reject dubious homologies in case a structure appeared to correspond to a structure in a few isolated other species but is not present in other closely related species.

So far the discussion has only covered one aspect of homology's inferential role: inferences that

[39] A contemporary explanation of this fact is given by evolutionary theory, which explains the occurrence of homologies based on inheritance from a common ancestor and interprets the hierarchical structure of taxonomical system in terms of the branching structure of the phylogenetic tree. Even though pre-Darwinian biologist could not offer an adequate, evolutionary explanation of this fact, the comparative study of organisms showed that — as a matter of fact — homologues exist across relatively large groups of organisms.

promote the establishment of homologies (the homology concept embodying homology criteria and assumptions about the existence of homologues). Yet this by itself does not explain why discovering homologies had any relevance for biology. A further aspect of homology's inferential role, which was essential for the successful use of this concept, is how knowledge about homologies was used for the purposes of taxonomy and morphology. Comparative biology is concerned with the study of similarities and differences between species, and comparing species and their structures usually consists in comparing homologous (rather than non-homologous) structures in different species. Biologist often express this by saying that homology enables 'meaningful' comparison. The reason is that each homologue is a unit of morphological variation across species. An organism is composed of different homologues, and what makes different homologues distinct morphological units is that fact that they can in principle vary independently from each other across different species.

The idea that homology enables meaningful comparison became increasingly relevant for pre-Darwinian taxonomy, as comparative biologists came to realize that homologies — but not analogies — are good guides to the taxonomic relatedness of species. The central task of taxonomy (systematics) is to arrange species hierarchically into higher taxa (genus, family, etc). While in the 18^{th} century many naturalists had endorsed a nominalism about the taxonomic system, conceiving of it is a human contrivance, in the first half of the 19^{th} century more and more biologists came to view the system as reflecting patterns that genuinely exist in nature (Amundson 2005). Similarities and taxonomic relations between species came to be viewed as exhibiting 'true affinities'. For instance, we saw that von Baer argued for an objective way of classifying species based on the idea that as a matter of natural law a parallel exists between the taxonomic hierarchy and the branching of the developmental trajectories of different species (Section 4.1.3). On this account, detailed comparison of development based on the embryological criterion of homology establishes the taxonomic relations of different species as they exist in nature. Homologies between different species exhibit true affinities, whereas comparing non-homologous structures that have the same function (analogies such as wings in insects and birds) do not reflect taxonomic relations. Charles Darwin, in the *Origin of Species* made reference to the taxonomic significance of homologies in contrast to analogies. His reason for doing so was that he could appeal to an idea that at this point in history was usually accepted, at least being implicit in classificatory practice, and based on his evolutionary theory he could explain why this practice is in fact effective. Given Darwin's idea that the traditional classification into natural groups is in fact classification according to genealogy, an interpretation of homologies in the light of common descent offers a justification of the accepted

idea that homologies are important to establish natural groups, whereas analogies are irrelevant:

> It might have been thought (and was in ancient times thought) that those parts of the structure which determined the habits of life, and the general place of each being in the economy of nature, would be of very high importance in classification. Nothing can be more false. No one regards the external similarity of a mouse to a shrew, of a dugong to a whale, of a whale to a fish, as of any importance. These resemblances, though so intimately connected with the whole life of the being, are ranked as merely "adaptive or analogical characters;" ... Again, no one will say that rudimentary or atrophied organs are of high physiological or vital importance; yet, undoubtedly, organs in this condition are often of high value in classification. ... All the foregoing rules and aids and difficulties in classification are explained, if I do not greatly deceive myself, on the view that the natural system is founded on descent with modification; that the characters which naturalists consider as showing true affinity between any two or more species, are those which have been inherited from a common parent, and, in so far, all true classification is genealogical; that community of descent is the hidden bond which naturalists have been unconsciously seeking, ... (Darwin 1859, pp. 414, 416, 426)

As a result, a central aspect of the use of the homology concept is that knowing that two structures are homologous justifies further comparison of these structures, and the degree of similarity of various homologous structures in different species indicates the taxonomic relatedness of these species, yielding stable classifications. This idea became more prevalent and explicit after the advent of evolutionary theory, but even in pre-Darwinian times classifications came to be based on the comparison of homologies rather than analogies. In sum, the homology concept was used by pre-Darwinian biologists to pursue one goal of comparative biology — the taxonomy of species.

The last type of inference that on my account constitutes homology's inferential role is a particularly important one. It is essential for morphology and comparative anatomy, and closed linked to the fact homologues are natural kinds and units of morphological variation across species. The inference is inductive: given some properties that hold of a structure in one species, these properties are likely to hold of the homologous structure in another species. The validity of this inference can best be explained in the context of homology across different species (rather than serial homology), based on the fact that homologous structures are derived from a structure in the common ancestor — yet knowing of the validity of this inference does not presuppose this phylogenetic explanation. A particular structure in an ancestral species has certain properties (e.g., morphological, histological, and developmental properties of this structure, how it is internally composed and connected to other structures). If this structure is inherited, then the corresponding structure in the descendant is likely to have the same properties, as long as no major modifications occur in the course of evolution. Thus, a structure in one descendant and its homologue in another descendant are likely to have the same features; and the more closely related the two species are (i.e., the more recent the ancestor is) the more likely it is that the two homologous structures share many properties. This permits an inductive inference from the properties of a structure in one species

to its homologue in another species. In other words, there is a *projectability of properties* from one homologue to another one (Goodman 1955). Projectability of many properties is a hallmark of natural kinds and this is my reason for claiming that homologues form a natural kind.[40]

Originally, philosophical theories of natural kinds were tied to physical and chemical kinds, despite biological species being some of the prime examples of natural kinds. These accounts typically assumed that natural kind are governed by laws of nature, which is problematic for biological kinds as laws of nature — as usually construed — are rare in biology.[41] Whereas natural kinds are sometimes taken to be have an existence that is independent of spatio-temporal restrictions, biological kinds such as species are essentially historical. In the past few decades, the notion of a natural kind has actually been used in different ways by philosophers.[42] The concept of a natural kind that I use in the present context is intended to cover biological kinds. It is basically the notion of a natural kind as it has been previously used and made prominent by Richard Boyd (1991, 1999), Paul Griffiths (1999a), and Rob Wilson (1999). A natural kind is a group of entities that are presumed to belong together due to some underlying mechanism or a structural property. The idea that these entities belong to a kind may be due to several interesting similarities and properties being shared by them. However, these similarities are not deemed to be what characterizes this kind. Instead, a natural kind is specified by some theoretically important, but yet unknown underlying feature or process that is presumed to account for the observed similarities.[43] This underlying property is what is often called the 'essence' of the kind — it defines kind membership and explains why the members have the properties that led to the introduction of the natural kind concept. It is this underlying causal or structural basis that accounts for many properties being co-instantiated in each kind member (Boyd calls natural kinds homeostatic property clusters for this reason). Thereby this 'essence' also accounts for the projectability of many properties from one instance of the kind to another one. In the case of a chemical kind, this essence is its chemical composition, which explains

[40] At the beginning of this chapter I pointed out that homology as a relation defines many equivalence classes. The members of one such are the so-called homologues — the structures that are homologous to a given structure. Each such class of homologues is a natural kind and homology as picking out these natural kinds is a natural kind concept.

[41] But see Mitchell (1997, 2000, 2003) for an account of laws that is adequate to understand biological theorizing.

[42] For different usages of this notion see Anderson 1994; Atran 1990; Brody 1976; Brown 1998; Browning 1978; Churchland 1982; Cocchiarella 1976; Collier 1996; D'Amico 1995; de Sousa 1984; Doepke 1992; Dupré 1993; Elder 1989; Graham and La Folette 1982; Granger 1989; Griffiths 1997; Hacking 1983; Hollinger 1974; Khalidi 1998; Kiester 1980; Kitcher 1979; Kripke 1980; Leplin 1988; Machery 2005; Matthen 1984; McGinn 1975; McKay and Stearns 1979; Meyer 1989; Putnam 1975; Quine 1969b; Reid 2002; Resnick 1960; Rorty 1988; Sankey 1997b; Savellos 1992; Shain 1993; Stuart 1999; Tienson 1977; Uzgalis 1988; Wilkerson 1995; Witmer and Sanecki 1998.

[43] Since this underlying feature is unknown, a natural kind concept is associated with a search for the basis of the kind. A full theoretical account of a natural kind can only be given after appropriate empirical study and might reveal a variety of complications. A natural kind concept may even change its reference throughout scientific investigation. In any case, a natural kind concept goes together with a scientific search which may be open-ended (Brigandt 2003b).

the typical properties of the kind such as the type of chemical reactions in which it takes place. So my account also fits with traditional physical and chemical kinds, but it is broader as it includes biological kinds. A higher taxon, for instance, is a class of species which are derived from an ancestral species. For this reason, the various species that belong to a taxon have many properties in common.[44] The case of homologues is perfectly analogous to this situation: homologues are a class of structures that are derived from a structure in a common ancestor. Common ancestry is the underlying property of this type of natural kind that accounts for homologous structures sharing many features. Thus, common ancestry explains the projectability of properties.

The fact that my notion of a natural kind is somewhat vague is not problematic as I do not assume that there is a clear-cut demarcation between natural kinds and other kinds. Rather, there is a continuum between natural kinds as we find them in physics and kinds that are clearly not natural kinds. But natural kinds are still quite different from most *functional* kinds, whose membership is defined in terms of the function of its members. For functional kinds typically do not have a projectability of many properties. This stems from the fact that functional kinds are multiply realizable. As different realizations of a functional kind may differ substantially in their material constitution and internal structure, two instances have only a few properties in common. For example, take two biological structures with the same function such as a bird wing and an insect wing. The internal structure of these two wings is completely different, so one cannot expect any projectability of properties. This applies even to functional properties such as biomechanical features about how bird wings and insect wings permit flight — these different types of wing operate in quite different ways to achieve their common function. The only interesting type of properties that different wing may have in common are probably a few ecological properties (e.g., properties that are associated with a flying life-style). Overall, insect and bird wings have hardly any biologically interesting properties in common — in contrast to homologues who share many properties in virtue of common ancestry. Individuating characters in terms of homology (rather than in terms of functional considerations such as analogy) is the best available individuation scheme for anatomical structures, as different homologues (different parts of the body) are distinct units of variation across species, and each homologue has many projectable properties. The difference

[44] It is sometimes assumed that species and higher taxa cannot be natural kinds because a natural kind is defined by necessary and sufficient condition, whereas evolving biological units change their properties. Griffiths (1999a) points out that there is no need to make the common (implicit) assumption that the defining properties of natural kinds are *intrinsic* properties. In the case of a higher taxon, common ancestry is the essence that defines kind membership. Common ancestry is a relational property and all species belonging to a taxon have this property, even though due to evolution their intrinsic (phenotypic as well as genotypic) properties may be different (see also LaPorte 2004).

between natural and functional kinds as regards the projectability of properties is the reason why in many biological contexts natural kind concepts are more important than functional categories.

Let us return to the inferential role of the homology concept. I explained why properties of a particular structure are likely to hold for the homologous structure in another species. My appeal to common inheritance offers an *explanation* of why the inductive inference from one homologue to another one is a good one, but a justification of the inference's validity does not presuppose phylogenetic considerations. Even before the advent of evolutionary theory, biologists realized that — as a matter of fact — homologues share many properties. Their biological practice of individuating characters by homology was based on this fact, independent of whether we nowadays have a better explanation of why this practice was so successful. After all, the recognition of the unity of form among organisms was one of the reasons to introduce the homology concept in the first place.[45] This type of inference that is supported by the homology concept is of fundamental importance for comparative biology for the following reason. Given that biological characters are individuated in terms of homology, many biological properties hold for a character that is present in a relatively large class of species. For example, take the cerebrum, a part of the brain, which is present in all vertebrates. Neurobiological textbooks simply talk about 'the' cerebrum, actually referring to individual homologues present in species from a taxon as large and diverse as the vertebrates. Talk about 'the' cerebrum is possible as many biological descriptions apply to any concrete cerebrum. This includes morphological and histological descriptions such as the internal structure of the cerebrum and out of which smaller structures it is composed and how it is connected to other structures. This also includes how the cerebrum develops. Thus, basing biological descriptions on structures individuated by homology permits descriptions that apply to large classes of organisms, despite differences between species. This basic type of inference is so important because it yields *unified knowledge*. As a result, the homology concept is used to pursue a goal of anatomy and comparative biology, namely providing systematic and unified descriptions of different species.

My account of the homology concept's *inferential role* (conceptual role) has mentioned two basic sets of inferences that constitute the successful use of this concept: a) how homologies were established, and b) how knowledge about homologies was used for taxonomic purposes (classification

[45]The explanation of property projectability based on common ancestry applies to homologous structures from different species, but does not work for serial homologues (the different vertebrae in one individual are the same morphological element but obviously not inherited from an ancestor that had only one vertebra). But as a matter of fact serial homologues still share many properties. An example is the right and the left forelimb, which have the same structure due to the body's overall symmetry. Morphological unity as occurring both within an individual and between species was the motivation to introduce the notion of homology. (Probably the fact that serial homologues have many properties in common has to be explained based on developmental in addition to phylogenetic considerations.)

of species are to be based on the comparison of homologous structures) as well as for morphological purposes (homologous structures in related species share many properties, supporting unified descriptions). On my theory of concepts, apart from inferential role, another component of a concept's content is the epistemic goal pursued with its use. The above discussion has actually covered the scientific purpose of this concept's usage. The two *epistemic goals* pursued with the use of the homology concept are 1) the classification of species and 2) the morphological description of species, so as to arrive at unified structural descriptions applying to large groups of organisms.

4.3 HOMOLOGY FROM 1859 UNTIL 1950: AN INSTANCE OF CONCEPTUAL STABILITY

Nowadays two structures are usually defined to be homologous in case they are inherited from a structure in the common ancestor. This modern definition is a consequence of the advent of evolutionary theory. In the *Origin of Species*, Charles Darwin (1809 –1882) did not propose a redefinition of the homology concept along phylogenetic lines. Instead, he used the traditional definition of homology as a pattern of morphological correspondence, but explained the existence of homologies by common descent. In general, Darwin took over many traditional concepts from taxonomy, morphology, and embryology, but approached them from an evolutionary point of view. Naturalist have long before Darwin attempted to classify species into natural (rather than artificial) groups that reflect their biological relations as they exist in nature. Darwin argued that the groupings that we find in nature are best explained by the idea of common ancestry, and that his evolutionary theory explains prior classificatory practices (see p. 168 above). Thus, Darwin endorsed a parallel between the hierarchical system of classification and the consecutive branching of species in the tree of life. We saw that Karl Ernst von Baer had drawn a parallel between the taxonomic system and the development of animals, based on his branching or divergence model of comparative development. Darwin actually addressed the issue of embryology, by using a model quite similar to von Baer's. Darwin claimed that his theory of descent with modification can explain why in development the more general features of an organism usually develop first, and later the more specific features (Darwin 1859, p. 442). His basic explanation is that the early embryo is not exposed to the struggle for life. For instance, mammalian embryos develop in the uterus and thus

environmental demands do not act on the embryo. For the most part, natural selection acts only on the later stages of life, which is the reason why different species diverge in the later parts of their development.[46]

As far as the homology concept is concerned, Darwin defined this term as his predecessors — homology is a certain pattern in nature, a correspondence of body plans:

> All physiologists admit that the swim-bladder is homologous, or 'ideally similar,' in position and structure with the lungs of the higher vertebrate animals: ...
>
> We have seen that the members of the same class, independently of their habits of life, resemble each other in the general plan of their organisation. This resemblance is often expressed by the term "unity of type;" or by saying that the several parts and organs in the different species of the class are homologous. (Darwin 1859, pp. 191, 434)

Darwin built on the prior results of transcendental anatomy, i.e., comparative anatomy based on the notion of homology. In particular, he emphasized the claim — previously made by Geoffroy and Owen, among others — that homologies cannot be explained based on functional considerations:

> What can be more curious than that the hand of a man, formed for grasping, that of a mole for digging, the leg of the horse, the paddle of the porpoise, and the wing of the bat, should all be constructed on the same pattern, and should include the same bones, in the same relative positions? Geoffroy St. Hilaire has insisted strongly on the high importance of relative connexion in homologous organs: the parts may change to almost any extent in form and size, and yet they always remain connected together in the same order. ... Nothing can be more hopeless than to attempt to explain this similarity of pattern in members of the same class, by utility or by the doctrine of final causes. The hopelessness of the attempt has been expressly admitted by Owen in his most interesting work on the 'Nature of Limbs.' On the ordinary view of the independent creation of each being, we can only say that so it is; — that it has so pleased the Creator to construct each animal and plant.[47]

Consequently, Darwin seeks to explain the existence of homologies is by common ancestry. Geoffroy and Owen had expressed similar ideas during some parts of their life, but Geoffroy's views were embedded in a speculative theory of evolution, and Owen had never been quite explicit about his belief in descent, masking his allusions to common ancestry in theistic rhetoric. Unlike Owen, Darwin is very explicit about his conviction that all animals are bound together by descent:

> By unity of type is meant that fundamental agreement in structure, which we see in organic beings of the same class, and which is quite independent of their habits of life. On my theory, unity of type is explained by unity of descent. (Darwin 1859, p. 206)

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[46] "We may sum up by saying that Darwin interpreted von Baer's law phylogenetically." (Russell 1916, p. 237)

[47] Darwin 1859, pp. 434–435. A main target of this remark are the zoologists belonging to the tradition of natural theology, assuming the "independent creation" of each species, whereby species have been created by functional considerations so as to fit their ecological niche. Amundson (2005) gives a revealing discussion of how the statement quoted has been misconstrued by proponents of what Amundson calls "Synthesis Historiography," i.e., the use if the conceptual framework of neo-Darwinism to interpret the history of biology. Synthesis Historiography tends to lump together different pre-Darwinian approaches as 'typological', conflating in particular the often opposing camps of natural theology and idealistic morphology. As a consequence, Darwin has repeatedly been interpreted as criticizing Owen (or more generally idealistic morphology) in the above statement, though he clearly uses Owen's work and theoretical ideas in support of his critique of natural theology. As mentioned in my previous discussion, unlike natural theology, pre-Darwinian morphology stressed the morphological relations between species and their structures and viewed them as reflecting real relations in nature, thereby yielding crucial support to the idea of common ancestry.

Darwin also offers an evolutionary explanation of the validity of the positional criterion of homology (Geoffroy's 'principe de connexions'). The particular shape of a structure (as well as its function) may change due to adaptation, but the relative positions of structures usually remain the same:

> In changes of this nature, there will be little or no tendency to modify the original pattern, or to transpose parts. The bones of a limb might be shortened and widened to any extent, and become gradually enveloped in thick membrane, so as to serve as a fin; or a webbed foot might have all its bones, or certain bones, lengthened to any extent, and the membrane connecting them increased to any extent, so as to serve as a wing: yet in all this great amount of modification there will be no tendency to alter the framework of bones or the relative connexion of the several parts. If we suppose that the ancient progenitor, the archetype as it may be called, of all mammals, had its limbs constructed on the existing general pattern, for whatever purpose they served, we can at once perceive the plain signification of the homologous construction of the limbs throughout the whole class. (Darwin 1859, p. 435)

Following previous anatomical theorizing, Darwin uses the notion of serial homology. The existence of repeated structures in extant organisms can be explained by the ancestor possessing these serial homologues. While in an ancestral, primitive organism the different serial homologues were quite similar, in a more evolved and complex individual the different serial homologues diverge in shape so that they can fulfill different functions in different regions of the body (Darwin 1859, pp. 437–438).

4.3.1 A Novel Homology Concept?

In the *Origin of Species*, Darwin defined homology in the traditional way and invoked common ancestry merely as an explanation. Soon homology came to be defined in terms of common inheritance by some biologists. In the 1860s, the German morphologists Carl Gegenbaur and Ernst Haeckel were among the first to base morphology on the theory of descent. I will take a closer look at these figures below. A clear instance of an early post-Darwinian biologist defining the homology concept in terms of ancestry is the British anatomist Edwin Ray Lankester (1847–1929). In fact, in 1870 Lankester rejected the term 'homology' and suggested the introduction of the a new term, because he viewed the old term as being connected to a pre-evolutionary, idealistic approach to morphology.

> ... certain terms and ideas are still in use which belonged to the old Platonic school, and have not been defined afresh in accordance with the doctrine of descent. ...
> The term "homology" belongs to the Platonic school, but is nevertheless used without hesitation by those who reject the views of that school. Professor Owen ... would understand by *homologue* "the same organ in different animals under every variety of form and function;" ... But how can the sameness (if we may use the word) of an organ under every variety of form and function be established or investigated? This is, and always has been, the stumbling-block in the study of homologies without the light of evolutionism; for, to settle this question of sameness, an ideal "type" of a group of organisms under study had to be evolved from the human mind, after study of the component members of the group; and then it could be asserted that organs might be said to be the "same" in two animals which had a common representative in the ideal type. This reference to an

> ideal type was the only criterion of homology; and yet we find those who have adopted the doctrine of evolution making use of the term 'homology' without any explanation. (Lankester 1870, p. 34–35)

Refusing to continue to use the term 'homology', Lankester suggested introducing the new term 'homogeny', referring to structures in different species which are inherited from the common ancestor.

> Structures which are genetically related, in so far as they have a single representative in a common ancestor, may be called homogenous. (Lankester 1870, p. 36)

Whereas homology had traditionally been contrasted with analogy, Lankester viewed 'homogeny' as opposed to what he termed 'homoplasy'. While homogeny is similarity due to common ancestry, homoplasy is similarity due to the action of similar forces or environments. Lankester argued that many of the structures viewed as serial homologues were not homogenous (i.e., not phylogenetically homologous), but homoplastic. The idea seems to be that serial 'homologues' develop based on similar developmental and environmental forces. Lankester's neologisms did not catch on, though.

Lankester explicitly distinguished between a post-Darwinian homology concept (his 'homogeny') and a pre-Darwinian 'Platonic' homology concept. Many contemporary biologists and historians of biology apparently agree with this idea that Darwinism brought about a new homology concept. At least this assumption is implicit in historical discussion and implied by statements about an 'idealistic' homology concept and a 'phylogenetic' homology concept. Even though this traditional assumption is not explicitly argued for and in particular not based on an explicit account of concepts and concept individuation, it is apparently driven by the idea that after the advent of Darwinism definitions of homology usually made reference to common ancestry, unlike pre-Darwinian definitions of homology, which rather made reference to the notion of a type.[48] However, it is far from clear that what biologist call definitions actually fully characterize what a concept is, so that different definitions amount to different concepts. Instead, there are many cases where individual biologists choose to advance their favorite definition of a concept, which is not equivalent to other definitions. But these different (sometimes quite idiosyncratic) definitions are advanced even though the term so defined is usually not used differently in biological practice. The standard implicit assumption that there is an idealistic as opposed to a phylogenetic homology concept is not only based on the mere fact that before and after Darwin different homology definitions were preferred. The history of 19$^{\text{th}}$ and early 20$^{\text{th}}$ century morphology is typically divided into three phases: the pre-Darwinian idealistic (or transcendental) morphology, the post-Darwinian evolutionary morphology, and the experimental (or causal) morphology that emerged in the 1880s. This

[48] Below, however, we shall see that the notion of common ancestry was not always included in definitions of homology, even in those that stemmed from a phylogenetic approach to homology.

division was made by early discussions of the history of anatomy such as E. S. Russell (1916) and Hans Spemann (1915), and it is still viewed as valid by contemporary historical accounts (Nyhart 1995). Surely the distinction between idealistic and evolutionary morphology fits with the view that these two approaches used different homology concepts.[49]

However, in what follows I shall resist this conventional wisdom about the history of homology, arguing that there is no need to view the homology concept as used by most researchers in comparative and evolutionary biology before 1950 as a concept distinct from the homology concept of pre-Darwinian anatomy. In the presentation of my semantic framework (Section 3.1), it was emphasized that even though one part of my account is a version of inferential role semantics according to which semantic content is determined by how a concept figures in inference, my notion of inference does not boil down to inferential relations between theoretical statements and how a concept figures in an explicit theory. Rather, inference also includes the way in which a concept is applied to objects and how it is used in scientific practice. The motivation for this was the idea that the rationale of semantic analysis and the ascription of concepts is to account philosophically for the successful use of language in communication and world-engaged practice. Consequently, it may be the case that standard theoretical definitions of the homology concept put forward by biologists may fail to fully capture the way in which this concept underwrites successful biological practice, so that the content of the homology concept is insufficiently specified by such theoretical statements. Thus, the heuristic impact of my framework on concepts is that one should not only look at definitions put forward, but rather at how a concept is actually used in biological practice

[49] Hans Spemann (1915) distinguishes between the 'geometric conception' of homology, used in the 'idealistic period' of anatomy, and the 'genetic conception' of homology, used in the 'historical period' of anatomy.

The physiologist John Tait (1928) states even more explicitly that a new homology concept emerged: "Structural likeness being seen to depend, not on unity of plan, but on descent from common ancestors, the original geometrical conception of homology, which for the sake of distinctness we might now call 'positional homology,' was allowed quietly to lapse. One might suppose that the term homology, having outlived its em raison d'être, would ultimately have died out. Instead, it adapted itself to its new surroundings and emerged in a new guise and with transformed meaning, which we shall here designate as 'embryological homology.'" (Tait 1928, p. 156)

O. Haas and G. G. Simpson (1946) defend a phylogenetic definition of homology. They apparently view the pre-Darwinian concept of homology as distinct from the modern concept: "After the advent of evolutionary ideas — all but ridiculed by Owen as late as 1866 . . . — Owen's concept of homology proved no longer satisfactory, lacking, as it did, any phylogenetic implications" (p. 321). Interestingly enough, they point to Spemann (1915) and Tait (1928) for "excellent presentations of the change of meaning undergone by this term after the advent of Darwinism" (p. 322).

The contemporary biologist Günter Wagner (1989a) distinguishes between 'the idealistic homology concept' and the 'the historical homology concept' (in addition to his 'biological homology concept', which is a variant of what I call the developmental homology concept, to be discussed in Section 5.2).

The biologist Gerd Müller (2003) keeps three pre-20$^{\text{th}}$ century 'conceptualizations' of homology apart (in addition to three 20$^{\text{th}}$ century conceptualizations): The 'idealistic' conceptualization used before the 19$^{\text{th}}$ century, which is used without any definition (Camper, Cuvier, Goethe), the 'ahistorical' conceptualization, which based on an explicit, comparative definition of homology as sameness (Owen), and the 'historical' conceptualization, which views homology as an indicator of common descent (Darwin, Gegenbaur, Haeckel).

and thereby brings about crucial biological knowledge. In what follows, I attempt to show that regards these features, the continuity in the use of the term 'homology' throughout the 19$^{\text{th}}$ century is larger than usually granted. This claim does not mean that I deny that many crucial theoretical changes took place with the advent of evolutionary theory. Darwin's ideas changed biology in fundamental ways. Even though the overall history of homology in comparative and evolutionary biology before 1950 exhibits in fact certain changes in the conception of homology and the use of the homology concept, I still argue that these changes are not substantial enough to warrant the postulation of a new homology concept. My suggestion is that one can account for the change that occurred by appeal to the introduction of novel concepts or changes in concepts apart from the homology concept. Another motivation for my tenet that Darwinism did not create a distinct homology concept in the 19$^{\text{th}}$ century is to highlight the fact that the homology concept as already used before the advent of evolutionary theory yielded crucial evidence for the idea of common ancestry and had the epistemic potential to underwrite the establishment of phylogenetic trees.

My following historical discussion of the homology concept since Darwin discusses some aspects of the use of homology focusing on the field of morphology, where the continuity is the largest. Substantial changes took place in other branches of biology — evolutionary biology and systematics, but for the most part only in the second half of the 20$^{\text{th}}$ century, to be discussed in the following chapter. Section 4.4 will present this philosophical argument based on the historical evidence presented in this section and finally summarize the overall discussion of this chapter.

Before I focus on the homology concept after the advent of evolutionary theory, I first want to briefly address the historical development of biology in general. The assumption that Darwin's theory brought about a new homology concept is surely driven by the idea that this theory reshaped biology as a whole.[50] But it would be a misinterpretation of the history to assume that a pre-Darwinian paradigm was replaced by a Darwinian paradigm. Even though more and more biologists accepted the very idea of evolution after the publication of the *Origin of Species*, this does not mean that biologists subscribed to Darwin's particular version of evolutionary theory. Late 19$^{\text{th}}$ century biologists held quite different views about the mechanisms of evolution, and the evolutionary theories they endorsed were often at variance with those views of Darwin that we view nowadays as most fundamental to the theory of evolution. Nowadays biologists agree that

[50] In the last four decades, the idea that pre- and post-Darwinian biology are different paradigms has been supported by the 'essentialism' historiography, as mentioned in footnote 37 (p. 161). At this place I pointed out that the essentialism story has recently been shown to be inadequate, so that an overall motivation for distinguishing between two 19$^{\text{th}}$ century biological paradigms and homology concepts turns out to be inadequate. The subsequent two pages will provide some historical evidence against making a clear distinction between pre- and post-Darwinian biology.

natural selection is the main mechanism of evolutionary change. The variation in a population on which selection acts is essentially random and unbiased (and there is no Lamarckian inheritance of acquired characters), so that evolution does not proceed in a progressive fashion towards a certain goal. Darwin held this modern view to a substantial extent — but unlike most 19$^{\text{th}}$ century biologists. Our modern understanding of evolution became the dominant theory not in the 19$^{\text{th}}$ century but in the 1940s based on the establishment of the Modern Synthesis, or neo-Darwinism as it is often called.

This case has been made in a bold and somewhat popularized form by Peter Bowler in his *The Non-Darwinian Revolution: Reinterpreting a Historical Myth* (1988). It is well-known that the majority of 19$^{\text{th}}$ century biologists viewed evolution as a strongly progressive or even goal-directed process. Bowler emphasizes that this fact has implications for how the very contribution of Darwin's theory on evolution should be historically viewed.

> My suggestion is that Darwin's theory should be seen not as the central theme in nineteenth-century evolutionism but as a catalyst that helped to bring about the transition to an evolutionary viewpoint within an essentially non-Darwinian conceptual framework. This was the "Non-Darwinian Revolution"; it was a revolution because it required the rejection of certain key aspects of creationism, but it was non-Darwinian because it succeeded in preserving and modernizing the old teleological view of things. ... The antiteleological aspects of Darwin's thinking prized by modern biologists were evaded or subverted by the majority of his contemporaries. (Bowler 1988, p. 5)

Bowler points out that most 19$^{\text{th}}$ century biologist were either what he calls 'pseudo-Darwinists' or 'anti-Darwinists'. Anti-Darwinists accepted the idea of descent, but openly opposed natural selection as the main mechanism of evolution. One prominent alternative view of evolution was Lamarckism, which flourished particularly towards the end of the 19$^{\text{th}}$ century. Lamarckism assumed adaptation to the external environment, albeit independent of natural selection. Another prominent view was orthogenesis, a doctrine assuming that organisms have internal developmental and evolutionary tendencies, which drive evolution in a certain direction even if it is maladaptive (Bowler 1983). Pseudo-Darwinists are biologists who officially endorse Darwin's theory but have actually a different agenda. Bowler views Ernst Haeckel and Thomas Henry Huxley as pseudo-Darwinists. Haeckel ('Darwin's German Bulldogge') made the theory of descent with modification popular in Germany. However, Haeckel viewed evolution as a fundamentally progressive process, and emphasized Lamarckian mechanisms of evolution more than natural selection. His famous doctrine of recapitulation postulated a parallel between evolution and development — given the orderly, goal-directed nature of development, this fitted with his progressivist view of evolution. Huxley is usually known as one of Darwin's supporters in the debate against the natural theolo-

gians. However, Huxley's emphasis on a natural mechanism of descent was primarily a reaction against a Platonic construal of the archetype. Bowler (1988) states that it appears that Huxley was interested in selection only as a possible mechanism of evolution, a hypothesis that allowed the general idea of descent to become respectable. Later Huxley's research focused on embryology and he ignored evolution and in particular the phenomenon of adaptation. Only by the influence of Haeckel did he become interested in phylogenetic research again.

An idea unifying both the anti-Darwinians and the pseudo-Darwinians was that they often used the idea of development as an orderly and teleological process as a guideline to think about evolution. For this reason, they actually continued a fundamental pre-Darwinian way of thinking about living organisms and their relations. In the discussion above we saw that developmental ideas were pervasive among pre-Darwinian anatomists. Goethe and Oken used developmental metaphors such as the notion of metamorphosis to think about the morphological differences between the serial homologues occurring in an organism (e.g., the skull being composed of transformed vertebrae). Geoffroy developed a developmental theory of evolution based on his teratological studies. Owen's developmental ideas on evolution were based on his studies on parthenogenesis. Von Baer and Owen later criticized Darwin's particular theory of evolution. What they rejected was the idea of evolution as being guided by environmental demands acting external to the organism, and the fact that Darwin's theory did not imply a teleological mode of evolution. Development promised both internal factors as guiding the process and a teleological mode of evolution. Bowler puts this continuity between pre-Darwinian and post-Darwinian biology as follows:

> The similarities that can be discerned between pseudo- and anti-Darwinism lie in the fact that both were largely expressions of the morphological approach to biology and the developmental view of the history of life. Both movements tended to picture evolution as the unfolding of orderly trends, without the element of haphazard divergence introduced by Darwin's concern for the accidents of migration. ...
>
> The anti-Darwinian theories of the period around 1900 must be treated as the final product of the developmental viewpoint that had flourished throughout the preceding century. (Bowler 1988, pp. 75, 103)

Bowler is right in claiming that the analogy between development and evolution, which had pre-Darwinian origins, was destroyed not before the beginning of the 20^{th} century. This was brought about by the emergence of Mendelian genetics and its integration into evolutionary theory.

In sum, it is not the case that the history of biology can be neatly divided into pre-Darwinian period and a subsequent period where Darwinian views were held. Post-Darwinian biologist differed sometimes strongly in their views about evolution. In addition, they often used certain basic ways to think about evolution, which are actually continuous with pre-Darwinian ideas about organismal

life. Let me now focus on the homology concept in order to assess the degree of continuity between its pre-evolutionary and post-evolutionary usage.

4.3.2 Evolutionary Morphology in the 19th Century

Now it is time to address post-Darwinian morphology, or evolutionary morphology, as it is usually called. I can discuss a few selected persons only. I start with Carl Gegenbaur and Ernst Haeckel, who were the founders of evolutionary morphology in the 1860s. In the next subsection, I fast-forward to a prominent representative of this tradition working in the middle of the 20th century, Adolf Remane. The characteristic feature of this tradition was that it embedded the concepts and theories of pre-Darwinian comparative anatomy and morphology in a phylogenetic framework. Taxonomic relationships between species and homologous relations between structures were clearly viewed as being due to common ancestry. However, evolutionary morphology — at least the tradition of evolutionary morphology on which I focus — was not concerned much with the mechanisms of evolutionary change. The study of natural selection and adaptation did not play an important role; instead, morphological research was primarily concerned with genealogical relationships of species and the phylogenetic transformation of structures — in particular by determining the structure of the common ancestor of a group of animals. [51] Edward Stuart Russell likewise stresses the continuity between pre- and post-evolutionary morphology in his history of animal morphology *Form and Function*, when he states at the beginning of the chapter discussing Gegenbaur and Haeckel that

> In what follows we shall see that the coming of evolution made surprisingly little difference to morphology, that the same methods were consciously or unconsciously followed, the same mental attitudes taken up, after as before the publication of the *Origin of Species*. (Russell 1916, p. 247)

Carl Gegenbaur (1826–1903) and Ernst Haeckel (1834–1919) have to be discussed together, because as colleagues and friends they jointly established the tradition of evolutionary morphology in Germany.[52] Later however, their approaches diverged somewhat, with Haeckel focusing on embry-

[51] The label 'evolutionary morphology' as used nowadays refers primarily to a tradition that became popular in the second half of the 20th century, primarily in the United States and Great Britain. This type of evolutionary morphology, or functional morphology as it more commonly called, deals in fact with the function of structures, how functions evolve and how the functioning of structures contribute to adaptation (Wake 1982; Liem and Wake 1985; Gans 1985b; Herring 1988). Many of the practitioners of this more recent tradition view themselves simply as evolutionary biologists. For this reason, my later discussion on homology in contemporary evolutionary biology and systematics (Section 5.1) will cover this approach. The tradition stemming from Gegenbaur and Haeckel that is presently discussed is a phylogenetic rather than a functional morphology.

[52] On Gegenbaur and Haeckel, see Coleman (1976), Laubichler (2003), Laubichler and Maienschein (2003) and Nyhart (2002). The authoritative treatment of the institutional history of German anatomy is Nyhart (1995).

ology as the primary means of establishing phylogenetic trees, while Gegenbaur viewed embryology as a subordinated tool and instead relied on the comparative anatomy of adults. This is another prominent instance of two researchers respectively favoring the embryological criterion and the positional criterion of homology. Carl Gegenbaur was arguably the most respected anatomist in the second half of the 19$^{\text{th}}$ century. Gegenbaur studied in Würzburg under prominent anatomists and physiologists such as Albert von Kölliker and Rudolf Virchow. In 1855, he became professor at the University of Jena's medical faculty, where he received a chair in anatomy and physiology in 1858. Originally, Gegenbaur's research focused on invertebrates. Due to his teaching commitments in the curriculum of the medical faculty, his interests shifted toward vertebrates, focusing on the comparative anatomy and embryology of the vertebrate skeleton and the nervous system. In 1873, Gegenbaur accepted a chair in anatomy in Heidelberg.

The shift from a non-phylogenetic towards a phylogenetic approach towards anatomy is reflected by the subsequent editions of Gegenbaur's main work, *Grundzüge der vergleichenden Anatomie* (Fundamentals of Comparative Anatomy). The first edition of the *Grundzüge* was published in 1859, before the publication of Darwin's *Origin*. Even though Gegenbaur had expressed proto-evolutionary ideas at his dissertation defense (Laubichler 2003), his early work followed the tradition of pre-evolutionary, 'transcendental' comparative anatomy. In the first edition of the *Grundzüge*, Gegenbaur used the traditional notion of a type: the structures of an animal within a type are arranged so as to adhere to a "determinate form of the overall nature of the animal which, as much in its deeper structure as in its external aspects, represent the type of the animal."[53] Gegenbaur divided the animal kingdom into seven basic types (*Grundtypen*), or phyla as we would nowadays say: vertebrates, mollusks, arthropods, worms, echinoderms, coelenterates, and protozoans. Like von Baer and Owen, he homologized adult structures only within such a type, but not between different body plans. Yet he saw certain morphological connections between the types by pointing out that the primitive members of each type could be viewed as structurally related. In the case of the most primitive representatives of each type there was the possibility to conceive of "intermediate forms which, like bridges, cast themselves over the gaps between the basic types."[54] As a consequence, the usually single-celled protozoans, as the most primitive type, were viewed as most closely related to the coelenterates (polyps), while the vertebrates were considered most similar to the mollusks. To be sure, these morphological relations were not yet viewed as genealogical

[53]Gegenbaur (1859), pp. 33–34; translation quoted from Coleman (1976).
[54]Gegenbaur (1859), pp. 38; translation quoted from Coleman (1976).

relations. After the publication of Darwin's *Origin*, Gegenbaur came to endorse the notion of common ancestry in the 1860s. He did not necessarily view the idea of all animals as being genealogically related as a proven scientific fact (unlike Ernst Haeckel who at the same time started to preach this idea to German zoologists and non-academics). But Gegenbaur took the notion of common ancestry as an important principle of studying and interpreting the morphological relations among extant species. For evolutionary theory permitted a much better explanation and integration of anatomical facts. The second edition of the *Grundzüge der vergleichenden Anatomie*, published in 1870, clearly presents this evolutionary morphology. Homology as a relation within a type was claimed to be due to common ancestry. In addition, the morphological and taxonomic relations between types were now interpreted as based on descent. The most primitive type of animals, protozoans, was viewed as the most ancestral form. They gave rise to both the coelenterates and worms as more complex types. The worms (included tunicates) were the ancestor of the remaining types: the mollusks, the arthropods, the echinoderms, and the vertebrates. But Gegenbaur still used the notion of a type, it was simply reinterpreted based on the notion of an ancestral form. The historian William Coleman (1976) emphasizes the ease with which Gegenbaur reinterpreted his prior work and the large degree of continuity between the very early, pre-evolutionary and the later evolutionary and mature phase of his intellectual career.

Based on his phylogenetic approach, Gegenbaur defined the homology concept in terms of common ancestry. More precisely, special homology — as homology between structures from different species — is defined as

> the relations which obtain between two organs which had a common origin, and which have also a common embryonic history. ... Homology ... corresponds to the hypothetical genetic relationship. In the more or the less clear homology, we have the expression of the more or less intimate degree of relationship. Blood-relationship becomes dubious exactly in proportion as the proof of homologies is uncertain. (Gegenbaur 1878, pp. 64, 63)

Gegenbaur distinguished between the situation where two special homologues are exactly alike in that they have the same subcomponents (complete homology), or where a structure is composed of some additional parts or has some missing parts compared to its homologue in another species (incomplete homology). He continued the previous tradition in distinguishing homology from analogy. Homology was viewed as a 'genetic' (i.e., phylogenetic) and 'anatomical' relation, while analogy was viewed as a 'physiological' relation. Comparative anatomy is concerned with homology only:

> We distinguish, accordingly, physiological likeness, or Analogy, from morphological likeness, or Homology, and only consider the proof of the latter as our task. (Gegenbaur 1878, p. 63)

Countering arguments that reject the idea of evolution, Gegenbaur pointed out that in the course of history the function of a structure may gradually change, so that it is possible that extant species have homologues with quite different functions:

> An organ can be changed by the gradual modification of its function that it becomes, from the physiological point of view, a new one, and then is placed in quite another physiological category of organs. (Gegenbaur 1878, p. 10)

Biologist had been well aware of the morphological and taxonomic importance of rudimentary organs. In agreement with Darwin, Gegenbaur stressed that these non-functional structures are important in determining evolutionary relationships:

> These organs are valuable objects, since phylogenetic relationships can be very generally recognized by their aid. They show, too, how little physiological significance ought to be regarded in a morphological discussion, for in most of them a function is not to be made out at all, or, if it can be made out, is found to be quite different from the primitive one. (Gegenbaur 1878, p. 7)

Like previous anatomists, Gegenbaur makes use of the notion of serial homology. He calls the repeated occurrence of the same morphological unit within an individual 'general homology' (not to be confused with Owen's general homology that referred to the relation between a structure in an organism and the archetype). Three types of general homology are distinguished: homotypy (due to the left-right symmetry of most animals), homodynamy (structure repeated along the long axis of the body, i.e., Owen's serial homology), and homonomy (structure repeated along the traverse axis, such as the fingers of a hand). Even though Gegenbaur conducted embryological studies, in his later practice he relied for the most part on the positional criterion of homology as the primary way of establishing homologies. In turn, establishing taxonomic relations and phylogenetic trees was based on the detailed comparative study of adults, with embryological studies being an additional support. The mature Gegenbaur viewed embryology as being subordinated to anatomy (1878, p. 7).

Ernst Haeckel was a student of Johannes Müller at Berlin. Then he moved to Jena, teaching in zoology for Carl Gegenbaur. In 1965, Haeckel obtained a chair in zoology in the philosophical faculty. He collaborated with Gegenbaur until the latter moved to Heidelberg in 1873. While Gegenbaur was more methodologically careful and politically conservative, Haeckel was creative, speculative, and politically left leaning. Lynn Nyhart (1995) characterizes their relationship as the founders of evolutionary morphology in Germany by stating that "Gegenbaur was its [evolutionary morphology's] greatest practitioner", while "Haeckel was evolutionary morphology's most voluble spokesman" (p. 153). In 1863, Haeckel for the first time publicly endorsed the theory of evolution in his talk "On Darwin's Developmental Theory" (Haeckel 1864). From this point on, he boldly defended the theory of descent. Haeckel's main work was the *Generelle Morphologie der Organismen*

(General Morphology of Organisms), published in 1866. This work clearly reflects the fact that Haeckel's evolutionism was not only inspired by Darwin. The subtitle of the *Generelle Morphologie* states that it is founded on 'the descent theory *reformed* by Charles Darwin'. The second volume of the *Generelle Morphologie* is dedicated to Charles Darwin, Wolfgang Goethe, and Jean-Baptiste Lamarck (the first volume being dedicated to Gegenbaur). Haeckel's evolutionism made use of Lamarckian ideas, and he strongly supported the idea that evolution is a progressive progress, directed toward man as the perfection. Towards the end of his career, Haeckel founded the Monist League in 1906, which endorsed pantheism and social Darwinism.

One of Haeckel's fundamental evolutionary tenets is that all organisms — animals, plants, and single celled organisms — are descended from a single ancestral form. Due to his phylogenetic approach, Haeckel introduced the term 'phylum' for a basic type — the term we still use nowadays (though we recognize more than 20 phyla). He divides the field of morphology in two subbranches: anatomy and 'morphogeny'. The latter is divided into 'ontogeny' and 'phylogeny', terms that he introduced to refer to the developmental history of the individual, and the evolutionary history of the species. Haeckel is well known for his version of the recapitulation theory — the so-called biogenetic law. In short, it states that ontogeny recapitulates phylogeny; and Haeckel even maintained that phylogeny was the mechanical cause of ontogeny:

> Ontogeny or the development of organic individuals, as a sequence of form changes through which every individual organism goes during its individual existence, is immediately determined by the phylogeny or the development of the organic group (phylum), to which it belongs. Ontogeny is a short and fast recapitulation of phylogeny, determined by the physiological function of inheritance (reproduction) and adaptation (nutrition). (Haeckel 1866, Vol. 2, p. 300; my translation)

In its basic form, this model assumes that evolutionary modifications of organisms occur in adult characters (rather than in embryonic features). The descendants will inherit evolutionary modifications as so-called terminal additions — they recapitulate the ancestral developmental sequence and the novelty is added at the end of this sequence. Thus, evolution proceeds by adding more and more structures to the developmental sequence, which is in turn condensed in the sense that descendant species run faster through this sequence so that they are able to recapitulate the whole phylogeny in their life-time. However, there clearly are exceptions to this pattern. As discussed above (Section 4.1.3), Karl Ernst von Baer criticized the pre-evolutionary version of the recapitulation theory, which assumed that the development of higher organisms runs through the adult stages of all lower forms. Von Baer's critique relied among other things on examples of features in higher animals that do not exist in lower animals, but that develop in the higher animals very early in development. For instance, the mammalian embryo develops the placenta long before adulthood is reached; and thus

a character that is a relatively late evolutionary novelty (emerging with the origin of mammals) occurs very early in development. Ernst Haeckel later addressed these counterexamples by arguing that they are merely exceptions to the rule. In 1875, he introduced the notion 'palingenesis' for an evolutionary pattern that conforms to recapitulation. 'Cenogenesis', however, refers to an evolutionary scenario where an evolutionary change takes place in early development, so that a novel features is inserted into the ancestral developmental sequence rather than being a terminal addition. Haeckel acknowledged the existence of cenogenesis, but argued that it happened not very often and did not invalidate the biogenetic law. Despite critique, overall the idea of recapitulation in one way or another was very influential throughout most parts of the 19$^{\text{th}}$ century. Unlike von Baer's branching and divergence model, many zoologists endorsed a linear model of recapitulation where the development of the higher animals recapitulates the lower forms, in accordance with the idea that evolution is a progressive process that brings about more and more complex forms.[55]

The biogenetic law was of fundamental importance for Haeckel because it provided a way to establish phylogenetic trees and reconstruct ancestral form. Since ontogeny recapitulates phylogeny, the evolutionary history of an organism could be read off from its embryology — as long as cenogenesis did not complicate the matter. Haeckel did not primarily use detailed comparative studies of adult organisms to establish genealogical relations; instead he relied on embryological studies. One illustration of his approach is his famous Gastraea theory — which he viewed as his most important contribution to biology. Proposed in 1874, gastraea was Haeckel's name for the putative ancestor of all animals (Haeckel 1874, 1875). Embryological studies show that in the early development of multicellular animals a process called gastrulation takes place, at which the different germ layers are formed. Figure 5 shows gastrulae (the embryo at the stage of gastrulation) from various phyla of the animal kingdom, as drawn by Haeckel. Haeckel's fundamental claim was that the gastrula stage represents the ancestral form of all animals, and he christened this ancestor the Gastraea (an idea that is not accepted any longer). The 1874 paper also addressed the embryological criterion of homology based on the germ layer theory. Haeckel argued that the different germ layers in different animals are in fact homologous to each other, and that homologous structures develop out of the same germ layers.

Like former anatomists, Haeckel stressed the study of animal form. Recall that he divided morphology into 'anatomy' and 'morphogeny'. Anatomy was defined as the science of the completed form of organisms, and contained 'promorphology' as the study of the basic forms. Haeckel's

[55]See Gould (1977) for a historical discussion of the dominance and the decline of the recapitulation doctrine.

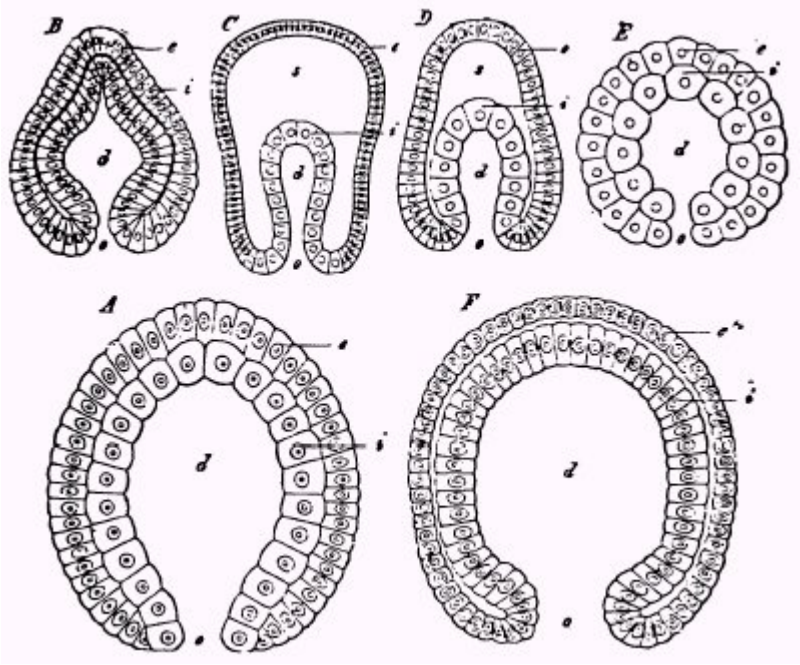

Figure 5: Gastrulae Across the Animal Kingdom (from Haeckel 1879)
A zoophyte; *B* worm; *C* starfish; *D* arthropod; *E* pond snail; *F* vertebrate
o primitive mouth; *d* intestinal cavity; *e* ectoderm; *i* entoderm

promorphology emphasized the various symmetries of organisms and the repeated occurrence of the basic morphological units within an organism. Consequently, Haeckel made use of the idea of serial homology, distinguishing the different types of serial homology by using Gegenbaur's terms (homotypy, homodynamy) in addition to his own neologisms. Haeckel defined (special) homology and analogy in evolutionary terms. Homology is similarity due to common ancestry, while analogy is similarity due to adaptation to similar environmental conditions:

> Apparently this question — even though nobody has addressed it so far — is of the highest importance for comparative morphology. For it concerns the final decision as to whether the striking similarities, which we find between the phyla of every kingdom (e.g., the similarities between vertebrates and segmented animals, . . .), are homologous — acquired by means of common ancestry — or analogous — originated due to similar adaptation. If all organisms of the three kingdoms are derived from one and the same moneres [most primitive forms], thus if each kingdom is a unique phylum [a monophyletic group], then it is possible that homologies exist between all parts of the phylum [i.e., the kingdom], i.e., similarities that are due to common descent and the inheritance from a common ancestral form. If however, each kingdom consists of different phyla, which originated from different moneres, then it is possible that similarities that occur in different parts of different phyla are merely analogies, i.e., acquired by means of similar adaptation to similar environmental conditions. (Haeckel 1866, Vol. 1, p. 204; my translation)

The modern reader needs to keep in mind that 19$^{\text{th}}$ century biologists did not make a real distinction between ontogeny and phylogeny. We nowadays view development and evolution as two

fundamentally different processes. For instance, a popular way to make the distinction is to say that in ontogeny the genetic information is expressed so that the animal develops. Evolution, on the other hand, is the modification of the genetic information inherited over generations. The modern understanding that views ontogeny and phylogeny as fundamentally distinct processes that should not be conflated originated in the 20$^{\text{th}}$ century based on the emergence of genetics. 19$^{\text{th}}$ century biologists understood 'inheritance' and reproduction as including development. Mendelian genetics, however, restricted the notion of 'inheritance' to the transmission of features over generation, which excluded development. Ideas such as the phenotype–genotype distinction and the rejection of the inheritance of acquired characters supported this development. A historical consequence was that during the first half of the 20$^{\text{th}}$ century, developmental biology and genetics split and became separate disciplines that did not influence each other much. Neo-Darwinism emerged in the 1930s as a synthesis of genetics and evolutionary biology, so that evolutionary and developmental biology were distinct enterprises — one studying phylogeny, the other ontogeny. 19$^{\text{th}}$ century biologists, however, viewed evolution and development as two sides of the same coin — to an extent that the modern reader will find 19$^{\text{th}}$ century biologist constantly conflating ontogeny and phylogeny. The term 'evolution' originally referred to the unfolding of the organism in development. The German word 'Entwicklung' was used to refer to both evolution and development, and continued to be used with this double meaning throughout the 19$^{\text{th}}$ century. This usage is illustrated by the title of Haeckel's first evolutionary treatise: "On Darwin's Developmental Theory [Entwicklungstheorie]." When Haeckel terminologically distinguished between ontogeny and phylogeny, he defined both as subtypes of *Entwicklung*, or as subdisciplines of the field morphogeny. The fact that Haeckel's two new terms were simply two species of the genus 'development' were the reason why other biologists accepted his neologisms (Nyhart 1995). The relative widespread acceptance of the idea of recapitulation (in different versions) reinforced the close connection that 19$^{\text{th}}$ century biologists saw between evolution and development — in continuity with how pre-Darwinians used developmental notions to propose (proto-)evolutionary ideas. This has consequences on how homology was viewed and defined. Nowadays, an evolutionary biologist defines homology in terms of common ancestry, but views the idea that homologous structures develop from the same precursor structures as a mere criterion of homology. In post-Darwinian 19$^{\text{th}}$ century biology, both phylogenetic and embryological formulations of homology were in use (the latter aligning with pre-Darwinian formulations). For instance, we saw above that Gegenbaur defines homologies as "the relations which obtain between

two organs which had a common origin, and which have also a common embryonic history."[56] Even more striking is the purely developmental definition of homology, which W. S. Dallas gives in the glossary appended to the 6th edition of Darwin's *Origin of Species*:

> Homology.—That relation between parts which results from their development from corresponding embryonic parts, either in different animals, as in the case of the arm of man, the fore leg of a quadruped, and the wing of a bird; or in the same individual, as in the case of the fore and the hind legs of quadrupeds, ... The latter is called *serial homology*. The parts which stand in such a relation to each other are said to be *homologous*, and one such part is called the *homologue* of the other. (Darwin 1890, p. 512)

Originally, Carl Gegenbaur and Ernst Haeckel had roughly the same approach in evolutionary morphology. A subtle difference in their academic style is pointed out by Lynn Nyhart:

> As a zoologist, Haeckel was more concerned to ascertain the true evolutionary tree of life, a historical pattern he dubbed "phylogeny." As a comparative anatomist, Gegenbaur was more concerned to explain present-day similarities and differences in vertebrate form through tracing their evolutionary history. (Nyhart 2002, p. 6)

While starting as colleagues and friends, their approaches came to diverge during their career, which was reinforced when Gegenbaur left Jena for Heidelberg while Haeckel stayed in Jena. Gegenbaur came to rely on comparative anatomy, while Haeckel used embryology to establish phylogenetic trees and evolutionary ancestors. Initially, both Gegenbaur and Haeckel endorsed the idea of recapitulation, and assumed that results from comparative anatomy and embryology would reinforce each other. But as we saw in the discussion of some prior anatomists, researchers differed in their training, the type of anatomical information they had available, and their preferred method. In actual practice, one of the criteria of homology (the positional or the embryological) was given slight preference. The same held for Gegenbaur and Haeckel. It became clear among morphologists that the different methods may yield different results, and the question as to whether comparative evidence is to be trusted more than embryological evidence led to a debate in German morphology (Nyhart 1995, 2002; Laubichler and Maienschein 2003). The conflict centered for instance on the question of how the vertebrate limbs evolved. The limbs of limbed vertebrates (i.e., the legs) are apparently derived from the paired fins of fish (the two pairs of fins located on the left and right side of the belly, as opposed to the single set of fins on the back and at the tail). However, primitive fish such as lampreys and hagfish do not have fins or appendages at all, so the question was how vertebrate appendages evolved in fish. In the 1870s, Gegenbaur developed and defended his famous archipterygium theory (the archipterygium is the primitive, ancestral form of the fin as

[56] In Section 4.3.1 I laid out Lankester's phylogenetic definition of homology, and his rejection of a Platonic conception of homology. In spite of this rhetoric, Lankester made the idea of recapitulationism popular in Great Britain, and his anatomical practice he strongly relied on embryological evidence (the embryological criterion of homology).

postulated by Gegenbaur). He argued that the paired fins in fish were derived from the gill arches (skeletal structures): the two hindmost gill arches had migrated from the head towards the tail and were transformed into the girdles of the two pairs of fins. Gegenbaur used detailed comparative study of the adult skeletons of vertebrates to support his view (Gegenbaur 1874). This theory was rejected by other anatomists, including the American James K. Thacher, the British zoologists St. George Mivart and Francis M. Balfour, and the German anatomists Anton Dohrn, Carl Rabl, and Robert Wiederheim. Gegenbaur's opponents used primarily studies about the development of fins to support their rival position (the side-fold hypothesis).

Overall, the situation led to a methodological dispute among German evolutionary morphologists in the 1880s and 1890, which came to be called the *Kompetenzkonflikt* (conflict of competence). Apart from denoting academic qualification, *Kompetenz* had a legal connotation, referring to administrative authority. The question was whether embryology or comparative anatomy was the arbiter over phylogenetic hypotheses:

> As the split widened, comparative anatomists and embryologists quarreled with increasing bitterness over the relative value of their different kinds of evidence for solving major morphological questions. ... As these men argued with each other, the terms of the debate shifted so that it came to signify a division between comparative anatomy on the one hand and embryology on the other. (Nyhart 1995, pp. 244–245)

Based on the biogenetic law, Haeckel and his supporters favored embryological evidence. Ancestral characters were those that can be found in the embryo. Gegenbaur, however, argued that those characters are ancestral that exists in the adult of a large group of animals (whereas characters that exist in a smaller group evolved more recently). He viewed the biogenetic law as being of low utility due to the existence of cenogenesis, i.e., adaptations and evolutionary novelties that occur in the embryo rather than in the adult as terminal additions. His fundamental objection was that any evolutionary modification in early development had profound influences on the subsequent steps of development. Thus, one cenogenetic event as an exception to the biogenetic law gave rise to further cenogenetic events (Gegenbaur 1889). One historical consequence of this debate was that the biogenetic law came under fire, contributing to its abandonment at the beginning of the 20^{th} century. A further result was that the methodological dispute was never really settled. Instead, a split between embryology and comparative anatomy occurred. The debate supported the decline of evolutionary morphology in favor of the new approach of experimental (or causal) morphology. This approach emerged in the 1880s and focused on the experimental study and the mechanistic explanation of ontogeny. Haeckel's contention that ontogeny was mechanically caused by phylogeny was vehemently rejected by the proponents of this new tradition, who abandoned the

study of phylogenetic and evolutionary questions in favor of embryological questions.

My discussion of early evolutionary morphology illustrates the following points. Anatomy in general and homology in particular came to be embedded in a phylogenetic framework. We saw that Darwin had given a similar interpretation of morphological notions in the *Origin*, using prior anatomical results as support for this position. However, in his research practice Darwin did not focus on anatomy, his primary concern were the mechanisms of evolutionary modification and inheritance, and the study of variation and the biogeographic distribution of species. Gegenbaur and Haeckel were hardly concerned with the mechanisms of evolution and the adaptation to environmental demands. Instead they focused on phylogeny and the patterns of evolutionary modification, using anatomical and embryological studies to establish ancestral forms and phylogenetic trees.

> Many of Darwin's contemporaries followed a different course. Carl Gegenbaur and his intimate friend Ernst Haeckel believed that the primary obligation imposed by Darwin was less the ever-wider extension and validation of the hypothesis of natural selection than a demonstration and detailed elaboration of the historical record of life. (Coleman 1976, pp. 149–150)
>
> The emphasis of evolutionary morphology as perceived by Gegenbaur and Haeckel differed from Darwin's original program in crucial ways; not individual variation and it consequences for gradual change by means of natural selection was the main focus of study, rather it was the idea that common ancestry could provide a new foundation for comparative anatomy and systematics as well as a new perspective for the search of morphological laws of transformation. (Laubichler 2003, p. 26)

Evolutionary biology brought a new perspective on anatomy. But especially in the case of Gegenbaur's intellectual development, we saw above the large extent of continuity between pre-Darwinian and the early evolutionary morphology (Coleman 1976). Traditional notions from 'idealistic' anatomy such as the homology concept and the notion of a type continued to be used, albeit from a phylogenetic point of view. Post-Darwinian definitions of the homology concept often included reference to common ancestry (as we saw in the case of Lankester, Gegenbaur, and Haeckel). However, despite this new definition the homology concept was used in largely the same way in biological practice as in pre-Darwinian times. Evolutionary biology did not create any new criterion of homology. For the condition of common ancestry as part of homology definitions did not yield an independent criterion to establish homologies: Knowledge about common ancestry and phylogenetic trees was based on prior studies in comparative anatomy and embryology — fundamentally based on the homology concept. Homologies used to be established based on the positional or embryological criterion. Only in a second step, homologies were interpreted as being due to common ancestry, and the taxonomic and morphological relations between different groups of living organisms were interpreted as genealogical relations.

> The interesting thing is that Gegenbaur defines it [the homology concept] genetically. Special homology is the name we give "to the relations which obtain between two organs which have had a

> common origin, and which have also a common embryonic history" ... This is his definition; but, in practice, Gegenbaur establishes homologies by comparison just as the older anatomists did, and infers common descent from homology, not homology from common descent. (Russell 1916, p. 266)

In his essay on the "History of Comparative Anatomy," the comparative anatomist Wilhelm Lubosch makes the point that evolutionary morphology merely reinterpreted prior notions:

> Viewed from the outside ... nothing more happened than that the previous conceptions were reinterpreted in accordance with the theory of descent. What had hitherto been called the basic forms [Urformen] (or as the type), now became called the ancestral forms [Stammformen]. The 'scale of forms' [Stufenfolge] became the genealogical tree; the metamorphosis became the real transformation. The manifold [of form] became the variation; the specification became called the inheritance. The homology of position became the homology due to common origin; the parallel between embryonic forms and the animal series became the biogenetic law. (Lubosch 1931, p. 38; my translation.)

The same point about anatomical practice is expressed by Edward Stuart Russell as follows:

> The close analogy between evolutionary and transcendental morphology has already been remarked upon and illustrated in the last three chapters. We have seen that the coming of evolution made comparatively little difference to pure morphology, that no new criteria of homology were introduced, and that so far as pure morphology was concerned, evolution might still have been conceived as an ideal process precisely as it was by the transcendentalists. The principle of connections still remained the guiding thread of morphological work; the search for archetypes, whether anatomical or embryological, still continued in the same way as before, and it was a point of subordinate importance that, under the influence of the evolution-theory, these were considered to represent real ancestral forms rather than purely abstract figments of the intelligence. The law of Meckel-Serres was revived in an altered shape as the law of the recapitulation of phylogeny by ontogeny; the natural system of classification was passively inherited, and, by a *petitio principii*, taken to represent the true course of evolution. It is true that the attempt was made to substitute for the concept of homology the purely genetic concept of homogeny, but no inkling was given of any possible method of recognising homogeny other than the well-worn methods generally employed in the search after homologies. (Russell 1916, pp. 302–303)

4.3.3 Evolutionary Morphology in the 20th Century

The goal of the discussion of evolutionary morphology so far has been to illustrate my claim that in the decades after the publication of Darwin's *Origin* basically the same homology concept was still used as in pre-Darwinian morphology. I do think that the use of an evolutionary approach ultimately led to the emergence of a distinct phylogenetic concept, used in evolutionary biology and systematics. However, my view is that this concept became predominant only in the second half of the 20th century. Thus, my claim is that well into the 20th century many biologists used the same homology concept as in the pre-Darwinian era. A justification of this claim would require a detailed review of the use of the homology concept in the first half of the 20th century — which is clearly beyond the scope of my dissertation. Rather than offering real evidence for this idea, I restrict my discussion to the more limited goal of illustrating that the tradition of Gegenbaur and Haeckel was

continued by some morphologists in the 20th century. I discuss in detail a single representative, the German morphologists Adolf Remane (1898–1976). His work has never been translated, but Remane was (together with Rupert Riedl) the most influential 20thcentury morphologist in German-speaking countries. Apart from his overall influence, I chose Remane because he gave very explicit theoretical reflections on the homology concept and explained and clarified the criteria of homology in a virtually unprecedented manner. One could view Remane as a transitional figure between a traditional 19thcentury and a contemporary homology concept (Laubichler 2000; Müller 2003). But I feel that Remane is still rooted in an approach like Gegenbaur's. Even though my brief discussion of evolutionary morphology deals with representatives from Germany only (Gegenbaur, Haeckel, Remane), similar approaches could be found in other countries as well (see for instance Hyman 1922; de Beer 1928; Goodrich 1930; Romer 1949).

Adolf Remane's main work is the treatise *Die Grundlagen des natürlichen Systems, der vergleichenden Anatomie und der Phylogenetik* (The Fundamentals of the Natural System, Comparative Anatomy, and Phylogenetics), originally published in 1952. Remane continues the tradition of Gegenbaur and Haeckel in that he approaches anatomy within a phylogenetic framework. His main aim is the study of phylogenetic and taxonomic relationships, but he is not much concerned with discussions of the mechanisms of evolutionary change, and the way in which organisms adapt to their environment. Remane uses the term 'phylogenetics' (*Phylogenetik*) for his approach in morphology. Due to his clear-cut and sophisticated phylogenetic framework, his work foreshadowed some ideas that are nowadays standard notions in phylogeny and phylogenetic systematics (cladistics). In line with previous post-Darwinian anatomists, Remane states that taxonomy and comparative biology is prior to phylogeny, as phylogenetic trees are established based on comparative information and classifications, but not the other way round. He also emphasizes the continuity between pre- and post-evolutionary anatomy regards research practice:

> The similarity between pre-phylogenetic morphology and systematics, on the one hand, and phylogenetics, on the other hand, that my discussion just emphasized appears to contradict the often stressed opposite between idealistic morphology and phylogenetics. However, both conceptions are valid. The identity of these two fields concerns the research principles, the method; w.r.t. these aspects the year 1859 (the year in which Darwin's Origin of Species appeared) does not amount to a radical change; morphology and systematics before and after [Darwin] worked based on the same guidelines. The situation is different as regards the biological view of life [Weltbild], which was erected on the knowledge gained. ... The work of morphologists and systematists in those days was only slightly influenced by this metaphysical [idealistic] approach, as it was simply used as an explanatory interpretation of the results gained in a methodical way. For this reason, it is regrettable that the whole period of pre-phylogenetic morphology came to be called 'idealistic morphology'. This important period should better be called 'pure morphology', the idealistic philosophy was simply an interpretative superstructure, which was very influential in the philosophy of nature in those days,

but hardly in the domain of methodical research. (Remane 1956, pp. 12–13; my translation)

Remane reasserts that homologous structures may look quite different in different species and may have a different function — emphasizing that "the independence of homologous type characters from the analogical agreement in structure and function is the most important principle of morphology" (1956, p. 28).[57] However, this merely tells us what homology is not. Remane offers a positive characterization of the homology concept by giving a detailed discussion of the criteria of homology. His discussion of homology criteria alone makes Remane's treatise so important for 20th century morphology. Remane addresses the fact that different criteria and definitions had been in use (positional, embryological, phylogenetic). Some biologists, such as Meyer (1926) and Bertalanffy (1932, 1934) have argued that different criteria yield different results and consequently different homology concepts. For instance, Bertalanffy suggested distinguishing between typological, typological-ontogenetic, phylogenetic, and developmental-physiological homology. Remane, however, replies that if there were in fact different homology concepts, one would obtain different taxonomies and phylogenetic trees. There is only one concept and phenomenon of homology, even though there are several criteria of homology. Whereas some biologists in the past have focused on one criterion of homology, Remane claims that homologies have to be established based on the use of all criteria. What he has in mind is a probabilistic approach according to which the degree of confirmation of homology is proportional to the number of criteria that are met and the degree to which they are satisfied.

Remane also addresses critiques of the homology concept directed against the phylogenetic definition of homology. Oskar Hertwig and Hans Spemann belong to the tradition of experimental morphology, rejecting the prior evolutionary morphology because the establishment of phylogenetic trees and the postulation of ancestors were viewed as speculative business in contrast to the experimental study and causal explanation of development. Homology was the main concept of evolutionary morphology; this is the reason why Hertwig (1901–1906) and Spemann (1915) criticized the phylogenetic understanding of homology from the point of view of developmental biology. Hertwig actually made the circularity objection against a homology concept that is defined in term of common ancestry that creationists nowadays put forward (see Section 4.0.2). The objection is that homology has to be established based on phylogenetic trees (as it is defined in terms of

[57] An important method of Remane to establish phylogenetic relations is what he calls the 'ethological' method. This method starts with disagreements between the structure of organisms and their lifestyle and their functions. In other words, non- or mal-adaptive structural features tell about phylogenetic relations. A special example is the well-known importance of rudimentary organs, but Remane's 'ethological' method is more general.

common descent), but the establishment of phylogenies presupposed comparative knowledge, in particular knowledge about homologies. Given Remane's assumption that pre- and post-evolution morphology are basically identical in their methods, he upholds the criteria of homology, which do not make reference to phylogeny, as a crucial ingredient of this concept:

> If one requires of a definition that it includes all methodical criteria of a concept, then in fact the phylogenetic definition of homology does not meet the standards of a definition; but in this case this does not tell anything against the homology concept, as there are methodical criteria for this concept. What the phylogenetic researchers wanted to give with their "definition" of homology, was an "explanation" of homology, the theory of this concept. The "common ancestry" can only be understood in this way; in this sense it is fully valid, it is in fact the only "explanation" of homology that can be given as of now. (Remane 1956, pp. 61–62; my translation)

Thus, despite definitions of homology in terms of common ancestry, Remane does not think that the standard definition exhausts the homology concept. Instead, he views the criteria of homology as constitutive of the homology concept. As already indicated, I am very sympathetic to the idea that the homology concept is not to be conflated with definitions of homology. Remane's emphasis of the criteria of homology focuses on how the homology concept is actually used in biological practice, which I take to be features that guide the philosopher to a concept's actual content.

Remane's criteria of homology summarize both prior biological practice and give useful guidelines for future researchers. He discusses three main criteria and some subsidiary criteria. The first criterion is the well-known positional criterion, or the 'criterion of position', as Remane calls it. He gives a detailed discussion of what this criterion means and how it is to be applied in various practical cases. The second criterion is the 'criterion of special quality'. This refers to the idea that homologous structures often resemble each other in structural detail, i.e., this criterion is about the intrinsic morphological qualities of a structure rather than its topological relation to others. If a biologists does not have a completely arranged skeleton, but only some individual bones, she is still in a position to assess the homology of these bones — even though an individual bone is not part of any structural assembly so that the positional criterion cannot be used. Otherwise it would be impossible to reconstruct a skeleton from individual bones. However, this criterion is of limited validity. Structures from closely related species in fact resemble each other to a large extent, but as it is well-known, characters from less closely related species can be quite dissimilar due to evolutionary change. In addition, the similarity of evolutionary pressures may bring about similar structures (analogies), even though these structures are not phylogenetically related. The last main criterion is the 'criterion of connection by intermediate forms'. Two structures that are not apparently homologous may still be homologous in case they can be connected by a series of intermediate

forms, such that two adjacent structures in this series are apparently homologous (according to the above two criteria). On Remane's account, intermediate forms can be adult structures from existing species or embryological structures. The subsidiary criteria of homology basically state that homology is likely to obtain if similar structures are present in many closely related species, whereas homology is unlikely if the similar structures occur only in unrelated species. These subsidiary criteria foreshadow the way in which homology is nowadays assessed in phylogenetic systematics (cladistics). It is worth quoting Remane's summary of his three main criteria:

> 1) Homology results from the same position in comparable structural systems. 2) Similar structures can be homologized independent of the same position, if they agree in numerous special features. 3) Even structures that are dissimilar and have a different relative position can be declared homologous, if it is possible to establish intermediate forms between them, such that in the case of two adjacent forms criterion 1 or 2 is satisfied. The intermediate forms may be obtained either from the ontogeny of structures or they may be real taxonomic intermediate forms. (Remane 1956, pp. 58; my translation)

The reader may have noticed that Remane does not mention the embryological criterion among his criteria. This is due to the fact that he does not think that the embryological criterion — as usually understood — is a real criterion of homology. Remane argues that we should not view the idea of recapitulation as stating that the development of the whole organisms repeats its phylogeny; instead, recapitulation obtains for individual organs. However, even in this weaker sense, recapitulation occurs only in 70% of all cases, on Remane's estimate, so that the embryological criterion is not very reliable. Remane points to several examples where related organisms develop in different ways. Their adult structures are homologous, but these structures develop out of different precursor structures and in a different fashion, so that the embryological criterion is invalidated. Homologous structures may even develop from different germ layers:

> When we postulate that in normal development the homologous organs usually originate from identical germ layers, we are justified in doing so, but only based on an empirically established rule, not because of an ontogenetic definition of homology. (Remane 1956, pp. 66; my translation)

This does not mean that embryological evidence does not play any role for establishing homologies. For we saw that Remane assumes that embryonic forms are important intermediate forms according to the third homology criterion. The point is that embryology yields the intermediate forms, but whether structures in a sequence of intermediates are homologous depends on the other, non-embryological criteria, in particular the positional criterion. Thus the use of embryological information is subordinated to the positional criterion. Developmental biology yields only indirect evidence, as it is usually invalid to directly read homology off the ontogeny of an individual, as the embryological criterion assumes. Thus Remane reasserts the often held position that embryology is

subordinated to comparative anatomy in the case of homology assessment. In line with Gegenbaur,

> We conclude that ontogenetic correspondence cannot possibly be used as a definition or criterion of homology. (Remane 1956, pp. 67; my translation)

Remane acknowledges the existence of serial homologues, i.e., the repeated occurrence of the same morphological elements within an organism. His first criterion (the positional criterion) does not apply to serial homologues, while the other two criteria can be used to establish serial homologies. But Remane still views serial homology of a different nature than special homology (homology between species), apparently due to his phylogenetic approach. Establishing serial homologues does not contribute to the classification of species and the establishment of phylogenetic trees — one has to compare structures in different species to do this. For this reason, Remane prefers to reserve the term 'homology' for homologies between different organisms, and to use the distinct term 'homonomy' for what Owen called serial homologues. Like his forerunners in anatomy, Remane uses the idea of a type. He distinguished between four notions of a type or four methods that were used to obtain the type of a group of animals. The 'diagrammatic type' represents organisms that correspond to each other in all their structures, i.e., these organisms have exactly the same number of homologues. The 'generalized type' represents what all different organisms in a group have in common by abstracting from variation. The 'central type' is the mean of a set of species arranged in a series. Finally, the 'systematic type' describes the features that characterize a taxonomic group. Remane argues that among the four this last notion of a type best represents the ancestral form, and thus is particularly useful for taxonomic and phylogenetic studies. This notion of type points again towards current taxonomic practice, for Remane's systematic type bears some similarities to what we nowadays call the set of synapomorphies that characterize a taxon.

4.4 A SEMANTIC CHARACTERIZATION OF THE HOMOLOGY CONCEPT USED BEFORE 1950

Given this review of some aspects of the history of the homology until 1950, it is time to draw philosophical conclusions. I combine a semantic characterization of the homology concept used in this period with the argument that despite the adoption of a novel definition of homology, the term 'homology' as used in pre-Darwinian and as used in post-Darwinian biology (until the middle of

the 20th century) expressed the same concept. In a nutshell, the argument is based on the historical stability of the concept's *inferential role* and the *epistemic goal* pursued with its use. The post-Darwinian adoption of a novel theoretical characterization of homology was a moderate change in inferential role occurring internal to the concept (rather than amounting to the advent of a distinct concept). Still, this particular conceptual change can be accounted for as proceeding in a rational fashion based on the stable epistemic goal for which the concept was used.

One aspects of a term's inferential role (conceptual role) are theoretical characterizations of the phenomenon referred to. In fact, the conventional wisdom among biologists, historians and philosophers of biology, assuming that a pre-Darwinian, 'idealistic' homology concept was replaced by a post-Darwinian, 'phylogenetic' homology concept, is predicated on the idea that before Darwin geometric definitions of homology prevailed, while after Darwin homology came to be defined in term of common ancestry (Section 4.3.1). It is true that preferred definitions of homology changed, but this account ignores that some continuity regards theoretical characterizations of homology obtained. We saw in Section 4.1 that in addition to purely geometric interpretations of morphological phenomena, homologies and morphological types were viewed as reflecting laws existing in nature, which were typically interpreted using ideas about development. For instance, von Baer argued for a theoretical account of homology and taxonomic relations in terms of laws of development. (I also mentioned that many pre-Darwinian evolutionary hypotheses were essentially developmental theories of evolution.) With the advent of Darwinian evolutionary theory, common ancestry often became a part of homology definitions. At the same time, developmental characterizations of homology were typically combined with phylogenetic ones, and I pointed out that even purely developmental definitions were put forward in the second half of the 19th century. Overall, throughout post-Darwinian 19th century biology, ontogeny and phylogeny were viewed as two aspects of one phenomenon, and many theories of evolution used developmental principles (rather than natural selection) to understand the patterns and mechanisms of evolution (Sections 4.3.1 and 4.3.2). Thus, even as regards definitions and theoretical characterizations of homology, there was some continuity between pre- and post-Darwinian biology.

Rather than theoretical definitions, a more crucial aspect of inferential role is the term's actual usage in practice. Chapter 3 motivated this semantically by the idea that a central task of a theory of concepts is to explain how a concept underwrites successful practice. Section 4.2 emphasized that the way in which the homology concept figured in biological practice and made successful practice possible in the first place was essentially constituted by how homologies were established

in practice, and how this knowledge was used for taxonomic and morphological purposes. In what follows I focus on these features of homology's inferential role (as used until 1950), which are more central to the concept's content than theoretical definitions. But before this, let me point out that even from a purely theoretical point of view, a definition of homology in terms of common ancestry is incomplete. The contemporary evolutionary biologist Ernst Mayr (1982) — using what I call the phylogenetic homology concept — criticizes Adolf Remane for not sharply distinguishing between the definition and the criteria of homology (Remane assumes that homology criteria are part of the concept; see Section 4.3.3). Mayr prefers a definition purely in terms of common ancestry. However, such a definition is to a certain extent circular, as pointed out by Jardine (1967), Wagner (1994), and Brigandt (2002). For structures in two extant species are defined as homologous in case they are derived from the same structure in the common ancestor. But to say that a structure in the descendant is 'derived' or 'inherited' from an ancestral structure is simply to say that these structures are homologous. One can consider a lineage of species leading from the ancestor to the descendant and re-identify the homologue in each species of this lineage. But then one still has to explain what makes a structure in an immediate descendant species homologous to a structure in the ancestral species. At least one needs an account of what makes a structure in an individual the same structure as the homologue in its parent. The criteria of homology obviously permit finding out which of the many structures in an offspring is homologous to a given parental structure. However, the criteria — construed in opposition to the definition — of homology do not yield an account of in virtue of what a structure of an individual is homologous to a structure of its parents. Homology definitions based on the notion of inheritance or common ancestry can reduce the notion of homology between extant species to the notion of homology between ancestor and descendant (or parent and offspring), but there is still an unexplained remainder.[58] Thus, even from a purely theoretical standpoint, a definition in terms of common ancestry is incomplete, and *a fortiori* does not capture the content of the homology concept as it underwrites actual research practice.

