

TOBIT REGRESSION AND CENSORED CYTOKINE DATA

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Submitted to the Graduate Faculty of

the Graduate School of Public Health in partial fulfillment

of the requirements for the degree of

Master of Science

University of Pittsburgh

2005

UNIVERSITY OF PITTSBURGH
THE GRADUATE SCHOOL OF PUBLIC HEALTH

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Well designed clinical studies theoretically produce accurate data from which a reasonable conclusion(s) may be drawn. Data accuracy may be hindered by the measurement tool or device. Additionally, the data may be in such a form that it is problematic from an analytic and interpretive point of view. An example of such a problematic form may be seen in censored, sample-selected, or truncated data.

Clinical data may be particularly prone to censoring or truncation since various assays used to measure patient parameters have limited sensitivity. Lower and upper limits of assay sensitivity may have a direct impact on the clinical diagnosis and prognosis of the patient, especially if the patient is a high risk critical care patient.

The aim of this report is to estimate mean cytokine levels using various approaches, including the arithmetic and geometric mean, and mean estimation from a tobit model. The data set is from the Department of Critical Care Medicine and contains values for several cytokines from 1753 patients (discharge status) or 1610 patients (follow-up status), including Interleukin 6 (IL-6), Interleukin 10 (IL-10), and Tumor Necrosis Factor (TNF). A brief overview of the immune system and its relationship to cytokine production will be presented prior to an explanation of the estimation procedures. Finally, recommendations for estimating a mean from the censored data set will be presented.

Although not specific to Critical Care Medicine, the problem of censored data is evident in many areas of study, specifically Public Health. Guidelines for dealing with censored data would be a significant and valuable tool for Public Health professionals.

TABLE OF CONTENTS

1. INTRODUCTION	1
2. BACKGROUND AND REVIEW	3
2.1. Immunology	3
2.1.1. Overview of Immune System	3
2.1.2. Overview of Cytokines	7
2.1.2.1. TNF	8
2.1.2.2. IL-6	9
2.1.2.3. IL-10	10
2.2. The Data – Censored, Sample-Selected, Truncated data	13
2.2.1. The Tobit Model	15
2.2.2. Maximum Likelihood	16
2.2.3. Tobit Model and Maximum Likelihood	17
2.2.4. The Delta Method for Standard Error Determination	19
2.3. Additional Analysis	21
2.3.1. Arithmetic Mean	21
2.3.2. Geometric Mean	21
3. RESULT	22
4. CONCLUSION / RECOMMENDATION	24
5. APPENDIX A: STATA Output	26
6. BIBLIOGRAPHY	46

LIST OF TABLES

Table 1. Definitions of Censored, Sample-Selected, and Truncated Variables.....	14
Table 2. Frequency of censored cytokine values and dead/alive status at discharge and follow-up.....	22
Table 3. Comparison of mean estimates for TNF, IL6, and IL10 for death at discharge based on the tobit model, the arithmetic and the geometric mean. Note that the population is the 1753 individuals with both complete lab and follow up data with 78 reported deaths at discharge and 1675 subjects alive at hospital discharge. Standard errors are given in parentheses below the mean.	23
Table 4. Comparison of mean estimates for TNF, IL6, and IL10 for death at follow-up based on the tobit model, the arithmetic and the geometric mean. Note that the population is the 1753 individuals with both complete lab and follow-up data with 231 reported deaths at follow-up and 1379 subjects alive at follow up and 143 with missing values. Standard errors are given in parentheses below the mean.....	23

1. INTRODUCTION

Well designed clinical studies theoretically produce accurate data from which a reasonable conclusion(s) may be drawn. However well intentioned investigators may be, the data may fail to accurately characterize the population from which the parameters were measured. Additionally, the data may be in such a form that it is problematic from an analytic and interpretive point of view. An example of such a problematic form may be seen in censored, sample-selected, or truncated data.

The problem of censored, sample-selected, or truncated data is evident in business/economic, social science, and medical literatures.¹ However, it was in the economics literature where the seminal paper by Tobin² in 1958 laid the foundation for the contemporary analysis and interpretation of censored, sample-selected, or truncated data. But no matter what problematic form the data may take, the ultimate goal of the analysis is to provide the best estimate of the population parameters.

Clinical data may be particularly prone to censoring or truncation since various assays used to measure patient parameters have limited sensitivity. Lower and upper limits of assay sensitivity may have a direct impact on the clinical diagnosis and prognosis of the patient, especially if the patient is a high risk critical care patient. In this situation it is essential that the clinician have a tool that best estimates the parameter in question to provide the patient with a reliable diagnosis and effective treatment plan that will, in turn, offer the most accurate prognosis.

One major factor in the management of the Critical Care Patient is the assessment of laboratory values. One measurable parameter that may be pertinent in Critical Care patient management is serum Cytokine level. Cytokine levels may be pertinent since cytokine

production is associated with immune response, inflammation, and sepsis, which are significant events for high risk patients. However, cytokine assay sensitivity may hinder the clinician's ability to effectively and efficiently treat their patients when the limited sensitivity results in a cytokine level cutoff value.

The aim of this report is to estimate mean cytokine levels using various approaches, including the arithmetic and geometric mean, and mean estimation from a tobit model. The data set is from the Department of Critical Care Medicine and contains values for several cytokines from 1788 patients, including Interleukin 6 (IL-6), Interleukin 10 (IL-10), and Tumor Necrosis Factor (TNF). A brief overview of the immune system and its relationship to cytokine production will be presented prior to an explanation of the estimation procedures. Finally, recommendations for estimating a mean from the censored data set will be presented.

2. BACKGROUND AND REVIEW

2.1. Immunology

The human immune system acts as a protective mechanism against pathogens which cause disease, and tissue damage. At the core of the immune system is the body's ability to recognize "non-self" molecules. Non-self molecules (antigens) are foreign molecules composed of protein(s) and/or carbohydrate(s) that stimulate an immune response. The immune system is regulated through the innate and adaptive immune responses.

2.1.1. Overview of Immune System

Innate Immunity

The innate immune response functions through physical barriers to entry, mechanical actions, biochemical defenses, and the actions of specialized cells. The epidermis and mucous membranes act as physical barriers against pathogen entry into the host's body, while the mechanical actions of sneezing, coughing and vomiting physically expel the pathogens. Additionally, the cilia that line the respiratory tract also brush pathogens along with a sweeping motion to eliminate them from the body.

The acidic environment of the stomach and the digestive enzymes found in mucus and tears provide biochemical barriers. Additional biochemical defense is possible through complement (anti-bacterial) and interferon (anti-viral). The specialized cells that afford innate defense include phagocytes, Natural Killer (NK), M, and Langerhan's cells found in the blood and

various organ systems. Finally, the inflammatory response attracts leukocytes to the site of an infection.

The inflammatory response is a series of events that results in redness, swelling, and occasionally, pain at the infection site. When common bacterial antigens are present, macrophages are stimulated to produce signaling proteins called cytokines. Examples of cytokine effects include increased production of leukocytes in the bone marrow, increased attraction of leukocytes to the infection site, increased expression of adhesion molecules found in the membranes of epithelial cells that line the blood vessels, and an increase in the amount of fluid that enters the tissue from the circulation. Leukocytes possess receptors to adhesion molecules that place them in a favorable position to enter the surrounding tissue. Excess fluid in the tissue results in increased levels of antibacterial molecules that are naturally occurring in lymph fluid.

Adaptive Immunity

The adaptive immune response functions essentially through antibody production and various actions of T cells. Adaptive immunity, although not permanent, can be very enduring. A characteristic that differentiates adaptive immune response from innate response is that adaptive immunity is antigen-specific and provides an efficient and effective defense against repeat infection(s).

Exposure and heredity play crucial roles in each individual's adaptive immune response. Exposure may be classified as either active or passive. Examples of active immunity are the natural infection with the influenza virus, or vaccination with an attenuated influenza virus. Active immunity requires a couple of weeks after infection to become established, but once

established may last for years. Passive immunity occurs with the direct transfer of antibodies or T cells (cellular immunity). Examples of passive immunity include antibody transfer from mother to child through breast milk, mother to fetus through the placenta, the infusion of animal antibodies into humans as a treatment for poisonous venom, and bone marrow transplantation.

Immunity at the cell and organ level

Immune cells are commonly called white blood cells or leukocytes. Leukocytes play a key role in both the innate and adaptive immune system. Leukocytes of the innate system are phagocytes and are *not* antibody specific. Phagocytes are either macrophages or polymorphonuclear leukocytes. Macrophages and polymorphonuclear leukocytes bind to protein surface molecules that are common on many pathogens, and engulf and kill them. Large granular lymphocytes that offer protection from virus infected cells and cancer cells are the Natural Killer (NK) cells of the innate system. NK cells lyse the infected cell or cancer cell, whereas macrophages engulf them. The NK cells are part of the innate system since they lack antigen specificity. Macrophages are also responsible for cytokine production (see below).

Leukocytes that *are* antigen-specific are part of the adaptive immune system. Leukocytes begin development in the bone marrow, whereas T cells complete their development in the Thymus. During development each cell acquires specific individual antigen receptors and co-receptors, receptors to cytokines, and receptors to adhesion molecules (found on epithelial cell membranes). Antigen-specific lymphocytes multiply when their receptors encounter the antigen. Their progeny, or clones, contain the same antigen specificity as the parent cell that was activated.

The organs of the immune system are classified as either primary or secondary. The primary organs include the bone marrow and the Thymus. The secondary organs are meeting places for antigen and leukocyte. The secondary organs include the spleen and the lymph nodes. Special clusters of epithelia cells (M cells) and lymphocytes also occur where exposure to antigen is most likely. Exposure is most likely at the membranes lining respiratory, digestive, and urogenital systems.

Antibodies

Antibodies, or immunoglobulins, are Y-shaped proteins that are composed of two identical binding regions at the upper part of the Y, but vary according to antigen specificity, and an invariable region on the lower portion of the Y. The invariable lower portion accounts for the five different isotypes of antibody including, IgA, IgD, IgE, IgG, and IgM. Antibodies are either membrane bound as receptor sites on B cells or unbound molecules that are secreted by B cells after stimulation from cytokines from T cells.

Antigen elimination is the primary function of the antibodies. The binding of antibodies to antigen results in neutralization and opsonization. Neutralization occurs when the antibodies bind to bacterial toxins or extracellular proteins and inactivates them. Opsonization occurs when antibodies (or complement) form a coat surrounding the pathogen which then enables binding to phagocytes and elimination (or lysing).

Isotypes

The IgM and IgD antibodies (immunoglobulins) are membrane bound and function as receptors on B cells. IgM, the first unbound antibody secreted by an activated B cell, is a very efficient

antigen-binder and a complement activator, but is also a very large molecule. Its large size limits its efficiency of infiltration into various tissues.

