

**ASSESSING PROGNOSIS FOR CHRONIC KIDNEY
DISEASE USING NEURAL NETWORKS**

by

Michael R. Zeleny

B.S. Biology, Juniata College, 2012

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

2016

UNIVERSITY OF PITTSBURGH
GRADUATE SCHOOL OF PUBLIC HEALTH

This thesis was presented

by

Michael R. Zeleny

It was defended on

April 22nd 2016

and approved by

Douglas Landsittel, PhD, Professor of Medicine, Biostatistics, and Clinical and Translational
Science, School of Medicine, University of Pittsburgh

Stewart J. Anderson, PhD, Professor of Biostatistics, Graduate School of Public Health,
University of Pittsburgh

Ada O. Youk, PhD, Associate Professor of Biostatistics, Epidemiology, and Clinical and
Translational Science, Graduate School of Public Health, School of Medicine, University of
Pittsburgh

Thesis Advisor: Douglas Landsittel, PhD, Professor of Medicine, Biostatistics, and Clinical
and Translational Science, School of Medicine, University of Pittsburgh

Copyright © by Michael R. Zeleny
2016

ASSESSING PROGNOSIS FOR CHRONIC KIDNEY DISEASE USING NEURAL NETWORKS

Michael R. Zeleny, M.S.

University of Pittsburgh, 2016

ABSTRACT

Neural networks can be used as a potential way to predict continuous and binary outcomes. With their ability to model complex non-linear relationships between variables and outcomes, they may be better at prognosis than more traditional regression methods such as logistic regression. In this thesis, the prognostic abilities of neural networks will be assessed using data from the Consortium for Radiological Imaging Studies of Polycystic Kidney Disease (CRISP) using clinically significant variables such as BMI, Blood Urea Nitrogen (BUN), Height Adjusted Total Kidney Volume (htTKV), baseline estimated glomerular filtration rate (eGFR), and type of PKD.

Both a logistic regression and variations of neural networks were modeled. The neural networks had hidden units from 2 to 10, and weight decays from 0.01 to 0.05. Each of these models was assessed by looking at Receiver Operator Characteristic (ROC) curves, specifically the area under the curve (AUC). The complexity of these models was also looked at by calculating the degrees of freedom for each model. More complex models could lead to an overfitting of the data, and were therefore examined in this study.

The study showed that neural networks have the capability to predict the outcome of stage 3 kidney disease better than a more traditional logistic regression, however, the models become increasingly complex as the predictive ability increases.

These findings could have a great impact on public health in the future. They could greatly impact the methods that are used for prognosis. The use of neural networks might lead to better prognosis and earlier treatment for kidney disease based on an individuals

baseline measurements of the aforementioned variables, or any other new biomarkers that are discovered in the future.

TABLE OF CONTENTS

PREFACE	x
1.0 INTRODUCTION	1
2.0 METHODS	3
2.1 DATA AND VARIABLES	3
2.2 MULTIVARIABLE LOGISTIC REGRESSION	3
2.3 ARTIFICIAL NEURAL NETWORKS	4
2.4 ROC CURVES	6
2.5 COMPLEXITY OF THE MODEL	6
2.5.1 DEGREES OF FREEDOM FOR BINARY VARIABLES	7
2.5.2 DEGREES OF FREEDOM FOR CONTINUOUS VARIABLES	7
2.5.3 DEGREES OF FREEDOM FOR BOTH BINARY AND CONTINUOUS VARIABLES	7
3.0 RESULTS	9
3.1 DESCRIPTION OF DATA	9
3.2 MULTIVARIABLE LOGISTIC REGRESSION	10
3.3 NEURAL NETWORKS	12
3.3.1 NEURAL NETWORKS WITH TWO HIDDEN UNITS	12
3.3.2 NEURAL NETWORKS WITH THREE HIDDEN UNITS	14
3.3.3 NEURAL NETWORKS WITH FOUR HIDDEN UNITS	16
3.3.4 NEURAL NETWORKS WITH FIVE HIDDEN UNITS	18
3.3.5 NEURAL NETWORKS WITH SIX HIDDEN UNITS	20
3.3.6 NEURAL NETWORKS WITH SEVEN HIDDEN UNITS	22

3.3.7 NEURAL NETWORKS WITH EIGHT HIDDEN UNITS	24
3.3.8 NEURAL NETWORKS WITH NINE HIDDEN UNITS	26
3.3.9 NEURAL NETWORKS WITH TEN HIDDEN UNITS	28
3.4 SUMMARY OF MODEL COMPLEXITY	30
4.0 DISCUSSION	32
APPENDIX. R CODE	34
BIBLIOGRAPHY	46

LIST OF TABLES

1	Descriptive Statistics for Continuous Variables	9
2	Descriptive Statistics for Continuous Variables	10
3	Multivariable Logistic Regression	11
4	AUC Values for Neural Networks with Two Hidden Units	14
5	AUC Values for Neural Networks with Three Hidden Units	16
6	AUC Values for Neural Networks with Four Hidden Units	18
7	AUC Values for Neural Networks with Five Hidden Units	20
8	AUC Values for Neural Networks with Six Hidden Units	22
9	AUC Values for Neural Networks with Seven Hidden Units	24
10	AUC Values for Neural Networks with Eight Hidden Units	26
11	AUC Values for Neural Networks with Nine Hidden Units	28
12	AUC Values for Neural Networks with Ten Hidden Units	30
13	Summary of Model Complexity	30

LIST OF FIGURES

1	Diagram of Simple Neural Network	5
2	ROC Curve for Multivariable Logistic Regression	12
3	ROC Curves for Neural Networks with Two Hidden Units	13
4	ROC Curves for Neural Networks with Three Hidden Units	15
5	ROC Curves for Neural Networks with Four Hidden Units	17
6	ROC Curves for Neural Networks with Five Hidden Units	19
7	ROC Curves for Neural Networks with Six Hidden Units	21
8	ROC Curves for Neural Networks with Seven Hidden Units	23
9	ROC Curves for Neural Networks with Eight Hidden Units	25
10	ROC Curves for Neural Networks with Nine Hidden Units	27
11	ROC Curves for Neural Networks with Ten Hidden Units	29

PREFACE

I would like to express my thanks and gratitude to Dr. Douglas Landsittel, who brought this topic to my attention and lead me throughout the entire learning process for this thesis. I would also like to thank both Dr. Stewart J. Anderson and Dr. Ada O. Youk for sitting on my thesis committee and giving me important suggestions to succeed in this thesis.

I would also like to thank my family, especially my parents Robin and Ray Zeleny for pushing me to achieve this degree and supporting me throughout the process. They have always pushed me to be my best.

1.0 INTRODUCTION

Polycystic kidney disease (PKD) is a group of disorders that result in renal cyst development. PKD is one of the leading causes of end stage renal failure. Most forms of the disease are inherited although it is possible to develop the disease in other ways. Of the hereditary types of PKD, the PKD1 genotype accounts for about 85% of PKD cases. PKD2 is another less common genotype¹. The significance of PKD in leading to renal failure strongly motivates the need to study prognostic factors for renal decline within this population.

One way to determine if an individual has chronic kidney disease (CKD) is by measuring glomerular filtration rate (GFR). The GFR can be estimated in a number of ways including serum-creatinine based estimates, which can be based on Cockcroft-Gault equations, Modification of Diet in Renal Disease, or the CKD-EPI equation that uses information from demographics and measured values of serum-creatinine². It has been found that the CKD-EPI equation results in a more accurate prediction of GFR than the MDRD estimate³.

The estimation of GFR is used for diagnosing stage 3 kidney disease. When looking at a value of GFR, the larger the number indicates better functioning of the kidney. When the GFR value drops below a threshold value of $60 \frac{mL/min}{1.73m^2}$ the individual is classified as having stage 3 kidney disease, which is considered chronic kidney disease. At this point half of the normal adult kidney function is lost⁴.

There are many variables which can be used as potential predictors to predict stage 3 kidney disease. One measure that could be a potential predictor of the onset of kidney disease is the total kidney volume, which can be measured as height adjusted total kidney volume. In one study, it was found that a height adjusted total kidney volume (htTKV) $600 \frac{cc}{m}$ was a significant predictor of developing renal sufficiency in PKD patients⁵. Blood urea nitrogen (BUN) levels can also indicate the onset of kidney disease with higher BUN

concentrations indicating advancement of disease in the kidney⁶. Body Mass Index (BMI) can also be considered a potential predictor as one study showed that study participants who developed kidney disease had a higher mean BMI than those who did not develop kidney disease⁷.

The Consortium for Radiological Imaging Studies of Polycystic Kidney Disease (CRISP) was established to use imaging techniques to determine if certain markers, such as the ones above, can be used to determine the progression of kidney disease in a cohort of individuals. Individuals enrolled in the CRISP study had some form of PKD and were followed prospectively⁸. Measurements of different variables were obtained to determine if there was any significance between possible markers and stage 3 kidney disease.

Neural networks, with the potential predictors mentioned, can be explored as a classification technique alongside a more traditional logistic regression approach to determine the predictive ability of each different model in turn. Neural networks allow for the modelling of complex non-linear relationships through the use of a component called the hidden layer, and in some studies show better predictive performance than techniques such as logistic regression⁹. When non-linear relationships are present the network will automatically adjust its weights in order to reflect this, a feature not present in traditional logistic regression. Neural networks, because of this ability to utilize non-linear relationships and complex interactions, are prone to overfitting. Weight decay is one way to address this problem with neural networks as it penalizes large weight terms to reduce complexity of the model¹⁰.

In this thesis, we will assess whether neural networks can improve on the prognostic ability of logistic models specific to the CRISP study and CKD outcomes. We will also assess the utility of different variations of network model fitting for these data. The prognostic ability of neural networks will be assessed and compared to prognostic abilities of logistic regression to analyze binary outcomes. When examining neural network prognostic abilities, models with different number of hidden layers will be assessed and overfitting considerations will be assessed by using different values of weight decay. Model complexity using degrees of freedom will also be assessed in relation to prognostic abilities.

2.0 METHODS

2.1 DATA AND VARIABLES

In this study, data from CRISP was used to develop a predictive model for the outcome of chronic kidney disease. For purposes of this analysis, the glomerular filtration rate (GFR), as estimated by the CKD-EPI equations (i.e. eGFR), was categorized as either eGFR of $<60 \frac{mL/min}{1.73m^2}$ i.e. reached Stage 3 CKD, or eGFR $\geq 60 \frac{mL/min}{1.73m^2}$. Participants who reached CKD Stage 3 or worse at any time during through the study were categorized as having the event of Stage 3 kidney disease (even if they were lost to follow-up because renal function can only decline over time). Participants who had an eGFR $\geq 60 \frac{mL/min}{1.73m^2}$ at 10 years or more past baseline were categorized as no event. Participants who had no available eGFR measurements at 10 years or more past baseline were excluded from the analysis.

The predictor variables of interest for this study were height adjusted total kidney volume (htTKV), eGFR at baseline, body mass index (BMI), Blood Urea Nitrogen (BUN), and their genotype of PKD (i.e. PKD1, PDK2, and no mutation detected, or NMD). For this study, PKD2 and NMD were grouped together as the reference category.

2.2 MULTIVARIABLE LOGISTIC REGRESSION

Multivariable logistic regression was used to predict the outcome that a patient would reach stage three kidney disease in the duration of the study. The model for this logistic regression

was defined as follows:

$$\ln\left(\frac{p}{1-p}\right) = X\beta \quad (2.1)$$

Where X is the matrix of covariates used in this study and β is the vector of parameters estimated through maximum likelihood estimation. When constructing this model, the variables used were based on clinical significance. In this case, the predictor variables used to build the model were BUN, PKD type, BMI, eGFR, and htTKV, and the outcome variable was an indicator of type 3 kidney disease (CKD).

2.3 ARTIFICIAL NEURAL NETWORKS

Feed forward neural networks with a single hidden layer were also used to model the data with the clinically significant variables (named a-priori). Feed forward neural networks do not form a cycle and are diagramed in Figure 1. To describe the model, we use the following notation:

1. X_{ik} : $i=1,2,\dots,r$, $k=1,2,\dots,n$ where i corresponds to each input, in this case variables and k corresponds to each observation
2. W_{ij} : $i=1,2,\dots,r$ $j=1,2,\dots,h$ defined as weights, where i corresponds to the weight for each input and j corresponding to the hidden unit number in which the data feeds to
3. H_j : $j=1,2,\dots,h$ corresponding to hidden units, where j corresponds to hidden unit number
4. V_j : $j=1,2,\dots,h$ corresponding to weights, where j corresponds to the hidden unit number
5. W_{0j} : intercept term
6. V_{0j} : intercept term
7. Y : outcome

Model coefficients are fit by minimizing the log likelihood of the data using an iterative process called back propagation, where coefficients are adjusted in small steps until they reach a local minimum. Feed forward neural networks can essentially be thought of as a set of nested logistic models, as shown in Figure 1. For this study 1000 iterations were used.