Throughout my discussion I paid attention to the criteria of homology, emphasizing that how

[58] A similar issue is *bona fide* instances of homology that do not fall under a purely phylogenetic definition. Hans Spemann (1915) discusses the regrowing of experimentally removed lenses in amphibians. The regenerated lens is in fact made from a different type of tissue than the original lens. Spemann's discussion is predicated upon the assumption that the regenerated lens is homologous to the original lens, but this case cannot fall under a definition of homology in terms of common ancestry or the inheritance of structures, as the regenerated lens is not inherited from any organism. In my view, for some scientific concepts, once a theoretical definition of the concept is gained some of the initial examples are rejected (if they do not fall under the new definition) and certain criteria viewed as highly fallible. In such cases, the new theoretical definition takes over and primarily constitutes the concept. The homology concept is very different in that biologists may stick to agreed upon examples and criteria even if they are not directly supported by a particular definition such as a definition in terms of common ancestry (Griffiths forth.).

homologies were established in biological practice was important for the content and successful usage of the homology concept. We saw that in pre-Darwinian comparative anatomy two main criteria were in use. The positional criterion assumes that a homologue across different species is connected with and has the same topological relations to other structures of the organism. The embryological criterion assumes that homologous structures in different species develop in the same way, e.g., by developing out of the same developmental precursors or the same germ layers. The pre-Darwinian history showed that some biologists relied in their practice more on one than the other criterion, and the same applies to the post-Darwinian period. Some anatomists argued for the primacy of the positional criterion by pointing to examples of homologous structures that develop in a different manner. This was the case for Richard Owen, and for Carl Gegenbaur and Adolf Remane in the case of evolutionary morphology (Tait 1928). Remane (1961) argued that sameness of developed structure and sameness of development are not coextensional. In a similar vein, Alan Boyden's review of the concept of homology asserted that relative position rather than developmental similarity is the most important criterion of homology (Boyden 1943). Overall, the positional criterion proved to be more important and widely used than the embryological criterion.[59] But the embryological criterion was still viewed as having some legitimacy despite potential exceptions. The idea of linear recapitulation as well as von Baer's divergence model of comparative development offered some explanation of why the embryological criterion holds in many cases. Even Remane, who argued that the embryological criterion is not a real criterion, admitted that the study of animal development is important for establishing homologies. He can be interpreted as using the embryological criterion as an auxiliary criterion.

Remane's influential discussion made a criterion explicit that appears to be distinct from both the positional and embryological as construed in pre-Darwinian anatomy. This is the criterion of connection by intermediate forms, according to which two structures are homologous if one can construct a transformation series of intermediate forms such that two adjacent forms in series are clearly homologous. Remane was surely not the first one to use this criterion, but he gives a particularly clear account of it. The intermediate forms can be intermediate stages of development. In this case, this criterion is similar to the embryological one, but it is more general as it does not assume that we can directly read homologies off the development of an individual in every case. In addition, the intermediate forms may be structures found in adult organisms. An obvious motivation for the criterion of connection by intermediate forms is the idea of descent with modification,

[59] Section 5.2.1 will explain why it is nowadays an important fact that homologous structure may develop differently.

so that evolutionary theory could potentially be viewed as having brought about a new homology criterion.[60] However, this idea was not totally new. For pre-Darwinian anatomists were aware of the variation that a homologue shows across different species. Geoffroy Saint-Hilaire, for instance, used as a point of reference the most developed and complex structure that exists in a group of animals, studying other structures that are homologous to this exemplar in terms of the degree to which they approach the most complex one. Thus, Geoffroy was aware of the fact that homologues across different species can be ordered into a series. The same idea was implicit in the practice of pre-Darwinian morphologists that strongly relied on embryological studies (such as Rathke and Müller), as they studied embryological intermediates and developmental series and made use of knowledge as to how the same structure is differently developed and functionally differentiated in different species. For this reason, I do not view Remane's criterion of connection by intermediate forms as a totally new criterion of homology. But evolutionary morphology made this criterion more explicit and widely used compared to pre-Darwinian anatomy. I view this as a refinement of the criteria of homology used rather than a substantial change in the way in which homology was assessed. Remane emphasized that the different criteria of homology cannot be used in isolation and that they do not constitute different homology concepts. I completely agree with this account. For the most part, the different homology criteria were used in combination to establish homologies. Apart from hard cases, biologists came to recognize and agree on many homologies.[61]

Another type of inference that was important for the homology concept's usage is based on the assumption that for any given structure in a species, there exist structures in other species that are homologous to it. My discussion of pre-Darwinian anatomy emphasized the importance of this assumption because of its heuristic impact. Based on this idea, biologists were able to discover structures in new species, or to break a known structure down into subunits in case these subunits can be homologized with known structures in other species. This heuristic impact of the homology concept did not diminish with the advent of evolutionary theory. Pre-Darwinian anatomists had a very good understanding of homologies in vertebrates, in particular the vertebrate skeleton. But other animal phyla were still in need of detailed comparative study. In addition, other vertebrate

[60] However, Remane did not require that the series of intermediate forms reflects the real evolutionary transformation series of the two structures involved, in contrast to contemporary phylogenetic approaches to homology (Section 5.1.3).

[61] In my discussion of the pre-Darwinian period (Section 4.2), I used Anil Gupta's (1999) notion of a frame to offer a semantic account of the interplay of different homology criteria. The same interpretation applies to the homology concept as used in the post-Darwinian period. Different criteria of homology are some of the inferences that constitute the content of the homology concept. Even though different criteria are empirically non-identical, due to the existence of a frame these criteria are used in appropriate circumstances and not conflated in practice, which accounts for the successful establishment of homologies in biological practice despite the availability of several criteria.

structures apart from the skeleton such as the muscular and nervous system had to be explored in more detail; and the homology concept also became applied to lower levels of biological organization by homologizing tissues, embryonic structures, and germ layers. Pre-Darwinian biologists were aware of the fact that a homologue of a given structure does not always exist in other species. For the most part, structures from different types (phyla) were never homologized. And as taxonomically closely related species are more similar than more remote species, the expectation was that the existence of homologues is more likely the closer two species are related taxonomically. After the advent of evolutionary theory, it became clear that taxonomic groups are genealogical groups, so that it could be stated that the occurrence of homologues is more probable the closer two species are related genealogically. The idea of common descent also yielded an explanation of the previously known fact that this inductive inference is valid in many cases.

A further influential aspect of the use of the homology concept stems from the idea that homology individuates characters by breaking down an organism into natural units (different homologues). One such unit can occur with a different shape and function in a different species, independently of how other units (structures) differ across species. From a phylogenetic point of view this means that a homologue is a unit of morphological evolution as it can undergo modification relatively independently of other units. In virtue of individuating biological characters and picking out units of morphological variation across species, the homology concept makes 'meaningful' comparison possible. Section 4.2 explained why this idea was already relevant for pre-Darwinian taxonomy. The classification of species proceeds by comparing the corresponding, i.e., homologous, structures in different species. Only the comparison of homologues is of use for taxonomic practice and guarantees stable classifications. Evolutionary theory yields an explanation for why this is so. For homologous structures in different extant species are derived from the same structure in the common ancestor; and the degree of dissimilarity between these structures informs biologists about how closely related two species are. While pre-Darwinian biologists were often aware of the fact that the similarity of analogous structures in two species does not imply that these two species have to be put into closely related taxonomic groups, evolutionary theory gave an explanation of why this prior practice of comparing homologous characters was so effective in establishing natural groupings of species. Evolutionary theory also revealed another sense in which homology makes 'meaningful' comparison possible. The reason is that hypotheses of homology are necessary for expressing claims about evolutionary patterns, i.e., for stating what changes took place in the course of phylogeny. Most claims about morphological evolution are about whether a homologous structure exists in

another species and whether a homologue of the ancestor was inherited or lost, or whether and how a homologue was modified in its structure or function in the course of evolution. Thus phylogenetic statements as made by evolutionary morphologist and post-Darwinian biologists in general presupposed the homology concept. In sum, the homology concept as individuating characters and relating structures from different species was important for classifying different species and studying the phylogenetic relations between species as well as their evolution. For this reason, the homology concept served some of the basic purposes of taxonomy and evolutionary biology.

My prior philosophical discussion of the homology concept as used in pre-Darwinian biology made clear what I view as one of the most important inferences supported by this concept. It stems from the idea that homologues are natural kinds (with homology individuating biological characters). For my purposes, the important feature of homologues as natural kinds is the projectability of properties from one instance of a natural kind to another instance. Many descriptions that hold of one structure hold of the corresponding structure in another species. This is the case for morphological and histological properties, such as how the structure is connected and related to adjacent structures and out of what subunits or types of tissue the structure is composed. It also holds for the development of structures, as homologous structures in many cases develop in a similar manner. Thus, the homology concept embodies an inductive inference from the properties of one structure to the properties of another structure. As one infers from one structure or species to another one, this inference is more precisely a form of analogical reasoning. In the case of special homologues, i.e., homologous structures from different species, the idea that these structures are derived from an ancestral structure can explain why this inductive inference is a good one. But the validity of this inference was clearly recognized by pre-Darwinian anatomists, even though they did not have an explanation of this fact as we have nowadays. In the case of serial homologues, i.e., the occurrence of the same structure within one individual, common ancestry cannot account for the shared properties of different instances of serial homology. But the inference is still valid as a matter of fact.[62] After all, the reason that the idea of homology — between species as well as within an individual — was introduced in the first place is that comparative anatomist were able to uncover a unity of form within and between organisms.

This inductive inference is so important for biological practice because it yields systematic descriptions of the features of organisms. Biological properties apply to most instances of a class of homologues such as the epithalamus, a part of the brain which exists across the large and di-

[62]Section 5.2 will discuss contemporary attempts to explain the validity of this inference.

verse group of vertebrates. Biological discussions can simply talk about 'the' epithalamus and give descriptions of it — as if it were a single token-structure rather than a large class of individual instances. Individuating characters by means of homology (rather than another principle of individuation) and applying predicates to names of homologues yields unified knowledge. This fact is important for all branches of biology and shows the fundamental importance of the homology concept. To illustrate this with a prominent example, the current research on model organisms is based on this inductive inference supported by the homology concept. Current research on animals primarily focuses on six species: the house mouse *Mus musculis*, the chicken *Gallus gallus*, the frog *Xenopus laevis*, the zebrafish *Brachydanio rerio*, the fruit fly *Drosophila melonogaster*, and the nematode worm *Caenorhabditis elegans*. These few species are experimentally studied in great detail. However, the assumption is that the knowledge gained from these organisms carries over to other species. For instance, the house mouse is a representative for all mammals in that we are permitted to draw conclusions about many biological properties of other mammals from the information gained on the mouse by means of analogical reasoning. The possibility of such an analogical inference depends on the fact that the many structures of these different species are homologous.

> Homology is the central concept for *all* of biology. Whenever ... we argue that discoveries about a roundworm, a fruit fly, a frog, a mouse, or a chimp have relevance to the human condition — we have made a bold and direct statement about homology. (Wake 1994, p. 265)

The inferential role of the homology concept as used until the first half of the 20$^{\text{th}}$ century exhibits some modifications — additions in fact — compared to the situation before the emergence of evolutionary theory. These additions to the inferential role primarily boil down to the fact that the results of comparative anatomy (homologies, morphological descriptions of types, taxonomic groupings) came to be interpreted in light of common descent. In addition, the idea of common ancestry provided an explanation of principles about animal form that had been previously been taken for granted without an explanation acceptable to our modern understanding. Likewise, a phylogenetic approach also offered some corrections to previous ideas and a sophistication of prior practice, including assessment of hypotheses of homology, development of morphological accounts (such as the status of vertebrate limbs), and revision of classifications. Overall, on my interpretation these changes in the actual use of the homology concept in biological practice were moderate and do not warrant the assumption that the advent of evolutionary theory created a new and distinct homology concept. My view is that the important changes that took place after the emergence of Darwinian theory are due to other new concepts that were introduced and ideas that gained acceptance such as the notions of 'common ancestry', 'phylogeny', and 'natural selection'. Unlike

these novelties, the changes in the homology concept itself were relatively small and immediately followed from changes that these other concepts brought about. Thus, in spite of my assumption that one and the same homology concept was used throughout the 19$^{\text{th}}$ century, a philosophical explanation of the theoretical and practical differences between pre- and post-Darwinian biology is still possible if one appeals to collateral beliefs and the content of other biological concepts. My claim that the homology concept used by most biologists before the middle of the 20$^{\text{th}}$ century is the same concept as the pre-Darwinian concept embodies two basic claims. First, the introduction of the idea of common ancestry did not bring about a new homology concept in the 1860s that was subsequently used by the large number of 19$^{\text{th}}$ century biologists working within a phylogenetic framework. Second, even in the first half of the 20$^{\text{th}}$ century, no distinct homology concept emerged that gained widespread acceptance.

Let my explain this second claim first. So far, Adolf Remane is the only 20$^{\text{th}}$ century biologists that I have discussed in detail. Surely this single case — despite the prominence of Remane's work on homology — cannot substantiate the claim that still the same homology concept was used in the first half of the 20$^{\text{th}}$ century. I pointed to other examples that in my view would yield the same picture as Remane (Hyman 1922; de Beer 1928; Goodrich 1930; Romer 1949), but a historical review of the understanding of the homology concept in the first half of the 20$^{\text{th}}$ century is beyond the scope of my dissertation. Instead of offering a direct argument for the claim that in the first half of the 20$^{\text{th}}$ century no novel homology concept came to be widely used, my strategy is as follows. In the next chapter I shall grant (and argue) that new homology concepts emerged during the 20$^{\text{th}}$ century. For the present context, the important concept is what I call the *phylogenetic homology*, as predominantly used in contemporary evolutionary biology and taxonomy. As argued in Section 5.1, what I take to be symptomatic of this novel concept is the fact that its extension does not include serial homologues (in contrast to homologies between different species). This contraction of the original homology concept used in the 19$^{\text{th}}$ century is due to fact that in 20$^{\text{th}}$ century evolutionary and systematic biology the homology concept became embedded in a particular phylogenetic approach that used this concept solely for the purposes of the comparison of different species and the study of their evolution. In biology taken as a whole, the notion of serial homology surely showed an overall decline after the advent of evolutionary theory, despite the fact that it still remained important in morphology. In the middle of the 20$^{\text{th}}$ century, one still finds disagreement about the very idea of serial homology.[63] It is in fact the case that some 19$^{\text{th}}$ century biologists abandoned the idea

[63]We saw that Adolf Remane (1956) accepted this idea, but viewed it as separate from homology between species

of serial homology based on their phylogenetic framework. My assumption, though, is that what I call the phylogenetic homology concept gained widespread acceptance only in the second half of the 20$^{\text{th}}$ century. I view this as a result of the emergence of new approaches that became particularly influential. In the case of evolutionary biology, this is the emergence of the Modern Synthesis (neo-Darwinism) in the 1930s, which became the dominant theory of evolution. In the case of systematics, this is the advent of cladistics (phylogenetics systematics) as the dominant theory of taxonomy. I acknowledge that it is possible that individual biologist already used the phylogenetic homology concept in the first half of the 20$^{\text{th}}$ century — as opposed to the original concept used by most 19$^{\text{th}}$ century biologists. But my assumption is that the widespread use of a distinctively phylogenetic homology concept is a feature of the second half of the 20$^{\text{th}}$ century. Section 5.1 will explain the emergence of this concept is due to the fact that neo-Darwinism and cladistics for the first time brought about a dominant theory in evolutionary and systematic biology, respectively, creating unified disciplines with a distinct method. My focus will be on the characterization of the phylogenetic homology concept and the explanation of its origin, but I will not attempt to settle the question to which extent this concept was already in use in the first half of the 20$^{\text{th}}$ century.

My basic claim about the history of the homology concept before 1950 is that no distinct homology concept emerged in the 19$^{\text{th}}$century with the advent of evolutionary theory. The homology concept was often defined in terms of common ancestry, but many different definitions of homology have been offered in the past and different definitions do not amount to different concepts.[64] Instead, the previous historical discussion has emphasized the way in which the homology concept was used in actual research practice and I have stressed the continuity between the pre- and post-Darwinian usage. According to my framework on concepts, the task of semantics is to account for how the possession of empirical concepts makes successful scientific practice possible. One central aspect of the content of the homology concept is how it enabled biologists to reliably discover new homologies. An important historical fact is that despite a phylogenetic definition of homology, throughout the 19$^{\text{th}}$ century biologists did not establish homologies based on a consideration of phylogenetic trees (exhibiting common ancestry), but instead assessed homologies using the comparative methods of pre-Darwinian anatomy. The homologies established based on the old practice were simply

and thus uses the term 'homonomy' instead of 'serial homology' — for serial homologues such as the vertebrae of one individual are not inherited from a structure in the common ancestor. In a similar vein, Alan Boyden (1943) argued for strict separation between 'homology' and 'homotypy', which is his term referring to serial homologues. Others, such as Carl Hubbs (1944) and Gairdner Moment (1945) replied that serial homology should not be viewed as a distinct notions, homology between species and within an individual being instances of the same phenomenon.

[64] We also saw that in spite of a phylogenetic understanding of homologies, sometimes post-Darwinian biologists gave definitions appealing to developmental features without explicitly invoking phylogenetic considerations (Section 4.3.2).

interpreted as being due to common descent. My previous discussion pointed to early 20th century biologists explicitly making this point (Russell 1916; Lubosch 1931; see p. 191 above). Even in the middle of the 20th century we find biologist stating the same about their own research practice:

> ... current definitions of homology almost unanimously stress common ancestry as a prerequisite and may even go so far as to state that "the sole condition which organs must fulfill to be homologous is to be descended from one and the same representative in the common ancestor" ... One would be led to believe from the current definitions of homology ... that we first *know* the ancestry and then decide that the corresponding organs or parts may be called homologous! (Boyden 1947, p. 657)
>
> The often endorsed assumption, homology can now be established based on the detection of common ancestry, construes the only possible procedure the wrong way round. Common ancestry of two species or two structures is not directly observable or graspable, but has to be found out and justified in a complicated logical manner. The central method for this is exactly the homological research. Thus, phylogeny is based on homological research, not the other way round. (Remane 1961, p. 447; my translation)

Once homologies had been established, this knowledge could be used to arrive at taxonomic groupings of species and morphological descriptions of groups of organisms. This is another important type of knowledge that biologists could generate in virtue of possessing the homology concept. While the advent of evolutionary theory did not modify the way in which homologies were established, as regards the scientific use of known homologies a certain change in scientific practice occurred. Morphological relations of characters and taxonomic relations of species came to be interpreted in light of common ancestry, and this phylogenetic interpretation yielded a sophistication of morphological and taxonomic practice. Still, the continuity in research practice is large and can be viewed as consisting largely in a mere re-interpretation of previous ideas in terms of phylogeny (see p. 191). The contemporary functional morphologist George Lauder, who uses what I call a phylogenetic homology concept, is aware of the continuity between pre- and post-Darwinian comparative anatomy (and like me, he views the Modern Synthesis of the 1930s as bringing about a real change):

> The advent of an evolutionary perspective made little immediate difference to the morphologist's view of the problem of organic form. Ancestry and descent with modification of structure provided a causal basis for unity of plan, but the analysis of design and diversity was little changed. In the 1930s, however, the emerging evolutionary "synthesis" focused the aim of morphological research on the relationship of organisms to the environment. In the process, the problem of form was redefined. It became less a question of intrinsic relationships and principles of construction (the focus of Cuvier, Owen, and Milne Edwards) and more an issue of explaining form as the product of extrinsic environmental selection. (Lauder, "Introduction" in 1982 [1916] 1982, pp. xix–xx)

Overall, the inferential role of the homology concept changed only moderately with the advent of evolutionary theory: theoretical characterizations of homology changed to some extent, while the actual use of the concept hardly changed. This continuity in inferential role provides a basis for my tenet that the advent of Darwinism did not introduce a novel and distinct homology concept.

Yet in Section 3.3.2, I suggested a pluralism about concept individuation. According to this idea, concepts may be individuated in more than one way, depending on the particular philosophical purposes underlying concept ascription and the study of conceptual change. Consequently, one could use the historical change regards theoretical views of homology to distinguish two homology concepts. One could ascribe a post-Darwinian, non-idealistic homology concept to those biologists who made actual use the idea of phylogeny in their research practice. For instance, we saw that Carl Gegenbaur came to accept the notion of common descent as he found that it was helpful in interpreting morphological facts and revising biological classifications. The philosophical motivation for this distinction between a pre- and post-Darwinian homology concept would be to mark the fact that despite large continuity in biological practice, a phylogenetic understanding of homology yielded a more sophisticated biological practice.

My preference is to not make use of this more fine-grained scheme of concept individuation and instead to posit a single homology throughout the 19^{th} century. For my philosophical aim is to underscore the scientific achievements based on the homology concept and its epistemic potential, which were already present in pre-Darwinian biology. Idealistic morphologists were in a position to determine homologies, and later evolutionary morphologists assessed homology independent of the notion of common ancestry. This is an important fact as many important aspects of biological theory and practice are built on the recognition of homologies.[65] The ability to reliably discover homologies permitted biologists to enhance their understanding of morphological and taxonomic phenomena by a systematic study of known homologies. My discussion of the homology concept as used in pre-Darwinian biology (Section 4.2) showed how important this concept was despite the absence of a phylogenetic understanding. Homology is the basis of comparative biology because it individuates characters as units of anatomical variation, thereby permitting meaningful and effective comparison. Knowledge about homologies provided the basis for the taxonomy of species, as species are classified based on the comparison of homologous features. Moreover, unified descriptions which apply to large groups of organisms can be based on known homologies. Most of these important biological tasks are supported by the homology concept independent of a phylogenetic definition (Section 4.2), and the discussion in this section showed that a phylogenetic understanding added only little to the actual achievements based on the concept's use. A good deal of the intellectual work in comparative anatomy had been done prior to the advent of evolutionary theory; and the inferential role of the homology concept used before 1859 embodied these epistemic abilities

[65] It also avoids the circularity claim put forward by contemporary creationists (see Section 4.0.2).

so that this concept supported a powerful scientific practice. The advent of a phylogenetic framework did modify homology's inferential role, however, the additions to the inferential role follow quite straightforwardly from newly introduced notions such as 'common ancestry' and the idea that taxonomically and morphologically related organism are related by descent. Thus, on my account the new inferences that the homology concept of the post-Darwinian period supports are simply corollaries to the inferential role present before Darwin.[66] The post-Darwinian biologists were in a position to immediately re-interpret prior taxonomic and morphological fact so as to establish phylogenetic trees. This was neither based on novel evidence, nor was it the case that originally the novel evolutionary ideas were theoretical speculations so that the genealogical trees inferred from these ideas and the prior evidence were in the beginning unconfirmed. Instead, the morphological and other biological evidence available before Darwin's publication of the *Origin* actually supported the phylogenetic claims put forward later on. Thus, my account of the homology concept emphasizes the epistemic potential of this concept as already used before the emergence of Darwinism. The homology concept was able to provide a large body of the evidence for the establishment of phylogenetic trees and thereby had the potential to enable later evolutionary research (where this potential became immediately manifest once homologies were re-interpreted phylogenetically).

So far my argument for evolutionary theory not introducing a novel homology concept in the 19$^{\text{th}}$ century has relied on continuity in homology's inferential role (conceptual role). But there is another significant part of a scientific concept's content: the *epistemic goal* pursued with its use. Section 4.2 argued that once the homology concept was established in pre-Darwinian biology, it was used to pursue two epistemic goals: the classification of species, and the morphological comparison of structures (so as to arrive at unified descriptions of groups of organisms). The discussion on post-Darwinian biology indicated that the homology concept continued to be used for the purposes of classification and morphological description. A seemingly new biological goal emerged with the advent of Darwinism, namely the establishment of phylogenetic trees (the homology concept being obviously used for this purpose). However, my above discussion made plain that pre-Darwinian

[66] Brandom (1994) offers a systematic account of this by distinguishing between a concept's inferential significance (the inferences that a person may draw using a concept) and the concept itself (which parallels my distinction between the total inferential role endorsed by an individual and a concept as shared among individuals). On Brandom's account, different individuals that possess the same concept may make different inferences as they endorse different collateral beliefs. Concept sharing is viewed as the ability to navigate between different doxastic perspectives, i.e., the ability to determine the inferences that follow given another person's set of background beliefs. I view the (different) inferences that pre- and post-Darwinian biologists drew using the homology concept in the same way. Even some post-Darwinian biologists endorsed a non-phylogenetic understanding of homology and taxonomy. Communication between biologists with a phylogenetic and non-phylogenetic approach was possible as different biologists were able to interpret statements involving the homology concept and inferences endorsed from either perspective.

taxonomic relations were simply re-interpreted as phylogenetic relations. After Darwin, the use of the homology concept to arrive at both phylogenetic trees and biological classifications was part of the same process, given that species are classified in terms of their phylogeny (as established from homologies). Thus, the establishment of phylogenetic trees is not a novel and distinct epistemic goal, but simply how the traditional goal of classifying species was spelled out after the advent of evolutionary theory. This strong continuity regarding the epistemic goals that were pursued with the homology concept's use between pre- and post-Darwinian is significant for the question of concept individuation. Section 3.3.3 suggested that epistemic goal as one of the dimensions of conceptual content is often the most significant factor for concept identity, as it reflects what biologists are trying to achieve by a concept's use. In spite of differences in beliefs about a phenomenon, which may be due to different empirical background information (and reflected by a difference in inferential role), scientists do not use incommensurable concepts and may be able to rationally settle empirical disagreements, provided that they pursue the same epistemic goal. (If, however, scientists are attempting to achieve quite different things when using a certain term, they are prone to talk past each other. In particular if researchers are unaware that the rival approach uses the term to pursue a different epistemic goal, then they are likely to fail to recognize the empirical merits of the rival account and concept use, which obtains relative to the rival scientific goal.) *The advent of evolutionary theory and the introduction of a novel theoretical account of homology (reflected in a certain change in inferential role) did not at all change what biologists were trying to achieve when using the homology concept.* Before and after Darwin, the concept was used for the epistemic goals of the classification of species and the systematic morphological description of groups of organisms. This stability regards this central component of conceptual content provides essential support for my tenet that the homology concept as used in post-Darwinian biology (before the middle of the 20^{th} century) is the same concept as used in pre-Darwinian biology.

On my account, the moderate change that occurred — the adoption of a novel theoretical characterization of homology — was a change taking place internal to the single homology concept used throughout the 19^{th} century. However, this way of semantically phrasing things is not to sweep conceptual change under the carpet. No matter whether a change in a term's inferential role is so substantial that it leads to the advent of a novel concept or whether it is merely a change internal to the concept, this modification of inferential role is in need of philosophical explanation. My semantic framework permits counting the post-Darwinian adoption of a new theoretical characterization of homology as rational. This instance of accounting for the rationality of conceptual change

proceeds based on homology's stable epistemic goals. We saw that evolutionary morphologists such as Gegenbaur came to adopt the phylogenetic interpretation of homology (and of taxonomic and morphological relations) precisely because they realized that it improved their previous practice of morphologically comparing the structures of different species and interpreting the morphological relations between species by classification. The phylogenetic interpretation provided a more sophisticated way to assess homologies, to interpret morphological findings and scrutinize morphological hypotheses (e.g. about the nature and origin of the vertebrate limb), and to establish and revise classifications in the light of genealogy. Thus, it was rational to adopt the novel characterization of homology, as it provided comparative biologists with a more effective method of pursuing and actually meeting the two traditional epistemic goals of this concept's use: the morphological comparison of structures and the classification of species. As a result, *change regards one semantic property — inferential role — can be philosophically accounted for as occurring in a rational fashion with reference to another semantic property — epistemic goal (at least if the latter is stable).*

To sum up the discussion of this chapter, I argued that evolutionary theory did not introduce a novel homology concept in the 19$^{\text{th}}$ century because of 1) unchanging epistemic goals being pursued with the use of the term 'homology', and 2) a strong continuity in the term's inferential role (conceptual role). As regards inferential role, it was emphasized that the content of the homology concept depended crucially on how homologies were established in practice, and how knowledge of homologies was used for morphological description and taxonomic classification. An upshot of this case study is that theoretical definitions can be peripheral to the content of a scientific concept and how it underwrites successful practice. To the extent that the advent of Darwinism transformed biology in general and morphology in particular, this change in biological practice need not be explained based on the advent of a novel homology concept; instead the differences between pre- and post-Darwinian practice can be explained with reference to the emergence of other concepts (such as 'common descent'). My preferred scheme of individuating the homology concept highlights the fact that the homology concept as already used before the advent of evolutionary theory supported taxonomic and morphological practice, yielded evidence for the idea of common ancestry and had the potential to underwrite later evolutionary research such as the establishment of phylogenetic trees. While arguing that the moderate change in inferential role that occurred with the advent of evolutionary theory was a change internal to the homology concept, this change can nonetheless be accounted for as occurring in a *rational fashion* based on the fact that it helped biologists to actually meet the epistemic goals associated with the concept.

5.0 HOMOLOGY IN CONTEMPORARY BIOLOGY: THE PHYLOGENETIC, THE DEVELOPMENTAL, AND THE MOLECULAR HOMOLOGY CONCEPT

> *There are concepts of such a central importance that their origin, change, and disintegration, in short their history, characterizes the development of the science they are part of. Such a concept is the concept of 'homology' in comparative anatomy.* (Hans Spemann 1915, p. 63; my translation)

The foregoing chapter discussed some key episodes of the homology concept in the 19$^{\text{th}}$ century, and took a brief look at some aspects of its history in the first half of the 20$^{\text{th}}$ century. My main claim was that the advent of evolutionary theory did not bring about a new and distinct homology concept. Instead, the homology concept of pre-Darwinian biology was used well into the 20$^{\text{th}}$century by most biologists. One reason for this claim is that the same criteria of establishing homologies were used before and after the introduction of evolutionary theory. Moreover, once homologies were established, this knowledge provided the basis for the effective comparison and classification of species, and it provided unified anatomical descriptions of taxa. The introduction of the idea common descent did modify the interpretation of homologies, morphological relations, and natural classifications. But these were reinterpretations in the light of evolutionary theory, which did not necessitate a fundamental redesign of the homology concept and hardly changed this concept's usage in actual practice. Moreover, the homology concept was used to pursue the same epistemic goals before and after the introduction of evolutionary theory.

Still, the homology concept did change throughout its history, and novel homology concepts actually emerged. My account asserts, though, that this happened much later than is usually assumed. I view the origin of new homology concepts as a feature of the 20$^{\text{th}}$century. In this century, new biological disciplines or specialized subdisciplines emerged. Compared to 19$^{\text{th}}$ century biology, these modern disciplines are characterized by a shared but relatively narrow set of biological goals, specific methods, and a united theoretical framework. Some 20$^{\text{th}}$ century biological disciplines came to use the homology concept for their particular purposes, reshaping and modifying it so as to create a novel homology concept peculiar to this discipline. In what follows, I shall argue that currently

three distinct homology concepts are used throughout biology. The *phylogenetic* homology concept is used in contemporary evolutionary and systematic biology. It is the product of the emergence of the modern synthetic theory of evolution in the 1930s, and phylogenetic systematics in the 70s. The *developmental* homology concept emerged in the early 1980s, being used in the relatively new field of evolutionary developmental biology. The *molecular homology* concept was created in the 1970s due to the use of the homology concept in molecular biology. In accordance with my semantic framework, the discussion will pay particular attention to inferential (conceptual) role (the inferences and explanations characterizing a concept) and the epistemic goal pursued with a concept's usage. Because of these inferences and explanations supported by a particular homology concept, such a concept yields a specific epistemic product: certain items of knowledge characteristic of a biological field. I shall explain the origin of the current homology concepts due to the distinct scientific goals of these disciplines and the fact that each of these fields uses their homology concept for particular epistemic purposes. In each case a specialized homology concept originated that actually *meets the epistemic goal* pursued with its use by a certain subdiscipline *to a larger extent* than the 19$^{\text{th}}$ century or other contemporary homology concepts. For this reason, each of these homology concepts originated in a *rational* fashion. Rather than leading to incommensurability, the usage of several homology concepts in overall biology is conducive to scientific theory and practice.

Sections 5.1, 5.2, and 5.3 will discuss the phylogenetic, the developmental, and the molecular homology concept, respectively. Each of these sections will first present the recent history and biological understanding of the homology concept discussed. At the end of each section, I shall give a semantic summary that lays out the inferential role of the respective homology concept and the epistemic goal pursued with its usage. The account on the developmental homology concept (Section 5.2) will mention some features of evolutionary developmental biology, such as the theoretical goal of this discipline pursued with the developmental homology concept. Yet evolutionary developmental biology as a quite recent field is not well known among philosophers. Appendix B gives a more detailed discussion of the history, theoretical aims, and modes of explanation of this discipline, and can be consulted before reading Section 5.2. In Section 5.2.4 I will use the discussion of the phylogenetic and the developmental homology concept to criticize both the descriptive and the causal theory of reference. I shall argue that pragmatic and epistemic aspects of concept use such as a concept's epistemic goal are a crucial factor of reference determination. Finally, Section 5.4 will summarize the whole discussion of homology (Chapters 4 and 5), emphasizing the rationality of the origin and practical usage of the three homology concepts in contemporary biology.

5.1 HOMOLOGY IN EVOLUTIONARY BIOLOGY AND SYSTEMATICS: THE STUDY AND EXPLANATION OF DIFFERENCES BETWEEN SPECIES

The *phylogenetic* homology concept is used in contemporary evolutionary biology and systematics. A diagnostic feature of the novel phylogenetic homology concept is that the idea of serial homology is not used any longer. What used to be called 'serial homologues' in the 19$^{\text{th}}$century, i.e., the repeated occurrence of the same structure within one individual (Section 4.1.2), is not viewed as an instance of homology at all in modern evolutionary and systematic biology. The very idea of serial homology is rejected and instead only structures of different organisms or species are viewed as homologous. It is true that the influence of the notion of serial homology decreased immediately after the advent of evolutionary theory — despite its continued use in post-Darwinian morphology. But only in the 20$^{\text{th}}$ century has there been a systematic usage of the homology concept within a distinctively phylogenetic and evolutionary framework that leads to a widespread and principled rejection of the notion of serial homology. The Modern Synthesis and phylogenetic systematics brought about dominant theories in evolutionary biology and systematics, respectively, characterized by clear-cut and shared research goals and distinct scientific methods. The goal of evolutionary biology is the explanation of the origin of new species and the differences between existing species. The goal of systematics is the classification of different species. In both disciplines, the focus is on the relations of different species, and the phylogenetic homology concept is used for these purposes. For this reason, homology is viewed as a relation between the characters of different species — unlike the idea of serial homology. In this sense, the phylogenetic homology concept is a contraction of the original homology concept, at least with respect to a certain aspect. The dropping out of the notion of serial homology is a diagnostic feature, but it is not my justification for postulating the emergence of a new (phylogenetic) homology concept. My reason for assuming a novel homology concept is the new usage of the homology concept within a distinct comparative and phylogenetic framework, as it is widespread only in modern systematic and evolutionary biology. This new usage of the homology concept for distinct biological purposes explains why the idea of serial homology came to be abandoned. A further reason for postulating a novel, phylogenetic homology concept is that a new criterion of establishing homologies emerged in the second half of the 20$^{\text{th}}$ century, namely the assessment of homologies based on phylogenetic trees.

In spite of the fact that the related fields of evolutionary biology and systematics use the same homology concept, these are two biological fields and each has a somewhat different perspective

on the phylogenetic phenomenon of homology. This is due to the different research focus of these disciplines. Evolutionary biology has a so-called *transformational* approach to biology, while phylogenetic systematics has a *taxic* approach to homology. (Biologists themselves sometimes talk about 'transformational homology' and 'taxic homology'.) For this reason, I first discuss the understanding of homology in evolutionary biology, and then turn to systematics. I explain why these are merely two perspectives on the same phenomenon, which are in fact complementary, and why a unique homology concept is used across these two disciplines. I conclude with a semantic characterization of the phylogenetic homology concept and an explanation of its origin.

5.1.1 Evolutionary Biology: Transformational Approach to Homology

One reason for the emergence of the phylogenetic homology concept and is the origin of the Modern Synthesis, which used new models of population genetics to study and explain the evolution of species. Until the 1920s, two different theoretical schools competed about the proper view of inheritance (Section 6.1.1). The Mendelians emphasized the inheritance of discrete, Mendelian genes. Due to the idea that genes are discrete units, they rejected continuous variation and a gradual evolution based on it. Consequently, the Mendelians endorsed a saltational, non-Darwinian picture of evolution. The biometricians, on the other hand, used the methods of statistics to study the distribution of phenotypic traits between generations. They emphasized the continuous variation of features, which was more congenial for a Darwinian, gradual account of evolution. In the 1930s, Ronald A. Fisher, J. B. S. Haldane and Sewall Wright synthesized these seemingly contrary approaches and founded the statistical theory of population genetics as we know it nowadays. The basic idea is to point out that many genes are involved in the production of a phenotypic trait, so that a quasi-continuous phenotypic variation within a population is consistent with a discrete mode of inheritance. Population genetics explains the evolution of populations based on a study of the distribution of genotypes and phenotypes, and their change due to mutation, genetic drift, migration, and in particular natural selection (Section 6.1.4). What is relevant for the impact on the homology concept is not the mathematical framework of population genetics. Instead, it is the fact that in the 1940s the ideas of early population genetics were promoted by students of natural populations and other biologists as an approach to evolution that came to be called the Modern Synthesis. The early proponents of this account were the geneticist Theodosius Dobzhansky, the

zoologists Ernst Mayr and Julian Huxley, and the paleontologist George Gaylord Simpson.[1] The Modern Synthesis stressed natural selection as the main mechanism of evolution, and evolution as a process of gradual change operating on variation within populations, where new species emerge in a gradual fashion out of founding populations belonging to an old species. The important aspect of this history for the emergence of the phylogenetic homology concept is that the Modern Synthesis succeeded in creating a dominant theory of evolution, not only defining a theoretical and practical approach for evolutionary biology as a discipline within biology, but exerting a large influence on biology as a whole. Neo-Darwinism is another name for this approach.

In modern evolutionary theory, the focus is on the study and explanation of the modification of traits in the course of history. Structural traits, i.e., homologues, are viewed as forming a lineage from an ancestral character to a character in the descendant. In between ancestor and descendent, there are intermediate species, each of which has a representative of this structure. Thus, the focus is on a sequence of characters from the ancestor to the descendant. While the structures in this sequence may vary in their particular shape and other properties, they are still homologous to each other. Due to this phylogenetic-evolutionary approach, structures in two extant species are viewed as homologous if and only if they are inherited from the same structure in the common ancestor. Definitions that define homology exclusively in terms of common ancestry are an expression of this idea (see also Haas and Simpson 1946):

> Homology is resemblance due to inheritance from a common ancestry. (Simpson 1961, p. 78)
>
> A feature in two or more taxa is homologous when it is derived from the same (or a corresponding) feature of their common ancestor. (Mayr 1982, p. 45)

This evolutionary and phylogenetic focus on homology is shown by the fact that proponents of this homology concept explicitly argue that standard criteria of homology are not to be confused with the nature and definition of homology, which is common ancestry (Bock 1973). Ernst Mayr (1982) explicitly criticizes Adolf Remane (who I discussed in Section 4.3.3) for viewing homology criteria as a part of the concept of homology. It is acknowledged that criteria are indispensable for assessing homologies, but criteria — making reference to the structure of extant organisms — are not to be confused with homology itself, which is viewed as a phylogenetic phenomenon.

Approaches in evolutionary biology are usually so-called *transformational* approaches to homology, which emphasize that characters form long lineages from the ancestor to the descendent, while substantial change and transformation of such a character is possible. Definitions of homology

[1] A series of books expresses this institutional establishment of the Modern Synthesis: Dobzhansky's *Genetics and the Origin of Species* (1941), Mayr's *Systematics and the Origin of Species* (1942), Huxley's *Evolution: The Modern Synthesis* (1942), and Simpson's *Tempo and Mode in Evolution* (1944).

reflect this perspective:

> Different characters that are to be regarded as transformation stages of the same original character are generally called homologous. "Transformation" naturally refers to real historical processes of evolution, and not to the possibility of formally deriving characters from one another in the sense of idealistic morphology. (Hennig 1966, p. 93)

An example that illustrates that massive transformation is possible is the ear ossicles in mammals. These are actually derived from parts of jaw of ancestral amphibians, so that mammalian ear ossicles are homologous to parts of the jaw of extant amphibians. For instance, the stapes (one of the ear ossicles) as we find it in mammals is homologous to the amphibian quadrate (a part of the jaw). This example and the transformational approach in general reassert that homology is independent of the particular shape and internal structure of a character as well as its function. The idea is that while the individual structures in a historical lineage of homologues may change, the homology concept refers to this lineage in the first place and in fact conceptualizes the character that underlies and undergoes the modification. Viewed from this angle, a homologue is like an individual who undergoes change in the course of its history. The transformational understanding of homology is summarized by a recent review in the following words:

> *Transformational homology.* A more popular view is that structures are homologous if they can be traced to a particular condition that originated once in a common ancestor ... This includes retention in a more or less unchanged form or transformation, directly or sequentially (and possibly radically), from an ancestral condition. (Donoghue 1992, p. 173)[2]

I now turn to the discussion of the use of the phylogenetic homology in systematics, later I will characterize the phylogenetic homology concept in more detail and explain its emergence.

5.1.2 Systematic Biology: Taxic Approach to Homology

The theory and method of taxonomy accepted nowadays is phylogenetic systematics or cladistics, as it commonly called. One fundamental tenet of cladistics is that every higher taxon (every group of organisms above the species level) is to be a *monophyletic group*, i.e., an ancestral species and all of its descendant species. For example, the reptiles as traditionally conceived — including snakes,

[2] I mentioned above (p. 198) that some have argued that a phylogenetic definition is to some extent circular. The objection is that the notion of two immediately following structures in a transformation series being homologous is not explained. This definitional gap can be closed in a pragmatic fashion by an appeal to the criteria of homology, which settle whether a structure in the descendant is homologous to a structure in the precursor species. (This solution does not conform to the official account according to which homology is to be defined in terms of common ancestry only without any reference to criteria, though.) Michael Ghiselin's definition embodies such a pragmatic approach, reflecting also the transformational approach of evolutionary biology: "Entities are homologous when they are elements of members of a group of precursors and derivates having a common source, and when these entities can, in principle, be traced back through the derivational series to the same element of a precursor from which the members derive, the sense in which they are homologous being stipulated so as to avoid ambiguity." (1976, p. 138)

lizards, and crocodiles, but excluding birds — do not form a monophyletic group. For birds are more closely related to crocodiles than lizards are related to crocodiles. Thus, if one takes the most recent common ancestor of crocodiles, lizards, and snakes, then the class of all species descended from this ancestor includes birds as well. For this reason, nowadays reptiles are often viewed as including birds so that the taxon name 'reptiles' actually denotes a monophyletic group. In sum, phylogenetic systematics assumes that monophyletic groups are natural kinds of organisms, and that they are the *only natural* taxa. Phylogenetic systematics gained dominance in the 1970s, replacing the prior systematic theory, the so-called evolutionary systematics. Evolutionary systematics used to be championed by founders of the Modern Synthesis such as Ernst Mayr, and among other things it permitted non-monophyletic groups as biological taxa. While for phylogenetic systematics the only relevant feature for classification is the branching structure of evolutionary trees, evolutionary systematics takes also the manner of subsequent divergence into account, so that considerations about adaptation and ecology play a role for classification (Mayr 1982). Nowadays there are still some biologists using the theory and method of evolutionary systematics, but phylogenetic systematics is clearly the generally accepted approach.[3]

Phylogenetic systematics was proposed by the German entomologist Willi Hennig in the 1950s (Hennig 1950). However, only after the translation of his work into English did his approach gain supporters (Hennig 1966). Hennig proposed a method of classification that is designed to identify monophyletic groups; and together with his allies, he succeeded in arguing that this method is the appropriate one by yielding the most stable classifications. The basic outlines of the method of phylogenetic systematics (cladistics) are as follows. (It is necessary to introduce the neologisms of cladistics to understand the taxic perspective on homology.) A plesiomorphy is a feature of a species that is historically old, i.e., an ancestral or primitive feature, while an apomorphy is a feature that emerged in more recent times, i.e., a more derived condition or an evolutionary novelty.[4] A *synapomorphy* is an apomorphy shared by a monophyletic group, while a *symplesiomorphy* is a plesiomorphy shared by a monophyletic group. The basic method is that one classifies species not by

[3]In the 1970s, a fierce debate about the theory and methods of taxonomy took place (Hull 1988). Apart from evolutionary systematics and cladistics, phenetics (also known as numerical taxonomy) was involved as a third approach. Pheneticists argued that species are not to be classified according to their genealogy, but simply according to their overall similarity (Sokal and Sneath 1963). Philosophically, phenetics took a nominalist stance towards biological classification and taxa. In addition, it leaned towards operationalism regards scientific concepts and methods, recommending an operational homology concept instead of a concept defined in terms of common ancestry (Jardine 1967; Jardine and Jardine 1970; Sneath and Sokal 1973; Donoghue 1992; Brigandt 2002). Phenetics was quite short-lived.

[4]The distinction between plesiomorphy and apomorphy ('old' and 'new') is not absolute, but always relative to a considered level of the systematic hierarchy. In the context of mammals as a subtaxon of tetrapods (the limbed vertebrates), the ear ossicle malleus, which we find in mammals, is an apomorphy. Relative to this, the amphibian articular — a part of the lower jaw from which the malleus is derived — is a plesiomorphic character.

comparing all of their characters; instead, we focus on apomorphies only. The underlying idea is that a synapomorphy characterizes a taxon (a monophyletic group), whereas a plesiomorphy provides no evidence for a group of species being monophyletic. For a symplesiomorphy characterizes a higher, more encompassing taxon, but it is not peculiar to the taxon in question. In a sense, plesiomorphies are too generic to be diagnostic of the taxon under consideration. If one is interested whether an organism is a bird, then its having a spinal column is uninformative, as this property is a plesiomorphy, possessed by all vertebrates. What one needs is apomorphies of birds.[5]

Many systematists and other biologists relying on cladistics use a *taxic* approach to homology. Characteristic of this view is the statement that homology is nothing but synapomorphy (Donoghue 1992; Rieppel 1992; Panchen 1992; Nelson 1994). The picture is as follows. Due to evolutionary change, a certain novelty or morphological structure with qualitatively new features emerges — an apomorphy originates in a certain species. This novelty is inherited by all the descendants of the species, thus the novelty is a synapomorphy of this monophyletic group. But as my earlier discussion already made plain, since these structures are inherited from an ancestral structure, they form a class of homologues — yielding the connection between synapomorphy and homology. The taxic perspective also emphasizes a certain parallel that exists between higher taxa and classes of homologues: A monophyletic group is a class of species derived from an ancestral species, while a synapomorphy (a class of homologues) is a class of structures derived from an ancestral structure. Taxa are hierarchically organized in that one monophyletic group is contained in other more encompassing groups (e.g., a genus is contained in a family). The same applies for classes of homologues, as synapomorphies are contained in the encompassing set of symplesiomorphies (which are synapomorphies at a higher level of analysis).

> ... homology is the relation which characterizes monophyletic groups. ... Corollaries of this definition are that synapomorphy and homology are the same; that every worthwhile proposal of homology is a hypothesis of a monophyletic (natural) group; that homologies form a hierarchy; and that paraphyletic (unnatural) groups are not characterized by homologies. (Patterson 1982, p. 21)

Homology has traditionally been contrasted with analogy, a usage originating in pre-Darwinian anatomy. Based on the idea of evolution, analogy is usually defined as the similarity of structures that is not due to common ancestry, but instead due to similar function and selection pressure. Taxic approaches contrast homology with *homoplasy*, though. Homoplasy is the existence of the same feature or similar structures in different species, where this similarity is not due to common ancestry. Thus homoplasy is a less restrictive notion than analogy — it refers to similarities that evolved

[5]The relativity of the plesio-/apomorphy distinction reappears in this context. If we talk about animals as whole, then having a spinal column is an apomorphy characterizing the subtaxon vertebrates.

independently, without requiring that this similarity is due to a shared selection pressure. Due to the large influence of phylogenetic systematics on overall biology, most contemporary biologists contrast homology with homoplasy rather than analogy. The distinction between homology and homoplasy is closely tied to the way in which cladistics establishes monophyletic groups and genealogical trees. For the purposes of illustration, consider a single character that is present in more than one extant species. Then there are some phylogenetic hypotheses where these structures are homologous, i.e., they can be explained by inheritance from a common ancestor, provided that the species that have this character are closely related according to the phylogeny. In other phylogenetic trees, though, the species that have this character are not closely related and thus these structures are homoplasies (for if the ancestor had the character, then most of its descendants would have the trait and not only some unrelated species). The idea is that the first scenario is the more likely one as it is more parsimonious to assume that a novel character (an apomorphy) originated *once* and was passively inherited by the descendants (a synapomorphy), whereas in the case of a homoplasy one is forced to assume that the novel character originated *several times* independently. The idea is that the best phylogenetic scenario is the one that requires the postulation the lowest number of evolutionary transformations and novelties. Thus, given the distribution of many characters among different extant species (i.e., the data is whether a certain character is present or absent in a particular species), among different possible phylogenetic trees the true (or most likely) phylogeny is that which maximizes the number of homologies and minimizes the number of homoplasies.

The relation between the transformational and the taxic perspective on homology is as follows. The standard distinction between a *character* and a *character state* is useful to explain this. A character is a set or lineage of homologues. It is a unit that may undergo evolutionary modification independent of other characters (homologues). A character state is the particular features a character can have in individual species. For instance, a homologue in one species may have a quite different shape (be in a different state) than the same character in another species. The transformational approach to homology focuses on how a character is gradually transformed in the course of evolution. It deals with the stepwise modification within a lineage, where this change may be smaller or larger. The taxic approach, in contrast, deals with the difference between the plesiomorphic state of a character and the apomorphic state that the character has in a more recent taxon. Thus, the focus is on two qualitatively different states of a character, thereby ignoring subtle changes in a lineage that occurred either before the origin of the apomorphy or after the origin of this novelty. For instance, the stapes (one of the ear ossicles) as we find it in mammals

is homologous to the amphibian quadrate (a part of the jaw). A transformational approach may emphasize how the amphibian quadrate was gradually modified so as to become what we call the stapes in mammals, and how the stapes of the mammalian ancestor was modified so as to yield the different stapi in different mammalian species. A taxic approach will emphasize that 'the' stapes is a feature shared by all mammals, a synapomorphy distinct from the amphibian quadrate (which as a plesiomorphy). The reason why a taxic approach is not interested in studying smaller modifications of a character is obvious: systematics distinguishes different taxa in terms of certain characters that qualitatively differ between these taxa (and that show only minor variation within a taxon). Some biologists argue that a taxic approach has precedence over a transformational approach (Sluys 1996). However, I agree with Olivier Rieppel (1987) that both approaches are complementary ways of looking at the same phenomenon.

The taxic and phylogenetic approach to homology actually brought about a new criterion of homology, namely, the idea that homologies (vs. homoplasies) have to be evaluated based on a phylogenetic tree. The idea is if one wonders whether two structures in two different species are homologous, then one needs a well-confirmed phylogeny that includes these two species. In addition, the character distribution of this structure *for every species in this tree* has to be taken into account. Based on the information as to whether the structure is present or absent in these different extant species one can infer which of the ancestral species had the structure and in which ancestor it emerged for the first time. Then it is clear whether the presence of the character in two species is due to common ancestry, so that the structures are homologous, or whether the structures are homoplasies. Former criteria such as the topological and the embryological did not require a phylogenetic tree. Instead, homology was assessed by comparing primarily the *two species under consideration*. Adolf Remane's criterion of intermediates includes further structures as it deals with a series of characters where the first and the last part are the structures evaluated for homology. However, Remane did not require that this series represent the real evolutionary transformation of this homologue (Section 4.3.3). Biologists with a taxic approach argue that only homology assessment based on a phylogenetic tree yields reliable results. Joel Cracraft (1981) states that morphological similarity is not evidence for homology. Similarity is the reason to postulate hypotheses of homology, but *phylogenetic distribution* is the evidence for homology. George Lauder (1986, 1994) even labels traditional criteria that do not make use of a phylogenetic tree 'a priori criteria' of homology, viewed as inferior to an 'a posteriori' analysis based on phylogenetic analysis. The evaluation and re-evaluation of homologies based on taxonomic and phylogenetic relations was

to some extent implicit in biological practice before the advent of phylogenetic systematics (e.g., Remane's auxiliary criteria of homology were hinting in this direction). Nevertheless, only the taxic and phylogenetic approach of cladistics made this criterion explicit because of its focus on establishing monophyletic groups in terms of synapomorphies. Due to the general acceptance of the methods of phylogenetic systematics, most contemporary biologists outside taxonomy agree that an evaluation of homologies based on phylogenetic trees is a mandatory procedure.[6]

5.1.3 A Semantic Account of the Phylogenetic Homology Concept

My claim is that what I call the *phylogenetic homology concept* is the homology concept used by most contemporary evolutionary biologists and taxonomists. I have discussed that in evolutionary biology a transformational understanding prevails, while in systematics a taxic perspective is used. This difference is recognized by biologists, who talk about 'phylogenetic homology' as opposed to 'taxic homology' (Rieppel 1987; Donoghue 1992; Sluys 1996). Yet the existence of these two perspectives on homology does not mean that two distinct concepts are used. Instead, the two perspectives simply emphasize different aspects of what is explicitly viewed as one phenomenon. A transformational approach focuses on a single lineage of homologues, stressing the stepwise potential modification of a trait in this lineage from species to species. A taxic approach stresses the origin of a novel structure or the qualitatively new features of an existing structure (the apomorphic condition as opposed to the plesiomorphic state) that emerged with the origin of a new taxon, and it emphasizes the fact that this apomorphy is inherited by all descendants — rather than focusing on a particular lineage from the species founding the taxon to a particular descendant.

[6] An issue that I cannot discuss in detail is the fact that nowadays also behavioral characters are homologized. By 'behavior' biologists refer to the movement of certain parts of the body. In a sense, whereas a morphological structure is a three-dimensional entity in space, a behavioral character is a four-dimensional entity — the spatial movement of structures over time. These four-dimensional entities can be homologized just like three-dimensional characters. One way to establish behavioral homologies is to quantitatively record the relative movement of structures in different species and to assess their similarity. Another criterion is to compare recordings of the electrical activities of muscles from different species. This notion of behavior and the very idea of behavioral homology emerged in the 1930s with the rise of ethology as a distinct biological field studying animal behavior (Brigandt 2005, forth. a).

Behavioral homology shows that even behavioral characters are individuated in terms of structural and phylogenetic considerations, but not in terms of their function. Functional categories used in behavioral biology such as 'mating behavior' do not refer to homologues. The individuation of behavioral characters in terms of homology proved to be important precisely because homologues are natural rather than functional kinds. In addition, Section 5.2.1 will discuss that homology exists on different levels of biological organization, where structures at higher levels cannot be reduced to features on the molecular level. Behavior is another relatively independent level of biological organization. Behavioral homologies can be established by means of comparative study using phylogenetic trees, but behavior cannot be reduced to certain morphological, neurological, or genetic features (Lauder 1994). For literature on behavioral homology see Atz 1970; Baerends 1958; Eibl-Eibesfeldt 1970; Gans 1985a; Golani 1992; Greene 1994; Hodos 1976; Lauder 1986; Lorenz 1931, 1932, 1935, 1937, 1950, 1996; Tinbergen 1963; Wenzel 1992.

The phylogenetic homology concept is used for somewhat different, though complementary purposes in these two fields: evolutionary biologists focus in the explanation of character transformation, while systematists focus on how different states of a character distinguish different taxa. There is only one concept used in these two related fields as a biologist possessing the phylogenetic homology concept (i.e., someone being able to identify the same character in different species) is able to both study phenotypic evolution and to classify species.

One difference between this modern *phylogenetic* homology concept and the *original* homology concept that prevailed in the 19$^{\text{th}}$ century is a difference in extension: the phylogenetic homology concept does not include serial homologues. While homology as originally understood was also a relation between structures of one and the same organism (Section 4.1.2), the phylogenetic homology concept only refers to structures of different individuals or species. Thus, in the course of history there occurred a contraction of the homology concept and its extension. The dropping out of the notion of serial homology is a diagnostic feature for the emergence of the new phylogenetic homology concept — a synapomorphy of this concept, as it were. The idea of serial homology became less important already in the 19$^{\text{th}}$ century, before the widespread usage of the phylogenetic concept. But only in the 20$^{\text{th}}$ century was this based on principled reasons about the new usage and scientific function of the homology concept, which were provided by neo-Darwinism and cladistics as dominant approaches with a united methodology in evolutionary biology and systematics. My subsequent discussion of the use of the phylogenetic homology concept and the epistemic goal pursued with its use provides the best semantic justification for the assumption often made by biologists that the extension of 'homology' — as used in these contemporary fields — does not include what was traditionally called serial homologues.[7]

As far as the *inferential role* (conceptual role) of the phylogenetic homology concept is concerned, a new criterion of homology emerged. Traditional criteria that were established before the advent of evolutionary theory (such as the positional and the embryological criterion) are still in use. However, they are often viewed as being subordinated to the new criterion, which is the assessment of homologies based on a phylogenetic tree. Given a well-confirmed phylogenetic tree (established by means of some previously known homologies), whether an occurrence of a certain feature in several species is a homology is assessed based on the distribution of this feature among extant

[7]Similarly, the increasing emphasis on definitions of homology referring to common ancestry combined with the claim that criteria of homology are to be distinguished from this definition could be viewed as another diagnostic feature of the phylogenetic homology concept. As in the case of the rejection of the idea of homology, the popularity of this idea among biologists is by itself not a justification for the semantic tenet that a distinct concept is in use.

species. Depending on the character distribution and the phylogeny, the presence of the character in different extant species is either best explained by inheritance from a common ancestor or by independent origination and parallel evolution of this trait. For evolutionary biologists this new criterion fits with the idea that common ancestry is the nature of homology, and that traditional criteria are mere criteria that are to be distinguished from the phylogenetic definition of homology. In the case of phylogenetic systematists, this novel and nowadays predominant criterion is tied to cladistic analysis, which seeks to distinguish between homologies and homoplasies in order to classify species into monophyletic groups by establishing phylogenetic trees.

Many of the inferences that characterized the original, 19$^{\text{th}}$ century homology concept (Sections 4.2 and 4.4) are still accepted by users of the phylogenetic homology concept. However, since not all of these inferences are as central to current research practice, I focus on those that are characteristic of the inferential role of the phylogenetic homology concept. The goal of *phylogenetic systematics* is to establish phylogenetic trees and to classify species into monophyletic groups accordingly. Classification proceeds by comparing the structures of different species, and by establishing whether a character is in a primitive (plesiomorphic) or more derived (apomorphic) state. The homology concept is necessary for this task as it refers to the same structure in different species. Recall the distinction that is often made between a 'character' and a 'character state'. A character is a homologue across different species, i.e., a unit or dimension of possible phenotypic variation, whereas a character state is the particular set of properties (the shape and internal structure) that a homologue in a particular species has. In the context of taxonomy, the distinction between characters and their states applies as follows. Different species are classified based on the comparison of various characters. The taxonomic data consists of the distribution of the *states* of each of these characters across different species. For the most part, the relevant character states are the plesiomorphic condition and the apomorphic condition. The homology concept is important because it individuates characters. It picks out the characters (homologues) that may vary between species and take different states. A phylogenetic definition of homology reflects the idea that related species have the same *character* due to common ancestry (so that characters to be individuated in this fashion), and that the descendants often inherit the particular character state of the ancestor, which suits the goal of phylogenetic systematics to classify species into groups descended from an ancestral species. A synapomorphy is the particular (apomorphic) state of a class of homologues which emerged in a species and was inherited by all descendants of this monophyletic group (unless substantial evolutionary change occurred). In sum, the homology concept is necessary to individ-

uate the characters on which systematists base their classifications. Apart from this, the fact that homology individuates characters is important for representing phylogenetic hypotheses, i.e., how a certain character is distributed on a whole phylogenetic tree and how it changed in the course of evolution. For instance, a phylogenetic scenario has to specify at what point in a phylogenetic tree a certain structure emerged as a novelty, in which branches of the tree it was inherited without major modification, at what points it changed substantially or was lost.

In *evolutionary biology*, the focus is on the modification of characters in the course of phylogeny. Homology is a concept that temporally links structures in different species, given that an ancestral and a descendant character are defined as being homologous in case they are connected by a transformation series of intermediate homologues (in a lineage of species leading from the ancestor to the descendant). In accounts of morphological evolution, homologues become historical units that may undergo change. A main goal of evolutionary biology is to explain the adaptive modification of traits. The concept of homology is necessary to conceptualize a lineage of characters. As the process of adaptation operates over many generations, the entity that is subject to change has to be identified. The various homologues of an organism are the entities underlying change. For instance, in order to talk about the same (type of) selection pressure operating on some morphological structure over time one needs to identify the lineage of characters on which this selection pressure operates. Due to different adaptive histories homologues in different species may differ in shape and function. Identifying homologous structures in ancestor and descendant is a precondition for giving an adaptation explanation of the change of this structure. The explanatory force of such an explanation essentially comes from other concepts, such as the notions of natural selection and adaptation. But the homology concept is still a necessary precondition, as adaptation explanation of the transformation of an ancestral trait into a descendant trait can be defeated by arguing that these two traits are not homologous (which may happen as in some cases where homology is not obvious). Thus, phylogenetic homology is used to yield (together with other concepts) an epistemic product of evolutionary biology — descriptions and explanations of the adaptive modification of characters. While homology in taxonomy allows for inferences, in evolutionary biology it is in addition a conceptual precondition for explanations by justifying which character transformations need to be explained. In short, a crucial aspect of the inferential role of the phylogenetic homology concept is that this concept links characters across species in order to conceptualize the natural units that underlie variation across species or evolutionary change. This serves the epistemic goals of arriving at effective classifications and making adaptation explanations possible.

My exposition of the inferential role of the phylogenetic homology has already indicated that this concept is used to pursue certain *epistemic goals* of evolutionary and systematic biology. In the case of taxonomy, this is the classification of different species; in evolutionary biology, it is the explanation of the adaptive modification of species and their characters. In the 20$^{\text{th}}$ century, the original homology concept as used in the 19$^{\text{th}}$ century was gradually modified and shaped to support inferences and explanations that precisely meet these goals as they are nowadays understood, leading to the emergence and widespread use of the phylogenetic homology concept in these two fields. In the 20$^{\text{th}}$ century, 'homology' came to be used for clear-cut phylogenetic purposes, characterized by the classification of *different species* and the evolutionary study of changes *from species to species*. One consequence of these epistemic goals is that homology is solely viewed as a relation of structures between *different species*, which led to an abandonment of the idea of serial homology. Walter Bock's (1973) phylogenetic approach makes explicit that the homology concept is used to express relations between species:

> Homology is, without question, the most important principle in all comparative biology. Moreover, it is possible that homology is the only method of comparing attributes of different species and that all other methods of comparison are reducible to homology. ... Here I must emphasize that the defining criterion for homology is phylogeny, but the recognizing criterion for homology is similarity. I do not advocate a definition for homology based on similarity. (Bock 1973, pp. 386–387)

In his essay "Homology in Biology – A Relational Term in the Comparison of Species", Peter Ax (1989) rejects the idea of serial homology based on the claim is that homology is *about* the comparison of different species:

> From the very beginning, homology is a relational concept in the comparison of structures of different species. ... If we decide in continuity with historical conceptions [of homology] to define homology as a relation of characters in the comparison of different species, then it is simply impossible to use the term homology at the same time for a conceptual characterization of the repetitive occurrence of characters in individuals of a single species. (Ax 1989, p. 488; my translation)

If one assumes that characters of one and the same individual (alleged serial homologues) cannot be homologous, this does not necessarily imply that characters of different species are the only features that can be homologized. For structures of different individuals of the same species are homologous. Often these so-called intra-specific homologies are quite obvious, and names such as 'the human humerus' refer to a type of structure possessed by all humans rather than token-structures in individuals. Still, the notion of intra-specific homology may be important in cases of non-obvious homologies such as sexual dimorphism, where sexes differ structurally. For instance, in the case of a mammalian species, it is a relevant question whether the male penis is homologous to the female clitoris. Even though intra-specific homologies may be recognized by evolutionary biologists,

taxonomist often restrict the notion of homology to a relation between characters of different species as taxonomy is about the comparison and classification of different species (Wagner 1989a). To illustrate this, while Michael Schmitt (1989) assumes that different approaches to homology can be used, he clearly expresses the phylogenetic understanding of homology as used in systematics:

> "Homologous are characters whose similarity is based on common ancestry." In virtue of this each establishment of homology supports a phylogenetic inference. ... It is trivial that Owen's homology concept is pre-phylogenetic and thus does not support any phylogenetic inferences. ...
>
> It is obvious that homonomies [serial homologies] do not conform to the phylogenetic homology concept: ... More difficult is the case of intra-specific "homologies": ... Thus, homonomies are clearly to be characterized as non-homologies, probably intra-specific similarities likewise ... In phylogenetics intra-organismic and intra-specific similarities of a certain species are uninteresting, ... (Schmitt 1989, pp. 506–508; my translation)

Serial homologues do not fall under phylogenetic definitions of homology. This by itself does not show that the phylogenetic homology concept does not include serial homologues in its extension. For my account of homology in the 19$^{\text{th}}$ century explicitly argued that standard 'definitions' can be peripheral to the actual content of a concept (Section 4.4). After all, evolutionary morphologists such as Gegenbaur gave a phylogenetic definition of homology and still clearly employed the notion of serial homology. The best semantic justification for the widespread assumption that the contemporary phylogenetic homology concept excludes serial homologues (and that common ancestry is central for this modern homology concept) is its being integrated in a modern phylogenetic framework. In particular, the phylogenetic concept is used for the comparison and classification of *different species* and for the explanation of the modification of traits *from species to species*. I view the increasing focus on these two epistemic goals as driving the emergence of the phylogenetic out of the original homology concept. Thus, this *difference in the epistemic goals* for which the term 'homology' has been used is the best semantic evidence for these actually being two distinct concepts. This is in line with my general suggestion that a concept's epistemic goal is a genuine component of a concept's content and crucial determinant for concept individuation (Section 3.3.3).

To summarize my discussion, in the case of systematics and evolutionary biology, the epistemic goals pursued with the homology concept's use are the comparison and taxonomy of species and the explanation of descent with modification. The inferential role of the homology concept in taxonomy and evolutionary biology permits the individuation of characters across species and the conceptualization of a lineage of species characters despite variation and potentially unlimited evolutionary change. This allows for stable classifications in the case of systematic biology, and is a precondition for explaining adaptation in the case of evolutionary biology. The phylogenetic homology concept is thereby *successfully used* to pursue the epistemic goals of these fields. As a

result, the emergence of the phylogenetic homology concept out of the 19th century concept and the associated change in inferential role occurred in a *rational* fashion, as the inferential role changed so as to meet the concept's epistemic goal.

5.2 HOMOLOGY IN EVOLUTIONARY DEVELOPMENTAL BIOLOGY: THE SEARCH FOR AN ACCOUNT OF MORPHOLOGICAL UNITY

The phenomenon of homology has been approached from a developmental point of view from the very introduction of the homology concept. The embryological criterion, according to which homologous structures usually develop in the same fashion and from the same precursor structures, used to be one of the main criteria of homology. In the discussion of the work of the comparative embryologist Karl Ernst von Baer (Section 4.1.3), we saw that when putting forward his model of comparative development, von Baer assumed morphological types and relations betweens species to fall under developmental laws. He argued that the nature of an individual structure is constituted by its mode of development, so that structures are to be individuated and homology is to be defined in terms of development. In spite of the emergence of evolutionary theory and phylogenetic views and definitions of homology, a developmental understanding of homology continued. My discussion pointed out that throughout the 19th century, ontogeny and phylogeny were viewed as two sides of one coin (Section 4.3.2). Ernst Haeckel's biogenetic law postulated a strong parallel between evolution and development, claiming that ontogeny recapitulates phylogeny; and many 19th century biologists accepted some form of recapitulationism. Even if the embryological criterion was viewed as a mere criterion that may fail in certain cases, developmental considerations were part of biological accounts of homology throughout the homology concept's entire history.

However, the traditional use of an embryological criterion and the developmental considerations did not lead to a novel homology concept. What I call the *developmental homology concept*, to be discussed in this section, originated in the last two decades. It is the product of modern biological approaches that attempt to account for morphological unity and evolvability based on mechanistic explanatory agendas. The idea is to use knowledge from developmental biology to explain the developmental origin and nature of characters and their phylogenetic stability and transformation. The distinctive feature of this novel approach to homology is to attempt to causal-mechanistically

explain homology as a phylogenetic phenomena using knowledge about developmental processes. The developmental homology concept is the homology concept used in contemporary evolutionary developmental biology (evo-devo), and it originated based on the emergence of the research agenda that characterizes current evo-devo.[8] As an independent and visible discipline, evolutionary developmental biology is only two decades old. While traditional neo-Darwinism focused on the explanation of speciation and adaptation, evo-devo attempts to account for morphological evolvability and the evolutionary origin of novel structures and total body plans. The central tenet of evo-devo is that knowledge about development is a necessary part of any explanation addressing these evolutionary questions. (While this section focuses on how the developmental homology concept relates to the agenda of evo-devo, a more detailed discussion of the history, theoretical ideas, and explanatory aims of evo-devo can be found in Appendix B.)

In the case of the phylogenetic approach in evolutionary and systematic biology (Section 5.1), we saw that during the 20$^{\text{th}}$ century, the notion of serial homology became irrelevant or came to be explicitly rejected. A characteristic feature of developmental approaches is that serial homology becomes an important idea again. Developmental approaches view serial homology as a genuine aspect of homology. Consequently, the developmental homology concept includes serial homologues in its extension, unlike the phylogenetic homology concept.

5.2.1 Irreducible Levels of Morphological Organization

Comparative anatomists often homologize adult features or features of gross morphology only (such as skeletal features, organs, muscles, blood vessels). But we saw that already in the 19$^{\text{th}}$ century, biologists compared and homologized developmental features and structures at lower levels of organization. For instance, tissue types and germ layers in different multi-cellular animals were viewed as homologous. During the 20$^{\text{th}}$ century, the homology concept became applied to still lower levels of biological organization, in particular in the comparative study of development. In current developmental biology the focus is on how differentiation takes place and structures are formed in

[8]Developmental biology as such is not concerned with comparative and evolutionary questions. Many developmental biologists study model organisms, and thus a single species only. For this reason, the homology concept need not play an important part for the research practice of many developmental biologists. Some developmental biologists who use the notion of homology have a relatively generic homology concept that does not clearly distinguish between the different contemporary homology concepts that are discussed in this chapter. Most developmental geneticists use the molecular homology concept, discussed in Section 5.3. The present section on the developmental homology concept is about the homology concept of those biologists who take developmental as well as evolutionary issues seriously. This is in particular the case for representatives of the discipline of evolutionary developmental biology.

the course of ontogeny by means of developmental resources such as genes, cytoplasmic factors, and extracellular signals. This branch of biology addresses most completely all levels of biological organization. It takes into account molecular and biochemical mechanisms in the nucleus and cytoplasm. It analyzes cell-cell adhesion and signal transduction. Developmental biology studies different cell types, cell lineages, and differentiation. It deals with tissue types and tissue formation. It describes transient structures, developmental precursors, and changing structures. Finally, developmental biology attempts to account for adult morphology.

As a result, when the issue of homology arises conceptually in the comparison of the development in different species, it becomes apparent that homology exists on different levels of organismal organization. Nowadays, genes and proteins in different species can be homologous (if they are derived from a common ancestral gene or protein). An important method in comparing the development of distantly related organisms is to compare their gene expression patterns in different kinds of tissues. Subparts of individual cells, so-called ultrastructures, are homologized (Rieger and Tyler 1979; Paulus 1989). Calling types of cells and tissues the same amounts to an implicit statement of homology. Some contemporary evolutionary developmental biologists attempt to homologize developmental processes (Gilbert et al. 1996; Gilbert and Bolker 2001; Minelli 2003). And, of course, standard morphological structures are homologized. Not only was the homology concept applied to different levels of organization, it actually turned out that *homology at one level need not translate into homology at another level*. For instance, homologous structures may develop in a different fashion and out of different precursor structures. In addition, homologous structures in different species may develop based on non-homologous genes, and the same gene in different species may be involved in the production of non-homologous structures. I will discuss why this finding is important for the way in which evolutionary developmental biologists think about homology and organismal organization. But first I want to review the evidence for this fact.

In the previous chapter, I pointed out that some biologists preferred to assess homology based on the comparison of adult structures, while embryological studies played only a minor role for their research practice. In fact, some argued that the positional criterion has precedence over the embryological criterion. We saw that a few 19^{th} century biologists such as Richard Owen and Carl Gegenbaur defended their methodological preference by pointing to exceptions to the embryological criterion — there are cases where homologous structures in different species develop from different precursor structures. In the 20^{th} century, the morphologist Adolf Remane (1956) discussed several examples where the same adult character in different species can originate in

quite different developmental ways. Some 20th century embryologists discussed homology from a developmental point of view, suggesting that the facts of development create puzzles for our way of thinking about homology. A prominent case is the experimental embryologist Gavin de Beer (1899–1972). In fact, de Beer's claims about homology can be viewed as setting the stage for current debates of homology (Brigandt 2006; Hall 2000; Laubichler 2000). De Beer stated his views on homology for the first time in the essay "Embryology and Evolution" (1938). This early account already contained most of de Beer's arguments and conclusions on homology. While his position is briefly restated in famous work *Embryos and Ancestors* (1958), the essay *Homology, An Unsolved Problem* (1971) offers a succinct account of de Beer's position.

In spite of recognizing that homology is a phylogenetic phenomenon, de Beer argued that the facts of developmental biology and genetics have profound implications for standard criteria and definitions of homology.[9] He presented different ways in which the embryological criterion of homology fails. First, homologous structures need not develop from the same part of the egg or the same part of the embryo. De Beer discussed several descriptive and experimental studies that show this point. To give an example, a homologue such as the alimentary canal in different vertebrates can be formed from the roof of the embryonic gut cavity (as in sharks), the floor (lampreys), the roof and floor (amphibians), or from the embryonic disc (reptiles). Second, the differentiation of a tissue (so that it develops further into a certain structure) may be contingent on the causal influence of an adjacent tissue (induction by an organizer). Referring to tissue grafting experiments conducted by the school of Hans Spemann, de Beer pointed out that homologous structures need not be induced by the same organizers or induction-processes. For instance, the development of eye lens in the common frog (*Rana fusca*) presupposes induction by the adjacent optic cup, whereas in the close related edible frog (*Rana esculata*) the lens develops autonomously without any inductive influence. Finally, de Beer's own observations showed that homologous structures need not even

[9] Prior to de Beer, an earlier discussion making similar points is Hans Spemann's 1915 essay "On the History and Critique of the Homology Concept" (Brigandt 2006; Laubichler 2000). As a practitioner of experimental embryology, Spemann's target is 19th century evolutionary morphology and what he calls the 'genetic conception' of homology, which views two structures as homologous in case they have a common origin. It is important to keep in mind that for 19th century biologists common origin meant both common evolutionary origin and common developmental origin, so that Spemann's critical considerations concern both the embryological criterion and the idea that homologous structures are inherited from parent to offspring. Based on examples from experimental embryology similar to the ones that de Beer was to use, Spemann concludes that "it appears that the homology concept in the version of the historical [evolutionary] period [of morphology] dissolves in our hands, if we want to work with it using a causal approach. This does not happen for the quite general reason that the changing [e.g., development] cannot possibly be fully expressed using fixed concepts [feste Begriffe], but it happens due to the much profounder reason that development occurs in a different manner than was assumed — probably to some extent implicitly — at the original introduction of the [homology] concept and its later usage." (Spemann 1915, p. 83–84; my translation)

develop from the same germ layers, previously assumed to be a necessary condition for homology (de Beer 1947). Thus, *homologous structures in different species may originate from different developmental precursors or by means of different developmental processes.*

Homologous structures need not originate from the same part of the fertilized egg. Given that the cytoplasm does not help us any further, what about searching for homology in the genes? Appeal to the inheritance of genes could be a way to spell out the idea that homologous structures are inherited from the parent without making the erroneous assumption that the structures themselves are materially transmitted or that structures are preformed in the egg. However, de Beer's claim was precisely that it is futile to try to pin down sameness of structure by the sameness of a limited set of genes. This remarkable insight is already present in his 1938 essay. On the one hand, phenotypic characters that are controlled by identical genes can be non-homologous. De Beer supported this claim by several examples. The *Antenna* gene in the fruit fly *Drosophila*, for instance, can control the production of an additional antenna instead of an eye, structures that are not homologous. In fowl, a particular gene controls the formation of crest feathers in some species; in other species it also causes a cerebral hernia, with upswelling of the skull. On the other hand, *homologous characters can be controlled by non-identical genes.* Phenocopies and the *Eyeless* gene in *Drosophila* show this point. Other genes of a gene complex can apparently 'deputize' and make up for the missing gene that normally controls the formation of the character (de Beer 1971, p. 15).

> It is now clear that the pride with which it was assumed that the inheritance of homologous structures from a common ancestor explained homology was misplaced; for such inheritance cannot be ascribed to identity of genes. (de Beer 1971, p. 16)

De Beer's claim about the independence of homology among morphological structures, homology among genes, and sameness of developmental processes is nowadays well-confirmed.[10] Wagner and Misof (1993) discuss several examples of homologous structures arising from different developmental processes. A striking class of examples is given by the phenomenon of *direct development.* Many animal groups have a larval form, which is retained for some while, while later the larva develops into the adult form by metamorphosis. The adult morphology is very different from the structure of the larva. This process proceeding from egg to larva to adult is called indirect development, as in such animal groups there is also direct development, where the adult directly develops from the egg without passing through the larval stage. Direct development occurs in insects, amphibians,

[10]To some extent, these ideas had to be rediscovered. For instance, V. Louise Roth, taking a developmental approach to homology, formerly proposed that "a *necessary* component of homology is *the sharing of a common developmental pathway*" (1984, p. 17). She quickly abandoned this requirement, since there are several cases of homologous structures arising by means of different developmental processes, as discussed in Roth (1988).

and sea urchins (Raff and Kaufman 1983; Raff 1996). For instance, *Heliocidarus tuberculata* and *Heliocidarus erythrogramma* are sea urchins that are very closely related, belonging to the same genus. While *H. tuberculata* develops indirectly, in the ancestral mode of development, *H. erythrogramma* is a direct developer (Love and Raff 2006). The adult forms of these two species are very similar, which is the reason why they were originally taken to be the same species. Yet the indirect developer has a larval body plan which is bilaterally symmetric, and then metamorphoses into a radial symmetric adult form. The two species develop in a radically different way, but still end up with the same adult morphology. Consequently, their adult structures exhibit clear homologies, but some of them develop out of non-homologous embryonic structures. It is nowadays beyond doubt that sameness of adult structures in different species and sameness of developmental processes do not map onto each other (Abouheif 1997; Hall 1992; Hall 1995; Meyer 1998).

The same situation applies for the relation of homology among genes and homology among structures. Nowadays, expression studies are an important tool for developmental biology. Molecular methods permit scientists to determine, even in a living and developing organism, at which particular part of a body and in which type of tissues a certain gene is expressed. If a characteristic gene is expressed in one structure, and its homologue it expressed in a structure in another species, then this is some evidence for the two structures being homologous. However, correspondence of expression patterns is merely a defeasible criterion. Abouheif et al. (1997) had to admonish developmental biologists that sameness of expression patterns is not to be confused with homology. For homologous structure may develop based on non-homologous genes and homologous genes may by involved in the production of non-homologous structures in different species. The reason is that the effect and function of a gene depends on how it interacts with other genes and cellular/developmental factors. In the course of evolution, a gene that used to be important for the production of a certain structure may additionally become involved in the development of another structure in a different part of the body, and finally become irrelevant for the production of the first structure. Genes may be co-opted for new functions while losing its original function. Such an evolutionary scenario leads to the situation where a gene is involved in the production a structure in one species, while it produces primarily another, non-homologous structure in different species. Conversely, by the same historical process two extant species can evolve such that the same structure is produced involving non-homologous genes in these different species. It is nowadays well known (though not always respected in practice) that homology of genes or identity of gene expression patterns is not to be equated with homology among morphological structures (Abouheif

1997; Bolker and Raff 1996; Dickinson 1995; Meyer 1998; Müller and Wagner 1996; Nielsen and Martinez 2003; Roth 1988; Svensson 2004; Newman 2006).