IgG and IgA are secreted by the B cells after they are activated by cytokines from the T cells. IgG and IgA neutralizes toxins and viruses by blocking the host cells binding capabilities. IgG is predominantly in the serum, thus neutralization and opsonization by IgG prevents the toxins and viruses from entering the host's cells. IgA is present in mucus secretions, including breast milk and those found in the lining of the digestive, respiratory, and urogenital systems.

IgE is the immunoglobulin responsible for histamine release that occurs with allergic reactions by binding to mast cells. IgE also functions as protection against antigens associated with parasites.

2.1.2. Overview of Cytokines

A key component in the immune response is cell-to-cell signaling. Cell-to-cell signaling is achieved through cytokine secretion. Cytokine is a generic term for a family of small proteins with short half lives that regulate and modulate the immune system. They are predominately produced by helper T cells and macrophages and result in activation, inhibition, inflammation, differentiation, proliferation, and cell death. Specific cytokines include lymphokines, monokines, chemokines, and interleukin. Lymphokines and monokines are produced by lymphocytes and monocytes, respectively. Chemokines produce chemotactic activity, i.e. they attract leukocytes to the site of an infection. Interleukins are cytokines produced by one type of leukocyte that causes a response in a different type of leukocyte.

Cytokines are capable of producing a variety of actions, including autocrine, paracrine and endocrine actions. Autocrine, paracrine and endocrine refer to actions upon, the same cells that

secrete the cytokine, cells in close proximity, and distant cells, respectively. Additionally, cytokines exhibit redundancy and pleiotropy. Redundancy refers to different cytokines producing similar functions or effects. Pleiotropy refers to one cytokine activating many different types of target cells, or for many different cytokine-producing cells to produce the same cytokine. Other characteristics of cytokines are their ability to behave in a synergistic or antagonistic fashion, and for the production of one cytokine to initiate production of another cytokine in a different cell.

Cytokines may also be categorized by function. Immune cell proliferation and differentiation characterizes the largest group of cytokines. This group includes TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, interferon gamma ($\text{IFN}\gamma$), and Granulocyte Monocyte Colony-Stimulating Factor (GM-CSF). Another group is characterized by its ability to inhibit viral replication in infected cells and simultaneously stimulating antigen-presenting MHC expression. This group includes Interferon alpha ($\text{IFN}\alpha$) and Interferon beta ($\text{IFN}\beta$). Interleukin-8, MCP-1, MIP-1 α , MIP-1 β , Lymphotactin, and Fractalkine represent the chemokine group. Finally, there is also a group that is composed of cytokines that inhibit inflammatory cytokine production by macrophages and includes IL-10 and IL-13.

Additional details concerning IL-6, IL-10, and TNF are provided since they are the focus of this analysis and report.

2.1.2.1. TNF

TNF is a superfamily of molecules first recognized when certain cancer patients exhibited regression of tumors following infection. Tumor Necrosis Factor alpha (α) and beta (β) are only two types of the many specific molecules found within this superfamily.

TNF α is a bioactive nonglycosylated transmembrane or soluble polypeptide. The transmembrane form is 233 amino acids long, has a mass of 26 kDa and consists of cytoplasmic, transmembrane, and extracellular regions composed of 29, 28 and 176 amino acids respectively.³ A soluble homotrimeric molecule of 157 amino acids is formed when a proteolytic TNF α converting enzyme cleaves the membrane bound protein.⁴ The soluble, circulating form is reported to be more potent than the membrane bound form and normal levels are 10-80 pg/mL.^{5 6}

Many different cells express TNF α . The various cell types include T helper cells⁷ (CD4 and CD8), macrophages, mast cells,⁸ osteoblasts,⁹ pancreatic cells,¹⁰ fat cells,¹¹ dendritic cells,¹² neurons,¹³ astrocytes,¹⁴ and monocytes.¹⁵ The effect of the TNF α expressed by these cells is cytotoxic to tumor cells and induces other cell types to secrete other cytokines involved with the inflammatory response.

TNF β is a circulating 25 kDa glycosylated polypeptide; one composed of 171 amino acids, the other of 194 amino acids.¹⁶ TNF β binds to the same receptors as TNF α and circulating levels are reported to be ~150pg/mL.¹⁷ Unlike TNF α , TNF β is not a transmembrane protein and only has a circulating or membrane-associated form. NK cell, and T and B cells express TNF β .¹⁸ While the effects of TNF β are similar to those of TNF α , TNF β also increases the phagocytic activity of macrophages and neutrophils.

2.1.2.2. IL-6

IL-6 is a relatively recent name given to a cytokine that was associated with many different functions and having equally many different names. It was only after a common gene was identified that these differently named molecules based on different functions became known collectively as IL-6.¹⁹ This phenomenon is the basis of the pleiotrophic characteristic of this

cytokine. Membership in the IL-6 family is related to its helical structure and receptor characteristics.^{20 21}

IL-6 is a secreted glycoprotein with a mass of 22-27 kDa. IL-6 is originally translated into a molecule of 212 amino acids, ending as a mature molecule of 184 amino acids.²² Normal circulating levels of IL-6 are reported to be ~1 pg/mL.²³ Elevations of IL-6 are also reported in association with menstruation,²⁴ melanoma,²⁵ and post-surgery.²⁶

As seen with TNF, various cell types express IL-6. Expression of IL-6 is seen in T cells (CD8),²⁷ fat cells,²⁸ fibroblasts,²⁹ osteoblasts,³⁰ mast cells,³¹ astrocytes,^{32 33} pigment cells in the retina,³⁴ cerebral cortex and sympathetic neurons,^{35 36} eosinophils,³⁷ neutrophils,³⁸ monocytes,³⁹ epithelial cells of the large intestine,⁴⁰ synoviocytes,⁴¹ pancreatic cells,⁴² and others.

IL-6 has been associated with various activities. IL-6 is described as both a pro- and anti-inflammatory molecule⁴³ as well as a co-stimulator (with IL-1) in T cell activation and plasma cell proliferation.⁴⁴ IL-6 also increases hematopoiesis⁴⁵ and modulates resorption of bone.⁴⁶

2.1.2.3. IL-10

IL-10 is a nonglycosylated molecule that weighs 18 kDa and is composed of 178 amino acids with a mature length of 160 amino acids.⁴⁷ Normal circulating levels of IL-10 are reported to be ~0.5 pg/mL.

As seen with TNF and IL-6, various cell types express IL-10. Expression of IL-10 is seen in T cells (CD8),⁴⁸ macrophages that have been activated,⁴⁹ B cells,⁵⁰ melanoma cells,⁵¹ NK cells,⁵² eosinophils,⁵³ dendritic cells,⁵⁴ and others. The secretion of IL-10 suppresses cytokine production by the T_H1 subset of T helper cells. IL-10 modulates function in various cell types including neutrophils, monocytes, dendritic cells, and mast cells and NK cells, as well as T and B cells.

IL-10 has an anti-inflammatory effect on neutrophils:

- Blocks IL-1 β and TNF α and inhibits secretion of IL-8, MIP-1 α , MIP-1 β ⁵⁵
- Results in less superoxide being produced, which hinders anti-body dependent cytotoxicity.⁵⁶

IL-10's effect on monocytes:

- Results in decreased IL-8 production⁵⁷
- Results in increased hyaluronectin in connective tissue (which is associated with decreased migration of metastatic tumor cells)⁵⁸
- Reduces MHC-II expression on the cell surface.⁵⁹

IL-10 has an immunosuppressive effect on dendritic cells. IL-10 results in:

- Increases in macrophages (while this may appear beneficial, macrophages are not good antigen presenting cells)⁶⁰
- Dendritic cells being less efficient at stimulating T cells⁶¹
- Immobile dendritic cells.⁶²

In NK cells, IL-10:

- Promotes TNF α and GM-CSF production⁶³
- May increase IL-2 induced NK cell proliferation⁶⁴
- Increases NK cells cytotoxicity with the aid of IL-12 and IL-18.⁶⁵

IL-10 has the opposite effect in mast cells compared to NK cells. In mast cells, IL-10 results in:

- Blocked production of TNF α and GM-CSF⁶⁶
- Increased release of histamine.

IL-10 effects T cell function by:

- Suppressing IL-2⁶⁷

- Inhibiting T cell apoptosis⁶⁸
- Induction of CD8 chemotaxis.⁶⁹

IL-10 effects B cell function by:

- Initiating differentiation/growth and promotes plasma cell formation⁷⁰
- Inducing the production of IgA⁷¹
- Inducing the production of IgG1 and IgG3 (in the absence of TGF β).⁷²

2.2. The Data – Censored, Sample-Selected, Truncated data

Many investigators use ordinary least squares (OLS) regression in the event of a continuous outcome variable. However, deviation from the assumptions of ordinary least squares will result in biased estimates. Uninformed investigators may also perform OLS on limited datasets, or datasets with missing values, while others may sort their data to eliminate groups with missing values and then perform OLS. These types of datasets often have a problem commonly referred to as a censoring problem, but may be categorized as either censored, sample selected, or truncated. To delineate the differences between these types of data see Table 1.⁷³

Table 1. Definitions of Censored, Sample-Selected, and Truncated Variables

Data/Sample	Dependent Variable	Independent Variable(s)
Censored	y is known exactly only if some criterion defined in terms of the value of y is met, such as $y > c$ (or $y < c$). y is a truncated random variable.	x variable values are observed for all of the sample, regardless of whether y is known exactly.
Sample selected	y is observed only if some criterion defined in terms of another random variable, z , is met such as if $z = 1$. y is a truncated random variable.	x and w are observed for all the sample, regardless of whether y is observed or not.
Truncated	y is observed only if some criterion defined in terms of the value of y is met, such as $y > c$ (or $y < c$). y is a truncated random variable.	Independent variables are observed only if y is observed

The dataset in this report is classified as censored from below. A variable is left censored (censored from below) if for some value y , the exact value of y taken is $y > c$. For other values of y it is only known that $y \leq c$. A variable may be right censored (censored from above) if for

some value y , the exact value of y taken is less than some threshold, $y < d$. For other values of y it is only known that $y \geq d$. A final example of censored data is where the data is censored from the left and the right (ie. from below and above). In this instance, $c < y < d$; where the exact values of y are known between the lower and upper limits. However, if outside of the specified range, it is only known that $y \leq c$ and/or $y \geq d$.

2.2.1. The Tobit Model

The simplest method for analysis for censored data is the Tobit model.⁷⁴ The Tobit model may be interpreted in terms of an underlying latent variable, y^* , of which y is the realized observation. Another way of saying this, is that y^* is the true value, and y is the value that is observed (remembering that the value is limited or censored). The model may be written in terms of the latent variable y^* :

$$y_i^* = x_i^T \beta + u_i$$

where the error term u_i is assumed to be independent and normally distributed with a mean of zero and a constant variance, σ^2 .