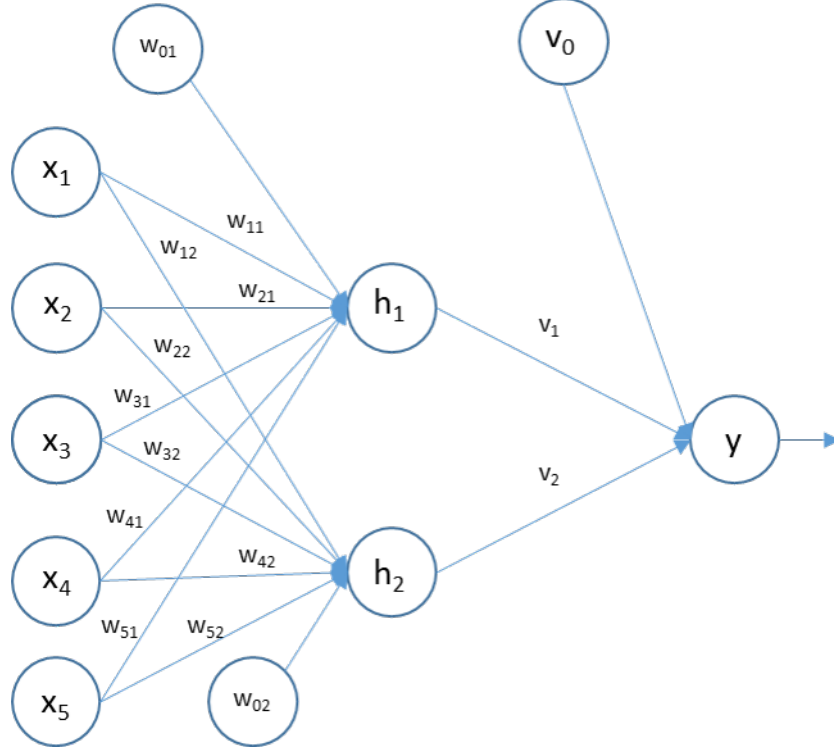


Figure 1: Diagram of Simple Neural Network

Each of the h_j 's are referred to as hidden units. The network can have any number of hidden units or hidden layers. The final output, or predicted response, with a single hidden layer, is given by equation 2.2 for the k^{th} observation .

$$\hat{y}_k = f(v_0 + \sum_{j=1}^H v_j f\{w_{0j} + \sum_{i=1}^p w_{ij}x_{ik}\}) \quad (2.2)$$

Weight decay, which is a penalty term that is multiplied by the sum of squared weights was also used to minimize over-fitting and optimize model convergence. This penalizes larger weights more and the backpropogation algorithm minimizes the error using these penalized weights, rather than unpenalized weights. The weight decay values in this thesis were varied from 0.01 to 0.05.

A neural network may have a number of hidden layers. In this study, one hidden layer was used and the number of hidden units in this hidden layer was allowed to vary. The number of hidden units chosen were 2 through 10 for the hidden layer. Based on these different numbers of hidden units, the predictive ability of each network was assessed.

2.4 ROC CURVES

Receiver Operating Characteristic (ROC) curves graph the sensitivity (y-axis) by 1-sensitivity (x-axis). Each specific cutoff value yields a different sensitivity and specificity for model prediction¹³.

$$sensitivity = \frac{TruePositives}{TruePositives + FalseNegatives} \quad (2.3)$$

$$specificity = \frac{TrueNegatives}{TrueNegatives + FalsePositives} \quad (2.4)$$

We will also calculate the AUC, which is the probability that the classifier will rank a randomly chosen positive instance higher than a randomly chosen negative instance¹⁴. The values of these AUCs will be assessed in this study and confidence intervals will be calculated.

2.5 COMPLEXITY OF THE MODEL

The effect of weight decay and number of hidden units on the complexity of the model was also of interest. To determine the complexity of the model, a calculation was used to determine the number of degrees of freedom there were for each of the neural networks tested. An estimate of the degrees of freedom was used based on both degrees of freedom calculations for binary variables and degrees of freedom calculations for continuous variables proposed by Landsittel (2009)¹⁵. Landsittel calculated the mean likelihood ratio test for model independence and associates that mean with degrees of freedom (df) for the associated

chi-squared distribution, and derived equations for interpolating the degrees of freedom over a range of models.

2.5.1 DEGREES OF FREEDOM FOR BINARY VARIABLES

For binary variables the degrees of freedom calculation relies on both the maximum number of terms, given by $2^i - 1$ where i corresponds to the number of variables, and the number of model parameters, given by $h(i + 1) + (h + 1)$, where h is the number of hidden units. Using these values, the degrees of freedom can be calculated using the interpolated equation $\frac{df}{p} = 0.6643 + 0.1429 \times \log_2(m - p)$, where m is the maximum number of terms and p is the number of model parameters.

2.5.2 DEGREES OF FREEDOM FOR CONTINUOUS VARIABLES

For continuous variables the degrees of freedom calculation relies on the number of hidden units, h , and the number of variables, i . Using these values, the degrees of freedom can be calculated using the interpolated equation $df = h \times [3 \times (i - 2) + 5]$.

2.5.3 DEGREES OF FREEDOM FOR BOTH BINARY AND CONTINUOUS VARIABLES

No established methods exist to calculate degrees of freedom for both binary and continuous variables in the same model. Therefore estimation of the degrees of freedom for these models was accomplished by the following steps:

1. Let i be the number of variables in the model
2. Let i_b be the number of binary variables in the model
3. Let i_c be the number of continuous variables in the model
4. Let $prop_b$ be the proportion of binary variables in the model, $\frac{i_b}{i}$ and $prop_c$ be the proportion of continuous variables in the model, $1 - prop_b$

5. Determine the degrees of freedom if all i variables were binary variables
6. Determine the degrees of freedom if all i variables were continuous variables
7. Estimate model degrees of freedom using $prop_b \times df_b + prop_c \times df_c$

The above method was used for each of neural network models. This method assumes the degrees of freedom varies proportionally between what it would be with all binary variables versus all continuous variables. Future studies will need to validate this approach.

3.0 RESULTS

3.1 DESCRIPTION OF DATA

In this section we report the results of the analysis performed in the thesis. There were a total of 241 patients who were examined for the presence of stage 3 kidney disease. Of these, 203 patients had complete data for the variables of interest and 38 patients had incomplete data for these variables. Of the 38 patients with missing data, 33 were missing the outcome variable, that is, Stage 3 kidney Disease. Patients with missing data were dropped for this analysis.

Table 1: Descriptive Statistics for Continuous Variables

Variable	Mean (Std. Dev)
Estimated GFR	91.57 (22.94)
BMI	25.96 (5.28)
Height Adjusted Total Kidney Volume	637.47(377.98)
BUN	14.59(4.30)

On the set of complete data, descriptive statistics were calculated. From Table 1, the mean estimated GFR was 91.57 with a standard deviation of 22.94. This mean puts the average patient into the category of no Stage 3 kidney disease. The average BMI of the patients was 25.96 with a standard deviation of 5.28. The mean height adjusted total kidney volume was 637.47 with a standard deviation of 377.98. The average BUN of the patients was 14.59 with a standard deviation of 4.30.

Table 2: Descriptive Statistics for Continuous Variables

Variable		Total (%) (N=203)
Stage 3 Kidney Disease	Yes	123(61%)
	No	80(39%)
Type of PKD	PKD1	162(80%)
	Other	41(20%)

From Table 2 of the patients in the study, 123 were diagnosed with stage 3 kidney disease (61%) and 80 did not reach stage 3 kidney disease during the course of the study (39%). Out of the patients that were in the study who suffer from PKD, 162 of them have PKD1 (80%), whereas only 41 have PKD2 or another classification of the disease (20%).

3.2 MULTIVARIABLE LOGISTIC REGRESSION

A multivariable logistic regression was run with the clinically significant variables mentioned in Section 1.

Table 3: Multivariable Logistic Regression

Variable	Odds Ratio	p-value
eGFR	0.9424	<0.00001
Type of PKD	1.976	0.1578
Height Adjusted TKV	1.004	<0.0001
BMI	1.029	0.4838
BUN	1.130	0.0476

Table 3 shows the results of the multivariable logistic regression. Height adjusted total kidney volume and the estimated GFR were the most significant predictors with BUN also being significant at the 0.05 level. Type of PKD and BMI were not statistically significant based on these data, but were left in the model because they were deemed to be clinically significant.

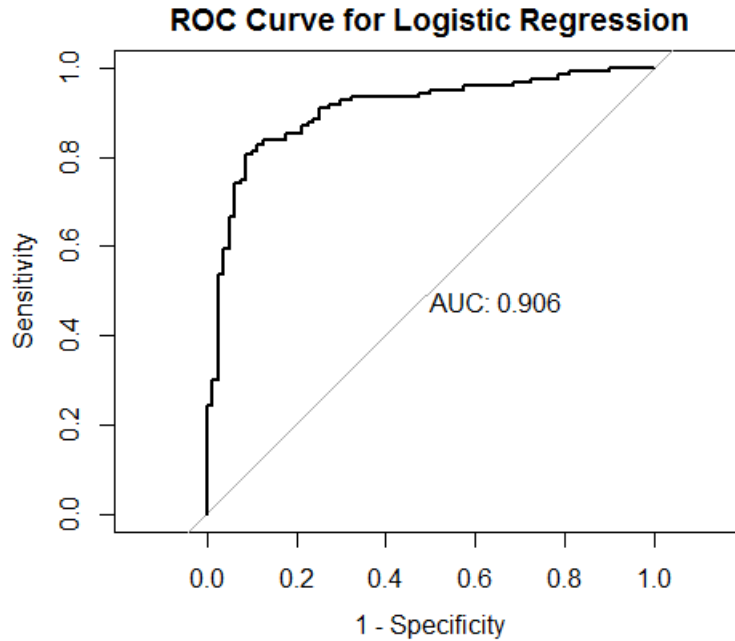


Figure 2: ROC Curve for Multivariable Logistic Regression

The ROC curve was also plotted for the multivariable logistic regression and the area under the curve was calculated. As seen from Figure 1 the discrimination exhibited by the multivariable logistic regression is excellent with an AUC of 0.906.

3.3 NEURAL NETWORKS

3.3.1 NEURAL NETWORKS WITH TWO HIDDEN UNITS

Feedforward neural networks were constructed with a single hidden layer in which the number of hidden units was 2. These neural networks were then varied with multiple values of weight decay to explore how weight decays affect the predictive abilities of these networks.