It is indeed surprising that homology among morphological structures cannot be reduced to homology among genes. De Beer formulated the puzzling nature of homology as follows:

> But if it is true that through the genetic code, genes code for enzymes that synthesize proteins which are responsible for the differentiation of the various parts in their normal manner, what mechanism can it be that results in the production of homologous organs, the same 'patterns', in spite of their *not* being controlled by the same genes? I asked this question in 1938, and it has not been answered. (de Beer 1971, p. 16)

Contemporary biologists can live very well with this fact. It is one of the fundamental assumptions of evolutionary developmental biology that organisms are structured in a hierarchical fashion in that there are *different levels of organization* (Stotz 2005). Among other things, there are molecules, cell parts, cells, tissues, and organs, each of which occupy different levels and stand in whole-part relationships. The idea of hierarchical organization does not mean that there is a fixed and clearly delimited set of levels and that every particular biological entity unambiguously occupies a certain level. Just as different entities emerge and are transformed in the course of both development and evolution, so can different levels be fluid. But it is still important to recognize different levels of organization, as entities on these level have a relative independence from each other. In particular, evolutionary change can occur on one level independent of change at a different level, as the issue of homology shows (Brigandt 2006). Homology among one level is compatible with non-homology at another level. A structure at one level of organization can be evolutionarily stable and be found in many species, while structures at other levels undergo substantial evolutionary change at the same time. For instance, a structure at higher levels of organization can be evolutionarily stable while its underlying molecular and developmental basis changes — resulting in homologous structures in different species that develop from non-homologous genes and by different developmental processes. Thus, structures at one level of organization need *not be reducible* to features at a lower level such as the molecular level. This irreducibility claim is not to deny that entities on different levels influence each other, and that entities on a higher level are mereologically composed of entities on a lower level. Token-token reduction obtains, but not the type-type reduction of a structure as it occurs across many species — which is the relevant feature for the explanation of the development of larger groups of organisms and the study of the evolution of development. Georg Striedter and Glenn Northcutt (1991) make this point, including behavior as an independent level:

> We contend that attempts to reduce behavioral homology to morphological homologies, and morphological homology to genetic and developmental homologies, are misguided and based on a failure to

> recognize the hierarchical nature of biological organization. Genes, developmental processes, morphological structures, physiological functions and behaviors all constitute different levels of biological organization. These levels are causally interrelated, but there is no one-to-one correspondence between characters at different levels. Furthermore, the causal relationship between characters at different levels may change during the course of evolution. As a result, higher level characters may be homologous, even though some of their constituent lower level characters are not homologous. (Striedter and Nothcutt 1991, p. 177)

The relative autonomy of structures on different levels implies that biological entities are best studied on the level at which they are stable features. A structure or developmental module as it exists across species may have a stable causal influence on development, morphological organization and functional integration, while the causal relevance of its underlying molecular basis varies from species to species. Thus, developmental explanations attach best to these stable entities, which may reside on higher levels of organization (Laubichler and Wagner 2001; Brigandt and Love in prep.). Günter Wagner connects this idea with his notion of shifting pluralism, i.e., the idea that the relative evolutionary importance of a certain causal feature may shift from situation to situation:

> This idea [shifting pluralism] is related to the broader concept that each level of biological organization has it own emergent mechanisms and that we have to identify the level and relative importance of those mechanisms that contribute to the explanation of any particular phenomenon. Any a priori assumption of what the mechanisms are or on what level they have to reside, be it reductionistic or holistic, is a metaphysical commitment that fails to appreciate the hierarchical nature of biological organizations. (Wagner 2000, p. 97)

Given that homologies at one level need not translate into homologies at a lower level, the implication is that while homology among genes can be a criterion of homology at higher levels, ultimately homology on one level as a relatively independent phenomenon is best studied using the comparative method, i.e., by comparing structures at this level across different species and determining whether a particular structure is present in other species and homologous to a structure in other species. De Beer made this point based on the idea that embryological origin and genetic basis are highly defeasible criteria of homology: "comparative anatomy, not comparative embryology, is the primary standard for the study of homologies" (1971, p. 14).[11] Nowadays, the comparative method includes cladistic and phylogenetic analysis. Characters across species are to be studies using a phylogenetic tree of the species involved, and the character distribution and character transformation on this tree is the basis for assessing homologies (Sections 5.1.2 – 5.1.3). A biological entity on one level of organization can be stable in evolution and homologous across species, while others are not. Ehab Abouheif (1997) makes this point in his essay "Developmental Genetics and Homology: A Hierarchical Approach", arguing that genes, gene expression patterns, embryonic

[11] Remane (1961) came to the same conclusion when arguing that identity of developed structures, identity of developmental trajectories, identity of causal determinants in development, and identity of genetic factors are independent.

origin, and morphology must simultaneously be analyzed within a phylogenetic framework:

> However, these conflicting aspects of 'sameness' [at different levels] should not be viewed as problematic, rather, it reveals the context dependence and hierarchical nature of homology. ... The recognition that homology can exist independently at each of these levels has allowed the integration of developmental genetic data into a meaningful framework for the analysis of homology. However, this class of data must be placed within the context of the comparative method, as it provides an explicit methodology to determine homology at several hierarchical levels of biological organization. (Abouheif 1997, p. 405)

5.2.2 Developmental Approaches to Homology

In the last two decades, several biologists have approached the homology concept from a distinctively developmental point of view. This led to what I call the developmental homology concept. A feature of this recent development is that quite a few developmental definitions or theories of homology have been proposed. These definitions reflect a search for the biological nature of homology as a principle of morphological organization. Common ancestry is sometimes viewed as a necessary, but not sufficient condition for two structures being homologous. Instead, developmental considerations are viewed as relevant for the origin and maintenance of the correspondence of structures in different species. Many biologists with a developmental understanding of homology are actually aware that they have a different approach and use a different concept of homology, which is shown by the fact that the developmental understanding is contrasted with a 'phylogenetic', 'historical', or 'evolutionary' homology concept. In addition, the difference in perspective is viewed as being due to the different theoretical and practical goals of evolutionary developmental biology as opposed to systematics and evolutionary biology. A characteristic feature of developmental approaches is that the notion of serial (= repetitive or iterative) homology is revived and viewed as important. The idea is that not only homologous structures in different species, but also homologous structures within one organism are governed by the same developmental principles. When apparently the same structure occurs repeatedly within an organism, this is surely intriguing for a developmental approach and calls for an explanation. Rupert Riedl (1978) gave an early and prominent expression of this idea. While Adolf Remane assumed that we should terminologically distinguish between homology (between species) and homonomy (serial homology), Riedl argued that both phenomena are due to the same fundamental mechanism for the formation of order in organisms.

In what follows, I illustrate developmental approaches to homology by reviewing some developmental definitions of homology that have been proposed in the last two decades. This plethora of definitions does not mean at all that there are different homology concepts in use. In fact, these

definitions should not be understood as definitions in the traditional sense. Sometimes such a 'definition' expresses a tentative hypothesis that is stressed by a particular developmental approach to homology. Rather than giving a genuine account of the biological nature of homology, often these definitions merely set out some boundary conditions within which further theoretical work on homology has to operate. Some of the 'definitions' of homology should be viewed as programmatic in that they single out a certain relevant biological feature, suggesting that research on homology has to focus on this feature. Thus, developmental 'definitions' of homology are best viewed as research proposals for future theoretical work (Brigandt 2002).

In his essay "Homology and Causes", Leigh van Valen (1982) suggests the following definition:

> All homologies involve a continuity of information. In fact homology can be defined, in a quite general way, as correspondence caused by a continuity of information. (van Valen 1982, p. 305)

While some may think that the concept of genetic information is a vacuous notion, Van Valen explicitly states that he does not understand 'information' as 'genetic information'. Instead, by information he means "more and less than the nuclei acid of the genotype" (p. 305). Information is more than genetic information because it can be carried and inherited in non-genetic ways. Biological information is less then genetic information as homologous structures can be produced by non-homologous genes. Von Valen does not offer a precise account of the notion information. In fact, his very point is to make use of a broad notion that encompasses different aspects of homology. In particular, it includes both homologues in different species and serial homologues:

> Homology is resemblance caused by a continuity of information. In biology it is a unified developmental phenomenon. Homologies among and within individuals intergrade in several ways, so historical homology cannot be separated from repetitive homology.
> However, homologies also occur within individuals. ... These resemblances also produced by a continuity of information. Such repetitive or modular homologies ... simplify development in that the same subprogram can be used many times, perhaps in modified ways. (van Valen 1982, pp. 305, 307)

Among many others, Haszprunar (1992) favors van Valen's definition as the placeholder notion of 'biological information' includes different types of homology such as serial homology, ontogenetic homology (identity of a structure during development), di-/polymorphic homology (homology between structures of different organisms in one species), and supraspecific homology (homology between different species). In sum, van Valen's definition emphasizes that there are different aspects and levels of homology, including serial homology. A developmental approach is able to show that different types of homology are in fact different aspects of one and the same unified phenomenon:

> Here I argue that a consideration of the causes of homology provides a unifying thread and that the apparently disparate relations called homology really can be considered as one. (van Valen 1982, p. 305)

Another well-known theoretical position is the work of V. Louise Roth (1984, 1988, 1991, 1994). Roth does not propose a definition of her own; instead she uses Van Valen's definition as a guideline. In her view, this definition is "the most succinct, comprehensive, and idealogically neutral definition of homology yet proposed. Its beauty lies in its flexibility: the definition can be used by adherents to any school of thought by simply specifying the relevant kind of information" (1988, p. 2). Homology surely exists on different levels and homologies are created and maintained by different mechanisms at each level, but this does entail that homology is not a single phenomenon: "But what is needed is not differing *definitions*, but different explanations" (1994, p. 307). Roth's work is of particular importance as her research works towards a developmental approach to homology, and she explicitly states that this approach is distinct from the traditional phylogenetic approach:

> The currently most widely used definitions of homology, which concentrate exclusively on what I call phylogenetic homology, involve comparisons between taxa. Although they share important conceptual relationships with phylogenetic homology and their role in evolutionary biology is significant, serial and other forms of iterative homology have been, by comparison, overlooked. There is need for a more inclusive definition of homology. (1984, p. 13)

Van Valen's account allows Roth to integrate serial homology in one definition: serial homologues develop when biological information is expressed repeatedly in different parts of the body (Roth 1988, p. 3; 1991, p. 169). In addition, this definition does not commit one to the idea that homologous structures develop in the same way. Roth calls this developmental approach "The Biological Basis of Homology," the title of her 1988 essay. Homologues are viewed as elements of phylogenetic stability. A developmental approach is supposed to specify what homologues are, given that they reappear in different generations and species and also occur several times within an individual. The task of a developmental approach is to find out about the biological basis of this phenomenon. Roth (1991) explicitly contrasts "Homology in systematics" and "The biological basis of homology" (p. 171). Both approaches differ in their objects of focal interest, their objectives, their empirical undertakings, their methods, and their research products. While the research objectives in systematics is to find homologous characters and to identify taxa, a developmental approach attempts to "discern what types of phenotypic features of organisms tend to be conserved, why they are, and how." The research product in systematics is patterns and distributions of characters and arrangements of taxa. In the case of a developmental approach it is the "clarification of similarities & differences in the developmental processes that produce phenotypic features" (p. 171). According to Roth, apart from accounting for how structures develop and are inherited, a challenge for understanding the biological basis of homology is the fact that organisms are hierarchically organized and that entities on different levels can evolve independently from each other (1991, p. 167).

A prominent account of homology is the one of Günter Wagner. Wagner views homologues as invariant, semi-autonomous characters of organisms, which is due to their being governed by developmental constraints. A developmental constraint is a feature of an organism's developmental and material constitution which determines the dimensions along which phenotypic variation can occur, thereby biasing or restricting the way in which further morphological evolution can proceed. For instance, due to a developmental constraint one feature of an organism may vary only together with another feature (see Appendix B.1 for a detailed discussion of developmental constraints).

> The concept of homology thus is restricted to those invariants of form that have been acquired during evolution and which are therefore the best indication of historical relations among organisms. *Homology implies the existence of historically acquired and genetically determined developmental constraints.* Constraints of phenotypic evolution most probably are caused by ... developmental mechanisms. Nevertheless, homology does *not* imply *identity* of developmental mechanisms. (Wagner 1986, p. 153)

In accordance with the morphological tradition, homologues are viewed as building blocks of organisms. A developmental approach, however, addresses new questions about the behavior of homologues in evolution and development:

> It is the central thesis of this paper that the evolutionary origin, maintenance and modification of these building blocks of "higher" animals is equivalent to the biological content of the homology concept. ... A biological homology concept is expected to explain three properties of homologs: 1) the *conservation* of those features that are used to define a homolog, 2) the *individualization* of the homolog with respect to the body, 3) the *uniqueness* of homologs, i.e., their specificity for monophyletic groups. (Wagner 1989b, pp. 1158, 1157)

Just like Louise Roth, in the beginning Wagner used the term 'biological basis of homology'. Then he proposed his own definition of homology, his 'biological homology concept'. Wagner distinguishes between the idealistic homology concept, the historical homology concept (which I call the phylogenetic homology concept), and the new biological homology concept:

> However, there are also quite problematic aspects of the current homology concept, which has been in use since the time of Darwin. This here is called the *historical homology* concept, since it is defined by historical continuity of descent from a common ancestor. The historical homology concept explicitly ignores iterative homology. ... More importantly a large body of developmental data seems to contradict certain implications of the current homology concept. ... It is more significant that most of these authors [with a developmental approach to homology] share a host of arguments which call for a new concept of homology. This may be called the "biological homology concept," because it refers to biological mechanisms rather than to genealogical connection alone. (1989a, pp. 51, 55)

Wagner offers the following definition of homology, his 'biological homology concept':

> Structures from two individuals or from the same individual are homologous if they share a set of developmental constraints, caused by locally acting self-regulatory mechanisms of organ differentiation. These structures are thus developmentally individualized parts of the phenotype. This definition is both more inclusive and more restrictive than the historical homology concept. It is more inclusive because it allows homology between parts of the same organism, i.e., iterative homology, and between individuals of the same species. ... The proposed homology concept is more restrictive than the historical one because it is restricted to individualized parts of the phenotype. (1989a, pp. 62)

The idea is that homologues reliably reappear in different generations and are relatively stable over evolutionary time because they are governed by developmental constraints, which are specific to a particular homologue and historically emerged with the origin of this structure. Not only does the same developmental constraint apply to structures in different species, but it may also pertain to different structures within an individual, this is why serial homologues may be genuine homologues as it is empirically plausible that they fall under this developmental definition.

Like former developmental approaches, Wagner stresses the fact that homologous structures may emerge by means of different developmental pathways. It is important to realize that shared developmental constraints do not imply shared developmental mechanisms. A morphological structure is a character on a particular level of biological organization, and it may be developmentally constrained and thereby evolutionarily stable independent of processes and entities on other levels of organization, such as genes and developmental processes. Wagner and Misof (1993) attempt an explanation of why two characters can be developmentally constrained in spite of the fact that they develop in a different fashion.[12] Wagner's account also ties up with the concept of evolutionary novelty, a crucial concept and feature to be explained by evolutionary developmental biology. As discussed in Appendix B.2, Müller and Wagner (1991) define a novelty as a structure that is non-homologous to any structure in the ancestor (including serial homologues). They assume that novelties arise when ancestral developmental constraints are overcome, so that the evolutionarily stable morphology of the ancestor is replaced by a modified morphology. This fits with Wagner's (1989a) identification of homologues with structures governed by a set of developmental constraint. For on such a view the emergence of a novel homologue is precisely the creation of a new set of constraints. Finally, note that Wagner's definition does not make explicit reference to phylogeny or common ancestry. It is by no means the case that Wagner has a non-historical approach to morphology — he explicitly views developmental constraints as historical products of evolution. Common ancestry is a sufficient condition for homology, for common ancestry implies that developmental

[12] A profound example of the evolutionary dissociation of development and adult form is given by Wagner and Gauthier (1999). In limbed vertebrates that still have all five digits of their hand, digits D1,...,D5 develop from condensation C1,...,C5, respectively. In birds, two digits have been lost in the course of evolution. Paleontological studies suggest that digits 1,2,3 have been retained; embryological studies, however, suggest that 2,3,4 have remained. Wagner and Gauthier argue that both position are based on relevant evidence and propose the following solution to this conflict. After the loss of C5/D5, condensation C1 was lost due to developmental constraints (determining that C1 is the second condensation to be lost). Yet this did not result in the loss of digit D1, as functional considerations (selection) favored retaining D1. Instead, a developmental frameshift took place such that D1 develops from C2, D2 from C3, and D3 from C4 (and D4 being lost). Thus it is possible that a character changes its identity during development, leading to an evolutionary dissociation between a character's developmental origin and its subsequent individualization: Embryological evidence suggests that digits 2,3,4 have been retained, but it are condensations C2,C3,C4 only that have remained. From them develop D1,D2,D3, as the paleontological evidence rightly asserts.

constraints are shared by structures in two species. Still, common descent is not constitutive of homology. It is not a necessary condition as for instance serial homologues are not derived from an ancestral structure.[13] Overall, the goal of a developmental account of homology is as follows:

> Hence the problem is to explain why there are individualized parts of the body that retain their structural identity despite variation in form and function. (Wagner 1994, p. 279)

Georg Striedter (1998) offers a further developmental definition, which he calls 'epigenetic homology'. His motivation is to combine phylogenetic and developmental aspects. Striedter thinks that the dichotomy between evolutionary and developmental approaches to homology is "based on false conceptualizations of development as being based on genetic blueprints" (p. 219). His account derives from the idea of epigenetic landscapes (see Waddington 1957). In an epigenetic landscape the process of development is represented by a topography including a series of valleys that usually branch. Moving downwards in this landscape represents the developing phenotype, which may end up at different end points. An epigenetic landscape tries in particular to take into consideration the fact that development is buffered against disturbances (environmental influences and genetic changes). The shape of an epigenetic landscape is determined by several developmental factors and resources (including genes). Striedter focuses more precisely on energy landscapes, which are used in modeling developmental processes as complex dynamical systems. An energy landscape depicts the stable states of the dynamical system by troughs. The bottom point of such a valley — a point of locally minimum energy — is an attractor: once the system is in a state close to such an attractor it tends to converge towards it. Based on these notions epigenetic homology is defined as follows:

> Characters that represent corresponding valley bottoms (attractors) in the epigenetic landscapes of two or more organisms are homologous if they have continuously reappeared in the ontogenies of individual organisms since their origin in a single population of ancestral organisms. (1998, p. 224)

[13] An approach outside the mainstream is process structuralism, as defended by Brian Goodwin. Structuralism is a modern version of idealistic morphology, attempting to recover as pre-Darwinian definition of homology. Species are not to be classified in terms of their genealogy, but according to their intrinsic structural features. This is in analogy to chemical elements being classified in terms of their intrinsic chemical properties, rather than in terms of the historical emergence of different chemical elements. Process structuralism assumes that organisms belong to a taxonomic group in virtue of falling under a set of developmental laws which govern the ontogeny of these organisms. Phenotypic variation within such a taxon is due to the changes in the parameters and initial conditions of these universal laws. The same applies to homology: two structures are homologous in virtue of being produced by the same developmental-generative laws. Because of its anti-evolutionary philosophy and the assumption that generative laws rather than natural selection is the determining factor in evolution, process structuralism has been endorsed by a handful of biologists only (Goodwin 1982, 1984, 1993, 1994a, 1994b; Webster 1984). Process structuralism agrees with mainstream evo-devo in emphasizing the fact that homologous structures are governed by certain developmental principles. But process structuralists fail to see that these developmental principles ('laws') are the product of evolutionary history and subject to change (Griffiths 1996a). While Wagner defines homology in terms of shared developmental constraints, he views developmental constraints not as universal laws, but as fundamentally historical. Developmental constraints do not exist before the organisms that are governed by these constraints. Instead, they phylogenetically originate together with developing system that characterizes a particular group of organisms and they are transformed by evolution or vanish in case of the emergence of evolutionary novelties.

An important feature of Striedter's approach is the focus on how ontogeny brings about structure over phylogenetic time. In addition, an account is given of how different developmental pathways can create homologous structures, as different developing structures may converge on an attractor state from a number of different initial positions. Striedter's idea is that homology as correspondence of epigenetic valleys is not defined by any intrinsic criteria but by their overlap in multidimensional state space, where this overlap is detected by phylogenetic analysis.

Following Rupert Riedl, Gerd Müller's (2003) account focuses on morphological organization:

> The evolution of organismal form consists of a continuing production and ordering of anatomical parts: the resulting arrangement of parts is nonrandom and lineage specific. The organization of morphological order is thus a central feature of organismal evolution, whose explanation requires a theory of morphological organization. Such a theory will have to account for (1) the generation of initial parts; (2) the fixation of such parts in lineage-specific combinations; (3) the modification of parts; (4) the loss of parts; (5) the reappearance of lost parts; and (6) and the addition of new parts. ... Only a few of the processes listed above are addressed by the canonical neo-Darwinian theory, which is chiefly concerned with gene frequencies in populations and with the factors responsible for their variation and fixation. ...
> I argue that comparative anatomy has always dealt with organization implicitly: the essence of this vast body of knowledge is embodied in what has been called the "concept" of homology. I propose that homology is not merely a concept or a conceptual tool, as it is often understood, but rather the manifestation of morphological organization processes. (Müller 2003, p. 51)

Müller stresses that homology exists on different levels of biological organization and that structures on the same level only can be homologous. Homologies on one level cannot be reduced to homologies on another level, and the "Search for a Locus" of homology (p. 56), i.e., a privileged level or set of entities (such as genes) in terms of which homology can be defined, is misguided:

> *Morphological homology* is a manifestation of structural organization that maintains identical building elements despite variation in their molecular, development, and genetic makeup. (Müller 2003, pp. 58–59)

Müller proposes a three-step model of the origin of homologues and structural novelties (see also Müller and Newman 1999; Newman and Müller 2000, 2001). The first step is 'generation', i.e., the origination of a new entity that could become a homologue. This process is largely epigenetic and developmental, and not necessarily based on genetic inheritance. It is only in the second step ('integration') that these units become genetically stabilized in terms of Mendelian inheritance. Thus, the existence of the stable re-occurrence of structures that is partially based on genetic control and inheritance is viewed as an evolved state of affairs, but not as the original condition. The final step is a structure's 'autonomization' as a central feature of structural organization:

> Homology, in its most evolved form, is characterized by an increasing independence from the underlying developmental, molecular, and genetic processes that led to the first appearance (generation) and subsequent fixation (integration) of basic, individual homologues. (Müller 2003, p. 63)

Based on these ideas, Müller proposes his 'organizational homology concept', which involves seven assumptions (some established by former authors, some proposed by Müller):

1. Homologues are constant elements of organismal construction; they are independent of changes in form and function (Owen, 1843);
2. Homology signifies identity, not similarity (Owen, 1843);
3. Homologues are fixated by hierarchically interconnected interdependencies ("burden"; Riedl, 1978);
4. Homologues are developmentally individualized building units (Wagner, 1989a,b);
5. Homology denotes constancy of constructional organization despite changes in underlying generative mechanisms;
6. Homologues act as organizers of the phenotype; and
7. Homologues act as organizers of the evolving molecular and genetic circuitry.

(Müller 2003, p. 64)

During the last decade, Günter Wagner's ideas on homology have evolved and developed. Like in his prior work and in Gerd Müller's account, homologues are viewed as individualized morphological building blocks that make up an organism. Müller's work on homology focuses on evolutionary novelty (the very origin of homologues) as well as on the developmental role of homologues (the way in which one homologue interacts with other homologues and organizes development). Wagner's recent work emphasizes the evolutionary behavior of homologues, in particular morphological evolvability. The different homologues of an individual are viewed as distinct characters that can vary and evolve relatively independently from each other, as different parts have a different contribution to fitness so that selection may act on some homologues without affecting others:

> It is suggested that homologues are building blocks of phenotypic adaptation, i.e., parts which provide independent contributions to the performance of an organism. Under this premise the individualization of characters makes adaptive sense since it is the structural prerequisite for a character to act as a building block of adaptation. (1995, p. 279)

The notion of *modularity*, which has been emphasized in the recent evo-devo literature, explains how it is possible that an organism is composed out of units that evolve relatively independently.[14] A module is a part of the body that is semi-autonomous in the following sense. It is internally integrated and it subparts have a high developmental and physiological influence on each other (e.g., there is a distinct set of genes primarily involved in bringing about this structure). The structure has causal connections with other modules, but the developmental and physiological connections between modules are smaller than within a module. This makes a module developmentally and morphologically semi-autonomous, and this feature in turn explains why a module can vary and change in evolution without other modules being affected. The concept of homology is connected to the notion of modularity because in a sense, modules are simply homologues and exist on different

[14]For some recent discussions of modularity, see Minelli (1998), von Dassow and Munro (1999), Bolker (2000), Raff and Raff (2000), Carroll (2001), Gilbert and Bolker (2001), Winther (2001), West-Eberhard (2003).

levels of the biological hierarchies, so that the cell as a module is a part of larger modules.[15] Wagner discusses different ways in which a module can be created out of existing ones. For instance, one module may split into two in case the internal effects within the original module are reduced; or two previously independent modules may merge into a larger module (Wagner and Altenberg 1996).

> The fact that phenotypic evolution can be studied on a character by character basis suggests that the body is composed of locally integrated units. These units can be considered as modular parts of the body which integrate functionally related characters into units of evolutionary transformations. These units may either emerge spontaneously by self-organization, or may be the product of natural selection. (Wagner 1996, p. 36)

Wagner's collaborator Manfred Laubichler (2000) puts this idea as follows:

> The core assumption of the biological homology concept is that homologues are the units of phenotypic evolution. As such they are individuated quasi-autonomous parts of an organism that share certain elements and variational properties. (Laubichler 2000, p. 783)[16]

Recently, Wagner and his collaborators have worked towards quantitative models that give a mathematical account of homologues as units of evolution, explicating the concept of a character (Fontana and Schuster 1998; Cupal et al. 2000; Wagner and Laubichler 2000, 2001; Stadler et al. 2001; Wagner and Stadler 2003). Prior accounts in quantitative genetics (studying heritability) model the phenotypic properties of an organism in terms of the $\mathbb{R}^n$, the n-dimensional space of real numbers. Each dimension of such a space is a character, a feature that can vary relatively independently from other characters. The state of each character in a particular individual is represented by a real number (corresponding to a homologue having a certain shape or other properties in an individual). What Wagner and collaborators find wanting about this traditional model is that it assumes a particular dimension of the $\mathbb{R}^n$, thus the number of characters (the morphological organization into a certain number of homologues) has to be known in advance. However, the goal of a developmental approach is to have an explication of the character concept that defines the number of characters an organisms has in term of its developmental make-up, which determines its structural evolvability. Wagner and collaborators address this issue by modeling possible phenotypes as elements of a pre-topological space. Given its topological properties, the phenotype space H can be factorized into different components, where the number of factors (the

[15] Notions such as module and modularity are also used in cognitive science and in evolutionary psychology. Evolutionary psychologists define modules in terms of their *function* and adaptive value only. Modules in the context of evo-devo, however, are purely developmental and *structural* modules. This is why Griffiths (forth.) argues that the evo-devo notion of a module as a homologue is more fruitful than the functional notion of a module used by evolutionary psychology. Evolutionary psychologists postulate a distinct module for every perceived adaptive behavioral task and then go on to assume that distinct modules can evolve and adapt differently. However, this is possible only if these functional modules are developmentally dissociated, i.e., if they are modules in the sense of evo-devo.

[16] See also Wagner (1999, 2001). Based on these ideas, the philosopher of biology Robert Brandon (1999) argues that modules are the units of selection (even though in his previous work he took organisms to be the units of selection, arguing against the gene as the unit of selection; see Brandon 1996 for his earlier position).

dimension of H) is the numbers of characters. A central feature of this model is that the topology of the phenotype space is essentially dependent on the genotype-phenotype map — i.e., development. Thus, an organism's development determines the number of characters that this organism has, which determines the dimensions along which evolutionary change may occur.[17]

5.2.3 A Semantic Account of the Developmental Homology Concept

It is time for a semantic characterization of the developmental homology concept, in terms of 1) its reference, 2) the epistemic goal pursued by its use, and 3) its inferential (conceptual) role. We shall see that the developmental homology concept, as it emerged in the last two decades in evolutionary developmental biology (evo-devo), differs as regards all these three components of content from the phylogenetic homology concept of systematics and evolutionary biology.

Biologists both from systematic/evolutionary biology and evo-devo use the *same criteria of homology* (Roth 1994), and consider the same structures of different species as homologous. Nevertheless, the homology concept of evolutionary developmental biology has a *wider extension*. Two points are worth mentioning. First, biologists focusing on development apply homology to lower levels of biological organization than systematists or evolutionary biologists usually do. Apart from organs and gross morphological structures, nowadays genes, proteins, cell and tissue types are homologized. Due to the explanatory focus of a developmental approach, homology has to be studied on different levels of biological organization, and thus the concept of homology became explicitly applied to different levels. As it turned out, homology on one level is not reducible to homology at other levels. In particular homologous morphological structures in different species can develop by means of quite different developmental pathways, and different homologues can be produced by non-homologous genes in different species. (We shall see below why this poses a challenge for a developmental account of homology and morphological evolvability.) Evolutionary developmental biologists assume that despite these different levels of homology, homology is a unified phenomenon and that there is one homology concept that encompasses these different levels.

Second, there is the issue of *serial homology*. This is telling evidence for the existence of different homology concepts in different contemporary biological fields. The multiple occurrence of

[17] Such an account should also allow for evolutionary novelties, i.e., the origin of completely new characters. As this means to add a new dimension to the space, novelties cannot be represented in the classical framework that assumed $\mathbb{R}^n$ having a fixed dimension. Wagner and collaborators address this issue by considering local factorizations of the total phenotype space, where a certain part of it can have a different dimension than other parts.

basically the same structure is referred to by the term serial homology (or also iterative or repetitive homology). This type of homology was recognized by pre-Darwinian morphology because of their geometrical-structural approach to homology (Section 4.1.2). For instance, Owen considered the different vertebrae of an organism as derived from a unique geometric scheme, the 'ideal vertebra', or serial homologues were viewed as developing based on the same laws of the generation of form. We saw in Section 5.1 that the idea of serial homology dropped out of favor in 20$^{\text{th}}$ century systematics and evolutionary biology. Biologists from these fields ignore the notion of serial homology or explicitly reject it as misunderstanding of what homology is about (Ax 1989; Bock 1989; Schmitt 1989). In the recent evolutionary developmental biology, however, the idea of serial homology became quite popular again. It is an idea that is widely accepted and utilized by developmental approaches to homology (Riedl 1978; van Valen 1982; Roth 1984; Wagner 1989a; Minelli and Peruffo 1991; Haszprunar 1992; Gilbert et al. 1996; Minelli 2003). Thus, there is a difference in extension between the two homology concepts: while the phylogenetic homology concept refers to homologous structures of different species only (excluding alleged serial 'homologues'), the developmental homology concept refers to homologues in different species and serial homologues. This difference in reference is a diagnostic feature in that it points to the existence of different homology concepts. But it is not the most profound reason for the existence of distinct concepts of homology. It is heuristically fruitful to take a look at the issue of serial homology, because this debate between the two biological fields reveals the real conceptual difference — which are distinct *epistemic goals* being pursued by different homology concepts. It is not just the case that serial homologues do not fall under standard phylogenetic 'definitions' of homology (as two structures in an individual are not inherited from a single structure in an ancestor), while serial homologues fall under developmental 'definitions' (e.g., two serial homologues are governed by the same developmental constraints so that Wagner's definition is met). There is more to these two homology concepts than standard definitions.[18] Both the phylogenetic and the developmental homology concepts are embedded in different research agendas, being used for different theoretical purposes and epistemic goals.

Regards the epistemic goal of the phylogenetic homology concept, Section 5.1 explained in detail that this concept is used to compare different species, in order to classify them or explain the evolutionary modification from one species to another. The focus on different species is the reason

[18] My above discussion of developmental definitions of homology (Section 5.2.2) emphasized that these definitions do not exhaust the content of the developmental homology concept and that instead they are best viewed as programmatic statements outlining some crucial features of a developmental understanding of homology or some issues viewed as promising for future research on homology.

why phylogenetic homology only includes between-species homologies.[19] If a systematist boldly states that developmental approaches do not understand what homology is 'about', then this does not merely express the idea that the developmentalists get the extension of 'the' homology concept wrong, it in fact expresses the tenet that developmental approaches are confused about what the homology concept is to be used for — namely, comparison of *different species*. The developmental homology concept is likewise used to achieve a particular epistemic goal. The different homologues of an organism — despite being developmentally and functionally connected parts of an organism — are morphologically individualized and semi-autonomous, so that one homologue may phenotypically vary and change in evolution without affecting other characters. A successful developmental account of homology is to explain why there are homologues as units of phenotypic variability, thereby shedding light on morphological evolvability as a central explanandum of evolutionary developmental biology (Appendix B). In addition, we saw that homologues exist on different levels of organization and that structures on one level may evolve relatively independently of other structures (Section 5.2.1). For instance, gross morphological structures may evolve independently of their developmental and molecular basis. A central task for evo-devo is to understand the developmental principles in virtue of which homologues gain their morphological individuality and relative independence from other structures on the same and other levels of organismal organization. This makes it necessary to account for the relation of homologues *within an organism*. When similar structures are present several times within an organism, it is natural to ask whether this is due to similar developmental processes, or the use of the same developmental resource in different parts of the organism. The occurrence of serial homologues is seen by evo-devo biologists as being due to the same mechanisms that generate morphological order in organisms as the presence of between-species homologues. To be sure, this is an empirical hypothesis, and further research into the developmental-morphological nature of structures has to reveal to which extent serial homologues in an organism are governed by the same developmental principles.

In sum, while the phylogenetic homology concept is about the relation of different species, evolutionary developmental biology attempts to account for *morphological unity within as well as between individuals* with its homology concept. Accounting for the morphological organization of individuals is crucial for understanding the *developmental basis of morphological evolvability*. It is

[19] It may also refer to structures of different organism of one species. But we saw above that while intra-specific homology is an idea used by most evolutionary biologists, taxonomist may restrict the notion of homology to between-species homology. For a developmental approach, intra-specific homologies are obviously important, as it is crucial to understand why the same structure develops in parent and its immediate offspring (Wagner 1989a).

this explanatory agenda that drives the emergence of the developmental homology concept. This *difference in epistemic goals* pursued by the developmental and the phylogenetic homology concept the real evidence for both being two distinct concepts. In turn, it implies that these two concepts have a different extension, so that the existence of different epistemic goals and research agendas is the justification for my semantic claim that both concepts differ in reference. In what follows, I expand on the difference between both concepts, focusing on their inferential role, and explain the emergence of the developmental homology concept based on the research goals of evo-devo.

The phylogenetic and the developmental homology concept differ in their conceptual role (inferential role), as the phylogenetic homology concept supports *inferences only*, while the developmental concept supports *explanations* as well.[20] In a nutshell, the inferences as supported by the phylogenetic homology concept are inductive inferences, more precisely analogical inferences from one species to another, yielding unified descriptions (Sections 4.4 and 5.1.3). The developmental homology concept, in contrast, also supports explanations in the sense of causal-mechanistic explanations or explanations involving laws of development. The phylogenetic homology concept fundamentally makes reference to the common ancestry of homologues. Based on this it supports an inductive inference from the properties of the structures of one species to the features of another species. This is the basis of unified descriptions that apply to large groups of organisms. In the context of systematics, the homology concept individuates characters in different species. Homologous structures are the characters in different species that systematists have to compare to arrive at classifications. And homologues as being derived from an ancestral structure characterize taxonomic groups as monophyletic groups, consisting of an ancestral species and all its descendant species. In evolutionary biology, homology conceptualizes a lineage of characters from an ancestral structure to a structure in the descendant. This permits evolutionary biologists to state evolutionary scenarios. In addition, it is a precondition for the explanation of the adaptive modification of structures by referring to the character across evolutionary time that undergoes adaptive change. This involves evolutionary explanations (which are causal or law-based explanations), but the homology concept is merely a conceptual precondition for these explanations in that it refers to the pattern in the

[20]This reference to explanations as opposed to inferences is not committed to a philosophical theory of explanation that would view explanations and inferences as totally distinct, not belonging to a common genus. Salmon (1970, 1971) argued that explanations are not arguments (neither deductive nor inductive), whereas Kitcher (1981, 1989) maintained that explanations are deductive inferences. I do not intend to settle the debate about the precise relationship between inference and explanation. Section 3.1.4 explained that my version of inferential role semantics views inferences as material inferences, which are endorsed in virtue of their content (rather than merely their logical form). Inferences construed in this broad fashion can encompass explanations, as material inferences can be counterfactually supporting and involve causal concepts. The difference between inferences and explanations I appeal to in the present context is not a particular philosophical distinction but more of a difference of scientific relevance.

first place that is in need of explanation (an evolutionary explanation of why an ancestral structures was transformed into a structure in the descendant can by rejected by pointing out that the two structures actually are not homologous). The explanation itself is not given by the homology concept but involves other concepts such as the notion of natural selection. It is in this sense that the phylogenetic homology concept supports inferences only.

In contrast, developmental definitions of homology usually do not make explicit reference to common ancestry. Several evolutionary developmental biologists view common ancestry as a sufficient condition for two structures to be homologous, but not as a necessary condition. Schmitt (1989), arguing from the perspective of a taxonomist, points out that while van Valen's definition of homology — based on the idea of continuity of information — may be broad enough to include serial homologues (which does not matter for a taxonomist anyway), "with [van Valen's definition] phylogenetic inferences are impossible" (p. 508). Definitions of homology proposed by evolutionary developmental biologists make reference to common developmental features rather than to common ancestry. In the case of developmental approaches, knowledge about developmental processes is generalized by concepts that refer to commonalities of different concrete developmental mechanisms. Explanations of the formation of a class of structures are based on considerations about a corresponding causal origin or a common maintenance of structures, or about the way in which a structure developmentally interacts with other structures as an integrated and individualized part of the body. Referring to repeated or corresponding structures of organisms, the developmental homology concept is used to account for the similarity of structures within and between organisms by pointing to an (as yet barely understood) common underlying developmental basis. It focuses on the mechanistic underpinnings of the structural identity of homologous characters in the course of development and evolution. For instance, the developmental constraints governing a structure are determined by the development and material constitution of an organism and manifest themselves in phylogeny by keeping the identity of a structure fixed despite its evolutionary modification. A developmental homology concept is intended to causally *explain* why the same structures (homologues including serial homologues) reliably reappear in different parts of the organism and in subsequent generations (Wagner 1996), by referring to those causal factors and developmental features that account for this reappearance of morphological units.

The important issue is that the phylogenetic homology concept cannot deliver these explanations (due to its particular inferential role). Günter Wagner puts this point as follows:

> Taking Mayr's definition as a reference point, we realize that [compared to Owen's definition] the

> historical homology concept [phylogenetic homology concept] only adds a termporal dimension to homology but in so doing relies also on an unspecified concept of "sameness." Mayr writes:
>
> > A feature in two or more taxa is homologous when it is derived from the same (or corresponding) feature of their common ancestor (Mayr, 1982, p 45).
>
> Hence the "sameness" of characters in two recent species is "explained" by the sameness of each of these features with the same character in a common ancestor. The question raised by Owen's definition of homology, "What does it mean to call two organs in different species the same," is not answered by the historical homology concept, but is used in the same unexplained manner as in Owen's definition. (Wagner 1994, pp. 277–278)

The idea is that the phylogenetic homology concept, using notions such as inheritance and common ancestry can reduce the relation of homology in general to the homology of a structure in a species and its immediate descendant or a parent and its offspring. But is does not give an account of what makes a structure in the offspring homologous to a structure in the parent, i.e., what constitutes that fact that a structure in the offspring corresponds to a particular part in the parent. Appeal to ancestry or the inheritance of genetic information is completely non-explanatory for a developmental approach, as it does not provide a mechanistic explanation of how and why the same morphological units are formed in different organism (Wagner 1989b; Roth 1994). In particular, the idea of genetically based inheritance does not explain how the different structures in an organism are differentiated from each other — so as to enable evolution on a character-by-character basis — and yet are functionally and developmentally connected. These considerations illustrate that 'homology' is clearly treated as a *natural kind concept* by evolutionary developmental biologists (Wagner 1996). It refers to a certain phenomenon perceived in nature, an explanation of which is sought. The assumption is that the phenomenon is brought about by some non-obvious, but scientifically significant underlying mechanism. Thus, a natural kind concept always goes together with the search for the underlying basis of the kind.[21] Roth's (1988) notion of the 'biological basis of homology' makes plain that this situation obtains for the homology concept (see Section 5.2.2). While phylogenetic accounts of homology appeal to common ancestry, evolutionary developmental biologists often view common ancestry as a sufficient condition for two structures being homologous, but not as a necessary condition.[22] From this perspective, the phylogenetic account is incomplete

[21] Philosophical accounts of natural kind terms usually focus on their reference or on the account of the natural kind (knowledge of its 'essence') once it has been established. My account, however, emphasizes the prior search for an adequate account that is characteristic of natural kind *concepts*, which leaves room for a change of the concept involved and change of its reference. To highlight this issue terminologically, in Brigandt (2003b) I used the term 'investigative kind concept' rather than 'natural kind concept'.

[22] Common ancestry is a sufficient condition for two structures being homologous, as the common ancestry of two structures is likely to imply shared developmental principles. It is not a necessary condition as for a developmental approach the constitutive feature of homology is structures being governed by certain morphological-developmental principles. For instance, serial homologues are considered as being governed by the same developmental principles, but the serial homologues in an individual are not derived from the same ancestral structure.

and falls short of a full account of the phenomenon to which the homology concept refers.

Wagner (1994) acknowledges that the phylogenetic homology concept, due to its reference to common ancestry, has something to offer beyond Owen's notion of homology. For it can show why the characters of extant organisms form a nested set in accordance with the taxonomic hierarchy. For instance, the species having the characters of primates form a proper subset of the species having the characters of the mammals, which form a subset of the species possessing the features of vertebrates, etc. From the fact that taxonomic groups have a common ancestor we can infer and in this sense explain the taxonomic distribution of characters. But the phylogenetic homology concept cannot explain why the same structures emerge in different generations and why a homologue can vary in form and function across generations and species while retaining its morphological identity:

> The discussion in this chapter of the relationship between homology and development presumes that the main goal of a biological [=developmental] homology concept is to explain why certain parts of the body are passed on from generation to generation for millions of years as coherent units of evolutionary change. Hence the problem is to explain why there are individualized parts of the body that retain their structural identity despite variation in form and function. (Wagner 1994, p. 279)

Evolutionary developmental biology has not offered yet a satisfactory explanation of this question. For this reason, the developmental homology concept's inferential/conceptual role (the particular inferences and explanations supported by it) is subject to change and future improvement. Given that homologues exist on different levels of morphological organization, a particular empirical and conceptual challenge is to explain how characters on different levels can evolve relatively independently from each other even though they are developmentally connected. For instance, an adequate account is yet to be given for why morphological structures can be dissociated and evolve independently from the developmental processes that bring them about. As of now, the developmental homology concept has still a limited explanatory potential and it remains to be seen whether empirical and theoretical progress will bring about a substantial improvement on the phylogenetic homology concept (in terms of inferential/explanatory role). In any case, the phylogenetic homology concept simply cannot explain why the same structure emerges in different places of an organism or in different generations. A developmental homology concept — having a different inferential/explanatory role by making reference to developmental processes — is needed to yield these types of explanations.

While comparative and evolutionary biologists sometimes attack the developmental homology concept, or more precisely the idea of serial homology, evolutionary developmental biologists are also aware of these two distinct understandings of homology, which is manifested by them talking about 'biological homology' or 'developmental homology' as opposed to 'historical homology', 'phy-

logenetic homology', or 'evolutionary homology' (Wagner 1989a; Minelli and Peruffo 1991; Roth 1991; Donoghue 1992; Shubin 1994; Sluys 1996; Striedter 1998). The discussion already pointed to the fact that this conceptual difference has something to do with the different theoretical goals of these fields. Different homology concepts are used to pursue different epistemic goals — they are intended to generate different types of biological knowledge or to explain different types of phenomena. Each homology concept serves the theoretical interests of the field in which it is used by being a necessary conceptual ingredient in bringing about the epistemic product characteristic of that field (such as certain descriptions or explanations). The developmental homology concept originated and is still developing because evo-devo uses this concept to pursue its epistemic goals. Biologist with a developmental approach to homology may be clearly aware of the fact that they have different goals compared to other approaches (Wagner 1994; Sluys 1996). Roth (1991), for instance, contrasts "Homology in systematics" and "The biological basis of homology" (p. 171). On her account, both approaches differ in their objects of focal interest, their objectives, their empirical undertakings, their methods, and their research products. While the research objective in systematics is to find homologous characters and to identity taxa, a developmental approach attempts to "discern what types of phenotypic features of organisms tend to be conserved, why they are, and how." The research products in systematics are patterns and distributions of characters and arrangements of taxa. In the case of a developmental approach it is the "clarification of similarities & differences in the developmental processes that produce phenotypic features" (p. 171).

In sum, the theoretical aim of taxonomy is to establish the phylogenetic relationship of species and to group species into taxa, and evolutionary biology is concerned with accounting for the origin and transformation of species. In evolutionary developmental biology, some of the explanatory goals are to understand how structures emerge in ontogeny and to account for structural identity in ontogeny and phylogeny. The important point is that these two disciplines do not only have different epistemic goals, they use their homology concept to pursue these goals. In contrast to homology in systematic and evolutionary biology, the epistemic goal pursued with the use of the homology concept in evolutionary developmental biology is to explain the formation of similar structures within and between organisms and how structures obtain their morphological individuality so as to function as units of phenotypic variation and morphological evolvability. Given the aim of accounting for morphological unity within and between individuals, the developmental homology concept actually continues the tradition of the homology concept used in 19^{th} and early 20^{th} century morphology. The difference is as follows. 19^{th} century morphologists either viewed themselves as

being engaged in description, but not explanation (unlike evolutionary biology), or they viewed themselves as discovering law-like generalities about form. Modern evolutionary developmental biologists make use of causal-mechanistic principles to explain the unity of form. The developmental homology concept emerged as a distinct concept when the homology concept derived from the 19$^{\text{th}}$ century became integrated into modern developmental-mechanistic approaches.

5.2.4 Implications for Theories of Reference

I close with some conclusions on theories of reference. Philosophers of science are particularly fond of the *causal theory of reference*, as it promises stable reference across theory change, so that no Kuhnian incommensurability arises (Section 2.1). The causal theory of reference is generally taken to be an adequate theory for natural kind concepts. The basic idea is that scientists pick out certain samples of the kind and then reference is fixed in accordance with the ontological structure of the world. Some natural kinds as we find them in physics or chemistry are not observable, so that they cannot be picked out by ostension or description of their observable appearance. But the causal effects of these kinds can be observed, so that the referent of an introduced term is that kind that is causally responsible for the observed effects (Newton-Smith 1981; Sterelny 1983). P. Kyle Stanford and Philip Kitcher (2000), however, point out that if we say that the referent is any object that has the same microstructural properties as those of the sample that cause the observed properties, then these causing microstructural properties cannot be the *total* cause of the properties (otherwise the kind would necessarily have the observed properties, which contradicts the idea that the descriptions used to introduce the term need not apply to all members of the kind). They solve this problem of picking out the relevant subset of the total cause by offering a very sophisticated causal theory of natural kind concepts. On their account, reference is determined based on a set of samples of the kind and a set of foils, and a set of stereotypical properties that is shared by all members of the kind, but not by all foils.[23] However, I do not think that even this sophisticated version of the causal theory is adequate to account for the reference determination of natural kind

[23]The precise account of Stanford and Kitcher (2000) is as follows: A natural kind concept T is associated with (i) a set of samples and a set of foils, (ii) and a set of stereotypical properties P_j that is shared by all samples, but each foil does not have all stereotypical properties. Then the reference of T is defined as follows:

extension of T = { x | x has the same inner constitution that is a common constituent in the total cause of each of the properties P_j in each of the samples, and that is absent from all of the foils }

In other words (leaving the foils aside), if $C_{i,j}$ is the total set of causes of sample i having property j, consider the features that are the intersection of the $C_{i,j}$. The natural kind term refers exactly to all objects having these features. (Note that on this account, a member of the natural kind need not have any of the stereotypical properties.)

concepts as we find them in biology. Homologues are natural kinds, and both the phylogenetic and the developmental homology concept are natural kind concepts.[24] But my claim is that the causal theory is not in a position to account for the reference of homology concepts (Brigandt 2004a).

The task of a theory of reference is to explain in virtue of what terms obtain their reference, more precisely, in virtue of what the users of a term count as referring to categories when using this term. As explained in Sections 3.1 and 3.2.2, the very rationale for making use of semantic notions such as 'concept', 'meaning', and 'reference' is to understand the successful use of language. From this perspective, a theory of reference has to offer an account of those features that determine a term's reference, such that these features explain the successful use of the term in communication and the successful practice surrounding the interaction with the referent. My discussion of the homology concept (the 19$^{\text{th}}$ century concept in addition to the contemporary phylogenetic and developmental homology concept) pointed out that the successful use of this concept depended on the establishment of homologies and the research with homologues — samples of the natural kind. This appears to be congenial for a purely causal theory of reference, which views the picking out of samples and their stereotypical properties as the only determinants of reference and — in contrast to descriptive theories of reference — assumes that a person's beliefs hardly bear on reference fixing. However, my case study showed that the successful use of the homology concept was based on more than picking out certain sample homologues, as it involved substantial empirical beliefs and sophisticated epistemic abilities. The establishment of homologies depended on the use of different criteria of homology and on the assumption that organisms belonging to the same taxonomic group possess corresponding structures — empirical criteria and assumptions that were not uncontroversial when the homology concept gained acceptance. My discussion showed that naming homologues involved more than considering individual homologues, as it depended on the originally controversial assumption that structures from different taxonomic classes (such as fishes and mammals) are the same ones. In fact, identifying structures across taxa and introducing a single name for structures that used to have different names in different groups of animals proved to be a progressive practice that was central for the success of morphology and its homology concept (Section 4.1.1). Once homologies had been established, they could be used to arrive at unified morphological descriptions and to effectively classify species into taxa. This successful usage of ho-

[24]The 'is homologous to' relation is an equivalence relation and each equivalence class is a class of homologues and thus a natural kind. Each class of token-homologues (a class of structures in individuals) is considered as a type-structure or a type-homologue ('the mammalian humerus') and given a certain name. This name refers to a particular natural kind, while the homology concept defines many such natural kinds.

mologies also involved empirical beliefs — the use of the homology concept as embodying inferences (Sections 4.2 and 4.4). Thus, the successful use of the homology concept in communication and scientific practice — including the early, pre-Darwinian usage — was based on more features than the picking out of samples and their stereotypical properties. In contrast to traditional causal theories of reference, I assume that these features determine the fact that biologists refer to homologues. It is the fact that the possessors of the homology concept have certain inferential abilities and engage in research on homologies based on certain epistemic abilities that permits the philosopher to count them as referring to homologues.[25]

A proponent of the causal theory of reference may insist that at least in the case of natural kind terms, the semantic issue of reference to a certain kind is independent from the epistemic issue as to whether or not the user referring to a kind is able to recognize the referent and find out about its properties. On such a causal account, what determines reference to a natural kind is merely interaction with some of its samples, while epistemic abilities and beliefs about the referent do not bear on reference fixing. Apart from the fact that this semantic theory does not account for the successful use of a natural kind concept (so that one may wonder what else the point of assigning referents to terms is), my further reply is to point out that nowadays there is more than one natural kind referred to by using the term 'homology'. The discussion in this chapter showed that the phylogenetic and the developmental homology concept differ in extension: the former excludes serial homologues unlike the latter. For this reason, an adequate theory of reference must at least account for this *difference* in extension, by showing that different factors determine the reference of the phylogenetic and the developmental homology concept so as to yield different extensions. Sophisticated causal theories such as Stanford and Kitcher (2000) view samples, foils, and some of their properties as the core determinants of the reference of natural kind concepts. While samples played some role when these two contemporary homology concepts emerged, my tenet is that samples, foils, and properties alone cannot account for reference. Proponents of the causal theory might try to argue that the reference of developmental homology was fixed by means of samples (and descriptions) that actually include serial homologues, while phylogenetic homology was defined using (besides standard between-species homologues as samples) alleged serial homologues as foils. However, this does not fit biological practice. Labeling alleged serial homologues as foils was of no

[25]This leaves out the inheritance of reference. A layman, for instance, can count as referring to homologues simply in virtue of using the term 'homology', without possessing any substantial epistemic abilities (as long as this individual is willing to defer to experts). Reference inheritance can be safely ignored as a trivial case because it is always parasitic on previously established reference (e.g., the use of the term 'homology' by biologists).

importance for 20$^{\text{th}}$ century systematists and evolutionary biologists, but their comparative research agenda determines the extension of the term 'homology'. The current debate with developmental biologists about the existence of serial homologues is not the origin but the consequence of the existence of two different homology concepts. When nowadays an evolutionary biologist insists that there are no such things as serial homologues, then this is not a statement that determined the reference of her homology concept in the first place, it is just the expression of the previously established fact that her homology concept does not refer to serial homologues. My discussion of the phylogenetic and developmental homology concept explained their difference — including the difference in reference — without relying on samples and foils; instead, my account was based on how these concepts are embedded in the conceptual practices of these fields and for what epistemic purposes they are used. The phylogenetic homology concept supports inferences and is used to obtain unified comparative knowledge of different species. The developmental homology concept underwrites causal-mechanistic explanations and is used to explain why structures reappear in subsequent generations and sometimes several times within an individual. My claim is that these pragmatic and epistemic aspects of concepts are a crucial factor of reference determination, and that standard causal theories of natural kind concepts do not address these factors adequately.

To be sure, causal theories can acknowledge that pragmatic and epistemic factors have a certain influence on reference determination. Epistemic and pragmatic aspects can be claimed to influence which samples and stereotypical properties are used, while the latter are the real determinants of reference.[26] However, a traditional causal theory is committed to assume that the pragmatic and epistemic factors *themselves* do not determine reference — they are *causal* or *epistemic* features that influence which *semantic* determinants of reference are used. But it deserves emphasis that a causal theory has to offer an account in virtue of what picking out certain samples and stereotypical properties counts as determining reference. Scientists interact with many objects and make different statements when using a natural kind term, so an account is needed which of the objects are actually samples and which statements are descriptions of their stereotypical so that they actually determine reference. On my account, the pragmatic features of concept use bear on this question. Interaction with samples and statements about the referent are reference-fixing to the extent that this fits the epistemic purpose (epistemic goal) for which a natural kind concept is used. However, this assumes that the pragmatic and epistemic aspects of concept use are genuine determinants of reference, so that reference determination for natural kind concepts involves features that substantially go

[26] I owe this point to Dan Steel.

beyond picking out certain samples.

One could point out that current causal theories are not purely causal theories and instead allow for *descriptive factors* as additional determinants of reference. Most current theories intend to combine causal and descriptive factors, including the account of Stanford and Kitcher (2000).[27] So one could attempt to explain the difference between phylogenetic and developmental homology by using theoretical statements about the referents of these two concepts. Some descriptions of homologues surely have an impact on the reference of 'homology'. But if by descriptive elements one has some necessary or sufficient properties in mind that the user associates with the concept or that are analytically linked to the concept, then it is not clear whether this can really yield a satisfactory account. On standard descriptive approaches, what determines reference are descriptions of the *referent* (such as 'gold is a yellow metal' in the case of the concept 'gold'). While my account did make some use of descriptions of *homologues* — the referent of the homology concept — the crucial features of my account were those that specified the practical use of the *homology concept* and the epistemic goals pursued by the use of this *concept*. For instance, a description such as 'homologues are the building blocks of organisms' — if properly understood — is not simply a description of homologues. For a systematists or a traditional evolutionary biologists would assent to this claim (taken in isolation), despite the fact that such a description is supposed to determine the difference between the developmental and the phylogenetic homology concept. The statement 'homologues are the building blocks of organisms' — as used by evolutionary developmental biologists — is in fact a short-hand, referring to a larger explanatory agenda that attempts to explain the evolutionary and developmental origin, stability and modification of these building blocks. It is this latter fact about the use of the developmental homology concept that marks the difference from the phylogenetic concept. Our best evidence for there being two concepts that differ in reference is the fact that these two concepts are used for different scientific purposes (epistemic goals). And my claim is that the reference of these concepts is determined by the way these concepts are embedded in different conceptual practices. It is surely possible to use a very broad notion of 'description', including any type of *implicit* knowledge connected to a concept and its use. On such an account, the features to

[27] While more traditional causal theories of reference are still popular among philosophers of science, many analytic philosophers endorse a modern version of the descriptive theory of reference, which is usually called causal descriptivism. The idea is that reference is solely fixed by descriptions, which may include statements making reference to causal features and relations, such as the causal powers of kinds. The difference between the traditional causal theory and causal descriptivism is that while the latter appeals to descriptions of causes (inside the mind), the former appeals to causal relations between the speaker and the world. Prominent proponents of causal descriptivism are Loar (1976), McKinsey (1978), Lewis (1984), Kroon (1987), Jackson (1998a, 1998b), and Chalmers (2002a, 2002b). My subsequent remarks on descriptive reference determination apply to causal descriptivism as well.

which I appeal are in fact reference-determining 'descriptions'. While in this case one would have a descriptive theory of reference (that could include causal elements as well), my point is that it has to be recognized that these 'descriptions' are not descriptions as traditionally understood: they are neither traditional analyticities nor solely descriptions of the referent. Furthermore, as in the case of the samples and stereotypical properties of a purely causal theory, a descriptive theory of reference has to offer an account in virtue of what a certain statement is reference fixing. On my account, a certain statement involving a term contributes to reference determination to the extent this statement constitutes the fact that this term is used to pursue a certain epistemic goal.

This idea can be put in a more general way. I individuated current homology concepts primarily in terms of the epistemic goals for which they are used. *By considering the epistemic goal pursued as a genuine and independent aspect of a term's meaning, I also viewed this feature as a determinant of reference* (Section 3.2.2). From this perspective, traditional causal and descriptive theories of reference are inadequate as the features that constitute the fact that a particular concept is used for certain epistemic purposes do not boil down to particular causal relations or descriptions of the referent. For instance, the fact that the developmental homology concept is used to pursue certain explanatory goals is not exhausted by statements about homologues (i.e., by descriptions of the referent of the term 'homology'), but by the larger research agenda of evo-devo, which involves statements containing other central biological terms *in addition to* 'homology'. Neither is the epistemic goal for which a concept is used reducible to particular beliefs, nor is it determined by the total set of beliefs or the total language use of a single scientist. It is the whole scientific community that influences which epistemic goals are pursued with the use of certain concept. The fact that a concept is used for certain epistemic purposes supervenes on the total beliefs (and linguistic activities) of a language communities, but this fact does not reduce to certain analytic (meaning-constitutive) beliefs about the referent, as descriptive theories assume. In sum, I suggest that reference is determined on a broader base than traditional theories of reference usually acknowledge. This is in line with my moderate holism about the factors that determine reference, as suggested in my discussion of the reference of the contemporary gene concept (Sections 3.2.2 and 6.3.2). A moderate holism about reference determination assumes that the factors that determine the reference of a term form an open and unbounded set. My account of the phylogenetic and the developmental homology concept contrasts with approaches that assume that the set of factors that determine reference can be reduced to a limited and clearly delineated set of beliefs or causal relations.

Discussions about the reference of scientific terms in the philosophy of science have a curious dialectic (Section 2.1). In accordance with the history of accounts of reference, first purely descriptive theories are presented and it is pointed out that among other things, descriptive theories lead to semantic incommensurability. Then purely causal theories are introduced as they avoid incommensurability. However, purely causal theories of reference have drawbacks as well, as they fail to permit the possibility of referential change and reference failure. For this reason, it is usually agreed that a mixed theory is needed that combines causal and descriptive factors.[28] The interesting feature is that even though some accounts acknowledge that a mixed account is used, the overall theory is still presented as a primarily *causal* theory of reference (Sankey 1994; Devitt and Sterelny 1999; Psillos 1999). The reason is probably that the causal component is viewed as philosophically more important as it deals with the incommensurability threat. The discussion of Stanford and Kitcher (2000) illustrates this dialectic. Most of their discussion presents a purely causal theory of reference for natural kind concepts, a quite sophisticated version indeed. Then they point out that in order to account for real cases some refinements are necessary. These include descriptions (primarily stereotypical properties of the referent), the idea that tokens of the same type can refer differently, and the notion of partial reference. My point is that these refinements are actually quite crucial, and if the necessary additions to a causal theory of reference are given their proper place, then causal factors will play only a small role among other features. My discussion of the phylogenetic and developmental homology concepts — both natural kind concepts — suggests that even in the case of natural kinds the causal theory of reference is inadequate. We need a much broader account of reference determination that makes use of factors that are not acknowledged by standard accounts. Apart from samples, stereotypical properties, and descriptions of a kind, there are other factors that have a crucial influence on reference. These are *pragmatic* aspects of how concepts are scientifically used and for what *epistemic* purposes they are used.[29]

[28] The discussion in Section 2.1.1 pointed out that it is not clear how causal and descriptive factors combine, i.e., which causal factors are relevant and which descriptions are reference-fixing. This issue is non-trivial as both components are invoked for opposite reasons. Causal factors promise to avoid the incommensurability that descriptions may bring about, but they may prevent reference failure and referential change. Descriptions promise to permit referential change and reference failure, however, they could create incommensurability.

[29] My critique of standard causal theories of the reference of natural kind concepts was based on a single example — the term 'homology'. But I think that the same point applies to other natural kind concepts as well. Another likely candidate is the species concept, which has figured prominently in philosophical discussion as an example of a natural kind concept. Stanford and Kitcher (2000) actually mention the species concept and the taxon 'chimpanzee'. However, their account is very sketchy and it is neither clear to me how they intend to handle this case nor why they are confident that their causal theory with some refinements can deal with such an example. My assumption is that a close look at how reference is actually determined by scientific practice in the case of the species concept and other examples reveals that real cases cannot be adequately accounted for by current causal theories of reference.

5.3 HOMOLOGY IN MOLECULAR BIOLOGY: THE PRACTICAL SUCCESS OF AN OPERATIONAL CONCEPT

With the rise of molecular biology, proteins and in particular genes came to be addressed from an evolutionary point of view. This led to the emergence of fields like molecular evolution and molecular phylogeny in the 1970s. A consequence of this is that the concept of homology became applied to genes and proteins. The understanding of homology in molecular phylogeny and evolution is the application and extension of the phylogenetic homology concept to the molecular level. Yet the term 'homology' is used *in other parts of molecular biology* as well, but with a different meaning. Most branches of molecular biology attempt to gain knowledge about molecular mechanisms for the purposes of biomedical applications, but they are not concerned with evolutionary questions. What I call the *molecular homology concept* is the homology concept used by these non-evolutionary branches of molecular biology — and thus by the vast majority of molecular biologists. The molecular homology concept is tied to the *experimental* approach of molecular biology and the life sciences. On this concept, homology is similarity of gene or protein sequences. In contrast, molecular evolutionary biologist view sequence similarity merely as a criterion of homology, but do not think that sequence similarity should be the definition of homology. The reason is that the molecular homology concept — homology as sequence similarity — is a quite operational concept that does not support phylogenetic inferences, in which molecular phylogeny and evolution are interested. Still, the molecular homology concept, as I construe it, is used by most molecular biologists and biomedical researchers.

My philosophical account views homology as sequence similarity as a *bona fide* concept, which is expressed by the fact that I label this particular understanding of molecular homology 'the' molecular homology concept. My position is not that the operational molecular homology concept is superior to the phylogenetic homology concept (applied to the molecular level) used by molecular evolutionary biologists. The molecular homology concept should surely not replace or eliminate the homology concept used in molecular phylogeny and evolution. My overall account of the homology concept delineates three contemporary homology concepts, and the point of doing so is not to claim that one homology concept is superior to another. Instead, these different homology concepts emerged when the original homology concept entered new disciplines. Due to the distinct theoretical demands and the scientific goals of these disciplines, the homology concept underwent conceptual change. Thus, my philosophical point is to explain conceptual change based on a

concept changing such that it delivers the epistemic product (the conclusions of inferences and explanations) that a certain discipline demands in a better fashion. The history of the molecular homology concept is no exception. The term 'homology' became integrated into the practical and operational approach of molecular biology, which led to the molecular homology concept. The operational molecular homology concept does not support phylogenetic inferences, but it is in fact a highly effective conceptual tool *given* the theoretical and practical interests of molecular biology.

My subsequent analysis does not start out with discussing what I call the molecular homology concept. For the purposes of contrast, I begin with explaining how the *phylogenetic* homology concept applies to the molecular level (i.e., the phylogenetic understanding of homology as used in molecular evolution and molecular phylogeny). Then I lay out the *molecular* homology concept and how it is tied to the practice of molecular biology.

5.3.1 The Phylogenetic Homology Concept in Molecular Evolution and Phylogeny

The notion of homology as used in contemporary molecular evolution and phylogeny emerged in the 1970s, based on a molecular understanding of genes. Genes are linear DNA sequences (Section 6.2.1). Each position in this sequence consists of a nucleotide, and there are four types of nucleotides (containing one of the bases adenine, thymine, guanine, and cytosine, respectively, as their main ingredient). In terms of its basic structure a gene is like a very long word consisting of four letters. Many genes consist of more than 1 000 letters. Usually genes code for proteins, which are long sequences of amino acids (there are 20 amino acids). The linear DNA sequence, i.e., the order in which the nucleotides occur, determines the amino acid sequence of a protein. (The mapping from nucleotide to amino acid sequence is called the genetic code.) In cell division the genetic material is multiplied, resulting from a process called replication, in which the total DNA sequence and thus the various genes are copied. By means of cell divisions and eventually reproduction, an offspring inherits the genes of its parent. Due to this copying process, a gene of the offspring corresponds to or is homologous to a particular gene of the parent. As the replication mechanism usually has a high fidelity, the DNA sequence in the offspring is identical to the parental sequence. However, after some generations mutations may occur, in particular so-called point mutations where a single nucleotide is replaced by another nucleotide. Thus, over long spans of evolutionary time the sequence of a gene will become less and less similar to the sequence of the original gene. Still, the gene in the ancestor and the extant species are homologous, as the derived gene is inherited

from the ancestral gene by a process of copying with error. This is the notion of homology among genes used by molecular evolutionary biologists. It is the concept of phylogenetic homology applied to the molecular level: two genes in different extant species are homologous if they are derived or copied from one and the same ancestral gene. The idea that DNA sequence may change over time fits with the transformational understanding of homology in evolutionary biology, which focuses on a lineage of homologues leading from the ancestor to the descendant, whereby intermediate elements in the lineage may undergo gradual change (Section 5.1.1). Not only can the structure (DNA sequence) of a gene change, also its function is subject to change as a gene in a new species may become involved in the production of a trait for which is was not responsible in the ancestral species. This change of function is due to a gene changing its sequence such that it codes for a protein with a modified structure that has a modified biochemical or physiological effect. In sum, homology on the molecular level conforms to the traditional idea that homologous characters are the same or corresponding characters despite variation in their form (internal structure) or function. As proteins are produced by genes that code for them, the notion of homology (derivation from a molecule in the ancestor) carries over to proteins. *Analogous* genes or proteins, in contrast, are those similar in structure or function, where this similarity is not due to common ancestry.

This phylogenetic and transformational understanding of homology among molecules supports the idea that is nowadays called 'deep homology'. This is inheritance of a gene from a very distant ancestor and the resulting presence of homologous genes in quite unrelated species (such as species from different animal phyla). For instance, certain genes coding for metabolic enzymes that are necessary for the survival of any cell originally emerged in bacteria and were thus well established before the evolutionary origin of fungi, plants, and animals. As these enzymes are responsible for the very survival of any cell, selection strongly acted against mutations of these genes, so that their sequence changed very slowly over long spans of time. Thus, the same gene may exist in plants and animals with a moderate degree of sequence similarity between these groups of organisms.[30]

[30]This notion of homology among genes is fundamentally based on a *molecular* conception of genes, viewing a gene as a DNA sequence that is copied and may undergo gradual change due to point mutations. While this concept emerged in the 1970s, the term 'homology' had already been in use in *classical* genetics, albeit with a very different meaning, tied to the classical (Mendelian) concept of the gene. Classical genes are alleles, where an allele is a variant of a gene that has a distinct phenotypic effect (Section 6.1.3). In molecular terms, an allele is a copy of a gene that is *sufficiently* different in terms of its sequence from other variants of this gene such that it has a distinct phenotypic effect. Not everyone used the term 'homology' in the context of classical genetics, but those who did relied on the classical gene concept, by calling two genes in different organisms (or species) 'homologous' in case they are the *same allele* (Boyden 1935). 'Analogous' genes, in contrast, were conceived of as different alleles at the same chromosomal location in different organisms (Kosswig 1948). The standard test for 'homology' between different species was the test of allelism. Sometimes closely related species can be hybridized, so that due to cross-breeding an allele from one species can be brought into another species. If it had the same phenotypic effect in the new species as in the original

The modern notion of homology among genes and proteins emerged in the late 1960s and early 1970s due to the origination of the fields of molecular evolution and molecular phylogeny. These fields developed based on two factors. First, there were theoretical advances in molecular biology as well as the development of new experimental techniques in molecular genetics and biochemistry. Second, some molecular biologists addressed distinctively evolutionary and phylogenetic questions. Pioneers of this new approach were Emile Zuckerkandl, Walter Fitch, and Emanuel Margoliash, among others.[31] The discipline of *molecular evolution* is concerned with the evolution of genes and proteins. General questions addressed in this field are whether the mutation rate is the same in different parts of the genome, how fast genes and proteins evolve, and whether or not molecular evolution has the same pace in different phylogenetic lineages. A crucial set of questions are about the mechanisms of molecular evolution. The neutral theory of evolution, originally proposed by Motoo Kimura and James Crow, claims that most changes in genes and proteins are selectively neutral, i.e., do not make any difference in the overall fitness of an organism. Neutralism claims that most evolutionary changes on the molecular level are not due to natural selection, but to random drift. To give another example of an idea about molecular evolution, Susumu Ohno (1970) argued that gene duplications play an important role for molecular evolution. Specific studies in molecular evolution address the evolution of particular genes and proteins. Overall, molecular evolution addressed a new level of organismal organization, which led to new biological questions and new evolutionary principles. *Molecular phylogeny* (also called molecular systematics or molecular taxonomy) uses information about molecular substances such as genes or proteins to establish phylogenetic trees. Molecular features are taxonomic characters just like morphological characters and provide an independent (or relatively independent) set of evidence to support phylogenetic

species, then it was considered the same allele, i.e., a 'homologous' (classical) gene. This understanding of 'homology' individuates genes in terms of their function, not in terms of common ancestry, as contemporary usage has it. Two distinct classical alleles that exist in different organisms at the same chromosomal location are likely to be copied from an ancestral gene and are thus homologous according our contemporary phylogenetic concept of homology, while classical geneticists would count two distinct alleles as 'analogous'. Moreover, the test of allelism can only be applied to two closely related species, so that the notion of homologous genes between unrelated species — in particular the phylogenetically significant notion of 'deep homology' — was unintelligible in the context of classical genetics. Still, the notion of 'homology' among classical genes was used by several biologists (Harland 1936; Waddington 1940; Huxley 1942), in fact until the 1960s despite the emergence of a molecular concept of the gene in the late 50s (Kosswig 1961). For instance, Ernst Mayr (1963) stated that "Much that had been learned about gene physiology makes it evident that the search for homologous genes is quite futile except in very close relatives. If there is only one efficient solution for a certain functional demand, very different gene complexes will come up with the same solution, no matter how different the pathway by which it is achieved" (p. 606). Mayr means that different *alleles* in different species can bring about a similar structure or solve the same evolutionary problem (because many genes are involved in a structure). Yet being different alleles does not preclude common ancestry — homology of genes in our, but not Mayr's sense.

[31] For some early works in these fields see Margoliash (1963), Zuckerkandl and Pauling (1962, 1965), Margoliash and Smith (1965), Florkin (1966), and Fitch and Margoliash (1967).

hypotheses. The use of molecular data in phylogeny is nowadays widespread, but led to debates as some biologists prefer traditional morphological data while others view molecular data as the best evidence (Gura 2000). Originally, results in molecular evolution and phylogeny were obtained primarily based on information about proteins, as the main methods that were available permitted similarity assessment of variants of a protein. Due to the possibility of sequencing genes that emerged in the 1980s, nowadays most molecular data is based on genes and gene sequences.

The establishment of the phylogenetic understanding of molecular homology was due to the use of a phylogenetic perspective on the evolution of molecular genes and the application of the homology/analogy distinction to genes and proteins (Florkin 1962; Fitch 1970). For phylogenetic and evolutionary purposes, it is obviously vital to distinguish between similarity that is due to common ancestry (homology) and similarity brought about by common functional demands and convergent evolution (analogy). Homologous genes have a similar sequence due to their common ancestry, and the more closely related two species from which these genes are, the more similar the gene sequences. Sequence similarity is a criterion for homology on the molecular level, but in molecular phylogeny and evolution it is a mere criterion and not to be confused with the phylogenetic definition of homology (Reeck et al. 1987; Patterson 1988; Hillis 1994; Fitch 2000). For similarity is compatible with the phylogenetically distinct phenomena of homology and analogy.

A phylogenetic understanding of homology among genes is important for another reason. For there are different ways in which a genetic lineage can split leading to two homologous genes. First, as with traditional homology of morphological structures, a speciation event leads to two descendant species that have homologous structures and homologous genes. Molecular homology due to speciation is called *orthology*. Second, a genetic lineage may split without any speciation occurring, namely, due to gene duplication. Due to the way in which replication and other molecular processes work, single genes, sets of genes or whole chromosome may duplicate. In the case of the duplication of a single gene, the result is that two copies of the same gene are present in a chromosome. As a gene duplication takes place within an individual (in fact, within a single cell), a genetic lineage may split without speciation taking place. For instance, hemoglobin, which is the macromolecule responsible for the oxygen fixation in red blood cells, consists of a heme group and four globin proteins. In primitive vertebrates, these four globin chains are of the same type, as they are produced from one and the same globin gene. In higher vertebrates, however, there is α- as opposed to β-globin, and hemoglobin consist of two α- and two β-globin chains. This is due to the fact that a gene duplication occurred, leading to two copies of the original globin

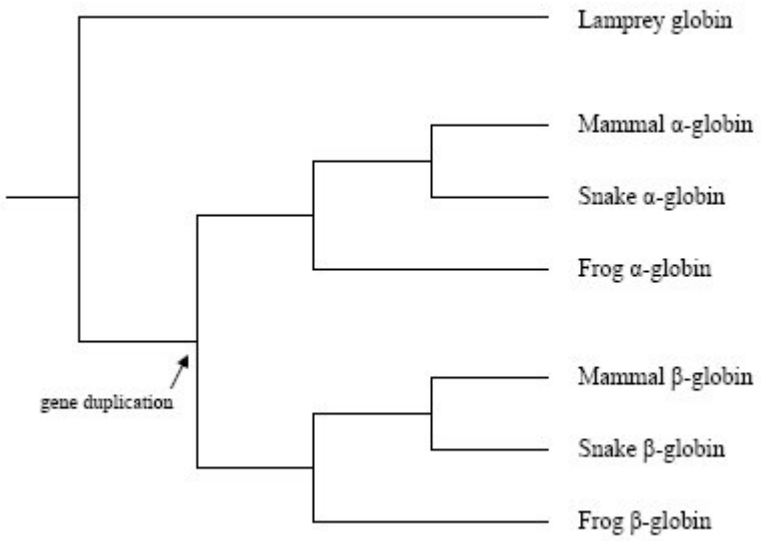

Figure 6: Phylogeny of the Globin Gene (after Hillis 1994)

gene. These two copied diverged in evolution, leading to the somewhat different and specialized α- and β-globin genes and their products. Molecular homology due to gene duplication is called *paralogy*. Paralogy is simply serial homology on the molecular level. In fact, even though the term 'paralogy' was introduced for genes and proteins, contemporary developmental biologists may use it as another term for 'serial homology', stating for instance that the human arm is paralogous to the human leg. The distinction between orthologous and paralogous genes is important for the following reason. Figure 6 shows a phylogenetic tree of the globin gene in four vertebrate species. This is not simply a standard phylogenetic tree of species, but it is a genetic tree showing the branching of genetic lineages. For instance, reference to mammals is made twice at the end of the tree, as there is mammal α- and mammal β-globin. Virtually all branching events in this genetic tree are due to speciation, but one is due to the duplication event that led to the difference between the two types of globin. Mammal α- and mammal β-globin are paralogous, while mammal α- and frog α-globin are orthologous. The situation is not always as simply as in this case, but the total genetic tree depicted permits one to read off the phylogenetic relationship of the species involved. Both the α- and the β-subbranch suggest that mammals are more closely related to snakes than they are to frogs. However, assume that we fail to distinguish between α- and β-globin. For instance, take the α-globin in mammals and frogs, but the β-globin in snakes. Figure 6 shows that the mammal α-globin is more closely related to the frog α-globin than it is to the

snake β-globin. So while some mammal globin is more closely related to some frog globin than to some snake globin, mammals are in fact not more closely related to frogs than to snakes. Thus, a phylogenetic tree of genes is not the same as a phylogenetic tree of species, and a genetic tree can be used to establish phylogenetic relations between species only if orthologous and paralogous genes are distinguished. In traditional systematics, homologous characters are compared to arrive at phylogenies and classifications. In molecular phylogeny, however, the establishment of phylogenetic relations between species requires something narrower: orthologies (homologies due to speciation) are needed, not paralogies (homologies due to gene duplications). The distinction between orthology and paralogy was introduced by Walter Fitch (1970), precisely in the context of addressing the phylogeny of proteins and the use of molecular data to establish phylogenetic trees.[32]

In sum, in the fields of molecular evolution and phylogeny it is important to distinguish between homologous and analogous genes, and different types of homology are to be distinguished according to the different mechanisms by which genetic lineages split. For the evolutionary purposes of these fields, a phylogenetic understanding of homology is necessary. The homology concept used in these fields is simply the phylogenetic homology concepts (used otherwise in evolutionary biology and systematics) applied to the molecular level.

5.3.2 A Semantic Account of the Molecular Homology Concept

Molecular evolution and phylogeny address phylogenetic questions, including the evolution of species, in terms of the phylogenetic history of genes and proteins. Most parts of molecular biology, however, are not concerned with the history and evolution of molecular substances at all. Instead, most molecular biologists investigate the structure of molecular entities and their function, i.e., their biochemical and cellular effects. Molecular biology is concerned with the way in which molecular substances figure in various biochemical pathways and how cellular processes are influenced by gene expression. Most of the knowledge gained about cellular processes, normal physiology and development, and abnormal physiology is relevant for the understanding of disease and other biomedical applications. Research in molecular biology focuses on how molecular entities operate and interact; the theoretical goal is to describe mechanisms and explain phenomena on the molecular level.

[32]Third, there is also a type of molecular homology called *xenology*. This arises from horizontal gene transfer, i.e., gene transfer from one species to another. Bacteria from different species may freely exchange genetic material, and viruses can insert a gene derived from a different species into a new host. In this case again, genetic lineages do not neatly map onto phylogenetic lineages of species.

What I call the *molecular homology concept* is the homology concept used by most molecular biologists, not the phylogenetic understanding of homology found in molecular evolution and phylogeny. My reason for viewing the molecular homology concept as an independent concept is not merely that it is used by the majority of molecular biologists. The term 'homology' became popular in molecular biology due to its previous usage by molecular evolutionary biologists. Though molecular biologists in general took over this term, they started using it with a different meaning (which happened in the early 80s). We can understand why this redefinition of the concept happened based on the theoretical goals and the practical focus of molecular biology. Its being used for a distinct *epistemic goal* is the main reason why I view the molecular homology concept as a separate concept. The concept of molecular homology refers to the degree of similarity between two DNA or amino acid sequences. For instance, a molecular biologist may say that there is '92% homology' between two genes, or that one sequence is '75% homologous' to another sequence. This means that this percentage of nucleotides is identical in the aligned sequences.[33] Thus molecular homology is not an all-or-nothing affair, but comes in degrees. Even more important is the fact that molecular homology is a statement about the mere similarity of genes and proteins, but not about their evolutionary origin — inheritance from a common ancestor.

The reason *why* this concept of homology is used in molecular biology is as follows. A good deal of easily accessible information about the structure as well as the function of genes and proteins is given by the mere DNA or amino acid sequence. Discovery in molecular biology depends to a large extent on the search for sequence correspondence among genes and proteins (and their parts). For similar genes have similar gene products and similar proteins are likely to be part of a similar pathway or to behave similarly in biochemical reactions. A certain part of a protein — a so-called domain — may be very important for the protein's particular function, i.e., its biochemical behavior. The reason is that a functional domain binds to other (macro-)molecules in biochemical reactions, and the structure and biochemical properties (such as charge, acidity) of a domain determine whether and how such a reaction takes place. Other parts of a protein may be substantially less important. For this reason, two variants of a protein in different species may have virtually identical functional domains, but vary in the rest of the amino acid sequence. Even within an individual there may exist many variants or forms of a proteins (so-called isoforms), that have the same

[33] In the course of evolution, a DNA sequence can change by one nucleotide being replaced by another nucleotide. But it also may happen that a nucleotide is lost (deletion) or inserted into the sequence (addition). Deletions and additions lead to sequences that are shorter or longer than the original sequence. For this reason, given two distinct gene and protein sequences, it is necessary to establish a correspondence of the individual sequences elements, i.e., to align them, such that additions and deletions are taken into account.

functional domain but differ in overall structure. As certain parts of the overall sequence determine the functional properties, genes and proteins are grouped into families and classes in the case of high similarity of relevant parts or domains. Knowing that a protein has a certain functional domain that is known from other proteins yields information about how it probably behaves in molecular and cellular processes. For instance, proteins with a so-called GPI anchor are known to be membrane bound, so when a newly studied protein is revealed to have such a domain it is very likely that it is membrane bound, too. To take another prominent example, the various homeotic genes have a certain segment called the homeobox, which is very similar among these different homeotic genes. The homeobox segment codes for a so-called homeodomain. All proteins with a homeodomain bind to DNA, and by binding to specific DNA segments such a protein regulates the expression of the genes that are located close to site where the protein binds. Thus in virtue of having a homeobox, homeotic genes regulate other genes, and any homeodomain in a protein is DNA-binding.