The observed and latent variables are related by the following relationship:

$$y_i = y_i^* \text{ if } y_i^* > c$$

$$y_i = c \text{ if } y_i^* \leq c$$

where c is the censoring threshold. In this report, the censoring thresholds for tnf , IL6 and IL10 , are 3.9, 4.9, and 4.9, respectively. The model written in terms of the observed variable y , using tnf for example is:

$$y_i = x_i^T \beta + u_i \text{ if } > 3.9$$

$$y_i = 3.9 \text{ otherwise.}$$

The purpose of regression is to estimate an intercept (α), a regression coefficient (β), and the standard error of the independent error term, σ (assumed normally distributed). In some circumstances (where certain assumptions met- no correlation between u and x , independence of u_i s, zero expectation of u_i , and homoscedasticity) ordinary least squares (OLS) provide estimates that are the best linear unbiased estimators (BLUE), i.e. the estimates have the smallest sampling variance (making them the most efficient) of all the linear unbiased estimators. However, in the case of censored data, maximum likelihood estimation is used to estimate α , β , and σ .

2.2.2. Maximum Likelihood

The goal of maximum likelihood is to find the set of parameters that would have generated the observed sample most often, if the parameters are true of the population. Maximum likelihood is applicable in both the discrete and continuous case. Regardless of type of variable, the first step is to formulate the likelihood function. Formulating a likelihood function first starts with the joint probability distribution

$$f(y_1, y_2, \dots, y_N).$$

And since the sample observations are assumed to be independent, the joint probability is equal to the product of the marginal probabilities

$$\begin{aligned} f(y_1)f(y_2)\dots f(y_N). \\ = \prod_1^N f(y_i). \end{aligned}$$

Although this equation is identical to the joint probability distribution of the sample, it is something completely different in terms of maximum likelihood estimation. In the case of a joint probability distribution, the parameters of the distribution are fixed, and the y values are variable. In the case of likelihood, the y values are fixed and the parameters are allowed to vary.

For simplifying calculations, the natural logarithm of the likelihood function is then taken, and maximized with respect to each parameter.

The dependent variables in this report (tnf, IL6, and IL10) are continuous, and therefore the probability density function is used to formulate the likelihood function (as opposed to probability mass function). Assuming the population y_i 's are normally distributed the density function is

$$f(y_i) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp \frac{-[(y_i - \mu)/\sigma]^2}{2}.$$

Taking the product of the densities of the y_i 's and then taking the natural logarithm of this function results in the log-likelihood function

$$\sum_1^N \log \left(\frac{1}{\sqrt{2\pi\sigma^2}} \right) - \frac{1}{2\sigma^2} (y_i - \mu)^2.$$

Let $\mu_i = \alpha + \beta x_i$, and substitute into the equation above. This substitution is made since μ varies over the sample resulting in

$$\sum_1^N \log \left(\frac{1}{\sqrt{2\pi\sigma^2}} \right) - \frac{1}{2\sigma^2} (y_i - (\alpha + x_i^T \beta))^2.$$

Parameter estimates of α , β , and σ are derived by maximizing the above equation.⁷⁵ This is the log-likelihood for the normal error regression model. However, in the tobit model, censored and uncensored observations make separate contributions to the log-likelihood function.

2.2.3. Tobit Model and Maximum Likelihood

Let y_i be the serum cytokine level (tnf, IL6, IL10) of the i^{th} patient in the population of study patients, and let x_i be the value of dead or alive status at discharge or follow-up. The goal is to estimate the vector β , which is the set of population regression parameters relating x_i to the level

of circulating cytokine. The sample is composed of N patients, of which N_0 have truncated cytokine (censored) values, and $N_1 (=N-N_0)$ with observed (uncensored) values.

To formulate the likelihood function for the tobit model it is assumed that

- u_i has a normal distribution,
- the error terms of each observation are independent of each other,
- the error term is independent of the independent variable(s) in the model.⁷⁶

We also have cytokine values for all patients (day 1), and that for uncensored (N_1) observations, the exact value is known.

Contributions to the likelihood come from censored and uncensored observations. The likelihood contains the product of N_0 observations that are censored and N_1 observations that are uncensored. The product of the N_0 observations is

$$\prod_{i=1}^{n_0} \left(1 - \Phi_i \left(\frac{y_i - (\alpha + x_i^T \beta)}{\sigma} \right) \right)$$

where Φ (unless stated otherwise) denotes the standard normal distribution function (*mean = 0, variance = 1*).

The product of the N_1 observations is

$$\prod_{i=n_0+1}^N \left(\Phi_i \left(\frac{y_i - (\alpha + x_i^T \beta)}{\sigma} \right) \right)$$

However, for the N_1 observations, the exact cytokine values are known, therefore the following term becomes part of the likelihood,

$$\prod_1 \frac{1}{\sigma} \frac{\Phi[(y_i - (\alpha + x_i^T \beta))/\sigma]}{\Phi_i \left(\frac{y_i - (\alpha + x_i^T \beta)}{\sigma} \right)}$$

When the three product terms are multiplied, the $\Phi_i(\cdot)$ term (in the second and third product-terms) cancels.

$$\prod_0 \left(1 - \Phi_i \left(\frac{y_i - (\alpha + x_i^T \beta)}{\sigma} \right) \right) \prod_1 \left(\Phi_i \left(\frac{y_i - (\alpha + x_i^T \beta)}{\sigma} \right) \right) \prod_1 \frac{1}{\sigma} \frac{\Phi[(y_i - x_i^T \beta) / \sigma]}{\Phi_i}$$

The result is the likelihood function:

$$\prod_0 \left(1 - \Phi_i \left(\frac{y_i - (\alpha + x_i^T \beta)}{\sigma} \right) \right) \prod_1 \Phi[(y_i - (\alpha + x_i^T \beta)) / \sigma].$$

The natural logarithm of the likelihood function is:

$$\sum_0 \log \left(1 - \Phi_i \left(\frac{y_i - (\alpha + x_i^T \beta)}{\sigma} \right) \right) + \sum_1 \log \frac{1}{\sqrt{2\pi\sigma^2}} - \sum_1 \frac{1}{2\sigma^2} (y_i - x_i^T \beta)^2 .$$

Notice that the circled portion (uncensored contribution) of the tobit log-likelihood function is same as the log-likelihood for the normal error regression model in the previous section (1.2.2).

2.2.4. The Delta Method for Standard Error Determination

The *predictnl* command is implemented as an ado-file following an estimation command (e.g. *tobit*) in STATA. The quantities generated by *predictnl* are not scalars, but functions of the data, and are therefore vectors over the observations within the data.

For general prediction,

$$g(\theta, x_i) \quad \text{for } i = 1, \dots, n$$

where θ are model parameters and x_i are data for the i^{th} observation (and are assumed to be fixed). In STATA, $g(\theta, x_i)$ is estimated by

$$g(\hat{\theta}, x_i)$$

where $\hat{\theta}$ are estimated model parameters stored as e(b) following the estimation command. In STATA, *predictnl* generates the estimated prediction, $g(\hat{\theta}, x_i)$, but also generates the standard error of $g(\hat{\theta}, x_i)$, using the “delta method”.⁷⁷

The delta method expands a function of a random variable about its mean with a one-step Taylor approximation, and then takes the variance.⁷⁸ When using *predictnl*, the transformation $g(\theta, x_i)$, is estimated by $g(\hat{\theta}, x_i)$, for $1 \times k$ parameter vector θ and the data x_i (which is assumed fixed). The variance of $g(\hat{\theta}, x_i)$ is estimated by

$$\widehat{Var}\{g(\hat{\theta}, x_i)\} = GVG'$$

where G is the vector of derivatives

$$G = \left\{ \frac{\partial g(\theta, x_i)}{\partial \theta} \Big|_{\theta=\hat{\theta}} \right\}_{(1 \times k)}$$

and V is the estimated variance-covariance matrix of $\hat{\theta}$.⁷⁹

For the instance presented here the mean is estimated by $\exp(x^T \hat{\beta})$. Using the delta method, the estimated variance is given by:

$$\begin{aligned} & \begin{pmatrix} e^{x\hat{\beta}} & xe^{x\hat{\beta}} \end{pmatrix} \begin{pmatrix} V(\hat{\beta}_0) & C(\hat{\beta}_0, \hat{\beta}_1) \\ C(\hat{\beta}_0, \hat{\beta}_1) & V(\hat{\beta}_1) \end{pmatrix} \begin{pmatrix} e^{x\hat{\beta}} \\ xe^{x\hat{\beta}} \end{pmatrix} \\ &= \left(V(\hat{\beta}_0)e^{x\hat{\beta}} + C(\hat{\beta}_0, \hat{\beta}_1)xe^{x\hat{\beta}}, C(\hat{\beta}_0, \hat{\beta}_1)e^{x\hat{\beta}} + V(\hat{\beta}_1)xe^{x\hat{\beta}} \right) \begin{pmatrix} e^{x\hat{\beta}} \\ xe^{x\hat{\beta}} \end{pmatrix} \\ &= \left(V(\hat{\beta}_0)(e^{x\hat{\beta}})^2 + C(\hat{\beta}_0, \hat{\beta}_1)x(e^{x\hat{\beta}})^2 + C(\hat{\beta}_0, \hat{\beta}_1)x(e^{x\hat{\beta}})^2 + V(\hat{\beta}_1)x^2(e^{x\hat{\beta}})^2 \right) \\ &= \left(e^{x\hat{\beta}} \right)^2 \left(V(\hat{\beta}_0) + 2C(\hat{\beta}_0, \hat{\beta}_1)x + V(\hat{\beta}_1)x^2 \right). \end{aligned}$$

2.3. Additional Analysis

In addition to tobit estimates of mean cytokine levels in the study population, the arithmetic and geometric mean are also provided.

2.3.1. Arithmetic Mean

The arithmetic mean of a set of numbers is the sum of all the members of the set divided by the number of items in the set. If the data set is denoted by $X = \{x_1, x_2, \dots, x_n\}$. The arithmetic mean is calculated as:

$$\bar{x} = (x_1 + x_2 + \dots + x_n) / n$$

or alternatively

$$\bar{x} = \frac{1}{n} \sum_{i=1}^n x_i$$

The arithmetic mean is greatly influenced by outliers.⁸⁰

2.3.2. Geometric Mean

The geometric mean is to multiplication as the arithmetic mean is to addition. Just as adding n terms all equal to the arithmetic mean yields the sum $x_1 + \dots + x_n$, so multiplying n factors all equal to the geometric mean yields the product $x_1 \dots x_n$ (these n numbers must be non-negative).

The geometric mean is

$$(x_1 x_2 \dots x_n)^{1/n}$$

or

$$\sqrt[n]{x_1 x_2 \dots x_n} .$$

The geometric mean is less affected by extreme values than the arithmetic mean and is useful for some positively skewed distributions.⁸¹

3. RESULT

The data set consists of serum cytokine levels measured on day 1 for 1753 critical care patients. Tumor necrosis factor, Interleukin-6, and Interleukin-10 are coded as *tnf*, *il6*, and *il10* respectively. Tobit estimates of mean cytokine levels are for dead or alive status at discharge and follow up. Dead and alive are coded as 0 and 1 respectively. Discharge and follow up are coded as “dc” and “fu”, respectively. Cytokine values were available for 1753 patients at discharge. However, 143 patients were lost to follow up.