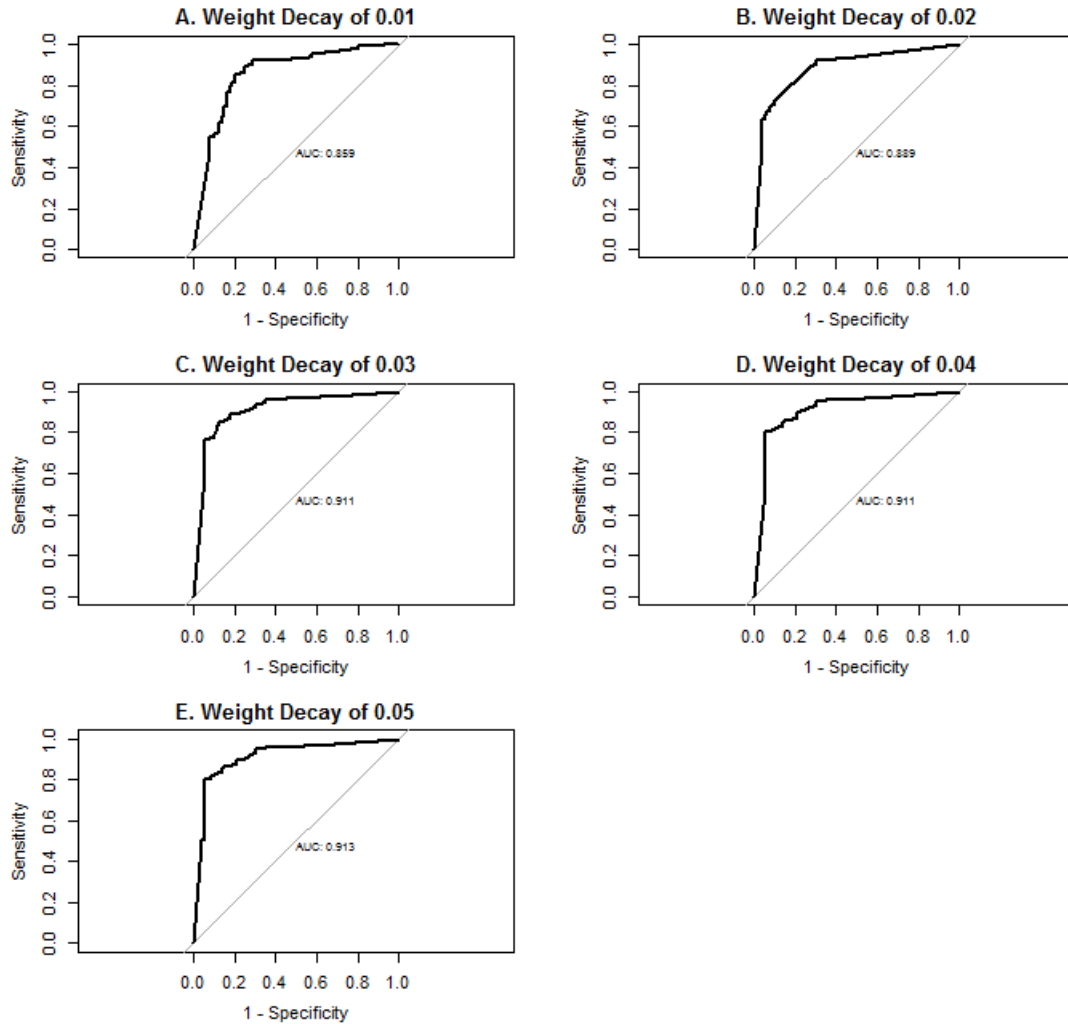


Figure 3: ROC Curves for Neural Networks with Two Hidden Units

From Figure 3, the AUCs of the ROC curves for these neural networks have a maximum value of 0.913 when weight decay of 0.05 is used. The minimum value of the AUC for this set of neural networks is 0.859 when the weight decay was set to 0.01. The other weight decay values gave values of 0.889, 0.911, and 0.911, for weight decay values of 0.02, 0.03, and 0.04 respectively. These results are summarized below in Table 4.

Table 4: AUC Values for Neural Networks with Two Hidden Units

Weight Decay	AUC	95% Confidence Interval
0.01	0.859	(0.804,0.914)
0.02	0.889	(0.843,0.935)
0.03	0.911	(0.868,0.954)
0.04	0.911	(0.867,0.955)
0.05	0.913	(0.870,0.956)

For neural networks with two hidden units the confidence intervals were reasonably narrow with widths ranging from ± 0.043 to ± 0.055 .

3.3.2 NEURAL NETWORKS WITH THREE HIDDEN UNITS

Feedforward neural networks were again constructed with a single hidden layer in which the number of hidden units was 3. These neural networks were then varied with multiple values of weight decay to again explore how weight decays affect the predictive abilities of these networks.

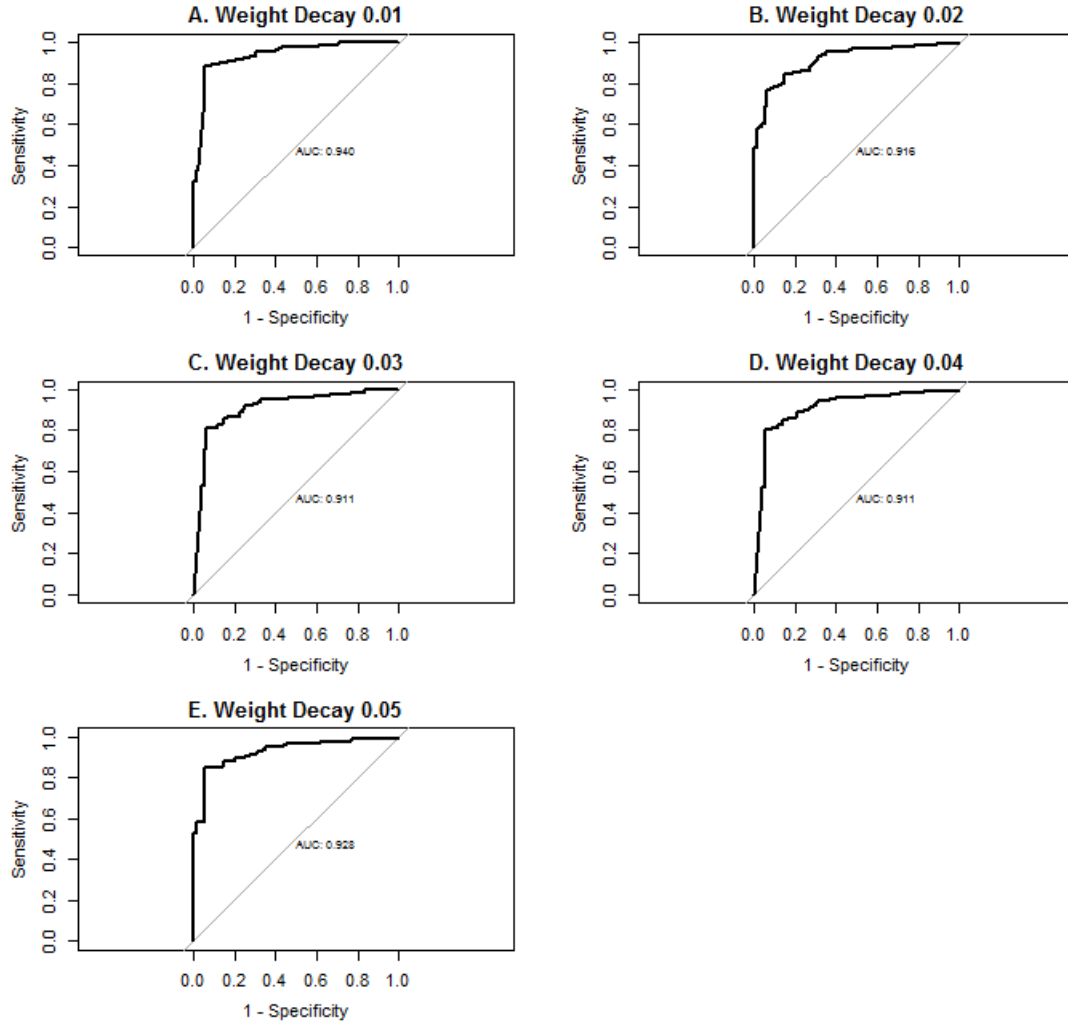


Figure 4: ROC Curves for Neural Networks with Three Hidden Units

From Figure 4, the AUCs of the ROC curves for these neural networks have a maximum value of 0.940 when weight decays of 0.01 and 0.03 are used. The minimum value of the AUC for this set of neural networks is 0.911 when the weight decay was set to 0.04. The other weight decay values gave values of 0.916 and 0.928, for weight decay values of 0.02 and 0.05 respectively. These results are summarized in Table 5 below.

Table 5: AUC Values for Neural Networks with Three Hidden Units

Weight Decay	AUC	95% Confidence Interval
0.01	0.940	(0.906,0.973)
0.02	0.916	(0.878,0.953)
0.03	0.911	(0.868,0.954)
0.04	0.911	(0.867,0.954)
0.05	0.928	(0.893,0.963)

For neural networks with three hidden units the confidence intervals were reasonably narrow with widths ranging from ± 0.034 to ± 0.038 .

3.3.3 NEURAL NETWORKS WITH FOUR HIDDEN UNITS

Feedforward neural networks were again constructed with a single hidden layer in which the number of hidden units was 3. These neural networks were then varied with multiple values of weight decay to again explore how weight decays affect the predictive abilities of these networks.

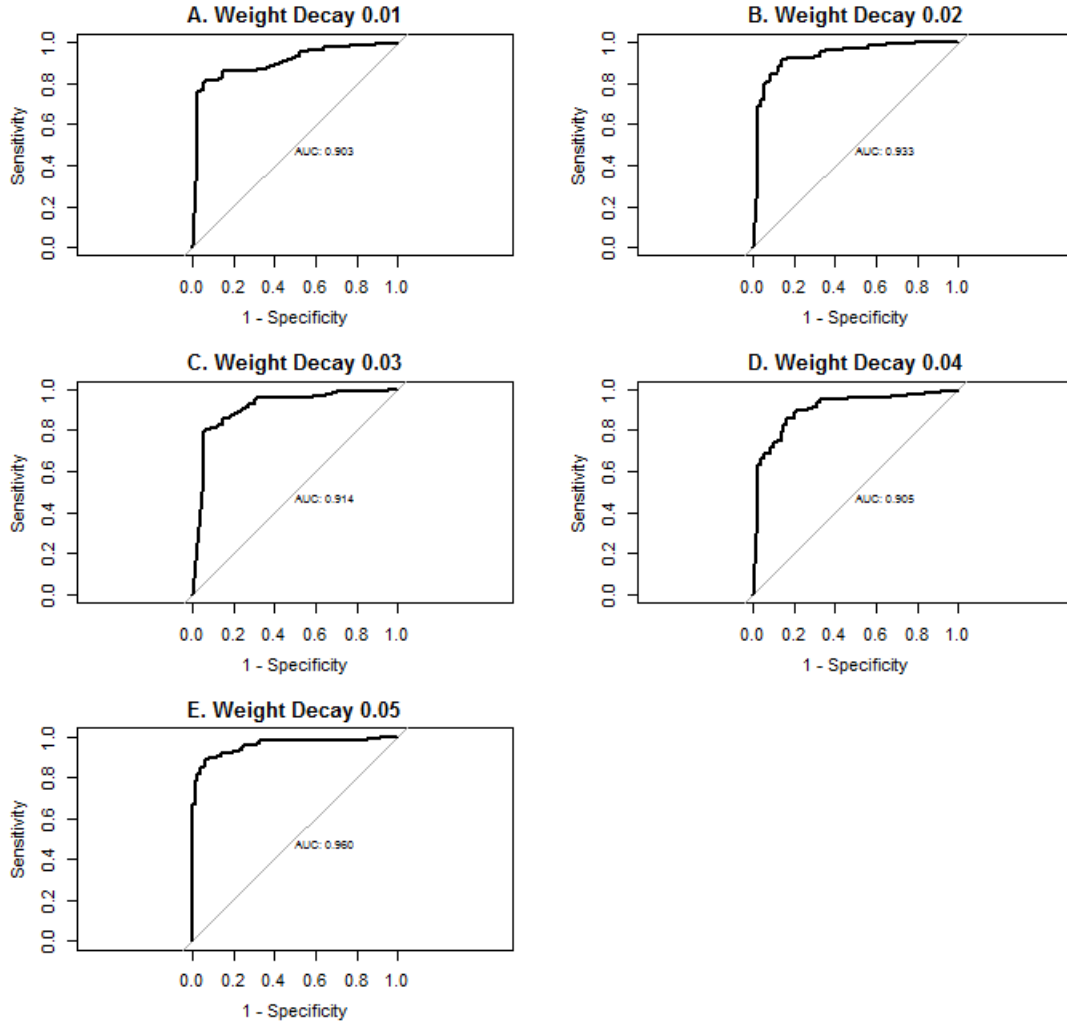


Figure 5: ROC Curves for Neural Networks with Four Hidden Units

From Figure 5, the AUCs of the ROC curves for these neural networks have a maximum value of 0.960 when weight decay of 0.05 is used. The minimum value of the AUC for this set of neural networks is 0.903 when the weight decay was set to 0.01. The other weight decay values gave values of 0.933, 0.914, and 0.905, for weight decay values of 0.02, 0.03, and 0.04 respectively. These results are summarized in Table 6 below.

Table 6: AUC Values for Neural Networks with Four Hidden Units

Weight Decay	AUC	95% Confidence Interval
0.01	0.903	(0.860,0.947)
0.02	0.933	(0.896,0.971)
0.03	0.914	(0.871,0.956)
0.04	0.905	(0.862,0.948)
0.05	0.960	(0.935,0.985)

For neural networks with four hidden units the confidence intervals were reasonably narrow with widths ranging from ± 0.025 to ± 0.043 .