Molecular biology often does not deal with the comparison of different species or with questions about the classification and evolution of organisms. Instead, the focus is on the structure of molecular substances and the mechanisms in which they figure. If the sequence of a new gene or protein is available, it is compared to known genes and gene products. For instance, GenBank is a database containing all publicly available DNA sequences, maintained by the National Institute of Health. It is one of the most important on-line tools for genomics. The most common way of using GenBank is by doing a so-called BLAST search. In such a query, one submits a certain DNA sequence to GenBank, and obtains a list of all sequences stored that resemble the submitted sequence, ordered from highest to lowest degree of sequence similarity ('homology'). Similarity allows for an inference or a hypothesis about the effect or function of a new molecular entity. This provides the opportunity to examine a new protein more effectively using knowledge about established proteins and their pathways. The knowledge about certain molecular systems can be employed to transfer experimental approaches and research strategies to other yet unstudied systems, provided that both are known to be similar. Often the similarity-based inference from one system to a new one yields effective ways of discovery rather than a direct confirmation of the properties of the new system. For instance, in order to sequence a particular gene, it is necessary to amplify it first (to make multiple copies of it). Amplification requires that among the total DNA of a cell, precisely the intended gene is multiplied. This is achieved by the use of a so-called primer, a short DNA segment that that binds to the particular part of the DNA to be amplified. The primer is added to the total cellular DNA; and if it has the right sequence it will bind at the

right spot where the amplification has to take place. If a gene is to be sequenced for the first time in a particular species, then it is not obvious what primer is to be used. But if the same gene has been sequenced before in another species, then the first thing to try out is to use the primer that worked for the original species with this new organism. As the same gene in different species can be assumed to have a relatively similar sequence, the primer is likely to work for both species. Thus, mere similarity of DNA or amino acid sequence yields clues as to which experimental design is to be tried out first and which practical procedure is likely to yield experimental results. The molecular homology concept precisely refers to the degree of sequence similarity.

The molecular homology concept is quite different from the homology concept used in molecular evolution and molecular phylogeny, which uses the *phylogenetic* homology concept from evolutionary and systematic biology applied to the molecular level. For the molecular homology concept does not support the phylogenetic inferences that are important for evolutionary biology and phylogenetic systematics. A collection of similar genes is not a lineage of characters from ancestor to descendant to which phylogenetic homology refers. The fact that two gene sequences are similar is not to be equated with the fact that they are derived from a common ancestral gene. For sequence similarity may be due to common ancestry (homology), but it also may be due to convergence (analogy). We saw above that for evolutionary and phylogenetic purposes it is vital to distinguish between homology and analogy of genes or proteins. In addition, different types of homology have to be distinguished, depending on the particular process that brought about a split in a genetic lineage (orthology vs. paralogy). Molecular homology as mere sequence similarity conflates these different phylogenetic and evolutionary reasons why genes or protein sequences can be similar. As a result, molecular evolutionary biologists and molecular systematists have repeatedly criticized the identification of molecular homology with sequence similarity. On their account, sequence similarity is a criterion of homology, but it is not to be conflated with homology as a particular phylogenetic phenomenon (Reeck et al. 1987; Hillis 1994; Fitch 2000). The *molecular* homology concept is an operational concept, in the sense that its definition (sequence similarity) is what a phylogenetic concept views as a mere criterion. Overall, the molecular homology concept is theoretically not as robust as the phylogenetic or the developmental homology concept. Structural similarity refers to a pattern, but does not include the ontogenetic or phylogenetic processes that brought about the similarity. For this reason, the molecular homology concept is not able to support the phylogenetic inferences and developmental explanations that the homology concepts of evolutionary and evolutionary developmental biology support. Moreover, we saw that both

the phylogenetic and the developmental homology concept are natural kind concepts. On either approach, homologues are natural kinds or real units of variation and evolution. The homology concept is a central theoretical concept — in traditional evolutionary and systematic biology and in evolutionary developmental biology. It is generally acknowledged to be the most important concept in comparative biology. In molecular biology, however, the situation is different. The molecular homology concept does not pick out natural kinds or units, it is merely a similarity relation. The term 'homology' is simply shorthand for sequence similarity, and does not play an important theoretical role for molecular biology and its theoretical principles. Rather, it is a *conceptual tool that directs experimental practice.*

Despite the fact that the molecular homology concept is merely an operational concept, I view this concept — which defines homology as sequence similarity — as an separate and *bona fide* homology concept, in addition to the phylogenetic and the developmental homology concept. My reason is that we can understand the emergence of this concept as used by the majority of molecular biologists based on the theoretical goals and the practical approach of molecular biology. In this field, the research focus is on the experimental level. The goal of this discipline is to discover mechanisms, which is crucial for explanations on the molecular level and basis for technological manipulation. Consequently, an operational account of homology is important. Molecular homology as mere similarity of DNA or amino acid sequence is an understanding of homology that is tied to the experimental approach of molecular biology. It is effective for organizing knowledge about the structure and function of molecular substances and to direct experimental practice. The *epistemic goal* pursued with this concept's use is to infer theoretical hypothesis about molecular entities and mechanisms, and its primary use is actually to infer experimental strategies.

There are two reasons why I call the molecular homology concept a *homology* concept despite its difference from the phylogenetic and developmental homology concept, which both agree on most instances of homology and have an evolutionary perspective on homology. Apart from the trivial fact that the molecular homology concept is referred to by the term 'homology', there is first a historical relationship: the molecular homology concept is historically derived from the phylogenetic homology concept applied to the molecular level. Second, there is a slight overlap in content between the phylogenetic and the molecular homology concept. Biologists with a phylogenetic understanding of homology among genes such as molecular evolutionary biologists or molecular systematists use the notion of sequence similarity themselves — albeit as a criterion of homology, which they terminologically do not identify with homology. Communication between different types

of molecular biologists is possible in many circumstances as molecular evolutionary biologists are typically aware of the peculiar usage of the term 'homology' among biomedical researcher and other biologists using the molecular homology concept. Thus, while I assume that the phylogenetic homology concept (applied to the molecular level) and the molecular homology concept are distinct concepts that differ in quite salient ways, it is not the case that these are incommensurable concepts in the sense that the current use of a the single term 'homology' does not lead to a breakdown of scientific communication (despite some misunderstandings).

5.4 SUMMARY OF THE DISCUSSION OF HOMOLOGY

Chapters 4 and 5 studied the change in meaning that the term 'homology' underwent along three dimensions or components of meaning: 1) inferential role, 2) the epistemic goal pursued with concept use, and also 3) reference. I delineated four homology concepts. The homology concept emerged at the beginning of the 19$^{\text{th}}$ century, and this original homology concept was used throughout the 19$^{\text{th}}$ century and the first half of the 20$^{\text{th}}$ century. During the 20$^{\text{th}}$ century, it was modified and ultimately abandoned, yielding to three new homology concepts that emerged due to the term 'homology' being integrated into new theoretical and methodological approaches or new biological fields. The first of these three, the phylogenetic homology concept, originated as a consequence of the emergence of neo-Darwinism as the dominant theory of evolution in the 1930s and of phylogenetic systematics as the dominant method of taxonomy in the 1970s. The developmental homology concept developed in the 1980s in the emerging field of evolutionary developmental biology. In the 80s, the advances in molecular biology brought about the molecular homology concept.

The original homology concept emerged at the beginning of the 19$^{\text{th}}$ century in comparative anatomy, long before the origin of Darwinian evolutionary theory (Sections 4.1 and 4.2). The origin of the homology concept proved to bring about a new and progressive practice of crucial importance for biology, making it the central concept of comparative biology. With the advent of Darwinian evolutionary theory, standard definitions of 'homology' changed as they came to include reference to the common ancestry of structures (Section 4.3). However, against the conventional wisdom among biologists and historians and philosophers of biology, my central claim in Chapter 4 was that this new definition did not bring about a novel homology concept. My argument was based on the idea

that *1) the concept's inferential role changed only moderately, and 2) the epistemic goals pursued with the use of homology concept were not modified by the advent of Darwinism* (Section 4.4).

The inferential role (conceptual role) of the homology concept changed with the advent of evolutionary theory and the integration of the notion of common ancestry into homology definitions. However, even post-Darwinian characterizations of homology included considerations about the common developmental origin of structures, just like pre-Darwinian accounts (Section 4.3.2). More importantly, the homology concept is a case where standard scientific definitions are peripheral to the content of a scientific concept, in contrast to its actual use in scientific practice. A central task of a philosophical theory of concepts is to account for how a concept underwrites successful practice, and I argued that it is primarily the semantic notion of inferential role that fulfills this philosophical function. Given that definitions were largely irrelevant for the homology concept's successful use, the following features constituted the concept's inferential role. Crucial were the basic homology criteria (the positional and the embryological criterion). The homology concept embodied the inductive inference that for any structure in a particular species there is a homologous structure in another, related species. This assumption proved to have an important heuristic impact for discovery in comparative anatomy. The homology concept supported the inductive inference that a structure in one organism shares many properties with its homologue in another species (or a serial homologue in the same individual). This inference was of central importance because individuating biological characters in terms of homology permits unified descriptions of the structure and properties of organisms that apply to large groups of species. Homology individuates characters by the viewing homologues as natural units of variation that are present in different organisms with a different shape and function. This was crucial for taxonomy as species are to be classified based on comparing the corresponding, homologous organs in different species. As a result, pre-Darwinian biologists — in virtue of possessing the homology concept — had crucial epistemic abilities, that permitted them to establish homologies and use this knowledge for morphological and taxonomic purposes (Section 4.2). The advent of evolutionary theory hardly changed the way in which the concept was used in practice (Section 4.4). Evolutionary theory introduced no novel way to establish homologies. Morphological descriptions of structures and taxonomic classification of species continued to be based on the comparison of homologous structures. The change that occurred consisted primarily in re-interpreting previous notions in the light of common ancestry, including a phylogenetic re-interpretation of previously established homologies, morphological relations, and taxonomic groupings. Character individuation by means of homology

also became relevant for stating phylogenetic hypotheses, which lay out how a certain structure changed in the course of evolution. This relative historical continuity in inferential role supports my tenet that the throughout the 19$^{\text{th}}$ century a single homology concept was used. In addition, given that theoretical work in pre-Darwinian anatomy yielded an important part of the evidential basis for the immediate acceptance of the notion of common ancestry, this way of individuating a homology concept underscores the fact that *the homology concept as already used before the advent of evolutionary theory yielded important evidence for the later establishment of phylogenetic trees and thereby had the potential to underwrite phylogenetic research.*

My second reason for the tenet that the origin of Darwinism did not introduce a novel homology concept was the stability of the concept's epistemic goal. Already pre-Darwinian biologists had used the homology concept to pursue two basic epistemic goals: 1) the comparison of the structures of different species (and the different structures of one individual), to arrive at general morphological descriptions; and 2) the classification of species into taxa (Section 4.2). The important point is that these epistemic goals remained stable throughout the whole 19$^{\text{th}}$ century — the advent of evolutionary theory did not modify what biologists were trying to achieve when using the term 'homology' (Section 4.4). A result of this account of concept identity is that the moderate change in inferential role occurring was a change taking place internal to the homology concept. The modified inferential role (the adoption of new inferences by post-Darwinian biologists) can be semantically construed as being due to the emergence of novel collateral concepts and beliefs, rather than consisting in a substantial change of the homology concept itself. Still, in spite of being a change in inferential role occurring internal to the homology concept, the historical adoption of a phylogenetic interpretation of homologies is in need of explanation. On my account (Section 4.4), it was rational to adopt the phylogenetic perspective as it provided a more effective way (relative to the pre-Darwinian inferential role) to actually meet the traditional epistemic goals (morphological comparison and taxonomic classification). Thus, *changes in a concept's inferential role can be assessed as rational relative to the (stable) epistemic goal pursued with the concept's use.*

In the case of the three contemporary homology concepts, the strategy suggested by my semantic framework was to delineate them based on the characteristic way any such concept is used in a particular field and for which epistemic purposes it is used. Scientists use concepts to justify claims and give explanations of phenomena. By supporting inferences and explanations concepts help to create specific kinds of scientific knowledge. This is an *epistemic product* of scientific practice, and obtaining certain kinds of knowledge may be characteristic for a particular branch of

science. Different scientific fields have different *epistemic goals*, and thus *demand* different epistemic products. Concepts are employed to pursue these goals; in fact, concepts are shaped and designed to bring about the intended epistemic product. The point of my semantic approach is precisely to link concepts to the epistemic products and the theoretical goals of a scientific field, by assuming that inferential role and epistemic goal are genuine components of the content of a scientific concept.

The discussion in Chapter 5 showed how the different contemporary homology concepts differ in their inferential role as well as the epistemic goals of their use. Given the variation in inferential role (conceptual role), different homology concepts support different inferences and explanations, so that they yield different epistemic products. And I made clear how this difference in epistemic products relates to the theoretical goals of the respective biological disciplines, so that the emergence of a particular homology concept can be explained by the fact that it came to be used to pursue certain epistemic goals (Brigandt 2003a). My discussion in Section 3.3.2 acknowledged that there may be more than one way to individuate a concept, and that a particular way of individuation depends on the philosophical interests that underlie the study of this concept. In the present case, the central philosophical interest guiding my study was to account for the rationality of conceptual change. Distinguishing between three homology concepts pointed to genuine differences as to how the term 'homology' is used across different biological fields. This variation in the inferential role of the term 'homology' across overall biology is conducive to scientific practice as the existence of three specialized homology concepts is necessary to fulfill different scientific tasks. In particular, my discussion offered a good account of the historical origin of this conceptual diversification. The justification for my claim that there are three distinct homology concepts used in contemporary biology was precisely that these concepts are tied to different theoretical agendas and that we can explain the emergence of the concepts individuated in this manner. It was epistemically warranted for different fields to use the (traditional) homology concept to pursue its specialized epistemic goals, leading to conceptual differences in the sense of differences in epistemic goals. The subsequent change in inferential role and divergence between the three homology concepts occurred likewise in a rational fashion. It was to a relevant extent progressive for these different biological communities to change their homology concept (the inferences and explanations supported by it), as such a novel homology concept is better suited to deliver the epistemic product required by a particular field. Thus, *studying and individuating concepts in terms of the epistemic goals for which they are used is one way in which changes in the meaning of scientific terms can be considered rational.*

Despite the emergence of new contemporary homology concepts, there is a large continuity be-

tween the original homology concept and the phylogenetic and developmental homology concept as its descendants. But still significant change occurred, due to the emergence of specialized fields in the 20th century. The origin of the *phylogenetic homology concept* (Section 5.1) is due to the emergence of neo-Darwinism as the dominant theory of evolution and cladistics as the dominant methods in systematics. In evolutionary biology and systematics, a new criterion of homology emerged. This is the assessment of homologies based on a phylogenetic tree (Section 5.1.3). The character distribution on a phylogenetic tree permits the biologist to establish whether the occurrence of the same trait in two species is due to common inheritance (homology) or due to independent evolution (homoplasy). A diagnostic feature of phylogenetic homology, which distinguishes it from the original homology concept, is the rejection of the idea of serial homology. Phylogenetic homology refers to corresponding structures in different species (or sometimes different organisms of one species), but not to the repeated occurrence of a structure within an individual. This is due to the fact that phylogenetic homology is used to compare and classify different species in taxonomy, and to explain the evolutionary changes between ancestor and descendant species in evolutionary biology.[34] The idea of common ancestry of structures is a constituent of the phylogenetic homology concept, because it is important for the way the homology concept is used in the practice of evolutionary and systematic biology (Section 5.1.3). In systematics, phylogenetic homology refers to the same characters in different species that are to be compared as they derive from an ancestral structure. Comparison of the similarities and dissimilarities of homologous structure is the basis for classification. In evolutionary biology, homology refers to a lineage of characters that underwent transformation in the course of evolution. Picking out such a lineage is a precondition for explaining this evolutionary change. Thus, the phylogenetic homology concept is used to pursue some of the central epistemic goals of evolutionary biology and systematics, namely, the explanation of the adaptive modification of traits and the classification and phylogenetics of species.

The *developmental homology concept* (Section 5.2) originated based on the phenomenon of homology being approached by developmental approaches in the 1970s and the emergence of evolutionary developmental biology in the 80s. Evolutionary developmental biology is concerned with phylogenetic questions, however, the main focus is not on the classification of species or the explanation of adaptation. Instead, the theoretical goal is to account for macroevolutionary phenomena such as the origin of body plans, the operation of developmental constraints and the evolvabil-

[34]The 19th century homology concept, in contrast, included serial homologues because of the traditional morphological aim of establishing morphological generalizations about structures within and between organisms.

ity of morphological form (Appendix B). A crucial tenet of evo-devo is that an answer to these questions must involve knowledge about the development and material constitution of organisms. The epistemic goal pursued specifically with the use of the developmental homology concept is to understand the developmental basis of morphological organization (Section 5.2.3). In virtue of its material and developmental make-up, an organism is partitioned into different units (homologues), where one such unit may undergo evolutionary change relatively independent of other characters. Understanding why morphological evolution can proceed along certain dimensions (evolvability of each character) but not along others (number of characters is fixed due to features of morphological organization such as developmental constraints) requires an account of how developmental organization permits and restricts phenotypic variation subsequent morphological evolution. From this perspective, evolutionary developmental biology continues to pursue the traditional goal of morphology (including pre-Darwinian morphology) to offer an explanation of biological form, though this is viewed from the point of view of the evolution of form. Evo-devo differs from some traditional approaches in morphology by strongly emphasizing development and approaching development from a causal-mechanistic point of view. While the original homology concept referred to morphological unity and yielded systematic descriptions and generalization of it, the modern developmental homology concept is intended to *explain* this morphological unity in a causal-developmental fashion. Despite being associated with a distinct epistemic goal, the inferential role of the developmental homology concept is still in flux as biological knowledge about developmental processes is changing and still insufficient to yield an adequate explanation of the origin of form. In this sense, a clearly delimited developmental homology concept is not fully established yet.

Nevertheless, there are significant differences between the developmental and the phylogenetic homology concept. One result of the distinct agendas of evolutionary developmental biology and traditional evolutionary and systematic biology is that developmental homology includes serial homologues in its extension, unlike the phylogenetic homology concept (Sections 5.1.3 and 5.2.3). The new re-emphasis on serial homology is due to the explanatory agenda of evo-devo. Similar to 19^{th} century morphology, evo-devo views homologues as governed by certain developmental-morphological principles — those accounting for morphological order. A central task for evo-devo is to explain how the different homologues of an individual — in spite of being developmentally and functionally connected parts of an organism — gain their morphological individuality, so that one structure may change in evolution without affecting other characters. An additional challenge is to understand why there are irreducible levels of morphological organization, in that homologues

on one level may evolve relatively independently of homologues on other levels — even though structures on different levels have developmental interrelations (Section 5.2.1). Thus, the developmental homology concept is intended to uncover the developmental principles in virtue of which homologues gain their morphological individuality and relative independence from other structures, which makes it necessary to account for the developmental properties of *individuals* and the relation of homologues *within* an organism. Evolutionary developmental biologists assume that not only structures between species, but also serial homologues are governed by the same developmental principles (Section 5.2.2). In contrast to the phylogenetic homology concept that is used to compare different species and therefore excludes serial homologues from its extension, the developmental homology concept includes serial homologues (just like the original homology concept). Another difference between the phylogenetic and the developmental homology concept is that the phylogenetic homology supports various inferences, but no explanations (Section 5.2.3).[35] Its reference to common ancestry does not yield a causal-mechanistic explanation of why a parental structure re-emerges in the offspring. The developmental homology concept supports some explanations by referring to developmental processes and features of the material constitution of organisms that account for the generation of morphological order. This concept is intended to explain why the same structure reappears in different organisms or within one and the same individual, and how it obtains its relative independence from other structures. Thereby the developmental homology concept is used to pursue a central epistemic goal of evolutionary developmental biology, namely, the explanation of morphological unity within and between individuals, and of how this organismal organization makes morphological evolvability possible.

In the 1970s, the phylogenetic homology concept came to be applied to the molecular level (Section 5.3.1). Out of it emerged in the 80s the *molecular homology concept* in those parts of molecular biology that are not concerned with phylogenetic and evolutionary questions — in fact, the largest part of molecular biology (Section 5.3.2). Researchers in molecular phylogeny and evolution continue using the phylogenetic homology concept, according to which the similarity of DNA or amino acid sequences is merely a criterion of homology, but not to be confused with its phylogenetic nature and definition. The molecular homology concept, however, as used by most molecular biologists, refers to nothing but the degree of similarity between two sequences. As a consequence, homology is not an all-or-nothing affair but comes in degrees. The referents of the

[35] We saw above that it is a conceptual precondition for adaptation explanations (a lineage of characters has to be referred to before one can describe the transformation in this lineage and then explain it). However, these explanations are given using other concepts, such as the concept of natural selection.

molecular homology concept are not natural kinds as they are in the case of the phylogenetic and developmental homology concept. The molecular homology concept refers to similarity, but not to the evolutionary and developmental processes that brought about this similarity. Therefore the molecular homology concept does not support phylogenetic inferences, conflating similarity being due to common ancestry (homology) and being due to convergent evolution (analogy). While the phylogenetic and developmental homology concept enjoy a central theoretical status in the disciplines in which they are used, the molecular homology concept is not of fundamental theoretical importance for molecular biology. Instead, it is an operational concept that is a short-hand for the notion of sequence similarity. My claim that the molecular homology concept is an independent homology concept does not mean that this concept is superior to the phylogenetic understanding of homology in molecular evolution and phylogeny. My delineation of three contemporary homology concepts is based on the idea that each of them is closely tied to the practice and theoretical goals of different subdisciplines, and that one cannot fully replace the other. My reason for viewing the operational molecular homology concept as a *bona fide* concept is that it is successfully used *within* the experimental approach of molecular biology, and that the operational re-definition that a phylogenetic account of homology underwent in most parts of molecular biology can be understood based on the practical demands of this field. Most parts of molecular biology are not concerned with the evolutionary history of molecular entities. Instead, the focus is on the biochemical and physiological effects of molecular substances, which are the relevant features for biomedical applications. In molecular biology, the epistemic goal is to explain normal and pathological cellular and physiological behavior by the discovery and study of the way in which molecular entities figure in mechanisms. Discovery in molecular biology depends to a large extent on the search for sequence correspondence among genes and proteins (and their parts). Similar genes and proteins (or similar parts of genes and proteins) behave similarly in biochemical pathways. The molecular homology concept precisely refers to this sequence similarity. Usually, this concept is not a tool of direct confirmation in that knowledge about one gene would permit a robust inductive inference about the molecular function of a new, but similar gene or protein. Rather, the inference suggests a starting hypothesis about how a newly investigated molecular substance is likely to behave or in which pathway it figures. Given this hypothesis, the new substance can be more effective investigated, but it is this further investigation that yields the experimental confirmation. Often, the molecular homology concept is not a tool of confirmation, but a tool of discovery. It permits the transfer of experimental strategies from one case to a new system that bears some similarities to an old case.

My tenet that currently there are different homology concepts in use and that there are genuine differences in content between them should not be construed as the idea that these are incommensurable concepts. For there is some overlap between each of these concepts (regards reference, inferential role, but also epistemic goals). In fact, I referred to these three concepts as *homology* concepts not just because all of them are referred to by the term 'homology' and are historically derived from the homology concept of the 19$^{\text{th}}$century. Each of the three concepts can be considered a homology concept as there is some overlap in content; at least biologists can to a relevant extent successfully communicate with each other using the term 'homology'. This holds in particular for the phylogenetic and the developmental homology concept. Traditional evolutionary biology and evo-devo address evolutionary questions and agree on many issues about the nature of evolution. Both approaches view homologues as structural units or characters that form phylogenetic lineages and may undergo evolutionary change. Both fields agree on the criteria of homology and on the main instances of homology. For this reason, in most general contexts, biologists from systematics, traditional evolutionary biology, and evolutionary developmental biology can perfectly communicate and convey information about homologues which can be successfully used by researcher from another field for biological theorizing and practical investigation. When it comes to more specialized ideas, though, that are peculiar to one approach (e.g., the question of whether homology is a purely phylogenetic or also a structural-developmental phenomenon, or the issue of serial homology), then discourse and understanding across fields can be problematic due to the different theoretical agendas and epistemic aims of these approaches. The conceptual overlap with other homology concepts is much lower in the case of the molecular homology concept. Still, communication is possible in many circumstances as biologists from other fields are typically aware of the peculiar usage of the term 'homology' among molecular biologists. Biologists with a phylogenetic understanding of homology among genes such as molecular evolutionary biologists or molecular systematists use the notion of sequence similarity themselves — albeit as one criterion of homology, which they terminologically do not identify with homology, unlike most molecular biologists.

Finally, my discussion of the phylogenetic and developmental homology concept offered some implications for *theories of reference determination* (Section 5.2.4). Both concepts are natural kind concepts in that they pick out natural kinds.[36] The causal theory of reference is often assumed

[36]The 'is homologous to' relation is an equivalence relation and each equivalence class is a class of homologues and thus a natural kind. Each class of token-homologues (a class of structures in individuals) is considered as a type-structure or a type-homologue ('the mammalian humerus') and given a certain name. This name refers to a particular natural kind, while the homology concept defines many such natural kinds.

to be an adequate theory of reference determination, at least in the case of natural kinds. I argued that my example suggests otherwise. My discussion of each of these two homology concept showed that assessing and studying homologies and the successful practice involving the term 'homology' depends on sophisticated epistemic abilities and genuine empirical assumptions (such as the idea that structures from different taxonomic classes such as fishes and mammals are the same ones). This suggest that the features that *determine* the reference of a homology concept include certain beliefs and epistemic abilities, which the causal theory focusing on causal interaction with individual samples ignores. Even if it is maintained that reference determination in the case of natural kinds does not involve epistemic features but is solely based on picking out certain samples, my discussion pointed out that the phylogenetic and the developmental homology concept differ in their extension (due to the exclusion or inclusion of serial homologues), so that any theory of reference determination has to account for this. I argued that standard causal theories, which focus on samples and their stereotypical properties, do not give a satisfactory account of this difference in extension that fits with biological practice. Despite my critique of the causal theory, my intention is not to recover a traditional version of descriptive theories of reference. Descriptions, as traditionally understood, are descriptions of the referent that are analytically tied to a concept. But in order to account for the reference of the phylogenetic and developmental homology concept, a broader construal of the features that determine reference is necessary. I pointed out that in the case of the term 'homology', some crucial features that influence reference are not statements about homologues — the referent of a particular homology concept — but instead features as to how a particular homology concept is used, in particular which epistemic goals are pursued by its use. In contrast to standard descriptive theories, the fact that a concept is used for certain epistemic purposes does not boil down to particular beliefs (analytic statements or other reference-fixing beliefs) and it may involve empirical beliefs apart from beliefs that are about the referent of the concept. The fact that a certain homology concept is used to serve certain theoretical interests depends on the larger research agenda of a scientific field, and not only on particular beliefs involving the homology concept.[37] In sum, in the case of natural kind concepts, apart from samples, stereotypical properties, and descriptions of a kind, there are other factors that have a crucial influence on reference determination. These are pragmatic aspects of how concepts are used by a whole scientific community and for what epistemic purposes they are used.

[37]Given that a concept being used for a certain epistemic purpose is determined by the practice of an overall scientific community, reference is not determined by the beliefs of an individual alone, but by the overall community (yielding a specific sense in which meaning is not inside any one head).

6.0 THE CHANGE OF THE GENE CONCEPT

> *It can, however, be questioned whether we should reconstruct the history of genetics as a history of gene concepts. My contention is that this would amount to a fallacious epistemological artifact, if such reconstruction were not tied to a history of the usages of these concepts.* (Hans-Jörg Rheinberger 2000, pp. 225–226)

Since its introduction not much more than a century ago, the gene concept has undergone substantial change, triggered by new empirical findings. This chapter offers a semantic interpretation of this history, distinguishing between three basic stages in the history of genetics. Section 6.1 will discuss the classical gene concept as used before the origin of molecular biology. I shall start out with an overview of the empirical and theoretical considerations that led to the origin and establishment of this early gene concept. Section 6.1.3 will offer a philosophical characterization of what I view as the classical gene concept, and which inferences and explanations it supports. The purpose of this way of delineating a classical gene concept is to highlight the contrast with the later molecular gene concept, so as to discern conceptual progress. In line with my pluralism about concept individuation, I will also offer an alternative scheme of individuation that distinguishes between different gene concepts used by classical geneticists. The rationale for this fine-grained way of individuation is that it provides a handle on explaining why certain research programs were pursued and certain empirical and theoretical changes took place within classical genetics leading to the development of the molecular gene concept. Section 6.1.4 will address the fact that the advent of the molecular gene concept did not lead to the elimination of the classical gene concept. In addition to still being used in molecular genetics, the classical gene concept figures prominently in the theory of population genetics. I shall discuss the use of the classical gene concept in (contemporary) population genetics in the overall section on classical genetics, as the theory of population genetics emerged well before the advent of molecular genetics. Yet the main function of the section on the classical gene concept is to prepare the contrast with the molecular gene concept.

Section 6.2 will discuss the molecular gene concept as used in the 1970s. This gene concept

is often called the 'classical' molecular gene concept, as opposed to the 'contemporary' molecular gene concept. I shall describe the empirical steps to the establishment of the molecular gene concept, and offer in Section 6.2.2 a semantic characterization of it. On my account, the molecular gene concept supports explanations in molecular biology by embodying what I call 'explanatory strategies.' I shall discuss this notion and the role the gene concept plays in molecular explanations. Section 6.2.3 will discuss the progress that occurred with the transition from the classical to the molecular gene concept. This case does not conform to some previous construals of how conceptual progress may occur. First, one sufficient condition for progress is theory reduction, e.g., classical genetics being reduced to molecular biology. However, neither did the molecular gene concept eliminate or fully replace the classical gene concept, nor can the classical gene concept be reduced to molecular genetics. Second, many accounts assume that unchanging reference of a term is a necessary condition for conceptual progress, the idea being that only in this case can one say that later scientists have an improved conception of the very same entity that earlier scientists referred to. However, while the extensions of the classical and molecular gene concept overlap, both concepts differ in reference. Still, even without reduction and stable reference there is a sense in which substantial conceptual progress occurred with the molecular gene concept largely replacing the classical gene concept. As Section 6.2.3 will discuss, the molecular gene concept supports causal-mechanistic explanations about the production of molecular substances and the development of phenotypic features, unlike the classical gene concept, which is primarily a tool of inference (the prediction of patterns of inheritance). On my account, the theoretical and explanatory progress that occurred from the transition of classical to molecular genetics occurred to a large extent in virtue of the change in the meaning of the term 'gene'. I view the change of reference that occurred with the advent of the molecular concept as a mere by-product of conceptual change. I shall explain why this meaning change (and thereby change in reference) occurred in a rational fashion.

Section 6.3 will address the change of the molecular gene concept that occurred due to empirical findings in the last two decades. The classical molecular gene concept assumed that genes form a homogeneous category, where a clearly defined structural kind fulfills the functional role of molecular genes. Recent findings from molecular genetics and genomics show that genes are in fact a very heterogeneous kind, where different types of genetic-structural elements figure in genetic processes. This led to a fragmentation of the molecular gene concept, in that the term 'gene' is used differently by different biologists or by the same geneticists on different occasions. Likewise, the reference of the term 'gene' changes from context to context. I shall describe the empirical reasons for this

conceptual development, and discuss in Section 6.3.2 some recent analyses of the contemporary molecular gene concept, some of which suggest that different molecular gene concepts are in use or that the molecular gene concept is to be abandoned. My own account will argue that there is a single contemporary molecular gene concept, but it deserves emphasis that its usage varies from context to context. I consider this context-sensitivity and flexibility of the molecular gene concept an epistemically significant feature of this concept in that it enhances successful experimental practice. I will explain the recent diversification and fragmentation of the molecular gene concept by differential epistemic pressures operating on different biological fields or research contexts. The fact that the reference of the molecular gene concept shifts from to context to context will provide an argument for a moderate holism about reference determination. Finally, Section 6.4 will summarize the discussion of this chapter.

6.1 THE CLASSICAL GENE CONCEPT

After sketching 19$^{\text{th}}$ century views of heredity and presenting Gregor Mendel's work, most of Section 6.1.1 will deal with the period between 1900 and 1910, from the rediscovery of Mendel's work until Johannsen's distinction between genotype and phenotype. This period is often referred to as 'Mendelian genetics'. The subsequent section addresses the main developments of 'classical genetics' (1910–1939), discussing in particular the work of the Morgan group and the establishment of the chromosome theory of inheritance. Section 6.1.3 gives my philosophical interpretation of classical genetics, characterizing the classical gene concept and laying out an alternative scheme of individuating classical gene concepts. Finally, Section 6.1.4 briefly discusses the way in which the classical gene concept was used and is still prominently used in population genetics. Before starting my historical discussion, I offer a brief primer of classical genetics for the unacquainted reader.

A Primer of Classical Genetics

Genetics distinguishes between the *genotype* and the *phenotype* of an individual, where the genotype is an individual's set of genes (or a part of it) and the phenotype is the set of observable traits of an organism, brought about by the interaction of genes with cellular and environmental factors in development. Apart from the fact that it is only the genotype that is directly and materially

transmitted between generations, the genotype and the phenotype ought to be distinguished as the relation between genes and traits is many–many: one gene may influence the development of several traits, and a trait develops based on the action of many genes. The failure of early Mendelian genetics to consistently distinguish these two notions caused confusion. Any gene occupies a particular position on a chromosome, such a position is called a *locus*. A locus may be occupied by different genes in different individuals; and the notion of a gene is synonymous to that of an *allele*. Classical genes (alleles) are best conceived of as difference makers: A particular trait (black fur) may be brought about by the action of different alleles at several loci, each of which is necessary for this phenotype to occur. But if only one of these alleles at a certain locus l is mutated (the locus is occupied by a different allele) then a different (mutant) phenotype results. Thus, given a certain total genetic (and environmental) background, the presence of a particular allele at locus l will result in black fur (though this gene does not bring about this trait on its own), while the presence of another allele at this locus results in a different phenotype. In spite of a trait being influenced by many genes, a genetic difference at one locus results in some phenotypic difference. In fact, classical genes are identified in terms of the phenotypic differences they bring about, which show up in mutation studies or experiments where individuals with different genotypes are crossed. The normal allele and its corresponding phenotype is called the *wildtype* allele or phenotype.

Higher plants and animals have a double (diploid) set of chromosomes. For each chromosome there is a corresponding, a so-called homologous, chromosome (this term has nothing to do with the notion of homology discussed in the previous chapters). Consequently, a locus is occupied by two alleles, one occupying a certain position on a chromosome, the other occupying the same position on the homologous chromosome. If there are two alleles A and a, then three genotypes are possible: AA, Aa, and aa (both chromosomes having A, one chromosome having A and the other a, and both chromosomes having a). A genotype such as AA and aa is called *homozygous*, whereas Aa is called *heterozygous*. (Across several individuals of a population, there may be more than two possible alleles that can be present at a certain locus: AA, AB, AC, BB, BC, CC are the possible genotypes for three alleles.) In the production of gametes (germ cells such as egg and sperm) the double set of chromosomes is divided in two halves, such that each gamete contains only one chromosome (one homologue) of a pair. Thus, an individual of genotype AA produces gametes containing allele A, and an individual of genotype aa produces gametes containing a. In a heterozygous individual (genotype Aa), 50% of its gametes contain allele A and 50% contain a. This process of splitting the genotype in the formation of gametes is called *segregation*. Fertilization,

the union of two gametes restores a double chromosome set. Two gametes containing allele A and a unite to form genotype Aa (but due to segregation, they fully separate into A and a again when the gametes are formed for the subsequent generation). To give some examples, crossing two individuals of genotype AA — written $AA \times AA$ — yields offspring of genotype AA only (all gametes are A). $AA \times Aa$ results in 50% AA and 50% Aa among the offspring (all gametes of the father are A, while 50% of the mother's gametes are A and the same proportion is a). $Aa \times Aa$ yields $50\% \cdot 50\%$ AA offspring, $50\% \cdot 50\%$ Aa plus $50\% \cdot 50\%$ aA (which is the same genotype as Aa), and $50\% \cdot 50\%$ aa. Thus, the offspring generation consists of 25% AA, 50% Aa, and 25% aa.

Often the phenotype of Aa is distinct from both AA and aa (AA having black fur, aa having white fur, and Aa having grey fur). In some cases, however, Aa has precisely the same genotype as AA (AA and Aa having black fur, and aa having white fur). In this case, allele A is said to be *dominant*, while allele a is *recessive*, because in the heterozygote Aa the influence of the recessive allele seems to be fully overshadowed by the dominant allele. Classical genetics identifies genes in term of their effects on phenotypes. Even though in the case of A being dominant the genotypes AA and Aa are phenotypically indistinguishable, they can be kept apart by carrying out breeding experiments and studying the phenotypes of the *subsequent* generation. For instance, crossing $AA \times AA$ yields only AA offspring (the dominant phenotype only), whereas $Aa \times Aa$ yields $\frac{1}{4}\,AA$, $\frac{1}{2}\,Aa$, and $\frac{1}{4}\,aa$, and thus $\frac{3}{4}$ of the dominant phenotype and $\frac{1}{4}$ of the recessive phenotype.

Consider not one but two loci, with possible alleles A and a at one locus and B and b at the other locus. Then there are $3 \cdot 3$ possible genotypes: $AA\,BB$, $Aa\,BB$, $aa\,BB$, $AA\,Bb$, $Aa\,Bb$, $aa\,Bb$, $AA\,bb$, $Aa\,bb$, $aa\,bb$. To understand the formation of gametes, consider for example genotype $Aa\,Bb$. Assume that the two loci are on the same chromosome pair, say pair 3, and that A and B (rather than A and b) are on the same homologue of chromosome pair 3. Given that A and B are physically on the same chromosome, a and b are on the other homologue of pair 3 (as in the left image of Fig. 7). To a first approximation, what happens in this case is that A and B (and likewise a and b) are fully linked and thus inherited together (full correlation): 50% of the gametes are AB and 50% of the gametes are ab. Now take the same basic genotype $Aa\,Bb$, but assume that the two loci are on different chromosome pairs (A and a are on one or the other homologue of pair 3, while B and b are on one or the other homologue of pair 5). In this case, there is no linkage between alleles at different loci. As it is random which homologue of chromosome pair 3 goes into a gamete with which homologue of pair 5 (stochastic independence), 25% of the gametes will be AB, 25% aB, 25% Ab, and 25% ab. In the previous case of two loci being on the same chromosome, a complication arises

Figure 7: Crossing Over

due to *crossing over*. Before the reduction of the chromosome set in the formation of gametes, the homologous chromosomes of each pair physically align and cross over, i.e., exchange some of their genetic material. For instance, if allele A and B used to be on different loci of one homologue of chromosome pair 3 and a and b used to be on the other homologue of this pair, then crossing over may result in one homologue of pair 3 having A and b and the other having a and B (see Figure 7). Thus, alleles on the same chromosome need not be fully linked and are separated with a certain probability — they are said to *recombine* before segregation occurs in gamete formation. Crossing over may occur at any part of the chromosome. The closer two loci are together on a chromosome, the less likely it is that crossing over occurs in between these two loci. This complication proved to be of fundamental importance for classical genetics. For systematic breeding studies (so-called linkage analysis) reveal *recombination frequencies*, which are a measure of how close two alleles are on a chromosome. This provided the basis for the establishment of *chromosome maps*, which show the relative positions of different loci (genes) on a chromosome.

6.1.1 From the Notion of Unit-Characters to the Genotype Concept

Before the rediscovery of the experiments of Gregor Mendel (1822–1884), there were two basic ways to theorize about heredity in the later part of the 19$^{\text{th}}$ century. The first consisted in somewhat speculative accounts of the particles that are materially transmitted in reproduction. Throughout the 19$^{\text{th}}$ century, heredity was seen as a part of development, and for this reason, a theory of the material basis of inheritance was primarily designed to *account for development*. A prominent case in point is Charles Darwin's (1868) theory of pangenesis. Darwin postulated the existence of 'gemmules', particles present in bodily fluids. Before reproduction, gemmules from different parts and all organs of the body move into the reproductive organs to form germ cells (such as egg and sperm). After fertilization, development proceeds under the guidance of gemmules which *spread out* into the developing organism. Pangenesis explains the resemblance between parent and offspring

and the development of the offspring's different structures by representatives from all parts of the parental body being transmitted. Furthermore, Darwin assumed that during the lifetime of an individual the gemmules change as the organism changes and physiologically adapts to the environment. This provided the basis for Lamarckian inheritance (where the changes in an organism's body are transmitted to the offspring), which was an ingredient of Darwin's theory of inheritance and evolution. Thus, Darwin's pangenesis offered a unified account of the material basis of inheritance, development, and evolution. Another material theory of heredity is August Weismann's (1892) doctrine of the germ plasm. Weismann assumed that the germ plasm transmitted in reproduction forms a mereological hierarchy of larger and smaller parts (biophores, determinants, ids, idants). Development as proceeding differentiation and the formation of specialized structures is explained by the idea that this germ material is consecutively *broken down* into smaller components, with one part of the hereditary material *going into one part* of the body, and other parts directing the development of other organs. The main difference to Darwin's theory is that Weismann assumed that there is also a cell line (called the germ-lime), where the total inherited germ plasm resides unchanged and in its entirety. It is this unchanged material from the germ line that forms germ cells and is transmitted to the next generation, whereas the broken down hereditary material in different parts of the body is not transmitted and does not have any influence on inheritance, thereby ruling out a Lamarckian mechanism of inheritance. In the 19^{th} century, several other theories of the material nature of heredity existed and many names for the supposed hereditary particles were proposed, but a common purpose of these theories of inheritance was to explain development.

Another basic way to theorize about inheritance was the quantitative and statistical study of the phenotypic variation across different generations, as pursued by the school of biometrics from 1870–1920. This school was founded by Francis Galton (1822-1911), and some of its main representatives were W. F. R. Weldon (1860–1906) and the famous statistician Karl Pearson (1857-1936). A central tenet of biometrics was the law of *ancestral inheritance*, which maintained that an individual inherits $\frac{1}{2}$ of its features from its parents, $\frac{1}{4}$ from its grandparents, $\frac{1}{8}$ from its grand-grandparents, and so on. This law accounted for the fact that an individual may have a character (such as a particular hair color), that neither of the parents possesses. The experience of breeders suggested that characters may be lost in some generations but reappear in later ones. Typically the idea of *blending inheritance* was endorsed, i.e., the notion that the character of the offspring is a mixture of or intermediate between the characters of both parents. Many biometricians were not concerned with the material nature of heredity and development — Karl Pearson was a phenomenalist — and

instead focused on the statistical study of phenotypic variation across generations, supporting Darwinian evolution by the study of continuous variation and gradual change.

Gregor Mendel's 1866 essay "Experiments on Plant Hybrids" remained without influence for 34 years. Mendel's work was conducted in the context of research on plant hybridization, which studied how to obtain variants with novel features by hybridizing existing variants. Mendel carried out his research on the garden pea *Pisum sativum*, one reason being that it showed clearly 'differentiating characters' (*differirende Merkmale*) in different species of this genus: the seeds are either round or they are irregularly angular and deeply wrinkled; the seed albumen is either yellow or green; the seed coat is either white or it is brown or grey; etc. Mendel chose seven such characters. For one such character Mendel denoted the two pure forms by A and a, respectively, and the hybrid that resulted from crossing by Aa (this first generation obtained by crossing came to be called the F_1 generation). For each character chosen, the hybrid Aa was phenotypically indistinguishable from a parent of type A, and Mendel called this character A the dominant character, and the other character a the recessive character. Inbreeding of hybrids Aa yielded the F_2 generation, consisting of plants with approximately $\frac{3}{4}$ having the dominant character and $\frac{1}{4}$ having the recessive character. The latter (recessive character) were pure forms a and further inbreeding of these resulted in nothing but peas of form a. Among the $\frac{3}{4}$ of F_2 plants with the dominant character, after inbreeding one third still yielded the dominant character (they were true breeding dominants), while the other two thirds yielded in F_3 $\frac{3}{4}$ of plants with the dominant and $\frac{1}{4}$ with the recessive character. Mendel's explanation was that the F_2 generation consisted of $\frac{1}{4}$ pure dominant forms A, $\frac{2}{4}$ hybrids Aa (having the dominant character), and $\frac{1}{4}$ recessive forms a. Thus, $A : Aa : a = 1 : 2 : 1$.

Mendel explained this pattern of inheritance by the following way of formation of egg and pollen cells. A pure form A produces egg/pollen cells of type A only, and a pure form a produces egg/pollen cells of type a only. Consequently, crossing a plant A with a plant a yields a hybrid Aa. A hybrid Aa forms egg/pollen cells such that $\frac{1}{2}$ of them are of type A and $\frac{1}{2}$ of type a. Thus, when hybrids are inbred ($Aa \times Aa$), with a frequency of $\frac{1}{2} \cdot \frac{1}{2}$ each, an A egg is fertilized by an A pollen, an A egg is fertilized by an a pollen, an a egg is fertilized by an A pollen, and an a egg is fertilized by an a pollen. This yields $\frac{1}{4}$ pure forms A, $\frac{2}{4}$ hybrids Aa, and $\frac{1}{4}$ forms a. Using these principles and combinatorics, Mendel predicted the frequencies of different forms for several subsequent generations, which he confirmed experimentally.

Mendel did not claim that the principles he discovered in *Pisum* were laws of heredity applying to all plants (or even animals). It also deserves emphasis that he did not postulate alleles or genes

on chromosomes. Nowadays, we write the pure form AA, because the genotype consists of two A alleles: one on each of two homologous chromosomes. Likewise, the hybrid Aa is interpreted as carrying a dominant allele on one chromosome and a recessive allele on the other. Mendel, in contrast, did not speculate much about the underlying material factors that account for the observed patterns of inheritance. While assuming that there are material factors transmitted by the egg and pollen, which he calls elements (*Elemente*), he did not offer a hypothesis about their nature. As the historian of genetics Robert Olby concludes in his essay "Mendel no Mendelian?",

> Mendel did not have the conception of pairs of factors or elements determining his pairs of contrasted characters. ... There is no case for the view that Mendel conceived of paired hereditary particles equivalent to the allels of classical genetics. He went no further than postulating *one kind* of element in the germ cell for any one trait. If we arbitrarily define a Mendelian as one who subscribes explicitly to the existence of a finite number of hereditary elements which in the simplest case is two per hereditary trait, only one of which may enter one germ cell, then Mendel was clearly no Mendelian. On the other hand, if by Mendelian we mean one who treats hereditary transmission in terms of independent character-pairs, and the statistical relations of hybrid progeny as approximations to the combinatorial series, then Mendel surely was a Mendelian. (Olby 1979, pp. 71–72)

Apart from mentioning 'elements' in his conclusion, Mendel's discussion concerned the phenotypic level, establishing statistical relations between phenotypic patterns of inheritance, for which Mendel had robust evidence. For instance, he distinguished dominant and recessive characters, not dominant and recessive alleles as later accounts. He refers to pure forms and hybrids by the symbols A, Aa, and a, and to the pollen and sperm of different types by the symbols A and a, without giving an account of the material factors that constitute these types.[1] Still, Mendel was able to make distinctions for which later terms relating to the genotypic level were introduced. While the pure form with the dominant character is phenotypically indistinguishable from the hybrid, Mendel conceptually distinguishes the two by denoting one form A and the other Aa, and he practically keeps them apart by what the phenotype distribution of the subsequent looks like: inbreeding A yields only offspring of dominant character, inbreeding Aa yields $\frac{3}{4}$ dominant and $\frac{1}{4}$ recessive.

Mendel's work supports what later became known as the *law of segregation* (or Mendel's First Law). While in the formation of hybrids the two alternative characters or their underlying elements are combined (A and a combine), in the formation of egg and pollen cells these characters or elements fully separate again (some gametes are of type A, others of type a). Later this came

[1] "The break, at 1900, between the earlier period of construction, by deductive reasoning, of speculative schemes to explain heredity and the later period in which theory was based on experimental investigation was also marked by sharp contrast between concepts of the nature of the living units employed in the two periods. Most of the 'deduced' units were conceived of as material elements—physiological units, gemmules, pangenes; while those arrived at inductively in the Mendelian scheme did not have this quality. The observed realities in Mendel's experiments were things grossly seen, the differentiating characters themselves. The Mendelian 'elements' within the reproductive cells were symbols only, inferred from statistical rules." (Dunn 1965, p. 48)

to be interpreted by the two alleles of an organism segregating in the formation of gametes. As already mentioned, Mendel studied seven contrasting characters and their combined distribution in breeding experiments. Unbeknownst to him, it is the case that the genes coding for these seven characters are located on different chromosomes, so that these traits are not genetically linked. In this case, each two characters are statistically independent in inheritance, which later came to be called the *law of independent assortment* (or Mendel's Second Law). Consequently, a plant that is hybrid in two characters ($Aa\,Bb$) produces four types of gametes in equal proportion: $A\,B$, $A\,b$, $a\,B$, and $a\,b$. Inbreeding of such a hybrid yields offspring with the following distribution:

$$A\,B : A\,b : a\,B : a\,b : A\,Bb : a\,Bb : Aa\,B : Aa\,b : Aa\,Bb \;\; = \;\; 1 : 1 : 1 : 1 : 2 : 2 : 2 : 2 : 4\,.$$

Because of dominance, these nine genotypes exhibit only four phenotypes, $A\,B$, $A\,b$, $a\,B$, $a\,b$, in the proportion $9 : 3 : 3 : 1$. Mendel confirmed this prediction experimentally, and did the same for the combined distribution of three characters.

After not having received much attention for several decades, Mendel's ideas were rediscovered in 1900 due to the research of the Dutch botanist Hugo de Vries (1848–1935), the German botanist Carl Correns (1864–1933), and the Austrian agronomist Erich von Tschermak (1871–1962). There are different accounts of why Mendel's work had been neglected for so long (Olby 1966; Brannigan 1979). Whatever the reasons for the original neglect, in March and April 1900 de Vries published two versions of a paper on "The Law of Splitting of Hybrids", the first publication appearing in France, the second in the German botanical journal *Berichte der deutschen botanischen Gesellschaft* (de Vries 1900b, 1900a). De Vries had worked with the evening primrose, discovering what came to be called Mendel's law of segregation, i.e., the splitting of contrasting characters being latently present in hybrids. These two papers did not discuss Mendel's work, though the German version acknowledged that de Vries had learned of Mendel's 1866 paper, but only after his own researches had been completed. Tschermak had worked on *Pisum*, the same plant Mendel used, and had already written up his results as a dissertation. On the appearance of de Vries' first paper, Tschermak urged the publication of his dissertation and published a summary in the *Berichte*, the same German journal in which de Vries' second paper was to appear (Tschermak 1900). Being aware of Mendel's paper, Correns had worked on maize and peas, finding in 1899 the principle of segregation, but he had decided to conduct further breeding studies as his results did not conform to Mendel's account in all respect, due to the fact that in the plants and characters he chose dominance did not always obtain. The receipt of de Vries' French paper prompted Correns to send his results to the *Berichte* (Correns 1900). Correns entitled his paper "G. Mendel's Law Concerning the Behavior

of Progeny of Varietal Hybrids". The explicit reference to Mendel, dubbing his results "Mendel's Law", was probably part of an attempt to undercut de Vries' priority on these matters.

Apart from rediscovering Mendel, de Vries showed that segregation and Mendelian inheritance hold for many other plants as well. Soon Mendelian characters were found in animals such as poultry. Lucien Cuénot (1902) showed that certain coat-color differences in mice obeyed Mendel's principles. Once Mendel's ideas gained popularity, the school of biometrics attacked their universality (Weldon 1901; Pearson 1904). The Mendelian school of genetics had to establish itself against this previous tradition studying inheritance. A major point of disagreement concerned the evolutionary implication of theories of heredity. While the biometricians emphasized continuous variation between individuals supporting gradual evolution, some Mendelians viewed discontinuous variation and mutation as the motor generating phenotypic change and producing new species. De Vries, for instance, defended his *Mutation Theory* of heredity and evolution (de Vries 1903). William Bateson (1861–1926) became the main popularizer of Mendelism in Britain. Before the rediscovery of Mendel's idea, Bateson had argued for a discontinuous mode of speciation (Bateson 1894). While unlike de Vries focusing less mutation, Bateson defended Mendelian discrete patterns of inheritance and the generation of discontinuous variation due to crossing (Bateson and Saunders 1902; Bateson 1902, 1906, 1909). Apart from alternative visions of evolution, the biometricians and the Mendelians disagreed about the way in which inheritance occurs. While biometrics endorsed continuous and quantitative variation, Mendelians argued for discrete, contrasting characters such as the dominant vs. recessive character. Mendelism advanced an atomistic conception of heredity, where patterns of inheritance are generated by discrete and distinct features. Biometrics endorsed blending inheritance, while Mendelians argued that characters do not blend: the hybrid exhibits the dominant character (rather than an intermediate phenotype), while the recessive character exists latently in the hybrid Aa and is fully recovered in the subsequent generation due to the law of segregation. The fact that the alleles do not blend in the hybrid and instead segregate in the formation of gametes (there are either A or a gametes) was referred to as the purity of the gametes:

> Such discontinuity will in fact primarily depend not on the blending or non-blending of the characters, as hitherto generally assumed, but on the permanent discontinuity or purity of the unfertilized germ-cells. (Bateson and Saunders 1902, p. 130)

Biometricians maintained regression to the mean, i.e., the idea that in a population the phenotypic variation of the offspring generation is lower than that of the parental generation. In contrast, Mendelian variation in a population does not decline: the discrete hereditary elements remain present, though their expression can be masked due to dominance.

To be sure, a conclusive explanation of why the Mendelian approach offers a better account of inheritance than biometrics requires a systematic distinction between the phenotype and the genotype. The *genotype* consists of discrete units (genes or alleles) which obey simple principles of inheritance, though the resulting *phenotypic* patterns of inheritance may be less straightforward and show more continuous variation. A clear-cut conceptual distinction between the genotype and the phenotype did not exist in early Mendelian genetics, though. Similarly, Mendelism appeared to be at odds with the law of ancestral inheritance championed by biometricians (which maintains that only $\frac{1}{2}$ of an individual's features are from its parents, $\frac{1}{4}$ from its grandparents, etc). For a proponent of Mendelian genetics, the features of the offspring (the *phenotype* distribution of the offspring generation) are fully determined by the parents (their *genotype* actually), and recourse to the grandparents is unnecessary. Overall, while the particulate, atomistic conception of inheritance favored by Mendelians clashed with the biometric approach, it aligned with late 19^{th}century theories of the material nature of inheritance, which offered various accounts of the particles or material hereditary units transmitted in reproduction. This furthered the acceptance of Mendelism.[2]

The term 'gene' was not used in early Mendelian genetics — it was suggested in 1909 by Wilhelm Johannsen and gained prominent usage in the 1920s. Instead, originally 'unit-character', 'allelomorph' (much later abbreviated to 'allele') and 'factor' were the terms used to denote the emerging gene concept. It was William Bateson who suggested the terms unit-character and allelomorph in 1902 as other terms for what Mendel called differentiating characters. Note that whereas according to later usage allelomorphs (alleles) are explicitly characterized as entities on the genotypic level, technically speaking Bateson introduced the notion of a *unit-character* and its synonym *allelomorph* as a character (*morph*ological feature), thus as a feature on the phenotypic level:

> Each such character, which is capable of being dissociated or replaced by its contrary, must henceforth be conceived of as a distinct *unit-character*; and as we know that the several unit-characters are of such a nature that any one of them is capable of independently displacing or being displaced by one or more alternative characters taken singly, we may recognize this fact by naming such unit-characters *allelomorphs*. (Bateson 1902, p. 22)

At the same time, Bateson also introduced the terms 'homozygote' and 'heterozygote':

> The purity of the germ-cells, and their inability to transmit both of the antagonistic characters, is the central fact proved by Mendel's work. We thus reach the conception of unit-characters existing in antagonistic pairs. Such characters we propose to call *allelomorphs*, and the zygote formed by the union of a pair of opposite allelomorphic gametes we shall call a *heterozygote*. Similarly, the zygote formed by the union of gametes having similar allelomorphs, may be spoken of as a *homozygote*. (Bateson and Saunders 1902, p. 126)

On the one hand, Bateson's discussion showed an implicit understanding that later came to be made

[2]For detailed histories see Olby (1966), Carlson (1966), Dunn (1965), Sturtevant (1965), and Darden (1991).

explicit by distinguishing the genotype and the phenotype. For when talking about "gametes having similar allelomorphs", though allelomorphs were defined as characters, he did not actually mean that a plant's the eggs and pollen exhibit a particular (unit-)character. Rather, he referred to a gamete containing a hereditary factor, which will bring about the character in the developed offspring. On the other hand, the unit-character terminology potentially conflated Mendel's 'differentiating characters' with the 'elements' which Mendel assumed to be transmitted in the gametes. As we shall see in a little while, this led to confusion among some early Mendelian geneticists.

Before the chromosome theory of inheritance gained acceptance, most Mendelian geneticists assumed that the unit-characters/allelomorphs were represented by factors freely floating in the nucleus or the cell (Carlson 1966). The debate about the *presence and absence hypothesis* illustrates that early Mendelians were unclear about what allelomorphs are and how they produce patterns of inheritance. Rather than assuming that the dominant character was due to the presence of a dominant allelomorph while the recessive character was due to the presence of another allelomorph, in 1903 Carl Correns and independently Lucien Cuénot suggested that the recessive trait could be represented as the loss or absence of the dominant character. In other words, what appears to be a pair of characters in Mendelian inheritance is really the presence and absence of a single character. Bateson (1906) became a main proponent of the presence and absence hypothesis. To this end, he used the term 'unit-factor' or simply 'factor', arguing that there are only factors or elements in the cell corresponding to the dominant character, and that in the production of gametes some of these factors are lost with a certain probability, such that the absence of a factor in the offspring results in the recessive character. The American geneticist William E. Castle (1867–1962), in contrast, rejected the presence and absence interpretation of allelomorphs (Castle 1906). While endorsing the hypothesis, George H. Shull (1909) acknowledged that it was not always obvious which of the two contrasting unit-characters in a Mendelian pair was due to presence rather than absence: "Yellow is described as present in the yellow pea and absent in the green pea. What is to hinder us from describing the green as present in the green pea and absent in the yellow one?" (pp. 411–412). While initially accepted by most geneticists, the presence and absence hypothesis was abandoned in the 1910s. Among other considerations, some empirical studies suggested that characters can consist not just in contrasting pairs, but that three alternative characters or states may exist, called multiple allelomorphs by Alfred Sturtevant (1913). While the presence and absence hypothesis admitted only two alternative unit-characters for any locus, finally the idea gained acceptance that there can be several alternative alleles for each locus.

Bateson, when introducing the term 'unit-character', was aware that the character should not be confused with the basis of its transmission (he later often used the term 'factor' for the latter; Carlson 1966). However, the notion of unit-character led some geneticists to conflate phenotypic patterns of inheritance with the underlying principles of genetic transmission. Bateson's unit-character terminology erroneously suggested a one–one relation between genes and traits, and "for the next fifteen years this [unit-character] fallacy would create a crisis among students of heredity" (Carlson 1966, p. 14). Due to this confusion, Castle (1905, 1906) prominently argued for his contamination theory, which explicitly acknowledged exceptions to Mendel's law of segregation and the purity of gametes. A heterozygous hybrid (Aa) results from the joining of two distinct alleles (A and a). But in the subsequent formation of gametes these alleles fully segregate again, which some gametes containing allele A and others a (the gametes are 'pure'), so that only one or the other factor is transmitted to a particular offspring. However, phenotypic patterns of inheritance do not always seem to follow the simple principle of segregation, in that some offspring shows intermediate phenotypes between the dominant and recessive. This led Castle to argue that the two alternative alleles A and a contaminate each other in the hybrid, so that half of the resulting gametes contain for the most part A but also some a and the other half contains largely a but also some A. On this conception, Mendelian factors are not constant and unchanging atoms of inheritance. Given that the *phenotypic* character he studied truly varied, for several years Castle would argue against the purity of gametes and the constancy of Mendelian *factors*, i.e., alleles (Castle 1912a, 1912b).

> In several recent papers I have pointed out the fact that the theoretical 'purity of gametes' of Mendelian inheritance does not exist. No more does the *purity of factors* exist. We cannot avoid the idea of impurity of the gametes by introducing the conception of factors, for the factors are as certainly impure as the gametes. To sum up the matter, it is certain that unit characters exist, but it is equally certain that the units are capable of modification; ... (Castle 1906, p. 280)

The results of breeding experiments that seemed to challenge segregation and the constancy of Mendelian alleles were later explained away by showing that phenotypic traits can be under the influence of several alleles (several alleles at different loci). An important step towards this was the work of the Danish botanist Wilhelm Johannsen (1857–1927).

Johannsen introduced the distinction between *genotype* and *phenotype* in his *Elemente der Exakten Erblichkeitslehre* (1909) (see also his 1911 essay "The genotype conception of heredity"). At the same time, he suggested the term *gene* for a factor transmitted in the inheritance, where the genotype is the total set of genes. Johannsen derived the term 'gene' from de Vries term 'pangene' (which de Vries had suggested based on Darwin's notion of pangenesis). 'Gene' became a generally used term — a synonym for 'allelomorph' — not before the 1920s, though.

> The "gene" is nothing but a very applicable little word, easily combined with others, and hence it may be useful as an expression for the "unit-factors," "elements" or "allelomorphs" in the gametes, demonstrated by modern Mendelian researchers. A "genotype" is the sum total of all the "genes" in a gamete or zygote. (Johannsen 1911, p. 132–133)

Johannsen developed these notions based on his studies of pure lines, hybrids, and selection acting on them. His experiments for instance showed that selection does not change the genotype of a pure line, phenotypic change can results only insofar a population already contains genotypic variation. Johannsen distinguished his genotype conception from the traditional transmission conception of heredity. The latter assumed that phenotypic characters are directly inherited from the parents, while the modern genotype conception showed that the personal qualities of an individual are determined from the genotype, i.e., the nature of the gametes that unite to form the fertilized zygote. An obvious target for Johannsen was the idea of ancestral inheritance endorsed by biometrics:

> Ancestral inheritance! As to inheritance, it is a mystical fiction. The ancestral influences are the "ghosts" in genetics; ... Ancestral influence in heredity is, plainly speaking, a term of the "transmission-conception" and nothing else. The characters of the ancestors as well as of the descendants are both in quite the same manner reactions of the genotypical constitution of the gametes in question. Particular resemblances between the ancestor and or more of his descendants depend — as far as heredity is responsible — on corresponding identities in the genotypical constitution, and, as we have urged here, perhaps to excess, the genotype is not a function of the personal character of any organism. (Johannsen 1911, pp. 138–139)

The fact that the same pure line of a plant shows phenotypic variation across different environmental conditions offers clear support for the idea that the genotype is to be distinguished from the phenotype (Woltereck 1909). Based on these ideas, Johannsen argues that instances of blending inheritance and problematic cases of phenotypic inheritance do not falsify the constancy of genes and the principle of segregation. One explanation for seemingly non-Mendelian patterns of inheritance is that a phenotypic feature is influenced by several genes:

> ... the instance exemplifies the two incident matters of fact, viz., that apparently simply "dimensional" characters may be determined by *several different genes*, and that one sort of gene may have influence upon *several different reactions*. (Johannsen 1911, p. 153)

The crucial conceptual innovation of Johannsen's genotype/phenotype distinction was to make room for the possibility that the relation between genes and traits is many–many, thereby, providing the basis for abandoning the notion of a 'unit-character', which sometimes referred to the trait that exhibits Mendelian patterns of inheritance and sometimes to the unit transmitted in the gametes, thereby misleading some geneticists to assume a one–one relation between genes and traits.

Note that for Johannsen the point of introducing the term 'gene' was *not* to endorse a particular view about the nature of genes. Neither did Johannsen identify inheritance with the chromosome or the cell nucleus, nor did he assume that genes are concrete particles localized in the cell:

> The question of *chromosomes* as bearers of "heredity qualities" seems to be an idle one. I am not able to see any reason for localizing "the factors of heredity" (i.e., the genotypical constitution) in the nuclei. The organism is in its totality penetrated and stamped by its genotype constitution. (Johannsen 1911, p. 154)

On Johannsen's account, the gene concept is "free from any hypotheses", a "calculating unit [*Rechnungseinheit*]", that does not involve defining genes as morphological units (Johannsen 1909).

> Only the simple conception should be expressed, that a trait of the developing organism is conditioned, or may be partly determined, through "something" in the gametes. ... No hypothesis about the nature of this 'something' should thereby be constructed or supported.[3]

The nature of genes is unclear and it is likewise impossible to know about the genotype — the *total* set of genes. Still, the existence of particular genes can be known and they can be studied since genotypic difference — differences in single genes — can be phenotypically detected.

> As to the nature of "genes" it is as yet of no value to propose a hypothesis; but that the notion "gene" covers a reality is evident from Mendelism. ... We do not know a "genotype," but we are able to demonstrate "genotypical" differences or accordances. (Johannsen 1911, p. 133)

In his chapter on the gene concept, the philosopher Marcel Weber (2005) broadly uses Kitcher's account of reference and conceptual change. Given that in Weber's view a purely causal theory of reference offers an extremely implausible interpretation, he largely relies on a descriptive theory of reference (Kitcher's descriptive modes of reference) to understand the classical gene concept. Consequently, he toys with the idea that "The term 'unit-character' [...] suffered reference failure" (p. 207). For on this interpretation the idea that there is a one–one relation between genetic factors and Mendelizing characters is considered as a reference-fixing, analytic statement. Since there are no entities that determine exactly one trait, reference failure follows. In my view, the period of Mendelian genetics between 1900 and 1910 — where the notion of unit-characters was widely used — demonstrates the limited usefulness of a semantic interpretation that boils down to assigning referents to terms. In Section 3.1.3 I restated Anil Gupta's (1999) point that for concepts involving misconceptions it may be impossible to assign a unique referent (or a unique truth value to statements containing such concepts). Making a forced choice when assigning one of several possible referents (or assuming reference failure) has the implausible consequence that particular statements were false (or meaningless) and thereby fails to account for how the concept figured in a partially successful practice. In the present case, *neither* assigning a referent (genes on chromosomes) to a tokening of the term 'unit-character' *nor* assuming that it was non-referential yields an interpretation that satisfactorily accounts for the usage of this term. The unit-character concept clearly involved misconceptions — at least among some geneticists — but at the same time

[3] Johannsen (1909), p. 124; translation quoted from Falk (1986).

it was part of a largely successful research practice, as the users of the unit-character notion studied Mendelian patterns of inheritance and could to some extent communicate their interpretations of them, which helped to finally clear up the misconception and abandon the term 'unit-character' when talking about the genetic basis of inheritance. A semantic interpretation such as Weber's that views this term as non-referential and the statement involving it as devoid of a truth value does not account for the partially successful use of this term. Rather than relying on the notion reference only (or meaning as constituted by analytic statements), a broader semantic interpretation is necessary that can take into account the actual usage of this term and the various (though sometimes misconceived) beliefs of geneticists. Something like an inferential role can be assigned to the term 'unit-character' as used by individual geneticists, and the rich structure of an inferential role is likely to account for instances where the term 'unit-character' was successfully used and cases where it led to theoretical confusions. This semantic explanation based on an inferential role is possible even in cases where a semantically fruitful assignment of a referent is impossible.

6.1.2 The Chromosome Theory and the Morgan Group

While the period from 1900 until 1910 is often referred to as Mendelian genetics, the period from 1910 or 1915 onwards is usually called classical genetics. The beginning of this stage in the history of genetics was marked by the so-called *Drosophila group*, the school of T. H. Morgan and his students. Before discussing the Morgan group and the acceptance of the chromosome theory of inheritance, let us take stock of the basic ideas of Mendel that survived and those that did not survive the period of Mendelian genetics. First, Mendel and the early Mendelians assumed that characters come in pairs where one character (or allelomorph) is dominant over the other. However, soon it became clear that dominance is no universal rule. The heterozygote Aa may have a phenotype that differs from both homozygotes AA and aa (e.g., by having an intermediate phenotype), so that in these cases it is impossible to consider an allele a dominant or a recessive one. (There also can be more than two alleles for one locus, as was clearly established later on.) Second, Mendel and the early Mendelians endorsed the principle of independent assortment, which assumed that distinct characters recombine independently (different characters are stochastically independent regards their representation in gametes). However, in Mendel's experiments independent assortment held because the characters he chose happened to lie on different chromosomes. During the period of Mendelian genetics there had been some indications that there are exceptions to independent

assortment, and as we shall see below the Morgan group established that different alleles can be linked, namely, in case they lie on the same chromosome. Third, it is only Mendel's principle of segregation that did survive all putative challenges, in particular Castle's attempt to show that there are exceptions to the purity of gametes as different allelomorphs may contaminate each other. (Castle himself conceded the universal validity of the principle of segregation around 1918.)

As I made plain above, in spite of the availability of the idea that the hereditary material resides in the nucleus and may even be identified with the chromosomes, many early Mendelians did not commit themselves to a hypothesis about the material nature of genes:

> Bateson, Castle, Johannsen, and East all worked with units which resided in the gametes. Their association with a material object other than the cell itself was purely speculative. (Carlson 1966, p. 30)

Even after the wide acceptance of the chromosome theory, many geneticists retained a cautious attitude towards theoretical assumptions about the nature of genes. For this reason, some historians have characterized classical genetics as taking an instrumentalist approach. Raphael Falk (1986), for instance, views several geneticists such as Johannsen, Castle, and E. M. East as endorsing an instrumental gene concept, while some classical geneticists such as H. J. Muller advanced a material concept of the gene. Jean Gayon (2000) maintains that classical genetics used an "operationalist (or more widely instrumentalist)" interpretation of genetics, in contrast to the realist interpretation used by molecular genetics (p. 70). In the subsequent section, I will offer my account of the classical gene concept, which assumes that this concept is largely independent of views about the material nature and internal structure of genes. However, to label classical genetics or some strands of it as 'instrumentalist' is somewhat misleading. The stance taken by most classical geneticists is more appropriately described as a *cautious realism* (sensu Amundson 2005). A cautious realist assumes that the phenomena she studies reflect genuine entities and true relations in nature, though she is unable to advance or withholds from advancing any account of the nature of these entities or phenomena, while assuming that future research will shed light in this question. Even someone like Johannsen, who argued that the gene concept was "free from any hypotheses", assumed that it denotes "something" that is present in the gametes, and that the very reality of genes had been inferred by their phenotypic effects in breeding experiments. William Castle was probably the only genuine operationalist in early Mendelian genetics, as will show up in the discussion below.

Before the acceptance of the chromosome theory and the idea that alleles are parts of chromosomes, there was no compelling reason to denote the homozygotes with double symbols (AA, aa). While Mendelism demanded from the outset that a hybrid Aa contains two elements or factors of

a different type, not before the 1910s did the idea gain some recognition that a homozygote contains two identical factors or genes, each of which was inherited from one parent, and that the two identical factors segregate in the formation of gametes, resulting in gametes of identical genotype. The chromosome theory built on late 19th century advances in cell biology. In these decades, the cell theory was established, i.e., idea that the cell is the fundamental structural building element of organisms, which develop based on subsequent cell divisions and differentiation. It was known that cell division included the division of the nucleus, and the idea became popular that the hereditary material resides inside the nucleus (Sapp 1987). Based on previous observations of chromosomes, Walter S. Sutton proposed in 1903 the chromosome theory of inheritance, which suggested that the segregation of Mendelian factors was due to the reduction division in meioses, i.e., the halving of the chromosome set that occurs when gametes are formed (Sutton 1903). The chromosome theory of Mendelian inheritance gained wide acceptance only in the 1910s based on the work of the Morgan group, which to a large extent relied on traditional Mendelian analysis — crossing and mutation studies — but combined them with some cell biological observations.

Originally, the American embryologist Thomas Hunt Morgan (1866–1945) was opposed to Mendelism and the chromosome theory, for he associated it with a preformationist view of development (Morgan 1909, 1910). Mendelism seemed to explain why an organism has a certain adult character by assuming that this (unit-)character or morphological structure (allelo*morph*) already resided in the fertilized egg, being transmitted as such in the gametes. Johannsen's genotype-phenotype greatly helped Morgan accept Mendelism. For Johannsen made explicit that the phenotype (or unit-characters) are not materially transmitted in the gametes; rather, it is the genotype that is passed on and the phenotype develops somehow based on the chemical action of the genes and their cellular environment — Mendelism was not committed to any view as to how the phenotype develops from the genotype. In fact, while 19th century views of heredity had been fundamentally concerned with explaining development, classical genetics changed the very notion of inheritance, leading to what is often called the transmission genetics (Amundson 2005). The task of genetics became the study of the transmission of genes between parents and offspring and the subsequent phenotypic patterns of inheritance, while black-boxing development (the genotype-phenotype relation), leading to the historical split between genetics and embryology (Allen 1985).

Using the fruit fly *Drosophila melanogaster* for Mendelian analysis, in 1910 Morgan discovered sex-linked inheritance patterns. The inheritance of a character (red eyes) departed from standard Mendelian expectations, but could be explained by assuming that Drosophila females possess two

sex factors (XX), males only one (XO), and that the character was linked to the sex factor. Originally, Morgan did not commit himself to the interpretation that the red eye allele was part of a chromosome (the X sex chromosome), but this finding spurred further studies, revealing more characters that were sex-linked. Together with his students Alfred Sturtevant (1891–1970), Calvin Bridges (1889-1938) and Hermann Joseph Muller (1890–1967), Morgan carried out extensive studies on *Drosophila*, setting the foundation for classical genetics (Kohler 1994). A novel experimental tool of the fly group was the use of X-rays to generate novel mutations whose genetic basis could be studies in subsequent crossing experiments, making *Drosophila* the central model organism of classical genetics. A crucial conceptual innovation of the Morgan group was the notion of *linkage* based on frequencies of crossing over. Since 1906, several characters had been known that violated Mendel's principle of independent assortment — they were coupled together (Bateson 1906). While Bateson and Punnet (1911) attempted to interpret this by differential multiplication of cells, the Morgan group explained linked characters as being associated with one chromosome. Any two linked characters were linked with a certain frequency, and conversely separated (recombined) with a certain probability. The suggestion was to view alleles as strongly linked to the extent that they are situated close to each other on the chromosome. In 1912, Sturtevant used these ideas and recombination frequencies obtained in cross-breeding experiments to construct the first genetic map. A genetic map consists of several linkage groups, each linkage group being a line showing the relative position of linked alleles, where the distance of different genes corresponds to recombination frequencies. A genetic map could be interpreted as a mere quantitative representation summarizing recombination frequencies, but a physical interpretation was to view a linkage group as representing a chromosome, in fact showing the relative position of genes on a chromosome. Recombination could be explained by the crossing over (chiasmata) of homologous chromosomes (see Fig. 7 on p. 285). Crossing over is more likely to occur between genes that are situated far apart on a chromosome, which established the correspondence between the relative chromosomal position of genes and the recombination frequencies represented on a genetic map.

In 1915, the Morgan group published its account in *The Mechanism of Mendelian Heredity* (see also Morgan 1917, 1922). By advancing what they called the 'factorial hypothesis', Morgan and his students preferred to use the term 'factor' for what is materially transmitted in the gametes (what Johannsen called 'gene'). A central idea is that the relation between factors and characters is *many–many*. Johannsen had already suggested that several genes influence a character, and E. M. East (1910) had offered good evidence for this idea in maize. In the terminology of the Morgan

group this idea became known as the 'multiple factor theory' (later 'polygenic inheritance'). While different factors at different loci are necessary to produce a certain character, a change in one factor (e.g., a mutation) leads to a phenotypic difference (a mutant phenotype):

> Mendelian heredity has taught us that the germ cells must contain many factors that affect the same character. Red eye color in Drosophila, for example, must be due to a large number of factors, for as many as 25 mutations for eye color at different loci have come to light. ... One can therefore easily imagine that when one of these 25 factors changes, a different end result is produced, such as pink eyes, or vermillion eyes, or white eyes, or eosin eyes. Each such color may be the product of 25 factors (probably many more) and each set of 25 or more differs from the normal in a different factor. It is this one different factor that we regard as the "unit factor" for this particular effect, but obviously it is only one of the 25 unit factors that are producing the effect. However, since it is only this one factor and not all 25 which causes the difference between this particular eye color and the normal, we get simple Mendelian segregation in respect to the difference. (Morgan et al. 1915, pp. 262–263)

Based on the rigorous distinction between factors and characters, Morgan and his students argued against the presence and absence hypothesis and the contamination theory (both discussed in Section 6.1.1). Factors obey Mendelian rules and are constant, even though their phenotypic expression may differ in different environments.

> Failure to realize the importance of these two points, namely, that a single factor may have several effects, and that a single character may depend on many factors, has led to much confusion between factors and characters, and at times to the abuse of the term "unit-character." It can not, therefore, be too strongly insisted upon that the real unit in heredity is the factor, while the character is the product of a number of genetic factors and of environmental conditions. The character behaves as a unit only when the contrasted individuals differ in regard to a single genetic factor, ... (Morgan et al. 1915, pp. 265–264)

From the 1920s onwards, the term 'factor' lost in popularity, and Johannsen's term 'gene' gained general acceptance, in tandem with the term 'allele' (or allelomorph). The philosopher of biology Lindley Darden (1991) rightly points out that while "Changes in terminology sometimes signal important theoretical developments", "the change in terminology from 'unit-character' to 'factor' indicated an important theoretical change, but the adoption of 'gene' was less important" (p. 178). The transition from the unit-character notion to the concept of a Mendelian factor marked the recognition of the genotype-phenotype distinction and the many–many relation between factors and characters. The shift from 'factor' to 'gene' was merely terminological.

Several empirical reasons emerged for a physical interpretation of a genetic map as representing the relative positions of genes on chromosomes, thereby furthering the position that genes are parts of chromosomes. The fact that an organism has several chromosomes could explain why there are different linkage groups in the first place, and studies showed that the number of an organism's linkage groups is identical to the number of its chromosomes (four in the case of Drosophila). The frequency of recombination of two genes within a linkage group could be explained by the physical

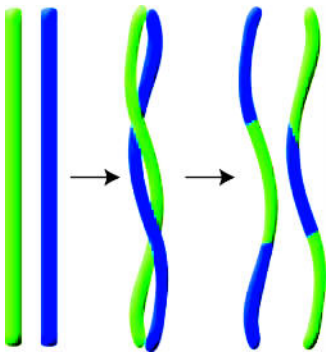

Figure 8: Double Crossover

crossing over of chromosomes and the resulting exchange of chromosome material (discovered by Janssens 1909). Moreover, sex-linked mutations and inheritance of certain traits could be explained by the fact that the gene for such a trait is situated on a sex chromosome and that males and females have different sex chromosomes (the latter could be observed by cell biological analysis). From 1913 onwards, chromosome defects and unusual chromosome behavior in gamete formation were found (Bridges 1913). Some unusual mutants and phenotypic patterns of inheritance could be correlated with underlying chromosome abnormalities. Finally, the non-additivity of recombination frequencies could be explained by the chromosome theory. Early models built linear linkage groups by assuming that if gene M is situated between A and B, then $f(A,B) = f(A,M) + f(M,B)$ (where f is the recombination frequency of two genes). However, more detailed studies showed that additivity does not exactly hold. This led William Castle (1919a, 1919b) to argue that Mendelian factors are not arranged on linear linkage groups, consequently rejecting the chromosome theory. Castle's objection was rooted in his operationalist interpretation of genetics, refusing to introduce entities into his theorizing (such as genes on chromosomes) that could not be directly ascertained through observation. (This attitude was also the source of his confusion between factors and unit-characters, which led him to argue against the purity of gametes, as discussed in Section 6.1.1). As result, Castle defended a non-linear genetic map, which represented genes as points in three-dimensional space, where the relative distance of two genes showed their mutual recombination frequency. The Morgan group, in contrast, defended the linear model based on the chromosome theory (Morgan et al. 1920; Muller 1922; Morgan 1926). Non-additivity could be explained due to double crossovers. If alleles A and B are on different ends of the same physical chromosome, then single crossing over in between them leads to recombination, so that A and B end up on different

chromosomes (see Fig. 7 on p. 285). Double crossing over between A and B, however, results in both ending up on the same chromosome, in spite of crossing over events occurring (Figure 8). Thus, in the case of a double crossover no recombination of A and B takes place and the recombination frequency obtained in breeding experiments concealed that double crossing over occurred. Double crossing over is particularly likely for genes that are far apart on the chromosome, explaining non-additivity of recombination frequencies. Taking this chromosomal phenomenon into account by correcting for double crossover frequencies permitted the Morgan group to establish linear gene maps from recombination frequencies, in contrast to Castle's three-dimensional model.