Laboratory values for *tnf*, *il6* and *il10* are left censored. The lower limit for *tnf*, *il6* and *il10* are 4, 4, and 5 respectively. The number of left censored cytokine values for *tnf*, *il6*, and *il10 at discharge*, were 670 (38.22%), 248 (14.15%), and 854 (48.72%), respectively. The number of left censored cytokine values for *tnf*, *il6*, and *il10 at follow up*, were 610 (38.89%), 230 (14.29%), and 788 (48.94%), respectively.

Microsoft Excel, Microsoft Access, and STATA 8.0 SE were used for all data analyses. A summary table for mean estimates of *tnf*, *IL6* and *IL10* for discharge status and follow-up status are presented below. The STATA output may be found in Appendix A.

Table 2. Frequency of censored cytokine values and dead/alive status at discharge and follow-up

	Discharge Status (N=1753)		Followup Status (N=1610)	
	Frequency	Percent	Frequency	Percent
tnf	670	38.22	610	38.89
IL6	248	14.15	230	14.29
IL10	854	48.72	788	48.94
dead	78	4.45	231	14.35
alive	1675	95.55	1379	85.65

N=1610 at follow up due to dead/alive status missing for 143 patients.

Table 3. Comparison of mean estimates for TNF, IL6, and IL10 for death at discharge based on the tobit model, the arithmetic and the geometric mean. Note that the population is the 1753 individuals with both complete lab and follow up data with 78 reported deaths at discharge and 1675 subjects alive at hospital discharge. Standard errors are given in parentheses below the mean.

Cytokine	Estimated tobit mean for dead at discharge	Estimated arithmetic mean for dead at discharge	Estimated geometric mean for dead at discharge	Estimated tobit mean for alive at discharge	Estimated arithmetic mean for alive at discharge	Estimated geometric mean for alive at discharge
TNF	8.2286 (1.0021)	17.6256 (3.9608)	9.70	5.1884 (0.1472)	10.4444 (0.7426)	6.90
IL6	167.1379 (38.3026)	2895.464 (1648.548)	172.46	37.0714 (1.8622)	329.1224 (33.4703)	43.28
IL10	11.3489 (2.2705)	47.11282 (13.2713)	15.64	4.9238 (0.2483)	22.34845 (1.6798)	9.61

Table 4. Comparison of mean estimates for TNF, IL6, and IL10 for death at follow-up based on the tobit model, the arithmetic and the geometric mean. Note that the population is the 1753 individuals with both complete lab and follow-up data with 231 reported deaths at follow-up and 1379 subjects alive at follow up and 143 with missing values. Standard errors are given in parentheses below the mean.

Cytokine	Estimated tobit mean for dead at follow-up	Estimated arithmetic mean for dead at follow-up	Estimated geometric mean for dead at follow-up	Estimated tobit mean for alive at follow-up	Estimated arithmetic mean for alive at follow-up	Estimated geometric mean for alive at follow-up
TNF	7.1808 (0.5058)	13.7311 (1.5252)	8.65	5.0828 (.01565)	10.0451 (0.7933)	6.77
IL6	77.9086 (10.4984)	1302.035 (575.8675)	83.81	35.2435 (1.9688)	318.4954 (33.0279)	41.62
IL10	7.7613 (0.9265)	30.8952 (5.1314)	12.17	4.7229 (.2623)	21.8598 (1.8900)	9.44

4. CONCLUSION / RECOMMENDATION

Three different methods were presented to estimate the mean cytokine levels of 1753 critical care patients. An accurate estimate of serum levels of TNF, IL6 and IL10 is important since elevated cytokine levels have been associated with tissue damage and a heightened immune response. However, when quantifying assays have a limited range of sensitivity, a large portion of the serum samples tested may fall below or above the accurate range of the assay. The tobit regression provides a method for estimation when dealing with censored data. The arithmetic and geometric means are presented for comparison.

I would not recommend using the arithmetic mean to estimate cytokine levels with this dataset since the data is highly skewed. The arithmetic mean does not take censored laboratory values into account and has a larger standard error associated with its mean when compared to the tobit estimate.

Although the geometric mean is less affected by extreme values than the arithmetic mean and is useful for some positively skewed distributions,⁸² I also would not recommend using the geometric mean for estimating the mean cytokine levels with this cytokine dataset. The geometric mean is similar to the arithmetic mean in that it does not account for the censored values.

Of the three estimation methods presented, I would recommend using the tobit model for estimation purposes. I would also recommend that the data be log transformed before the analysis and that the delta method be used to estimate the standard error. Although the tobit model accounts for censored values, it is assumed that the underlying latent variable of the model:

$$y_i^* = x_i^T \beta + u_i,$$

is the correct functional form for the relationship between the latent cytokine level, and discharge or follow-up status. However, other relevant variables may have been omitted from the specification⁸³ and further research may conclude that a more complex model, than the one presented here, may reveal a more clinically meaningful estimate.

5. APPENDIX A: STATA Output

```
-----
log: C:\Documents and Settings\RSITLO\Desktop\TOD\Tobit_LWDeltaSE.log
log type: text
opened on: 24 Feb 2005, 14:13:51

. do "C:\DOCUME~1\RSITLO\LOCALS~1\Temp\STD030000.tmp"

. * estimating mean tnf and the std error of the predicted value - from STATA manual
for "predictnl"
> pg 225)
.
. **Make sure to check that path for data file is correct before running on different
computers
.
. **** FOR TNF
. **** FOR TNF
. **** FOR TNF
.
.
. * FOR TNF DISCHARGE STATUS
. clear

. use "C:\Documents and Settings\RSITLO\Desktop\TOD\fullvalueslogtransformed.dta"

. tobit lntnf dc, ll

Tobit estimates                               Number of obs   =       1753
                                             LR chi2(1)     =       13.56
                                             Prob > chi2    =       0.0002
Log likelihood = -2120.2731                 Pseudo R2      =       0.0032

-----
      lntnf |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-----+-----
       dc |   -0.461206   .1246857    -3.70   0.000   -0.7057491   -0.2166521
      _cons |   2.107614   .1217833    17.31   0.000    1.868758    2.34647
-----+-----
      _se |   1.039942   .0242969                (Ancillary parameter)
-----

Obs. summary:      670  left-censored observations at lntnf<=1.360977
                  1083  uncensored observations

. predict lntnfdcxb, xb

. sort dc

. by dc: summarize lntnfdcxb
-----
```

```
-> dc = 0
```

Variable	Obs	Mean	Std. Dev.	Min	Max
lntnfdcxb	78	2.107614	0	2.107614	2.107614

```
-> dc = 1
```

Variable	Obs	Mean	Std. Dev.	Min	Max
lntnfdcxb	1675	1.646413	0	1.646413	1.646413

```
. generate esttnfdcxb=exp(lntnfdcxb)
```

```
. sort dc
```

```
. by dc: summarize esttnfdcxb
```

```
-> dc = 0
```

Variable	Obs	Mean	Std. Dev.	Min	Max
esttnfdcxb	78	8.228582	0	8.228582	8.228582

```
-> dc = 1
```

Variable	Obs	Mean	Std. Dev.	Min	Max
esttnfdcxb	1675	5.188336	0	5.188336	5.188336

```
.  
. **Calculation of standard error is based on Lisa DELTA Method when using predictnl  
. predictnl pxb=(xb()), se(pxb_se)
```

```
. sort dc
```

```
. by dc: summarize pxb_se
```

```
-> dc = 0
```

Variable	Obs	Mean	Std. Dev.	Min	Max
pxb_se	78	.1217833	0	.1217833	.1217833

```
-> dc = 1
```

Variable	Obs	Mean	Std. Dev.	Min	Max
pxb_se	1675	.0283636	0	.0283636	.0283636

```
. generate se=pxb_se*(exp(pxb))
```

```
. sort dc
```

```
. by dc: summarize se
```

```
-> dc = 0
```

Variable	Obs	Mean	Std. Dev.	Min	Max
se	78	1.002104	0	1.002104	1.002104

```
-> dc = 1
```

Variable	Obs	Mean	Std. Dev.	Min	Max
se	1675	.1471599	0	.1471599	.1471599

```
.  
.
.
```

```
. ** FOR TNF FOLLOWUP STATUS  
. clear
```

```
. use "C:\Documents and Settings\RSITLO\Desktop\TOD\fullvalueslogtransformed.dta"
```

```
. tobit lntnf fu, ll
```

```
Tobit estimates                               Number of obs   =       1610
                                                LR chi2(1)      =       20.41
                                                Prob > chi2     =       0.0000
Log likelihood = -1939.0459                    Pseudo R2      =       0.0052
```

lntnf	Coef.	Std. Err.	t	P> t	[95% Conf. Interval]	
fu	-.345545	.0761716	-4.54	0.000	-.4949509 - .1961391	
_cons	1.971414	.0704406	27.99	0.000	1.833249 2.109579	
_se	1.026036	.0249322	(Ancillary parameter)			

```
Obs. summary:      610 left-censored observations at lntnf<=1.360977
                   1000 uncensored observations
```

```
. predict lntnffuxb, xb  
(143 missing values generated)
```

```
. sort fu
```

```
. by fu: summarize lntnffuxb
```

```
-> fu = 0
```

Variable	Obs	Mean	Std. Dev.	Min	Max
lntnffuxb	231	1.971414	0	1.971414	1.971414

```
-> fu = 1
```

Variable	Obs	Mean	Std. Dev.	Min	Max
----------	-----	------	-----------	-----	-----

```
-----+-----
lntnffuxb |      1379      1.625869          0      1.625869      1.625869
```

```
-> fu = .
```

```
-----+-----
Variable |      Obs      Mean      Std. Dev.      Min      Max
-----+-----
lntnffuxb |          0
```

```
. generate esttnffuxb=exp(lntnffuxb)
(143 missing values generated)
```

```
. sort fu
```

```
. by fu: summarize esttnffuxb
```

```
-> fu = 0
```

```
-----+-----
Variable |      Obs      Mean      Std. Dev.      Min      Max
-----+-----
esttnffuxb |      231      7.180821          0      7.180821      7.180821
```

```
-> fu = 1
```

```
-----+-----
Variable |      Obs      Mean      Std. Dev.      Min      Max
-----+-----
esttnffuxb |     1379      5.082833          0      5.082833      5.082833
```

```
-> fu = .
```

```
-----+-----
Variable |      Obs      Mean      Std. Dev.      Min      Max
-----+-----
esttnffuxb |          0
```

```
.
. **Calculation of standard error is based on Lisa DELTA Method when using predictnl
. predictnl pxb=(xb()), se(pxb_se)
(143 missing values generated)
```

```
. sort fu
```

```
. by fu: summarize pxb_se
```

```
-> fu = 0
```

```
-----+-----
Variable |      Obs      Mean      Std. Dev.      Min      Max
-----+-----
pxb_se |      231      .0704406          0      .0704406      .0704406
```

```
-> fu = 1
```

```
-----+-----
Variable |      Obs      Mean      Std. Dev.      Min      Max
-----+-----
pxb_se |     1379      .030785          0      .030785      .030785
```

```
-> fu = .
```