3.3.4 NEURAL NETWORKS WITH FIVE HIDDEN UNITS

Feedforward neural networks were again constructed with a single hidden layer in which the number of hidden units was 5. These neural networks were then varied with multiple values of weight decay to again explore how weight decays affect the predictive abilities of these networks.

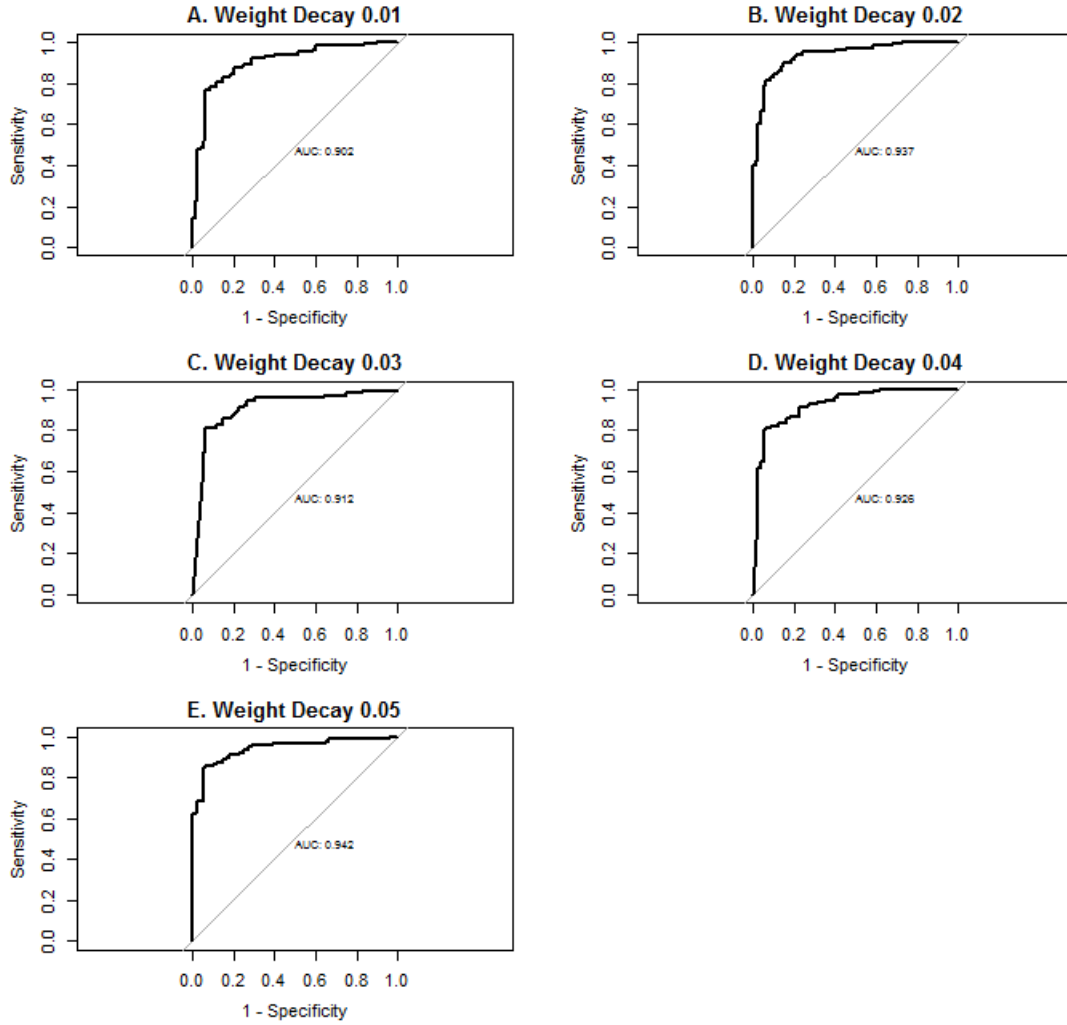


Figure 6: ROC Curves for Neural Networks with Five Hidden Units

From Figure 6, the AUCs of the ROC curves for these neural networks have a maximum value of 0.942 when weight decay of 0.05 is used. The minimum value of the AUC for this set of neural networks is 0.902 when the weight decay was set to 0.01. The other weight decay values gave values of 0.937, 0.912, and 0.926, for weight decay values of 0.02, 0.03, and 0.04 respectively. These results are summarized in Table 7 below.

Table 7: AUC Values for Neural Networks with Five Hidden Units

Weight Decay	AUC	95% Confidence Interval
0.01	0.902	(0.858,0.946)
0.02	0.937	(0.903,0.970)
0.03	0.912	(0.869,0.955)
0.04	0.926	(0.888,0.964)
0.05	0.942	(0.911,0.973)

For neural networks with five hidden units the confidence intervals were reasonably narrow with widths ranging from ± 0.031 to ± 0.044 .

3.3.5 NEURAL NETWORKS WITH SIX HIDDEN UNITS

Feedforward neural networks were again constructed with a single hidden layer in which the number of hidden units was 6. These neural networks were then varied with multiple values of weight decay to again explore how weight decays affect the predictive abilities of these networks.

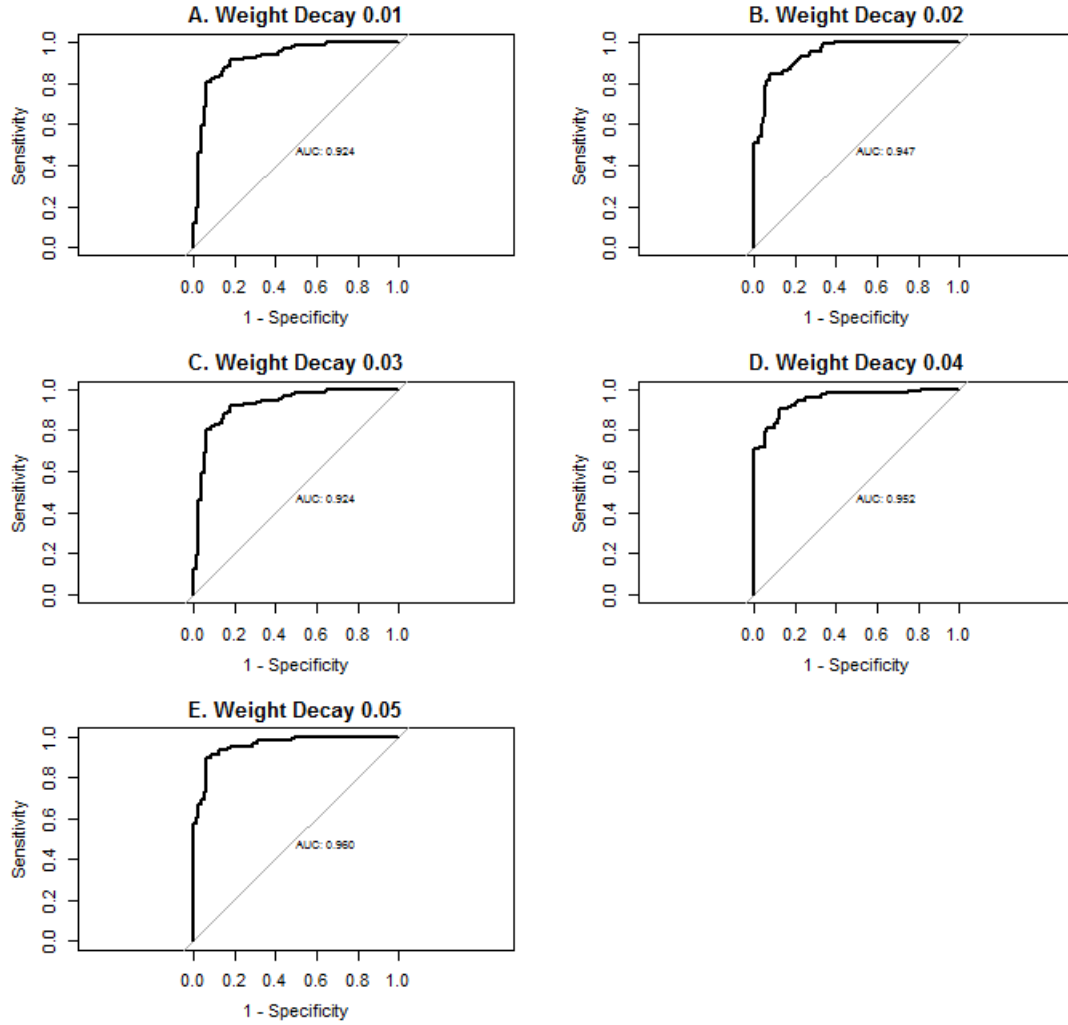


Figure 7: ROC Curves for Neural Networks with Six Hidden Units

From Figure 7, the AUCs of the ROC curves for these neural networks have a maximum value of 0.960 when weight decay of 0.05 is used. The minimum value of the AUC for this set of neural networks is 0.924 when the weight decay was set to 0.01 and 0.03. The other weight decay values gave values of 0.947 and 0.952, for weight decay values of 0.02 and 0.04 respectively. These results are summarized in Table 8 below.

Table 8: AUC Values for Neural Networks with Six Hidden Units

Weight Decay	AUC	95% Confidence Interval
0.01	0.924	(0.884,0.964)
0.02	0.947	(0.919,0.975)
0.03	0.924	(0.884,0.964)
0.04	0.952	(0.925,0.978)
0.05	0.960	(0.936,0.984)

For neural networks with six hidden units the confidence intervals were reasonably narrow with widths ranging from ± 0.024 to ± 0.040 .

3.3.6 NEURAL NETWORKS WITH SEVEN HIDDEN UNITS

Feedforward neural networks were again constructed with a single hidden layer in which the number of hidden units was 7. These neural networks were then varied with multiple values of weight decay to again explore how weight decays affect the predictive abilities of these networks.

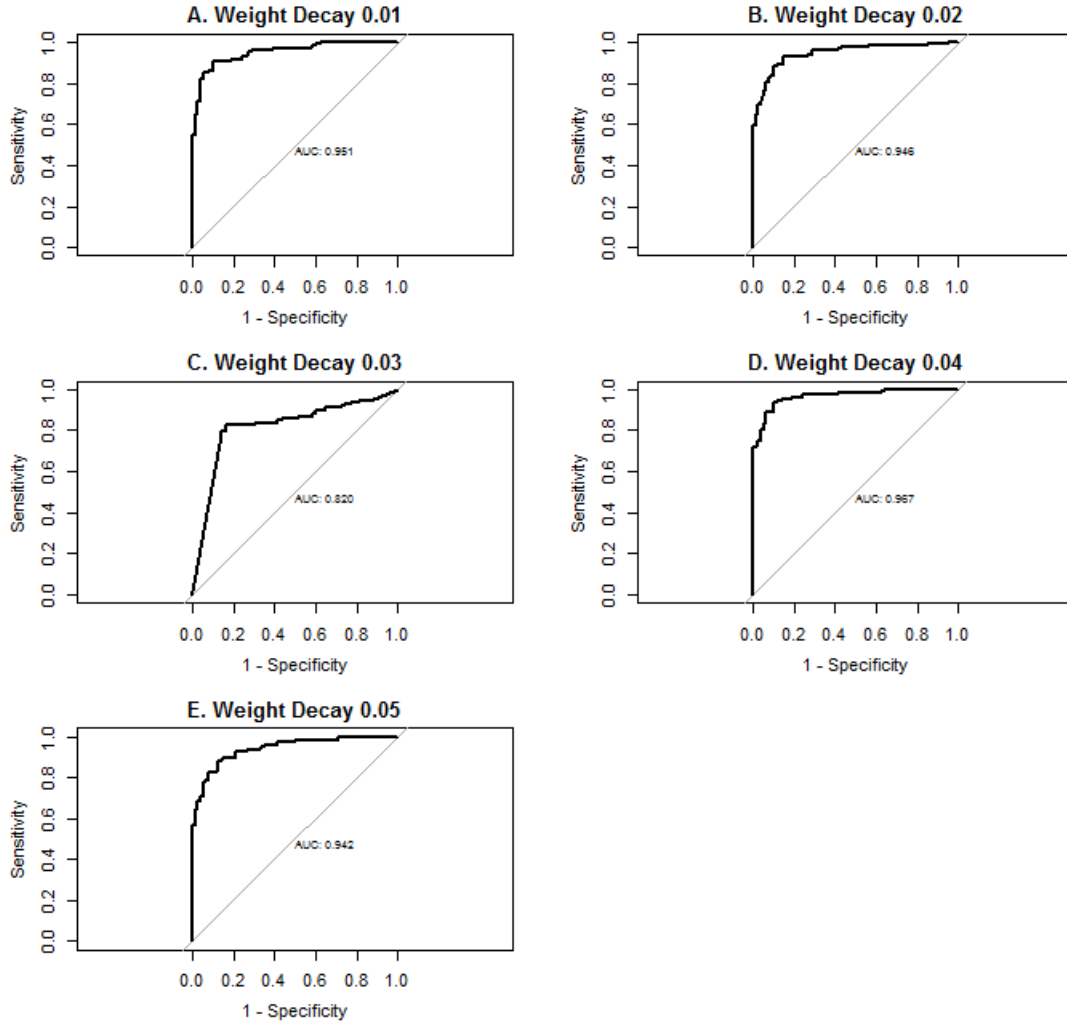


Figure 8: ROC Curves for Neural Networks with Seven Hidden Units

From Figure 8, the AUCs of the ROC curves for these neural networks have a maximum value of 0.967 when weight decay of 0.04 is used. The minimum value of the AUC for this set of neural networks is 0.820 when the weight decay was set to 0.03. The other weight decay values gave values of 0.951, 0.946, and 0.942, for weight decay values of 0.01, 0.02 and 0.05 respectively. These results are summarized in Table 9 below.