In addition to conceiving of genes as somehow being located on or being parts of chromosomes, some classical genetics endorsed more specific and sometimes speculative views about the material nature of genes such as their internal structure or their physico-chemical properties. A particularly bold case was H. J. Muller (Carlson 1981), as shown by his essay "The Gene as the Basis of Life" (Muller [1926] 1962). Muller clearly viewed genes as material particles, "strung as they are in myriad upon their tiny chains" (p. 202). In fact, based on mutation and crossover information Muller offered an estimate of the size of an individual gene. On this tentative account, a gene is not larger than a megamolecule such as a colloidal particle, but large enough to contain many typical protein molecules. (Before the discovery of the structure of DNA it was often assumed that genes are made of protein.) In any case, genes as molecules have a chemical substructure. Several years later estimates as to the size of genes were derived from mutation rates obtained when applying X-rays to genetic material. Overall, the fact that X-rays could be used to induce mutations furthered the idea that genes were physical particles, for it showed that genes could be hit and ionized by radiation. In addition to them being molecules, Muller made speculative suggestions regards the functional and chemical features of genes. First, given that genes have physiological effects so as to determine the phenotype, he assumed that genes have catalytic properties (similar to enzymes), so that they are able to support chemical reactions and influence physiological processes. Genes are the material units of physiological function. Second, given that the genetic material is duplicated in cell division, Muller maintained that genes have autocalytic properties, meaning that each gene can autonomously direct its own chemical duplication ([1926] 1962, p. 196). Genes are the material agents of inheritance. Third, given that genes mutate, Muller argued that the material nature of genes is such that they can change to a different allele without losing the above two powers. In particular, a mutation of a gene results in another gene that still has autocalytic properties, so that this mutation can be transmitted. Thus, genes are also the material units of evolution.

Despite views of genes as particulate entities, the stereotype conception of genes as beads aligned on a chromosome string mischaracterizes historical views about genes. Too numerous were empirical challenges that arouse from crossing and mutations studies and cytological observations.

> ... the gene has frequently been depicted as a spherical "bead" on a gene-string. This "classical gene concept" is a fiction. It is based on the analogies and illustrations used in the development and popularization of the factorial hypothesis. With the maturity of the experimental investigations in *Drosophila* between 1914 and 1918, this "classical" model ceased to exist. Multiple allelism, mosaicism, detailed mapping, and the cytological discoveries of chromosomal continuity throughout the mitotic cycle were all major contributions to the definition of the gene with a structure more complex than a factorial bead. A careful reading of the literature of the 1920's would not fail to reveal how much controversy and theory existed on the details of the gene concept. ... Whether Castle, Eyster, Demerec, Goldschmidt, East, Correns, or Muller is cited in the development of the gene concept ... the result is the same: each discussed uniquely different models or properties of the gene which were opposed to the straw-man model of the classical gene. (Carlson 1966, p. 253)

Often the gene was viewed as the smallest *unit of function* (a gene has a distinct physiological effect inside the cell), the smallest *unit of mutation* (a gene may mutate into an alternative allele), and the *unit of recombination* (crossing over may occur between any two genes, but not within a gene). However, while these three characterizations were sometimes identified, some geneticists were aware that they need not empirically coincide. Raffel and Muller (1940), for instance, state that

> ... no such understanding has been arrived at concerning the question of how the limits of a gene, as distinguished from its neighboring genes, shall be defined. In genetic theory, genes have been considered as (1) crossover units — hypothetical segments within which crossing over does not occur; (2) breakage units — again hypothetical segments within which chromosome breakage and reattachment do not occur ...; (3) mutational and functional units — those minute regions of the chromosomes, changes within one part of which may be so connected with changes in the functioning of the rest of that region as to give rise to the phenomenon of (multiple) allelism; or (4) reproductive units — the smallest block into which, theoretically, the gene-string could be divided without the loss of the power of self-reproduction of any part.
>
> Although it seems often to have been assumed, there is as yet no empiric evidence, and only doubtful theoretical ground, for assuming that the lines of demarcation between genes, as defined on any one of these systems, would coincide with those on any others, or even assuming, in case of some given one of these systems (especially the mutational one) that such lines of demarcation are necessarily invariable, non-overlapping, well-defined and absolute. (Raffel and Muller 1940, p. 570)

The precise nature of the putative boundaries between genes was unclear, as was the internal structure of genes. To give one example, in the 1920s the so-called genomere hypothesis was put forward which assumed that genes are composed of smaller particles (genomeres), which may segregate like genes. In order to account for certain patterns of inheritance, it was argued that the gene was not the smallest unit of heredity (Eyster 1924; Demerec 1928, 1938). Raffel and Muller (1940) acknowledge that genetic elements may have a complex internal structure and that there may be no unique answer as to which mereological part to call a gene:

> These parts, then, might themselves be called "genes," and the whole a "gene-complex," or the parts might be called "sub-genes" or something equivalent, and the whole a "gene," depending upon the taste of the writer and upon the criterion which he prefers (that of "allelism" or that of breakage) for defining the limits of a "gene." (Raffel and Muller 1940, p. 570)

Throughout his life, the eminent geneticist Richard Goldschmidt (1878–1958) argued against a particulate conception of genes (Goldschmidt 1927, 1928, 1937a, 1937b, 1938, 1940a, 1940b, 1944, 1950, 1954; Harwood 1993). In his early work, Goldschmidt offered a holistic view of genetic processes. He viewed the gene concept as a mere instrumental notion, with the chromosome being the real unit of inheritance and physiological function (Falk 1986). In the 1930s, the phenomenon of so-called *position effects* provided fuel for Goldschmidt's attack on the corpuscular view of the gene, and raised empirical and conceptual problems within the genetic community. A position effect obtains when the phenotypic effect of an allele changes with its position within the genome. This suggests that a gene's having a certain effect is not just an intrinsic property of a gene, challenging a simple particulate view of genes. Sturtevant (1925) had introduced the position effect hypothesis to account for unusual behavior at the bar eye locus. A possible interpretation was that the relative position of genes on a chromosome has an influence on their effect. Chromosomal rearrangements (translocations) could change the position of genes, and some genes appeared to be sensitive to which other genes they were close to on a chromosome (Muller and Altenburg 1930; Offermann 1935). Another interpretation of position effects was to postulate protosomes and episomes. On this hypothesis, a protosome was the main part of a gene firmly anchored in the chromosome, while episomes were putative smaller segments that can attach to it. Gene mutations could be interpreted as for the most part consisting in losses or additions of a small episome, and only in some cases in a change of the large protosome itself (Thompson 1931; Dobzhansky 1932). Among other empirical challenges of the 1930s and 40s, position effects forced geneticists to admit that genes may have a complex structure, that the boundaries between genes are not fully clear-cut, and that different genes may chemically influence each other (Dobzhansky 1941; Muller 1947; see the quotes in the previous paragraph by Raffel and Muller 1940). In spite of complexities, most geneticists still worked with a particulate conception of genes.

For the renegade Richard Goldschmidt, however, the whole chromosome was the unit of function, with certain rearrangements showing up as genetic effects and mutant phenotypes. While standard approaches distinguished between a gene mutation (a change internal to a particulate gene) and a position effect (a change in the relations of genes), Goldschmidt argued that there was just a continuum between position effect and mutation, both being minor or major rearrangements of

the chromosome, so that it was impossible to discern genes as distinct and independent entities (Goldschmidt 1938). One could still localize the production of a phenotypic effect and associate it with a chromosomal position, but it did not follow that at this position there was a wildtype allele that produced the phenotypic effect. Instead, the whole (wildtype) chromosome was the 'allele' for all mutant genes within this chromosome.

> The time has come to acknowledge that gene mutations have as little existence as genes themselves. ... The idea of a position effect, made to save the concept, will also have to disappear when it is recognized that the position effect is actually identical with what was called a gene. The chromosome as a unit will be found to control normal development or wild type. The changes of the correct order within its chain produce deviations from normal development, called mutations. Though they are localized, there is no such thing as a gene and certainly no wild type allelomorph. (Goldschmidt 1937b, p. 767)

In his more mature work from the mid-1940s onwards, Goldschmidt moved from a holistic to a hierarchical view of genetic processes. Now he attempted to replace the gene as a particulate entity with a hierarchy of fields. Unlike others who relied on the gene as the central notion that unified genetics, Goldschmidt developed an account of a whole hierarchy of sequential developmental processes. While most classical geneticists focused on the transmission of genes and phenotypic characters between generations, Goldschmidt's 'physiological genetics' was fundamentally concerned with the role of genes in development. Due to the recent developments in molecular genetics and the emergence of developmental genetics, Goldschmidt's holistic or hierarchical view of the genes comes to be viewed in a more positive light than by his contemporaries (Dietrich 2000a, 2000b).

In classical genetics, different and sometimes conflicting views about the material nature were endorsed. While many withheld from speculations about the structural properties of genes, a genuine instrumentalism or even operationalism about the gene concept was only endorsed by a few classical geneticists. Above we encountered William Castle as an operationalist among the early geneticists. Another prominent case was the American geneticist Lewis J. Stadler (1896–1954). When in the early 1950s new insights on the fine-structure of genes and chemical structure of the genetic material became available, Stadler still argued for an operational approach to genetics. He urged to keep the operational notion of a gene and the gene as a theoretical concept apart:

> The term *gene* as used in the current genetic literature means sometimes the operational gene and sometimes the hypothetical gene, and sometimes, it must be confessed, a curious conglomeration of the two. (Stadler 1954, p. 814)

Even though Stadler viewed his approach as following the operationalism of Percy W. Bridgman (1927, 1936), he apparently did not endorse a genuine operationalism, i.e., a semantic doctrine that maintains that non-operational definitions and theoretical concepts are meaningless. In fact,

Stadler viewed what he calls the hypothetical gene concept as meaningful. His approach was a methodological or epistemological operationalism, that carefully distinguished between what can directly discovered from experimental observation (the operational gene) and theoretical speculation that does not directly follow from the actual evidence.

> What is the gene in operational terms? In other words, how can we define the gene in such a way as to separate established fact from inference and interpretation? ... Operationally, the gene can be defined only as the smallest segment of the gene-string that can be shown to be consistently associated with the occurrence of a specific genetic effect. It cannot be defined as a single molecule, because we have no experimental operations that can be applied in actual cases to determine whether or not a given gene is a single molecule. It cannot be defined as an indivisible unit, because ... there is no operation that can prove that further separation is impossible. For similar reasons, it cannot be defined as the unit of reproduction or the unit of action of the gene string, nor can it be shown to be delimited from neighboring genes by definite boundaries. (Stadler 1954, p. 814)

Apart from isolated operationalist/instrumentalist tones and various material accounts of the gene, a common stance among classical geneticists was what I called above *cautious realism*. Geneticists assumed that genes have a certain material structure, while being aware of the fact that the advanced hypotheses about the internal structure and physiological effects of genes and the boundaries and material relations between genes lacked genuine verification, so that being cautious toward speculations about the nature of genes was reasonable. This strategy is nicely illustrated by T. H. Morgan's 1934 Nobel lecture. Morgan clearly assumed that future research would uncover the nature of genes as material entities. Yet he was aware that current evidence did not provide a characterization of gene structure. What had been established was how genes figure in inheritance and that they are associated with chromosomes. Morgan emphasized that the endorsement of a more concrete account about the nature of genes was largely irrelevant to genetic practice. The role of genes in inheritance could be studied by standard crossing and mutation studies:

> What is the nature of the elements of heredity that Mendel postulated as purely theoretical units? What are genes? Now that we locate them in the chromosomes are we justified in regarding them as material units; as chemical bodies of a higher order than molecules? Frankly, these are questions with which the working geneticist has not much concern himself, except now and then to speculate as to the nature of postulated elements. There is no consensus of opinion among geneticists as to what they are — whether they are real or fictitious — because at the level at which the genetic experiments lie, it does not make the slightest difference whether the gene is a material particle. In either case the unit is associated with a specific chromosome, and can be localized there by purely genetic analysis. Hence, if the gene is a material particle, it is a piece of the chromosome; if it is a fictitious unit, it must be referred to a definite location on a chromosome — the same as on the other hypothesis. Therefore, it makes no difference in the actual work in genetics which point of view is taken.
> ... As we do not know of any comparable division phenomena in organic molecules, we must also be careful in ascribing a simple molecular constitution to the gene. On the other hand, the elaborate chains of molecules built up in organic material may give us, some day, a better opportunity to picture the molecular aggregate structure of the gene and furnish a clue concerning its mode of division. (Morgan 1934, pp. 315–316)

6.1.3 The Content of the Classical Gene Concept and Its Limited Explanatory Potential

After this review of the use of the gene concept and the understanding of genes in classical genetics, it is time for a philosophical analysis. For the most part, this section gives a characterization of what I view as the classical gene concept, as being used by virtually all geneticists before the emergence of molecular genetics. I lay out the inferential role (conceptual role) of this concept — the inferences and explanations that are supported by the classical gene concept and that account for its successful use in scientific practice. The main purpose of this discussion is to prepare the comparison between the classical gene concept and the molecular gene concept. The later discussion on the classical molecular gene concept (Section 6.2.3) will argue that substantial progress occurred with the transition from the classical to the molecular gene concept precisely because the molecular concept supports explanations that the classical gene concept cannot yield. My analysis of the classical gene concept (and the subsequent contrast between the classical and molecular gene concept) resembles the account of Ken Waters (1994), the main difference being that Waters' discussion is not based on any theory of concepts. In addition to characterizing a single classical gene concept as shared by classical geneticists, the present section also sketches a more fine-grained scheme of individuation that distinguishes between several gene concepts being used by different classical geneticists, thereby illustrating my pluralism about concept individuation (Section 3.3.2). Ascribing distinct gene concepts to different classical geneticists underwrites an explanation of why certain lines of research and developments took place in genetics (while the ascription of a shared classical gene concept exhibits the progress the occurred with the origin of the molecular gene concept).

The above discussion indicated that during the history of classical genetics, especially its early history, views about genes changed relatively rapidly. And even at a particular time, geneticists differed widely as regards their beliefs about the structure and chemical effect of genes. Some biologists viewed genes as clearly delimited parts of the chromosome, thus endorsing an inference from 'is a gene' to 'is a delimited part of the chromosome'. H. J. Muller assumed that each gene has the power to direct its own replication, and thereby was willing to make the bold inference 'has autocatalytic properties' from 'is a gene' — a speculative claim about the chemical properties of genes that proved to be plainly wrong. Others rejected the idea that genes are distinct parts of the chromosome. Richard Goldschmidt, for instance, argued that the chromosome is the unit of

genetic function. While assuming that genetic phenomena such as distinct phenotypic differences and Mendelian patterns of inheritance are due to physiological changes that can be correlated with particular locations on a chromosome, Goldschmidt argued that this does not warrant postulating the existence of a discrete gene on that chromosome location. While a cautious realism about genes prevailed, a few classical geneticists took an instrumentalist stance and assumed that genes are abstract entities. My previous overview could address only some of the various accounts of the material nature of genes. Elof Carlson (1966) puts the differences in views as follows:

> The gene has been considered to be an undefined unit, a unit-character, a unit factor, a factor, an abstract point on a recombination map, a three-dimensional segment of an anaphase chromosome, a linear segment of an interphase chromosome, a sac of genomeres, a series of linear subgenes, a spherical unit defined by target theory, a dynamic functional quantity of one specific unit, a pseudo-allele, a specific chromosome segment due to position effect, a rearrangement within a continuous chromosome molecule, ... (Carlson 1966, p. 259)

At any particular point in time, different geneticists sometimes endorsed different inferences in which the term 'gene' figures. In semantic terminology (Section 3.1), different individuals endorsed different *total* inferential roles (or different total conceptual roles). This can be viewed as a difference between the mental representations each individual associated with the term 'gene'. Individuals may differ in their conceptions of a phenomenon or an entity.

Due to the disagreement about the nature of genes, the total inferential role of terms such as 'gene', 'factor', and 'allele' — as a property of an individual — exhibited interpersonal variation. However, the crucial step in my account is to delimit the classical gene concept by some inferences in which the term 'gene' figured and that were widely endorsed by geneticists — so as to account for the successful use of this concept in biological practice. In a nutshell, on my account particular beliefs about the material structure of genes were not constitutive of the classical gene concept. Instead, classical genes were functionally defined in terms of their role in *phenotypic transmission between generations*. The inferences that characterize the classical gene concept are those that specify how genes bring about *patterns of inheritance*. More precisely, possession of the classical gene concept presupposes knowledge of the genotype-phenotype distinction, of the fact that genetic loci are arranged into linkage groups and that each locus is occupied by two alleles (in the case of a diploid species), so that there are homozygous and heterozygous genotypes. Furthermore, segregation and linkage are the two basic principles characterizing the behavior of genes in inheritance. Segregation specifies that for each of two corresponding linkage groups (for each of two homologous chromosomes) half of the gametes will inherit this linkage group (chromosome). Alleles on distinct linkage groups assort stochastically independently, while alleles on the same linkage group recom-

bine with a certain frequency, which is given by the relative distance of the loci occupied by these two alleles. (A special principle obtains for case of sex-linked inheritance.) These principles involve some physical assumptions about the cellular basis of inheritance: knowledge about processes such as cell division (mitosis), gamete formation (meiosis), and fertilization. Finally, the classical gene concept involves a specification of the relation between the genotype and phenotype: a genotype at a certain locus entails a particular phenotype, assuming that the genotype at other loci is wildtype and that the environment is normal. (Which phenotype corresponds to a particular genotype has to be established empirically, in fact, classical genes are defined and experimentally detected by the phenotypic effect they have.) In addition to these abstract principles that specify the impact that classical genes have on *phenotypic* patterns of inheritance, the only idea about the material features of genes that I view as constitutive of the classical gene concept is their association with chromosomes. Linkage groups correspond to chromosomes, so that genetic loci are particular position on chromosomes. Likewise, the classical gene concept embodies knowledge about the behavior of chromosomes and cell division and gamete formation (including chromosomal crossing over). We saw in the foregoing section that the idea of associating genes with chromosomal locations was essential to account for recombination frequencies, to establish linear genetic maps, and to explain sex-linked inheritance. Apart from the idea that genes are parts of chromosomes, on my account no more specific views about the material nature of genes are constitutive of the classical gene concept, i.e., no assumptions about the internal structure of genes, the boundaries between genes and the chemical properties and physiological effects of genes. (Most such views turned out to be wrong, for instance, most classical geneticists assumed that genes are made of protein.)

Classical geneticists sometimes widely disagreed about the concrete nature of genes. Consequently, my account of the classical gene concept, which largely abstracts from beliefs about the material nature of genes, has the advantage that the gene concept thusly characterized was shared by virtually all classical geneticists. To be sure, the precise shape of the above listed principles characterizing genes changed in the history of classical genetics once exceptions to the simple patterns of inheritance became clear due to variable expressivity, position effects, and complex loci. The inferential role of the term 'gene' changed, but only slightly so that we can claim that these refinements in the way inheritance was explained do not amount to the emergence of a new concept and that instead change took place internal to the concept of the classical gene. My justification for this particular delineation of the classical gene concept is as follows. While speculative beliefs about the structure and physiological function of genes were largely irrelevant for the successful use of

the gene concept, the above specified inferences were strongly embedded in the practice of classical geneticists and account for the practical success of the usage of this concept. For instance, classical geneticists regularly carried out segregation and linkage analysis, thereby making use of the above specified genetic principles. In particular, these inferences yielded the *epistemic and experimental access* to classical genes. Whatever the material structure of genes, classical geneticists agreed on the fact that patterns of inheritance are to be predicted and explained by the inheritance of genetic factors or alleles. Whenever a trait mendelizes (yields a Mendelian pattern of inheritance), the default interpretation was that this is due to the effect of a single gene. This evidence for the action of a gene is valid even if the particular research was carried out by another geneticist who endorsed different beliefs about the nature of genes. The statement by Morgan (1934) quoted above on page 306 illustrates the idea that particular views about the material nature of genes were largely irrelevant for the experimental practice of classical genetics. Mature classical genetics was not only concerned with the study of patterns of inheritance, but investigated a larger range of biological phenomena using genetic analysis (Waters 2004b). Still, the basic experimental strategies for these investigations derived from the principles specifying the behavior of genes in inheritance. Thus, the inferences that I view as constitutive of the classical gene concept provide the basis for detecting the presence and operation of genes — reliable evidence and stable access to genes that was valid across different geneticists and different views of the nature of genes.

Given this semantic characterization, the classical gene concept underwrites certain *inferences*, namely the prediction of patterns of inheritance. Patterns of inheritance are predicted by inferring from the genotypes of parents the distribution of genotypes and thus phenotypes of the following generation. This prediction is possible because the inferential role of the classical gene concept includes an account of how genes behave in processes such as segregation and linkage (which entails the genotype distribution of the next generation) and it makes reference to the phenotypic impact of genes, including the notions of dominance and recessiveness (which entails the phenotype of the filial generation).[4] Apart from inference and prediction, the role of the classical gene concept in the *explanation* of phenotypic traits is as follows. Classical genetics was unable to explain the presence or development of particular traits by appeal to genes. One reason is that classical geneticists did not have any idea of *how* genes bring about their contribution to the phenotype. It was unknown by which physico-chemical properties or biochemical mechanisms genes bring about their physiological effects so as to determine a certain phenotypic property. Moreover, Ken Waters (1994) rightly points

[4]For a detailed example see Waters (1994), pp. 165–160.

out that "Geneticists did not even understand *what* the genes' contributions were" (pp. 171–172). For classical geneticists knew very well that the relation between genes and traits is many–many, in particular that many genes are involved in the production of a single phenotypic trait:

> The factorial hypothesis does not assume that any one factor produces a particular character directly and by itself, but only that a character in one organism may differ from a character in another because the sets of factors in the two organisms have one difference. (Morgan et al. 1915, pp. 265–266)

Relative to a total genetic background, a genetic difference at a particular locus shows up as a phenotypic difference (Waters 1994; Schwartz 2000). For instance, in *Drosophila* the presence of the *vermilion* allele results in an individual with pink eyes, whereas a wildtype allele at the same locus leads to the normal, red eye color (assuming in both cases that wildtype alleles occupy all other loci). Such a phenotypic difference provides a means of identifying a classical gene and locating it on a chromosome, but it does not have any implications about the individual contribution of this gene. The fact that the presence of the 'pink eye allele' (*vermilion*) corresponds to the development of a pink eye color does not entail that this gene directs the production of a pink eye pigment.[5] Section 6.1.1 mentioned that 19$^{\text{th}}$ century theories of inheritance had essentially been concerned with the explanation of development. Accounts of the material bearers of inheritance such as Darwin's and Weismann's had postulated particles representing different parts of the body and their properties, where these particles are materially transmitted as a whole but then physically split and move into different parts of the developing organism such that each particle determines the development of a specific character. Classical geneticists did not and could not conceive of genes in this way. First, Mendelians were not concerned with an explanation of development (the material relation between the genotype and the phenotype), but solely with patterns of inheritance. Second, classical geneticists viewed chromosomes as the material bearers of inheritance and were well aware of the fact that in a developing organism each cell acquires the full set of chromosomes, so that the 19$^{\text{th}}$ century way of explaining development was not available to classical genetics.

> Although there is little that we can say as to the nature of Mendelian genes, we do know that they are not 'determinants' in the Weismannian sense. ... All that we mean when we speak of a gene for pink eyes is a gene which differentiates a pink eyed fly from a normal one — not a gene which produces pink eyes *per se*, for the character pink eyes is dependent upon the action of many other genes. (Sturtevant 1915, p. 265)

Even if the many biochemical factors that are involved in the production of the wildtype red eye

[5] Even though since the origin of the molecular gene concept it is common to conceive of a gene as being the cause of a specific product, this did not hold for classical genetics: "In retrospect, one might have expected to find explicit definitions of 'factor' or 'gene' as an entity that *causes* characters. In retrospect, it sounds correct to claim that genes *cause* hereditary characters, although the relation is not one cause, one effect. ... With hindsight, it seems geneticists were postulating an underlying, unobservable causal factor to explain their data. Causal language, however, was used surprisingly infrequently in the literature." (Darden 1991, p. 182)

color had actually been known to classical geneticists, the basic conclusion that could have been drawn about the *vermilion* locus is that the wildtype allele is *somehow* involved in the overall production of red eyes, while the absence of the wildtype allele and presence of the pink eye allele at this locus *somehow* modifies the overall set of biochemical factors involved *such that* pink eyes result. (In Section 6.2.1 we shall see that on the way toward the molecular gene concept biologist did acquire insight into the individual contribution of genes for some genes in microorganisms.)

Thus, the classical gene concept does not underwrite a mechanistic explanation of how genes bring about their effects. Classical geneticists were ignorant of how a certain eye color develops based on the interaction of various molecular substances produced by several genes. The classical gene concept does not even specify what the individual causal contribution of a gene is. In this sense, the explanatory potential of the classical gene concept is severely limited. Still, classical genetics could explain phenotypic *differences* by means of genotypic *differences*. For instance, one can explain why a fruit fly has orange eyes (differing from the normal eye color) with reference to the fact that a certain gene is mutated (it has a *cinnabar* rather than the wildtype allele). Such an account does not causally explain how a certain eye color develops based on the molecular effects of several genes; rather, it explains phenotypic differences based on genotypic differences relative to a normal genetic and environmental background. While falling short of a real explanation of how characters originate based on gene action, these explanations are still useful. For instance, as discussed in Section 6.1.4, population genetics makes use of the classical gene concept in its explanations of phenotypic evolution, as the existence of genetically based phenotypic differences between individuals is the only relevant presupposition for accounting for the effect of natural selection. In sum, *the inferential role of the classical gene concept supports the prediction of patterns of inheritance and the explanation of phenotypic differences by means of genotypic differences.*

In Section 3.3.2 I suggested a pluralism about meaning, i.e., the idea that there may be different ways to individuate a concept. The suggestion was that each instance of concept individuation is guided by certain philosophical interests, and since the same concept can be approached with different explanatory interests in view, different individuation schemes may be legitimate. In the remainder of this section I illustrate this idea in the context of classical genetics. So far my account of the classical gene concept largely abstracted from particular views of the material nature of genes, yielding a single classical gene concept shared by geneticists. This construal of the classical gene concept is in many cases sufficient to account for its successful use in genetic practice. But actually my main rationale for this characterization of the classical gene concept is to contrast it

with the molecular gene concept so as to *discern conceptual progress*, which will be carried out in Section 6.2.3. This comparison of two periods in the history of genetics favors contrasting 'the' classical gene concept with 'the' molecular gene concept. However, this minimalist construal of the classical gene concept makes unintelligible certain developments within classical genetics. I acknowledged above that during the history of classical genetics the precise understanding of principles of inheritance changed once Mendel's original rules had to be modified. This discussion viewed all these changed as occurring within the boundaries of 'the' classical gene concept — as a cluster consisting of different and historically changing total inferential roles endorsed by different individuals. But understanding these changes internal to 'the' classical gene concept is significant as well, and this makes it necessary to take into account the discovery of exceptions to standard Mendelian patterns of inheritance (due to linkage, variable expressivity, and position effects), which yielded some preliminary insights into the structure and function of classical genes and provided important clues for further experimental research. Apart from the principles of phenotypic inheritance, particular views about the structure of genes endorsed by an individual explain why this scientist opted to carry out certain experiments and pursue certain lines of research. Thus, if we are interested in *explaining scientific change* (why particular experimental and theoretical changes took place in classical genetics and how molecular genetics could grow out of it in the first place), we have to make use of a more fine-grained scheme of individuation. Now we have to discern several classical gene concepts, each of which embodies certain relatively specific views about the internal structure and causal functioning of genes. Each of these concepts was possessed only by a subset of classical geneticists, and some individuals changed from one concept to another in their scientific career. This permits the philosopher to track the development of classical genetics in a more fine-grained manner, and it puts her in a position to explain why certain historical developments occurred with reference to the different gene concepts used by different research groups.

One could distinguish several such particular gene concepts throughout the history of classical genetics, but I put forward only two examples as an illustration. One specific classical gene concept is given by what was sometimes called the 'genomere hypothesis'. Before 1920, several seemingly unstable characters were found that yielded a spectrum of traits or varying phenotypes in patterns of inheritance (Correns 1919). For instance, the hue of the kernel color in maize — a Mendelian character — was found to vary. While these patterns of inheritance did not seem to contradict the principle of segregation, an interpretation of this phenomenon was needed (Emerson 1917). In 1920, E. G. Anderson suggested that genes may be made up of smaller particles of a different

kind, such as red-determining and white-determining particles, where a gene having a different particle composition in different individuals accounts for color variegation across individuals (Demerec 1938). W. E. Eyster (1924) explicitly spelled out and defended this theory, suggesting the name 'genomere' for the particles composing a gene. M. Demerec (1926) explained some observed patterns of inheritance by the idea that during mitotic cell division before the formation of gametes the individual genomeres making up a gene divided randomly and unequally, resulting in daughter cells (and finally gametes) whose distribution of different genomeres differed, resulting in a phenotypic variegation within a Mendelian character across individuals. This genomere hypothesis of the structure of classical genes yielded a specific concept of the gene, which gave its proponents a new investigative approach during the 1920s (Carlson 1966). It led to experiments and studies on plant and animal heredity that attempted to confirm this hypothesis, investigate the nature of genes and genetic subunits, or to measure the rate of genomere assortment (Demerec 1928). Others, in contrast, defended an alternative gene concept and attempted to explain the phenomena that led to the genomere hypothesis in another fashion (Muller [1926] 1962).

Another example of a specific gene concept is Goldschmidt's holistic or hierarchical account of genes and genetic processes. It is important to realize that Goldschmidt was fundamentally concerned with the physiological action of genes, or with the nature of developmental processes, as one would say nowadays. Most classical geneticists, in contrast, focused on what I referred to above as transmission genetics — the study of patterns of inheritance, which ignores the way in which genes bring about the phenotype. From the point of view of transmission genetics it was largely possible to endorse the idea of genes as stable factors and unchanging genotypic units. Given an additional concern with development, however, one has to account for cellular and structural differentiation in development in spite of the fact that each cell in the body contains the same set of genes. Consequently, genes cannot solely be viewed as constant factors but one has to address the physiological rate of gene action in different cells. This led Goldschmidt and other researchers addressing the role of genes in development to study and speculate about the way in which gene activation influences rates of development (Goldschmidt 1927; de Beer 1930). Thus, Goldschmidt's dynamical concept of the gene that views genetic processes and their quantitative relations as the real units of genetics has to be viewed against the background of his explanatory concern with the physiology of gene action; and Goldschmidt's commitment to this particular gene concept helps to understand why he chose to conduct his specific experiments about the physiological action of genes and disagreed vehemently with most other geneticists about the nature of genes.

6.1.4 The Classical Gene Concept in (Contemporary) Population Genetics

The classical gene concept does not make assumptions about the material structure of genes, and it does not offer an account of what a gene's causal contribution is. Rather than explaining how a gene brings about its phenotypic effect, the classical gene concept explains phenotypic differences by means of genotypic differences (relative to a total organismal and environmental background). As discussed in the next section, in contrast to the classical concept the molecular gene concept embodies knowledge about the molecular structure of genes and thereby underwrites explanations of the causal effects of genes. The molecular gene concept has largely replaced the classical gene concept in that geneticists usually express the molecular concept when using the term 'gene'. However, the classical gene concept has not been eliminated and it is still important for a few biological tasks. This holds even for molecular genetics. Some experimental methods to uncover *molecular* genes — particular DNA sequences — make use of the tools of classical genetics, for instance by producing and analyzing mutants or by using maps that show the location of (classical) genes on the chromosome to zero in on and isolate molecular genes. Molecular biologist's design and description of these experimental procedures uses the classical gene concept (Section 6.2.3). In addition to molecular genetics, many theoretical accounts and experimental approaches in behavioral genetics, human genetics, and clinical genetics rely on the classical gene concept. For in these disciplines genes are often conceived of as difference makers that account for unusual behavioral traits or a abnormal condition or human disease — genes 'for' such and such a condition (Moss 2003).

A prominent example of a contemporary biological discipline that largely uses the classical gene concept is population genetics (and the related field of quantitative genetics). In fact, population genetics originated in the 1930s — well before the advent of molecular genetics. Before the 1920s, two different theoretical schools competed about the proper view of inheritance and its impact on evolution. The Mendelians emphasized that inheritance is due to the transmission of classical genes as discrete units, and that mutation consist in a genetic change from one to another allele, leading to a distinct phenotypic change. Consequently, the Mendelians often rejected continuous variation and a gradual evolution based on such a variation, and instead endorsed a saltational, non-Darwinian picture of evolution. The biometricians, on the other hand, used the methods of statistics to study the distribution of phenotypic traits between generations. They emphasized the continuous variation of features, which was more congenial for a gradual account of evolution. In the 1930s, Ronald A. Fisher (1930), J. B. S. Haldane (1931) and Sewall Wright (1931) synthesized these

seemingly contrary approaches and founded the statistical theory of population genetics. The basic idea is to use a Mendelian account of genes as discrete units, while pointing out that many genes are involved in the production of a phenotypic trait, so that a quasi-continuous phenotypic variation within a population is consistent with a discrete mode of inheritance (Fisher 1918). Population genetics became the central theoretical ingredient of the Modern Synthesis, the neo-Darwinian theory of evolution, combining classical genetics with evolutionary biology (Dobzhansky 1941; Mayr 1942; Huxley 1942; Simpson 1944). Population genetics explains the evolution of populations based on a study of the change in genotype and allele frequencies due to mutation, genetic drift, migration of organisms, and natural selection. Contemporary population geneticists also use the methods and knowledge of molecular genetics and for this reason sometimes make use of the molecular gene concept. Still, most theoretical models and applications in contemporary population genetics simply rely on the classical gene concept, with the same content as in the 1930s. The basic reason is that a difference on the genetic level within a population is relevant for population genetics only insofar as it makes a phenotypic difference, as selection acts on *phenotypic differences* among individuals. Which molecular structure accounts for the phenotypic difference and how a different gene brings about a variant phenotype is irrelevant for tracking the change in gene frequencies and the corresponding changes in phenotype frequencies. Population genetics may be defined as "the study of naturally occurring genetic differences among organisms" (Hartl 2000, p. 1).

Let me give you a flavor of what models and explanations in population genetics look like. According to Bruce Wallace (1981), "The population geneticist studies the frequencies of different alleles in a population, the interactions of alleles at the same or different loci, and the degree to which such interactions govern gene frequencies themselves" (p. 4). Textbooks in population genetics typically start out with how to measure and quantitatively describe allele frequencies. The notions of 'gene' and 'allele' (and correspondingly 'gene frequency' and 'allele frequency') are used synonymously (Crow and Kimura 1970; Crow 1986; Christiansen 2000). A basic starting point for theorizing is the well-known Hardy-Weinberg model. In a sexually reproducing, diploid species, consider a single locus with two alleles A and a. Assume that the following idealizations hold: 1) the population size is infinite, 2) generations do not overlap, 3) organisms mate at random, 4) no migration obtains, 5) no mutation occurs, and 6) no selection takes place. If in the parental generation the frequency $f(A)$ is p and $f(a)$ is q, then in any subsequent generation the allele frequencies stay the same, and the genotype frequencies are as follows: $f(AA) = p^2$, $f(Aa) = 2pq$, $f(aa) = q^2$. Thus, genotype frequencies do not change in later generations and the population

is in Hardy-Weinberg equilibrium. The above six idealizations never hold for a real population, but the Hardy-Weinberg model is still fruitful. For if measurement in a real population show that the genotype frequencies do not conform to Hardy-Weinberg expectations, then at least one of the idealizations must be substantially violated, which triggers investigation into which conditions are not met, i.e., the causes that disturb Hardy-Weinberg equilibrium. Furthermore, on the theoretical level more adequate models can be developed by abandoning one or several of the idealizations.

One way in which the condition of random mating in a population is violated is if inbreeding occurs. Inbreeding has the effect that the frequencies of AA and aa gradually increase across generations, while the frequency of Aa decreases (an increase in homozygosity and a decrease in heterozygosity). If a model assumes a finite and small population size, then random genetic drift due to sampling error results. Mutation and migration may bring novel alleles into a population. Various models study the effect of population structure and migration, which removes the idealization of random mating and takes gene-flow between populations into account. An important task is to model the effect of natural selection. To this end, population genetics assigns a *fitness* value w_x to each genotype x. This is the probability with which this genotype will be represented in the next generations, reflecting how likely an organism with a particular genotype is to survive and leave a certain number of offspring. (Reflecting the influence of natural selection, the fitness value is always is relative to a certain environment.) To take a simple model, assume that all Hardy-Weinberg conditions as stated above obtain apart from the influence of selection. If $w_{AA} > w_{Aa} > w_{aa}$, then $f(AA)$ and $f(A)$ will monotonically increase and converge to 1, that is, the allele A goes to fixation and allele a is eliminated. Likewise, if $w_{AA} < w_{Aa} < w_{aa}$, then a goes to fixation. If $w_{AA} > w_{Aa} < w_{aa}$ (called underdominance or heterozygote inferiority), then an unstable equilibrium exists: if in the first generation, $f(A)$ happens to be exactly $\hat{f}$, where $\hat{f} = \frac{w_{Aa}-w_{aa}}{2w_{Aa}-w_{AA}-waa}$, then the allele frequencies will not change. If the initial frequency of $f(A)$ is above $\hat{f}$, then it will converge to 1; if $f(A)$ is below $\hat{f}$, then it will converge to 0. Thus, the system has one unstable equilibrium $\hat{f}$ for $f(A)$, and two stable equilibria: 0 and 1. The last possibility is underdominance (heterozygote superiority): $w_{AA} < w_{Aa} > w_{aa}$. Now $f(A) = 0$ and $f(A) = 1$ are unstable equilibria, but for any other initial value of $f(A)$, the system will converge to the stable equilibrium $\hat{f}$. In this case both alleles A and a will be maintained in the population by virtue of selection.[6] Apart from this simple

[6] A classic example for underdominance is sickle-cell anemia. The sickle-cell mutation a, when occurring in a homozygous condition, leads to severe anemia (fitness w_{aa} is very low). In the heterozygous condition, however, it increases the resistance to malaria. Consequently, in high-malaria regions of Africa, the fitness of a person with the sickle-cell allele is even higher then that of a 'normal' person: $w_{AA} < w_{Aa}$. Thus, $w_{AA} < w_{Aa} > w_{aa}$ and natural selection maintains the presence of the sickle-cell allele a in these populations.

model, more sophisticated models in population genetics study the combined effect of population structure, migration, mutation, genetic drift, and selection. Rather than considering only a single locus with two alleles, various models address the presence of several alleles at a certain locus, and in particular study the change of allele frequencies at different loci (Christiansen 2000).

In sum, most applications in population genetics, including contemporary population genetics, rely on the classical gene concept (Christiansen and Feldman 1986; Ewens 2004; Gale 1990; Gillespie 2004). To be sure, for certain purposes the tools and concepts of molecular genetics are used. For instance, measuring migration and gene flow between populations may involve the use of molecular genetic markers, where an understanding of these experimental tools presupposes the notions of molecular biology. Still, many standard models in population genetics based on the notion of classical genes apply to molecular markers, as "the inheritance of most molecular traits, such as restriction fragment polymorphisms (RFPLs), follows simple Mendelian rules" (Crow 1986, p. 2). Population genetics views a gene as any entity that is inherited in a Mendelian fashion and that accounts for phenotypic differences between individuals, thereby using the classical notion of a gene. Population genetics tracks the change in allele and genotype frequencies, studying how genetic variation changes within a population and how this brings about phenotypic change. Genetic differences and between-individual variation on the molecular level is relevant only insofar as it brings about phenotypic differences and variation. For natural selection acts on phenotypic differences. Fitness values are assigned to a genotype based on the reproductive success of the organisms having this genotype (in a particular environment exerting a certain selection pressure). What the molecular structure of an allele is or how it causal-mechanistically brings about a certain phenotype (which determines fitness) is irrelevant for the theory of population genetics. The evolutionary developmental biologist Scott Gilbert makes this point by contrasting the notion of classical genes used by population genetics with the notion of developmental genes, i.e., the molecular gene concept used in developmental biology and evo-devo (see also Gilbert 2003; Falk 2000):

> The gene of the Modern Synthesis of the 1940s was an abstraction. It was not sequenced, its structure was unknown ... The genes of the Developmental Synthesis [evolutionary developmental biology] are specific sequences of DNA containing not only protein-encoding regions, but regulatory sequences such as promoters, enhancers, silencers, insulators, introns, 5' untranslated regions, and 3' untranslated regions ... (Gilbert 2000, p. 179)

Evolutionary developmental biology is interested in how the same molecular gene is present in quite unrelated species and controls their development, e.g., homologous developmental genes being present in species sharing the same body plan such as different vertebrates. In this sense, developmental genes are important because of the similar molecular, developmental and pheno-

typic influence they have on different organisms. This differs from the gene of population genetics:

> The genes of the Modern Synthesis are manifest by the differences they cause. These differences could be selected. The genes of the Developmental Synthesis are manifest by their similarities. (Gilbert 2000, pp. 179–180)

6.2 THE CLASSICAL MOLECULAR GENE CONCEPT

The discussion starts out with an overview of the basic steps that led to the origin of the molecular gene concept. I focus on the results of complementation studies (the *cis-trans* test) yielding insights into the fine-structure of genes, the evidence for the one gene–one enzyme hypothesis, the discovery of the molecular structure of DNA, and the genetic code. Section 6.2.2 offers my characterization of the classical molecular gene concept (as used in the 1970s) and its explanatory potential. To this end, I introduce the notion of an 'explanatory strategy', arguing that explanations in molecular biology and the molecular gene concept likewise involve and combine several such strategies. On my account, the molecular gene concept supports explanations of the molecular and cellular effects of genes, including the regulation of gene expression, which I illustrate with early work on gene regulation (the *lac* operon). Section 6.2.3 compares the classical with the molecular gene concept. Even though the molecular gene concept did not replace or reduce the classical gene concept, and even though both gene concept differ in reference, conceptual progress occurred with the way in which the meaning of the term 'gene' changed in the transition from the classical to the molecular gene concept. In a nutshell, while the classical gene concept can merely explain phenotypic differences by genetic differences, the molecular gene concept supports a direct, causal-mechanistic explanation of the origin of biological traits. I explain why the meaning change from one gene concept to a distinct concept and the related change in reference occurred in a rational fashion.

6.2.1 Genetics on the Way Toward a Molecular Gene Concept

Research in the 1940s and in particular the 50s and early 60s led to the origin of the molecular gene concept. The discovery of the chemical structure of DNA in the 50s and subsequent early work in molecular genetics such as the establishment of the genetic code essentially involved biochemical techniques, without relying much on the methods of classical genetics. I address this strand of

research later in this section, but first I have to discuss chronologically earlier research traditions and findings. Though these experimental traditions happened to be on the way towards molecular genetics, they were approaches that made primarily use of classical genetic analysis, thereby using the classical gene concept as the basis of uncovering the nature of genes. (Later research in molecular genetics likewise continued to use some methods of classical genetics; see Section 6.2.3.)

Early research in classical genetics had used higher plants and animals as experimental systems, *Drosophila* being the icon of classical genetics. While the study of higher organisms continued, a methodological novelty of mature classical genetics (from the 1940s onwards) was the increased use of microorganisms, such as fungi or bacteria. It became clear that bacteria like other organisms have stable phenotypic features that are genetically based, and that mutations of the genetic material occur. While bacteria neither reproduce sexually nor have a double set of linkage groups that recombine, they exchange genetic material. Ingenious experimental techniques permitted the demonstration that bacterial genomes are circular and that the individual genes are situated one after the other in a regular order, so that a bacterial genome is like a single linear linkage group of a higher organism whose ends are fused to form a circle (Wollman and Jacob 1955; Jacob and Wollman 1961). Fungi as eukaryotes have a chromosomal organization just like plants and animals and in many cases reproduce sexually. One advantage of using microorganisms for genetic research was the opportunity to handle, mutate and cross-breed huge number of individuals. This permitted the detection of rare mutations or rare recombination events (genes that are very close toward each other on the genetic material are very unlikely to recombine by crossing over, so that large sample sizes are needed). A new and very influential strand of research was phage genetics. Bacteriophages are viruses that use bacteria as their hosts. Like any virus, a phage carries a stretch of genetic material, inserts it into the host cell, where the inserted genetic material together with the cellular machinery of the host brings about the production of a huge amount of viruses, including replication of the viral genetic material. Upon destruction of the host cell, the viruses are released. The use of phages to study genetic phenomena was pioneered in the early 40s by the physicist Max Delbrück. Genetic analysis in higher organisms relied on the fact that these organisms have a double chromosome set, so that crossing over and recombination occurs, which provided the basis for establishing genetic maps. Even though nothing like this happens in phages, a bacterium could be experimentally infected with two distinct phage strains, modeling a classical Mendelian situation. X-rays were used to induce mutations in bacteria and phages, and in the early 50s genetic maps of some viral genomes were developed (Hershey and Rothman 1949; Benzer 1957).

One result of the genetic study of microorganisms was insights into the fine-structure of genes, as these experimental systems permitted the detection of rare recombination events. Classical genes are entities that have a physiological/phenotypic effect, that mutate, and between which recombination occurs. All three phenomena are obviously related as classical genetics is able to detect mutation and recombination only in terms of the phenotypic effect of genes, and to detect the phenotypic impact of genes in virtue of phenotypic differences between organisms due to mutations and recombination. Consequently, as mentioned in Section 6.1.2, in early classical genetics genes were often — though usually implicitly — understood to be *at the same time* 1) the smallest units of physiological function, 2) the smallest unit of mutation, and 3) the smallest unit of recombination. I also indicated that there was never real evidence for this assumption and soon so-called complex loci and other findings emerged that suggested a more complicated picture of genetic structure. As a result some classical geneticists questioned whether the units of physiological function, mutation, and recombination always aligned (Raffel and Muller 1940). Investigation into the fine-structure of genes of the 50s actually demonstrated that this is not the case. Mutations occur within a part of a gene as a macromolecule, so that the unit of mutation can be a tiny part of the chromosome that is smaller than a gene. More surprisingly, recombination may not only occur between distinct genes, but also within a gene (Oliver 1940; Lewis 1941, 1945; Green and Green 1949). There has to be a particular notion of 'gene' in play that permits one to state that mutation and recombination may occur within a gene. This is the idea that the gene is the *unit of physiological function*.

An operational definition of the gene as a unit of physiological function was given by the *cis-trans test*. Conceive of a gene as a continuous chunk of a chromosome (or a stretch of DNA) that has a distinct physiological effect (produces a genetic product by itself). Assume that you have two recessive mutations a and b that have the same phenotype (aa and bb yield the same mutant phenotype). These alleles could be mutations of distinct genes (loci) that happen to have the same phenotypic result. The *cis-trans* test establishes whether or not a and b are mutations of the same gene as follows. In a double mutant that has one a and one b allele, there are actually two possible situations (see Figure 9). Both mutations could be on one chromosome, which is called the *cis* position, so that the other, homologous chromosome is without any mutation: $a\,b\,/\,{+}{+}$ (writing $+$ for a wildtype allele). Or one of the mutations could be on one chromosomes and the other on the homologous chromosome, which is the *trans* position: $a{+}\,/\,{+}b$. If the two mutations are on loci belonging to *different* genes, then there is no phenotypic difference between the *cis* and *trans* situation. In each case the normal phenotype results, as mutation a is recessive and so is mutation

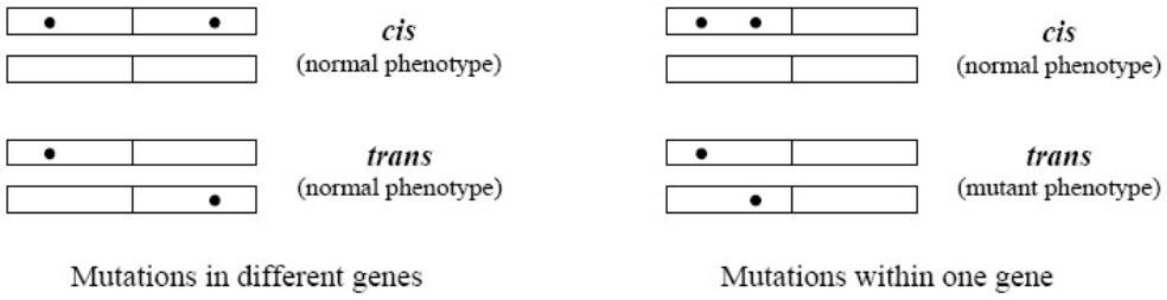

Figure 9: The *Cis-Trans* Test

b being on a distinct gene. However, if the two mutations are on two positions within the *same* gene, then a difference between the *cis* and *trans* case results. In this situation, the *cis* position ($a\,b\,/\,{+}{+}$) shows the normal phenotype — on one chromosome, there are two mutations within the same gene, while the gene on the homologous chromosome is wildtype, leading to normal phenotype as the mutation is recessive. In the *trans* situation ($a{+}\,/\,{+}b$), however, the mutant phenotype shows up — for on both chromosome the gene under consideration has a mutation (probably on different particular spots within each copy of this gene). Thus, the *cis-trans* test yields a different outcome depending on whether two mutations are part of the same gene (functional unit) or on separate genes, thereby providing an operational definition of a gene as a functional unit. This test was used in the 1940s in work on position effects, complex loci and pseudoallelism, when it was usually referred to as 'test of complementation' (Pontecorvo 1952; Carlson 1966). A basic version of it had actually been used by the Morgan school, where it was called the 'test of allelism', used to determine whether two alleles were variants of one gene or whether they belonged to two distinct genes (Waters 2004b; Weber 2005). The *cis-trans* test was refined by Seymour Benzer in his leading work in phage genetics, and he used it as part of his analysis of the genome of the T4 phage — examining the genetic fine-structure up to single nucleotides (Holmes 2000).

Building on previous work using classical genetic analysis, Guido Pontecorvo (1952), who studied the fungus *Aspergillus nidulans*, concluded that the unit of physiological function, the unit of mutation, and the unit of recombination are probably not identical.[7] Seymour Benzer (1957), focusing on phages that invaded the bacterium *Escherichia coli*, confirmed this idea and prominently drew terminological consequences by distinguishing three concepts: the *cistron* as the unit of physi-

[7]Interestingly enough, while the research tradition in which he worked led up to a picture of genes as particular stretches of DNA, Pontecorvo (1952) himself argued that the experimental results indicated that genes are neither sharply delineated portions of chromosome, nor megamolecules; rather, they are processes or functions (Holmes 2000).

ological function operationally defined by the *cis-trans* test, the *muton* as the unit of mutation, and the *recon* as the unit of recombination. This terminology did not catch on, but the term 'gene' came to be used (and had already been used to a substantial extent) in the sense of Benzer's cistron — a part of the chromosome with a distinct physiological function. The commentator Petter Portin (1993) refers to this as a 'neo-classical gene concept', which grew out of the classical gene concept and was used in the 50s before the advent of the molecular gene concept. This notion largely used a classical understanding of genes (being embedded in an experimental tradition that used classical genetic analysis in a refined fashion), but it embodied novel insights about the fine-structure of classical genes, namely, that mutation and recombination may occur within genes as units of physiological/phenotypic function. In the second half of the 50s these ideas were interpreted in the light of the then available knowledge that the genetic material is DNA, so that genes (cistrons) were conceived of as stretches of DNA consisting of nucleotides (Pontecorvo 1958).

The original implicit theoretical conflation of the unit of function, mutation, and recombination illustrates the semantic advantage of having a fine-grained type of content available, such as my notion of total inferential role (an individual's use of a term). In the case of some (though not all) classical geneticists their total inferential role of the term 'gene' allowed for an inference to each of these three characterizations of the gene. Originally, this did not create any contradictions in scientific practice, as the three units broadly align within the scope of the experimental tools of early classical genetics. Mature classical genetics' insights into the fine-structure of classical genes demonstrated the need to distinguish the gene concept from the smallest units of mutation and recombination, so that the total inferential role endorsed by geneticists was modified accordingly. There are different ways in which a concept can change, and studying the fine-grained total inferential roles of a term used by various individuals suggests ways in which the concept might change.

Whereas the work of Pontecorvo and Benzer used the concepts and tools of classical genetics to understand the *structure* of classical genes, earlier work of the 1940s shed light on the physiological *function* of genes. I am referring to the famous one gene–one enzyme hypothesis of George Beadle and Edward Tatum, who provided evidence that each gene determines the production of a particular enzyme, using classical genetic analysis of microorganisms combined with biochemical methods. While I stressed in Section 6.1.3 that for the most part classical geneticists did not have any idea of what the causal contribution of a gene is, this particular work in mature genetics established in some special cases which classical gene (identified by its phenotypic effect and chromosome location) has which functional effect in the sense of being responsible for a particular molecular

product. Beadle and Tatum suspected that each gene has a primary effect such as the production of a specific enzyme. Originally, they worked with eye color mutants of *Drosophila*, transplanting eye buds from one mutant onto an organism of a different genotype. For instance, eye buds from the mutant vermilion, which lacks the brown pigment of the normal red eye, became normal red on a wildtype host. Apparently, the wildtype host supplied a substance that was missing in the mutant eye bud, and the vermillion wildtype allele was responsible for producing precisely this substance. However, finding the precise biochemical effect of genes proved to be intractable with *Drosophila*, and soon Beadle and Tatum turned in the early 40s to *Neurospora crassa* (the pink bread mold) as a model organism. This fungus reproduces sexually and thus permitted Mendelian analysis. Furthermore, culturing techniques for fungi in strictly defined synthetic media had recently been developed. *Neurospora* needs nothing more than a minimal medium, consisting of minerals, glucose and the vitamin biotin, to grow. Several *Neurospora* mutants were found that did not grow on minimal medium, but on an enriched medium containing various chemical components. By selectively using differently enriched media, Beadle and Tatum could establish for several mutants which specific chemical substance each mutant failed to produce (such as a vitamin or an amino acid). Given biochemical knowledge that in organisms chemical substances are produced with the help of enzymes, a plausible interpretation was that in each mutant a particular enzyme was missing (normally produced by the wildtype allele), so that the mutant fails to generate a substance for whose production this enzyme is needed. Beadle and Tatum (1941) explicitly put forward the one gene–one enzyme hypothesis and offered preliminary support by showing for three *Neurospora* mutants that they had lost the ability to synthesize pyridoxin, thiamin, and para-aminobenzoic acid, respectively, and that each mutant differed from the wildtype by a single gene.

Subsequent studies offered more specific support for this assumption in the following way. Consider a biochemical pathway where one chemical substance S_{i+1} is produced from a previous substance S_i, where the reaction from S_i to S_{i+1} is catalyzed (made possible) by the enzyme E_i:

$$\ldots \xrightarrow{E_3} S_4 \xrightarrow{E_4} S_5 \xrightarrow{E_5} S_6 \xrightarrow{E_6} S_7 \xrightarrow{E_7} \ldots$$

In many concrete cases partial biochemical pathways were known, where several of the substances (chemical products) that were transformed throughout the pathway were established, though less was known about the structure of the individual enzymes involved apart from them being proteins consisting of amino acid chains. Take the case of a *Neurospora* mutant that fails to produce S_5, i.e., a mutant that grows on minimal medium only if S_5 or a later product in the synthesis (S_6, S_7, ...) is added to it. From these findings one can conclude that it is precisely enzyme E_4 is missing or

defective. (If an earlier enzyme such as E_3 were missing, then adding S_4 would restore growth; and if a later enzyme such as E_5 were missing, S_5 could not restore growth.) Thus, the likely interpretation is that in this mutant the gene that is mutated has the primary effect of producing enzyme E_4. Using this logic and experimental approach, Srb and Horowitz (1944) interpreted mutants that affected the ornithine cycle in *Neurospora crassa*. This biochemical cycle involves the substances ornithine, citrulline and arginine, among other then unknown intermediate components ($\ldots \longrightarrow$ ornithine $\longrightarrow \ldots \longrightarrow$ citrulline $\longrightarrow$ arginine $\longrightarrow \ldots$). Srb and Horowitz could point to four distinct genes (or the enzymes produced by them) that were involved in the synthesis leading up to ornithine. More importantly, they could show that two other genes were responsible for the steps between ornithine and citrulline, and another gene that determined the step from citrulline for arginine — apparently coding for the enzyme that transforms citrulline into arginine. Other studies offered similar results for different pathways in *Neurospora* and other microorganisms (Tatum and Bonner 1944; Tatum et al. 1944; Beadle 1945, 1946; Demerec and Demerec 1956). Even though the one gene–one enzyme hypothesis did not offer an account of how a genes produces an enzyme, it was a major step towards the molecular gene concept. While classical genetics until 1940 was unaware of the causal contribution of individual genes and had to conceive of them as difference makers — a mutated allele changes the overall constitution of an organism so as to bring about a mutant phenotype — the hypothesis put forward by Beadle and Tatum offered an account of the direct contribution of a gene. The one gene–one enzyme hypothesis had to be refined since an enzyme can be composed of several proteins/polypeptides, so that it in the 50s it became the one cistron–one polypeptide hypothesis. (While this idea was basically accepted until the end of the 70s, the Section 6.3 will discuss findings that show that a gene can code for several polypeptides and that some polypeptides are produced by several genes.)

The uncovering of the structure of DNA by James Watson and Francis Crick (1953b) triggered research that led to the establishment of the genetic code, the molecular gene concept, and molecular biology more generally.[8] Before the discovery of the double helix by Watson and Crick there had hardly been compelling evidence that DNA was the carrier of genetic information (Olby 1974). The genetic sequence of a whole chromosome consists of a single double-strand of DNA. Each strand of the double-stranded DNA consists of a long sugar-phosphate backbone, along which the four bases adenine, cytosine, guanine, thymine (A, C, G, T) are aligned, leading to a large string consisting of four letters (so-called nucleotides). Basically only one strand carries the genetic information (it

[8]For literature on the history of molecular biology see Judson (1980), Morange (1998), and Hausmann (2002).

came to be called the coding or sense strand), while the other strand (called antisense strand) is like its mirror-image due to complementary base pairing: A on one strand corresponds to T on the other strand, and C on one strand corresponds to G on the other one. Watson and Crick (1953a) immediately realized that this suggests a mechanism of genetic replication. The double strands disjoin, and the original sense strand acts like a template: it is complemented by a newly created antisense strand whose sequence is determined by base-pair correspondence. Likewise, the original antisense strand is complemented by a newly created sense strand, which consequently has the same sequence than the original sense strand. This way of creating two double strands out of one is called semi-conservative as one half of the original double strand goes into one daughter cell and the other half into the other daughter cell (Delbrück and Stent 1957).[9] Watson and Crick (1953a) already suggested a way in which mutations could occur, namely, inaccurate base pairing would lead to a modified DNA sequence which would be propagated.

Proteins, for which genes code, are polypeptides, i.e., long chains of amino acids (there are 20 amino acids). Thus, while a gene is a linear stretch of DNA written in a four-letter alphabet, a protein has likewise a linear sequence, written in a alphabet consisting of 20 letters.[10] Due to the one gene–one enzyme hypothesis, it was already known that a gene (now understood as a stretch of DNA) produces a protein. This triggered in the 50s a scientific race determined to solve the coding problem (Kay 2000). What is the *genetic code*, i.e. how does the DNA sequence of genes determine or map to the amino acid sequence of proteins? A first plausible assumption was the *colinearity hypothesis* (Gamow 1954). A codon is a set of nucleotides coding for one amino acid. The colinearity hypothesis maintains that the order of codons (along the DNA sequence) corresponds to the order of the amino acid chain.[11] Originally, researchers attempted to solve the coding problem in a theoretical-mathematical fashion, as a problem in cryptology. Numerous codes were proposed due to their chemical or logical plausibility. Let me give you a flavor of the 'code craze' by mentioning a few suggestions. Two nucleotides can code for at most 4×4 possibilities, so given that there are 20 amino acids, at least three nucleotides code for one amino acid (a set of three adjacent nucleotides is called a triplet). Given that the continuous nucleotide sequence is not physically structured into units (codons) that correspond to amino acids, does one of the

[9] In the early 60s, the enzyme that effects DNA replication was found (Kornberg 1960; Josse et al. 1961). The precise mechanism of DNA replication was uncovered later (Okazaki and Okazaki 1969; Kornberg and Gefter 1971).

[10] The first amino acid sequence of a protein to be determined was that of insulin, sequenced in 1955 by the group of Frederick Sanger (Ryle et al. 1955). Much later RNA (Brownlee et al. 1968) and DNA (Sanger et al. 1977) could be sequenced. Modern effective DNA sequencing methods became in the late 1980s (Saiki et al. 1985).

[11] Colinearity was proven by Sarabhai et al. (1964) for a gene of the T4 bacteriophage, by Yanofsky et al. (1964, 1967) for a gene of the bacterium *E. coli*, and by Sherman et al. (1970) in the eukaryote *S. cerevisae* (yeast).

bases symbolize a comma that structures the genetic message? Another suggestion was to assume that the code is overlapping, i.e., that some of the nucleotides coding for one amino acid are also part of another codon determining another amino acid (Gamow 1954; Gamow et al. 1955). Crick et al. (1957) concocted a comma-less code, where only some triplets were permitted, imposing a triplet structure on the continuous DNA. In their scheme, out of the 64 potential triplets, exactly 20 permitted ones remained to represent the 20 amino acids, which looked too perfect to be wrong (though it was wrong). Findings about the ratios of different bases in various microorganisms led to the suggestion that the code was degenerate, i.e., that several codons may code for the same amino acid (Crick 1963). Apart from the many speculations about the code, by studying mutants where one or more nucleotides were deleted or inserted Crick et al. (1961) demonstrated at least that a codon consisted of triplets. The various proposals and attempts to solve the coding problem in a information-theoretical fashion did not lead to any success (Sarkar 1996). The genetic code was established by biochemical research on protein synthesis. This work was not directed at solving the coding problem, rather biochemists attempted to create protein synthesis *in vitro* to understand its mechanism. Marshall Nirenberg was the first to develop a cell free *E. coli* system (Matthaei and Nirenberg 1961). A synthetic poly-U RNA (UUUUU..., corresponding to TTTTT... in DNA), which was added as a control, happened to produce a polypeptide chain consisting only of the amino acid phenylalanine (Nirenberg and Matthaei 1961). Apparently, the RNA triplet UUU (DNA triplet TTT) coded for phenylalanine. Soon other research groups used synthesized RNAs to determine which polypeptide chains they produced. Eventually, the coding problem was solved — purely experimentally rather than mathematically (Nirenberg et al. 1965; Khorana et al. 1966). It turned out the code is degenerate: every one of the 64 possible triplets codes for an amino acid (or a start or stop codon). As there are no commas in the DNA sequence and every arbitrary set of three adjacent nucleotides within a DNA sequence codes, the only feature that imposes a codon or triplet structure on a DNA sequence is the fact that genes begin with a particular triplet sequence, a so-called start codon. The genetic code is virtually universal, i.e., apart from a few exceptions, all species use the same DNA/RNA triplet $\rightarrow$ amino acid mapping (Hall 1979).

The polypeptide chain of a protein is not directly produced from the DNA sequence. Rather, there is an intermediate, messenger RNA (mRNA). RNA is chemically similar to DNA, and it likewise forms chains consisting of four bases (instead of thymine, it has uracil, yielding an A, G, C, U RNA alphabet). Gene expression proceeds in two steps (see Figure 10). First, a gene as stretch of DNA is *transcribed* into a single-stranded mRNA: The DNA double strand is opened and the mRNA

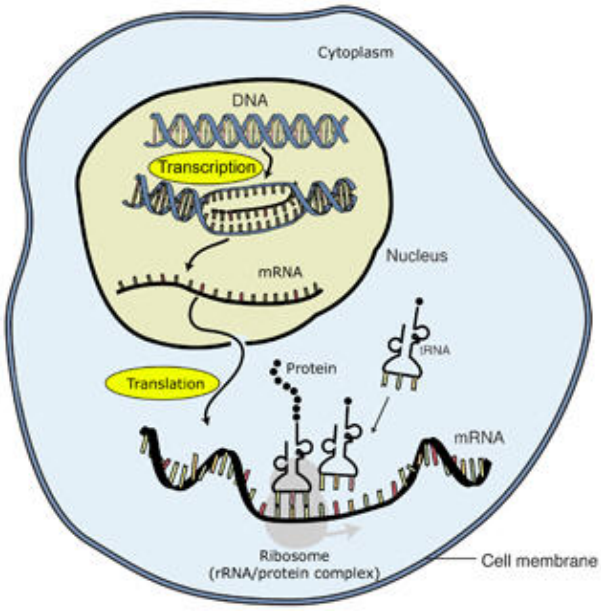

Figure 10: Transcription and Translation

forms at the antisense DNA strand due to complementary base pairing mediated by the enzyme RNA polymerase, which yields an mRNA with the same sequence as the sense DNA (though T being replaced by U). A gene as a stretch of DNA is delimited by a particular triplet sequence that marks its beginning, the start codon (which is preceded by a regulatory promoter sequence), and by a triplet that signals the end of the gene (a stop codon), so that transcription proceeds from the start to the stop codon. While transcription takes place directly at the DNA, the second step, *translation* occurs in the cytoplasm at the ribosomes. Then the polypeptide chain is produced from the linear mRNA sequence in accordance with the genetic code. The basic working of these mechanisms were uncovered in the 60s (Rheinberger 1997; Hausmann 2002). Francis Crick (1958) stated the basic causal order in the *central dogma of molecular biology*, which maintains that information flows from DNA to RNA, and from RNA to protein, but never the other way round (Thieffry and Sarkar 1998).[12] Due to this existence of the RNA intermediate, Jacob and Monod (1961) introduced the idea of a one gene–one messenger RNA hypothesis, in addition to the one gene–one polypeptide hypothesis. Thus, a gene came to be conceived of as a unit of transcription coding for messenger RNA, which is then translated to a polypeptide.[13]

[12]Information flow from RNA to DNA turned out to be possible, though. The genome of some viruses consists of RNA instead of DNA. These viruses come with the enzyme reverse transcriptase, which inside the host cell reversely transcribes the viral RNA to DNA (Baltimore 1970; Temin and Mizutani 1970).

[13]The one gene–one messenger RNA hypothesis is actually more widely valid, as not every gene codes for a

Apart from the basic structure of genes (sequence of DNA) and its function (production of a polypeptide in accordance with the genetic code), a further important aspect of the nature of molecular genes is the regulation of gene expression, i.e., the way in which genes are switched on and off. I shall address this issue in the subsequent section, as it is important for my account of explanations in molecular biology and the content of the molecular gene concept. Most early discoveries about the structure and function of genes were made in bacteria, in particular *Escherichia coli*, as the most simple living cells.[14] In 1968, the molecular biologist Gunter Stent published the controversial essay "That Was the Molecular Biology that Was", in which he announced that all important problems in molecular biology had been solved. However, as we shall see much later in the section on the contemporary molecular gene concept, research in animal and plant genetics from 1975 onwards revealed a whole range of surprising findings and novel challenges, which among other things showed that knowledge gained from bacterial genetics far from exhausts genetics.

6.2.2 The Content and Explanatory Potential of the Classical Molecular Gene Concept

This section gives my characterization of the classical molecular gene concept as established in the 1960s and used in the 70s. Though the 'classical' molecular gene concept differs from the contemporary molecular gene concept (discussed in Section 6.3), in the remainder of Section 6.2 I shall usually refer to it as the 'molecular gene concept', because at this stage the focus is on the contrast between the classical (Mendelian) gene concept and the molecular gene concept in general — thereby addressing features that do not set the classical molecular and the contemporary molecular concept apart. A central feature of the molecular gene concept is that it embodies knowledge about the function of genes, i.e., the way in which genes bring about their causal effects. Section 6.2.1 mentioned some features that bear on gene function: the fact that genes produce polypeptides (usually forming enzymes) with mRNA as an intermediate causal step. The structure of genes is relevant for understanding their function because the fact that genes are stretches of DNA together with the genetic code explains how the sequence of a particular gene brings about its product — a polypeptide with a specific amino acid sequence. A further significant aspect of genetic

polypeptide (or proteins and enzymes which largely consist of polypeptides). A few genes (so-called RNA genes) merely code for RNA, which is not translated into a polypeptide, but fulfills vital cellular functions as RNA.

[14] Among eukaryotes (fungi, plants, animals), the first species to be systemically studied by molecular geneticists was the yeast *Saccharomyces cerevisae*.

function is how gene expression is regulated: which conditions determine whether a gene's product is formed in a certain cell at a particular point in time? It turned out that it is gene transcription rather than translation that is primarily regulated. Thus, the central feature to understand is under what conditions a gene is transcribed to mRNA in a particular cell, which then immediately explains how the gene produces its final product: a polypeptide created from the mRNA.

The first major insights into the regulation of gene activity were obtained in the simplest living systems: single-celled bacteria. In the early 60s, the *lac* operon model provided an account of the regulation of one particular set of genes in *Escherichia coli*. This result grew out of the work of François Jacob, Jacques Monod, and their collaborators, who combined biochemical methods with the analysis of genetic mutants. The phenomenon that had been studied by Jacob and Monod for over a decade used to be called enzymatic adaptation (Monod 1947), and was later termed induction or repression of enzyme synthesis. It had been known since the beginning of the 20^{th} century that many enzymes of microorganisms were detectable only if their corresponding substrates (the chemical substance that the enzyme transforms into another substance) were available in the culture medium. Even simple organisms are apparently able to metabolically adapt to their environment and express certain genes coding for enzymes only under suitable conditions. In the case of *E. coli*, as soon as lactose is added to the medium, a galactoside-permease is produced inside the bacterium, an enzyme which increases the transport of the energy source lactose into the cell, and at the same time β-galactosidase is formed, which metabolically breaks down lactose into galactose and glucose. The induction of the synthesis of these two enzymes is very specific in that it is brought about only by lactose, hence called an inducer. The permease is coded for by the gene y (now *lacY*) and β-galactosidase by the gene z (now *lacZ*). The *lac* operon model of Jacob and Monod (1961) properly explained induction in the following way. The *lac* operon consists of three genetic elements immediately adjacent to each other on the genetic map: the *lac* operator o, gene y, and gene z. The operator DNA sequence does not code for a protein but has a regulatory function in the following sense. There is a further component inside the cell, a so-called repressor (later shown to be a protein), which binds to the operator sequence. If the operator is occupied by the repressor, the adjacent genes y and z are not transcribed into mRNA (the repressor blocks their expression). If the operator is unoccupied, expression of y and z occurs. The repressor is coded for by a different gene (i is the gene for this particular repressor). This gene is constitutively (constantly) expressed so that the repressor is always present in the cell. Induction occurs because the functioning of the repressor is sensitive to the presence of the inducer: While the repressor normally binds to

the operator, blocking expression, once the inducer (lactose) is present in the cell it binds to the repressor, which effects such a change in the three-dimensional structure of the repressor that it cannot bind any longer to the operator, so that the genes y and z adjacent to the operator are transcribed, leading to the production of galactoside-permease and β-galactosidase.

The operon model explains gene expression by making two important distinctions between different types of genetic elements (DNA sequences with different functions). First, there is the difference between genetic elements that are transcribed to mRNA and code for polypeptides and those that do not code for any product but serve a regulatory function. Whereas the genes i, y, and z code for products (the repressor, galactoside-permease, β-galactosidase, respectively), the DNA sequence of the operator is not transcribed, but it is such that a protein (the repressor) can bind to it, thereby regulating the transcription/expression of the adjacent genes. The second distinction is between structural genes and regulator genes (Jacob and Monod 1959, 1961). y and z are structural genes as they code for products that fulfill metabolic and similar functions. The gene i, in contrast, is a regulator gene as it codes for a product (a repressor in this case) that regulates other genes by binding to DNA. Thus, a regulator gene (mediated by its product) regulates structural genes. Later molecular genetic studies of eukaryotes (fungi, plants, animals) from the 1970s onwards revealed that the mechanism of gene expression and regulation in eukaryotes is substantially more complicated than in bacteria. Still, Jacob and Monod's two basic distinctions between different genetic elements are still valid. With respect to their distinction between regulator genes and structural genes, biologists nowadays usually talk about *regulatory genes* as opposed to *structural genes*. A regulatory gene codes for a so-called transcription factor, which directly binds to DNA. Structural genes code for other types of products, which may provide components of the cell structure, carry out biochemical reactions, or support cell-cell communication.

Jacob and Monod's distinction between coding genetic elements and non-coding, regulatory genetic elements (which they terminologically made by keeping genes apart from operators) is nowadays made terminologically explicit by distinguishing between the *coding region* and the *regulatory region* of a gene (or simply between 'coding sequences' and 'regulatory sequences'). Bacterial genes are often organized in operons, consisting of a regulatory sequence (an operator) and several adjacent genes (y and z in the above case) whose joint expression is regulated by the operator. In eukaryotes, however, different genes are typically regulated by distinct regulatory sequences.[15]

[15]Originally, operators by themselves were sometimes referred to as genes (so-called operator genes). This usage reflected a classical gene concept. An operator behaves in many ways like a Mendelian allele, for instance, mutations in an operator (non-coding sequence) just like a mutation in a gene (coding sequence) leads to a genetically based

There are two basic types of eukaryotic regulatory regions. Promoters are located immediately in front of the coding region of a gene (they have a characteristic DNA sequence that does not vary much across different genes and species). The promoter is the spot to which the RNA polymerase binds. RNA polymerase is the enzyme that produces the mRNA, so that the binding of the RNA polymerase starts transcription of the subsequent coding sequence of the gene. In addition, eukaryotic genomes contain enhancers and silencers as regulatory sequences, which can be located relatively far apart from the gene they regulate (they are often but need not be upstream of the particular gene). Transcription factors bind to enhancers and silencers, and thereby influence the ability of the RNA polymerase to bind to the promoter of the corresponding gene. A silencer is a sequence to which a transcription factor binds that represses or downregulates the transcription of the corresponding coding region. An enhancer, in contrast, upregulates gene expression. A eukaryotic gene can be under the influence of several enhancers and silencers, and the binding of many transcription factors can influence the transcription of a single gene, permitting fine-tuned gene regulation in multi-cellular organisms (Singer and Berg 1991; Alberts et al. 1994).

At this point I want to offer some remarks on explanation and theorizing in molecular biology by introducing the notion of an *explanatory strategy*. This idea is relevant in the present context as I conceive of the molecular gene concept as embodying such explanatory strategies, which accounts for how this concept supports explanations. An explanatory strategy is a conceptual/theoretical schema, which involves different concepts that make reference to certain structural entities and their functional relationship such that this schema gives an explanation encompassing several biological concrete mechanisms or processes. Explanations in molecular biology are often viewed as attaching to molecular mechanisms (Glennan 1996; Machamer et al. 2000; Tabery 2004). An explanatory strategy, however, is not a particular explanation that describes a specific (type of) mechanism, rather it is like a schema in that it gives a more abstract characterization that can be applied to many concrete cases, describing what several mechanisms have in common. An explanatory strategy obtains generality as it specifies only certain parts of a mechanism or only certain steps in a sequence of events, so that in order to advance a complete explanation of a molecular process, different explanatory strategies have to be combined and applied to a concrete situation.

One example of an explanatory strategy may be termed 'gene regulation'. As the genetic material in a cell is the same across time and across the different cells of an organism, an account

phenotypic difference. However, this early usage was soon abandoned. Nowadays a regulatory sequence by itself is never referred to as a gene. The term 'gene' either refers solely to the coding region of a gene, or to the coding region plus the sequences that regulate it (the context makes usually clear which usage is intended).

of differential gene expression has to invoke material factors apart from genes and DNA. This is achieved as the explanatory strategy of gene regulation makes the central distinction between regulatory and coding DNA sequences, and includes the idea that cellular entities (RNAs or proteins) bind to specific regulatory DNA sequences so that the transcription of the corresponding coding sequence is positively or negatively influenced. Given the idea that a DNA-binding entity has a particular specificity for its target, differential gene expression of a gene is thereby explained by the varying presence or binding-ability of entities that can bind to a particular regulatory region of this gene. Beyond the distinction between regulatory and coding sequences demanded by the basic explanatory strategy, different types of or subcomponents of such sequences may be distinguished, e.g., different parts of a coding region (start codon, stop codon, exon, intron) or different types of regulatory sequences (promoters, enhancers, silencers). Another distinction implied by this explanatory strategy is the distinction between regulatory and structure genes (only regulatory genes code for products that have a regulatory function by binding to DNA). My preceding discussion of the operon model of Jacob and Monod (1961) made plain that their account of the regulation of the *lac* operon already embodied what I call the 'gene regulation' explanatory strategy. An explanatory strategy is more abstract than an explanation of a type of mechanism or a molecular model. For instance, the operon model makes some more specific assumptions that do not hold for all cases of gene regulation (e.g., the idea that the DNA-binding molecule always acts as a repressor of gene expression, or the idea that an operator regulates several adjacent structural genes). An explanatory strategy can apply to various and quite different types of cases. Using the gene regulation strategy, biologists and biomedical researchers may account for a temporal change of a cell (e.g., the onset of the production of β-galactosidase due to the presence of lactose), for a spatial difference as in cellular differentiation (developmental biology explains differences between distinct cells of an organisms with reference to differential gene expression), or for a difference between two organisms (e.g., a healthy individual and one with a certain disease).[16]

My notion of an explanatory strategy bears some resemblance to the notion of an 'explanatory schema' as developed by Philip Kitcher (1981, 1989, 1993). There are some differences between these two accounts though, and my notion of an explanatory strategy can be viewed as such a modification of Kitcher's approach as to yield a more adequate account of explanation for the

[16]Many textbooks describe the genetics of prokaryotic and eukaryotic systems in different chapters. Alberts et al. (1994), however, start their overview of gene expression with an example of a single activator in bacteria. Their next case is the regulation of the *lac* operon by means of an activator and repressor, and then they turn to a broad account of the situation in eukaryotes. All these different examples make use of the one explanatory strategy considered here.

context of molecular biology. First, as Kitcher's account is part of his deductivist-unificationist theory of explanation, Kitcher assumes that explanations are formal, deductive inferences, so that an explanatory schema is a deductive inference scheme. Section 3.1.4, however, offered support for the suggestion that scientific inference is not formal, but material inference, i.e., an inference is good not in virtue of falling under a formal scheme of deduction, but in virtue of the empirical concepts occurring in it. I stated that I view material inference as the genus encompassing different forms of scientific reasoning: reasoning involved in confirmation, discovery, and also explanation. Material inference can capture explanation as material inferences may be counterfactual-supporting, and they may involve concepts specifying the causal properties of certain entities. In contrast to Kitcher formal-deductivist account of explanation, I assume that an explanatory strategy consists of several *material* inferences, thereby necessarily involving empirical concepts. Second, most of Kitcher's examples of explanatory schemata are quantitative (involving formulas or numerical relations). An explanatory strategy as used in molecular biology may, but need not be quantitative.

Third, Kitcher assumes that a particular explanation is an instance of a single explanatory schema. My account, in contrast, emphasizes that explanations in molecular biology (and in biology in general) typically involve *several* explanatory strategies. For instance, in their account of the regulation of the *lac* operon, Jacob and Monod (1961) did not just make use of the strategy that I termed 'gene regulation'. Another central principle was the idea that the functioning of the repressor is sensitive to the presence of lactose. The binding of lactose with the repressor so modifies the latter that it loses the capacity to bind to the DNA sequence of the *lac* operator (now permitting transcription of genes y and z). Monod (1966) used the term 'allosteric transition' to refer to the fact that a molecule can switch between two states (in which this molecule has different structures and functions) depending on whether other molecules bind to it. This yields in fact another significant explanatory strategy that applies to various cases in biochemistry and molecular biology beyond gene regulation. The particular biochemical function of a macromolecule such as an enzyme (its ability to bind to other molecules and support certain chemical reactions) depends essentially on its three-dimensional shape (conformation). An interaction of such a molecule with other ones (even the binding of a small molecule to a huge enzyme) can change the conformation and thereby the function of the former. In the case of explanations of development, an entity produced in one cell may influence gene expression in an adjacent cell. Consequently, a full account of such an instance of gene regulation has to address the interaction between cells (extracellular messengers, receptors, and signal transduction in the cytoplasm). Thus, an understanding of the different

causal steps in a particular mechanism or pathway may involve the usage of different explanatory strategies. Explanatory strategies are building blocks that can be combined in various ways to yield explanations of concrete cases. Unlike Kitcher, I assume that a successful explanation in biology involves several explanatory schemata/strategies and various empirical concepts, which typically refer to several levels of biological organization. Given traditional philosophical construals of a scientific theory, the body of knowledge of molecular biology is only poorly described as consisting of one or several theories (Sarkar 1998). As an alternative to 'theory', my suggestion is that the notion of an explanatory strategy captures one important aspect of theoretical knowledge (knowledge that has a certain generality and yields explanations) in molecular biology.