Variable	Obs	Mean	Std. Dev.	Min	Max
pxb_se	0				

```
. generate se=pxb_se*(exp(pxb))  
(143 missing values generated)
```

```
. sort fu
```

```
. by fu: summarize se
```

```
-> fu = 0
```

Variable	Obs	Mean	Std. Dev.	Min	Max
se	231	.5058214	0	.5058214	.5058214

```
-> fu = 1
```

Variable	Obs	Mean	Std. Dev.	Min	Max
se	1379	.1564751	0	.1564751	.1564751

```
-> fu = .
```

Variable	Obs	Mean	Std. Dev.	Min	Max
se	0				

```
.
```

```
. ***** IL6
```

```
. ***** IL6
```

```
. ***** IL6
```

```
.
```

```
. * FOR IL6 DISCHARGE STATUS
```

```
. clear
```

```
. use "C:\Documents and Settings\RSITLO\Desktop\TOD\fullvalueslogtransformed.dta"
```

```
. tobit ln16 dc, ll
```

```
Tobit estimates                               Number of obs   =       1753  
                                              LR chi2(1)      =        40.72  
                                              Prob > chi2     =        0.0000  
Log likelihood = -3461.2358                 Pseudo R2      =        0.0058
```

ln16	Coef.	Std. Err.	t	P> t	[95% Conf. Interval]
dc	-1.505972	.2345922	-6.42	0.000	-1.966083 -1.045862
_cons	5.118819	.2291676	22.34	0.000	4.669348 5.56829
_se	2.018852	.038088			(Ancillary parameter)

```

Obs. summary:      248 left-censored observations at ln16<=1.589235
                  1505 uncensored observations

. predict ln16dcxb, xb
. sort dc
. by dc: summarize ln16dcxb

```

```

-> dc = 0

```

Variable	Obs	Mean	Std. Dev.	Min	Max
ln16dcxb	78	5.118819	0	5.118819	5.118819

```

-> dc = 1

```

Variable	Obs	Mean	Std. Dev.	Min	Max
ln16dcxb	1675	3.612847	0	3.612847	3.612847

```

. generate estil6dcxb=exp(ln16dcxb)
. sort dc
. by dc: summarize estil6dcxb

```

```

-> dc = 0

```

Variable	Obs	Mean	Std. Dev.	Min	Max
estil6dcxb	78	167.1379	0	167.1379	167.1379

```

-> dc = 1

```

Variable	Obs	Mean	Std. Dev.	Min	Max
estil6dcxb	1675	37.07143	0	37.07143	37.07143

```

.
. **Calculation of standard error is based on Lisa DELTA Method when using predictnl
. predictnl pxb=(xb()), se(pxb_se)
. sort dc
. by dc: summarize pxb_se

```

```

-> dc = 0

```

Variable	Obs	Mean	Std. Dev.	Min	Max
pxb_se	78	.2291676	0	.2291676	.2291676

```
-> dc = 1
```

```
Variable |      Obs      Mean  Std. Dev.      Min      Max
-----+-----
pxb_se |    1675   .0502337         0   .0502337   .0502337
```

```
. generate se=pxb_se*(exp(pxb))
```

```
. sort dc
```

```
. by dc: summarize se
```

```
-> dc = 0
```

```
Variable |      Obs      Mean  Std. Dev.      Min      Max
-----+-----
se |        78   38.30259         0   38.30259   38.30259
```

```
-> dc = 1
```

```
Variable |      Obs      Mean  Std. Dev.      Min      Max
-----+-----
se |    1675   1.862235         0   1.862235   1.862235
```

```
.
```

```
. ** FOR IL6 FOLLOWUP STATUS
```

```
. clear
```

```
. use "C:\Documents and Settings\RSITLO\Desktop\TOD\fullvalueslogtransformed.dta"
```

```
. tobit lnil6 fu, ll
```

```
Tobit estimates              Number of obs   =      1610
                             LR chi2(1)       =       29.35
                             Prob > chi2      =       0.0000
Log likelihood = -3186.5002    Pseudo R2      =       0.0046
```

```
lnil6 |      Coef.  Std. Err.      t    P>|t|     [95% Conf. Interval]
-----+-----
fu |   -.7932545   .1458047   -5.44   0.000   -1.079242   -.5072673
_cons |  4.355537   .1347528   32.32   0.000    4.091227    4.619846
-----+-----
_se |  2.034854   .0400979                (Ancillary parameter)
```

```
Obs. summary:      230 left-censored observations at lnil6<=1.589235
                  1380 uncensored observations
```

```
. predict lnil6fuxb, xb
(143 missing values generated)
```

```
. sort fu
```

```
. by fu: summarize lnil6fuxb
```

```
-----+-----
      pxb_se |          231      .1347528          0      .1347528      .1347528
-----+-----
```

```
-> fu = 1
```

```
Variable |          Obs          Mean      Std. Dev.          Min          Max
-----+-----
      pxb_se |         1379      .0558627          0      .0558627      .0558627
-----+-----
```

```
-> fu = .
```

```
Variable |          Obs          Mean      Std. Dev.          Min          Max
-----+-----
      pxb_se |             0
-----+-----
```

```
. generate se=pxb_se*(exp(pxb))
(143 missing values generated)
```

```
. sort fu
```

```
. by fu: summarize se
```

```
-> fu = 0
```

```
Variable |          Obs          Mean      Std. Dev.          Min          Max
-----+-----
          se |          231      10.4984          0      10.4984      10.4984
-----+-----
```

```
-> fu = 1
```

```
Variable |          Obs          Mean      Std. Dev.          Min          Max
-----+-----
          se |         1379      1.968799          0      1.968799      1.968799
-----+-----
```

```
-> fu = .
```

```
Variable |          Obs          Mean      Std. Dev.          Min          Max
-----+-----
          se |             0
-----+-----
```

```
.
```

```
. ***** IL10
. ***** IL10
. ***** IL10
```

```
. * FOR IL10 DISCHARGE STATUS
. clear
```

```
. use "C:\Documents and Settings\RSITLO\Desktop\TOD\fullvalueslogtransformed.dta"
```

```
. tobit ln1l10 dc, ll
```

```
Tobit estimates                               Number of obs   =       1753
```

```

Log likelihood = -2346.2507
LR chi2(1) = 16.41
Prob > chi2 = 0.0001
Pseudo R2 = 0.0035

```

```

-----
      lnill10 |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-----+-----
           dc |   -0.8350396   0.2051793   -4.07   0.000   -1.237462   -0.4326176
          _cons |    2.429117   0.2000641   12.14   0.000    2.036728    2.821507
-----+-----
          _se |    1.692803   0.0442609                (Ancillary parameter)
-----

```

```

Obs. summary:      854 left-censored observations at lnill10<=1.589235
                  899 uncensored observations

```

```

. predict lnill10dcxb, xb
. sort dc
. by dc: summarize lnill10dcxb

```

```

-> dc = 0

```

```

-----
Variable |      Obs      Mean   Std. Dev.      Min      Max
-----+-----
lnill10dcxb |      78   2.429117         0   2.429117   2.429117
-----

```

```

-> dc = 1

```

```

-----
Variable |      Obs      Mean   Std. Dev.      Min      Max
-----+-----
lnill10dcxb |     1675   1.594078         0   1.594078   1.594078
-----

```

```

. generate estill10dcxb=exp(lnill10dcxb)
. sort dc
. by dc: summarize estill10dcxb

```

```

-> dc = 0

```

```

-----
Variable |      Obs      Mean   Std. Dev.      Min      Max
-----+-----
estill10dcxb |      78  11.34886         0  11.34886  11.34886
-----

```

```

-> dc = 1

```

```

-----
Variable |      Obs      Mean   Std. Dev.      Min      Max
-----+-----
estill10dcxb |     1675   4.923785         0   4.923785   4.923785
-----

```

```

. **Calculation of standard error is based on Lisa DELTA Method when using predictnl
. predictnl pxb=(xb()), se(pxb_se)

```

```

. sort dc

```

```
. by dc: summarize pxb_se
```

```
-> dc = 0
```

Variable	Obs	Mean	Std. Dev.	Min	Max
pxb_se	78	.2000641	0	.2000641	.2000641

```
-> dc = 1
```

Variable	Obs	Mean	Std. Dev.	Min	Max
pxb_se	1675	.0504257	0	.0504257	.0504257

```
. generate se=pxb_se*(exp(pxb))
```

```
. sort dc
```

```
. by dc: summarize se
```

```
-> dc = 0
```

Variable	Obs	Mean	Std. Dev.	Min	Max
se	78	2.270499	0	2.270499	2.270499

```
-> dc = 1
```

Variable	Obs	Mean	Std. Dev.	Min	Max
se	1675	.2482854	0	.2482854	.2482854

```
.
```

```
. ** FOR IL10 FOLLOWUP STATUS
```

```
. clear
```

```
. use "C:\Documents and Settings\RSITLO\Desktop\TOD\fullvalueslogtransformed.dta"
```

```
. tobit ln110 fu, ll
```

```
Tobit estimates                               Number of obs   =       1610
                                                LR chi2(1)      =       14.78
                                                Prob > chi2     =       0.0001
Log likelihood = -2147.814                    Pseudo R2      =       0.0034
```

ln110	Coef.	Std. Err.	t	P> t	[95% Conf. Interval]	
fu	-.4967164	.1289058	-3.85	0.000	-.7495573 - .2438755	
_cons	2.049144	.1193811	17.16	0.000	1.814985 2.283302	
_se	1.691228	.046283	(Ancillary parameter)			

```
Obs. summary:          788 left-censored observations at ln110<=1.589235
```

822 uncensored observations

```
. predict lnill10fuxb, xb  
(143 missing values generated)
```

```
. sort fu
```

```
. by fu: summarize lnill10fuxb
```

```
-> fu = 0
```

Variable	Obs	Mean	Std. Dev.	Min	Max
lnill10fuxb	231	2.049144	0	2.049144	2.049144

```
-> fu = 1
```

Variable	Obs	Mean	Std. Dev.	Min	Max
lnill10fuxb	1379	1.552427	0	1.552427	1.552427

```
-> fu = .
```

Variable	Obs	Mean	Std. Dev.	Min	Max
lnill10fuxb	0				

```
. generate estill10fuxb=exp(lnill10fuxb)  
(143 missing values generated)
```

```
. sort fu
```

```
. by fu: summarize estill10fuxb
```

```
-> fu = 0
```

Variable	Obs	Mean	Std. Dev.	Min	Max
estill10fuxb	231	7.761253	0	7.761253	7.761253

```
-> fu = 1
```

Variable	Obs	Mean	Std. Dev.	Min	Max
estill10fuxb	1379	4.72292	0	4.72292	4.72292

```
-> fu = .
```

Variable	Obs	Mean	Std. Dev.	Min	Max
estill10fuxb	0				

```
.  
. **Calculation of standard error is based on Lisa DELTA Method when using predictnl  
. predictnl pxb=(xb()), se(pxb_se)
```

(143 missing values generated)

```
. sort fu  
. by fu: summarize pxb_se
```

-> fu = 0

Variable	Obs	Mean	Std. Dev.	Min	Max
pxb_se	231	.1193811	0	.1193811	.1193811

-> fu = 1

Variable	Obs	Mean	Std. Dev.	Min	Max
pxb_se	1379	.0555424	0	.0555424	.0555424

-> fu = .