Table 9: AUC Values for Neural Networks with Seven Hidden Units

Weight Decay	AUC	95% Confidence Interval
0.01	0.951	(0.924,0.978)
0.02	0.9465	(0.915,0.976)
0.03	0.820	(0.761,0.879)
0.04	0.967	(0.945,0.988)
0.05	0.942	(0.912,0.971)

For neural networks with seven hidden units the confidence intervals were reasonably narrow with widths ranging from ± 0.022 to ± 0.059 .

3.3.7 NEURAL NETWORKS WITH EIGHT HIDDEN UNITS

Feedforward neural networks were again constructed with a single hidden layer in which the number of hidden units was 8. These neural networks were then varied with multiple values of weight decay to again explore how weight decays affect the predictive abilities of these networks.

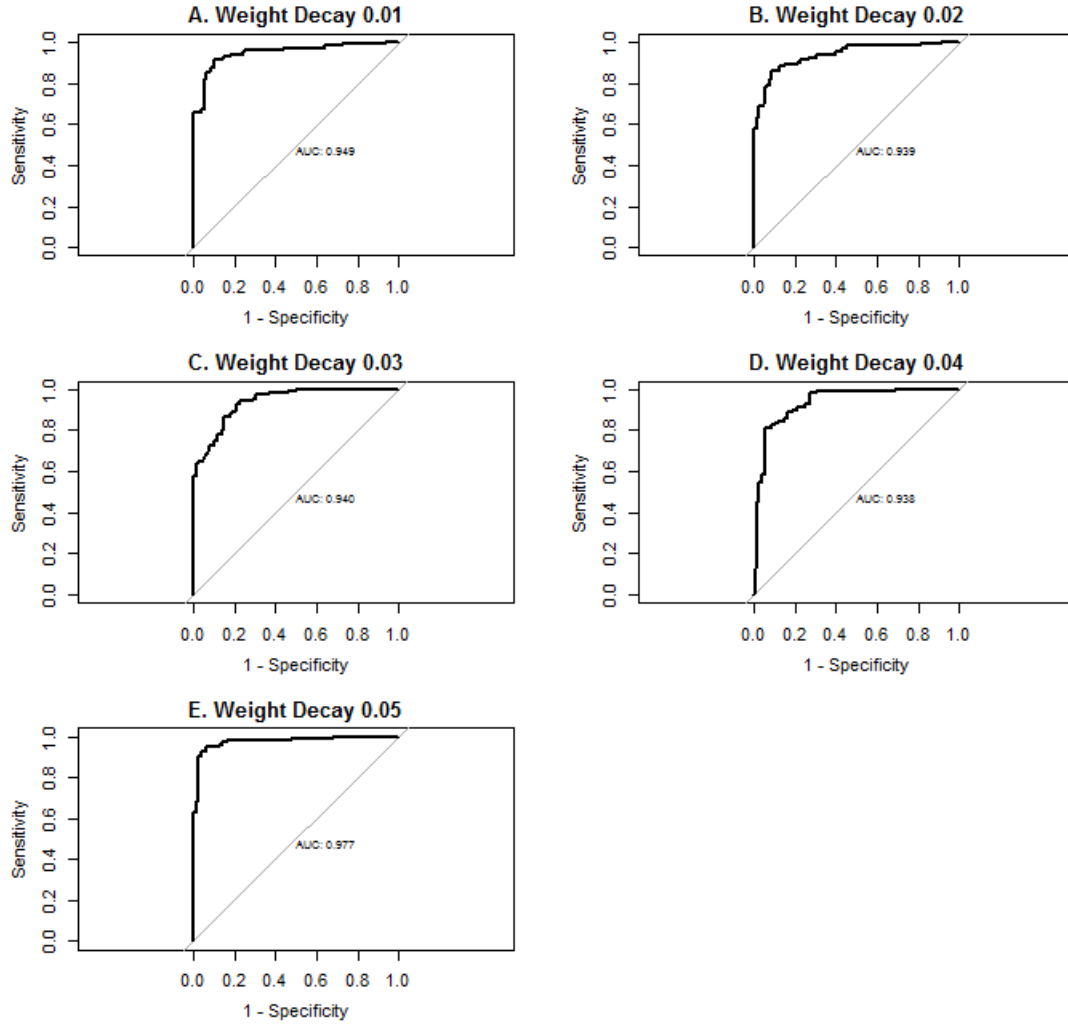


Figure 9: ROC Curves for Neural Networks with Eight Hidden Units

From Figure 9, the AUCs of the ROC curves for these neural networks have a maximum value of 0.977 when weight decay of 0.05 is used. The minimum value of the AUC for this set of neural networks is 0.938 when the weight decay was set to 0.04. The other weight decay values gave values of 0.949, 0.939, and 0.940, for weight decay values of 0.01, 0.02 and 0.03 respectively. These results are summarized in Table 10 below.

Table 10: AUC Values for Neural Networks with Eight Hidden Units

Weight Decay	AUC	95% Confidence Interval
0.01	0.949	(0.920,0.979)
0.02	0.939	(0.908,0.970)
0.03	0.940	(0.911,0.969)
0.04	0.938	(0.904,0.973)
0.05	0.977	(0.959,0.996)

For neural networks with eight hidden units the confidence intervals were reasonably narrow with widths ranging from ± 0.018 to ± 0.034 .

3.3.8 NEURAL NETWORKS WITH NINE HIDDEN UNITS

Feedforward neural networks were again constructed with a single hidden layer in which the number of hidden units was 9. These neural networks were then varied with multiple values of weight decay to again explore how weight decays affect the predictive abilities of these networks.

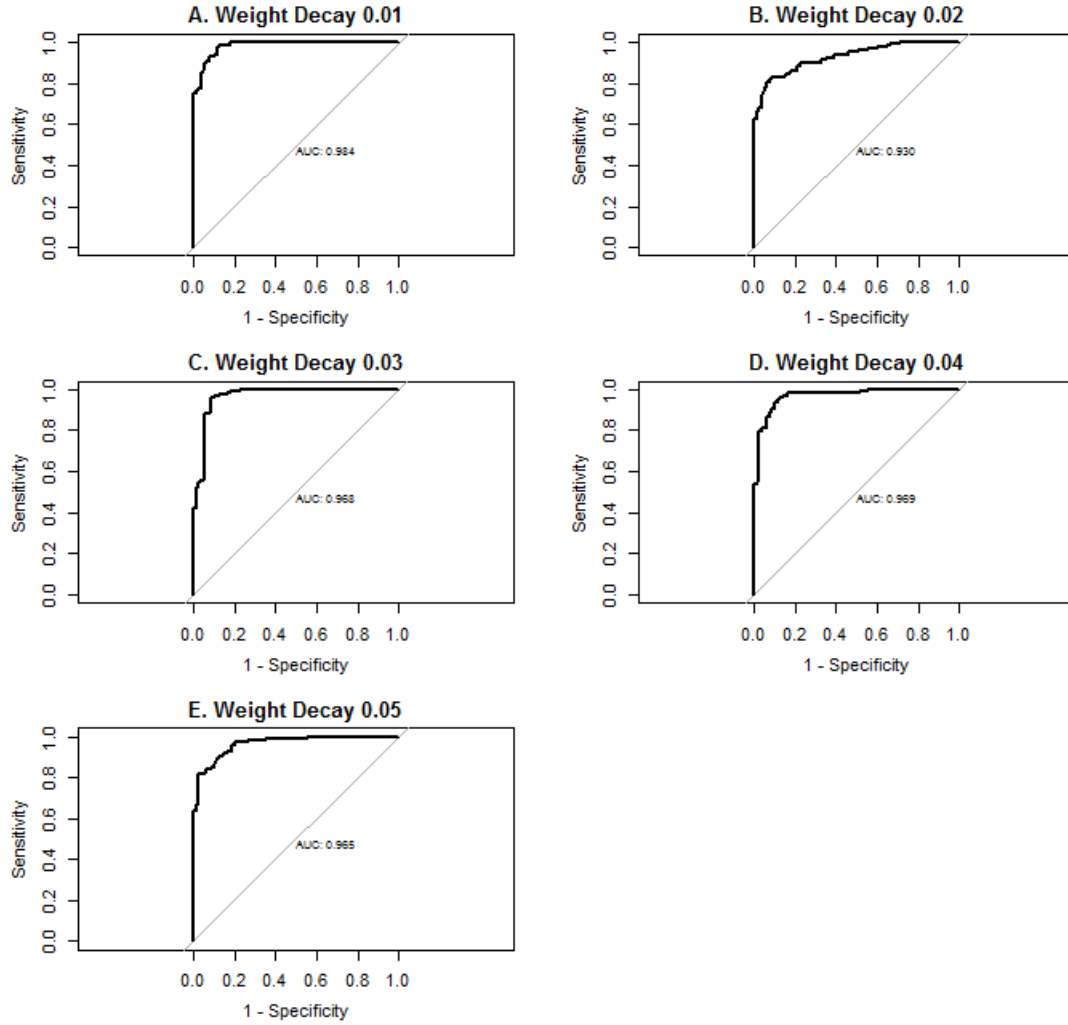


Figure 10: ROC Curves for Neural Networks with Nine Hidden Units

From Figure 10, the AUCs of the ROC curves for these neural networks have a maximum value of 0.984 when weight decay of 0.01 is used. The minimum value of the AUC for this set of neural networks is 0.930 when the weight decay was set to 0.02. The other weight decay values gave values of 0.968, 0.969, and 0.965, for weight decay values of 0.03, 0.04 and 0.05 respectively. These results are summarized in Table 11 below.

Table 11: AUC Values for Neural Networks with Nine Hidden Units

Weight Decay	AUC	95% Confidence Interval
0.01	0.984	(0.971,0.996)
0.02	0.930	(0.898,0.963)
0.03	0.968	(0.944,0.993)
0.04	0.969	(0.948,0.990)
0.05	0.965	(0.944,0.986)

For neural networks with nine hidden units the confidence intervals were reasonably narrow with widths ranging from ± 0.013 to ± 0.032 .

3.3.9 NEURAL NETWORKS WITH TEN HIDDEN UNITS

Feedforward neural networks were again constructed with a single hidden layer in which the number of hidden units was 10. These neural networks were then varied with multiple values of weight decay to again explore how weight decays affect the predictive abilities of these networks.