Now it is time to offer an account of the (classical) molecular gene concept. It is common to assume that unlike the classical gene concept, the molecular gene concept essentially involves knowledge about the structure of genes (Kitcher 1984; Waters 1994). Molecular genes are typically conceived of as stretches of DNA, bounded by specific structural elements such as a start codon, a stop codon, and a promoter (each of which is characterized by a certain sequence). Scientific definitions often characterize a gene in purely structural terms as an *open reading frame*, i.e., as a stretch of DNA within a start and stop codon preceded by a promoter (Fogle 2000; Stotz and Griffiths 2004; Stotz et al. 2006). I do not assume that the *classical* gene concept is functionally defined whereas the *molecular* gene concept is purely structurally defined, as some molecular 'definitions' of the gene may suggest. Rather, the content of both the classical and the molecular gene concept substantially involves functional considerations, though quite different functional considerations which have fundamentally different implications about the relevance of structural features for a concept of the gene. To explain this idea, a first point to make is about my prior characterization of the classical gene concept in Section 6.1.3. There I argued that the classical concept does not embody assumptions about the material nature of genes, and that it instead defines genes in terms of their function or role in phenotypic inheritance. However, this does not mean that the classical gene concept does not involve any beliefs about material entities and processes. For I pointed out that this gene concept embodies knowledge about the chromosome theory of inheritance, more specifically, about cellular processes such as cell division, gamete formation and fertilization, the behavior of chromosomes in each of the processes (including chromosomal crossing over), and the association of genes with chromosomal locations. These basic assumptions about a few cellular and organismic processes are necessary to account for patterns of inheritance. While some material assumptions are needed to account for the functional role of genes in inheritance, it does not presuppose any

knowledge of the material nature of genes as such, i.e., no assumptions about the internal structure of and boundaries between genes, and their chemical and physiological properties.

The second — and more central — point to make is that functional considerations are essential for the molecular gene concept as well. This is not the functional role of genes in inheritance, as molecular genetics is not concerned with explaining patterns and processes of inheritance. Rather, molecular biology attempts to explain the workings of biochemical and physiological processes occurring inside cells. Consequently, a molecular gene concept is intended to explain how genes figure in and influence these processes. At this point I recall my tenet from Chapter 3 that the content of a scientific concept is not (or not fully) given by certain analytical statements or definitions (be they structural or functional), and that concepts instead exhibit a more complex structure. Sections 3.1 and 3.3.3 suggested that one important aspect or dimension of the content of a scientific concept is the *epistemic goal* pursued with its use. In the case of the molecular gene concept, the central theoretical and explanatory purpose for which this concept is used is to account for the production of molecular substances important for the cellular machinery (such as RNA and polypeptides), which has to include an account of gene expression, i.e., of what determines the differential production of gene products. A structural understanding of genes is important for molecular biologists precisely because a gene's structure explains its molecular function. This involves the fact that genes are stretches of DNA delineated by certain structural elements (sequences) such as promoters, start codons, and stop codons, which determine where transcription begins and ends, thereby specifying a unit of transcription. Knowledge about these different structural elements is necessary to explain how a gene creates a messenger RNA, and further knowledge of the genetic code (the DNA/RNA sequence → amino acid sequence mapping) is essential for understanding how a gene determines a polypeptide with a particular sequence. In sum, both the classical and the molecular gene concept involve functional considerations as they are intended to explain biological processes (inheritance vs. synthesis of molecular entities). Both concepts consequently involve certain physical assumptions, though only in the case of the molecular gene concept knowledge about the physical structure of genes. One dimension of the content of the molecular gene concept is that the epistemic goal pursued with its use is to explain gene *function*, while another aspect of its content — inferential role — includes information about the molecular function and in particular the *structure* of genes as this knowledge is necessary to actually meet the epistemic and explanatory goal.

Molecular biology in the 1970s — and thus the *classical* molecular gene concept — assumed that there is a one–one correspondence between genes (characteristic DNA sequences) and genetic prod-

ucts. Consequently, a functional definition of genes (such as 'a gene is that molecular entity that codes for the production of a polypeptide') and a structural definition (such as 'a gene is an open reading frame, i.e., a stretch of DNA within a start and stop codon preceded by a promoter') appear to pick out the same entities. In the past this led many to assume that molecular genes are purely structurally defined entities. For instance, the biologist Christopher Epp (1997) argued that the decision of whether or not a stretch of DNA is a gene can be made independently of the functional consideration of whether this gene is expressed. However, my reply is that any structural characterization of genes gains it legitimacy from functional considerations — the rationale of 'gene' talk is to account for certain molecular processes, namely, the biosynthesis of specific RNAs and individual proteins. A structural characterization of genes as continuous open reading frames is adequate *to the extent to which* these and only these structural entities bring about a polypeptide. One item of evidence for this is the more recent development of the molecular gene concept — to be discussed in Section 6.3. Empirical findings of the last two decades show that the genetic entities coding for a product form a structurally very heterogeneous kind. This led to a change in the molecular gene concept changed (more precisely, its inferential role involving structural considerations): the *contemporary* molecular gene concept emerged due to the fact that the molecular gene concept is also functionally in nature, together with novel findings about the structural basis of genetic function. Thus, this later discussion will provide crucial evidence for my tenet that the content of the *classical* molecular gene concept already involved an essential functional component, even though in the 70s and 80s this fact was masked by the alleged availability of a unique, purely structural definition that picks out the seemingly homogeneous structural kind that fulfills this function.

At this stage of my historical discussion — molecular biology until the 1970s — the evidence for the idea that content of the classical molecular gene concept includes the epistemic goal of accounting for gene function is twofold. First, in the history that led to the establishment of the molecular gene concept, genes had been viewed as the materially inherited units of physiological function. The one gene–one enzyme hypothesis offered in the 40s the first concrete insights into the functional contribution that individual genes have for cellular biochemistry and physiology. Once it became clear in the 50s that the unit of physiological function, the unit of recombination, and the unit of mutation are not identical, the reaction was not that the unified, Mendelian concept of the gene had to be abandoned, rather the gene concept became immediately identified with the notion of a cistron, i.e., stretch of the genetic material that makes an independent functional contribution by being responsible for the production of an enzyme (Stotz and Griffiths forth.). Second,

molecular biologists in the 70s were fundamentally concerned with putting forward explanations of the influence genes have on cellular biochemistry and the regulation of physiological processes. (This explanatory concern is very different from the study of inheritance conducted by classical geneticists.) An account of the successful use of the classical molecular gene concept has to take into account that it was actively used to account for genetic function (coding).

In his discussion of the classical and the molecular gene concept, Ken Waters (1994) offers a characterization of the classical gene concept that is largely identical to mine in Section 6.1.3. For this reason, his contrast of the classical and the molecular gene concept, assuming conceptual progress, may seem like a forerunner of my present position. One difference between Waters' and my account is the fact that only my discussion makes use of a framework of concepts that offers an explicit semantic defense of my characterization of different gene concepts. For instance, my account of the content of the molecular gene concept semantically distinguishes between the epistemic goal of its use (which involves gene function) and particular definitions of genes as part of the term's inferential or conceptual role (which involves gene structure). Another difference between Waters' and my position is that only my account stresses the way in which the molecular gene concept figures in explanations of gene regulation. Waters (1994), in line with some biologists such as Epp (1997), argues that the term 'gene' should refer only to sequences that code for a product (the open reading frame), but not include regulatory sequences such as promoters and enhancers. This is a normative suggestion as in actual usage the term 'gene' often (though not always) refers to the coding region *plus* the regulatory sequences that influence its transcription (e.g., biologists may talk about the 'coding region of a gene', thereby using 'gene' so as to include regulatory regions). On the one hand, this terminological recommendation reflects the legitimate idea that the coding sequences and regulatory sequences are different in nature. Only in the case of the former the linear DNA sequence digitally encodes information about a polypeptide in accordance with the genetic code (while a regulatory region is not transcribed and the binding of transcription factors to such a DNA sequence is an instance of analogue control and works without anything like a genetic code). On the other hand, Waters' terminological suggestion ignores the functional significance of regulatory regions which are important structural components, determining that a gene creates a product in the first place and influencing how gene expression is regulated across time or across different cells. The fact that in some contexts the term 'gene' is used so as to include the regulatory regions of a gene as well shows that the actual usage of the gene concept is based on functional considerations. The point I want to make is that even if biologists exclusively used the term 'gene' to refer to

nothing but coding regions, the fact that the *referent* of the gene concept excluded regulatory sequences would not entail that the *meaning* of this concept would not involve knowledge about gene regulation. Unlike Waters' and many other previous construals of the molecular gene concept, my account emphasizes that this concept is essentially used to advance explanations about how the regulation of gene expression influences biological processes.

To sum up my characterization of the classical molecular gene concept, unlike the classical (Mendelian) gene concept, possession of the molecular gene concept presupposes detailed assumptions about the structure and molecular function of genes. This includes the idea that genes are stretches of DNA, knowledge of the structure of double-stranded DNA, mRNA, polypeptides, notions such as open reading frame, triplet, start codon, stop codon, promoter, enhances, silencer, and knowledge of entities such as DNA polymerases, RNA polymerase, and transcription factors. The molecular gene concept also embodies knowledge about the processes in which these entities figure, including transcription, translation in accordance with the genetic code, binding of transcription factors to DNA and their regulatory influence. (The precise set of beliefs embodied by the molecular gene concept changed somewhat in the course of the history of molecular genetics based on novel findings.) These detailed beliefs about molecular entities and processes are part of the inferences that specify the content of the molecular gene concept (its inferential role), as this concept supports explanations of how genes bring about products that are important for the cellular machinery and of how gene expression is regulated. In particular, the molecular gene concept embodies several explanatory strategies as discussed above, including how gene regulation is explained based on the difference between regulatory and structural genes, the difference between regulatory and structural sequences, and the modification of the action of transcription factors. The subsequent section, which deals with the difference between the classical and the molecular gene concept and the rationality of conceptual change, will offer additional discussion of the explanations supported by the molecular gene concept, i.e., its explanatory potential.

6.2.3 Conceptual Progress Without Reduction and Stable Reference

Based on my characterization of the classical and of the molecular gene concept (Sections 6.1.3 and 6.2.2), I argue that the transition from the classical to the molecular gene concept is an instance of rational semantic change and conceptual progress, even though it meets neither of two criteria that have often been viewed as either sufficient or necessary conditions for progress: 1) reduction of

the classical gene concept to molecular genetics as a sufficient condition for progress, and 2) stable reference across theoretical change as a necessary condition for conceptual progress.

When the first generation of logical positivists argued for a 'unity of science', they merely tried to show that concepts from different scientific fields (including mathematics) could be expressed in a common language. Some subsequent philosophers of science, however, tended to endorse the substantially stronger idea that some or all scientific knowledge could be derived from a basic theory, such as physics (Kemeny and Oppenheim 1956; Oppenheim and Putnam 1958). A prominent account along these lines was the notion of theory reduction, as developed by Ernest Nagel (1949, 1961). Theory reduction is the idea that the statements of one theory (the reduced theory) can be formally deduced from another theory (the reducing theory). Given a D-N model of explanation, such a deduction actually implies that the reducing theory can explain all the laws, principles and claims of the reduced theory — justifying the label *reduction*. The idea of theory reduction also yields a way in which theoretical *progress* can occur, namely, if a mature theory can reduce an earlier theory from the same domain, such as relativity theory being able to reduce classical mechanics. Theory reduction presupposes in particular that the concepts of the reduced theory can be reduced to the notions of the reducing theory, and this was one of the tenets that Paul Feyerabend (1962) attacked when putting forward the idea of incommensurability, arguing for instance that the concepts of classical and relativistic mechanics are incommensurable. In the philosophy of molecular biology, a prominent debate in the 1970s and 80s occurred regarding the question of whether classical genetics could be reduced to molecular biology (or biochemistry).[17]

For the most part, the reduction debate about genetics was settled in favor of the anti-reductionists. A central question was whether the classical (Mendelian) gene concept could be reduced to molecular biology. I do not want to rehearse the various arguments put forward in this debate (for a review see Brigandt and Love forth.); in fact, I assume that my account of the relation between the classical and molecular gene concept provides a more fruitful way of understanding these concepts. To give a brief overview, a very useful notion to understand the debate is Jerry Fodor's (1975) distinction between *token-token* and *type-type reduction*. While Steven Kimbrough (1978) applied this distinction to the reduction debate in genetics, unfortunately it has hardly been explicitly used ever since in the philosophy of biology. Token-token reduction is a very weak notion, it is about whether one can explain a token phenomenon in a reductive fashion. The stronger case of

[17]Balzer and Dawe 1986a, 1986b; Darden and Maull 1977; Goosens 1978; Hooker 1981; Hull 1972, 1974, 1976, 1979; Kimbrough 1978; Kitcher 1982, 1984; Maull 1977; Rosenberg 1985, 1993; Ruse 1971a, 1971b, 1973, 1976; Sarkar 1992, 1998; Schaffner 1967a, 1967b, 1969a, 1969b, 1974b, 1976, 1993, 1996; Vance 1996; Waters 1990, 1994; Wimsatt 1976.

type-type reduction obtains when it is possible to offer a reductive, though unified explanation that covers many instances of a type of phenomenon. Token-token reduction was never controversial in the reduction debate about genetics, as it directly follows from materialism/physicalism, i.e., the idea that the life processes of an organism supervene on physico-chemical processes. Reductionists, when arguing that classical genetics can be reduced to molecular biology, typically endorsed a variant of Nagel's strong notion of theory reduction — while anti-reductionist denied this. Thereby the reductionists committed themselves to showing that the concepts of classical genetics can be type-type reduced to molecular biology, while (being partially unaware of the distinction) they actually offered arguments for mere token-token reduction (Ruse 1973; Goosens 1978; Waters 1990).[18] An illustration of this is Ken Schaffner's (1993) 'general reduction-replacement model', a refinement of Nagel's account. Schaffner's main example that is offered as support for the possibility of reduction addresses the Mendelian concept of 'dominance'. According to his account, given certain classical genes a and b, the property 'allele a is dominant (relative to allele b)' can be expressed in molecular terms as follows. Assume that the genotype aa yields phenotype A and genotype bb corresponds to phenotype B, while ab yields A (because of dominance). We figure out that gene a consists of DNA sequence α and gene b consists of DNA sequence β, and that phenotype A is brought about by protein ℵ; while phenotype B is brought about by protein ⊐. This yields the following 'reduction':

> allele a is dominant (relative to b) iff
> the presence of two copies of DNA sequence α molecularly produces protein ℵ [thus phenotype A], the presence of two copies of sequence β produces protein ⊐ [phenotype B], and the presence of one copy of α and one copy of β produces ℵ [phenotype A]. (Schaffner 1993, p. 442)

While Schaffner explicitly claims to have shown that the *concept* of dominance (a binary predicate) can be reduced to the language of biochemistry, his evidence actually shows how a single *instance* of dominance (dominance of specific allele a over allele b) is brought about by particular states on the molecular level — restating the uncontroversial idea of token-token reduction/materialism.[19]

Anti-reductionist have shown that even single concepts from classical genetics such as 'gene' or 'dominance' cannot be reduced to the notions of molecular biology as required by a strong notion

[18] The same pattern re-emerges in a recent debate about whether developmental biology can be reduced to developmental genetics (Rosenberg 1997; Laubichler and Wagner 2001; Frost-Arnold 2004; Delehanty 2005; Weber 2005; Brigandt and Love in prep.).

[19] There is another striking defect of Schaffner's reductionism. Molecular genetics can avail itself of the notion of genes as causal difference makers: the *difference* between phenotype A and phenotype B in two organisms (referred to by Schaffner) can be explained by a difference in DNA sequences — relative to a genetic, cellular and environmental background. Schaffner, however, is committed to formally deduce a complete phenotype such as A from molecular premises — not just phenotypic differences. He may fail to realize that the presence of phenotype A follows deductively from the presence of protein ℵ only if a specification of the *total cellular and organismal* surrounding of this protein is added to the premises; at least he begs the question by simply assuming that a molecular specification is possible.

of reduction (Hull 1974; Kimbrough 1978; Kitcher 1984). This is due to the fact the phenomena of classical genetics are multiply realizable on the molecular level. In the case of the above example of dominance, Schaffner's biconditional holds for some but not for many other instances of dominance. The basic reason is that dominance is about gross phenotypic features, and since there are many steps in the causal network leading from DNA sequences to the production of such a phenotype there are different molecular ways in which a certain final phenotype can be brought about. For example, a mutant phenotype B may result whenever no protein similar to א (which yields normal phenotype A) is produced, which may happen if only protein ב is produced that does not fulfill the function of א, or if no protein is produced at all. Thus, in some individuals a being dominant over b is due to allele b corresponding to DNA sequence β_1 which produces protein ב (as Schaffner assumes in the above account), while in other individuals it is due to b corresponding to sequence β_2 which fails to produce a protein, resulting in phenotype B nonetheless. In this case Schaffner's molecular formula (the right-hand side of the above biconditional) gives a sufficient, but not a necessary condition for dominance. The example also shows that even a quite specific instance of dominance such as allele a being dominant over b — which can occur in different individuals of a species and thus encompasses several token cases — can be realized differently on the molecular level in different individuals. In general, a higher-level kind or process as studied by classical genetics usually corresponds to various different kinds and processes on the molecular level. Consequently, a different molecular account has to be given for each distinct molecular way in which the higher-level kind can be instantiated, which forfeits a unified reduction as required by type-type reduction (Fodor 1975). The same applies to the classical gene concept. A difference in a single Mendelian gene, leading to a phenotypic difference between individuals, can — depending on the particular case and molecular context — be due to differences that are of a different molecular kind: a mutation in an exon within a gene's coding region, a mutation in an intron (not translated/coding) within a gene's coding region, a mutation in a gene's promoter, or a mutation of the enhancers or silencers of a gene. Furthermore, a mutation may lead to the molecular situation that no mRNA is transcribed, that an mRNA is transcribed but not translated, that a polypeptide is produced which is nonfunctional, or that a polypeptide is produced that slightly differs in function so as to finally yield to a different organismic phenotype. In addition to the idea that the concepts of classical genetics cannot be reduced to molecular biology, anti-reductionists have argued that the phenomena studied by classical genetics are still explained in the most successful and unifying way by the traditional concepts of classical genetics — concepts that primarily refer to entities and processes above the molecular level, such as processes involving

the behavior of whole chromosomes and cells (Kitcher 1984).

Some disputants in the reduction debate such as Waters (2000) seem to have assumed the following false dichotomy: either everything can be explained using molecular notions only, or there is an autonomous theory/discipline of classical genetics that has its own laws, concepts, and level of explanation and therefore could not benefit from the idea of molecular biology. This dichotomy is highly inadequate as the notions of molecular biology shed some light on the phenomena of classical genetics, as due to the possibility of token-token reduction molecular notions can contribute to understanding exceptions to the principles of classical genetics that obtain in some cases. In such a case, enriching classical with molecular notions provides an improved explanatory framework. Vice versa, molecular biology benefits from classical notions. Section 6.1.4 discussed how the classical gene concept is still used in contemporary population genetics, but molecular genetics itself — in spite of developing the predominantly used molecular gene concept — has continued to make significant use of the classical gene concept (Vance 1996; Weber 2005). Though there are several examples from the practice of molecular biology, I only mention one case that illustrates the usage of the classical concept and its interplay with the molecular concept. This is the significant method of identifying molecular genes based on molecular cloning and chromosomal walking, as used before the 1990s (see Weber 2005 for a more detailed discussion). Molecular cloning consists in chopping up the whole genome of an arbitrary organism into smaller fragments of genetic material, each of which is stored within a different bacterial cell (yielding a so-called a genomic library). The repeated division of one such bacterium yield copies (so-called clones) of this genetic segment, which can be subjected to further analysis. Chromosomal walking used to be the main way of relating DNA fragments (containing *molecular* genes) with loci on genetic maps showing the position of *classical* genes on chromosomes. Given a target allele to be identified molecularly, chromosomal walking starts out with a previously known molecular gene (cloned DNA fragment) that is located on the chromosome map as closely as possible to the target locus. The first step is to find a DNA fragment from the genomic library that overlaps with the starting fragment on the end of the starting fragment that is closer toward the target locus. Given the known chromosomal location of the starting fragment, the physical overlap of the two DNA fragments yields the location of the new fragment, which happens to be a DNA fragment closer toward the target locus. Repeated use of this method yields a sequence of overlapping DNA fragments — a walk on the chromosome towards the target locus. If finally a DNA fragment is found that covers the target locus and that is small enough, its DNA sequence can be determined, yielding information about the number and structure

of the genes (thereby molecular genes) contained in this fragment (located at this classical locus). Molecular cloning, chromosomal walking and genetic sequencing are based on the idea that genes are particular stretches of DNA and thereby on a molecular understanding of genes. In particular, chromosomal walking involves *in situ* hybridization, i.e., checking whether a radioactively labeled small DNA fragment binds with chromosomal DNA and thus fits with its sequence. At the same time, chromosomal walking presupposes *classical* cytological and genetic techniques, in particular genetic mapping that identifies classical loci on chromosomes. Moreover, a standard way of verifying that a cloned DNA segment corresponds to the intended classical gene consists in inserting this segment into a mutant. If the inserted sequence recovers the normal phenotype, it is established that it in fact contains the wildtype allele that the mutant lacks. This method is similar to basic criteria of identifying classical genes as units of function: the test of allelism of early classical genetics or the method of complementation (the *cis-trans* test) of mature classical genetics. Given that the identification of molecular genes involves the classical gene concept, the example shows that the classical gene concept continues to be used at least for experimental purposes.

In sum, neither can the classical gene concept be reduced to purely molecular notions, nor has it been fully replaced by the molecular gene concept. Given that molecular biologists use both the classical and the molecular gene concept, the question of whether the classical concept can be reduced to molecular theory is not fruitful as such (Vance 1996). The relation between the classical and molecular gene concept is more complex: while each concept supports particular types of explanations and has specific virtues, in some cases their combined use is necessary to achieve successful experimental investigation and theoretical explanation.

While reduction is a sufficient condition for progress, *unchanging reference* has often been viewed as a necessary precondition for conceptual progress to occur, as discussion surrounding issues such as realism, incommensurability, and the pessimistic meta-induction show. The motivation for this idea is that only in the case of stable reference can one say that later scientists have an improved conception of the very same entity that earlier scientists referred to, whereas in the case of reference change the assumption is that our novel conception is simply about another object.[20] However, the reference of the gene concept has changed throughout its history (and the discussion on the contemporary molecular gene concept will explain how its reference changes from context to

[20] A referee for the *British Journal for the Philosophy of Science* insists on this tenet in general and regards the reference of the gene concept: "To show conceptual progress, one must show change while defending the claim that the change occurred between two representations *of the same thing*, so that the pessimistic meta-induction, and its sidekick, incommensurability, can be defeated."

context). In their semantic account of the gene concept, philosopher of biology have acknowledged unstable reference, either more implicitly (Kitcher 1982; Burian 1985) or in a very explicit fashion (Burian et al. 1996). Marcel Weber (2005) engages in a detailed discussion of the reference of the gene concept, using Kitcher's semantic framework involving causal and descriptive modes of reference. Weber focuses on descriptive modes of reference, assuming that in many cases certain descriptions were so salient that they fixed reference. In particular during the history of classical genetics, the endorsement of such descriptions pertaining to the identification and study of genes changed, leading to change of reference. Weber introduces the useful notion of 'floating reference' for the idea that the reference of the gene concept changed constantly, though in a gradual fashion from one category to another category overlapping with the former.

> As the practice of genetics continuously generated new ways of detecting, localizing (mapping), and describing genes, some DNA segments moved in, others out of the term's extension. This kind of conceptual change differs substantially from the typical cases that have been studied in the physical sciences, such as phlogiston, mass, temperature. The latter terms shifted in reference during scientific revolutions, but were fairly stable at most times. The reference of the term "gene" was never really stable, and perhaps is not even stable today. Remarkably, this floating of the term's reference seems not to have diminished its theoretical importance or practical usefulness. (Weber 2005, p. 224)

Given that it is difficult (and possibly not semantically necessary) to determine to which precise set of entities different geneticists were referring at different points in the history of classical genetics, it is not straightforward to assess the precise way in which the reference of the classical gene concept changed. A more clear-cut case is the difference between classical and molecular genetics. Classical genes are individuated by their position on the chromosome and in particular by the criterion of complementation (the *cis-trans* test), which characterizes them as units with a distinct function for the *overall adult phenotype*. A molecular gene is defined as a transcription unit, i.e., as a structure (an open reading frame) with a function on the *molecular level* (coding for RNAs or polypeptides). The extension of the classical and the molecular gene concept strongly overlap, but they are still different: some classical genes are not molecular genes and vice versa. For instance, the genes of bacteria and viruses are clearly molecular genes, but they arguably did not belong to the extension of the classical gene concept (at least until 1940), because the lack of sexual reproduction in bacteria implies that their genes do not show recombination and patterns of inheritance as a hallmark of the operation of classical genes, and before the 1940s biologists were ignorant of the fact that bacteria have genetically based stable phenotypic features that can mutate. Vice versa, some regulatory DNA regions behave like classical alleles, yet a regulatory region alone, without the corresponding coding region, is not a molecular gene (see footnote 15 above). A range of

cases that illustrate the difference in reference of the classical and the molecular gene concept and that are also epistemically significant are studies that molecularly sequenced genes whose loci have previously been subject to classical genetic analysis. Though there are cases where a gene was detected for the first time by molecular methods, in many other cases chromosomal loci had been subject to detailed classical genetic studies, which had provided well-confirmed expectations about the number and locations of classical genes at this area of the chromosome. Subsequent molecular studies succeeded in cloning and sequencing this segment of the genetic material, e.g., using the technique of chromosomal walking described above. In many cases, the molecular analysis confirmed previous classical counts of the identity of genes at a certain locus. In some other instances, however, it turned out that both the number and the positions of classical and molecular genes at a locus diverged. An example is the *achaete-scute* locus, a gene complex which had already puzzled classical genetics as at was an instance of a so-called step-allelism suggesting a complicated internal structure and relation between adjacent genes (Carlson 1966). Detailed classical studies carried out in the 1970s and 80s suggested five classical genes at this locus. Molecular research of the 80s instead revealed four molecular, protein-coding genes that responsible for the phenomena observed by prior classical studies, and some more transcription units with unclear function (Campuzano and Modolell 1992). The disagreement between the classical and molecular individuation of genes is due to the complex organization of eukaryotic molecular genes. The *achaete-scute* gene complex is one of the many cases where several regulatory and coding sequences are interspersed. As different regulatory sites influence the transcription of the same coding region and the same regulatory site acts on the transcription of different coding regions, classical analysis yields a different account than the molecular analysis. Overall, the history of genetics shows that there are several categories of chromosomal or DNA segments that may be legitimately termed 'genes'; in particular classical and molecular genes are overlapping, yet distinct kinds. Weber (2005) makes this fact explicit:

> I suggest that geneticists were not tracking a single natural kind of entities that they called "genes." Instead, different historic versions of the concept referred to *different* natural kinds, which were not coextensive. ... Yet these kinds are all different, perhaps even in ways that could generate incommensurable concepts in the sense of Kuhn and Feyerabend. But this appears not to have caused major theoretical problems; geneticists simply switched freely between different modes of reference and frequently changed the set of things to which they were referring to when using the term "gene." (Weber 2005, p. 224)

(Section 6.3 will explain in detail why molecular genes form a set of many overlapping categories, where biologists refer to one or the other of these categories depending on the context.)

The upshot of the discussion so far is that the transition from the classical to the molecular

gene concept meets neither of two conditions that have often been viewed as criteria for conceptual progress to occur: 1) reducibility of the classical gene concept to molecular genetics as a sufficient condition on theoretical progress, and 2) stable reference of the term 'gene' during theoretical change as an alleged necessary condition on conceptual progress. Nevertheless, I maintain that the change of the meaning of the term 'gene' that occurred with the origin of the molecular gene concept is an instance of both rational semantic change and conceptual progress. Let me first explain why the transition from the classical to the molecular gene concept is a case of genuine explanatory progress, and then I will indicate why non-reduction and changing reference are epistemically innocuous and do not forfeit rational conceptual change and progress in this particular case.

My semantic framework assumes that the epistemic goal pursued by a concept's use is an important aspect of the content of a scientific concept; and the previous discussion indicated that the theoretical and explanatory purposes for which the term 'gene' was used changed in the transition from classical to molecular genetics. The epistemic goal of the use of the classical gene concept is the explanation of patterns of inheritance. Molecular biology, in contrast, is usually not concerned with the study of inheritance between generations; rather, the molecular gene concept is primarily used to explain processes taking place within single organisms or even cells, namely, the production of genetic products and the regulation thereof. This shift in epistemic goals is one reason for considering the classical and the molecular gene concept as distinct concepts. Another reason is that these concepts embody substantially different bodies of knowledge about the structure and material properties of gene, so that these two concepts support different types of explanations.

The classical gene concept includes knowledge about basic cellular processes (such as the behavior of chromosomes), which is sufficient for advancing explanations of patterns of inheritance. We saw in Section 6.1 that classical genetics could make progress relative to 19^{th} century theories of heredity by focusing on intergenerational inheritance (genotype-genotype relations between parent and offspring and corresponding phenotype-phenotype relations) while bracketing the question of development (the genotype-phenotype relation). An acceptable account of the developmental role of genes was impossible given that the classical gene concept does not provide information about the material nature of genes. Section 6.1.3 made explicit that classical geneticists did not have any idea as to *how* genes bring about their products, and that they in fact did not even know *what* the particular contribution of an individual gene is. As a result, the explanatory potential of the classical gene concept is severely limited (including contemporary variants of the classical concept as used in population genetics): the classical gene concept can explain only phenotypic *differences*

between individuals by reference to genotypic differences. The molecular gene concept, in contrast, has a substantially enlarged explanatory potential, as it supports causal-mechanistic explanations of the phenotypic contribution of genes — explanations that directly account for the contribution of genes within an organism rather than explaining phenotypic differences. The ability to offer direct explanations of development comes at a price: molecular accounts cannot explain the development of higher-level phenotypes (such as adult morphological structures) by appeal to genes alone. As discussed in detail in Section 6.2.2, the gene concept *immediately* permits explaining which *molecular* product (RNA or polypeptide) is produced inside a cell at a particular time. *Mediated* by further items of knowledge (involving further concepts and explanatory strategies apart from gene regulation), the gene concept is an essential ingredient in physiological and developmental explanations above the cellular level. For instance, developmental biologists explain the emergence of a particular morphological structure and its properties by the temporal differentiation of precursor cells and tissues and the resulting spatial differences (the various cell and tissue types composing the developed morphological structure). Such an explanation necessarily involves an account of which novel cell types develop and what determines the change of cells and their differentiation in the interaction between different cells and tissues. An essential ingredient in such an account is the gene concept: the expression of a particular gene explains why a specific gene product is formed, which may change the physiological properties of a cell or bring about an influence on other cells (including a change in gene expression of other cells). Differences between cells across space and time are understood based on the differential regulation of certain genes in different cells.

The difference between the two concepts of the gene becomes apparent in the case of genes that are essential for the physiological functioning of any cell. As mutations in such a gene are lethal, no mutant organism develops in the first place. Given that classical genetics detects genes based on the phenotypic features of a mutant, the function of such genes is usually beyond the grasp of classical genetics. Molecular biology, in contrast, is in a position to understand the *function of any gene*, including genes that are indispensable for a cell's survival or for an organism's development. For this reason, only the molecular gene concept can actually contribute to a genuine *understanding of life processes*. In sum, the *molecular* gene concept underwrites explanations of the production of cellular substances vital for the cellular machinery, and when combined with other concepts and items of knowledge it supports explanations about the physiological properties of cells, tissues and organs, including the development of complex organisms. The *classical* gene concept — as it is still used nowadays — cannot yield any of these explanations, for it does not embody knowledge about

genetic structure, in particular not about the features of genes that determine which product is coded for by a gene and which conditions bring about a gene's expression.

In addition to underwriting molecular, cellular, and developmental explanations that are beyond the reach of the classical gene concept, the molecular gene concept can shed light on those phenomena that are the primary explanandum of the classical concept. For instance, genetically based phenotypic differences between individuals have a molecular basis and thus can also be accounted for using the molecular gene concept. Such a molecular explanation is more fine-grained and sophisticated than a Mendelian explanation. While classical genetics explains any phenotypic difference as being simply due to two distinct alleles occupying the same locus in different individuals, a molecular explanation can pinpoint the precise difference in molecular genes that accounts for a particular phenotypic difference (a difference in a regulatory region of a gene rather than in a coding region, or the specific mutation involved). For instance, an abnormal condition such as cystic fibrosis can be explained by being due to a particular point mutation in a coding region of a specific molecular gene.[21] The primary type of explanations that the classical gene concept supports is accounts of patterns of inheritance. The above tenet that the classical gene concept cannot be reduced to molecular biology (in the sense of type-type reduction) was supported by the idea that molecular biology — unlike classical genetics — cannot provide a unified explanation of patterns of inheritance. Thus there is a range of phenomena which the molecular gene concept cannot explain in a unified fashion. At the same time the molecular gene concept sheds light on understanding patterns of inheritance as token-token reduction is possible. A specific pattern of inheritance involving certain individuals has a specific molecular basis, which can be explained using the concepts of molecular genetics. In particular certain exceptions to standard patterns of inheritance, which cannot be understood using the resources of classical genetics alone, can be molecularly accounted for in this fashion. Thus, in a certain respect the explanation of patterns of inheritance is within the reach of the molecular gene concept, though in a limited fashion that cannot replace the classical gene concept. (This is no problem as we saw that molecular biologists can make use of the classical gene concept together with the molecular gene concept.)

The reference of the term 'gene' changed during its history, in particular, the classical and the molecular gene concept differ in extension. While some philosophers of science have implicitly

[21] Apart from merely explaining phenotypic differences based on specific differences in DNA sequences, a molecular account can offer a more direct explanation of why a certain phenotype (such as a disease phenotype) obtains in an individual. For instance, a mutation in a gene leads to a difference in the function of a chloride-ion conductance channel for which it codes, which is the first step in a causal sequence leading to the symptoms of cystic fibrosis.

or explicitly viewed unchanging reference as a necessary precondition for conceptual progress, the case of the gene concept shows that one should make room for a less restrictive understanding of progress. It is in fact not the case that geneticists changed their conception of the *very same* thing (referent) during theoretical change. But first there was *continuity of the research object in the sense of the scientific questions pursued*. Second, the reference change that occurred was rational and scientifically warranted. On my account, *change of reference was a mere by-product of the rational and progressive change that the gene concept underwent* with the advent of molecular biology. We saw above that while classical geneticists were originally primarily concerned with how genes bring about patterns of inheritance, mature classical genetics also used genetic analysis in an attempt to shed light on the material properties of genes. Given the fact that genes bring about phenotypic differences and patterns of inheritance, they had often been viewed by classical geneticists as units of function, i.e., as material entities that can be inherited and make an independent physiological contribution. Research during the emergence of molecular biology provided insights into the fine-structure of genes (still understood as classical genes) and the causal contribution of individual genes. This provided information about how genetic elements make an individual and specific causal contribution. This empirical knowledge about the structure and molecular function of genetic elements became integrated into to gene concept, leading to meaning change and ultimately to the molecular gene concept as a concept distinct from the classical gene concept. This semantic change was rational as it was based on those items of empirical information about genes that were relevant for the idea of genes as units of function, i.e., for understanding the physiological impact of genes. The semantic change was progressive as gradual changes in the concept of the gene endowed biologists with an increasing ability to explain genetically based phenomena. This finally led to the molecular gene concept, which supports explanations that the classical gene concept does not underwrite. A side-effect of this rational and progressive meaning change — involving an increase in the explanatory potential of the term 'gene' — is that reference shifted. The molecular and the classical gene concept individuates genes in different ways (relying on different specifications of the structure and function of genes, and methods of identifying genes), and as it turned out, classical and molecular genes are strongly overlapping, yet non-identical categories. This change in reference occurred largely unbeknownst to geneticists (the fact that some genetic elements counts as classical genes but not as not molecular genes and vice versa became apparent not before the 1980s).

In addition to having occurred in a rational fashion, the shift in reference does not lead to epistemic problems such as incommensurability. My above brief discussion on how the first molec-

ular genes in higher organisms have been identified (see pp. 343, 346) is instructive in this respect. Studies started with knowledge about classical genes, in particular their location on a genetic map. Then molecular analysis proceeded by zeroing into such a specific region of the genetic material, using e.g. chromosomal walking, which combined the use of the classical and the molecular gene concept. Finally, a cloned DNA segment was sequenced revealing the number and structure of molecular genes at this locus. In most cases, the prior account of the number and location of classical genes at this locus aligned with the later established number and position of molecular genes. In some cases a difference between classical and molecular genes became apparent. Yet this difference in the entities picked out by classical and molecular gene concept did not provide an obstacle for finding out about molecular genes based on prior classical genetic analysis. Thus, the shift in reference is epistemically innocuous, in fact, the combined use of the classical and molecular gene concept on the experimental level proved to be fruitful for the identification and investigation of genes.

In sum, the idea that concepts are used to pursue epistemic goals provides a basis for accounting for the rationality of semantic change (including change in reference), even though in the case of the term 'gene' the epistemic goal itself changed during the overall history of genetics. The occurring conceptual change was rational as it was based on empirical findings that bore on *some aspects* of the concept's epistemic goal as used in *classical* genetics (yet this led to change of the concept including eventually its epistemic goal). The molecular gene concept growing out of (though not fully replacing) the classical concept is an instance of progress as both concepts differ substantially in their explanatory potential. While the classical gene concept can explain phenotypic differences only, the molecular gene concept supports direct, causal-mechanistic explanations of the molecular effects of genes, which forms an essential ingredient in cellular and developmental explanations. Not only did explanatory progress occur in the history of genetics, but my semantic framework permits us to say that this progress occurred to a large extent due to change of the gene concept.

6.3 THE CONTEMPORARY MOLECULAR GENE CONCEPT

My account of the classical molecular gene concept as used especially in the 1970s (Section 6.2) emphasized that views about gene function — gene expression and its regulation — are an essential

aspect of the molecular gene concept. The fact that both the structure and the function of genes bear on concepts of the gene has not gone unnoticed by philosophers of biology. For instance, Burian et al. (1996) explicitly argue that in the history of classical as well as molecular genetics, various functional and structural definitions of genes (and combinations of both) have been used.[22] Also analyses of the molecular gene concept as currently used have emphasized an interplay between structural and functional considerations (Waters 2000; Burian 2004; Falk 2004; Stotz and Griffiths forth.). While my above account of the molecular gene concept acknowledges different features that bear on this concept, it does not assume that all such features operate on the same level. In contrast to Burian et al. (1996), I do not think that the content of the gene concept is properly construed as being simply constituted by various descriptions of genes, be they structural or functional. Instead I have argued that there are *different components or dimensions of the meaning of a scientific term*, which are not reducible to each other. In addition to descriptions of the referent as recognized by various traditional semantic accounts, my approach has stressed that another significant component of conceptual content is the epistemic goal for which a concept is used. In the case of the molecular gene concept this theoretical goal is the explanation of the production of molecular entities used by the cellular machinery from genetic elements, thereby essentially involving gene function. Beliefs about the referent bear on a concept, but on my account are to be viewed as a second, distinct dimension of meaning (which I call a concept's inferential role). These empirical beliefs are semantically relevant as they permit scientists to actually meet the epistemic goal associated with a concept's use to some extent. Regards this dimension of the molecular gene concept the knowledge about the structure of genes is important, as the structure of genetic elements explains their causal capacities and molecular function.

Beliefs about a term's referent (or a term's inferential role) are to be recognized by a semantic theory as they explain how a concept is successfully used in scientific practice. The epistemic goal pursued by a concept's use is a further important aspect of a term's meaning, because it is vital for understanding how a concept can change in a rational fashion — a revision of meaning-determining beliefs is a warranted semantic change to the extent to which these novel beliefs permit scientists to meet the respective epistemic goal to a larger extent. In the present case, the scientific goal

[22]Burian et al. (1996) point to a trade-off between structural and functional definitions, i.e., reference-fixing descriptions (descriptive modes of reference sensu Kitcher). A definition of a gene in terms of its putative structural properties is more likely to be false than a functional definition specifying the causal effect genes have on the phenotype. Consequently, a structural definition is more likely to lead to reference failure. However, a purely functional account largely strips the concept of the gene of empirical content, thus reducing its explanatory power. According to Burian et al., this trade-off between empirical commitment and explanatory power is the reason why sometimes structural, sometimes functional, and often both types of definitions have been used in the history of genetics.

associated with the use of the molecular gene concept philosophically explains why the *classical molecular* gene concept had to cede to the *contemporary molecular* gene concept, in particular why this change in meaning (inferential role) occurred in a rational fashion. Molecular biologists in the 1970s and 80s assumed that genes form a homogenous category, so that genes can be picked out by a uniform structural definition, which characterized molecular genes as open reading frames (a sequence of DNA delimited by a start and stop codon and preceded by a promoter). Past empirical beliefs — which the classical molecular gene concept reflected — assumed that there was a one–one correspondence between genetic elements and their products, where each open reading frame codes for a unique polypeptide and where for each gene product the DNA sequence coding for it is precisely one continuous open reading frame. Empirical findings about the structure and function of eukaryotic genes made in the last two decades, however, revealed that the relation between genetic elements and gene products is many–many, so that there is often no unique answer to the question as to which DNA element(s) counts as the one(s) being responsible for a particular product, i.e., as forming a gene. Genes form a very heterogeneous kind and are best viewed as consisting of a plethora of different, but overlapping categories. These empirical findings about the structural basis of genetic function led to change of the molecular gene concept precisely because the epistemic goal of this concept's use is to account for the molecular functioning of genes.

The discussion of the gene concept as used in contemporary molecular genetics starts out with an overview of the empirical discoveries about the nature of genes and their function that led to these conceptual changes. Then Section 6.3.2 presents my semantic analysis of the contemporary gene concept in an attempt to understand how the highly context-sensitive usage of the term 'gene' is conducive to biological practice; and I offer some reasons for why this current variation usage originated, based on the idea that different biological subdisciplines are subject to different epistemic pressures. Finally, I will use the fact that the reference of the term 'gene' varies from context to context to support a moderate holism about the features that determine reference.

6.3.1 Recent Empirical Findings and the Fragmentation of a Concept

This section gives a brief overview of some facts about genetic structure and function that have been discovered in the last two decades and which challenge the unified notion of the gene as used in the 1970s. Some of these empirical findings pertain to how gene expression is regulated.[23] However,

[23]For each gene there may be various DNA sequences (possibly of a different type) that influence its expression. Furthermore, gene expression is dependent on how the DNA double helix is physically packaged within a chromosome

in what follows I do not want to focus on the nature of regulatory sites, but on empirical findings concerning the relation between coding regions and their products. In a nutshell, while it was originally assumed that the each gene as a continuous stretch of DNA (an open reading frame) codes for a unique mRNA which determines a unique polypeptide, research on eukaryotes showed that the relation between genetic elements and gene products is many–many. First, the continuous sequence of one open reading frame may be used for the production of several polypeptides (even within one cell), so that it is unclear whether this genetic element is to be considered as one gene — yet coding for several products — or rather as many genes (one for each product) that happen to be physically identical. Second, several distinct and non-contiguous genetic elements may be involved in the production of a polypeptide, so that is unclear whether several genes count as working together to bring about a product or whether the polypeptide is coded for by a single gene that happens to consist of several distinct units, possibly located at different regions of the genome. In many cases there is no unique smallest (yet meaningful) genetic element that is involved in the coding for a certain molecular product. Due to the many–many relationship between genetic elements and their products, different biologists may consider a certain genetic element (a mereological part of the genome, possibly involving several non-contiguous parts) as constituting a single gene, as merely being a proper part of a gene, or as forming a collection of several genes. Typically, such a choice as to how to individuate genes depends on the research context, i.e., the considerations about the structure or function of genes that govern a particular usage of the term gene.

One surprising discovery, made in the late 1970s, was the finding that eukaryotic genes typically come in pieces (Gilbert 1978; Crick 1979). In gene transcription, a continuous stretch of DNA is transcribed to RNA. However, it is not the whole RNA stretch — called a pre-mRNA — that is translated to a polypeptide. Instead, in a process called *splicing* several parts are cut out of the pre-mRNA, and the other parts are joined together. This yields a so-called mature mRNA whose nucleotide sequence is translated to a polypeptide (with a corresponding amino acid sequence). The RNA stretches that are cut out (and their corresponding DNA segments) are called *introns*, the remaining parts that are actually translated are called *exons*. Consequently, a total eukaryotic gene is a stretch of DNA consisting of several alternating exons and introns. This continuous sequence is

(chromatin remodeling) and can be influenced by chemical modification of DNA, which does not change its nucleotide sequence (DNA methylation). Various types of proteins bind to DNA or use another way of positively or negatively influencing gene expression. In addition to proteins, RNAs are nowadays accorded regulatory functions as well (Mattick 2004). Finally, a single regulatory sequence (an enhancer or silencer) can influence the expression of several coding regions, each of which codes for a distinct product. Given that on the one hand regulatory sequences are sometimes considered part of a gene while on the other hand different coding regions are viewed as distinct genes (as they code for different products), such a case provides potential problems for a unique scheme of individuating genes.

transcribed to pre-mRNA (several alternating exons and introns), and then the introns are spliced out, yielding a mature mRNA as a sequence of several exons that are translated. As it turned out, the coding part of a gene is not a continuous stretch of DNA, rather it is a set of several exons between which non-coding introns are interspersed. Indeed, in a typical gene introns make up 95% of the transcribed sequence; only 5% are exons and code. The fact that a gene — conceived of as that DNA sequence that codes for a polypeptide — comes in several adjacent, yet distinct pieces was unanticipated, but could be quite easily accommodated. However, the subsequent discovery of *alternative splicing* provided a genuine challenge to the classical molecular gene concept (Lewin 1980; Portin 1993). In alternative splicing, only some exons of a gene's total exon set are joined to form the mature mRNA that is subsequently translated, and which exon subset is used varies from splicing instance to splicing instance. In other words, different tokens (transcripts) of the same pre-mRNA sequence yield mature RNAs consisting of different exon combinations (thus different in type). Alternative splicing provides a way for the cell to make flexible use of the exons constituting a gene, by combining them in different ways so as to yield different polypeptide products. In humans, 60% of genes are alternatively spliced; and there are some individual genes that have up to 100 different splice forms (Modrek and Lee 2003; Leipzig et al. 2004). Consequently, one genetic element that is transcribed as a unit (hence one gene?) can yield many different products, *violating the traditional assumption that each gene codes for exactly one product.*[24]

While alternative splicing is a way in which one genetic element can code for many different products, a more recently discovered, yet quite common variety of splicing reveals that also a *many–one relationship between genetic elements and gene products* obtains. Splicing as described so far is nowadays more precisely referred to as cis-splicing (intragenic splicing): given a single pre-mRNA (transcribed from a coding region), some of its parts (exons) are used to produce the mature mRNA. In *trans-splicing* (also called intergenic splicing), however, the mature mRNA is produced from *several* pre-mRNAs, where parts of two or more pre-mRNAs are fused together by splicing to form a mature RNA, which is in turn translated to a polypeptide. This may happen by a single coding region producing several pre-mRNA transcripts that are identical in sequence, but some of whose exons are spliced together. In most cases, however, each of two or more distinct coding

[24]There are some further ways in which a gene can produce several proteins. Added to one end of each pre-mRNA is a poly-A tail consisting of about 200 adenosine ribonucleotides (not coded for in the DNA), which is relevant for the further processing of the mRNA. Due to the existence of multiple polyadenylation sites, this tail can be added at different points, yielding different mature mRNAs from the same gene (Portin 1993). Furthermore, different tokens of the same translated amino acid sequence can be modified in different ways by proteolytic cleavage or a process called protein splicing (Liu 2000).

regions (genes?), possibly located on different chromosomes, produces a pre-mRNA, and some parts of these pre-mRNAs differing in sequence are trans-spliced together.[25] In sum, the overall relation between genes and their products is as follows (individuating them by type, i.e., in terms of their sequence). In transcription an open reading frame always produces the same pre-mRNA, so that up to this point a one–one relation between genetic elements and primary transcripts obtains. In step two, the process of splicing, the causal sequence may branch (alternative splicing leading to several mature RNAs) or merge (trans-splicing of several pre-mRNAs to one mature RNA), so that there is a many–many relation between pre-mRNAs (primary transcripts) and mature RNAs. In the last step, each mature RNA is usually translated to a unique polypeptide (protein product). Overall, a *many–many relation* between genetic elements and their protein products obtains.

Now I want to focus on further complexities, each of which provides a way in which *genes may overlap*. Apart from the fact that overlapping genes implies that the same physical stretch of DNA can code for distinct products, it also challenges the traditional idea that genes are arranged in a linear fashion on the chromosome or the DNA double helix. First, there are case of complex promoters and *multiple transcription initiation sites*. Imagine an open reading frame that is preceded by a promoter and is transcribed to mRNA. Within this open reading frame (gene 1), there may be another promoter that initiates the transcription of an mRNA (call this second stretch of DNA that is transcribed gene 2). In this case, gene 1 and gene 2 physically overlap (sharing some exons) and thus their products have a partially overlapping amino acid sequence. In addition, one gene may be totally contained within another one without sharing any coding sequence. For instance, the full sequence of gene 2 may be contained in an intron of gene 1 (Mottus et al. 1997). If gene 1 is transcribed (the whole intron-exon series), all introns — including the sequence of gene 2 — are subsequently spliced out and thus not translated to a polypeptide. Gene 2, however, can be transcribed as an independent unit, resulting in a functional product that has no overlap with the polypeptide product of gene 1. The fact that within one gene (transcription unit) there can be transcription initiation sites or transcription termination sites for other transcription units provides different ways in which genes can physically overlap.

Second, there is *antisense transcription*. Remember that one strand of the double helix is just the mirror-image of the other due to complementary base pairing: A on one strand corresponds to T on the other strand, and C on one strand corresponds to G on the other one (Section 6.2.1). This

[25] Blumenthal and Thomas 1988; Caudevilla et al. 1998; Magrangeas et al. 1998; Communi et al. 2001; Finta et al. 2002; Finta and Zaphiropoulos 2000; Flouriot et al. 2002; Pirrotta 2002; Takahara et al. 2002; Dorn and Krauss 2003; Zhang et al. 2003.

organization insures stability of the genetic information and provides a way to replicate the whole double helix and its sequence. Normally, only parts of one strand — the so-called sense strand — are transcribed. This strand was traditionally called the 'coding strand', while the complementary antisense strand was referred to as the 'non-coding strand'. However, there are cases where stretches of the 'non-coding' strand are transcribed to mRNA and translated to a polypeptide, so that antisense DNA may code for a product. An antisense element may independently code for a product, or in other cases a pre-mRNA from *antisense* DNA may be trans-spliced to a pre-mRNA from *sense* DNA, resulting in a polypeptide product that is coded for by both sense and antisense DNA elements (Dorn and Krauss 2003). Moreover, both a sense stretch of DNA and an *overlapping* antisense stretch may be independently transcribed, yielding two totally different transcripts and thus two structurally and functionally distinct products (Coelho et al. 2002). Yelin et al. (2003) estimate that more than 8% of human genes have an overlapping antisense partner.

Finally, there is another way in which overlapping genes code for totally different products, namely, *transcription in different reading frames*. Remember that in a continuous sequence of nucleotides, each set of three adjacent nucleotides (a triplet) codes for a specific amino acid. A sequence such as '...THEREDOLDHAT...' can be read in three different frames: '...THE RED OLD HAT...', '...T HER EDO LDH AT...', or '...TH ERE DOL DHA T...'. The internal structure of the DNA sequence does not determine which reading frame obtains (the genetic code does not have commas), the occurrence of a start codon and a promoter at the beginning of the open reading frame initiates transcription and thereby determine the particular reading frame (Section 6.2.1).[26] While an alternative reading frame usually would not code for a functional product, there are cases where a stretch of DNA is transcribed in two or three different reading frames, resulting in very different products (Sharpless and DePinho 1999). E.g., both '...THE RED OLD HAT...' and '...T HER EDO LDH AT...' would yield a functional product once translated to an amino acid sequence.

The above empirical findings revealed in particular the many–many relation between coding regions and gene products. Especially due to alternative splicing a token DNA sequence may code for several types of polypeptides (which differ in amino acid sequence), so that in one sense factors external to this DNA sequence determine which amino acid sequence the DNA sequence actually codes for. In another sense, however, this still leaves intact the basic idea that DNA sequence codes

[26] A mutation consisting in the deletion or insertion of a nucleotide results in a shifted frame from the point of mutation onwards, typically yielding a nonfunctional product. E.g., 'THE RED OLD HAT...' mutates by deletion of the 7th letter to 'THE RED ODH AT...', insertion of an 'A' at position 7 yields 'THE RED OAL DHA T...'.

for amino acid sequence; namely, in any of the above examples it was the case that for each type of gene product (a certain amino acid sequence) there is an overall DNA sequence that corresponds to the sequence of the product in accordance with the genetic code (though this coding DNA sequence may consist of several non-contiguous elements, and it may code for other products as well). However, there are prominent exceptions to the idea that a polypeptide's sequence is fully determined by some genetic sequence in accordance with the genetic code. One such type of case is *RNA editing* (Portin 1993; Gray 2003; Samuel 2003; Flomen et al. 2004; Kim et al. 2004). As always the DNA is transcribed to pre-mRNA (simple copying), but then the mRNA sequence is modified by enzymes ('edited'), before the edited, mature mRNA is translated to protein (according to the genetic code). Consequently, the sequence correspondence between the DNA and the mature RNA is disturbed, and thus the amino acid sequence of the polypeptide produced is not a function of DNA sequence based on the genetic code any longer. There are many cases and different ways in which the RNA sequence is edited by the substitution, insertion, or deletion of nucleotides. Moreover, there are cases of *translational recoding*, where the mature mRNA is translated to a polypeptide in non-standard ways (Baranov et al. 2003). For example, in frameshifting at the ribosome an alternative reading frame is used when the mRNA is translated. The reading frame shifts by one or two nucleotides relative to the way in which the mRNA is normally read, leading to a novel three-nucleotide codon structure and thus to an alternative amino acid sequence. Furthermore, there are cases of codon redefinition, where in special molecular contexts an RNA triplet is not translated to that amino acid that the genetic code prescribes, but to another amino acid, thereby yielding an exception to the genetic code. Thus, in addition to the many–many relation between coding genetic elements and its products, there are exceptions to the idea that protein sequence is fully determined by some genetic sequence in accordance with the genetic code.

Let us take a look at a concrete example that shows the possibility of individuating genes in different ways. Genetic complexity can be illustrated by the modifier of *mdg4* region in *Drosophila* (Dorn and Krauss 2003; Pirrotta 2002). At this locus there are several exons on the sense strand of the DNA: 4 so-called common exons that are transcribed as one unit (element A in Figure 11), followed by 19 so-called alternative exons each of which has an individual promoter and is transcribed to a separate pre-mRNA (elements $B-T$). Any of the alternative exons can be trans-spliced to the 4 common exons. Consequently, 19 different mature mRNAs are produced (each of which contains the 4 common exons plus one alternative exon) and 19 different protein isoforms result. In this case one could say that the region contains only one gene consisting of genetic element A, one gene

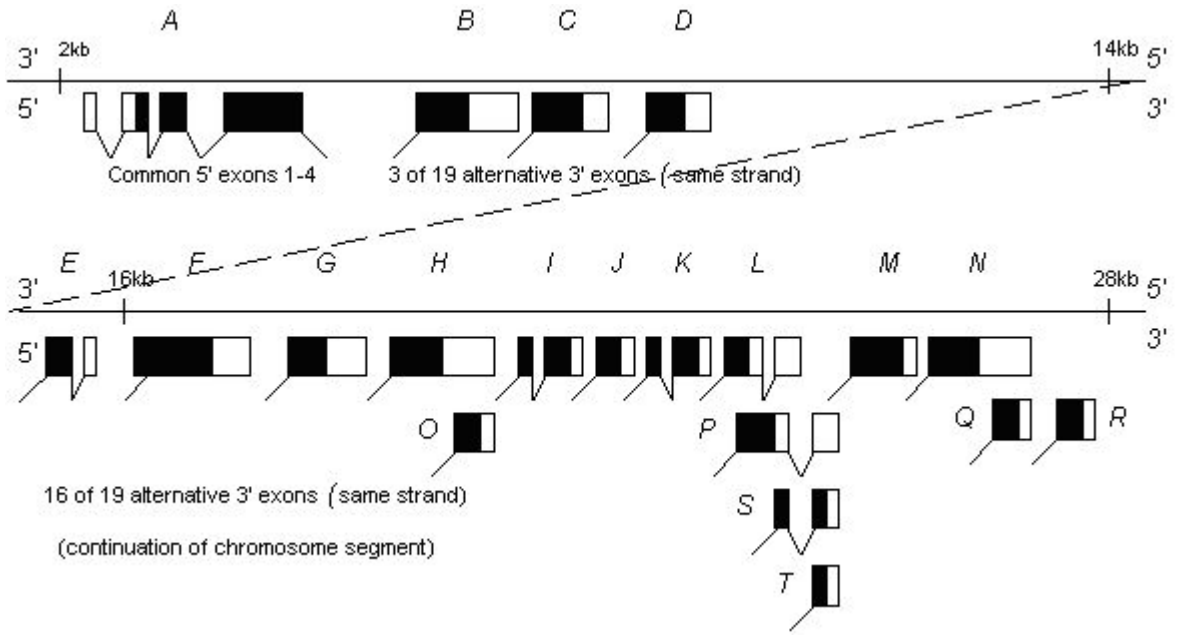

Figure 11: Region *mod(mdg4)* in *Drosophila*
4 common sense-exons (A) and 19 alternative sense-exons ($B-T$)
(Image courtesy of Karola Stotz. http://representinggenes.org)

consisting of all exons involved (A+...+T), two genes (A and B+...+T), 19 genes (A+B, ..., A+T), or 20 genes (A, ..., T). Each of these possible options of individuating genes at this locus picks out a structurally well-defined entity (an exon or set of exons) that is involved in the production of an mRNA or a polypeptide. Given that an alternative exon has a separate promoter and is independently transcribed, as a transcription unit it has some functional independence and could be considered a distinct, one-exon gene. At the same time, none of the alternative exons makes a polypeptide product on its own but has always to be joined with the 4 common exons, supporting a rival terminological choice according to which an alternative exon is just a proper part of a gene.

To complicate matters further, in this genetic region there are 7 further alternative exons, but which are located on the antisense strand of the DNA (these 7 additional exons are not depicted in Fig. 11). Any of these antisense-exons can be independently transcribed to a pre-mRNA and trans-spliced to the 4 common exons mentioned above, yielding 7 more possible mature RNA and thus polypeptides, each of which is based on both sense and antisense elements. The presence of the antisense-exons together with the common sense-exons yields several options as to how to individuate genes at this locus, which are the same basic options as in first part of this case. However, note that while in the first part one has the option to count a gene as consisting of several sense-exons

(such as $A+B$ in Fig. 11), now one has to decide whether a gene can consist of a combination of sense and antisense elements (such as A plus one of the alternative antisense-exons).

Karola Stotz and Paul Griffiths (2004) point out that the "dialectical development of the gene concept can be interpreted as reflecting a desire to keep the structural and functional definitions of the gene focused on a single entity" (p. 7). The classical gene concept could not ensure this because of the many–many relation between genes and the characters they determine. In contrast, the molecular gene concept changed the notion of 'genetic function' from the effect genes have on gross phenotypic characters (such as eye color) to a much more proximal effect of genes, namely, their producing of RNAs and polypeptides. Given the one–one relation between open reading frames and polypeptides assumed in the 1970s, the "process of conceptual evolution *seemed* to reach a stable resting point with the 'Classical Molecular Gene Concept'" (p. 7, my emphasis). However, as it turned out, the relation between genetic elements and their molecular products is many–many, resulting in the transformation of the classical into the contemporary molecular gene concept. There is more than one structurally defined kind that fulfills the function of coding for molecular products. The concrete example above illustrated that there are different legitimate ways to individuate genes by considering certain genetic elements as genes. As a geneticist puts it,

> What are the rules for deciding whether two partially overlapping mRNAs should be declared to be alternative transcripts of the same gene or products of different genes? We have none. (Gelbart 1998, p. 660)

As a result, nowadays the term 'gene' is used in a very context sensitive fashion, where depending on the context different structural criteria of individuating genes are used. One significant reason for this is the fact that different researchers (or the same scientist in different contexts) may focus on more proximal gene products such as RNAs or rather on more distal ones such as proteins. Take two transcription units (open reading frames), that are transcribed independently and then trans-spliced together to yield a functional protein. Given the simple one–one relation between transcription units and pre-mRNAs (primary transcripts), in a context where the scientific focus is on pre-mRNA it is common to view these two transcription units as separate genes. However, if the focus is on the protein produced, then it is more reasonable to consider the two transcription units as one gene (with non-contiguous parts) coding for the protein considered. In the past it was often assumed that proteins are the main functioning entities produced by genes, with RNAs only being an intermediate step. However, it not nowadays recognized that RNAs fulfill crucial cellular functions just like proteins (Mattick 2003, 2004), thereby increasing the legitimacy of focusing on either RNA or protein as the gene product of interest. Due to the many–many relation between genetic

elements and their protein products, a varying focus on more proximal or more distal gene products leads to shifting individuation choices (Waters 1994, 2000). Due to the different characterizations of genes and the high variation in usage, the contemporary molecular gene concept is a somewhat fragmented concept compared to the unified classical molecular gene concept (Pearson 2006).

> But beyond this belief [that genes are made of DNA], what is meant by the use of the terms can only be gathered from the context. Sometimes 'gene' is used to denote a specific unit, sometimes it is a collective term for genetic units and quite often it is avoided completely. (Falk 1986, p. 165)
>
> The particulate gene has shaped thinking in the biological sciences over the past century. But attempts to translate such a complex operational concept into a discrete physical structure with clearly defined boundaries were always likely to be problematic, and now seem doomed to failure. Instead, the gene has become a flexible entity ... (Dillon 2003, p. 457)

The Representing Genes Project (http://www.representinggenes.org), led by Karola Stotz and Paul Griffiths, is an attempt to determine the actual variation in usage in the gene concept across different biological disciplines (Stotz and Griffiths 2004; Stotz et al. 2006). The method used consists in having biologists from various fields fill out an on-line questionnaire, which contains actual cases that demand one to choose which of certain genetic elements with certain structural and functional properties count as forming one or several genes. One basic aim of the Representing Genes Project is to determine along how many dimensions the usage of the term varies. The questionnaire design took into account the following potential axes of variation, i.e., logically independent conditions that could be used to individuate genes. 1) Do separate DNA elements have separate promoters? (It is probably more likely that elements with separate promoters are counted as independent genes.) 2) Are all the separable genetic elements translated? (In which case they are more likely to be viewed as separate genes.) 3) Does a genetic element that forms a product in conjunction with other DNA elements (trans-splicing) also produce another product on its own in other cellular contexts? (In which case it is more likely to be considered an independent gene.) 4) How far from each other are the locations of the different genetic elements involved? 5) Are both sense and antisense elements involved? 6) Is the relation between genetic elements and their products one–one, one–many, many–one, or many–many? 7) How proximal or distal are causal branching points (if the relation is one–many) or merging points (if it is many–one)? 8) If different products are produced (e.g., one–many relation), how chemically diverse are the different products? (Chemically distinct products are more likely to be attributed to being coded for by different genes.)

One upshot of recent empirical findings is that genes do not form a unique, homogenous kind. Rather, what are called genes is best viewed as a set of various overlapping categories. Each

combination of yes/no choices on the conditions listed in the previous paragraph yields a structurally well-defined molecular category. Given that there several logically independent conditions, a large number of categories can be defined that differ yet strongly overlap in extension. Each thusly defined kind picks out entities that (at least in some cases) essentially contribute to the production of some RNA or some polypeptide (at some stage in the causal process), and thus is legitimately considered as fulfilling the function attributed to genes. Since there is no unique structural kind that fulfills the molecular function of coding for gene products, genes form actually a set of many overlapping categories, and depending on the context, a biologist may refer to one or the other of these categories.[27]

> The efforts to identify unique structural entities for the functionally defined genes that, following the Watson-Crick model of DNA, culminated in the notion of the cistron as a sequence of nucleotides that corresponds to a specified sequence of amino-acids, and in the Central Dogma of a one-way information flow from polynucleotides to polypeptides, increasingly failed. ...
> In the decades that followed [early molecular genetics] it became increasingly clear that there is no one, 'objective' functionally-independent way to define a material canonical gene. Various criteria have been used to identify genes in the monotonous DNA sequences ... Eventually, different research groups each defined their own 'gene' concept. Viewed from above, the 'gene' became rather a generic term, like 'chair' or 'table'. (Falk 2004, pp. 106–108)

6.3.2 A Semantic Analysis of the Contemporary Gene Concept

My discussion of the classical molecular gene concept (Section 6.2.2) already emphasized the centrality of gene function for the molecular gene concept, as on my account the epistemic goal pursued by this concept's use is to explain how genes bring about their molecular products. The previous section reviewing developments of the last two decades stressed that it turned out that there are different structurally defined categories that fulfill the function of genes by coding for genetic products. The fact that genes are ultimately defined in terms of their molecular function rather than by a particular structure is currently shown by the difficulty of deciding whether a genetic element is a gene rather than a pseudogene and the problem of offering gene counts for whole genomes.

There are several operational criteria used for predicting whether a stretch of DNA codes for a product that only rely on the sequence of this DNA stretch (i.e., purely structural criteria for

[27] One such structurally defined category could be considered a natural kind, so that genes are merely a set of overlapping natural kinds rather than a genuine natural kind. However, one such homogeneous category picks out the entities that fulfill the molecular function of genes only in some cases, while in other cases other such categories contain the relevant genetic elements. For this reason, the set of all genes as including all these categories is the explanatorily more relevant kind, so that my preferred position is to still view genes as a natural kind — though in contrast to stereotypical views about natural kinds as a very heterogeneous natural kind consisting of many overlapping structurally defined categories.

genehood). A good indicator is if an open reading frame can be identified, i.e., a stretch of DNA bounded by a start and stop sequence and preceded by a promoter sequence. A further criterion is codon bias, i.e., the presence of a nucleotide sequence within the open reading frame that shows a characteristic bias rather than a random sequence. The philosopher Dick Burian (2004) introduced the useful notion of a 'nominal gene' for a stretch of DNA that exhibits these structural hallmarks shared by many genes. However, these structural criteria are highly defeasible: their use detects only 50% of exons and 20% of whole genes (Snyder and Gerstein 2003; whole genes are particularly difficult to identify as the several coding parts (exons) of a gene may be interspersed by 20 times larger non-coding introns). Nominal genes need not be genes, as a gene is a stretch of DNA that actually codes for a functional product (Snyder and Gerstein 2003). In fact, the notion of a *pseudogene* is a common term used to denote a stretch of DNA that looks like a gene by meeting all structural hallmarks, yet is not expressed and thus does not produce a product. One explanation for the presence of such pseudogenes is that they used to be genes in the past, but that mutations internal or external to the gene (not affecting its status as nominal gene) rendered it non-functional. This raises problems for practically determining which DNA elements are genes in the genome of a newly sequenced organism and estimating the very number of genes in a whole genome. For the easiest way to predict genes in a newly sequenced genome is to use computational methods that use (highly fallible) structural criteria. In the case of the human genome, both the private enterprise Celera Genomics and the public genome consortium Ensembl offered their gene counts and prediction about which sequences are genes. Ignoring genes that have already been known previous to sequencing the total human genome, only 20% of the genes newly predicted by Celera were counted as genes by the Ensembl estimate and vice versa, due to the use of different algorithms and structural criteria (Hogenesch et al. 2001). As a result, computer-implementable structural criteria have to be supplemented by significantly more time-consuming experimental procedures that determine whether a DNA sequence is actually transcribed and produces a functional product. As a result, even though the *Drosophila* genome was sequenced in 2000, Oliver and Leblanc (2003) assert that "we still have no clear idea how many genes there are in *Drosophila*" (p. 204.1).

Apart from the practical problem of detecting genes in the genome, the fact that a gene's sequence provides only a defeasible estimate for whether it actually produces a product has some interesting metaphysical implications. Focus on the common usage according to which the term 'gene' refers to a coding region only (excluding regulatory regions). Especially in this case, whether a gene is actually transcribed and produces a product depends not only on the gene's sequence, but on

other factors such as DNA sequences more or less adjacent to the gene and the presence of non-genic macromolecules inside the cell (which are usually coded for by DNA sequences far apart from the gene under consideration). The same DNA sequence occurring in a different species or in a different cellular context may produce a different product or no product at all. Thus, the causal power of a gene, i.e., its ability to produce a molecular product, is *not an intrinsic property* of a gene. Given that the function of genes is essentially context-sensitive, contemporary molecular genetics becomes the best argument against genetic determinism (Gilbert and Sarkar 2000, Stotz forth.). Moreover, while philosophical discussions on dispositions and causal capacities have typically focussed on examples of intrinsic dispositions, ignoring possible extrinsic dispositions (Love 2003b), the causal capacities of genes do not fit this philosophical stereotype. I actually assume that many properties of living beings are extrinsic properties and that the function of biological entities is essentially context-sensitive, but it is interesting that even genes do not conform to the picture of causal properties derived from the Mechanical Philosophy. Indeed, given that genes are ultimately defined in terms of their function, *the very property of being a gene is an extrinsic property.* A gene may very well be a particular stretch of DNA with a clear-cut structure, but what makes this DNA sequence a gene (rather than a pseudogene) depends on features external to it. By suggesting that a DNA sequence should count as a gene if its transcription (in a certain cellular context) is above an arbitrary level, the biologists Finta and Zaphiropoulos (2001) even maintain that genes are not well-defined and clearly delimited regions of DNA but rather "statistical peaks within a genome-wide pattern of expression of the genetic information" (p. 160).

The fragmentation of the contemporary gene concept led some commentators to take an eliminativist stance, suggesting that the gene concept is about to be abandoned, or that it should be abandoned (Gray 1992; Neumann-Held 1999). Philip Kitcher prominently maintained that

> ... it is hard to see what would be lost by dropping talk of genes from molecular biology and simply discussing the properties of various interesting regions of nucleic acid. (Kitcher 1992, p. 130)

The idea is that given the strongly varying usage of the term 'gene', other notions from molecular genetics (such as open reading frame, exon, transcription unit) can jointly be used in a less ambiguous way to refer to certain genetic elements coding for RNAs and polypeptides. Why either erroneously suggest by the use of a single term that a unique category is referred to, or talk ambiguously about 'genes', if there are nowadays other prominent terms whose joint usage provides a more effective way of addressing the expression of genetic information? This skeptical stance towards the gene concept can not only be found among some philosophers, but also among geneticists:

> ... we may well have come to the point where the use of the term 'gene' is of limited value and might in fact be a hindrance to our understanding of the genome. Although this may sound heretical, especially coming from a cardcarrying geneticist, it reflects the fact that, unlike chromosomes, genes are not physical objects but are merely concepts that have acquired a great deal of historic baggage over the past decades. ... The classical concept of the gene ultimately forms a barrier to trying to understand phenotypes in terms of encoded functional products. (Gelbart 1998, p. 660)

At the same time, while clearly realizing that the monolithic classical molecular gene concept has ceded to a variety of terms, commentators of the contemporary gene concept acknowledge that 'gene' talk is still very prominent in molecular biology and that some shared gene concept is still in play. The biologist Thomas Fogle (2000) uses the term 'consensus gene' for this shared interpretation of what a gene is. The consensus gene functions as a stereotype across various usages and users, even though its application to actual cases demands an implicit departure from the stereotype and variation from case to case. In spite of empirical challenges the gene concept continues to be used:

> At present, there is strong momentum to absorb new molecular revelations into the consensus gene rather than effect a more fine grained description of molecular parts and processes. (Fogle 2000, p. 5)

In *The Century of the Gene* (2000), the philosopher Evelyn Fox Keller points to the limits of the current gene concept, arguing that in the future more new terms will be necessary for effective scientific discourse about molecular function. Yet she neither demands nor predicts the abandonment of the gene concept. Instead, in her concluding chapter she rightly shifts away from the question of what genes are and rather discusses what gene *talk* is good for. In subsequent paragraphs I address the question of why the gene concept is still significant for contemporary biological practice.

A prominent philosophical analysis of the contemporary gene concept is Ken Waters' (1994, 2000, 2004a) defense of a unified molecular gene concept. His move is to acknowledge that *genes* are not a unified, homogenous kind and that the reference the term 'gene' changes from context to context, while arguing that there is still a unified *concept* that underlies these varying usages. Waters' motivation is to point to an epistemic virtue of the molecular gene concept, which accounts for its continuing significance for explanations and experimental investigation. Waters focuses on the idea that a gene is a linear sequence of DNA that codes for another linear sequence, its product (be it RNA or polypeptide). He is well aware of the fact that due to processes such as alternative splicing one DNA sequence can code for several different products which differ in sequence. As explained in Section 6.3.1, due to the many–many relation between genes and their products, focusing on a more proximal product such as RNA or alternatively on a more distal product such as a polypeptide yields different accounts of what the particular DNA element is that codes for *this* product. However, Waters' point is that once one considers a specific product (at a certain

stage in the causal sequence), then there is a unique DNA sequence which codes for this product in accordance with the genetic code.[28] In a nutshell, while the traditional one gene–one product idea fails, one can still arrive at a unique coding gene by starting with a particular product and working backwards through the flow of information. On Waters' account of the molecular gene concept,

> **a gene *g* for linear sequence *l* in product *p* synthesized in cellular context *c*** is a potentially replicating nucleotide sequence, n, usually contained in DNA, that determines the linear sequence l in product p at some stage of DNA expression. (Waters 2000, p. 544)

Thus, when the term 'gene' is tokened, the particular epistemic context and particular case studied determine on which gene product a scientist focuses. This fixes l, p and c in the above definition, so that it is uniquely determined what the gene g with sequence n is. Waters' analysis covers many individual usages of the term 'gene', and it is philosophically fruitful as the core idea that the linear sequence of genes determines the linear sequence of a genetic product captures to a relevant extent how gene-based explanations account for how genes bring about specific molecular products. The account also captures to a large degree how the gene concept figures in experimental investigation and manipulation. For instance, stretches of DNA are experimentally inserted into model systems to bring about the production of novel products and study their effects.[29]

In my view, a philosophical analysis of the contemporary molecular gene concept should account for two related features: 1) why the usage of the term 'gene' varies from context to context (why variation in the gene concept is conducive to biological practice), and 2) why at the same time biologists still make use of the term 'gene' across these various contexts (why a shared gene concept is in play). Waters' analysis can be viewed as providing some answer to both issues. One can conceive of his accounts as assuming that the gene concept is a function from a certain epistemic context (specifying l, p, c) to the referent of the term 'gene' (DNA sequence n) in this context. The fact that the value of the function (the particular referent) changes from epistemic context to context explains why the use of the gene is sensitive to the particular context. At the same time, there is a unique gene concept shared by different biologists, as the same function applies to all usages of the term 'gene'. These different usages have a central idea in common (represented by Waters' function), namely, that the linear sequence of a gene determines the linear sequence of its product. While I think that Waters' analysis is fundamentally on the right track, in the following

[28] This DNA sequence may consist of several non-contiguous segments as coding exons are interspersed by non-coding introns or due to trans-splicing there can be a many–one relation between genetic elements and gene products.

[29] Another prominent philosophical account is Lenny Moss's (2001, 2003) claim that there are two distinct gene concepts used in molecular biology: *Gene-P* and *Gene-D*. While I assume that my account can cover this idea (the Gene-P and Gene-D distinction roughly corresponding to my notions of the classical, Mendelian gene and the nominal gene), I cannot interpret Moss's account and discuss its relation to my analysis at this place.

paragraphs I point to some limitations of his account and explain how to improve it.

First, while Waters' account addresses some of the variation that the gene concept exhibited in the 80s and 90s, his construal does not capture all of the variation, in particular novel usages that emerged due to findings of the last decade. For instance, in the modification of pre-mRNA due to RNA editing the resulting mature mRNA is not just determined by the sequence of the gene, and thus the amino acid sequence of the polypeptide product (translated from the edited mRNA) is not simply a function of the DNA sequence, thereby violating the genetic code (Section 6.3.1). This phenomenon is not captured by Waters' analysis that relies on the genetic code and the idea that the sequence of the product is fully determined by the sequence of the gene. As another complication mentioned above, DNA sequences on the antisense strand can be transcribed and trans-spliced to a pre-mRNA transcribed from the sense strand. Waters' construal needs to be refined to take a sense-antisense chimera into account, in particular given that biologists disagree on how to apply the term 'gene' to such cases. Furthermore, while in one cellular context a certain transcribed genetic element may be just one ingredient for the product as it is trans-spliced to other transcribed elements, it matters for biologists whether there are other contexts in which this genetic element independently produces a product (without being combined with other DNA segments), in which case this genetic element is more likely to be considered a separate gene (Paul Griffiths, personal communication). In such a situation, whether a genetic element is considered a gene depends not only on the single case of gene expression considered, but also on other items of knowledge biologists have about this genetic element (how it figures in other cases of gene expression). Waters' analysis, in contrast, does not take into account that the usage of the term 'gene' may depend on other cases apart from the one under consideration (modeled by l, p, c). In these pages, I cannot offer a precise account of the contemporary usage of the gene concept. The ongoing Representing Genes Project, led by Karola Stotz and Paul Griffiths, will shed light on this issue by charting some of the actual variation exhibited by the contemporary gene concept (Section 6.3.1). This empirical analysis of concept usage can be followed by a more detailed study of why the particular variation obtains, i.e., of the epistemic reasons that lead an individual biologists to adopt a particular usage in a certain biological case. Such an account can offer a better understanding of *why* the concept's usage exhibits the function implied by Waters' analysis or *why* there are legitimate usages that deviate from Water's account. (Further below I will also point out that in contrast to Waters', my account acknowledges that some feature of the molecular gene concept has actually changed in the course of history, namely its inferential role, and that this phenomenon can be explained.)

Second, while Waters' account acknowledges the variation in usage, his focus on securing a shared gene concept makes him downplay the actual variation that the gene concept exhibits. In particular, he recently made the astonishing suggestion that an empirical study of the actual use of the term 'gene' such as the Representing Genes Project has no bearing on a philosophical analysis of the molecular gene concept (Waters 2004a). For this reason, let me offer my own brief account of why the variation in usage is conducive to biological practice, and why in spite of the varying usage of the same term communication is still possible across different contexts. The use of the gene concept is context-sensitive because there are different legitimate explanatory and investigative interests that may underlie the study of one and the same genetic region and expression events involving this region. In one research context the focus may be on certain structural features of genes (such as sequences that usually lead to the initiation of transcription). In another context, researchers may be interested in the RNA transcript, while others may focus on the polypeptide finally produced from a gene. We saw above that due to the fact that genes are a highly heterogeneous kind and the many–many relation between genetic elements and gene products, different such explanatory and investigative interests may pick out different entities, in fact differently characterized entities. The core idea underlying various usages of the gene concept — the explanation of how genes bring about their products — can be applied differently and spelled out in different precise ways; and at the same time there is no single structurally clearly delineated category ('genes') that would explain the production of RNAs and polypeptides in all cases. An individual researcher may study different regions containing genes that have different structural and functional properties, or she may approach different cases with different investigative questions, so that an overall context-sensitive usage of gene concept may be conducive even for the practice of a single scientist. In addition to the fact that a flexible usage of genetic terminology is necessary to bridge different research contexts, this flexibility permits scientists to react more adequately to novel findings, thereby taking into account that scientific research is addressing entities (such as genes) and phenomena (gene function) that still are not fully understood. In sum, given the nowadays *known* complexities of genetic structure and function, meeting *different legitimate explanatory and investigative interests* makes a varying usage and reference of the term 'gene' necessary.

In spite of the strongly varying usage, communication across contexts is still possible — at least to a relevant extent. For biologists are aware of the flexible overall usage of this concept, and the particular research context disambiguates in that within a certain context it is relatively clear what characterization and understanding of 'genes' is in play and which entity is actually referred to.