Variable	Obs	Mean	Std. Dev.	Min	Max
pxb_se	0				

```
. generate se=pxb_se*(exp(pxb))  
(143 missing values generated)
```

```
. sort fu  
. by fu: summarize se
```

-> fu = 0

Variable	Obs	Mean	Std. Dev.	Min	Max
se	231	.9265467	0	.9265467	.9265467

-> fu = 1

Variable	Obs	Mean	Std. Dev.	Min	Max
se	1379	.2623224	0	.2623224	.2623224

-> fu = .

Variable	Obs	Mean	Std. Dev.	Min	Max
se	0				

```
.  
. end of do-file
```

```
. log close  
log: C:\Documents and Settings\RSITLO\Desktop\TOD\Tobit_LWDeltaSE.log
```

log type: text
 closed on: 24 Feb 2005, 14:14:07

STATA output

STATA 8.0 from dataset fulllabvaluesday1_recodecutoffs.dta

tabulate tnf

tnf	Freq.	Percent	Cum.
3.9	670	38.22	38.22
4	13	0.74	38.96
4.1	17	0.97	39.93
4.2	13	0.74	40.67
Total	1,753	100.00	

. tabulate il6

il6	Freq.	Percent	Cum.
4.9	248	14.15	14.15
5	3	0.17	14.32
5.1	5	0.29	14.60
Total	1,753	100.00	

tabulate il10

il10	Freq.	Percent	Cum.
4.9	854	48.72	48.72
5	5	0.29	49.00
5.1	6	0.34	49.34
5.2	12	0.68	50.03
Total	1,753	100.00	

FOR **dc** and **fu**, **dead = 0**, **alive=1**

tabulate dc

dc	Freq.	Percent	Cum.
0	78	4.45	4.45
1	1,675	95.55	100.00
Total	1,753	100.00	

. tabw dc

Variable	0	1	2	3	4	5	6	7	8	9	****	.
dc	78	1675	0	0	0	0	0	0	0	0	0	0

```
. tabulate fu
```

fu	Freq.	Percent	Cum.
0	231	14.35	14.35
1	1,379	85.65	100.00
Total	1,610	100.00	

```
. tabw fu
```

Variable	0	1	2	3	4	5	6	7	8	9 ****	.
fu	231	1379	0	0	0	0	0	0	0	0	143

FOR **dc** and **fu**, **dead = 0**, **alive=1**

```
bysort dc: means tnf il6 il10
```

```
-> dc = 0
```

Variable	Type	Obs	Mean	[95% Conf. Interval]	
tnf	Arithmetic	78	17.62564	9.73869	25.51259
	Geometric	78	9.696395	7.872858	11.94231
	Harmonic	78	7.121124	6.224914	8.318795
il6	Arithmetic	78	2895.464	-387.2139	6178.142
	Geometric	78	172.4636	106.6768	278.8207
	Harmonic	78	39.36164	28.12402	65.55615
il10	Arithmetic	78	47.11282	20.68629	73.53935
	Geometric	78	15.63691	11.6946	20.90821
	Harmonic	78	9.235005	7.924356	11.06512

```
-> dc = 1
```

Variable	Type	Obs	Mean	[95% Conf. Interval]	
tnf	Arithmetic	1675	10.44436	8.98779	11.90093
	Geometric	1675	6.895529	6.667764	7.131074
	Harmonic	1675	5.766919	5.639237	5.900517
il6	Arithmetic	1675	329.1224	263.4744	394.7704
	Geometric	1675	43.28377	39.77457	47.10257
	Harmonic	1675	15.82778	15.00716	16.74334
il10	Arithmetic	1675	22.34848	19.05381	25.64314
	Geometric	1675	9.614716	9.166154	10.08523
	Harmonic	1675	7.093285	6.91908	7.27649

```
.
```

```
bysort fu: means tnf il6 il10
```

```
-> fu = 0
```

Variable	Type	Obs	Mean	[95% Conf. Interval]	
tnf	Arithmetic	231	13.73117	10.72595	16.73638
	Geometric	231	8.650008	7.769028	9.630889
	Harmonic	231	6.684285	6.213401	7.232394
il6	Arithmetic	231	1302.035	167.3855	2436.685
	Geometric	231	83.81066	65.03224	108.0115
	Harmonic	231	24.4099	20.58427	29.98213
il10	Arithmetic	231	30.89524	20.78477	41.0057
	Geometric	231	12.17408	10.52017	14.08801
	Harmonic	231	8.156444	7.542953	8.878564

-> fu = 1

Variable	Type	Obs	Mean	[95% Conf. Interval]	
tnf	Arithmetic	1379	10.04511	8.488952	11.60126
	Geometric	1379	6.770655	6.530785	7.019334
	Harmonic	1379	5.709249	5.572955	5.852377
il6	Arithmetic	1379	318.4954	253.7051	383.2858
	Geometric	1379	41.61529	37.90955	45.68327
	Harmonic	1379	15.32583	14.46826	16.29146
il10	Arithmetic	1379	21.85975	18.15209	25.56742
	Geometric	1379	9.442556	8.963611	9.947093
	Harmonic	1379	7.019783	6.832954	7.217117

--more--

sort dc

. by dc: summarize tnf il6 il10

-> dc = 0

Variable	Obs	Mean	Std. Dev.	Min	Max
tnf	78	17.62564	34.9808	3.9	269
il6	78	2895.464	14559.58	4.9	126000
il10	78	47.11282	117.2089	4.9	896

-> dc = 1

Variable	Obs	Mean	Std. Dev.	Min	Max
tnf	1675	10.44436	30.39318	3.9	944
il6	1675	329.1224	1369.83	4.9	30215
il10	1675	22.34848	68.74748	4.9	1519

. bysort dc: centile tnf il6 il10, centile(25 50 75)

-> dc = 0

Variable	Obs	Percentile	Centile	-- Binom. Interp. -- [95% Conf. Interval]	
tnf	78	25	3.9	3.9	5.374954
		50	8.05	5.784426	11.21557
		75	18.125	12.60056	24.88224
il6	78	25	41.15	17.24517	67.69851
		50	133	72.16392	225.8034

il10	78	75	482	285.2542	1575.786
		25	4.9	4.9	5.9
		50	9.3	6.4	18.8451
		75	31.5	23.67533	64.73052

-> dc = 1

Variable	Obs	Percentile	Centile	-- Binom. Interp. -- [95% Conf. Interval]	
tnf	1675	25	3.9	3.9	3.9
		50	5.4	5.1	5.7
		75	10.2	9.4	10.72504
il6	1675	25	9.7	8.8	11.2
		50	35.5	31.2	39.71063
		75	121	105	134
il10	1675	25	4.9	4.9	4.9
		50	5.1	4.9	5.510629
		75	14.8	13.57768	16.52504

bysort fu: centile tnf il6 il10, centile(25 50 75)

-> fu = 0

Variable	Obs	Percentile	Centile	-- Binom. Interp. -- [95% Conf. Interval]	
tnf	231	25	3.9	3.9	4
		50	7.2	6.2	8.8
		75	15.4	11.77895	17.32885
il6	231	25	19.9	16.6	27.60132
		50	67.6	55.84014	93.561
		75	235	177.5987	350.0321
il10	231	25	4.9	4.9	4.9
		50	7.4	6.4	9.53532
		75	23	17.93947	30.52949

-> fu = 1

Variable	Obs	Percentile	Centile	-- Binom. Interp. -- [95% Conf. Interval]	
tnf	1379	25	3.9	3.9	3.9
		50	5.3	5	5.6
		75	9.7	9.1	10.50225
il6	1379	25	9.1	8.2	10.5
		50	34.1	29.7	39.4
		75	115	101	132
il10	1379	25	4.9	4.9	4.9
		50	4.9	4.9	5.4
		75	14.3	12.50047	16

-> fu = .

Variable	Obs	Percentile	Centile	-- Binom. Interp. -- [95% Conf. Interval]	
tnf	143	25	3.9	3.9	3.9
		50	5	3.953444	6.073278
		75	10.2	7.7	12.96807
il6	143	25	12.1	8.431926	17.66181
		50	32.5	25.63361	52.6854
		75	132	97.61475	202.3615
il10	143	25	4.9	4.9	4.9
		50	5.3	4.9	7.373278
		75	16.3	9.903646	24.91029

```
. bysort fu: summarize tnf il6 il10
```

```
-> fu = 0
```

Variable	Obs	Mean	Std. Dev.	Min	Max
tnf	231	13.73117	23.18153	3.9	269
il6	231	1302.035	8752.428	4.9	126000
il10	231	30.89524	77.9898	4.9	896

```
-> fu = 1
```

Variable	Obs	Mean	Std. Dev.	Min	Max
tnf	1379	10.04511	29.45811	3.9	944
il6	1379	318.4954	1226.487	4.9	14231
il10	1379	21.85975	70.18643	4.9	1519

```
-> fu = .
```

Variable	Obs	Mean	Std. Dev.	Min	Max
tnf	143	12.9021	47.59097	3.9	565
il6	143	259.7958	681.2462	4.9	4230
il10	143	26.76294	75.53486	4.9	769

```
. clear
```

```
. use "C:\Documents and Settings\RSITLO\Desktop\TOD\fullvalueslogtransformed.dta", clear
```

```
. bysort dc: ci tnf il6 il10
```

```
-> dc = 0
```

Variable	Obs	Mean	Std. Err.	[95% Conf. Interval]	
tnf	78	17.62564	3.960795	9.73869	25.51259
il6	78	2895.464	1648.548	-387.2139	6178.142
il10	78	47.11282	13.2713	20.68629	73.53935

```
-> dc = 1
```

Variable	Obs	Mean	Std. Err.	[95% Conf. Interval]	
tnf	1675	10.44436	.7426236	8.98779	11.90093
il6	1675	329.1224	33.47028	263.4744	394.7704
il10	1675	22.34848	1.679768	19.05381	25.64314

```

.
.
end of do-file

```

```
. do "C:\DOCUME~1\RSITLO\LOCALS~1\Temp\STD010000.tmp"
```

```
. clear
```

```
. use "C:\Documents and Settings\RSITLO\Desktop\TOD\fullvalueslogtransformed.dta", clear
```

```

.
. bysort fu: ci tnf il6 il10

```

```
-> fu = 0
```

Variable	Obs	Mean	Std. Err.	[95% Conf. Interval]	
tnf	231	13.73117	1.525233	10.72595	16.73638
il6	231	1302.035	575.8675	167.3855	2436.685
il10	231	30.89524	5.131352	20.78477	41.0057

```
-> fu = 1
```

Variable	Obs	Mean	Std. Err.	[95% Conf. Interval]	
tnf	1379	10.04511	.793273	8.488952	11.60126
il6	1379	318.4954	33.02788	253.7051	383.2858
il10	1379	21.85975	1.89004	18.15209	25.56742

-> fu = .