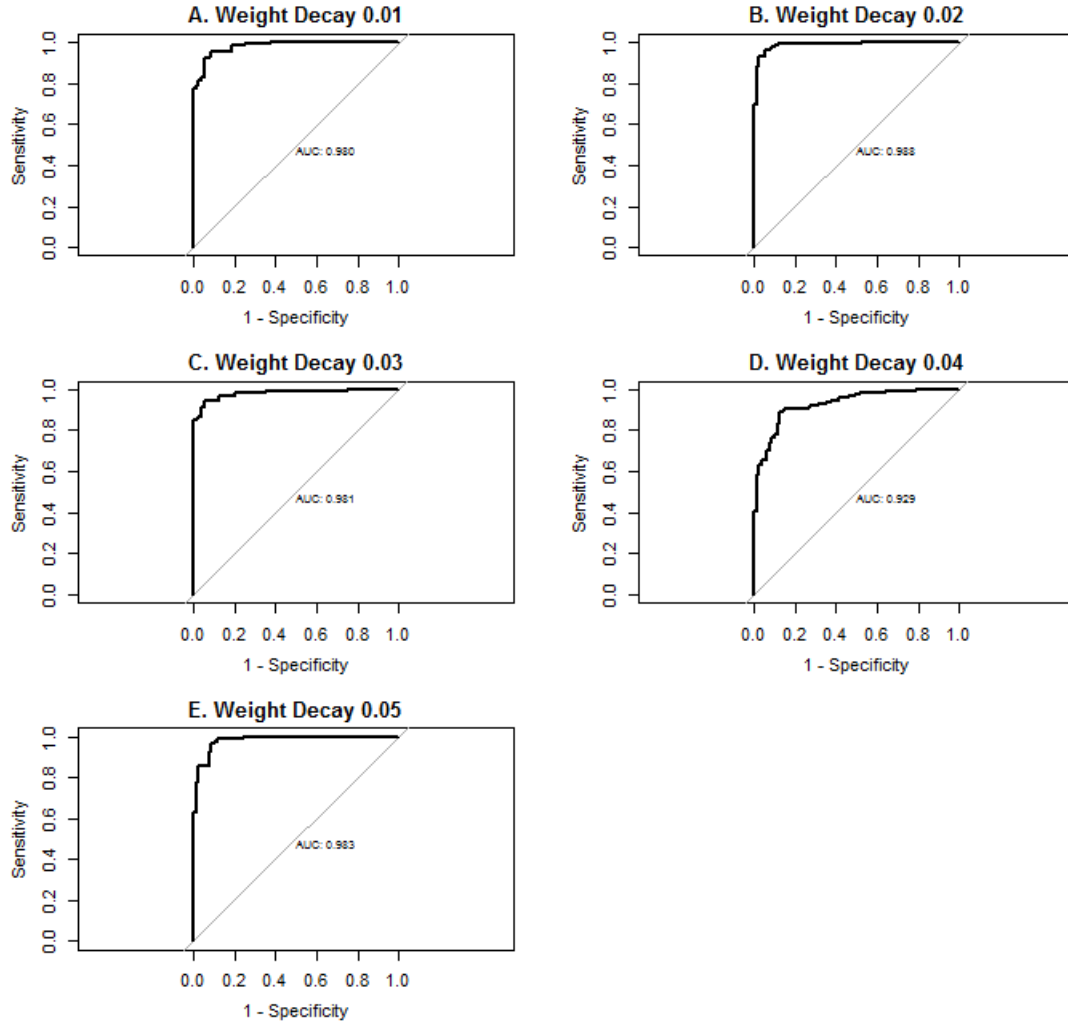


Figure 11: ROC Curves for Neural Networks with Ten Hidden Units

From Figure 11, the AUCs of the ROC curves for these neural networks have a maximum value of 0.988 when weight decay of 0.02 is used. The minimum value of the AUC for this set of neural networks is 0.929 when the weight decay was set to 0.03. The other weight decay values gave values of 0.980, 0.981, and 0.983, for weight decay values of 0.01, 0.04 and 0.05 respectively. These results are summarized in Table 12 below.

Table 12: AUC Values for Neural Networks with Ten Hidden Units

Weight Decay	AUC	95% Confidence Interval
0.01	0.980	(0.967,0.994)
0.02	0.988	(0.976,1.000)
0.03	0.981	(0.966,0.997)
0.04	0.929	(0.894,0.963)
0.05	0.983	(0.969,0.997)

For neural networks with two hidden units the confidence intervals were reasonably narrow with widths ranging from ± 0.012 to ± 0.035 .

3.4 SUMMARY OF MODEL COMPLEXITY

Degrees of freedom were estimated for neural networks with 2, 4, 6, 8, and 10 hidden units and a weight decay value of 0.01 to determine the model complexity.

Table 13: Summary of Model Complexity

Method	Hidden Units	Weight Decay	AUC	95% CI	Parameters	df	AIC
Logistic	-	-	0.906	(0.863,0.949)	5	5	165.84
NN	2	0.01	0.859	(0.804,0.914)	15	26.11	125.66
NN	4	0.01	0.903	(0.860,0.947)	29	49.48	160.10
NN	6	0.01	0.924	(0.884,0.964)	43	73.40	202.33
NN	8	0.01	0.949	(0.920,0.979)	57	95.8	240.01
NN	10	0.01	0.980	(0.967,0.994)	71	118.2	263.24

From Table 13, as the number of hidden units is increased in the model the degrees of freedom also increases. The maximum degrees of freedom calculated for this study were 118.20 when the number of hidden units was set to 10 and the minimum degrees of freedom calculated were 26.11 when the number of hidden units were set to 2. Table 13 also shows that as the number of hidden units increases the AIC value also increases with the maximum being 263.24 for a neural network with 10 hidden units and a minimum being 125.66 for a neural network with 2 hidden units. The logistic regression had a lower value for degrees of freedom and also had a lower AIC value than all but neural networks with 2 and 4 degrees of freedom.

4.0 DISCUSSION

When looking at the prediction of Stage 3 kidney disease, it has been shown that neural networks can perform better than standard logistic regression using the same variables. The maximum AUC value found in this study was 0.988 with a confidence interval of (0.976, 1.000) whereas the logistic regression gave an AUC of 0.904 with a confidence interval of (0.863, 0.949).

With new research being completed, new biomarkers and other potential predictors are being identified. With these new potential predictors being identified, the importance of prediction modeling becomes highlighted. Prediction models have the ability to both provide the ability to assess predictors in a model and the ability to estimate risk for individual patients¹⁶. Neural networks can potentially more accurately predict the risk of an individual to develop a certain disease and therefore allow for better medical treatment and prevention. This has already been shown in prediction of prostate cancer, where neural networks could be used in order to change the way patients are counseled for treatment options¹⁷.

The research to identify new biomarkers extends into the field of nephrology where both the PKD Foundation¹⁸ and the Consortium for Radiologic Imaging Studies of Polycystic Kidney Disease⁸ are both working to identify new markers. Once new markers are identified, neural networks will be able to use these markers to make predictions on outcome predictions and potentially change the way treatments are administered based on baseline values of biomarkers.

However, when looking at modern regression techniques such as neural networks the pros and cons must be weighed. Neural networks allow for the modeling of complex non-linear relationships between variables, detection of all possible interactions between variables, and

can be used with many different algorithms for training for specific types of data. All of these could be very useful when employed for prediction modeling. Neural networks have certain disadvantages as well. These disadvantages include the use of neural networks as a black box technique, leading to a limited ability for detecting casual relationships between variables and hence, making interpretation difficult. Neural networks are also prone to overfitting. However, to adress overfitting, weight decay can be used. Limiting the amount of training can also be a solution to overfitting. For looking at outcome prediction, neural networks are a good candidate for prediction modeling.

Overall, the use of neural networks is a promising technique in which known predictors and biomarkers can be used in order to create a prediction model. And with this prediction model, the way in which the condition is treated could be modified in a way that benefits patients with the disease.

APPENDIX

R CODE

```
##Libraries

require(mlogit)
require(nnet)
require(psych)
require(ROCR)
library(pROC)

##Data management

summary(thesis.data)
thesis<-cbind(thesis.data$ckd_epi, thesis.data$type, thesis.data$httkv0, thesis.data$bmi_c0, thesis.data$sbune_ca0, thesis.data$ckd3_120)
colnames(thesis)<-c("ckd_epi","type","httkv0","bmi","sbun","ckd3")
describe(thesis)
thesis.f<-data.frame(thesis)
thesis.final<-na.omit(thesis.f)

##Descriptives
describe(thesis.final)
summary(thesis.final)
t=table(thesis.final$type)
tcount=as.data.frame(t)
tcount
o=table(thesis.final$ckd3)
ocount=as.data.frame(o)
ocount

##multivariable logistic regression

full<-glm(ckd3~ckd_epi+type+httkv0+bmi+sbun, family=binomial(link=logit),data=thesis.final)
summary(full)
pred1<-predict(full, type=c("response"))
thesis.final$pred1=pred1
```

```

logisticROC<-roc(ckd3~pred1, data=thesis.final, plot=TRUE, print.auc=TRUE, legacy.axes=T, main="ROC_Curve_for_Logistic_Regression", ci=T)

#seed

set.seed(0625199016)

#2 Hidden Unit Network Variations

#neural network with 2 hidden units with weight decay 0.01

neural1<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=2, entropy=TRUE, maxit=1000, decay=0.01)
summary(neural1)
pred21<-predict(neural1, newdata=thesis.final, type=c("raw"))
thesis.final$pred21=pred21
n21<-roc(ckd3~pred2, data=thesis.final, print.auc=T, legacy.axes=T, plot=T, main="2_Hidden_Units_and_Weight_Decay_of_0.01")
plot(n21)

#neural network with 2 hidden units with weight decay 0.02

neural12<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=2, entropy=TRUE, maxit=1000, decay=0.02)
summary(neural12)
pred22<-predict(neural12, newdata=thesis.final, type=c("raw"))
thesis.final$pred22=pred22
n22<-roc(ckd3~pred22, data=thesis.final, print.auc=T, legacy.axes=T, plot=T, main="2_Hidden_Units_and_Weight_Decay_of_0.02")
plot(n22)

##neural network with 2 hidden units with weight decay 0.03

neural13<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=2, entropy=TRUE, maxit=1000, decay=0.03)
summary(neural13)
pred23<-predict(neural13, newdata=thesis.final, type=c("raw"))
thesis.final$pred23=pred23
n23<-roc(ckd3~pred23, data=thesis.final, print.auc=T, legacy.axes=T, plot=T, main="2_Hidden_Units_and_Weight_Decay_0.03")
plot(n23)

##neural network with 2 hidden units with weight decay 0.04

neural14<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=2, entropy=TRUE, maxit=1000, decay=0.04)
summary(neural14)
pred24<-predict(neural14, newdata=thesis.final, type=c("raw"))
thesis.final$pred24=pred24
n24<-roc(ckd3~pred24, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="2_Hidden_Units_and_Weight_Decay_of_0.04")
plot(n24)

##neural network with 2 hidden units with weight decay 0.05

neural15<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=2, entropy=TRUE, maxit=1000, decay=0.05)
summary(neural15)
pred25<-predict(neural15, newdata=thesis.final, type=c("raw"))
thesis.final$pred25=pred25
n25<-roc(ckd3~pred25, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="2_Hidden_Units_and_Weight_Decay_of_0.05")
plot(n25)

##plots for 2 Hidden units

```

```

par(mfrow=c(3,2))
n21<-roc(ckd3~pred21, data=thesis.final, print.auc=T, legacy.axes=T, plot=T, main="A.WeightDecayof0.01", ci=F)
n22<-roc(ckd3~pred22, data=thesis.final, print.auc=T, legacy.axes=T, plot=T, main="B.WeightDecayof0.02", ci=F)
n23<-roc(ckd3~pred23, data=thesis.final, print.auc=T, legacy.axes=T, plot=T, main="C.WeightDecayof0.03", ci=F)
n24<-roc(ckd3~pred24, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="D.WeightDecayof0.04", ci=F)
n25<-roc(ckd3~pred25, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="E.WeightDecayof0.05", ci=F)
par(mfrow=c(1,1))

##CI can be toggled to T to obtain confidence interval

##neural network with 3 hidden units with weight decay 0.01
neural21<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=3, entropy=TRUE, maxit=1000, decay=0.01)
summary(neural21)
pred31<-predict(neural21, newdata=thesis.final, type=c("raw"))
thesis.final$pred31=pred31
n31<-roc(ckd3~pred31, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="3HiddenUnitsandWeightDecay0.01")
plot(n31)

##neural network with 3 hidden units with weight decay 0.02
neural22<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=3, entropy=TRUE, maxit=1000, decay=0.02)
summary(neural22)
pred32<-predict(neural22, newdata=thesis.final, type=c("raw"))
thesis.final$pred32=pred32
n32<-roc(ckd3~pred32, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="3HiddenUnitsandWeightDecay0.02")
plot(n32)

##neural network with 3 hidden units with weight decay 0.03
neural23<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=3, entropy=TRUE, maxit=1000, decay=0.03)
summary(neural23)
pred33<-predict(neural23, newdata=thesis.final, type=c("raw"))
thesis.final$pred33=pred33
n33<-roc(ckd3~pred33, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="3HiddenUnitsandWeightDecay0.03")
plot(n33)

##neural network with 3 hidden units with weight decay 0.04
neural24<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=3, entropy=TRUE, maxit=1000, decay=0.04)
summary(neural24)
pred34<-predict(neural24, newdata=thesis.final, type=c("raw"))
thesis.final$pred34=pred34
n34<-roc(ckd3~pred34, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="3HiddenUnitsandWeightDecay0.04")
plot(n34)

##neural network with 3 hidden units with weight decay 0.05
neural25<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=3, entropy=TRUE, maxit=1000, decay=0.05)
summary(neural25)
pred35<-predict(neural25, newdata=thesis.final, type=c("raw"))
thesis.final$pred35=pred35
n35<-roc(ckd3~pred35, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="3HiddenUnitsandWeightDecay0.05")
plot(n35)