In addition to the general context, other terms apart from 'gene' (such as 'exon' or 'transcription unit') can be used to offer a more explicit and precise characterization of which type of entity is meant. The somewhat monolithic classical molecular gene concept has definitely ceded to a contemporary molecular gene concept that is just one among other terms used to effectively talk about genes and their function. Given this, one may wonder why should one talk about 'genes' at all rather than eliminating this notion in favor of a set of terms whose joint usage could support a less ambiguous usage? My reply is that communication across various contexts is scientifically necessary, and scientific notions and claims ought to have a basic generality across contexts. This requires a shared terminology and understanding such as the current gene concept. In contrast, using solely terms that may promise precision but apply to a particular experimental context only would due to this specificity make communication across contexts difficult. My claim that the flexible use of the gene concept is conducive for current biological practice does not imply that I think that the gene concept will be or should be with us until the end of time. Future science may find conceptually more appropriate ways to explain molecular function, and such a potential abandonment of the gene concept due to the emergence of empirically more appropriate notions could be philosophically understood as well. But currently, often making use of a single term 'gene' in various situations, while at the same time using it differently, is an appropriate way to meet a trade-off that exists between scientific precision and generality/communication across contexts.

A final remark on Waters is that my approach offers a refined account of what the shared molecular gene concept is and why it is used the way it is. My account explicitly argues that for each central biological concept there is an *epistemic goal* pursued by the use of this concept. The fact that the molecular gene concept is used to explain how genes bring about their product provides a philosophical account of what different usages of the term 'gene' have in common and why there is a shared gene concept. Moreover, it philosophically explains why the usage varies, as the epistemic goal is spelled out differently in different contexts (the kind of product whose synthesis is to be explained varies from case to case). Waters (2004a) offers an idea that may have some *prima facie* similarity to my notion of a concept's epistemic goal, by arguing that the task of a philosophical analysis of a scientific concept is to exhibit the "epistemic virtues" of a scientific theory (2004a, p. 30), such as the molecular gene concept figuring in important explanations. However, Waters' idea of a concept's epistemic virtue does not differentiate between two of my notions that have different philosophical functions: a concept's inferential role (accounting for how a concept figures in successful scientific theorizing and practice, such as gene-based explanations), and the epistemic

goal pursued with a concept's use (accounting for the rationality of conceptual change).[30]

In my discussion on reference in Section 3.2.2 I suggested what I called a *moderate holism about reference determination*, pointing to the contemporary gene concept as case supporting this idea. A radical holism about reference determination would assume that all of an individual's beliefs in which a concept occurs determine the reference of a term (potentially leading to referential incommensurability between different individuals). A localism instead assumes that the set of factors determining reference is well-defined and clearly limited, e.g., by assuming that for each concept there is a limited set of analytic statements determining the reference of this concept. Moderate holism takes an intermediate position by assuming that only some of an individual's beliefs, utterances, or interactions with the world determine what she refers to, but that this set of factors determining reference is unbounded in that in some contexts a factor is not reference determining, while in other cases it may be. More precisely, the idea is that for each factor bearing on reference determination (such as a description of the referent), the extent to which it determines reference together with other factors in a certain case is a matter of degree, and that the salience of a factor for reference determination can vary from context to context.

The fact that nowadays the reference of the term 'gene' may shift from context to context argues against a genuine localism about reference determination, for if there were a clear-cut set of conditions that determine reference , then these conditions would always pick out the same extension independent of the context (assuming that there is no relevant change of the world). In the case of the contemporary gene concept, it is in fact the case that various conditions and considerations bear on its reference, where the salience of different considerations depends on the particular context. For instance, the idea that genes typically consist of DNA bears on the reference of most 'gene' tokens (though other conditions are necessary to determine which stretch of DNA is referred to), while in some context, involving reference to viral genes consisting of RNA, this idea cannot bear

[30]In addition, while Waters tends to downplay the philosophical significance of actual term usage, I argued that a concept being used for a certain epistemic goal is determined by a term's usage. At the same time, for Waters an adequate philosophical analysis requires that scientists would explicitly approve of the analysis (Waters 2004a, p. 36). My account, in contrast, does not require that a concept has its particular epistemic goal because a scientist has an *explicit* belief to this effect ('I use my concept of X to pursue epistemic goal Y'). I also do not assume that a concept being used for a certain epistemic purpose is determined by the beliefs of a *single* scientist. Rather than a single explicit belief, it is a term's overall usage within a whole scientific community that determines the concept's epistemic goal. On my account, ascribing concepts to individuals or scientific communities serves the purposes of explaining how concepts make successful practice possible and how they can rationally change. Thus, a philosophical analysis of a concept (and its epistemic goal) is legitimate not because scientists may agree with it, but because it yields a philosophical explanation of scientific practice. (In contrast to Waters (2004a), Stotz et al. (2004) rightly assume that an account of concepts is about how scientists reason and act, rather than about what scientists *claim* how they reason. Their questionnaire study shows different results when the same question is asked in a direct way — explicit definition of one's gene concept — and in an indirect way — application of the gene concept to concrete cases.)

on reference determination. In certain research contexts, some stereotypical structural properties of genes (being an open reading frame delineated by promoter, start and stop codon) may encompass all considerations biologists use to refer. Most of the entities thereby referred to are genes and these conditions succeed in picking out many genes (relative to other legitimate characterizations of what a gene is), and researchers thereby rely on conditions that are significant in a research context that involves investigation of these structural properties of genes. In other research contexts that focus on gene function or particular gene products, however, further or other criteria are used. For as the previous discussion of the contemporary molecular gene made plain, a structural definition of a gene as an open reading frame often underdetermines its genetic function, and given that the relation between open reading frames and gene products is many–many, other conditions are necessary to pick out the stretch of DNA that produces a particular product. In one research context, the focus is on the mRNA being produced by a gene; whereas other researchers may be interested in the protein product, thereby using different considerations that bear on reference determination. Some biological questions may permit the inclusion of antisense-DNA as part of a gene or have to take RNA editing into account, others do not.

Localism is actually compatible with context-sensitive reference in two well-known semantic cases. If the meaning of a term is *ambiguous*, then it actually expresses distinct meanings (concepts) in different contexts, leading to a shift in reference. The term 'gene', however, is not adequately construed as referring to a small set of clearly distinct concepts. In the case of an *indexical*, a term can be viewed as having a constant meaning across different tokenings, but the reference depends on the context of the utterance. While the gene concept is not usually thought of as an indexical, one may wonder whether Waters' account of a unified gene concept as a function from context to a linear stretch of DNA is in line with the way in which the meaning of an indexical is explicated as a function from contexts of utterance to referents. The crucial difference is that in the case of an indexical different contexts of utterance can be specified in largely *non-intentional* terms. The difference between one utterance of 'I' and another utterance of this indexical is a mere difference in the *physical* location of the utterance. (Contexts of utterance are often modeled as centered worlds, where the context in a world is simply modeled by this world having a certain center or pointer in space-time.) In the case of an indexical such as 'there', unambiguous reference may also involve the speaker's beliefs and intentions, yet the difference in reference between two tokens of an indexical is still primarily accounted for by the physical difference between the two contexts of utterance. In contrast, the point in space and time at which the term 'gene' was uttered provides hardly any clue

to the referent of this tokening. Rather than a difference in location, what primarily accounts for the difference in reference of two utterances of the term 'gene' is their being made by two persons that have different beliefs, intentions, and research interests. In fact, one and the same person may refer to different categories using the term 'gene' on different occasions because it is her beliefs and research focus that differs between these occasions. Thus, the meaning of the gene concept is rather like a function from an *intentional/epistemic* context to an extension, preventing a straightforward application of theories of indexicals to such a biological concept. It is the semantic relevance of these various collateral beliefs and intentions that creates a moderate holism.

At the end of my discussion of the molecular gene concept, let me summarize my semantic characterization and explain how I account for the *rationality of the change that the molecular gene concept underwent* in the last three decades. On my account, in spite of substantial variation in usage, the term 'gene' corresponds to a single concept (ignoring the fact that the classical gene concept is still in use even in molecular biology). Moreover, I view the molecular gene concept as used in the 1970s and 80s (the classical molecular gene concept discussed in Section 6.2) and as used nowadays (the contemporary molecular gene concept) as the same concept. The reason is that the molecular gene concept used in different research contexts or different parts of the last three decades is used to pursue the same basic *epistemic goal*: the explanation of how genes bring about their molecular products. On my semantic approach, the epistemic goal or theoretical purpose for which a concept is used is an important component of a scientific concept, and I indicated that I view this feature as the main basis for concept individuation (Section 3.3.3). While the epistemic goal pursued with the use of molecular gene concept has been stable — implying that no novel gene concept emerged in recent years — another aspect of this concept has changed significantly: the inferential role (conceptual role) associated with the gene concept. The inferences and explanations in which the term 'gene' figures have changed in the last three decades, as structural characterizations of genes as open reading frames and the assumption that there is a one–one relation between genes and gene products have ceded to significantly more complex theoretical accounts. In addition, nowadays the inferential role of the term gene may change from biological subdiscipline to subdiscipline or even from context to context. On my preferred way of concept individuation, the historical change in inferential role is just a change internal to the molecular gene concept, which does not lead to a contemporary molecular gene concept being a concept distinct from the classical molecular gene concept. (In contrast, I argued that the classical gene concept is distinct from the molecular

gene concept as apart from differences in inferential role both concepts differ in the epistemic goal pursued with their usage.)

Still, the change internal to the molecular gene concept (change of its inferential role) is in need of explanation. On my account, the change occurred in a *rational* fashion, as the changes in inferential role that occurred were based on those new empirical findings about the structure and function of genes that bear on the concept's *epistemic goal*. The inferential role of the molecular gene concept changed such that the revised concept permitted an empirically more adequate explanation of how genes bring about their products. Initially available empirical information partially warranted the assumption that genes admit a unified structural characterization where every such structural unit brings about a genetic product and every gene product is coded for by one such structurally defined stretch of DNA. Subsequent empirical findings showed that further structural features internal and external to genes bear on which product a stretch of DNA codes for (if any), and that in different cases different types of structurally defined genetic elements account for a product. In particular, the inferential role of the molecular gene concept changed so as to accommodate the fact that a genetic element may code for several distinct products (due to alternative splicing), and that several distinct genetic elements may be jointly involved in coding for a single products (due to trans-splicing). The molecular gene concept's inferential role did not just change over history, but a consequence of the finding that genes do not form a unique and homogeneous structural category is that nowadays different characterizations of genes may be given by biologists and the use of the gene concept (in the sense of inferential role) varies substantially across current biology as whole. As explained above, this variation in actual usage is conducive to biological practice. In spite of a shared epistemic goal pursued with the use of the gene concept, different biological subdisciplines may spell it out in different ways. What counts as the relevant genetic product and what counts as a mechanistic explanation of the synthesis of such a product by genetic elements may vary across biological disciplines. From a historical point of view, due to their different research focus different subdisciplines were exposed to *differential empirical pressures*. A novel empirical finding that potentially challenged previous assumptions about genes (such as alternative splicing) was an actual conceptual challenge for some types of molecular biologists. Due to the latter's research focus this finding bore on how the relevant genetic product is brought about, leading to a change in the use of the gene concept and characterization of genes among these scientists. For other types of molecular biologists, however, this empirical finding was not a conceptual challenge to their usage of the gene concept. If for instance the focus was on the mRNA produced, subsequent alternative

splicing needed not be taken into account and did not demand a rethinking of what genes are. In sum, the *stability* of the epistemic goal pursued with the molecular gene concept explains both how the inferential role of the molecular gene concept changed in the last few decades in a rational fashion (the classical molecular gene concept transmutating into the contemporary molecular gene concept), and how the current variation in usage rationally originated.

This is another way in which my account improves on Ken Waters' analysis. While Waters (1994, 2000) in his attempt to secure a shared molecular gene concept maintains that the molecular gene concept has not changed throughout history, I explicitly acknowledge that one component of the molecular gene has substantially changed and is still changing: its inferential role. At the same time I agree that there is an important sense in which the classical molecular and the contemporary molecular gene are the same concept, as there is a stability of epistemic goal. This idea also provides a basis for explaining the change in inferential role that is to be acknowledged. The historian Hans-Jörg Rheinberger (2000), instead of "trying to codify precision of meaning," called for an "epistemology of the vague and exuberant" when arguing that the flexibility in use and definition of the gene concept from classical to molecular genetics proved to be important for the possibility of experimental and theoretical advance (p. 222).[31] My notion of the epistemic goal pursued with a concept's use explains why biologists never were hostages to their tentative definitions of the gene concept: definitions and usages of the term 'gene' (inferential roles) changed in accordance with the concept's epistemic goal and the currently available empirical beliefs as to how to meet this explanatory goal. How the epistemic goal of explaining the production of gene products is spelled out in actual research contexts accounts for the current variation in usage. Likewise, in Section 6.2.2 we saw that even the shift in epistemic goal occurring in the transition form the classical to the molecular gene concept can be understood in response to the advent of novel empirical information.

[31] "Boundary objects and boundary concepts operate on and derive their power from a peculiar epistemic tension: To be tools of research, they must reach out into the realm of what we do not yet know." "... it is not necessary, indeed it can be counterproductive, to try to sharpen the conceptual boundaries of vaguely bounded research objects while in operation." (Rheinberger 2000, pp. 222–223, 221)

6.4 SUMMARY OF THE DISCUSSION OF THE GENE CONCEPT

My discussion analyzed the gene concept and its historical change based on three semantic properties, or three components of conceptual content: 1) reference, 2) inferential role, and 3) the epistemic goal pursued by a concept's use. Inferential (conceptual) role, i.e., the inferences and explanations supported by a concept, proved to be important for explaining how different gene concepts made successful scientific practice possible and for evaluating conceptual progress. The epistemic goal pursued, i.e., the theoretical purpose of a concept's use, provided the basis for accounting for the rationality of the conceptual change that the term 'gene' underwent.

On my account of the *classical gene concept*, the *epistemic goal* that is pursued with its use is the explanation of patterns of phenotypic inheritance across generations. In the period until 1915, the gene concept involved empirical misconceptions, as geneticists conflated the genotype and phenotype based on the implicit assumption that there is a one–one correspondence between genes and phenotypic traits, thereby erroneously assuming that Mendel's law straightforwardly apply to the inheritance of phenotypic traits. For this reason, it is sometimes impossible to assign referents to terms or truth-values to statements made by geneticists in this period, at least not determinate referents or truth-values (Weber 2005). Nevertheless, I suggested that an explanation of how the gene concept figured in a partially successful practice is possible in terms of the concept's inferential role (Section 6.1.1, see also 3.1.3). Once the confusion was cleared up by an explicit distinction between the genotype and the phenotype, the *inferential role* of the classical gene concept made possible a fairly adequate prediction of patterns of inheritance. On my account (Section 6.1.3), the inferences that characterize the classical gene concept include principles specifying the transmission of genes (linkage, recombination, segregation), the idea that genetic loci correspond to positions on the chromosome (explaining some features of phenotypic inheritance), the assumption that the relation between genes and traits is many–many and other ideas about the relation between genotype and phenotype (such as dominance and recessiveness). My justification for this construal of the classical gene concept was that these ideas were shared by most biologists, and account for the successful use of most uses of the gene concept, as the inferential role thusly characterized supports an explanation of patterns of inheritance as demanded by the concept's epistemic goal. In particular, these inferences were strongly rooted in the experimental practice of geneticists, as they provided the epistemic access to the study of genes, paving the way for future genetic discoveries. I pointed out that the classical gene concept is still used in contemporary population genetics, as

this gene concept — hardly embodying any knowledge about the structure and material nature of genes — is sufficient to explain changes in the distribution phenotypic traits in populations based on changes in genotype frequencies due to mutation, drift, migration, and selection (Section 6.1.4).

While this characterization of the gene concept assumes that all classical geneticists shared the same concept, in line with my *pluralism about concept individuation* (Section 3.3.2) I acknowledged that — depending on the philosophical interests pursued — it is possible to ascribe different gene concepts to different groups of classical geneticists, by assuming that each such concepts embodies more specific hypotheses about the material nature of genes (Section 6.1.3). This latter, fine-grained scheme of individuation is legitimate if the philosophical interest is to explain certain developments within classical genetics, leading to the origin of molecular genetics. The idea was that ascribing different gene concepts explains why different research groups carried out different experiments and thereby gained insights into the structure and functions of genes. In contrast, my main way of characterizing the classical gene concept — ascribing it to all classical geneticists — was guided by the philosophical interest of contrasting it with the molecular gene concept in order to highlight the conceptual progress that occurred in the transition from classical and molecular genetics.

What geneticists were primarily trying to achieve when studying genes changed with the advent of molecular genetics (Section 6.2). In contrast to the classical gene concept, the *epistemic goal pursued with the molecular gene concept* is the explanation of how genes bring about their molecular products, thereby addressing mechanisms taking place within single cells rather than the relation between the phenotypic traits of different generations. This difference in epistemic goal is one reason why I viewed the classical and the molecular gene concept as distinct concepts. Another consideration is a substantial difference in *inferential role*. While the classical gene concept does not embody any knowledge about the material nature of genes (apart from their association with chromosomes), the molecular gene concept (at least from 1960 onwards) includes detailed knowledge about the molecular structure of genes. These ideas about gene structure are significant as they explain gene function, as demanded by the concept's epistemic goal. The inferential role of the molecular gene concept includes inferences specifying the molecular structure of genes (linear stretch of DNA or RNA, start/stop codons, promoters, introns/exons, regulatory regions), and the processes in which genes figure (transcription, translation, the genetic code, the process of gene regulation). I emphasized that even if many usages of the term 'gene' refer to the coding region of a gene only (excluding regulatory regions), the gene concept (its inferential role) includes knowledge about several non-genic entities and non-coding DNA regions that account for gene expression. I

explicated the way in which the gene concept supports explanations of the production of RNAs and polypeptides by the notion of an 'explanatory strategy', assuming that the molecular gene concept embodies several of these (Section 6.2.2).

Previous analyses have emphasized that the molecular gene concept involves both structural and functional considerations. My account agrees with this by assuming that the concept's epistemic goal is the explanation of molecular gene *function* and that the concept's inferential role includes inferences specifying the *structure* of genes. Nevertheless, my analysis goes beyond traditional philosophical accounts by distinguishing two aspects of the gene concept that are different in kind: *epistemic goal and inferential role operate on different semantic levels* (whereas traditional accounts appear to take into account inferential role only by assuming that the 'definition' combines structural and functional criteria). The notion of a concept's *epistemic goal* provides a basis for accounting for the *rationality of conceptual change*. In spite of a substantial difference in epistemic goal between the classical and molecular gene concept, this shift in epistemic goal can be conceived of as occurring rationally once one philosophically analyzes the individual historical steps that made the molecular concept grow out of the classical concept. On my account, *one aspect* of the epistemic goal of the classical concept was the idea that genes are units of physiological function, since genes must produce phenotypic traits to bring about patterns of phenotypic inheritance. In the 1940s and 50s, new empirical findings about the function and structure of genes became available that bore on the physiological function of genes. It was therefore *rational* to include these ideas into the gene concept. As a result the inferential role of the term 'gene' changed, and with this novel knowledge a change in epistemic goal resulted: geneticists came to focus exclusively on the physiological function of genes, largely abandoning the aim of explaining patterns of inheritance and instead attempting to account for the genetic production of molecular substances.

The notion of *inferential role* accounts for how a concept underwrites successful scientific practice and theorizing and permits one to evaluate the progressiveness of change in practice and theorizing. The classical gene concept supports inference and prediction, namely inferring the phenotype distribution of the offspring generation from the genotype the parents. The classical gene concept can 'explain' phenotypic features only in this sense: it can infer phenotype *distributions* and explain phenotypic *differences* between individuals based on genotypic differences. But it does not support a causal-mechanistic explanation of the development of a trait in an individual based on the influence of genes, as the classical concept does not involve knowledge about the molecular structure and function of genes. The molecular gene concept, in contrast, underwrites the

mechanistic explanation of the synthesis of gene products, and can thereby indirectly explain the development of traits, once combined with other concepts and other items of biological knowledge. This substantial increase of the explanatory potential of the gene concept (due to change in its inferential role) was the basis of my claim that significant *conceptual progress* occurred with the transition from the classical to the molecular gene concept (Section 6.2.3). Previous discussion of conceptual progress in the philosophy of science have sometimes assumes that theory reduction is a sufficient condition for conceptual progress, or that stable reference is a necessary condition. However, neither situation obtains in this instance of conceptual progress. The classical gene concept cannot be reduced to molecular biology (in the sense of type-type reduction), and I explained why it is significant that the classical gene concept is still used in molecular genetics. Progress still obtains due to the above consideration and the fact that the molecular gene concept can shed some light on the processes studies by classical genetics due to the possibility of token-token reduction. Moreover, the change of the term 'gene' changed in the course of history, as the extensions of the classical and molecular gene concept are not identical in spite of large overlap. On my account, this change in reference was simply a by-product of rational and progressive change of the gene concept. Thus, in contrast to a traditional assumption in the philosophy of science about conceptual progress and incommensurability, conceptual progress is consistent with *shifting reference* once epistemic considerations such as a concept's epistemic goal are taken into account.

In the 1970s the empirical assumption prevailed that genes form a homogenous and structurally clearly defined category. As a result it seemed that there is nothing more to the gene concept than a structural definition of genes as open reading frames. However, in addition to this *inferential role*, my account of the classical molecular gene concept emphasized that also the concept's *epistemic goal* must be taken into account (Section 6.2.2). Due to the original assumption that there is a one–one relationship between genes as open reading frames and their products, it may have seemed that the epistemic goal (the explanation of how genes code for their products) could be fully reduced to the inferential role (the structural definition). However, apart from understanding the above mentioned issues, the molecular gene concept's epistemic goal proves to be philosophically significant for explaining how the classical molecular gene concept of 70s and 80s ceded to the *contemporary molecular gene concept* (Section 6.3). The epistemic goal remained stable, and for this reason I favor the idea that the so-called classical molecular concept and the contemporary concept are the same concept. Yet substantial change has taken place (occurring internal to the molecular gene concept), namely a change in inferential role and also reference. The current use of

the gene concept (in the sense of inferential role) varies substantially. Biological characterizations of what genes are and what category is precisely referred to vary among different biological fields and even among different usages of the same scientist. One reason for this is that genes are a heterogeneous kind, actually consisting of many overlapping yet distinct structurally defined categories. But in particular the fact that there is a many–many relation between genetic elements and genetic products explains why different biologists may refer to different structural categories, as focusing on one of different types of possible gene products implies viewing a particular type of genetic elements as the gene coding for this product. Thus, the epistemic goal of the molecular gene concept and how it is differently spelled out in different research context (e.g., what the gene product is whose production is to be explained) accounts for why the current variation in usage and reference of the term 'gene' is actually *conducive to biological practice* (Section 6.3.2). Moreover, the historically stable epistemic goal of the molecular gene concept shows that the change in inferential role (and reference) that occurred since the 70s occurred in a *rational* fashion: contemporary characterizations of what genes are and usages of the term 'gene' are empirically more adequate as they offer an improved account of how genetic elements produce various gene products. Thus, the rationality of conceptual change is explained by the fact that the inferential role of the molecular gene concept as used nowadays permits scientists to meet the concept's epistemic goal to a higher degree than the inferential role as used in the 70s.

Finally, I used the fact that the reference of the contemporary gene concept varies from context to context to support a *moderate holism* about the features that determine reference, i.e., the idea that the set of factors determining reference is unbounded and that the salience of each factor for reference determination may vary from context to context (Section 6.3.2, see also 3.2.2). For what determines the reference of a particular utterance involving the term 'gene' depends on various collateral beliefs of a scientist, including the particular intentions and research interests underlying a particular study of genes. While the context-sensitive reference of indexicals can be accounted for by assuming that their meaning is a function from context of utterance to extension, I pointed out that this model does not simply carry over to a biological concept such as the gene concept. For an indexical's context of utterance can be characterized in physical, non-intentional terms, whereas in the case of the gene concept it is an intentional/epistemic context that determines reference.

7.0 CONCLUSION

The task of a study of scientific concepts is a semantic analysis of scientific language and the properties of terms as used in research practice. A crucial task of semantic analysis is to understand the role of language in successful communication and practice. Semantic notions such as 'meaning', 'concept', or 'reference' gain their legitimacy and fruitfulness from their capacity to describe and explain linguistic practice. A prominent way to conduct semantics is by using a representational approach. For representational semantics, semantic analysis reduces to or at least proceeds from assigning referents to terms and truth-conditions to sentences. This approach proved to be successful for understanding the semantic properties of logical and mathematical concepts. However, the present discussion proceeded from the assumption that this need not be the case for empirical concepts; and the case studies offered support for the idea that *a purely representational framework does not fully capture the semantic features of scientific concepts*, in particular as approached from perspective of conceptual change. If semantic analysis boils down to assigning referents to scientific terms and truth-values to scientists' claims, then this leads for instance in the case of concepts involving empirical misconceptions to an incomplete or partially inadequate description of the successful use of language (Sections 3.1.3 and 6.1.1; Gupta 1999).[1] We saw that even a representationalist like Philip Kitcher is aware of the fact that being semantically committed to a forced choice as to whether the term 'phlogiston' was referential or whether it was non-referential is problematic as either option fails to capture some important aspects of the practice of phlogiston chemists (Section 2.2.1). Kitcher, however, attempted to solve this issue within the bounds of a purely representational approach by assuming that the reference of a term may change from tokening to tokening.[2] The account pursued here used a broader approach by taking further semantic

[1] Burian et al. (1996) and Bishop and Stich (1998) illustrate some dilemmas originating in the study of cases from the history of science if one is committed to assign either this or that referent (or truth-value) to a given expression.

[2] However, if neither the assumption that the term type 'phlogiston' was non-referential nor the assumption that it referred (to oxygen) does justice to what scientists believed and did, then the same situation also arises for some term tokens of 'phlogiston'. See Section 2.2.2, Psillos (1997) and McLeish (2005) for a critique of Kitcher's account that reference changes from token to token or for his account of how the reference of a term tokening is determined.

properties into account. For I suggested that in addition to reference, a) a concept's inferential role and b) the epistemic goal pursued with a concept's use are genuine components of a concept. By using the notion of inferential role I included inferential (rather than representational) aspects of concepts, especially the way in which concepts confer epistemic abilities on their possessors — in virtue of concepts supporting inferences, explanations, and guiding practical investigation.[3] *The motivation was that using these additional, non-representational semantic features offers a richer philosophical account of successful scientific practice involving language use.*

The primary concern of this dissertation was the philosophical study of conceptual change. Philosophers of science have interpreted scientific terms and approached the phenomenon of conceptual change in science primarily in terms of representational notions such as reference (Section 2.1). The reason is that most accounts of conceptual change in the philosophy of science have attempted to address the incommensurability problem, by arguing that stable reference across theoretical change is the solution. As a consequence, semantic accounts of scientific concepts have focused on the reference of scientific terms — often assuming that unchanging reference is a precondition for scientific progress — while at the same time tending to ignore the notion of meaning or being reluctant to admit that the meaning of a term may vary across time or across different theories (Shapere 1966; Burian 1987).[4] The picture emerging from the traditional literature in philosophy of science is that semantic stability is a virtue, while semantic change is epistemically problematic and not conducive to conceptual progress. Apart from the philosophy of science literature, a similar picture is present in two-dimensional semantics, as endorsed by some metaphysicians and philosophers of mind. This semantic theory focuses on meaning in addition to reference (defining meaning in a representational way), but in Section 3.3.1 we saw that it endorses what I called a preformationist picture of concepts, according to which empirical concepts do not change under the influence of experience. A concept is viewed as already embodying an account of how the concept would apply to any possible empirical scenario. As a consequence, two-dimensional semantics assumes that semantic change usually does not occur: the concept itself remains unchanging under

[3] In the discussion of Anil Gupta's (1999) approach (Section 3.1.3), we saw that his semantic account starts out with the notion of the 'effective content' of a sentence (based on the sentence's inferential role and frame), which is intended to explain successful linguistic practice. Only in a second step is the representational notion of truth-value introduced. The virtue of Gupta's analysis is that it promises a semantic account of scientific practice (based on the notion of effective content) even in cases where it is impossible to assign a unique referent to scientific terms or where a certain assignment of referents or truth-values offers an inadequate account of scientific practice.

[4] Stable reference is supposed to be a precondition for conceptual progress as in this case our conception of the referent continuously denoted by a term can improve, whereas otherwise the assumption is that our novel conception is simply about another object: "To show conceptual progress, one must show change while defending the claim that the change occurred between two representations *of the same thing*, so that the pessimistic meta-induction, and its sidekick, incommensurability, can be defeated" (a referee for the *British Journal for the Philosophy of Science*).

the influence of new empirical findings, what changes is our beliefs about which objects in our world the concept applies to. Proponents of two-dimensional semantics do not deny that it is possible that the meaning of a term changes, however, this is usually viewed as a 'change of topic', thereby considering genuine change in meaning as philosophically prohibited or irrational.

In contrast, a fundamental point of departure for the present approach was the fact that conceptual change as the change in the meaning of scientific terms is a widespread phenomenon in science, at least in biology. Moreover, I assumed that it is rational for scientific communities to change their concepts; conceptual innovation was viewed as a hallmark of scientific progress. In some cases, change of reference may occur as a consequence of progressive meaning change, so that stability of reference is not always necessary for conceptual progress to occur. If it is actually the case that change and variation in the meaning (and other semantic properties) of terms is conducive to successful scientific practice, then a semantic study of scientific terms has to offer an account of why conceptual change is epistemically significant. *While traditional accounts within and beyond the philosophy of science have assumed that meaning change is epistemically problematic, the present discussion attempted to work towards an account of concepts according to which conceptual change in science is rational.* The case studies on the homology and the gene concept exhibited semantic change in biology and offered philosophical arguments for this change being rational.

From this point of view, any account of conceptual change involves two basic components: *conceptual phylogeny*, i.e., the historical study of concepts and their change; and *conceptual ecology*, an account of the intellectual and epistemic factors associated with concept use, which may bring about conceptual change and thus account for conceptual change as a rational process. Three desiderata for any theory of conceptual change emerged from this idea. An account of conceptual change should include: a) an account of concept identity that permits the philosopher to track meaning change and detect the emergence of novel concepts; b) an intellectual explanation of why conceptual change rationally occurred; c) an evaluation of the degree to which conceptual change was progressive. In Section 2.2.1 we saw that Kitcher's theory of conceptual change and progress — one of the most sophisticated recent accounts — goes beyond the mere study of reference. Kitcher introduced the notion of a 'mode of reference' (the way in which an individual refers to a category) as a proxy for the traditional semantic notion of meaning; and he suggested that a concept is a 'reference potential' (the set of modes of reference associated with a term). As Kitcher studies conceptual change in terms of changes of reference potentials, he explicitly acknowledges that the meaning of scientific terms is subject to change. However, I criticized Kitcher's reference

based theory of concepts for failing to meet the above three desiderata in an adequate manner (Section 2.2.3), and used this critique to motivate the strategy of pursuing an account that is not restricted to representational features. Apart from the fact Kitcher is not concerned with offering an account of concept individuation (desideratum a), his account was criticized as regards the other two desiderata. First, though Kitcher is actually not concerned with putting forward a rational explanation of conceptual change, I cast doubt on the idea that his framework has the potential to be used for this purpose. Kitcher views concept possession as a person's ability to refer to categories, but this referential semantic theory leaves out aspects of scientific concepts that bring about conceptual change. (Which include the feature that concepts are used to pursue particular epistemic goals. The way in which scientists use a concept for the purpose of scientific inference and explanation may lead to conceptual change in the face of novel evidence.) Second, Kitcher offers an account of conceptual progress that basically assumes that it consists in the addition of new modes of reference. However, the idea that progress boils down to scientists finding new ways to refer to old referents leaves out crucial aspect of conceptual progress. Progressive changes in a concept also improve the epistemic abilities of those that possess this concept. Novel concepts permit scientists to justify new hypotheses, explain novel phenomena, or conduct practical discovery in a more effective way. I used this as a motivation to view the way in which a concept supports inferences and explanations as a genuine semantic aspect of a concept.[5] In sum, *traditional referential and representational approaches to scientific concepts fail to take into account some semantic features of concepts that rationally bring about conceptual change and that constitute conceptual progress.*

Based on these preliminary motivations, Chapter 3 laid out a framework of concepts and conceptual change, which was used in the subsequent case studies. My account of concepts attempted to meet the following Two Constraints on Any Theory of Scientific Concepts: A) *A theory of concepts has to explain how concepts underwrite successful practice.* More specifically, concepts figure in rational reasoning and action and are ascribed for explaining intentional behavior. Concepts are shared among individuals and serve the purposes of communication. A semantic account has to capture these aspects of concepts. B) *A theory of concepts has to explain how it is possible for a*

[5]For instance, a natural kind concept supports inductive inferences from the properties of one instance of the kind to another instance (projectability of properties), or from one property of an instance to another property of the same instance (homeostatic property cluster). Yet traditional accounts have viewed the projectability of properties or the presence of homeostatic property clusters as a feature of *natural kinds*, but have not viewed the ability to support inductive inferences as a property of natural kind *concepts*. That it, it has not been assumed that supporting such inferences is a part of the *meaning* of natural kind terms, or that the ability to carry out such inferences is a constitutive feature of natural kind *concept possession*. Instead, traditional *semantic* accounts of natural kind terms have focused on the reference of natural kind terms, in particular in the context of the causal theory of reference.

concept to rationally undergo change in the course of history. To this end, I suggested that the content of each scientific concept has three components: *1) the concept's reference, 2) the concept's inferential role, and 3) the epistemic goal pursued by the concept's use.* Even though these three semantic features are related, they are distinct components of content, as a term may change in history in any of these components, sometimes independently of other components. In this sense, each of the three semantic properties is an independent dimension of meaning. Acknowledging all three components is necessary for the following reason. Inferential role is the way in which a concept supports inference, explanation, and practical investigation. Thereby the notion of inferential role (and to a lesser extent the notion of reference) explains how concepts underwrite successful practice (Constraint A). As discussed in detail below, the notion of a concept's epistemic goal is essential in accounting for the rationality of conceptual change, in particular change in a term's inferential role and reference (Constraint B). Conceptual progress is to be assessed based on the degree to which a concept's inferential role changed (relative to its epistemic goal). In sum, scientific concepts are to be studied in terms of several semantic properties as the historical change in one semantic component can philosophically be understood as rational relative to the other components.

My semantic approach endorsed *inferential role semantics* (IRS), also called conceptual role semantics, as a prominent non-representational approach from the philosophy of mind and language. IRS has sometimes been construed as an account of what a term's semantic property is (the semantic value being a total inferential role rather than an extension). However, I understood IRS as a doctrine of philosophical semantics *sensu* Brandom (1994), i.e., as an account of in virtue of which features a term has its semantic properties. On my approach, there are different semantic properties (reference, inferential role, epistemic goal), and a scientific term having any of these is determined by the term's overall use within a scientific community. A term's *total inferential role* was my name for the total set of the inferences (in which this term figures) as accepted by an individual (where different individuals may use different total inferential roles). A term's reference, inferential role, and epistemic goal are determined by the total inferential roles used by the members of the linguistic community. In this sense, concepts supervene on total inferential roles (rather than being identical to total inferential roles). The notion of inference used here was construed more broadly than usual. First, it is to be understood as *material inference* rather than as formal inference (being accepted in virtue of its content rather than its logical form), thereby capturing explanations (material inferences involving causal content). Second, my notion of inference does not only include inferential relations between concepts, but also how concepts relate to the world in

perception and action. Thus the total inferential role of a term is the way in which a term is used in epistemic and world-engaged practice (involving language use), which includes in particular the inferences and explanations in which this term figures. *Total* inferential roles operate on the level of individuals; they can be viewed as the idiolect meanings that different individuals associate with a term. In contrast, the *inferential role* of a term as a component of a communal concept operates on the level of language communities, being the set of inferences and explanations supported by a concept as shared by a language community. Inferential role semantics is often viewed as endorsing a radical holism, the idea being that whenever two persons disagree about some inferences in which a term figures, then they necessarily associate different concepts with this term. My version of IRS, however, endorsed a moderate holism about meaning *determination*, but not a radical holism about concept *individuation*. On my approach, a scientist associates a particular communal concept with a term t to the extent that the total inferential role of t as used by this scientist provides her with sufficient epistemic abilities so that she can effectively communicate with other members of her research community and conduct successful scientific investigation.

Chapter 3 addressed several criticisms of inferential role semantics (such as the compositionality of concepts, the relation between inferential role and reference, and the sharing of concepts), in order to show that IRS is a viable semantic approach. Yet in spite of endorsing IRS my semantic framework was not defended as the right metaphysical account of the nature of concept; rather, it was developed to be used a *methodological tool* for the semantic study of historical episodes in science, to be evaluated in terms of its fruitfulness for this task. Rather than offering a clear-cut metaphysical analysis (such as a naturalistic reduction) of the semantic properties of reference, inferential role, and epistemic goal, my primary aim in these pages was to show that these semantic properties can be ascribed to some scientific terms as actually used and that the historical change of these semantic features can be studied and accounted for as rational in actual cases.

The central novelty of my semantic approach was the idea that the *epistemic goal pursued with a concept's use* is a genuine and independent component of a concept. Reference, inferential role, and epistemic goal are all determined by a term's overall use; and historical change in one semantic property may correlate with change in others. Yet they are independent semantic components as one of them can in many cases change without the others, and as these different semantic properties fulfill different philosophical functions. The notion of a concept's epistemic goal is vital for accounting for the *rationality of conceptual change*. While it is well-known that scientific fields pursue certain scientific and explanatory goals, my point was that in many cases individual

scientific concepts are used to pursue certain epistemic goals. A concept is used for certain epistemic purposes, and it is intended to yield a certain epistemic product, i.e., certain types of knowledge such as explanations or confirmed hypotheses (the conclusions of inferences). Thus, while a concept's inferential role is the inferences and explanations actually supported by a concept, its epistemic goal is the inferences and explanations that it is supposed to yield. Given that concepts are changed and shaped by scientists so as to succeed in yielding the intended epistemic product, this provides a basis for viewing conceptual change as rational and progressive. A change in a concept's inferential role (and reference) is rational if the revised inferential role (the inferences and explanations supported by the concept at this later point) meets the given epistemic goal to a higher degree than the old version of the concept.[6] Overall, traditional semantic accounts have construed concepts in terms of reference and/or assumed that a concept consists in certain *beliefs about the referent* (a definition, analytic statements, an inferential role). By introducing the notion of epistemic goal and conceiving of it as an independent component of a concept's content, my account maintained that in addition to the beliefs scientists have, another important feature of a concept is *what scientists are trying to achieve by having those beliefs* (as it accounts for the rationality of semantic change).

While the notion of a concept's epistemic goal is not part of traditional inferential role semantics, it broadly aligns with this semantic approach. First, it fits with a *non-representational* semantic approach such as IRS. For a particular concept being used to pursue some epistemic goal is *not* the idea that this concept is intended to refer to a certain category. Instead, it is the idea that the concept is intended to deliver a certain epistemic product, i.e., to yield certain inferences and explanations. Second, the idea that an aspect of a term's meaning is the epistemic goal pursued with its use supports a *moderate holism about meaning determination*, in line with traditional versions of IRS.[7] Moderate holism assumes that the factors (such as beliefs and inferences) that determine meaning form an open and unbounded set, which is explained by the idea that the degree to which a particular factor is salient is context-sensitive: in one context where a term is used by a person a statement may be salient for determining the meaning of this term, in another context (e.g., as used by another person) the same statement may be less salient. Non-holist semantic theories assume that the factors that determine the meaning of a term can be reduced to a limited and clearly delineated set of features, such as the set of analytic statements in which a particular term occurs, certain meaning-constitutive beliefs, or certain causal relations between a mental symbol

[6] Also a term's epistemic goal may change. As discussed below, in some cases this can be accounted for as rational.

[7] Moderate holism differs from *radical* holism about meaning determination, which assumes that *all* inferences (or beliefs) in which a concept figures are *necessary* to determine the meaning of this concept.

and its referent.[8] However, often the fact that a concept is used to pursue a certain epistemic goal is not constituted by *particular* beliefs that the users of this concept have. Scientists usually do not have a belief or intention that p, where p involves semantic notions such as 'concept' and 'epistemic goal pursued with concept use'. Rather, a concept being used to pursue a certain epistemic goal is determined by the overall use of this concept or larger and unbounded sets of beliefs. Out of the total set of beliefs endorsed by scientists, some are more relevant and others are quite irrelevant for making it the case that a concept is used for a certain epistemic aim, but this does not mean that a limited and precise set of beliefs can be isolated that fully constitutes the epistemic goal of concept use.[9] Neither is the epistemic goal for which a concept is used reducible to particular beliefs, nor is it determined by the total set of beliefs or the total language use of a *single* scientist. It is the whole scientific community that influences whether or not certain theoretical interests are pursued with a particular concept. In this sense, a concept cannot be identified with what a particular individual has grasped (such as a total inferential role). As a consequence, scientific concepts and conceptual change are to be studied based on how a term is used in a whole scientific community and how this usage varies within the community. In sum, *I view the epistemic goal for which a scientific concept is used as an emergent semantic property determined by the overall use of this concept in a scientific community, which cannot be reduced to particular beliefs or the total mental state of an individual scientist.* Assuming that the epistemic goal associated with a concept is a component of meaning, a moderate holism about the factors that determine meaning follows.

Given that on my account terms may change and differ in several semantic properties (reference, inferential role, epistemic goal), dissimilarity with respect to several or simply one of these features

[8]We saw another such proposal in the discussion of Kitcher's theory of concepts (Section 2.2.2). In the case of descriptive modes of reference, Kitcher appealed to a speaker's 'dominant intention' to use a certain statement as a reference-fixing (and thereby meaning-determining or analytic) statement. As a consequence, Kitcher assumes that there is a single feature — a reference-fixing statement or a dominant intention — that determines the meaning for a particular term token. My above discussion of Kitcher criticized his notion of a dominant intention to refer.

[9]Some traditional theories assume that what determines the meaning of a concept is a subset of the beliefs *involving this concept*, or a descriptive theory of reference assumes that what determines reference is a subset of the descriptions *of the referent* (statements *containing the term expressing the concept*). On my approach, in contrast, even statements that do not contain the term expressing the concept may bear on determining the concept's epistemic goal. For instance, the fact that the developmental homology concept is used for certain explanatory goals is not exhausted by statements about homologues, but by the larger research agenda of evolutionary developmental biology, which involves statements containing other central biological terms apart from 'homology'. Moreover, while biologists using different homology concepts — including users of the molecular homology concept — will assent to the statement 'characters derived from an ancestral character are homologous', this statement is highly relevant for determining the epistemic goal pursued with the phylogenetic homology concept, it is less relevant for determining the epistemic goal of the developmental homology concept, and it is irrelevant for determining the epistemic goal of the molecular homology concept. Thus, a statement being a factor determining the concept's epistemic goal *is not an intrinsic property* of this statement. Rather, the degree to which a statement is salient for determining the epistemic goal depends on the relation of this statement to other statements, i.e., on how it is embedded in a larger theoretical agenda. This context-sensitivity of a factor's relevance for meaning determination is a hallmark of moderate holism.

could be philosophically relevant and thus the basis for postulating different concepts being in use. As a result, there need not be unique criteria of *concept individuation*, and the labeling of two scientists' term use as expressing the same or a different concept may not be fruitful without further explanation. My discussion on concept individuation in Section 3.3 criticized the meaning monism that is endorsed by most contemporary semantic approaches. Meaning monism is the idea that concepts have unique and determinate meanings and that a concept can be individuated in a unique and clearly delineated way. The standard strategy is to arrive at this position by developing an analytic/synthetic distinction or another distinction between meaning-constitutive and non-constitutive features (such as beliefs or inferences). I criticized some such proposals as to how to individuate concepts, in order to motivate an alternative approach — *meaning pluralism*, i.e., the idea that some scientific concepts can be individuated in more than one way. My claim was not to have refuted meaning monism; rather, my intention was to provide a way to individuate concepts and to show that conceptual change can be studied without making use of a pre-given notion of analyticity or another individuation criterion. As an analogy, I used the individuation of languages and the change of dialects as studied in linguistics. My suggestion was that each instance of concept ascription is based on particular philosophical purposes, which may vary from case to case. Since the same concept can by approached in different studies with different philosophical aims in mind, different studies may individuate this concept in a different way. An implication of my approach is that the philosophical burden is not to spell out and defend a unique criterion of concept individuation that can be applied to every concrete case. Rather, on my account the task for each instance of concept individuation is to spell out the particular individuation criteria used in this case and to offer a philosophical defense for this manner of individuation. Consequently, my cases studies made explicit the philosophical purposes that underlay my individuation decisions, and pointed to the philosophical insights that each such way of individuation yielded.

Critics of inferential role semantic have constructed a straw man by assuming that IRS individuates meaning in terms of total inferential role, so that two persons always possess different concepts (Section 3.3.2). My account definitely does not conform to the straw man position, as my case studies used two basic guidelines for individuating scientific concepts as suggested by Section 3.3.3. *First*, I construed the *inferential role* of a concept as consisting of those inferences and explanations that account for the successful use of this concept in biological practice. I did not assume that for two persons to share a concept it is necessary that they endorse the same set of inferences. For while concept possession presupposes having certain epistemic abilities (such as carrying out infer-

ences), in the case of a scientific concept these epistemic abilities may be spread out over a whole community, so that the successful communal use of a concept may be dependent on some scientists making different inferences. Thereby I did not endorse the traditional picture according to which two persons share a concept if they have grasped the same definition or accept the same analytic statements. Rather, concept possession consists in having a minimal set of inferential dispositions and epistemic abilities so as to be able to meaningfully communicate with other scientists and to conduct scientific research. *Second*, apart from the semantic feature of inferential role, in my case studies *epistemic goal* was the most salient semantic property for concept individuation, in that I usually ascribed the same concept to different scientists provided that they used a certain term to pursue the same scientific goals. The idea was that scientists count as investigating the same phenomenon and pursuing the same scientific problem not if they merely happen to refer to the same entity with a term, but if they use this term for the same epistemic purpose. Different scientists will react to novel empirical findings and challenges in similar ways and be able to communicate with each other to the extent to which they use a term to pursue the same epistemic goal, so that this semantic property is significant for concept individuation. In several cases my discussion explained a rational change in a concept's inferential role (and reference) relative to its stable epistemic goal. This shows that a concept's epistemic goal is historically more stable than its inferential role. Thus, individuating concepts in terms of the epistemic goals pursued by concept use yields an account of conceptual stability despite theoretical change (such as change in inferential role).

7.1 PHILOSOPHICAL INSIGHTS YIELDED BY THE APPLICATION OF THE FRAMEWORK OF CONCEPTS TO THE CASE STUDIES

Chapter 4 discussed the homology concept as used until 1950. I challenged the common assumption that the advent of Darwinism brought about a novel homology concept, a 'phylogenetic' or 'evolutionary' homology concept being distinct from the pre-Darwinian 'idealistic' homology concept. While this assumption among biologists and historians and philosophers of biology has never been explicitly argued for, it is based on the fact that unlike pre-Darwinian biologists, post-Darwinian biologists often defined homology in terms of common ancestry. (My discussion showed that this was not exclusively the case, though.) Against this common wisdom I argued that evolutionary theory did not bring about a novel homology concept in the 19$^{\text{th}}$ century. Motivated by my seman-

tic framework, my historical discussion paid attention to those features of the homology concept's actual use that were *the basis of its successful use in biological practice* (inferential role).

My claim that there was a single homology concept used throughout 19$^{\text{th}}$ century biology was backed by two reasons (Section 4.4). *First*, the actual usage (inferential role) of the homology concept did not change much with the advent of evolutionary theory. The main criteria of homology were established in pre-Darwinian anatomy, and Darwinism did not add a novel homology criterion. (A genuinely novel criterion was introduced not before 1960.) Despite the fact that many post-Darwinian biologists defined homology in terms of common ancestry, they did not establish homologies based on phylogenetic trees; instead they arrived at homologies in the same way pre-Darwinian morphologists had done. Apart from establishing homologies, I emphasized that the homology concept supported important types of inferences and yielded significant items of biological knowledge. The concept underwrote inductive inferences from the properties of a structure in one species to the properties of the corresponding structure in another species. As a consequence, the homology concept yielded unified comparative and morphological descriptions of the properties of groups of organisms. Comparison of homologous structures in different species also provided the basis for classification of species into higher taxa. Post-Darwinian biologists — in addition to establishing morphological generalizations and taxonomic classifications — used the homology concept to establish phylogenetic trees. Yet this proceeded simply by reinterpreting previously known morphological relations between structures and taxonomic relations between species as reflecting common ancestry — no genuinely new evidence was needed to arrive at phylogenetic trees apart from the kind of evidence available to pre-Darwinian biologists. In addition to this continuity in usage, my way of individuating the homology concept highlights the epistemic potential of this concept as already used before the advent of Darwinism. For the homology concept enabled pre-Darwinian biologists to establish various morphological and taxonomic facts that formed a good deal of the evidential basis for the acceptance of the idea of common ancestry, and that provided the evidence for the establishment of phylogenetic trees. *Second*, in addition to this substantial continuity in inferential role, the concept exhibited strong stability with respect to the *epistemic goals* pursued with its use. Throughout the 19$^{\text{th}}$ century the concept's epistemic goals were the morphological description of groups of organisms and the classification of species. The advent of evolutionary theory did not introduce so much a novel epistemic goal for the homology concept — the study of phylogeny — but phylogeny became an essential tool for pursuing the traditional goals of morphological generalization and taxonomic classification. Thus, despite introducing novel theoretical

interpretations of homology, the advent of evolutionary theory did not change what biologists were trying to achieve by the use of the homology concept. This provides a further reason for the idea that the term 'homology' as used by pre- and post-Darwinian biologists was the same concept.

Apart from the question of concept identity, *the stability in the homology concept's epistemic goal accounts for the rationality of the historical change in inferential role.* In spite of continuity, the concept's inferential role did change to some extent due to the advent of phylogenetic interpretations of homology. Even though this was a change occurring internal to the concept (given my account of concept identity), the change in inferential role has to be accounted for. The historical study discussed that phylogenetic interpretations of morphological and taxonomic relations (including homology) came to be accepted precisely because the phylogenetic approach provided a more sophisticated way of pursuing the traditional morphological and taxonomic goals. Thus, the revised inferential role provided a more effective way of meeting the stable epistemic goals.

The homology concept is an eminently theoretical concept, in that it is based on a theoretically sophisticated practice of establishing homologies and provides the conceptual and theoretical basis for various domains of knowledge (morphology, systematics, evolutionary biology, among others). However, it is far from the case that the content of the homology concept is given by certain theoretical definitions, or by how it figures in statements of a putative theoretical language (as it has been contrasted by a putative observational language). For some scientific concepts, it may the case that their meaning is largely given by theoretical definitions; and for such a concept it is possible that what used to be considered an instance of the kind (denoted by the concept) according to previously used criteria comes to be rejected as kind member in case it fails to satisfy a novel theoretical definition. The homology concept is not a concept of this type. *It is a theoretical concept whose content is significantly determined by how homologies are established in practice.* The successful use of the homology concept in biological practice and theory is strongly tied to criteria of homology and the morphological and taxonomic practice organized around well-established instances of homology. Overall, possessing the homology concept is a practical ability that does not boil down to knowing statements expressing definitions or basic criteria of homology. This feature of this biological case supports my choice to construe the notion of 'inference' (and thereby 'inferential role') used here in a broad fashion. I emphasized that in addition to inferential relations between concepts, *my notion of inference includes how concepts relate to the world by being practically applied to objects and figuring in action.* Only on this broad construal — which views inference as world-engaged practice — is it possible to maintain that the content of the homology concept is determined by

how it figures in inference. A more traditional construal of the meaning or reference of theoretical terms, which assumes that a theoretical term is defined by explicit theoretical statements or how it figures in an overall theory construed as a set of sentences (Ramsey 1931; Carnap 1966; Lewis 1970; Papineau 1996), fails to give a satisfactory account of the content of the homology concept as a central theoretical concept. Finally, the homology concept is a natural kind concept, referring to classes of natural kinds (each class of homologues forms a natural kind). The case study also showed that a crucial aspect of scientists possessing a *natural kind concept* is their ability to carry out important types of *inferences*, in addition to the property of referring to a category.

Chapter 5 was concerned with the development of the homology concept during the last 60 years. This study was strongly guided by the heuristic focus of my framework of concepts: studying semantic change in terms of the inferences and explanations supported by concepts, and the epistemic goals pursued by concept use. I maintained that nowadays the term 'homology' corresponds to three distinct concepts, which are used in evolutionary biology and systematics, in evolutionary developmental biology, and in molecular biology, respectively. The argument was that each homology concept supports different types of inferences and explanations and is used for different epistemic goals in these different fields.

The *phylogenetic homology concept* (used in systematics and evolutionary biology) primarily supports inferences. It yields unified descriptions of organisms and provides the evidence for classification and the establishment of phylogenies. In evolutionary biology, the fact that homology refers to a lineages of characters that can undergo evolutionary transformation is the basis for describing evolutionary change, and in this sense a precondition for explaining evolutionary change. The epistemic goals for which the phylogenetic homology concept is used are the comparison and taxonomy of species and the study of descent with modification. *Evolutionary developmental biology* (evo-devo) attempts to explain evolutionary phenomena, and for this reason some of its theoretical aims overlap with the ones of traditional evolutionary biology. However, evo-devo has some distinct explanatory goals that are peculiar to this approach. This is the explanation of the evolutionary origin of body plans and structural novelties, and the explanation of how phenotypic variation and morphological evolvability is possible. One ingredient to solve these problems is a developmental account of homology, i.e., an account of the developmental and morphological factors that constitute the organization of organisms into morphological units or characters (homologues), such that variation and evolutionary change within a unit is possible, while the overall number of units and their relative functional integration and developmental organization is stable. In sum, the epistemic

goal pursued with the *developmental homology concept* is the explanation of morphological unity within and between organisms. A central assumption of evo-devo biologists is that developmental considerations and causal explanations are necessary to arrive at an account of morphological unity and an explanation of why the same structure develops repeatedly in different generations and species, and in different parts of an individual. As a consequence, the developmental homology concept is intended to support causal-mechanistic explanations. Due to ongoing empirical research, the conceptual role (inferential role) of the developmental homology is changing, and currently its explanatory potential is still limited, but it differs from the phylogenetic homology concept which does not support causal-mechanistic explanations, but inferences only. Finally, the *molecular homology concept* is tied to the experimental agenda of molecular biology (molecular biology excluding molecular phylogeny and molecular evolutionary biology, which use the phylogenetic homology concept as it applies to genes and proteins). It is an operational concept in that it uses sequence similarity between genes and proteins — which phylogenetic approaches would view as a mere criterion of homology — as its definition. The molecular homology concept does not distinguish between similarity due to common ancestry and to evolutionary convergence, thereby failing to make the homology/analogy distinction of phylogenetic approaches. For this reason, the molecular homology concept does not support phylogenetic inferences as the phylogenetic homology concept does. (And it also does not support the explanations of the developmental homology concept as molecular biology is not concerned with higher-level development and morphological organization.) In molecular biology the epistemic goal is the discovery of molecular mechanisms and the explanation of molecular phenomena. The molecular homology concept permits biologists to infer information about the molecular behavior of genes and proteins (and their parts), particularly in order to guide further experimental investigation and technological manipulation.

The differences between these homology concepts are genuine differences in meaning as they are rooted in different epistemic goals, rather than disagreements about particular biological facts. Thus, this way of individuating homology concepts highlights semantic differences between different biological fields that have a significant epistemic basis — namely, *how the same term is used for distinct explanatory and theoretical goals in different biological fields.* It also provides a *basis for the rational explanation of conceptual change.* On my account, in the second half of the 20$^{\text{th}}$ century the original homology concept became integrated into newly developed specialized subdisciplines. It is not surprising that different fields use a term in slightly different ways, and that different disciplines have different scientific aims. Chapter 5 showed something stronger, namely, that the different

biological fields discussed actually used the homology concept to pursue their specific epistemic goals. This led to conceptual variation among these fields in the use of the term 'homology', and to conceptual change as the homology concept within a particular field came to support specific types of inferences or explanations differing from the homology concept used by another discipline. Eventually, three distinct homology concepts originated. This instance of conceptual change is rational as each specialized homology concept (more precisely its inferential role) changed so that it came to meet the epistemic goals associated with its use to a higher degree. Different biological fields demand for particular epistemic products (certain types of knowledge), and the homology concept as used in a biological subfield changed so as to yield this epistemic product to a higher extent in virtue of underwriting inference, explanation, and discovery of a certain kind.

The philosophical tenet that the development of novel homology concepts is rational and to some extent progressive does not imply that one of these concepts is superior to others and can or should replace them. The molecular homology concept, for instance, as an operational concept is incapable of underwriting phylogenetic research as done in evolutionary biology. My claim that the emergence of the molecular homology concept is rational refers to the fact that this novel concept is an effective tool for molecular and biomedical research. In the case of the species concept, philosophers have prominently debated the issue of pluralism, i.e., whether the contemporary existence of different species concepts reflects the fact that several concepts are scientifically useful and necessary, or whether there is only one true species concept, to be established in the future.[10] My present discussion supports a *pluralism about homology concepts*. An implication for biological practice is that the debate between different fields about the right understanding of 'the' homology concept is of limited use. Different homology concepts can coexist because each is an effective tool for certain purposes. A biologist can stick to the homology concept used by her field — as long as it is explicitly recognized that there are other homology concepts that satisfy different theoretical needs. This upshot is not to be construed as the idea that the current situation has to persist. I do not claim that biology in general must necessarily have three or more homology concepts or that none of the current homology concepts might disappear in the future. My pluralism about homology concepts is based on a philosophical reflection on the current empirical situation, leading to the claim that the emergence of different homology concepts is rational and to some extent progressive.

My tenet that currently there are different homology concepts in use was reflected by the ter-

[10]See Brigandt 2003b; Dupré 2001; Ereshefsky 1998; Ghiselin 1987; Hull 1987; Kitcher 1984; Mayden 1997; Mayr 1987; Mishler and Brandon 1987; Mishler and Donoghue 1982; Mishler and Brandon 1987; Stanford 1995.

minological distinction between the phylogenetic, the developmental, and the molecular homology concept. However, this argument for the existence of different homology concepts must not be construed as the idea that these are incommensurable concepts. For there is some overlap between each of them. In fact, I referred to these three concepts as *homology* concepts. One reason is terminological: each of the three concepts is expressed by the term 'homology'. Another reason is historical: the three concepts are historically derived from the original homology concept, as used in the 19$^{\text{th}}$ century. Apart from these more trivial issues, each of the three concepts can be considered a homology concept as there is some overlap in content, including reference and inferential role, but also epistemic goal (generically construed). At least biologists can to a relevant extent successfully communicate with each other using the term 'homology'.[11] This holds in particular for the phylogenetic and the developmental homology concept. Traditional evolutionary biology and evo-devo address evolutionary questions and agree on many issues about the nature of evolution. Both approaches view homologues as characters that form phylogenetic lineages and may undergo evolutionary change. Both fields agree on the criteria of homology and on the main instances of homology. For this reason, in most general contexts, biologists from systematics, traditional evolutionary biology, and evolutionary developmental biology can perfectly communicate and convey information about homologues which can be successfully used by researchers from another field for biological theorizing and practical investigation. When it comes to more specialized ideas, though, that are peculiar to one approach (e.g., the question of whether homology is a purely phylogenetic or also a structural-developmental phenomenon, or the issue of serial homology), then discourse and understanding across fields can be problematic due to the different theoretical agendas and epistemic goals of these approaches. In the case of the molecular homology concept, the conceptual overlap with other homology concepts is much lower. Still, communication is possible in many circumstances as biologists from other fields are typically aware of the peculiar usage of the term 'homology' among molecular biologists. Biologists with a phylogenetic understanding of homology among genes such as molecular evolutionary biologists or molecular systematists use the notion of sequence similarity themselves — albeit as one criterion of homology, which they terminologically do not identify with homology, unlike most molecular biologists.

One semantic upshot is that the homology discussion illustrated the fruitfulness of my framework of concepts, as an approach that is not restricted to representational aspects of content (reference).

[11] For this reason, my terminological distinction between 'phylogenetic homology', 'developmental homology', and 'molecular homology' belongs to the philosophical metalanguage used for a semantic analysis of science; it is not the terminological recommendation that biologists should stop using the term 'homology' and instead use different terms.

The case study showed that studying concepts in term of inferences and explanations supported by them yields a good account of how the successful biological use of the homology concept. In addition, the appeal to the epistemic goals pursued with concept use — which likewise relate to inferences, explanations, and other epistemic products of concept use — proved to be instrumental for the rational explanation of conceptual change. Another semantic issue addressed in Chapter 5 was theories of reference. I used the discussion of the phylogenetic and the developmental homology concept to *criticize both causal and traditional descriptive theories of reference* (Section 5.2.4). The causal theory of reference offers an inadequate account as it leaves out several features that constitute the successful use of a concept and thereby determine the meaning and reference of this concept. On my account, both causal and standard descriptive approaches use too narrow a basis for accounting for reference determination, as they leave out pragmatic and epistemic features associated with concept use. I suggested that the epistemic goals pursued with concept use are an important determinant of reference. This idea supports a *moderate holism about the factors that determine reference*, as the features that constitute the fact that a particular concept is used for certain purposes do not boil down to particular causal relations or beliefs/descriptions. For instance, the fact that the developmental homology concept is used for certain explanatory purposes is not exhausted by statements about homologues (i.e., by descriptions of the referent of the term 'homology'), but by the larger research agenda of evo-devo, which involves statements containing other central biological terms apart from 'homology'. This is in conflict with descriptive theories of reference as traditionally construed, which assume that reference is *fully* determined by certain descriptions *of the referent*. An advantage of my approach is that it uses a feature relevant for reference determination that yields clear differences between different concepts. In spite of the moderately holist way in which it is determined that the phylogenetic homology concept is used for certain purposes, it is quite clear-cut that the phylogenetic and the developmental homology concept are used for distinct epistemic goals — which was important for my claim that both concepts have different extensions. In addition, the fact that a certain concept is used for certain epistemic purposes yields a more principled way of determining to which extent a certain causal relation or a belief/description is actually relevant for reference determination — an individual factor is salient for and bears on reference fixing to the extent it is relevant for the epistemic goal. Finally, beliefs and causal relations may vary between individuals, even if they bear on reference determination. The epistemic goals associated with concept use are subject to less variation across individuals and across time. Overall, my homology case suggests that theories of reference that include descriptive

factors should not focus exclusively on beliefs about the referent as determinants of reference, but also take into account what individuals try to achieve by having currently certain beliefs — a stable feature that points at more fundamental factors of reference determination.

Chapter 6 discussed the history of the *gene concept*. In the 20$^{\text{th}}$ century, the term 'gene' changed along all three dimensions of content (reference, inferential role, and epistemic goal), and I used similarity of epistemic goal as the main criterion of concept individuation. I distinguished a classical and a molecular gene concept and maintained that the transition from the classical to the molecular concept was an instance of rational semantic change and conceptual progress. The classical gene concept has been largely, but not fully replaced by the molecular gene concept. The classical gene concept cannot simply be reduced to molecular biology, and I offered some considerations about their relation by showing how both concepts are used and needed for certain biological tasks in molecular biology. I also pointed out that the extensions of these two gene concepts overlap, but are not identical, so that a shift of referring from one to another kind occurred with the transition from the classical to the molecular gene concept. Discussions about incommensurability and the pessimistic meta-induction have often assumed that stability of a term's reference is a necessary precondition for conceptual progress, where progress consists in improved views about the unchanging referent. In contrast to this traditional assumption, I argued that *the molecular gene concept largely replacing the classical gene concept is an instance of conceptual progress, despite a shift in reference. A satisfactory case for this tenet cannot be made, however, if one uses a purely representational semantics.* This instance of semantic change cannot adequately be understood based on the idea that the novel molecular gene concept enabled geneticists to refer to a new kind, or the idea that molecular geneticists acquired new intentions to refer. My account of conceptual change essentially relied on non-referential semantic features, assessing the progressiveness of concept change based on the semantic property of inferential role, and accounting for the rationality of conceptual change based on the semantic notion of epistemic goals being pursued by concept use. On this account, the change in reference that occurred (largely unbeknownst to geneticists) was a mere by-product of rational and progressive change in meaning (Section 6.2.3).

More precisely, in order to discern conceptual progress, Sections 6.1 and 6.2 contrasted a classical and a molecular gene concept. I explicated the inferential role of the two concepts (the inferences and explanations they support). The classical gene concept primarily supports inferences, namely, the prediction of Mendelian patterns of inheritance. This feature of the classical gene concept was strongly entrenched in the practice of classical geneticists who carried out experimental studies of

special features of inheritance. It also provided the basic epistemic access to classical genes, which were detected in terms of the patterns of phenotypic inheritance they bring about. On my account, classical genes were defined in a functional way, in terms of their functional role in phenotypic inheritance. This construal of the classical gene concept as a tool of inference and prediction fits with the fact that this concept could support explanations only in a very limited way. Classical geneticists could explain phenotypic *differences* in terms of genotypic *differences* (e.g., explaining an abnormal phenotype with reference to a mutated gene); but a direct explanation of how and why certain phenotypic traits develop was impossible. On my account, the molecular gene concept filled precisely this gap. While beliefs about the material nature of genes were irrelevant for the content of the classical gene concept beliefs about the material structure of genes are meaning-constitutive for the molecular gene concept and account for its explanatory potential. I explicated the molecular gene concept (its inferential role) as supporting inferences about the structural properties of genes, which account for how genes figure in molecular mechanisms and bring about their products. I construed the molecular gene concept as embodying so-called explanatory strategies, which are schemata referring to types of molecular mechanisms and ways in which genes and other structural elements causally interact. Even if the molecular gene concept refers to DNA segments with a certain structure (coding regions), the concept itself involves knowledge about other entities (such as regulatory regions) and gene function, so that the molecular concept underwrites the explanation of how the expressions of genes is regulated. As a result, the molecular gene concept supports causal-mechanistic explanations and a direct explanation of the origin of phenotypic traits (at least on the lower levels of organization) when combined with other notions. The transition from the classical to the molecular gene concept is an instance of conceptual progress as the molecular gene concept supports significant types of explanations that the classical gene concept cannot support.

Apart from a significant difference in inferential role, my main reason for considering the classical and the molecular gene concept as distinct concepts was the fact that both are used to pursue distinct *epistemic goals*. In the case of the classical concept, this is the prediction of patterns of inheritance; in the case of the molecular concept, it is the explanation of how genes bring about their molecular products. The molecular gene concept growing out of the classical gene concept can be accounted for as rational, even if in this case the very epistemic goal pursued by a term's use changed (Section 6.2.3). On my account, *one aspect* of the classical gene concept's epistemic goal was the idea that genes are units of physiological function (as genes bring about patterns of inheritance in terms of their phenotypic function). Novel findings about gene structure and

function modified the term's inferential role in the 1940s and 50s, and this occurred in a rational fashion because these new ideas shed significant light on the cellular and physiological function of genes, thereby bearing on the epistemic goal of the *classical* gene concept. Yet this semantic change eventually led to a change in the term's epistemic goal, with the molecular gene concept focusing exclusively on the molecular function of genes (which is a modification of what used to be only one aspect of classical concept's goal). Thus, taking the classical gene concept's epistemic goal into account provides a basis for viewing the transition from the classical to the molecular gene concept — including the occurring change in inferential role and reference — as rational.

This account was guided by the philosophical aim of studying conceptual progress. As a consequence, I contrasted 'the' classical gene concept with 'the' molecular gene concept. This construal of the classical concept viewed it as shared among classical geneticists, thereby abstracting from all disagreements among biologists regards genes, in particular their material nature. Yet Section 6.1.3 also suggested another way of individuating the classical gene concept, in accordance with my *meaning pluralism*. If the philosophical aim is not to study conceptual progress, but to offer an epistemological account of the intellectual development in classical genetics, then a more fine-grained scheme of individuation is advisable. I distinguished several gene concepts, each of which was used by a part of the total community of classical geneticists, e.g., a particular research group or geneticists with a certain approach. Different such classical gene concepts embody different beliefs about the material nature of genes. This way of individuation permits a more fine-grained study of conceptual change, e.g., in case some scientists changed from using one concept to another in their scientific career. In particular, the differences between alternative gene concepts highlighted the epistemic factors that determined biological practice and the epistemic differences that brought about intellectual change. Differences in views about the material nature of genes explain why different geneticists chose to side with different research approaches and conduct different experiments. Some of this research yielded insights into the structure and function of classical genes and provided important clues for further experimental investigation.

Previous philosophical accounts of the molecular gene concept have pointed out that its definition includes both structural and functional considerations. While this is true, on my account the fundamental distinction is not between structural and functional considerations (being part of the concept's definition or inferential role), but between the concept's *inferential role* and the *epistemic goal* pursued by its use.[12] The novelty of my approach is to introduce the notion of epistemic goal

[12]Structural and functional considerations are both relevant on my account, precisely because the molecular gene

as a genuine component of a concept; and we saw above that acknowledging this semantic property provides a way to distinguish the classical and molecular gene concept, and to account for how the latter emerged rationally out of the former. Furthermore, distinguishing a concept's epistemic goal from its inferential role is vital for understanding the rational change that the molecular gene concept underwent in the last few decades (Section 6.3). On my account, the *classical molecular* gene concept (used in the 1960s and 70s) and the *contemporary molecular* gene concept can be considered the same concept as they are used to pursue the same epistemic goal (the explanation of how genes bring about their products). Yet their inferential roles differ, and this change that recently occurred in the *inferential role* of the term 'gene' (change internal to the molecular gene concept on my account) can be counted as rational relative to the concept's *stable epistemic goal*.

Geneticists of the 1960s and 70s believed that there is a one–one correspondence between genes and their products and that genes form a homogeneous category. The classical molecular gene concept, more precisely its inferential role, reflected the assumption that there is a unique structural definition (characterizing genes as open reading frames) that picks out genes as the entities that code for gene products. However, it turned out that the relation between genetic elements and gene products is many–many and that genes form a very heterogeneous category in that in different cases different types of structural entities produce a product. As a result, the usage (inferential role) of the contemporary gene concept varies strongly, in particular across the various biological subbranches that study genes or use findings from molecular biology. Different biologists — or also one and the same person in different contexts — may make use of different considerations and criteria of what characterizes and individuates a gene. Genes are best viewed as forming a set of various overlapping, yet different structurally defined categories. As the term 'gene' may refer to one or the other of these categories, nowadays the reference of the gene concept varies from context to context. On my account, *this variation and context-sensitivity in usage and reference is conducive to biological practice*, which can be explained by the molecular gene concept being used for a generic epistemic goal: the explanation of how genes bring about their products. This epistemic goal may be spelled out differently in different research contexts, e.g., the focus can be on RNAs as a proximal gene product or on proteins as a more distal gene product. Due to the many–many relations between genetic elements and their products, focusing in the same case (genetic region) on different products may lead to different accounts of what the gene is that codes for the product considered. As it is

concept's epistemic goal is the explanation of gene *function*, while its inferential role (in addition to ideas about gene function) includes information about gene *structure*, which is essential to account for gene function.

legitimate to focus on different types of products and different aspects of gene function in different contexts, different characterizations of genes may be necessary in different cases.

The contemporary molecular gene concept (its context-sensitive inferential role and reference) originated in a rational fashion out of the classical molecular concept. For the inferential role of the molecular gene concept changed in the last few decades so as to integrate novel findings about the *structural* basis of gene *function*, which was epistemically warranted precisely because the concept's (unchanging) epistemic goal has been to account for gene function. As a result, nowadays the molecular gene concept meets the epistemic goal to a higher extent than the molecular gene concept as used in the 70s. The discussion explained the historical emergence of the concept's diversification and current fragmentation by differential epistemic pressures operating on different biological fields or research contexts. Biologists from different fields may have different research interests and consequently react differently to novel findings that challenge traditional assumptions about genes, leading to a different usage of the molecular gene concept across different biologists. My account of the *variation* in the molecular gene concept showed that this concept and its historical development can be philosophically understood only if one *studies how this concept is used across a whole scientific community*, rather than how a seemingly representative individual scientist uses the concept. Overall, the discussion illustrated that a semantic account of the gene concept has to take into account the *epistemic and pragmatic features associated with concept use*.

Apart from the idea that the context-sensitive reference of the contemporary molecular gene concept is conducive to biological practice, I also used the fact that reference shifts from context to context to argue for a *moderate holism about the factors that determine reference* (Section 6.3.2). Moderate holism is the idea that the features that determine reference (such as utterances and beliefs) form an open and unbounded set, and that the degree to which one such factor is relevant for reference determination depends on the particular context. As a particular factor may be irrelevant in most contexts but turn out to bear on reference determination in certain special contexts, the total set of features that influence reference is unbounded. Moderate holism is able to explain the context-sensitivity of the contemporary gene concept in terms of how a particular epistemic context in which the term 'gene' is uttered influences the salience of factors determining reference. In different epistemic contexts different factors are salient, which may in some cases lead to reference to a different category. In contrast, an alternative approach that assumes that the reference of a concept is determined by a unique and clearly delineated set of reference fixing conditions cannot account for reference shift from context to context. Furthermore, while indexicals are a well-known

type of case where a word's reference is essentially context-dependent, I argued that standard semantic accounts of indexicals do not straightforwardly carry over to a biological concept such as the gene concept. The reference-determining context of an indexical can to a relevant extent be specified by the physical location of the utterance, and thus in non-intentional terms (so that an indexical can be formally modeled as a function from centered worlds to referents). In contrast, the context that determines the reference of the term 'gene' is fundamentally an epistemic and intentional context, which involving many of the speaker's collateral beliefs and intentions.

7.2 SUMMARY AND IMPLICATIONS OF THE CASE STUDIES: CONSTRAINTS ON ANY THEORY OF CONCEPTS

My discussion studied the historical change of concepts along 3 dimensions of content: *reference, inferential role, and epistemic goal*. Acknowledging different components of content and studying concepts in these terms proved to be fruitful for explaining how concepts make successful practice possible, and especially for understanding semantic change. Overall, reference was the least important semantic property for these philosophical tasks. While many traditional accounts of conceptual change have focused on reference and chosen not to talk about meaning, this is inadequate for two reasons. First, my case studies showed that a term's meaning in the sense of inferential role (and also its epistemic goal) may change in the course of history. Pointing to stability of reference (while sweeping meaning change under the carpet) does not explain why change of meaning can occur in a rational fashion and why variation of meaning within an overall community may be compatible with successful communication. Second, my case studies showed that even a term's reference may change in the course of history, and may vary within a scientific community. It is therefore in need of explanation why reference can rationally change and why context-sensitive reference may be conducive to scientific practice. A theory of reference alone cannot account for this.

Despite the traditional focus on reference, the notion of reference is of low importance in explaining conceptual change. My case studies showed that primarily the notion of *inferential role* accounted for how concepts make successful practice possible, and it provided the basis for assessing conceptual progress as increase in success. The notion of *epistemic goal* yielded the basis for accounting for the *rationality* of change in inferential role and reference. Given an unchanging epistemic goal being pursued with a concept, this concept demands certain inferences and expla-

nations, and a change in the concept's inferential role is rational provided that the revised concept (in virtue of its novel inferential role) is in a better position to yield these inferences and explanations. (Examples were the advent of a phylogenetic definition of homology in the 19$^{\text{th}}$ century, and the change internal to the molecular gene concept leading to the contemporary molecular gene concept.) Reference may change together with a modification of a concept's inferential role, and in this case change in reference is rational as well. While such an account of the rational change in inferential role and reference presupposes stability of epistemic goal, we saw that even this component of content may change, eventually leading to novel concepts such as the three contemporary homology concepts growing out of the 19$^{\text{th}}$ century concept, or the molecular gene concept emerging out of the classical gene concept. Yet even change in epistemic goals can be rational. In the case of the advent of the contemporary homology concepts, a more generic goal was replaced by more specific goals, or an epistemic goal came to be pursued that had not been addressed before. For in the case of the emergence of the molecular gene concept, novel findings became available that were relevant for *one aspect* of the *classical* gene concept's epistemic goal, leading to a rational change in inferential role, but eventually transforming even the epistemic goal (the molecular gene concept exclusively addressing what used to be only one aspect of the gene concept's epistemic goal).

The dissertation attempted to demonstrate the fruitfulness of my framework of concepts by pointing to the philosophical insights that it yields once applied to concrete cases of conceptual change from the history of biology. However, my claim is not that alternative semantic accounts cannot possibly yield equivalent insight. Still, apart from illustrating the merits of my approach, the case studies entail certain constraints for *any* theory of concepts, at least biological concepts. Independently of whether one favors a representational or a non-representational semantics (such as IRS), independently of whether one uses an atomist, a localist, or a holist semantic theory, the discussion of my two case studies revealed the following features of some biological concepts that any theory of concepts and conceptual change must take into account and account for.

The case studies gave examples of how concepts figure in actual scientific theorizing and research practice. The different cases and historical episodes considered showed that the kind of concept usage and the way in which a concept underwrites successful practice may vary from concept to concept. For instance, in contrast to some other theoretical concepts (as found in physics) whose content is largely given by theoretical definitions, the homology concept is a theoretical concept whose content is strongly dependent on criteria of homology and how homologies are established in practice and used for further research. While the homology concept as used in the 19$^{\text{th}}$ century,

does not exhibit much variation in actual usage (despite different theoretical interpretations of homology), the contemporary molecular gene concept varies strongly in usage and its successful use is fundamentally dependent on the context-sensitivity of practical usage. Thus, any semantic theory has to account for how concepts enable successful communication and research practice, which makes it necessary to capture the peculiar usage of particular concepts.

Semantic changes in biology are widespread, including changes in the meaning of concepts, changes in reference, and the emergence of novel concepts. Not every instance of semantic change need be rational, but for the most part conceptual change is rational. Semantic change and conceptual innovation is a hallmark of scientific progress, at least in biology. The case studies discussed several cases of conceptual change: the 19$^{\text{th}}$ century homology concept acquiring a phylogenetic interpretation of homology, the origin of three novel homology concepts in the 20$^{\text{th}}$ century, the advent of the molecular gene concept, and the emergence of the contemporary molecular gene concept (out of the classical molecular gene concept). My account offered some philosophical ideas supporting the idea that each of these instances of semantic change was rational and to varying degrees progressive. Therefore, any theory of concepts must be able view semantic change as rational and to offer an intellectual explanation of why conceptual change rationally occurred.

The case studies illustrated that an important characteristic of conceptual progress is that novel concepts permit scientists to justify new scientific assumptions (phylogenetic trees established by the homology concept), to explain novel phenomena (cellular functions explained by the molecular gene concept), and to carry out discovery in an improved manner (clues for further experimental research yielded by the molecular homology concept). Thus, any account of concepts should offer an account of conceptual progress that captures all aspects of conceptual progress, including how it enhances scientists' abilities to confirm hypothesis, explain phenomena, and conduct discovery. I also argued that the transition from the classical to the molecular gene concept is an instance of conceptual progress in spite of change of reference. Any account of conceptual change should make room for varieties of conceptual progress that occur without historical stability of reference.

Viewing concepts as shared between persons and ascribing mental contents to groups of individuals presupposes an appropriate account of concept identity. I made use of a pluralist and pragmatic approach to concept individuation. But even alternative accounts that promise a principled and unique way of individuation have to yield a defensible semantic account when applied to concrete cases. In the case of the contemporary molecular gene concept, we saw that the term 'gene' as currently used refers to many overlapping yet distinct categories. An account such as Jerry

Fodor's informational semantics secures clearly individuated concepts by assuming that content is constituted by how a mental symbol refers to a category. However, in the case considered Fodor seems to be committed to the idea that nowadays the term 'gene' denotes a plethora of concepts (as many as there are categories of possible referents), and that scientists using this term constantly switch from one concept to the other. This is precisely in conflict with Fodor's intention to have an account that secures stable meanings and concepts which are usually shared between persons (as these underwrite the intentional laws of thought and action that Fodor postulates). Any philosophical account of concept individuation has to be able to offer a semantic interpretation of scientific concepts such as the contemporary gene concept (or of the term 'gene' as used nowadays).