Variable	Obs	Mean	Std. Err.	[95% Conf. Interval]	
tnf	143	12.9021	3.979757	5.034871	20.76932
il6	143	259.7958	56.96867	147.1795	372.4121
il10	143	26.76294	6.316542	14.27633	39.24955

.
.

end of do-file

6. BIBLIOGRAPHY

-
- ¹ Gourieroux, C. (2000). Econometrics of qualitative dependent variables. New York, New York: Cambridge University Press.
- ² Tobin, J. (1958). Estimation of relationships for limited dependent variables. Econometrica, 26, 24-36.
- ³ Shirai, T., Yamaguchi, H., Ito, H., Todd, C.W., & Wallace R.B. (1985). Cloning and expression in *Escherichia coli* of the gene for human tumour necrosis factor. Nature, 313, 803-806.
- ⁴ Kreigler, M., Perez, C., DeFay, K., Albert, I., & Lu, S.D. (1988) A novel form of TNF/cachectin is a cell surface cytotoxic transmembrane protein: ramifications for the complex physiology of TNF. Cell, 53, 45-53.
- ⁵ Els Decoster, B., Vanhaesebroeck, P., Vandenaabeele, J.G., & Fiers, W. (1995). Generation and Biological Characterization of Membrane-bound, Uncleavable Murine Tumor Necrosis Factor. J. Biol. Chem., 270, 18473 - 18478.
- ⁶ Spengler, U., Zachoval, R., Gallati, H., Jung, M.C., Hoffmann, R., Riethmuller, G., & Pape G. (1996). Serum levels and in situ expression of TNF-alpha and TNF-alpha binding proteins in inflammatory liver diseases. Cytokine, 8, 864-872.
- ⁷ Ware, C.F., Crowe, P.D., Grayson, M.H., Androlewicz, M.J., & Browning, J.L. (1992). Expression of surface lymphotoxin and tumor necrosis factor on activated T, B, and natural killer cells. J. Immunol., 149, 3881 - 3888.
- ⁸ Bissonnette, E.Y., Enciso, J.A., & Befus, A.D. (1996). Inhibitory effects of sulfasalazine and its metabolites on histamine release and TNF-alpha production by mast cells. Journal of Immunology, 156(1), 218-23.
- ⁹ Modrowski, D. (1995). Involvement of interleukin 1 and Tumour Necrosis Factor α as endogenous growth factors in human osteoblastic cells. Cytokine, 7(7), 720-726.
- ¹⁰ Yamada, K., Takane, N., Otabe, S., Inada, C., Inoue, M., & Nonaka, K. (1993). Pancreatic beta-cell-selective production of tumor necrosis factor-alpha induced by interleukin-1. Diabetes, 42, 1026-1031.
- ¹¹ Kern, P. A., Saghizadeh, M., Ong, J., Bosch, R., Deem, R., & Simsolo, R. (1995). The Expression of Tumor Necrosis Factor in Human Adipose Tissue: Regulation by Obesity, Weight Loss, and Relationship to Lipoprotein Lipase. J. Clin. Invest., 95, 2111-2119.

-
- ¹² Zhou, L-J. & Tedder, T.F. (1995). A distinct pattern of cytokine gene expression by human CD83+ blood dendritic cells. Blood, 86, 3295-3301.
- ¹³ Tchelingierian, J-L., Le Saux, F., & Jacque, C. (1996). Identification and topography of neuronal cell populations expressing; TNF and IL-1 in response to hippocampal lesion. J. Neurosci. Res., 43, 99-106.
- ¹⁴ Lee, S.C., Liu, W., Dickson, D.W., Brosnan, C.F., & JW Berman, J.W. (1993). Cytokine production by human fetal microglia and astrocytes. Differential induction by lipopolysaccharide and IL-1 beta. J. Immunol., 150, 2659 - 2667.
- ¹⁵ Frankenberger, M., Sternsdorf, T., Pechumer, H., Pforte, A., & and Ziegler-Heitbrock, H.W. (1996). Differential cytokine expression in human blood monocyte subpopulations: a polymerase chain reaction analysis. Blood, 87, 373-377.
- ¹⁶ Aggarwal, B.B., Kohr, W.J., Hass, P.E., Moffat, B., Spencer, S.A., Henzel, W.J., Bringman, T.S., Nedwin, G.E., Goeddel, D.V., & Harkins, R.N. (1985). Primary structure of human lymphotoxin derived from 1788 lymphoblastoid cell line. J. Biol. Chem., 260, 2334-2344.
- ¹⁷ Sriskandan, S. et al. (1996) Cytokine 8:933.
- ¹⁸ Ware, C.F. et al. (1992) J. Immunol. 149:3881.
- ¹⁹ Poupart, P., Vandenabeele, P., Cayphas, S., Van Snick, J., Haegeman, G., Kruys, V., Fiers, W., & Content, J. (1987). B cell growth modulating and differentiating activity of recombinant human 26-kd protein (BSF-2, HuIFN-beta 2, HPGF). EMBO J., 6, 1219-1224.
- ²⁰ Hibi, M., K. Nakajima, K., & Hirano, T. (1996). IL-6 cytokine family and signal transduction: a model of the cytokine system. J. Mol. Med., 74, 1-12.
- ²¹ Hirano, T., T Matsuda, T., & Nakajima, K. (1994). Signal transduction through gp130 that is shared among the receptors for the interleukin 6 related cytokine subfamily. Stem Cells, 12, 262-277.
- ²² May, L., David, T., Helfgott, C., & Sehgal, P.B. (1986). Anti- β -interferon Antibodies Inhibit the Increased Expression of HLA-B7 mRNA in Tumor Necrosis Factor-Treated Human Fibroblasts: Structural Studies of the β 2 Interferon Involved. Proc. Natl. Acad. Sci. USA, 83, 8957-8961.
- ²³ D'Auria, L., Bonifati, C., Mussi, A., D'Agosto, G., De Simone, C., Giacalone, B., Ferraro, C., & Ameglio, F. (1997) Cytokines in the sera of patients with pemphigus vulgaris: interleukin-6 and tumour necrosis factor-alpha levels are significantly increased as compared to healthy subjects and correlate with disease activity. Eur. Cytokine Netw., 8, 383-387.

-
- ²⁴ Angstwurm, M.W.A. (1997). Cyclic plasma IL-6 levels during normal menstrual cycle. Cytokine, 9(5), 370-374.
- ²⁵ Mouawad, R., Benhammouda, A., Rixe, O., Antoine, E.C., Borel, C., Weil, M., Khayat, D. & Soubrane, C. (1996). Endogenous interleukin 6 levels in patients with metastatic malignant melanoma: correlation with tumor burden. Clin. Cancer Res., 2, 1405-1409.
- ²⁶ Sakamoto, K., Arakawa, H., Mita, S., Ishiko, T., Ikei, S., Egami, H., Hisano, S., & Ogawa, M. (1994). Elevation of circulating interleukin 6 after surgery: factors influencing the serum level. Cytokine, 6, 181-186.
- ²⁷ Sad, S., Marcotte, R., & Mosmann, TR. (1995). Cytokine-induced differentiation of precursor mouse CD8+ T cells into cytotoxic CD8+ T cells secreting Th1 or Th2 cytokines. Immunity, 2, 271-279.
- ²⁸ Fried, S.K., Bunkin, DA., & Greenberg, A.S. (1998). Omental and subcutaneous adipose tissues of obese subjects release interleukin-6: depot difference and regulation by glucocorticoid. Endocrinology, 83, 847-850.
- ²⁹ May, L.T. (1986). Proc. Natl. Acad. Sci. USA, 83, 8957.
- ³⁰ Ishimi, Y., Miyaura, C., Jin, C.H., Akatsu, T., Abe, E., Nakamura, Y., Yamaguchi, A., Yoshiki, S., Matsuda, T., & Hirano, T. (1990). IL-6 is produced by osteoblasts and induces bone resorption. J. Immunol., 145, 3297-3303.
- ³¹ Gagari, E., Tsai, M., Lantz, C.S., Fox, L.G., & Galli, S.J. (1997). Differential Release of Mast Cell Interleukin-6 Via c-kit. Blood, 89, 2654-2663.
- ³² Lee, S.C. et al (1993) J. Immunol. 150:2659.
- ³³ Lafortune, L., Nalbantoglu, J., Antel, JP. (1996). Expression of tumor necrosis factor alpha (TNF alpha) and interleukin 6 (IL-6) mRNA in adult human astrocytes: comparison with adult microglia and fetal astrocytes. J. Neuropathol. Exp. Neurol., 55, 515-521.
- ³⁴ Kuppner, M.C., McKillop-Smith, S., & Forrester, JV. (1995). TGF-beta and IL-1 beta act in synergy to enhance IL-6 and IL-8 mRNA levels and IL-6 production by human retinal pigment epithelial cells. Immunology, 84, 265-271.
- ³⁵ Ringheim, G.E., KL Burgher, K.L., & Heroux, J.A. (1995). Interleukin-6 mRNA expression by cortical neurons in culture: Evidence for neuronal sources of interleukin-6 production in the brain J. Neuroimmunology, 63, 113-123.
- ³⁶ Marz, P., Cheng, J., Gadiant, R.A., Patterson, P.H., Stoyan, T., Otten, U., & Rose-John, S. (1998). Sympathetic neurons can produce and respond to interleukin 6. Proc. Natl. Acad. Sci. USA, 95, 3251-3256.