```

```

##plots 3 Hidden Units
par(mfrow=c(3,2))
n31<-roc(ckd3~pred31, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="A. Weight Decay 0.01", ci=F)
n32<-roc(ckd3~pred32, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="B. Weight Decay 0.02", ci=F)
n33<-roc(ckd3~pred33, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="C. Weight Decay 0.03", ci=F)
n34<-roc(ckd3~pred34, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="D. Weight Decay 0.04", ci=F)
n35<-roc(ckd3~pred35, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="E. Weight Decay 0.05", ci=F)
par(mfrow=c(1,1))

##neural network with 4 hidden units with weight decay 0.01
neural31<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=4, entropy=TRUE, maxit=1000, decay=0.01)
summary(neural31)
pred41<-predict(neural31, newdata=thesis.final, type=c("raw"))
thesis.final$pred41=pred41
n41<-roc(ckd3~pred41, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="4 Hidden Units and Weight Decay 0.01")
plot(n41)

##neural network with 4 hidden units with weight decay 0.02
neural32<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=4, entropy=TRUE, maxit=1000, decay=0.02)
summary(neural32)
pred42<-predict(neural32, newdata=thesis.final, type=c("raw"))
thesis.final$pred42=pred42
n42<-roc(ckd3~pred42, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="4 Hidden Units and Weight Decay 0.02")
plot(n42)

##neural network with 4 hidden units with weight decay 0.03
neural33<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=4, entropy=TRUE, maxit=1000, decay=0.03)
summary(neural33)
pred43<-predict(neural33, newdata=thesis.final, type=c("raw"))
thesis.final$pred43=pred43
n43<-roc(ckd3~pred43, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="4 Hidden Units and Weight Decay 0.03")
plot(n43)

##neural network with 4 hidden units with weight decay 0.04
neural34<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=4, entropy=TRUE, maxit=1000, decay=0.04)
summary(neural34)
pred44<-predict(neural34, newdata=thesis.final, type=c("raw"))
thesis.final$pred44=pred44
n44<-roc(ckd3~pred44, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="4 Hidden Units and Weight Decay 0.04")
plot(n44)

##neural network with 4 hidden units with weight decay 0.05
neural35<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=4, entropy=TRUE, maxit=1000, decay=0.05)
summary(neural35)
pred45<-predict(neural35, newdata=thesis.final, type=c("raw"))
thesis.final$pred45=pred45
n45<-roc(ckd3~pred45, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="4 Hidden Units and Weight Decay 0.05")

```

```

plot(n45)

##plot 4 Hidden Units
par(mfrow=c(3,2))
n41<-roc(ckd3~pred41, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="A.WeightDecay0.01", ci=F)
n42<-roc(ckd3~pred42, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="B.WeightDecay0.02", ci=F)
n43<-roc(ckd3~pred43, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="C.WeightDecay0.03", ci=F)
n44<-roc(ckd3~pred44, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="D.WeightDecay0.04", ci=F)
n45<-roc(ckd3~pred45, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="E.WeightDecay0.05", ci=F)
par(mfrow=c(1,1))

##neural network with 5 hidden units with weight decay 0.01
neural41<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=5, entropy=TRUE, maxit=1000, decay=0.01)
summary(neural41)
pred51<-predict(neural41, newdata=thesis.final, type=c("raw"))
thesis.final$pred51=pred51
n51<-roc(ckd3~pred51, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="5HiddenUnitsandWeightDecay0.01")
plot(n51)

##neural network with 5 hidden units with weight decay 0.02
neural42<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=5, entropy=TRUE, maxit=1000, decay=0.02)
summary(neural42)
pred52<-predict(neural42, newdata=thesis.final, type=c("raw"))
thesis.final$pred52=pred52
n52<-roc(ckd3~pred52, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="5HiddenUnitsandWeightDecay0.02")
plot(n52)

##neural network with 5 hidden units with weight decay 0.03
neural43<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=5, entropy=TRUE, maxit=1000, decay=0.03)
summary(neural43)
pred53<-predict(neural43, newdata=thesis.final, type=c("raw"))
thesis.final$pred53=pred53
n53<-roc(ckd3~pred53, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="5HiddenUnitsandWeightDecay0.03")
plot(n53)

##neural network with 5 hidden units with weight decay 0.04
neural44<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=5, entropy=TRUE, maxit=1000, decay=0.04)
summary(neural44)
pred54<-predict(neural44, newdata=thesis.final, type=c("raw"))
thesis.final$pred54=pred54
n54<-roc(ckd3~pred54, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="5HiddenUnitsandWeightDecay0.04")
plot(n54)

##neural network with 5 hidden units with weight decay 0.05
neural45<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=5, entropy=TRUE, maxit=1000, decay=0.05)
summary(neural45)
pred55<-predict(neural45, newdata=thesis.final, type=c("raw"))
thesis.final$pred55=pred55
n55<-roc(ckd3~pred55, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="5HiddenUnitsandWeightDecay0.05")

```



```

plot(n55)

##plots 5 Hidden Units
par(mfrow=c(3,2))
n51<-roc(ckd3~pred51, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="A.WeightDecay0.01", ci=F)
n52<-roc(ckd3~pred52, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="B.WeightDecay0.02", ci=F)
n53<-roc(ckd3~pred53, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="C.WeightDecay0.03", ci=F)
n54<-roc(ckd3~pred54, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="D.WeightDecay0.04", ci=F)
n55<-roc(ckd3~pred55, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="E.WeightDecay0.05", ci=F)
par(mfrow=c(1,1))

##neural network with 6 hidden units with weight decay 0.01
neural51<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=6, entropy=TRUE, maxit=1000, decay=0.01)
summary(neural51)
pred61<-predict(neural51, newdata=thesis.final, type=c("raw"))
thesis.final$pred61=pred61
n61<-roc(ckd3~pred61, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="6HiddenUnitsandWeightDecay0.01")
plot(n61)

##neural network with 6 hidden units with weight decay 0.02
neural52<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=6, entropy=TRUE, maxit=1000, decay=0.02)
summary(neural52)
pred62<-predict(neural52, newdata=thesis.final, type=c("raw"))
thesis.final$pred62=pred62
n62<-roc(ckd3~pred62, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="6HiddenUnitsandWeightDecay0.02")
plot(n62)

##neural network with 6 hidden units with weight decay 0.03
neural53<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=6, entropy=TRUE, maxit=1000, decay=0.03)
summary(neural53)
pred63<-predict(neural53, newdata=thesis.final, type=c("raw"))
thesis.final$pred61=pred63
n63<-roc(ckd3~pred63, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="6HiddenUnitsandWeightDecay0.03")
plot(n63)

##neural network with 6 hidden units with weight decay 0.04
neural54<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=6, entropy=TRUE, maxit=1000, decay=0.04)
summary(neural54)
pred64<-predict(neural54, newdata=thesis.final, type=c("raw"))
thesis.final$pred64=pred64
n64<-roc(ckd3~pred64, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="6HiddenUnitsandWeightDecay0.04")
plot(n64)

##neural network with 6 hidden units with weight decay 0.05
neural55<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=6, entropy=TRUE, maxit=1000, decay=0.05)
summary(neural55)
pred65<-predict(neural55, newdata=thesis.final, type=c("raw"))
thesis.final$pred65=pred65

```

```

n65<-roc(ckd3~pred65, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="6_Hidden_Units_and_Weight_Decay_0.05")
plot(n65)

##plots 6 Hidden Units
par(mfrow=c(3,2))
n61<-roc(ckd3~pred61, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="A_Weight_Decay_0.01", ci=F)
n62<-roc(ckd3~pred62, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="B_Weight_Decay_0.02", ci=F)
n63<-roc(ckd3~pred63, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="C_Weight_Decay_0.03", ci=F)
n64<-roc(ckd3~pred64, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="D_Weight_Decay_0.04", ci=F)
n65<-roc(ckd3~pred65, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="E_Weight_Decay_0.05", ci=F)
par(mfrow=c(1,1))

##neural network with 7 hidden units with weight decay 0.01
neural61<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=7, entropy=TRUE, maxit=1000, decay=0.01)
summary(neural61)
pred71<-predict(neural61, newdata=thesis.final, type=c("raw"))
thesis.final$pred71=pred71
n71<-roc(ckd3~pred71, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="7_Hidden_Units_and_Weight_Decay_0.01")
plot(n71)

##neural network with 7 hidden units with weight decay 0.02
neural62<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=7, entropy=TRUE, maxit=1000, decay=0.02)
summary(neural62)
pred72<-predict(neural62, newdata=thesis.final, type=c("raw"))
thesis.final$pred72=pred72
n72<-roc(ckd3~pred72, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="7_Hidden_Units_and_Weight_Decay_0.02")
plot(n72)

##neural network with 7 hidden units with weight decay 0.03
neural63<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=7, entropy=TRUE, maxit=1000, decay=0.03)
summary(neural63)
pred73<-predict(neural63, newdata=thesis.final, type=c("raw"))
thesis.final$pred73=pred73
n73<-roc(ckd3~pred73, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="7_Hidden_Units_and_Weight_Decay_0.03")
plot(n73)

##neural network with 7 hidden units with weight decay 0.04
neural64<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=7, entropy=TRUE, maxit=1000, decay=0.04)
summary(neural64)
pred74<-predict(neural64, newdata=thesis.final, type=c("raw"))
thesis.final$pred74=pred74
n74<-roc(ckd3~pred74, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="7_Hidden_Units_and_Weight_Decay_0.04")
plot(n74)

##neural network with 7 hidden units with weight decay 0.05
neural65<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=7, entropy=TRUE, maxit=1000, decay=0.05)
summary(neural65)
pred75<-predict(neural65, newdata=thesis.final, type=c("raw"))

```

```

thesis.final$pred75=pred75
n75<-roc(ckd3~pred75, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="7 Hidden Units and Weight Decay 0.05")
plot(n75)

##plots 7 Hidden Units
par(mfrow=c(3,2))
n71<-roc(ckd3~pred71, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="A Weight Decay 0.01", ci=F)
n72<-roc(ckd3~pred72, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="B Weight Decay 0.02", ci=F)
n73<-roc(ckd3~pred73, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="C Weight Decay 0.03", ci=F)
n74<-roc(ckd3~pred74, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="D Weight Decay 0.04", ci=F)
n75<-roc(ckd3~pred75, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="E Weight Decay 0.05", ci=F)
par(mfrow=c(1,1))

##neural network with 8 hidden units with weight decay 0.01
neural71<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=8, entropy=TRUE, maxit=1000, decay=0.01)
summary(neural71)
pred81<-predict(neural71, newdata=thesis.final, type=c("raw"))
thesis.final$pred81=pred81
n81<-roc(ckd3~pred81, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="8 Hidden Units and Weight Decay 0.01")
plot(n81)

##neural network with 8 hidden units with weight decay 0.02
neural72<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=8, entropy=TRUE, maxit=1000, decay=0.02)
summary(neural72)
pred82<-predict(neural72, newdata=thesis.final, type=c("raw"))
thesis.final$pred82=pred82
n82<-roc(ckd3~pred82, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="8 Hidden Units and Weight Decay 0.02")
plot(n82)

##neural network with 8 hidden units with weight decay 0.03
neural73<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=8, entropy=TRUE, maxit=1000, decay=0.03)
summary(neural73)
pred83<-predict(neural73, newdata=thesis.final, type=c("raw"))
thesis.final$pred83=pred83
n83<-roc(ckd3~pred83, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="8 Hidden Units and Weight Decay 0.03")
plot(n83)

##neural network with 8 hidden units with weight decay 0.04
neural74<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=8, entropy=TRUE, maxit=1000, decay=0.04)
summary(neural74)
pred84<-predict(neural74, newdata=thesis.final, type=c("raw"))
thesis.final$pred84=pred84
n84<-roc(ckd3~pred84, data=thesis.final, print.auc=T, plot=t, legacy.axes=T, main="8 Hidden Units and Weight Decay 0.04")
plot(n84)

##neural network with 8 hidden units with weight decay 0.05
neural75<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=8, entropy=TRUE, maxit=1000, decay=0.05)
summary(neural75)