A concept is shared by many individuals and in this sense a feature on the group level. At the same time, possessing a concept is a property of an individual. Many semantic accounts assume that concept possession involves having certain epistemic abilities (being able to carry out inferences, having knowledge about the concept's referent, having grasped a definition). However, in the case of scientific concepts it need not be the case that every scientist possessing a concept has the same epistemic abilities. Due to specialization and the scientific division of labor, the various epistemic abilities that determine the successful use of a concept in an overall scientific community may be spread out over that community. We saw that some 19$^{\text{th}}$ century anatomists used embryological criteria to establish homologies, whereas others preferred the comparative analysis of adult structures. The combined use of both approaches and different types of criteria in overall biology proved to be significant. My discussion suggested that it is not the case that possessing a scientific concept consists in the same definition being grasped by every scientist, and in this sense a scientific concept as a property of a community cannot be construed as having a monolithic content (a unique and clear-cut definition) and not exhibiting variation. Thus, a task for any study of scientific concepts is to understand how various epistemic abilities integrate within a community so as to underwrite communication and the successful use of a concept. Furthermore, the variation within a concept as used in an overall community is a determinant of conceptual change. We saw that the varying use of the term 'homology' within 20$^{\text{th}}$ century biology rationally led to the formation of three distinct contemporary homology concepts, and that an originally moderate variation in use and epistemic aims associated with the term 'gene' led — due to differential epistemic pressures acting on different biological subdisciplines — to the contemporary molecular gene concept exhibiting substantial variation. As a result, any account of scientific concepts has to understand how *variation* internal to a concept underwrites it successful use and accounts for its rational change.

APPENDIX A

CONCEPTS IN PSYCHOLOGY

Not only are theories of concepts proposed in the philosophy of mind and language, but concepts are extensively studied in cognitive psychology. In fact, the experimental study of concepts and the development of theories of concepts has been one of the most fruitful activities in cognitive psychology during the last few decades (Murphy 2002). Even though philosophy and psychology need not pursue identical aims when studying 'concepts', both approaches ought to be consistent and complementary. While my semantic notion of a concept's epistemic goal does not have an equivalent in psychology, the notion of *inferential role* — an essential component of a concept on my account — bears parallels to some theoretical ideas in the psychology of concepts. This appendix section gives a brief overview of the psychology of concepts and contemporary psychological theories of concepts, relating it to the philosophy of concepts and in particular inferential role semantics (IRS). The aim is to show that contemporary psychological theories of concepts and IRS are not incommensurable and that there is a possible convergence between both approaches. The similarities that my semantic approach (especially the notion of inferential role) and recent trends in the psychology of concepts exhibit are explained by analogous aims of both approaches.

The philosophy of concepts and the psychology of concepts need not have identical aims. As discussed in Section 3.1, the fundamental task for the philosophy of mind and language is to account for the intentionality of thought and language. Concepts make intentional thought possible by being the basis of propositional attitudes. A philosophical theory of concepts has to account for the representational dimension of intentionality, i.e., how concepts make thoughts possible that represent states of affairs. The psychology of concepts, in contrast, takes it for granted that concepts refer to the world, and it does not aim at explaining how concepts do so. Instead, psychological re-

search studies the cognitive properties of concepts. Concepts are viewed as cognitive structures that embody knowledge or certain information (and for this reason psychologists talk about 'knowledge structures', 'data structures', or 'mental representations' in addition to 'concepts'). These cognitive structures figure in cognitive processes, and thereby bring about the different conceptual performances of individuals, which involve verbal and non-verbal behavior and can be experimentally investigated. Among others, these conceptual performances are categorization (how individuals decide whether an object falls under a concept), induction (how individuals infer the properties of a category from information about other categories), conceptual combination (how individuals combine primitive to complex concepts), concept learning, and conceptual development (including child cognitive development). The central task of the psychology of concepts is to causally explain these conceptual performances, by developing an account of the cognitive structures (concepts) and the cognitive processes that bring about conceptual performances. This can be achieved only by studying the internal structure of cognitive structures and by breaking down larger cognitive modules into its components. Different structures such as different concepts have different causal effects on conceptual performance in virtue of their different internal structures.[1] As a consequence, different psychological theories agree on a non-atomistic picture of concepts (they disagree regards the internal structure concepts have). This is the reason why the atomist Fodor (1998a) rejects most approaches to concepts in cognitive science (ignoring that the psychology of concepts does not attempt to offer an account of intentionality like Fodor's atomist informational semantics).

Despite the different aims of philosophical and psychological theories, there are two basic ways of viewing them as consistent. The traditional approach is to view them as complementary, yet quite distinct enterprises (Peacocke 1989; Margolis 1998). The philosophy of concepts is about offering an account of intentionality, whereas psychology has nothing to contribute to this question. Instead, the psychology of concepts is about the causal mechanisms that underlie thought, e.g., by explaining how cognitive structures, some of which permit intentional thought, are causally acquired and maintained. Philosophy, in turn, is taken not to be concerned with empirical questions such as concept learning and how intentional thought is causally established in humans.[2] A stronger connection between the philosophy and the psychology of concepts can be made by some versions

[1] Obviously, the mere fact that two cognitive structures have different referents — for Fodor the primary difference concepts can have — cannot account for the different psychological properties of these structures.

[2] Also atomists take this position (Laurence and Margolis 2002): An atomistic semantic theory offers an account of intentionality by maintaining that informational relations between cognitive structures and the external world are meaning-constitutive, whereas conceptual connections and epistemic/cognitive abilities (as stressed by my approach and the psychology of concepts) are metaphysically independent of content. The latter merely form the causal basis for the acquisition and maintenance of the content-constitutive informational relations in creatures like us.

of inferential role semantics. According to IRS, what constitutes intentional thought (including the reference of concepts) is the way in which concepts figure in reasoning, perception, and action. The psychology of concepts addresses similar features by the study of how cognitive structures figure in different cognitive processes and conceptual performances. From this perspective, psychology may actually contribute to the study of those features that account for the intentionality of thought.[3] My semantic approach emphasized that scientists possess different epistemic abilities in virtue of possessing scientific concepts. Cognitive psychology can contribute to the study of these epistemic abilities by the empirical study of the cognitive abilities of individuals.

In what follows, I want to give an overview of some recent developments in the psychology of concepts, focusing on how psychology can contribute to philosophical approaches to concepts, in particular to the study of conceptual change in the philosophy of science. A standard philosophical argument against psychological research bearing on the semantics of concepts is based on the idea that psychology cannot offer individuation criteria of concepts and the related claim that concepts are intrinsically normative, in that they tell us how we have to reason, while psychological research can only uncover how people actually reason (Hampton 1989; Smith 1989). My discussion on concept individuation challenged the philosophical assumption that there is a unique way to individuate concepts, arguing that concept are to be individuated based on the philosophical and explanatory fruitfulness of such an individuation (Section 3.3). From this perspective, we can dispense with this argument for the irrelevance of psychology for philosophy.

The so-called classical theory of concepts, which assumed that concepts embody definitions of a category in terms of necessary and sufficient properties, was replaced in the 1970s by novel approaches.[4] For the classical theory failed to account for effects which were reliably demonstrated in different psychological experiments. One prominent example are typicality effects, i.e., the fact that categorization is strongly influenced by the degree to which an object categorized is a typical instance of the category (e.g., typical instances are categorized faster and more reliable than untypical members). Given that typicality has an influence on conceptual performances such as categorization, it has to be somehow represented in cognitive structures (probably in concepts, given that concepts are the cognitive structures that are immediately and by default activated in conceptual performances). This led to the development of so-called prototype theories of concepts,

[3]This does not mean that every cognitive structure has semantic / intentional properties. Rather, psychology sheds light on concepts by breaking concepts (structures that have genuine semantic properties) down into cognitive substructures and studying their interaction, which accounts for the conceptual performances underlying intentionality.

[4]Murphy (2002) gives a good overview of the psychology of concepts in the last three decades.

which assume that concepts are statistical feature lists describing the likelihood of an arbitrary category instance having certain properties (Rosch and Mervis 1975; Rosch 1978; Hampton 1979; Smith and Medin 1981).[5] Another prominent approach is exemplar theories (motivated by exemplar effects, i.e., the situation that those *particular* instances of the category based on which the person learned the concept bear on later conceptual performances). Exemplar theories assumes that a concept contains information about particular instances of the category that the individual was acquainted with (Medin and Schaffer 1978). Whereas the prototype approach assumes that a concept encodes information about properties of the category, the exemplar approach maintains that a concept encodes information about particular instances of the category.

In the last two decades, the prototype theory and the exemplar theory, which are still popular, have been challenged by the so-called *theory theory* of concepts. This approach is neither a unique psychological theory of concepts, nor does it offer an account of concepts that is as clear-cut and quantitative as the prototype and exemplar theories. Rather, it is a general approach to concepts, motivated by drawbacks of former accounts. The theory theory is motivated and supported by so-called *knowledge effects*, i.e., the fact that various conceptual performances depend on a substantial body of an individual's background knowledge. While previous approaches have ignored this background knowledge and in particular not viewed the collateral beliefs relating to a category as part of a concept, the theory theory suggests a picture of concepts according to which concepts embody substantial background knowledge. Gregory Murphy (2002) puts this idea by stating that concepts are more like entries in an encyclopedia, rather than entries in a dictionary (as former theories of concepts assumed). According to the theory theory of concepts, concepts are basically mental theories (thence the name of this theory). More precisely, concepts are representations whose structure consists in their relations to other concepts *as specified by a mental theory* (Murphy and Medin 1985; Carey 1985; Keil 1989a; Gopnik and Meltzoff 1997; Murphy 2002).[6]

[5]Since psychology has to explain cognitive performances, it views concepts as closely connected to the cognitive abilities that account for these performances. Given that categorization is influenced by the typicality, psychologists maintain that concept possession presupposes the ability to recognize typical instances, which is a recognitional / epistemic ability of an individual. This is the basis for Fodor's compositionality critique against psychological theories of concepts (see Section 3.2.1). Fodor argues that instancehood (concepts) compose, whereas good-instancehood (typicality) does not compose (due to emergent properties). Likewise, this is the basis for his claim that recognitional and epistemic abilities have nothing to do with concept possession (Fodor 1998a, 1998b, 2001, 2004).

[6]Gopnik (1988) characterizes a mental theory as an abstract cognitive structure which includes entities and rules for manipulating those. Further accounts relating to the theory theory are Ahn et al. 2001; Brewer et al. 1998, 2000; Carey 1988, 1991; Carey and Gelman 1991; Carruthers et al. 2002; Evans 1989a, 1989b, 2002; Gelman 2003, 2004; Gelman and Markman 1986, 1987; Gelman and Wellman 1991; Gopnik 1996; Gopnik et al. 1999; Gopnik and Wellman 1994; Hirschfeld 1996; Hirschfeld and Gelman 1994; Johnson-Laird 1983; Johnson and Keil 2000; Karmilloff-Smith 1988; Keil 1989b, 1995; Keil and Wilson 2000a, 2000b; Margolis 1988; Medin and Ortony 1989; Murphy 2000; Wellman 1990.

Knowledge effects are relevant for *concept learning*. For instance, concepts of coherent categories are learned better than of incoherent categories, where a coherent category consists of different properties that are connected in a causal or functional manner (Murphy and Allopenna 1994). Thus, an individual's background knowledge about the properties that may or are likely to co-occur in different types of natural objects and artifacts affects the way in which she learns such types of concepts. Closely related to this is how knowledge effects show up in *categorization*. Some categorization experiments proceed by forming different groups of subjects, where the subjects in each group become acquainted with the same artifact category in that they are shown the same instances of the category. The only difference is that subjects from different groups obtain different information as to the function or use of the category members. This has an effect on how subjects subsequently categorize novel objects as falling or not falling under the category (Lin and Murphy 1997; Wisniewski 1995). For instance, individuals from two groups are shown the same selection of category members, including a description of the different parts of any such artifact. But as different groups obtain different information as to the use of the artifact, different subjects take different parts of the artifact to be more or less relevant for category membership, depending on how important the part is for performing the alleged function of the artifact. Thus, background knowledge about which different parts can perform a certain function influences whether or not a certain part or property of an object is viewed as important for the category, influencing categorization.

Not surprisingly, background knowledge strongly effects *induction*, i.e., whether a person is willing to infer that a category has certain properties given that another category has the same property. Whether a person carries out the induction depends on the type of property that is to be inferred from one category to the other, and how this property relates to the sort of categories to which the two categories belong (animals from the same taxonomic group, artifacts with a common use, etc). For instance, an individual may be willing to transfer a biochemical property from one type of food to another type of food of the same biological kind (two taxonomic categories), but not from one type of food to another type of food that is eaten on the same occasion such as breakfast (two script-based categories). Induction as a cognitive process does not depend on the overall similarity of the two categories involved, but on substantial causal or functional background knowledge that is used to assess the salience and relevance of the properties involved (Evans 1989a; Heit and Rubinstein 1994; Lassaline 1996; Proffitt et al. 2000; Ross and Murphy 1999). This with my recommendation made in Section 3.1.4 to construe scientific inference as material inference.

There I pointed out that formal models of induction and analogical reasoning are of limited value, because they have to appeal to an unexplained notion of 'relevance' of properties. This relevance is given by the causal and functional features that depend on the particular domain to which a case of induction belongs. Psychological experiments demonstrate that this background knowledge is relevant not only for scientific, but also for everyday life contexts. Finally, knowledge effects show up in *conceptual combination*. As mentioned in the discussion on compositionality (Section 3.2.1), noun-noun combinations exhibit emergent properties. These emergent properties are to be explained by a person's collateral knowledge. Individuals use their explanatory knowledge to understand combined concepts. For instance, Johnson and Keil (2000) gave some of their subjects information that challenges explanatory knowledge that is part of a combined concept (such as 'arctic rodents'), while other subjects received information that challenges non-explanatory knowledge about this combined concept.[7] Even though both items are equally typical of the combined concept, contradicting non-explanatory vs. explanatory knowledge has a different effect (e.g., on replying to questions such as 'arctic rodents are white'). On this basis, Johnson and Keil argue that causal knowledge is part of the core (rather than prototypical identifying) features of concepts.

The theory theory departs in two basic ways from more traditional psychological theories of concepts. First, it adopts a *more holistic view of concepts*. While a traditional approach such as the prototype theory assumes that a concept is given by a few properties that characterize the category denoted, the theory theory assumes that a concept is closely related to large bodies of knowledge. In fact, given the assumption that a concept is a representation whose cognitive structure consists in their relations to other concepts as specified by an individual's mental theory, the theory theory closely aligns with inferential role semantics, which assumes that conceptual content is determined by the inferences and explanations (the theory endorsed by an individual) in which the concept figures. Second, while traditional theories tended to assume that the features that define concepts are perceptual features of a category, the theory theory stresses the relevance of theoretical (as opposed to perceptual and superficial) knowledge, which includes *knowledge about the causal, functional and use properties of a category*. Conceptual performances are influenced by knowledge about the causal properties and causal connections between properties of natural kinds, about the functional connections of different animal parts and features, about the function of artifacts and the functional relations of their parts, and about the rules and procedures of

[7]While explanatory knowledge is information that is used for explaining the properties of the category, non-explanatory knowledge is information that is part of a person's concept, yet does not have causal and functional relations to other features of the category, so that the person does not use this knowledge for explanations.

human social activities. Thus, concepts are viewed as embodying theoretical and practical modal knowledge about which properties must or may not co-occur in natural kinds, functionally defined categories, and human social behavior.

Some support for the theory theory comes from the study of concepts in children; in fact, the theory theory is particularly popular among cognitive psychologists studying *child development*. The received view, stemming from the work of Jean Piaget, was that cognitive development in children proceeds from the concrete to the abstract, from cognitive processes that are based on superficial, perceptually given information to more theoretical reasoning (Piaget and Inhelder 1969). This general picture has been rejected due to findings of the last two decades. As it turns out, reasoning in children may involve substantial theoretical assumptions. Prominent in this context is the group of reasoning patterns often labeled *child essentialism*, which may be found in children as young as $2\frac{1}{2}$ years of age.[8] Essentialism refers to the fact that children treat different kinds of objects such as artifacts and animals in a different way. In the case of artifacts, the outer appearance of an object determines kind membership, while animals are treated as if they possessed a natural kind essence, a non-perceptual property (such as inner structure or genealogy) that determines category membership. Frank Keil (1989a) demonstrated this in his prominent transformation paradigm, a categorization task that involves a strong counterfactual element (using thought experiments à la Putnam 1975). Experimenters describe how mad scientists transform the outside of certain artifacts or animals so that they *look like* a different artifact or another type of animal, respectively. Children will say that once a cup is transformed into something that looks like a plate, it is a plate. Young children react the same way in the case of animals, assuming that outer appearance determines category membership. Older children, however, state that if the outer features of a raccoon are transformed such that it comes to look and smell like a skunk, it is still a raccoon. Similarly, if a newborn pig is described as being moved to a cow community and raised by cows only, children assume that this pig will develop a curly tail and say 'oink', rather than 'moo'. Thus, children respond in psychological experiments as if they assumed that different species have internal essences that determine how the animal looks like and how it behaves, while these internal essences cannot be influenced by external influences (Gelman and Wellman 1991). This way of treating animals as natural kinds also shows up in induction tasks (projectability of properties). For instance, children are shown a picture of a flamingo and told that its legs get cold at night. They are also shown a

[8]See Ahn et al. 2001; Gelman 2003; Gelman 2004; Gelman and Markman 1986; Gelman and Markman 1987; Gelman and Wellman 1991; Hirschfeld 1996; Hirschfeld and Gelman 1994; Keil 1989a; Medin and Ortony 1989.

bat, being told that its legs stay warm at night. Then the children have to decide in the case of a depicted owl, whether it has warm or cold legs. Despite the owl and the bat being perceptually more similar (both regards their legs and their overall body shape), children assume that the owl has the same property (cold legs at night) as the flamingo — because both are birds (Gelman and Markman 1986, 1987).

In sum, experiments in child conceptual development show that children do not always judge based on perceptual features (such as perceptual similarity), but make use of *causal and modal knowledge* about certain types of categories. Based on such findings, Alison Gopnik and her collaborators endorse a particularly bold version of the theory theory of concepts for children (Gopnik 1996; Gopnik and Meltzoff 1997; Gopnik et al. 1999). On her account, children as young as 18 months possess genuine mental theories of certain domains of objects, where these mental theories are very much like scientific theories. For they have some structural aspects of theories: they are abstract, internally coherent, contain causal knowledge and support counterfactuals, and make ontological commitments. They have functional features of genuine theories, as they are used to make predictions and explanations. Finally, mental theories in children conform to scientific theories in their dynamic aspects, as mental theories change in the face of novel evidence.

Some developmental psychologists that are favorable toward the theory theory suppose strong parallels between *scientific theory change* and *conceptual development in children*. It is suggested that philosophical accounts of theory change may bear on psychological theorizing or that psychological findings about cognitive development shed substantial light on scientific reasoning and rationality. For example, Susan Carey (1985, 1988, 1991) studied the way in which folk scientific concepts (such as 'animal', 'alive', or 'heavy') develop in children. On her account, the development from children to adults is not just the acquisition of novel beliefs; instead, it involves substantial conceptual change. The child and the adult concept of a living object are based on differing ontologies and embedded in different conceptual schemes. Carey used the work of Thomas Kuhn (1962) to interpret her experimental findings, by arguing that child and adults concepts are incommensurable. From this perspective, concepts in children are not just rough approximations of the adult concepts, which children have not yet properly grasped. Child development is not a gradual convergence to the adult use of the concept, but involves shifts between incommensurable concepts. Gopnik's above mentioned version of the theory theory apparently uses ideas from the philosophy of science for her psychological theorizing, by maintaining that human cognition involves genuine theories all the way down to children. In particular, cognitive development in children is driven

by experience and evidence (a claim that is controversial among developmental psychologists who emphasize the role of innate mental modules in development). The converse — though complementary — strategy is to maintain that a fundamental ingredient in understanding scientific reasoning and scientific theory change is adult and child cognitive psychology. This idea endorsed by some psychologists is inspired by Quine's (1969a) naturalistic epistemology, stressing the continuity between folk reasoning and scientific reasoning. Gopnik (1996) pushes this 'the scientist as child' analogy, suggesting that a cognitive approach bridges that gap between traditional philosophical-normative and sociological approaches to scientific change, both of which leave something out. On her realistic view of science, science is successful and arrives at the truth because scientists use cognitive mechanisms that usually get things right (being designed by evolution). From this perspective, the psychological study of the cognitive mechanisms underlying learning in children and adults sheds substantial light on conceptual change in science. In my view, one obvious drawback of Gopnik's cognitive approach is the fact that a good deal of scientific rationality and success stems from its particular social, institutional, and technological organization, which does not have parallels to how children learn. The psychological approach focusing on cognitive mechanisms of individuals fails to capture the social and collaborative nature of scientific reasoning, and thus the 'scientist as child' analogy is valid only up to a certain point.

However, my concern here is not to discuss the adequacy of some of the bolder analogies between conceptual development in children and conceptual change in science.[9] Instead of assessing the similarities of scientific change and child development as processes, I want to point to similarities between my framework on concepts and conceptual change and cognitive psychology as methodological approaches. I do not view any incompatibility between the psychological and philosophical study of concepts. In the remainder of this section, I want to highlight some similarities between both approaches, focusing on how psychological ideas can contribute to the study of conceptual change in science. I also offer some reasons for the similarities between my semantic account — in particular the notion of inferential role — and the theory theory of concepts.

In Section 3.1.4, I recommended to view inference as material (rather than formal) inference, pointing to some advantages this approach has for studying scientific inference and reasoning. The picture of inference and reasoning that emerges from recent psychology (in particular the theory theory) aligns to a large extent with the notion of material inference. First, psychologists deny that

[9]For discussions of these issues, see Carey and Spelke 1996; Downes 1999a, 1999b; Fine 1996; Giere 1996; Kitcher 1988; Nersessian 1996; Stich and Nichols 1998; Solomon 1996.

general and domain-independent reasoning processes can account for most instances of reasoning. Instead, in many cases inference is viewed as domain-specific, in that many cognitive structures and processes apply only to certain domains of knowledge (such as animals, but not other types of categories). The particular empirical information that is contained in concepts determines whether or not an inference is drawn. This fits with my critique of formal models of scientific reasoning and the idea that scientific reasoning in confirmation and discovery is based on types of inferences that are specific to the particular scientific field, domain, or case. If inference is material inference, then it is based on the empirical principles that apply to a particular case, which cannot be captured by formal or domain-general models of inference.[10] Second, the theory theory emphasizes inference and cognitive processes that involve counterfactual and modal elements. Reasoning in adults and children alike is viewed as being based on knowledge about what is causally necessary, functionally necessary, or necessary given human conventions. Reasoning essentially involves giving causal or functional explanations. This psychological account fits with the idea that material inference includes counterfactual and causal inference (as well as moral reasoning). Different proposals of conceptual role semantics have emphasized the semantic significance of inference. However, often the notion of 'inference' has been left somewhat unexplained, thereby implicitly endorsing a traditional understanding of this notion.[11] The labels 'conceptual role semantics' and 'inferential role semantics' are usually treated as synonyms; and most versions of inferential role semantics have not stressed that the notion of conceptual role ought to include the explanatory role of concepts as well. In contrast, I emphasized that the way in which scientific concepts support particular explanations is an important aspects of their content, so that conceptual role is to include explanatory role. I achieved this by using a broader construal of the notion of inference — inference as material inference which includes causal, nomological and modal reasoning and thereby scientific explanation. Likewise, psychological accounts of reasoning in children and adults have from the outset focused on explanation and explanatory understanding (in particular causal and functional explanation). In sum, the picture of inference and reasoning that emerges from contemporary psychology closely aligns with the notion of material inference. In this respect, psychology can offer new perspectives to the philosophy of science — which has tended to study scientific reasoning in terms of formal and domain-independent models of inference — as well as to standard versions of inferential role

[10] Murphy and Medin (1985), in one of the first proposals of the theory theory, point to the drawbacks of formal models of inference such as Bayesianism.

[11] The exceptions are Sellars (1974), Brandom (1994), and Gupta (1999), who explicitly state that they view inference as material inference.

semantics — which have focused on inference without emphasizing explanation.

Not only does psychology study inference and explanation, the theory theory of concepts views conceptual connections such as inferential and explanatory relations as an important part of the cognitive structure of concepts. Some of the explanatory and theoretical background knowledge that influences conceptual performance involving a concept is taken to be part of conceptual structure. This is in line with inferential role semantics (or any semantic account that views inferential role as part of a concept's content), while traditional approaches to scientific terms in the philosophy of science have focused on studying the reference of terms. The psychologist Gregory Murphy (2002) argues that while referential semantics is very popular in linguistics, it "is not suitable as a psychological theory" of meaning (p. 387), since referential semantics does not yield an account of an individual's understanding of a concept (linguistic approaches merely yield what I call a formal as opposed to philosophical semantics). Psychology studies the cognitive abilities individuals have in virtue of understanding (possessing) certain concepts, which makes it necessary to take into account an individual's inferential and explanatory abilities that are related to understanding a concept. In Chapter 2, I criticized the referential approach to concepts, which traditional philosophy of science has used to study conceptual change, for leaving out some crucial aspects of conceptual change and progress. Referential approaches ignore how novel concepts contribute to justification, explanation, and discovery in science. For similar reasons, I am skeptical towards the suitability of Fodor's atomist semantics for studying conceptual change. In a similar vein, developmental psychology uses a non-referential and non-atomistic account of concepts to study conceptual development. Conceptual development from children to adults is viewed as change in mental theories in which certain concepts are embedded, and conceptual change proceeds by change in explanatory relations between concepts embodying causal, functional, or ontological assumptions. The psychologist Frank Keil and the philosopher Rob Wilson (2000a) discuss the way in which a theory theory view contributes to the explanation of conceptual development, and question the fruitfulness of Fodor's atomism for this task and the study of conceptual change in science:

> Conceptual change, in history and in development, follows patterns that would make little sense if concepts had no internal structure. ... Concepts, whatever they are, seem to have the property of being tightly connected to one another as they travel along trajectories of conceptual change. ... it is difficult to see how informational atomism provides *any* substantive theory of conceptual change. (Keil and Wilson 2000a, pp. 310, 317)

In the last two decades, conceptual development has been fruitfully studied by using a non-referential and non-atomist account of concepts, emphasizing how concepts figure in explanation and theoretical reasoning. Thus, the psychology of concepts could recommend this approach to the

philosophy of science as a potentially fruitful way to address the question of conceptual change. While the tradition in the philosophy of science has focused on stability of reference and has been reluctant to admit meaning change in order to avoid the incommensurability threat (Section 2.1), theory theorists such as Gopnik emphasize that substantial conceptual change occurs in children (and in science), and that it is driven by new evidence. This fits with the very starting point of my discussion that for the most part conceptual change in science is rational and based on experience.

Overall, my framework of concepts — to be used for the study of conceptual change in the philosophy of science — is much more similar to some recent accounts of concepts in cognitive science than to traditional referential approaches to concepts in the philosophy of science. More specifically, there is a parallel between the theory theory of concepts and the semantic notion of inferential role, which according to my theory of concepts is an important component of a concept's content. There are reasons for this convergence, which have to do with two similar goals of both approaches. *First, both approaches are broadly concerned with the explanation of behavior.* Inferential role semantics as a philosophical approach focuses on the *rational* explanation of verbal and non-verbal behavior involving language use — concepts are ascribed for the intentional explanation of action. The theory theory as a psychological approach focuses on the *causal* explanation of behavioral and conceptual performances. Psychological theories attempt to understand how a concept can contribute to the way in which people reason and navigate in the world. A psychological theory of concepts has to account for the various types of conceptual performances studied in experiments. Inferential role semantics endorses a holistic picture of the way in which conceptual content is determined as an agent's intentional behavior and rational reasoning depends on her collateral beliefs. Likewise, the theory theory emphasizes rich inferential and explanatory connections between concepts — implicit mental theories — as an individual's conceptual performances in various experiments depend on these. In sum, a holistic account of concepts, or at least of concept determination, underwrites the explanation of behavior both in philosophy and psychology. *The second aim on which my semantic account and the theory theory broadly converge is the study and explanation of conceptual change.* My framework is fundamentally concerned with the study of conceptual change in science. To this end, I focus on the change and improvement of scientist's *epistemic* abilities that they have in virtue of possessing certain concepts (such as changes in inferential and explanatory abilities). This yields a non-atomistic and non-referential approach to concepts. Developmental psychology, studying cognitive and conceptual development of individuals, focuses on the change of *cognitive* properties and abilities. A non-atomistic and non-denotational picture of concepts is congenial for

pursuing this aim as well. Both my framework of concepts and the theory theory view themselves as evaluable not in terms of their metaphysical credentials as a theory of semantic content, but in terms of their fruitfulness for understanding conceptual change.[12]

Despite non-identical aims and theories of concepts in philosophy and psychology, I view both approaches as compatible. Psychological research can contribute to inferential role semantics by offering an account of how concepts are learned and modified, which may be bear on the philosophical question of how individual scientists change their views. Psychology also sheds light on the causal and cognitive basis of reasoning and concept possession, which may influence the way in which the notion of an inferential role is spelled out by philosophers.[13] Conversely, philosophical accounts to conceptual change like mine can offer some perspectives for cognitive psychology, as due to the philosophical focus on the communal use of language and the social and institutional underpinnings of scientific practice they can broaden the individualistic focus of psychology.

[12]In my brief comparison of Fodor's atomism with my approach (Section 3.1.2, p. 59), I pointed out that even if Fodor were right about the nature of concepts, so that other approaches were not about 'concepts' but just features related to 'concepts', rival approaches would still focus on features that are more significant than the 'concepts' that an atomist approach could study. Given that in understanding conceptual change and conceptual development the explanatory force resides in those features that are studied by my approach or by cognitive psychology, I chose to assume that the content of 'concepts' includes those features (inferential role and epistemic goal on my account).

[13]It has to be admitted, though, that presently proponents of the theory theory have not arrived yet at a well-understood notion of a mental theory.

APPENDIX B

CRITIQUES OF NEO-DARWINISM AND THE EMERGENCE OF EVOLUTIONARY DEVELOPMENTAL BIOLOGY

Evolutionary biology and developmental biology used to be completely separate for most of the 20th century. One historical reason for this is the way in which classical genetics emerged at the beginning of the 20th century (see Section 6.1). Originally, 19th century biologists had viewed heredity and development as a single phenomenon (Section 6.1.1). Classical genetics, however, restricted the notion of 'inheritance' to the transmission of features over generation, which excluded development as the way in which inherited factors such as genes bring about the phenotypic features of the adult. Ideas such as the phenotype–genotype distinction and the rejection of the inheritance of acquired characters supported this historical development. A consequence was that during the first half of the 20th century, developmental biology and genetics split and became separate disciplines that did not influence each other much. Neo-Darwinism emerged in the 1930s as a synthesis of genetics and evolutionary biology, the so-called Modern Synthesis (Section 6.1.4), so that evolutionary and developmental biology were distinct enterprises — one studying phylogeny, the other ontogeny. Contemporary *evolutionary developmental biology* attempts to reunite these two disciplines. The current label 'evo-devo' used to designate this new discipline came to be used in the 1990s, reflecting an increasing interest in this approach. Even though evolutionary developmental biology as a genuine discipline is quite recent, it has its intellectual precursors. There are several 20th century biologists who approached evolution from a developmental point of view, and in many respects current evo-devo continues the tradition of 19th century evolutionary morphology. The main tenet of evo-devo is that knowledge about the development of organisms is vital to answer certain evolutionary questions. As traditional neo-Darwinism ignored development, the claim is

that traditional evolutionary theory is incomplete and the developmental approach of evo-devo will transform and refine evolutionary theory. Evo-devo biologists have a broader understanding of the causes of evolution. Given that evo-devo addresses questions about evolution that were neglected by neo-Darwinism (to be discussed below), the *novel explananda* make it necessary to develop several new modes of explanation, with development being a central part of the explanans.[1]

The basic tenets of classical neo-Darwinism are as follows. While Darwin defined evolution as descent with modification, referring to morphological modification, neo-Darwinists and in particular population geneticists often characterize evolution as *change in gene frequencies*. John Maynard Smith (1983), for instance, acknowledges two ways of seeing evolution — as a series of adult forms or as change in gene frequencies — while arguing that the second option is more adequate for the process of evolution. Neo-Darwinism stresses evolution as being based on variation within populations and species, brought about by the mutation of genes and the migration of individuals. Natural selection acts on the phenotypic properties of organisms, influencing their reproductive rates and thus changing the genotype frequencies and subsequently the phenotype frequencies. Natural selection is claimed to be the main mechanism of evolutionary change, at least the only creative, non-random mechanism that produces adaptation. Selection pressure as a force acting on the reproductive capacity of an organisms is viewed as being determined by the *environment* of this organism, where the environment may include abiotic factors as well as other organisms such as predators and conspecifics. A fundamental tenet of neo-Darwinism is that evolution is *gradual*, i.e., that it proceeds in many small and continuous steps rather than jumps.[2]

Critiques of neo-Darwinism are not new. Despite the dominance that neo-Darwinian evolution-

[1] Evo-devo practitioner Günter Wagner uses the name 'developmental evolution' instead of 'evolutionary developmental biology' to make explicit that the explanandum of evo-devo is evolution (not just development), while developmental biology is part of the explanans.

[2] It has to be pointed out that the since the dominance of traditional neo-Darwinism in the 60s and 70s, evolutionary biology has been transformed. This is primarily due to the emergence of the disciplines of molecular evolutionary biology and phylogenetic systematics. Advances in molecular biology led to the new field of molecular evolution. Among other things, it became clear that large parts of the genome evolve much more unconstrained by selection than adult morphological traits (Section 5.3.1). Phylogenetic systematics (cladistics) gained acceptance as the proper theory of classification (Section 5.1.2), but it also strongly influenced and transformed evolutionary biology. Cladistics emphasizes the importance of phylogenetic trees, and that evolutionary hypotheses have to be evaluated based on confirmed phylogenies (Lauder 1981). Neo-Darwinism, in contrast, focused on adaptation and relied on optimality models assuming that an organism is designed such that it meets environmental demands (coming to be in equilibrium with the environment). Yet this proceeded without studying in detail how the organism historically evolved to obtain its current characteristics and without taking into account that the phylogenetic history of an organism imposes certain constraints on its further evolution. Cladist George Lauder makes this case by talking about "the nature of the modern synthesis as a nonhistorical, equilibrium program" ("Introduction" in Russell [1916] 1982, p. xxxv). Nowadays, many evolutionary biologists view studying the evolution of species and the modification of characters based on phylogenetic trees as mandatory, thereby reviving a crucial practice of 19$^{\text{th}}$ century evolutionary morphology. One consequence of the emergence of molecular evolution and phylogenetic systematics is that nowadays evolutionary theory is less adaptationist than original neo-Darwinism and the biology pictured by some philosophers.

ary theory enjoyed for many decades, there have been dissenters since the very origin of the Modern Synthesis. In the past, the critics were to be found primarily in morphology and paleontology; and debates centered for the most part on macroevolutionary phenomena. The notion of *microevolution* refers to evolution below the species level, while *macroevolution* is evolution above the species level, such as the emergence of higher taxa (families, orders,...). Morphology and paleontology are solely concerned with macroevolution. The models of population genetics used by the Modern Synthesis deal with the change of gene frequencies within a population and are thus microevolutionary models. While neo-Darwinists maintain that macroevolution is nothing but microevolution on a large scale, in the past some paleontologists and morphologists have questioned whether a simple extrapolation of neo-Darwinian theory to macroevolution can yield an adequate account. A good deal of the criticisms dealt with the question of gradualism, with some paleontologists arguing that a gradual theory of evolution does not fit the non-gradual pattern that the gappy fossil record suggests (Stanley 1979; but see Rensch 1959, Levinton 1988). The most prominent debate surrounded the theory of punctuated equilibrium, which was proposed by the paleontologists Niles Eldredge (1971) and then defended together with Stephen Jay Gould (Eldredge and Gould 1972; Gould and Eldredge 1977). The model of punctuated equilibrium assumes that during its lifetime a species does not change much (evolutionary statis), while at the point of the emergence of a new species substantial phenotypic change occurs in a comparatively short period of time. In what follows, we shall see that evolutionary developmental biology deals to a large extent with macroevolutionary questions and challenges neo-Darwinism on these grounds.

Evolutionary developmental biology is a quite recent discipline, and developmental biology and evolutionary biology used to be distinct domains for most of the 20^{th} century. In spite of this, the study of the connection between evolution and development was undertaken by some biologists who can now be considered 20^{th} century forerunners of evo-devo. Many of these early studies dealt with the evolution of development. Rather than solely studying the evolution of adult form from species to species, the change in the evolution of whole ontogenies was addressed. The most prominent notion in this domain until the 1970s was the idea of *heterochrony*. Heterochrony refers to changes in relative timing of different ontogenetic events in the descendant, as compared to the timing of these events in the ancestral ontogeny. A quite striking type of heterochrony is what is called *neoteny* or *paedomorphosis*. This refers to the situation when the sexual maturation of a species proceeds much faster than its somatic (i.e., overall morphological) development, compared to the development of the ancestor. The result of paedomorphosis is that in the descendant the adult

looks like the juvenile form (larva or newborn) of the ancestor, due to the fact that the general morphological development is strongly retarded. But the adult of the descendant is still fertile, as sexual maturation is accelerated relative to the ancestor and sexual organs are fully developed. Paedomorphosis occurred with the origin of humans. In terms of their morphology, adult humans are much similar to newborn chimpanzees than humans are to adult chimpanzees.

The notion of heterochrony was made popular by the evolutionary embryologist Gavin Rylands de Beer (1899–1972).[3] Most of de Beer's views on developmental evolution were already contained in his *Embryology and Evolution* (1930). His discussion started out by criticizing Haeckel's biogenetic law, which assumed that descendant ontogenies usually recapitulate ancestral ontogenies in a condensed fashion and that evolutionary modification occur only among adult characters as terminal additions to the ontogenetic sequence (Section 4.3.2). In contrast, de Beer emphasized that evolutionary novelties can occur at any stage of development, including early development. Paedomorphosis actually clashes with the idea of recapitulation, as the descendant does not recapitulate the whole ancestral ontogeny, but only a part of it. For de Beer, heterochrony provided a causal link between evolution and development, as an evolutionary change from an ancestral to a descendant structure can be explained by changes in development. De Beer viewed evolution by paedomorphosis as an important mode of evolution, as it allows for large phenotypic changes and the origin of new morphological forms. By arguing that heterochrony accounts for the origin of many higher taxa, he built on the prior work of Walter Garstang (1922, 1929). Garstang suggested that one can explain the origin of chordates (and thus vertebrates) from an echinoderm-like ancestor, provided that paedomorphosis took place so that the ancestral chordate is morphologically similar to an echinoderm larva.[4] De Beer argued that several taxa have originated by paedomorphosis, including many lower taxa such as humans. But paedomorphosis also accounts for the origin of higher taxa such as chordates and insects. Thus, heterochrony is a principle of developmental evolution that was used to explain macroevolutionary phenomena. The notion of heterochrony figured prominently in Stephen Jay Gould's seminal *Ontogeny and Phylogeny* (1977), who substantially improved upon de Beer's account and his evolutionary explanations of why heterochrony occurs. Despite a decline in significance (Love 2006b), heterochrony is still one of the concepts of evolutionary developmental biology, as it is the cause of many developmental alterations and can bring about major novelties (McKinney and McNamara 1991; McKinney 1988; McNamara 1995; Zelditch 2001).

[3]For discussions of de Beer's work see Gould (1977), Ridley (1986), Hall (2000), and Brigandt (2006).
[4]Chordates include the vertebrates, echinoderms include sea urchins and star fish.

B.1 Developmental Constraints and Evolvability

A central tenet of evolutionary developmental biology is that knowledge about the development of organisms is fundamental for explaining morphological evolution. Proponents of the neo-Darwinian orthodoxy, however, have repeatedly argued that developmental biology has nothing to contribute to evolutionary biology. In the *Selfish Gene*, Richard Dawkins, states that "The details of the embryonic developmental process, interesting as they may be, are irrelevant to evolutionary considerations." (1976, p. 66). This claim is based on a conceptual framework that emerged with the origin of classical genetics and population genetics. Its very origin is the conceptual separation between inheritance and development. While 19$^{\text{th}}$ century biologists viewed these two as one phenomenon, classical geneticists came to conceive of two processes: development as the creation of the adult out of the fertilized egg, and inheritance as the transmission of genes from one generation to the other. The idea that these two processes are separate is supported by Weismannism, i.e., the idea that acquired characters cannot be inherited (Maynard Smith 1983; Wallace 1986). Features acquired by an individual during development (due to environmental influences) are not genetically inherited, thus development has no influence on inheritance. Nowadays the notion of 'genetic information' can be used to make plain the neo-Darwinian conceptual framework.[5] Inheritance is the transmission of genetic information from one generation to the next, and evolution is the change of the genetic information of the different individuals within a population due to selection. Development is simply the unfolding of this information, and has no influence on the way in which the genetic programs within a population are changed. Ernst Mayr, one of the main founders of neo-Darwinism, made this point as early as 1959:

> Or, let us look at the problem of the relation between embryology and evolution which has been a source of endless disputes since the 18$^{\text{th}}$ century. Most pre-Darwinian evolutionists and many of Darwin's contemporaries considered the development of the individual and phylogenetic change merely as two aspects of a single phenomenon. Stating this problem in terms of genetic information has greatly clarified the issue. The genetic material, handed down from generation to generation, can be considered as coded norms of reaction [i.e., a function from environment to phenotype]. Individual development is the uncoding of the information made available through fertilization. Evolution, on the other hand, is the generating of ever-new codes of information, of ever-new norms of reaction. Stated in these terms it is at once evident that the superficial similarity between individual and phylogenetic development is entirely spurious. (Mayr 1959b, p. 4)

[5] Despite it popularity, the notion of 'genetic information' is actually untenable given that facts of molecular and developmental biology. It is a non-explanatory metaphor that promotes a highly distorted picture about the role of genes in development. I cannot discuss this issue here. For the debate about genetic information, see Falk 1984, 2000; Gerhart et al. 1982; Godfrey-Smith 1999, 2000; Gray 1992; Griffiths 2001; Griffiths and Gray 1994, 1997; Griffiths and Knight 1998; Griffiths and Neumann-Held 1999; Griffiths and Sterelny 1999; Hall 2001; Keller 2000; Moss 2001, 2003; Neumann-Held 1999; Maynard Smith 2000; Müller 1994; Newman and Müller 2000; Nijhout 1990; Oyama 1985; Robert 2001, 2004; Sarkar 1996, 2000; Sterelny 2000; Strohman 1993.

A further way to express this idea is Mayr's distinction between *proximate* and *ultimate* causes (Mayr 1982). A proximate cause is a developmental or physiological cause, it explains how a certain factor influences an individual's ontogeny. Gene action in development and environmental triggers of behavior are proximate causes. An ultimate cause is an evolutionary cause, it answers to evolutionary questions. Mutation, genetic drift, and natural selection are ultimate causes (modifying populations rather than individuals). Mayr's claim is that since proximate causes and ultimate causes are distinct and independent types of causation, development has no impact on evolution:

> ... what amazes me is in how much of the current literature that distinction is still ignored or confused. I must have read in the last two years four or five papers and one book on development and evolution. Now development, the decoding of the genetic program is clearly a matter of proximate causations. Evolution, equally clearly, is a matter of evolutionary causations. And yet, in all these papers and that book the two kinds of causations were hopelessly mixed up. All I can say that I hope that the day will come when people realize that the decoding of a genetic program is something very different from the making and changing of genetic programs that is done in evolution. (Mayr 1994, p. 357)

Another clear expression of the argument that knowledge about development has no influence on the explanation of evolution is made by the neo-Darwinian population geneticist Bruce Wallace:

> I shall further argue that problems concerned with the orderly development of the individual are unrelated to those of the evolution of organisms through time ... Evolution consists of changing, within the genetic resources of populations, the frequencies of those genetic programs that lead to successful development, and survival of individuals under prevailing environmental conditions. This claim ... is merely a verbose paraphrase of the terser statement: evolution is a change in gene frequency. (Wallace 1986, p. 149–150)

Wallace (1986) uses the following pictorial illustration to support his argument, which nicely captures the conceptual framework of neo-Darwinism. Wallace represents the genotype within a population across different generation by a horizontal line — the germ-line as an unbroken thread of inheritance across generations. Different ontogenies are represented by vertical lines branching of from the genetic information of the germ line, ending with the adult form, which is represented by different geometric shapes (triangle, star, square). The selective demand imposed by the environment at a particular time is represented by a mould to which the adaptive phenotypes fit, but not other unfit phenotypes: "At each time level, the environment assumes a different shape, thus excluding the previously adapted phenotype while placing a selective premium on one that is compatible with new demands" (Wallace 1986, p. 153). The process of development as such does not have an influence on how evolution proceeds, as Wallace stresses that characters acquired during development are not inherited.

Even if one buys into this conceptual framework, then there are still compelling reasons that show that developmental biology is relevant for evolutionary biology. The developmental and internal constitution of organisms influences evolution, as the phenomenon of *developmental constraints*

shows. Historically speaking, the notion of developmental constraint became probably the second crucial concept used by developmental approaches to evolution after the notion of heterochrony. This idea can be illustrated with an example. Many organisms have a bilateral symmetry in that the exterior organs and many internal organs occur in a symmetric and pairwise fashion. Tetrapods (limbed vertebrates) have a right forelimb and a left forelimb, which are perfectly symmetric in their internal structure. This is no accident, as tetrapods develop and are built this way. In the course of evolution, the right forelimb may change. But any such change will virtually always correlate with a corresponding change in the left forelimb. This is a developmental constraint. Due to the way in which tetrapods are built, certain changes (such as a change in the left limb without change in the right limb) are impossible. A developmental constraint is a *constraint on phenotypic variation*, thereby influencing subsequent morphological evolution. A 'developmental' constraint is constituted by the developmental make-up of organisms, but it manifests itself in evolution.

> A developmental constraint is a bias on the production of variant phenotypes or a limitation on phenotypic variability caused by the structure, character, composition, or dynamics of the developmental system. (Maynard Smith et al. 1985, p. 266)

One way to explain this notion is as follows. The genotype space is the set of all possible genotypes, and the phenotype space is the set of all possible phenotypes. Ignoring selection for the moment and taking into account the effect of mutation only, evolution starts out with a certain genotype and then random mutation is applied, yielding a trajectory in genotype space that is a random walk. To this corresponds a trajectory in phenotype space representing the morphological evolution of this lineage. The idea of developmental constraints is that the genotype–phenotype map is far from unbiased: certain phenotypic changes are very likely to occur given random mutation on a particular genotype, while other changes are highly unlikely. Due to the particular structure of the genotype–phenotype map, the random walk in genotype space yields a non-random, biased walk in phenotype space, introducing a non-random, possibly directional influence on evolution. Even if the effect of selection is taken into account, a bias remains. For due to developmental constraints the very phenotypic variation that selection presupposes and acts on is biased. One among other reasons why the genotype–phenotype map is biased is that there are impossible phenotypes that do not develop from any genotype whatsoever, the dynamics of development making the origination of such formally possible adult forms impossible (Alberch 1982).

Some developmental constraints apply to any organism. Physical constraints arise from the operation of the laws of physics which govern organisms as physical systems. For instance, physical constraints prohibit organisms being made out of cells of an enormous size because the diffusion of

biochemical substances from one such cell to another is virtually impossible. Other developmental constraints are specific to certain groups of organisms — such constraints emerged historically together with the material make-up and the mode of development of a group of organisms. A morphogenetic constraint is a bias due to the particular principles that govern modes of development. Such a bias occurs for instance as certain developmental interactions and steps in early development constrain subsequent development, with some further steps being likely, whereas other being unlikely. While a developmental constraint as a bias on phenotypic variation is brought about by an organism's internal constitution, it manifests itself in evolution. There are several prominent phylogenetic patterns that suggest the operation of developmental constraints. The paleontologists David Raup (1967) studied the distribution of existing and fossil ammonoid shells in phenotype space (morphospace).[6] Vast chunks of this space of theoretically possible shell shapes are and were unoccupied. This probably cannot be explained based on functional considerations (e.g., the operation of natural selection making these non-existing shell forms maladaptive). Instead, it appears that the unoccupied parts of morphospace correspond to developmentally impossible phenotypes. Pere Alberch's studies of morphological variation in salamanders offer another example (Alberch 1980, 1982, 1983). In this case, certain morphological features did not show continuous variation across different species, instead certain traits are either present or absent, without any functional or adaptive reason why intermediates should by impossible. Alberch argued that

> ... the observed patterns of variation are not necessarily a reflection of some direct environmental selection but that, rather, they are the result of the structural organization of the intrinsic mechanisms generating the trait. In other words, the definitely bounded variation is the result of constraints imposed by the way the organism develops. (Alberch 1983, p. 913)

A final example is patterns of digit reduction in tetrapods. Many extant tetrapods have less than 5 digits, due to digit loss in certain evolutionary lineages. Digit loss shows certain phylogenetic patterns (e.g., which digit is lost first), which is believed to be due to the way in which the tetrapod limb develops (Alberch and Gale 1985; Holder 1983a, 1983b; Oster and Alberch 1982; Shubin 1994).

While traditional neo-Darwinism maintains that developmental biology has nothing to offer to evolutionary biology, the existence of developmental constraints contradicts this assumption. In accordance with the conceptual framework of neo-Darwinism outlined above, phenotypic evolution can be explained in terms of the change of genotype frequencies, effected by selection acting on phenotypes. Mutation and genetic drift cause random changes in gene frequencies, while natural selection makes evolution proceed in a certain direction. However, natural selection is not the

[6] All possible shells can be represented by a three-dimensional space, whose axes refer to different parameters that influence shell-coiling in development and thus the final shell shape.

only source of non-random change, developmental constraints are another. Bruce Wallace's model illustrates the neo-Darwinian assumption that the environment generates certain adaptive problems, and that organisms phenotypically adapt to these demands in the course of evolution. However, solving an adaptive problem is possible only if the phenotype that solves this problem to the highest degree can actually originate. The existence of developmental constraints shows that certain phenotypes may not evolve because they cannot originate due to developmental reasons. Thus, explaining phylogenetic patterns and understanding how adaptation is possible makes it necessary to know about the action of developmental constraint in certain groups of organisms.[7] Whereas neo-Darwinism focuses on natural selection as being brought about by the environment *external* to the organism, developmental constraints are created by the material make-up and factors *internal* to the organism. Since its introduction, the notion of developmental constraints has been vital for developmental approaches to evolution.[8]

Former developmental approaches to evolution stressed developmental constraints, thus suggesting that development has a somewhat negative and constraining impact on evolution. Nowadays, it is widely recognized that the flipside of developmental constraints are developmental opportunities. The developmental constitution of organisms makes certain phenotypic variations likely and opens evolutionary pathways (Bürger 1986; Carroll 2001; Müller 1989; Sander 1983; Wagner 1984, 1988). *Development does not only constrain phenotypic variation (and evolution), it makes phenotypic variation and thereby evolution possible.* The contemporary concept for this is *evolvability*. Evolvability is the capacity of organisms and species to evolve, i.e., to bring about phenotypic variants, and to respond flexibly to natural selection (McKinney and McNamara 1991; Gerhart and Kirschner 1997, 1998). The close connection between developmental constraints and morphological evolvability can be put as follows — making use of the idea of *homology* (Section 5.2). An organism is composed of several homologues or characters. A character is a unit of evolution in that it can

[7] In his masterful discussion on constraints, Ron Amundson (1994) also makes explicit that evo-devo and traditional evolutionary biology differ in their explanatory goals (morphological evolvability vs. adaptation). Amundson points out that whereas developmental approaches view developmental constraints as *constraints on form* (constraints on the generation of phenotypic variation), neo-Darwinians reduce this notion to *constraints on adaptation*. Consequently, neo-Darwinians argue that a constraint (on adaptation) has to be invoked *only once* the features of an actual organism turn out to be suboptimal relative to a certain optimality model, supporting the idea that the notion of constraint is conceptually posterior to the notion of adaptation. Amundson, however, points out that a developmental approach is necessary to account for the morphological evolution of even perfectly adapted traits. In my terms this means that developmental constraints have to be studied as they are at the same time the developmental basis of morphological evolvability — the evolvability of any structure, including adapted ones.

[8] See Amundson 1994; Carroll 2001; Goodwin 1984; Gerhart et al. 1982; Gould 1989; Gould and Lewontin 1979; Gerhart and Kirschner 1998; Hall 1992; Kauffman 1983; Lauder 1981; Lauder and Liem 1989; Maderson et al. 1982; McKinney and McNamara 1991; Müller 1994; Raff et al. 1990; Resnik 1995; Roth 1991; Sander 1983; Seilacher 1990; Trueb 1996; Wagner 1984, 1986, 1988; Wagner et al. 2000; Wagner and Misof 1993; Wake et al. 1991.

vary within a population and thereby undergo evolutionary modification *independently of other characters*. Given that an individual is organized into several morphological units or characters, selection can act on some but not other characters, so that evolution can proceed along several dimensions. If an organism had only one character, so that one part of the body could change only if every other part of the body changed at the same time, genuine evolution and adaptation could not occur. Thus, explaining evolvability makes it necessary to understand the developmentally constituted morphological organization of individuals into different characters. At the same time, the existence of certain characters implies that evolution can occur only along these, but not along other dimensions — one type of developmental constraint. If it were the case that the number of characters were infinite (no constraints existed), any possible variation could occur, for instance an insect could gradually evolve into a vertebrate. But evolution as we know it does not (and cannot) proceed this way — a fact which is in need of explanation as well. Given that the material constitution of organisms makes certain morphological variations possible and others impossible, understanding why morphological evolution (as we know it) can occur makes it necessary to study its developmental basis.

Accounting for evolvability is one of the most important features on the agenda of contemporary evolutionary developmental biology. Understanding evolvability was not part of the neo-Darwinian program, which focused on adaptive changes (how selection acting on variation leads to evolutionary modifications), but not on the very precondition of such evolutionary changes (the morphological variation on which selection can act). Note that whereas explanations of adaptation proceed from *differences* between individuals (on which selection can act), an individual shares its developmental-morphological constitution with many other organisms of the same taxon, so that accounts of the developmental basis of evolution appeal to features that are shared by organisms.[9]

My argument based on the notions of developmental constraints and evolvability shows that developmental biology has to contribute to evolutionary biology. This argument is valid even if one accepts the neo-Darwinian framework outlined above. However, the empirical results and new concepts of evo-devo strongly suggest abandoning the received conceptual framework. Neo-Darwinism stressed the external environment as the agent of evolution. Modern notions such as developmental

[9]Even though the study of evolvability gained interest only recently, some forerunners of modern evo-devo actually addressed this issue. A case in point is Gavin de Beer's (1930, 1958) developmental theory of evolution. Even after the evolution of higher taxa, further evolution and diversification on lower taxonomic levels occurred. De Beer offered two developmental explanations of why in the case of paedomorphosis, macroevolution can occur without obstructing further microevolution: one account based on cellular differentiation, the other on the developmental function of genes (Brigandt 2006). De Beer called the capacity for further microevolution after the emergence of a higher taxon 'plasticity', offering a developmental-mechanistic account of how macro-evolvability and micro-evolvability combine.

opportunities and evolvability suggest that factors internal to the organism are relevant evolutionary forces as well. In particular the following feature of the neo-Darwinian conceptual framework turns out to be defective. The traditional tenet was that only the environment imposes selection pressure. Bruce Wallace's (1986) pictorial sketch of the process of evolution by natural selection reflects this idea, by representing the adaptive problems to be solved by moulds (see above). The fundamental assumption is that these moulds are determined by the environment only — they are given before and are independent of the organism that is to occupy this environment. Adaptive problems are ontologically prior to the organism and its developmental and evolutionary potential. However, the above considerations show that the developmental constitution of an organism determines which characters it has, which determines along which independent dimensions phenotypic variation and thus selection pressure can arise in the first place. Consequently, development influences what selection pressure and which adaptive problems can arise. Current research undermines a conceptual framework that was built on a dichotomy between factors internal and external to the organism. Selection does not act only on the adult organism, instead it can act at any point during ontogeny and the lifetime of an individual. Moreover, it can act on different levels of organismal organization. A fundamental assumption of modern evo-devo is that organisms are hierarchically structured, in that there are different levels of organization (molecules, cells, tissues, organs). Different levels need to be recognized as processes on one level may have a certain independence from processes of other levels (Section 5.2.1). In particular, selection can act differently on one level than on others. Certain levels are not only subject to evolutionary pressures, they may create selection pressure on their own, for instance, due to cell-cell competition (Buss 1987; Lauder and Liem 1989; Gerhart and Kirschner 1997; Winther 2001). There may actually be a conflict between different levels, and the evolutionary outcome is dependent on the way in which developmental constraints and selective forces operate on different levels. Thus whereas neo-Darwinism assumed that only the environment external to the organism determines selection pressure, evolutionary developmental biologists assume that there is multi-level selection in which selection may act differently on different stages of development and levels of organization, and in which not only the environment, but features internal to the organism create selection pressures.

In general, whereas neo-Darwinians tended to define evolution as change in gene frequencies, the proponents of evo-devo tend view evolution as descent with modification, the explanandum being morphological evolution. In this respect, evo-devo links up with traditions such as 19$^{\text{th}}$ century evolutionary morphology. While neo-Darwinians stressed genetic inheritance and black-boxed de-

velopment, evo-devo biologists emphasize the importance of *epigenetic* factors, i.e., cellular and developmental resources that include genes as only one among many developmental resources. To account for development, it is crucial to study epigenetic interactions, in particular developmental features above the molecular level (Laubichler and Wagner 2001; Robert 2004). Consequently, many evolutionary developmental biologist also stress the causal importance of epigenetic factors and higher levels of organismal organization for evolution (Løvtrup 1974; Riedl 1978; Ho and Saunders 1979; Müller 1990; Newman and Müller 2000, 2001; Wagner 2000; West-Eberhard 2003). In sum, evolutionary developmental biology makes use of a more powerful conceptual framework than traditional neo-Darwinism, as it takes into account the developmental influences on evolution and attempts to understand the developmental basis of evolution.

B.2 The Explanation of the Origin of Body Plans and Evolutionary Novelties

In spite of the fact that evo-devo became a genuine discipline attracting substantial attention not much more than a decade ago, in the recent past there have been some biologist who can be considered forerunner of the new discipline. We saw above that Gavin de Beer (1930) used knowledge from developmental biology to address questions of macroevolution and evolvability such as the origin of higher taxa. Another person who is viewed as important by modern evo-devo biologist was Conrad Hal Waddington (1957), whose evolutionary models of gene physiology stressed the way in which developmental issues such as the epigenetic interaction of genes and the genotype–phenotype map bear on evolution. Søren Løvtrup, in his *Epigenetics: A Treatise on Theoretical Biology* (1974) argued that factors internal to the organism such as cytoplasmic factors and developmental genes determine phylogeny. Løvtrup urged the need to use knowledge from different biological disciplines to explain evolution, rather than the narrow resources of orthodox neo-Darwinism (Løvtrup 1977). An important forerunner of evo-devo is the Austrian marine biologists and morphologists Rupert Riedl (Wagner and Laubichler 2004). Philosophers usually know Riedl because in his later career he became one of the prominent proponents of evolutionary epistemology. His prior biological work, however, was less adaptationist and more developmentally oriented. Riedl's main work in the context of developmental evolution is his *Order in Living Organisms: A Systems Analysis of Evolution* (1978, originally published in German in 1975). Arguing that the conceptual framework of standard evolutionary biology has to be substantially enlarged if one is to explain macroevolutionary phenomena, he was particularly interested in the explanation of the origin and modification

of body plans. For Riedl, a body plan is a source of both evolutionary constraints and potentials. Body plans are ontologically prior neither to the homologues that make-up a body plan, nor to the group of organisms that share a body plan. Instead, a body plan is the product of evolutionary history and can be transformed in the course of phylogeny. It constituted by the developmental interaction and functional integration of different parts of the body. (Riedl calls his approach a systems theory because of the idea that the organism is a system of various causally interconnected parts.) A central concept of Riedl was the notion of 'burden'. This refers to the degree to which one part of an individual is a developmental and functional precondition for other parts. If a character with high burden were to change, many other characters would be influenced as well. Thus, the higher the burden of a structure, the less likely it is that it can change in evolution. In this sense, a structure with a high burden is developmentally and functionally constrained. In the course of evolution, newly acquired characters may be based on and become dependent on an existing structure, which increases the burden of this older structure. Riedl also addressed the question of evolvability by arguing that developmental constraints and an increase in the burden of structures may be necessary for the adaptive origin of complex and functionally integrated characters. Riedl directly influenced some contemporary practitioners of evolutionary developmental biology such as Gerd Müller, Günter Wagner, and Manfred Laubichler.[10]

One possible way to date the origin of evolutionary developmental biology is the 1981 Dahlem Conference on *Evolution and Development* (Bonner 1982). The workshop group Maderson et al. (1982) argued for an integration of developmental biology into evolutionary theory, maintaining that a new framework is needed to explain the origin of evolutionary novelties. Emphasized were notions such as developmental constraint and heterochrony. Gerhart et al. (1982) addressed evolutionary potentials and the explanation of the evolvability of morphological structures and developmental mechanisms. They argued that macroevolutionary changes arise as an escape from prior developmental constraints. Since then, there have been several biologists urging a synthesis of evolutionary and developmental biology. In his "Syllabus for an Embryological Synthesis", T. J. Horder (1989) argued that the primary explanandum for evolutionary biology is the change of developmental processes. He complained that development has often been viewed as a one-step process from the genome to the adult organism rather than as the subsequent interaction of many changing factors. In addition, Horder rejected a dichotomy between genetic and environmental factors, which neglects the internal environment of the organism. In "Development and Evolution: The Emergence of a

[10]See Maderson (1975), Raff and Kaufman (1983) and Horder (1983) for some other precursors of current evo-devo.

New Field", Wake et al. (1991) summarized a conference discussion symposium, suggesting that not only the integration of evolution and development necessitates a multidisciplinary approach, but may also create a new field with central principles and new biological goals. They stressed that developmental constraints provide evolutionary opportunities, and that the new field of evolutionary developmental biology should not be reduced to the functioning of genes. In a similar vein, Gerd Müller (1991) suggested the name 'evolutionary embryology' for the emerging field, stressing the idea that organism are epigenetic systems so that explanations in development and evolution cannot be reduced to the molecular level. Müller (1994) argued that many disciplines such as genetics, molecular biology, cellular and developmental biology and morphology are necessary to successfully account for morphological evolution.[11] Nowadays, evolutionary developmental is a small but progressing field that attracts more and more attention. It has its own journals, among others the *Journal of Experimental Zoology: Molecular and Developmental Evolution* (edited by Günter Wagner) and *Evolution & Development* (edited by Rudolf Raff). There are also several evo-devo textbooks (Arthur 1988; Hall 1992; Rollo 1994; Raff 1996; Arthur 1997; Gerhart and Kirschner 1997; Schlichting and Pigliucci 1998; Hall 1998; Carroll et al. 2001; Davidson 2001; Wilkins 2002; Minelli 2003; West-Eberhard 2003).

Many proponents of evolutionary developmental biology assume that a developmental approach will transform evolutionary biology in one way or another, or even that traditional evolutionary biology is incomplete and in need of new modes of explanation (Robert 2002). As evolutionary developmental biology is a relatively recent field, it yet has to offer substantial success in the explanation of morphological evolution and macroevolution. As of now it is an open question to which extent evo-devo will actually transform biology. This is ultimately an empirical question and will depend on the ability of evolutionary developmental biology to generate results of fundamental evolutionary impact that go beyond the capacity of traditional evolutionary biology.

Apart from explaining evolvability, possibly the most important goal of evolutionary developmental biology is the explanation of the *origin of body plans*. Many phyla and thus body plans probably emerged in a relatively short period of time (the Cambrian explosion), and only a few new body plans originated after that. It is hard to see how this could be explained by selection alone, and it does not appear to be an accident either. Evo-devo attempts to get a better understanding of how the physical features of ancestral multicellular organisms might have made possible the origin

[11]For other early programmatic accounts on the integration of evolution and development see Wake and Roth (1989), Hall (1992), Gilbert et al. (1996), and Wake (1996).

of the current body plans, and why the origin of further body plans did not occur, while change within the established body plans was possible. Findings from developmental genetics made in the last decade suggest that progress can be made on this question. It was discovered that there are developmental genes that play fundamental roles in establishing the overall structure of the body. Paradigmatic are the so-called *Hox* genes. This is a family of genes the different members of which are expressed in early development at different parts of the body along the body axis. Any such gene regulates many other developmental genes and thus controls how a specific segment of the body develops in contrast to a different segment which is regulated by another *Hox* gene. The astonishing discovery is that *Hox* genes are conserved among large classes of animals. A particular *Hox* gene may be shared by a large part of the animal kingdom, e.g., a homologue of this genes exists in vertebrates, in insects, and in crustaceans (Burke and Brown 2003; Carroll et al. 2001; Gehring 1998; Holland 1992; Schierwater and Kuhn 1998). One task is to understand what higher taxa such as phyla have in common, in particular what developmental features they have in common. Once biologists have gained a better understanding of what characterizes the developmental modes and body plans of different animal groups, it can be attempted to explain how different body plans emerged. This is surely a question that cannot be adequately addressed with the traditional research methods and conceptual resources of neo-Darwinism.

A closely related question is the explanation of *evolutionary novelties*. An evolutionary novelty (or an innovation, as it is sometimes called) is a qualitatively new character, such as feathers in birds or the turtle carapace. Thus, an explanation of a novelty may be an account of the evolutionary origin of a single structure rather than a whole body plan. Practitioners of evo-devo stress that accounting for the origin of novelties necessarily involves knowledge about the development of organisms. Actually, the problem of novelty has been a focal question of evolutionary biology from the very beginning. Darwin's assumption that one species transmutates into another implies that a fortiori individual characters transform into the relatively different structures of another species. Darwin had to show that the main mechanism of his theory — natural selection operating on small variations of traits — can account for the emergence of new characters over time. A particular challenge for Darwin was to make plausible that the complex and highly functional characters of extant species (such as the vertebrate eye) can be explained as being derived from much more primitive evolutionary precursors. Critics of Darwin, Darwinism and later neo-Darwinism sometimes argued that the Darwinian theory cannot account for novelties. Despite the fact that the very question of novelty is an old one, evolutionary developmental biology uses a very specific

notion of novelty and thus attempts to explain something quite specific. This becomes clear if one takes a look how 'novelty' was usually understood during large parts of the 20th century in neo-Darwinism. The neo-Darwinian concept of novelty is tied very closely to the theoretical and explanatory framework of neo-Darwinism. Mayr (1960) is probably the best expression of this understanding of novelty, defining novelty as "any newly acquired structure or property that permits the assumption of a new function" (p. 351). Note the emphasis on function, which is due to the neo-Darwinian focus on the explanation of adaptation. The problem of novelty is how to account for evolutionary change by means of selection, even though the primitive/emerging structure cannot really perform the later function. What has to be explained is the origin of new functions or a change of function in a gradual and adaptive manner. The core notion that neo-Darwinism offers in this case is the idea of 'pre-adaptation' (Bock 1959). A structure is pre-adapted for a new function if it is in principle capable of performing that function to a relevant extent, although so far it does not have to perform this function. The idea is that we start out with a certain structure that has and performs a particular original function. Evolutionary change (driven by the demands of this original function) may as a by-product partially pre-adapt this structure to a prospective function. Once it is beneficial to perform this new function (because it solves a new adaptive problem) the structure can partially perform this new function without interference with the old function. Further evolutionary modification can make this new function the main function of the structure. For instance, insect wings are believed to have emerged for thermo-regulatory purposes. Once they had a certain length, they were pre-adapted to gliding. This second function brought about a further increase in the length of wings, and finally flight became the main function of wings. Pre-adaptation serves as a bridge between two functions. In this manner, we can explain the emergence of structures with complex and new functions based on a framework that is committed to gradual change and natural selection as the only creative force in evolution.

Is neo-Darwinism really in a position to explain the origin of novelties? Bock (1959) explains the "appearance of radically new structures" as follows: "the evolution of most, if not all, new structures involved old structures which were preadapted for the new function" (p. 200). It appears to be analytic that a novelty is a novel structure, i.e., a structure that did not exist before. But if Bock assumes that the structure emerged from a precursor structure, why is it a novelty? We find the same idea in Mayr (1960) (who also stresses pre-adaptation): "The emergence of new structures is normally due to the acquisition of a new function by an existing structure. In both cases the resulting 'new' structure is merely a modification of a preceding structure" (p. 377). If Mayr attempts

to explain novel structures by assuming that they are not new, then he seems to beg the question, provided that the problem of novelty is to account for structures that did not exist hitherto. This is exactly the problem that evolutionary developmental biology addresses.[12] For neo-Darwinism, a novelty is not really a structure that did not exist in the precursor species. Rather it is a modified structure with a qualitatively *new function*. Neo-Darwinism has this perspective on novelty due to its focus on explaining complex adaptations; and as it is non-obvious how new and complex functions can be acquired in a gradual manner, a convincing explanation of the possibility of functional shifts is important. Evolutionary developmental biology, in contrast, has a structural (rather than functional) understanding of novelty. Gerd Müller and Günter Wagner (1991) give the clearest account of this perspective by explicitly contrasting it with the neo-Darwinian understanding of novelty. They spell out what is meant by saying that a novelty is a structure that did not exist before: "A morphological novelty is a structure that is neither homologous to any structure in the ancestral species nor homonomous [i.e., serially homologous] to any other structures of the same organism" (p. 243). (Thereby the concept of novelty is connected to the homology concept. Note that they talk about a 'morphological' novelty, thus stressing structure but not mentioning function.) Not every evolutionary developmental biologist may use the notion of novelty exclusively in this strong sense that views novelties as structures that are not homologous to any structure in the ancestor. Often novelties are simply viewed as substantial structural changes. Nevertheless, the explanation of novelties in the strong sense of Müller and Wagner (1991) is an important biological question. Just like the evolutionary origin of new body plans, the origin of a completely new morphological structure is in need of explanation.

Apart from the fact that neo-Darwinism does not view the explanation of structural novelties as a central goal for evolutionary biology, its theoretical framework based on mutation and selection cannot account for the origin of novelties. The reason is as follows. Given a certain structure which is an independent character (a homologue), this character can vary within a population so that natural selection can act on it. *Given that this character already exists*, natural selection can explain why a certain state of this character (the particular form or function of a homologue in some individuals) becomes more frequent in a population until this trait becomes eventually predominant in a species. Neo-Darwinism explains evolutionary change by considering the frequency of a certain property (a state of a character) in a population, and explains change of frequency (change in a

[12]This idea was already foreshadowed by Maderson et al. (1982), who argued that the neo-Darwinian explanation of novelty by means of pre-adaptation does not explain genuine evolutionary novelties.

character) by appeal to natural selection. However, this presupposes the existence of this character, so that the notion of natural selection cannot explain how the character came into being in the first place. Since natural selection does not explain the very origin of novelties, one may wonder whether appeal to mutations does the job. However, mutations occur all the time in the course of phylogeny, and for the most part they either do not bring about any difference in the adult phenotype, or they bring about regular, small changes in existing structures. Thus, appeal to mutation does not explain why a novelty emerged at a particular point in history, rather than mutation modifying existing structures without creating a novel structure. Instead, an explanation of how an evolutionary novelty originated has to appeal to the mode of development that existed before the origin of the novelty, and to point to a way in which development could have been changed so as to lead to a mode of development according to which the novel structure develops.

This can be illustrated by a possible evolutionary scenario. Gerd Müller (1990) argues that many novelties emerged as an epigenetic by-product of adaptive evolution.[13] Assume that in the ancestor two tissues or developmental modules are spatially distant and therefore do not exert a developmental influence on each other. On Müller's hypothesis, standard modification of the ancestor (e.g., its adult features) due to mutation and selection may have the side-effect that these embryonic tissues get closer to each other. This is a mere by-product of selection as — in Elliot Sober's (1984) terminology — there is no selection *for* these tissues being close to each other. If these tissues are close enough a threshold may be passed and one tissue may exert a developmental influence on the other, inducing a change in the development and adult morphology of the organism so as to bring about a novelty. On this possible evolutionary scenario, both natural selection and mutation are somehow causally involved in bringing about the novel structure. However, they are not the causally most relevant features; instead, the explanatory force resides in understanding the change in development. In this side-effect scenario selection acts on a certain (adult) trait that is not the tissues under consideration. But there is neither selection for these tissues getting closer, nor selection for the novelty. As a consequence, the origin of this novelty cannot be explained by appeal to environmental demands and natural selection — as long as it is not explained how selection acting on one structure can *due to particular developmental connections* bring about *another* structure. Mutations have occurred during this shift from the original mode of development to another, but appeal to mutation is non-explanatory — as long as it is not specified which particular mutations

[13] 'Epigenetic' factors are any type of developmental factors, including in particular non-genetic ones. See also Müller and Newman (1999), Newman and Müller (2000, 2001) and the contributions in Müller and Newman (2003).

can bring about *a particular mode of development* so as to create a novelty. The explanatory force resides in an account of how it was *developmentally* possible that the evolutionary novelty originated (while it may be impossible to know about which particular mutations and what selection pressure actually brought about the new mode of development).

The entry on "Innovation" in the recent encyclopedia *Keywords and Concepts in Evolutionary Developmental Biology* makes this point as follows:

> ... the transitions [from an ancestral state to the presence of a novelty] often require developmental modifications that are not within the mutational reach of the ancestral character state. An example is the origin of feathers, a radically different morphology that cannot be explained by a smooth shape change of the reptilian scale. In such cases, natural selection alone is of limited explanatory value. The real problem lies in understanding the mechanisms for the origin of the new phenotypic state. Many innovations may involve a breaking up of developmental or functional constraints that prevailed in the ancestral lineage. ... These consequences [the origin of novelties] can neither be considered the direct result of natural selection nor the result of speciation per se. By implication, the research on key innovations requires methodological tools that go beyond those used in the adaptationist and the origin of species program. (Müller and Wagner 2003, pp. 220, 227)

The idea is that given the stable organization and developmental constraints of the ancestral morphology, variation *internal* to its characters (homologues) is possible due to the effects of mutation. Since the origin of a genuinely novel homologue is beyond phenotypic variation due to regular mutations, a novelty arises when ancestral developmental constraints are overcome, so that a stable ancestral morphology eventually cedes to a novel stable morphology. As a result, explaining the evolutionary origin of novelties requires understanding morphological organization and the operation of developmental constraints. For any such explanation, the crucial feature is to offer an account of which changes in the ancestral mode of development occurred and why these changes in *overall development* led to a new morphology in the descendant.

Stressing the importance of explaining novelties, Günter Wagner (2000) concisely answers the question "Why Is Developmental Biology Necessary to Explain Evolutionary Innovations?"

> ...the most promising areas for *Developmental Evolution* is the explanation of evolutionary innovations and the evolution of body plans. Indeed, the most exciting research in developmental evolution is directly or indirectly aiming at these questions, which proved to be out of the reach of ... classical population genetics. Why is this the case? Why is it that evolutionary innovations eluded the only causal theory of evolution we have, namely population genetics? And what is it about developmental evolution that makes it look more promising? (Wagner 2000, p. 95)

Wagner acknowledges that both population genetics as the main tool of neo-Darwinism and developmental biology are necessary to explain evolution. However, he argues for a 'shifting pluralism', according to which in some cases the explanations of population genetics have a higher 'explanatory force', whereas in other cases developmental explanations have a higher explanatory significance. Wagner illustrates this with two examples. In species with different sexes there is a stable sex ration

(usually about 50% of males and females). The evolution of stable sex ratios is best explained by the mathematical models of population genetics. For while the different sexes are established in quite different developmental ways in different species, one and the same basic mathematical model from population genetics explains sex ratios in various cases. A different situation is the explanation of an evolutionary novelty such as the origin of the butterfly eye spot patterns. The genes and gene networks that are involved in butterfly pigment patterns radically change during the origin of eye-spots. Because of this substantial change on the genetic level, any attempt to explain this novelty at the level of genes by using the concepts of variation and selection is not very promising. It is more informative to use a level of description that changes less during the process that is to be explained. In this case the origin of a morphological structure called the eyespot organizer is the explanatory relevant feature. The eyespot organizer is a stable feature of development in spite of a radical change in the underlying genetic basis. Wagner concludes his discussion by stating that

> The perspective proposed above is one of "shifting pluralism," i.e., the idea that there are multiple causes and mechanisms involved in every evolutionary process and that their relative importance for the outcome of evolution shifts from situation to situation. This idea is related to the broader concept that each level of biological organization has it own emergent mechanisms and that we have to identify the level and relative importance of those mechanisms that contribute to the explanation of any particular phenomenon. (Wagner 2000, p. 97)

B.3 Morphology or Developmental Genetics?

Very recently, some evo-devo biologists have pointed out that they focus increasingly on microevolutionary questions, as macroevolutionary questions turn out to be hard and more progress can be made on microevolutionary issues (Corley 2002; Pennisi 2002). Since a microevolutionary approach deals with short spans of time and smaller taxonomic groups, it is more feasible to obtain sufficient biological information about these groups. However, if evolutionary developmental biology is to solve substantial evolutionary questions that are beyond the reach of traditional neo-Darwinism, it has to address macroevolutionary questions (Wagner and Larsson 2003). Among the central goals on the agenda of evo-devo are the explanation of morphological evolvability and the operation of development constraints, and the explanation of the evolutionary origin of structural novelties and body plans (Wagner, Chiu, and Laubichler 2000). An important reason of why evolutionary developmental biology received increased attention and originated as an independent discipline is due to advances in developmental genetics. In the 1980s, substantial progress took place in developmental genetics, based on new experimental methods from genetics and molecular biology. Comparative

studies of the development and its molecular basis in different species received great attention among biologists, recruiting many young researchers. The new methods of developmental genetics provide evolutionary developmental biology with some of the important tools to work on its questions. A drawback of the methodological importance of developmental genetics is that this field is sometimes viewed as the core of evo-devo. Given that evo-devo is typically considered the synthesis of evolutionary and developmental biology, developmental genetics is viewed as the link between these two traditional disciplines (Love 2003a, forth.). Apart from the fact that development and the developmental basis of morphological evolution cannot be accounted for by studying gene expression and processes on the molecular level only (Dawid et al. 1982; Horder 1983; Müller 1991; Wake et al. 1991), the assumption that evo-devo boils down to developmental genetics ignores the fact that the identity of a scientific discipline does not only reside in the type of experimental tools it uses, but consist also in the scientific problems it attempts to solve (Love and Raff 2003). The macroevolutionary questions addressed by evolutionary developmental biology predate the origin of developmental genetics and evo-devo itself by many decades (Müller 2006).

In fact, in terms of its conceptual framework and its modes of explanation, evolutionary developmental biology continues in many ways the tradition of 19$^{\text{th}}$ century evolutionary morphology, as practiced by Gegenbaur and Haeckel, for instance (Amundson 2005; Hall 1998). As it intends to account for morphological evolution, evo-devo continues the goal of pre-Darwinian morphology to explain organismal form and the goal of evolutionary morphology to explain the evolution of form. The goal of neo-Darwinian evolutionary theory, in contrast, is the explanation of adaptation and speciation. In Section 4.3.2, we saw that 19$^{\text{th}}$ century evolutionary morphology explained evolution based on the study of phylogenetic trees and the phylogenetic changes of organismal structure (without relying much on the notion of selection). Evo-devo also makes substantial use of phylogenetic studies, thereby using a tool that was not part of the approach of traditional neo-Darwinism (though it is nowadays part of mainstream evolutionary biology influenced by phylogenetic systematics). Above I discussed in detail that developmental considerations were vital for 19$^{\text{th}}$ century morphology. In fact, evolutionary morphology explained evolution in terms of how ontogenies (modes of development) have changed in the course of phylogeny. This aligns with modern evo-devo which views ontogenies as the entities that undergo evolutionary change — while neo-Darwinians focus on populations as the entities that change. Evo-devo assumes that an account of evolvability and the operation of developmental constraints makes it necessary to understand how an organism is composed of different units or characters, so that evolutionary change can occur along several di-

mensions (but not proceed in other directions). An account of the origin of body plans and novel structures also requires understanding how an ancestral morphological organization could give rise to a novel morphology, and how ancestral constraints could have been overcome. In both cases, an account of the organization of an organism into structural units or homologues is necessary, in line with the goal of 19$^{\text{th}}$ century morphology to understand morphological organization. Furthermore, 19$^{\text{th}}$ century morphology focussed on the study of types, i.e., on morphological features shared by larger groups of organisms. Similarly, the knowledge about the developmental-morphological constitution of organisms that enters explanation of morphological evolution in evo-devo focuses on those features that are shared by the species of a taxon. Neo-Darwinian explanations based on natural selection, in contrast, appeal to differences between individuals. Finally, like traditional morphology evo-devo emphasizes higher levels of organizations, assuming that features on higher levels are relevant for explaining development and evolution (Love 2006a).

These considerations show how evo-devo can be viewed as pursuing the tradition of evolutionary morphology, and at the same time offers conceptual tools and modes of explanations that complement the framework of traditional, neo-Darwinian evolutionary theory. Overall, if evo-devo is to pursue biological problems that go beyond the framework of traditional evolutionary theory and if it is to be successful, then it has to be a multidisciplinary approach, using resources from molecular genetics, molecular biology, cellular biology, developmental biology, ecology, population genetics, paleontology, morphology, and theoretical biology (Müller 1994; Laubichler 2005; Love 2005).

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