-
- ³⁷ Melani, C., Mattia, G.F., Silvani, A., Care, A., Rivoltini, L., Parmiani, G., & Colombo, M.P. (1993). Interleukin-6 expression in human neutrophil and eosinophil peripheral blood granulocytes. Blood, 81, 2744-2749.
- ³⁸ Ericson, S.G., Zhao, Y., Gao, H., Miller, K.L., Gibson, L.F., Lynch, J.P., & Landreth, K.S. (1998) Interleukin-6 Production by Human Neutrophils After Fc-Receptor Cross-Linking or Exposure to Granulocyte Colony-Stimulating Factor. Blood, 91, 2099-2107.
- ³⁹ Kestler, D., Agarwal, S., Cobb, J., Goldstein, K.M., & Hall, R.E. (1995). Detection and analysis of an alternatively spliced isoform of interleukin-6 mRNA in peripheral blood mononuclear cells. Blood, 86, 4559-4567.
- ⁴⁰ Jung, H.C., Eckmann, L., Yang, S., Panja, A., Fierer, J., Morzycka-Wroblewska, E., & Kagnoff, M. (1995). A Distinct Array of Proinflammatory Cytokines Is Expressed in Human Colon Epithelial Cells in Response to Bacterial Invasion. J. Clin. Invest., 95, 55-65.
- ⁴¹ Miyazawa, K., Mori, A., Yamamoto, K., & Okudaira, H. (1998). Constitutive transcription of the human interleukin-6 gene by rheumatoid synoviocytes: spontaneous activation of NF-kappaB and CBF1. Am. J. Pathol., 152, 793-803.
- ⁴² Campbell, I.L., Cutri, A., Wilson, A., & Harrison, L.C. (1989). Evidence for IL-6 production by and effects on the pancreatic beta-cell. J. Immunol., 143, 1188-1191.
- ⁴³ Kishimoto, T. (1989). The biology of interleukin-6. Blood, 74, 1-10.
- ⁴⁴ Van Snick, J. (1990) Interleukin-6: An Overview. Annu. Rev. Immunol., 8, 253-278.
- ⁴⁵ Hirano, T., Matsuda, T., & Nakajima, K. (1994). Signal transduction through gp130 that is shared among the receptors for the interleukin 6 related cytokine subfamily. Stem Cells, 12, 262-277.
- ⁴⁶ Barton, B.E. (1997). IL-6: Insights into Novel Biological Activities. Clin. Immunol. Immunopathol., 85, 16-20.
- ⁴⁷ Vieira, P., de Waal-Malefyt, R., Dang, M., Johnson, K.E., Kastelein, R., Fiorentin, D.F., de Vries, J.E., Roncarolo, M., Mosmann, T.R., & Moore, K.W. (1991). Isolation and Expression of Human Cytokine Synthesis Inhibitory Factor cDNA Clones: Homology to Epstein-Barr Virus Open Reading Frame BCRF1. Proc. Natl. Acad. Sci. USA, 88, 1172-1176.
- ⁴⁸ Varney, M.L., Ino, K., Ageitos, A.G., Heimann, D.G., Talmadge, J.E., & Singh, R.K. (1999). Expression of Interleukin-10 in Isolated CD8+ T Cells and Monocytes from Growth Factor-Mobilized Peripheral Blood Stem Cell Products: A Mechanism of Immune Dysfunction. J. Interf. Cytokine Res., 19, 351-360.

-
- ⁴⁹ Panuska J.R., Merolla, R., Rebert, N.A., Hoffmann, S.P., Tsivitse, P., Cirino N.M., Silverman, R.H., & Rankin, J.A. (1995). Respiratory syncytial virus induces interleukin-10 by human alveolar macrophages. Suppression of early cytokine production and implications for incomplete immunity. Journal of Clinical Investigation, *96*, 2445-2453.
- ⁵⁰ Spencer, N.F.L. & Daynes, R.A. (1997). IL-12 directly stimulates expression of IL-10 by CD5+ B cells and IL-6 by both CD5+ and CD5- B cells: possible involvement in age-associated cytokine dysregulation. Int. Immunol., *9*, 745-754.
- ⁵¹ Sato, T., McCue, P., Masuoka, K., Salwen, S., Lattime, E.C., Mastrangelo, M.J., & Berd, D. (1996). Interleukin 10 production by human melanoma. Clin. Cancer Res., *2*, 1383-1390.
- ⁵² Mehrotra, P.T., Raymond, P., Wong, S., Kanegane, H., Geremew, A., Mostowski, H.S., Furuke, K., Siegel, J.P., & Bloom, E.T. (1998). Production of IL-10 by Human Natural Killer Cells Stimulated with IL-2 and/or IL-12. J. Immunol., *160*, 2637-2644.
- ⁵³ Nakajima, H., Gleich, G.J., & Kita, H. (1996). Constitutive production of IL-4 and IL-10 and stimulated production of IL-8 by normal peripheral blood eosinophils. J. Immunol., *156*, 4859-4866.
- ⁵⁴ Iwasaki, A. & Kelsall, B.L. (1999). Freshly isolated Peyer's Patch, but not spleen, dendritic cells produce Interleukin 10 and induce the differentiation of T helper type 2 cells. J. Exp. Med., *190*, 229-240.
- ⁵⁵ Wang, P., Wu, P., Anthes, J.C., Siegel, M.I., Egan, R.W., & Billah, M.M. (1994). Interleukin-10 inhibits interleukin-8 production in human neutrophils. Blood, *83*, 2678-2683.
- ⁵⁶ Capsoni, F., Minonzio, F., Ongari, A.M., Carbonelli, V., Galli, A., & Zanussi, C. (1997). Interleukin-10 down-regulates oxidative metabolism and antibody-dependent cellular cytotoxicity of human neutrophils. Scand. J. Immunol., *45*, 269-275.
- ⁵⁷ Gesser, B., Leffers, H., Jinqun, T., Vestergaard, C., Kirstein, N., Sindet-Pedersen, S., Jensen, S.L., Thestrup-Pedersen, K., & Larsen, C.G. (1997). Identification of functional domains on human interleukin 10. Proc. Natl. Acad. Sci. USA, *94*, 14620-14625.
- ⁵⁸ Girard, N. (1999). Hyaluronectin secretion by monocytes: downregulation by IL-4 and IL13, upregulation by IL-10. Cytokine, *11(8)*, 579-585.
- ⁵⁹ Chadban, S.J., Foti, T., Atkins, L., & Paterson, N. (1998). Interleukin-10 differentially modulates MHC class II expression by mesangial cells and macrophages in vitro and in vivo. Immunology, *94*, 72.
- ⁶⁰ Buelens, C., Verhasselt V., De Groote, D., Thielemans, K., Goldman, M., & Willems, F. (1997). Interleukin-10 prevents the generation of dendritic cells from human peripheral blood mononuclear cells cultured with interleukin-4 and granulocyte/macrophage-colony-stimulating factor. Eur. J. Immunol., *27*, 756-762.

-
- ⁶¹ Enk, A.H., Angeloni, V.L., Udey, M.C., & Katz, S.I. (1993). Inhibition of Langerhans cell antigen-presenting function by IL-10. A role for IL-10 in induction of tolerance. J. Immunol., 151, 2390-2398.
- ⁶² D-Amico, G., Frascaroli, G., Bianchi, G., Transidico, P., Doni, A., Vecchi, A., Sozzani, S., Allavena, P., & Mantovani, A. (2000). Uncoupling of inflammatory chemokine receptors by IL-10: generation of functional decoys. Nature Immunol., 1, 387-391.
- ⁶³ Shibata, Y., Foster, L.A., Kurimoto, M., Okamura, H., Nakamura, R.M., Kawajiri, K., Justice, J.P., Van Scott, M.R., Myrvik, Q.N., & Metzger, W.J. (1998). Immunoregulatory Roles of IL-10 in Innate Immunity: IL-10 Inhibits Macrophage Production of IFN--Inducing Factors but Enhances NK Cell Production of IFN. J. Immunol., 161, 4283-4288.
- ⁶⁴ Carson, W. E., Lindemann, M.J., Baiocchi, R., Linett, M., Tan, J.C., Chou, C.C., Narula, S., & Caligiuri, M.A. (1995). The functional characterization of interleukin-10 receptor expression on human natural killer cells. Blood, 85, 3577-3585.
- ⁶⁵ Cai, G., Kastelein, R.A., Hunter, C.A. (1999). IL-10 enhances NK cell proliferation, cytotoxicity and production of IFN- when combined with IL-18. Eur. J. Immunol., 29, 2658-2665.
- ⁶⁶ Lin, T.J. & Befus, A.D. (1997). Differential regulation of mast cell function by IL-10 and stem cell factor. J. Immunol., 159, 4015-4023.
- ⁶⁷ Taga, K., Mostowski, H., & Tosato, G. (1993). Human interleukin-10 can directly inhibit T-cell growth. Blood, 81, 2964-2971.
- ⁶⁸ Cohen, S.B.A., Crawley, J.B., Kahan, M.C., Feldmann, M., Foxwell, B.M.J. (1997). Interleukin-10 rescues T cells from apoptotic cell death: association with an upregulation of Bcl-2. Immunology, 92, 1.
- ⁶⁹ Gesser, B. (1997). Proc. Natl. Acad. Sci. USA, 94, 14620.
- ⁷⁰ Agematsu, K., Nagumo, H., Oguchi, Y., Nakazawa, T., Fukushima, K., Yasui, K., Ito, S., Kobata, T., Morimoto, C., & Komiyama, A. (1998). Generation of plasma cells fFrom peripheral blood memory B cells: Synergistic effect of Interleukin-10 and CD27/CD70 interaction. Blood, 91, 173-180.
- ⁷¹ Rousset, F., Garcia, E., Defrance, T., Peronne, C., Vezzio, N., Hsu, D., Kastelein, R., Moore, K.W., & Banchereau, J. (1992). Interleukin 10 is a Potent Growth and Differentiation Factor for Activated Human B Lymphocytes. Proc. Natl. Acad. Sci. USA, 89, 1890-1893.

-
- ⁷² Briere, F., Servet-Delprat, C., Bridon, J.M., Saint-Remy, J.M., & Banchereau, J. (1994). Human interleukin 10 induces naive surface immunoglobulin D+ (sIgD+) B cells to secrete IgG1 and IgG3. J. Exp. Med., 179, 757-762.
- ⁷³ Breen, R. (1996). Regression models: Censored, sample-selected, or truncated Data (Sage University Paper series on Quantitative Applications in the Social Sciences, series no. 07-111). Thousand Oaks, CA: Sage.
- ⁷⁴ Tobin, J., (1958). Estimation of relationships for limited dependent variables. Econometrica, 26, 24-36.
- ⁷⁵ Fomby, T.B., Hill, R.C., & Johnson, S.R. (1984). Advanced econometric Methods. New York, New York: Springer-Verlag. pp. 358-366.
- ⁷⁶ Davidson, R., & Mackinnon, J.G. (1993). Estimation and inference in econometrics. Oxford, New York: Oxford University Press. pp534-542.
- ⁷⁷ StataCorp. (2003). STATA base reference manual volume 3 N-R release 8. College Station, TX: Stata Corporation.
- ⁷⁸ <http://www.stata.com/support/faqs/stat/deltam.html>
- ⁷⁹ StataCorp. (2003). STATA base reference manual volume 3 N-R release 8. College Station, TX: Stata Corporation.
- ⁸⁰ <http://www-micro.msb.le.ac.uk/1010/1011-18.html>
- ⁸¹ <http://www-micro.msb.le.ac.uk/1010/1011-18.html>
- ⁸² <http://www-micro.msb.le.ac.uk/1010/1011-18.html>
- ⁸³ Breen, R. (1996). Regression models: Censored, sample-selected, or truncated Data (Sage University Paper series on Quantitative Applications in the Social Sciences, series no. 07-111). Thousand Oaks, CA: Sage.