```

```

pred85<-predict(neural75, newdata=thesis.final, type=c("raw"))
thesis.final$pred85=pred85
n85<-roc(ckd3~pred85, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="8_Hidden_Units_and_Weight_Decay_0.05")
plot(n85)

##plots 8 Hidden Units
par(mfrow=c(3,2))
n81<-roc(ckd3~pred81, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="A_Weight_Decay_0.01", ci=F)
n82<-roc(ckd3~pred82, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="B_Weight_Decay_0.02", ci=F)
n83<-roc(ckd3~pred83, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="C_Weight_Decay_0.03", ci=F)
n84<-roc(ckd3~pred84, data=thesis.final, print.auc=T, plot=t, legacy.axes=T, main="D_Weight_Decay_0.04", ci=F)
n85<-roc(ckd3~pred85, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="E_Weight_Decay_0.05", ci=F)
par(mfrow=c(1,1))

##neural network with 9 hidden units with weight decay 0.01
neural81<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=9, entropy=TRUE, maxit=1000, decay=0.01)
summary(neural81)
pred91<-predict(neural81, newdata=thesis.final, type=c("raw"))
thesis.final$pred91=pred91
n91<-roc(ckd3~pred91, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="9_Hidden_Units_and_Weight_Decay_0.01")
plot(n91)

##neural network with 9 hidden units with weight decay 0.02
neural82<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=9, entropy=TRUE, maxit=1000, decay=0.02)
summary(neural82)
pred92<-predict(neural82, newdata=thesis.final, type=c("raw"))
thesis.final$pred92=pred92
n92<-roc(ckd3~pred92, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="9_Hidden_Units_and_Weight_Decay_of_0.02")
plot(n92)

##neural network with 9 hidden units with weight decay 0.03
neural83<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=9, entropy=TRUE, maxit=1000, decay=0.03)
summary(neural83)
pred93<-predict(neural83, newdata=thesis.final, type=c("raw"))
thesis.final$pred93=pred93
n93<-roc(ckd3~pred93, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="9_Hidden_Units_and_Weight_Decay_of_0.03")
plot(n93)

##neural network with 9 hidden units with weight decay 0.04
neural84<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=9, entropy=TRUE, maxit=1000, decay=0.04)
summary(neural84)
pred94<-predict(neural84, newdata=thesis.final, type=c("raw"))
thesis.final$pred94=pred94
n94<-roc(ckd3~pred94, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="9_Hidden_Units_and_Weight_Decay_0.04")
plot(n94)

##neural network with 9 hidden units with weight decay 0.05
neural85<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=9, entropy=TRUE, maxit=1000, decay=0.05)

```

```

summary(neural85)
pred95<-predict(neural85, newdata=thesis.final, type=c("raw"))
thesis.final$pred95=pred95
n95<-roc(ckd3~pred95, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="9_Hidden_Units_and_Weight_Decay_0.05")
plot(n95)

##plots for 9 Hidden Units
par(mfrow=c(3,2))
n91<-roc(ckd3~pred91, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="A_Weight_Decay_0.01", ci=F)
n92<-roc(ckd3~pred92, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="B_Weight_Decay_0.02", ci=F)
n93<-roc(ckd3~pred93, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="C_Weight_Decay_0.03", ci=F)
n94<-roc(ckd3~pred94, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="D_Weight_Decay_0.04", ci=F)
n95<-roc(ckd3~pred95, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="E_Weight_Decay_0.05", ci=F)
par(mfrow=c(1,1))

##neural network with 10 hidden units with weight decay 0.01
neural91<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=10, entropy=TRUE, maxit=1000, decay=0.01)
summary(neural91)
pred101<-predict(neural91, newdata=thesis.final, type=c("raw"))
thesis.final$pred101=pred101
n101<-roc(ckd3~pred101, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="10_Hidden_Units_and_Weight_Decay_0.01")
plot(n101)

##neural network with 10 hidden units with weight decay 0.02
neural92<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=10, entropy=TRUE, maxit=1000, decay=0.02)
summary(neural92)
pred102<-predict(neural92, newdata=thesis.final, type=c("raw"))
thesis.final$pred102=pred102
n102<-roc(ckd3~pred102, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="10_Hidden_Units_and_Weight_Decay_0.02")
plot(n102)

##neural network with 10 hidden units with weight decay 0.03
neural93<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=10, entropy=TRUE, maxit=1000, decay=0.03)
summary(neural93)
pred103<-predict(neural93, newdata=thesis.final, type=c("raw"))
thesis.final$pred103=pred103
n103<-roc(ckd3~pred103, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="10_Hidden_Units_and_Weight_Decay_0.03")
plot(n103)

##neural network with 10 hidden units with weight decay 0.04
neural94<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=10, entropy=TRUE, maxit=1000, decay=0.04)
summary(neural94)
pred104<-predict(neural94, newdata=thesis.final, type=c("raw"))
thesis.final$pred104=pred104
n104<-roc(ckd3~pred104, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="10_Hidden_Units_and_Weight_Decay_0.04")
plot(n104)

##neural network with 10 hidden units with weight decay 0.05
neural95<-nnet(ckd3~ckd_epi+bmi+type+httkv0+sbun,data=thesis.final,size=10, entropy=TRUE, maxit=1000, decay=0.05)

```

```

summary(neural95)
pred105<-predict(neural95, newdata=thesis.final, type=c("raw"))
thesis.final$pred105=pred105
n105<-roc(ckd3~pred105, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="10 Hidden Units and Weight Decay 0.05")
plot(n105)

##plots 10 Hidden Units
par(mfrow=c(3,2))
n101<-roc(ckd3~pred101, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="A. Weight Decay 0.01", ci=F)
n102<-roc(ckd3~pred102, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="B. Weight Decay 0.02", ci=F)
n103<-roc(ckd3~pred103, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="C. Weight Decay 0.03", ci=F)
n104<-roc(ckd3~pred104, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="D. Weight Decay 0.04", ci=F)
n105<-roc(ckd3~pred105, data=thesis.final, print.auc=T, plot=T, legacy.axes=T, main="E. Weight Decay 0.05", ci=F)
par(mfrow=c(1,1))

###degrees of freedom calculations###

##2 Hidden Units
k2<-2^5-1
p2<-2*(5+1)+(2+1)
df2<-(0.6643+0.1429*log2(k2-p2))*p2

df2c<-2*(3*(5-2)+5)
edf2<-df2*.2+df2c*.8

##4 Hidden Units
k4<-2^5-1
p4<-4*(5+1)+(4+1)
df4<-(0.6643+0.1429*log2(k4-p4))*p4

df4c<-4*(3*(5-2)+5)
edf4<-df4*.2+df4c*.8

##6 Hidden Units
k6<-2^5-1
p6<-6*(5+1)+(6+1)
df6<-(0.6643+0.1429*log2(k6-p6))*p6

df6c<-6*(3*(5-2)+5)
edf6<-k6*.2+(df6c*.8)

## 8 Hidden Units
k8<-2^5-1
p8<-8*(5+1)+(8+1)
df8<-(0.6643+0.1429*log2(k8-p8))*p8

df8c<-8*(3*(5-2)+5)
edf8<-k8*.2+df8c*.8

##10 Hidden Units
k10<-2^5-1
p10<-10*(5+1)+(10+1)
df10<-(0.6643+0.1429*log2(k10-p10))*p10

```

```
df10c<-10*(3*(5-2)+5)
edf10<-k10+((df10c-k10)*.8)
```

```
##AIC values
```

```
AIC11<-(73.44+2*edf2)
```

```
AIC41<-(61.14+2*edf4)
```

```
AIC61<-(55.53+2*edf6)
```

```
AIC81<-(48.41+2*edf8)
```

```
AIC101<-(26.84+2*edf10)
```

BIBLIOGRAPHY

- [1] Harris, Peter C., and Vicente E. Torres. "Polycystic kidney disease.", *Annual review of medicine* 60 (2009): 321.
- [2] Rule, Andrew D., Vicente E. Torres, Arlene B. Chapman, Jared J. Grantham, Lisa M. Guay-Woodford, Kyongtae T. Bae, Saulo Klahr et al. "Comparison of methods for determining renal function decline in early autosomal dominant polycystic kidney disease: the consortium of radiologic imaging studies of polycystic kidney disease cohort." *Journal of the American Society of Nephrology* 17, no. 3 (2006): 854-862.
- [3] Stevens, Lesley A., Christopher H. Schmid, Tom Greene, Yaping Lucy Zhang, Gerald J. Beck, Marc Froissart, Lee L. Hamm et al. "Comparative performance of the CKD epidemiology collaboration (CKD-EPI) and the modification of diet in renal disease (MDRD) study equations for estimating GFR levels above 60 mL/min/1.73 m²." *American Journal of Kidney Diseases* 56, no. 3 (2010): 486-495.
- [4] Levey, Andrew S., Josef Coresh, Ethan Balk, Annamaria T. Kausz, Adeera Levin, Michael W. Steffes, Ronald J. Hogg, Ronald D. Perrone, Joseph Lau, and Garabed Eknoyan. "National Kidney Foundation practice guidelines for chronic kidney disease: evaluation, classification, and stratification." *Annals of internal medicine* 139, no. 2 (2003): 137-147.
- [5] Chapman, Arlene B., James E. Bost, Vicente E. Torres, Lisa Guay-Woodford, Kyongtae Ty Bae, Douglas Landsittel, Jie Li et al. "Kidney volume and functional outcomes

- in autosomal dominant polycystic kidney disease." *Clinical Journal of the American Society of Nephrology* 7, no. 3 (2012): 479-486.
- [6] Liu, Kathleen D., Jonathan Himmelfarb, Emil Paganini, T. Alp Ikizler, Sharon H. Soroko, Ravindra L. Mehta, and Glenn M. Chertow. "Timing of initiation of dialysis in critically ill patients with acute kidney injury." *Clinical Journal of the American Society of Nephrology* 1, no. 5 (2006): 915-919.
- [7] Fox, Caroline S., Martin G. Larson, Eric P. Leip, Bruce Culleton, Peter WF Wilson, and Daniel Levy. "Predictors of new-onset kidney disease in a community-based population." *JAMA* 291, no. 7 (2004): 844-850.
- [8] "NIDDK Central Repository." NIDDK: Consortium for Radiologic Imaging Studies of Polycystic Kidney Disease. Accessed March 16, 2016. <https://www.niddkrepository.org/studies/crisp/>.
- [9] Tu, Jack V. "Advantages and disadvantages of using artificial neural networks versus logistic regression for predicting medical outcomes." *Journal of clinical epidemiology* 49, no. 11 (1996): 1225-1231.
- [10] Bartlett, Peter L. "The sample complexity of pattern classification with neural networks: the size of the weights is more important than the size of the network." *Information Theory, IEEE Transactions on* 44, no. 2 (1998): 525-536.
- [11] Zweiri, Yahya H. "Optimization of a three-term backpropagation algorithm used for neural network learning." *Int J Comput Intell* 3 (2007): 322-327.
- [12] Dreiseitl, Stephan, and Lucila Ohno-Machado. "Logistic regression and artificial neural network classification models: a methodology review." *Journal of biomedical informatics* 35, no. 5 (2002): 352-359.
- [13] Bradley, Andrew P. "The use of the area under the ROC curve in the evaluation of machine learning algorithms." *Pattern recognition* 30, no. 7 (1997): 1145-1159.

- [14] Fawcett, Tom. "An introduction to ROC analysis." *Pattern recognition letters* 27, no. 8 (2006): 861-874.
- [15] Landsittel, Douglas. "Estimating Model Complexity of Feed-Forward Neural Networks." *Journal of Modern Applied Statistical Methods* 8, no. 2 (2009): 13.
- [16] Steyerberg, Ewout W., and Yvonne Vergouwe. "Towards better clinical prediction models: seven steps for development and an ABCD for validation." *European heart journal* (2014): ehu207.
- [17] Djavan, Bob, Mesut Remzi, Alexandre Zlotta, Christian Seitz, Peter Snow, and Michael Marberger. "Novel artificial neural network for early detection of prostate cancer." *Journal of Clinical Oncology* 20, no. 4 (2002): 921-929.
- [18] "Home - PKD Foundation." PKD Foundation. Accessed March 21, 2016. <http://www.pkdcure.org/page.aspx?pid=329>.