Design Improvements for the University of Virginia Transplant Center

Omkar G. Kharkar

December 12th, 2011

Honor Pledge: On my honor, I pledge that I am the sole author of this paper and I have accurately cited all help and references used in its completion.

Summary:

In this report, I have included analysis for design improvements for the University of Virginia's transplant center for kidney and liver transplants. My analysis has been based on Response Surface Methodology (RSM) using the EISE approach. The models for the response surface have consisted mainly of linear and time series models, with bootstrapping techniques used to when mathematical assumptions have been violated. Based on the results, the University of Virginia should definitely consider expanding its transplant service to other demographics. It should also consider designing a transplant center for increasing liver transplants, in the 2-year time horizon, for a projected increase starting in year 3 and beyond. The transplant center should be further evaluated based on time-value of money and deterministic projections.

1 Problem Description

1.1 Background

The purpose of this report to evaluate several designs for the University of Virginia's organ transplantation system for liver and kidney transplants, in comparison to other major centers, such as MCV, UNC and Duke which comprise of the Region 11 transplant centers. From [3], Brown, D. E (2011) provides a more detailed description about the transplant center:

"Organ transplantation replaces diseased or damaged organs with functioning organs from either deceased or living donors. The complexity of these procedures requires highly skilled teams of physicians, nurses, and support staff as well as facilities for the surgery and recovery. The University of Virginia has conducted organ transplantation for more than 30 years and now provides services for kidney, pancreas, liver, islet, heart and lung transplantation [1].

> 'The UVA Health System is consistently ranked as one of the Top 100 Hospitals in America[1].' The availability of first-rate transplantation services is a component of these rankings. The Transplant Center desires to continue to increase the number of transplants in all categories but needs guidance on how to achieve this goal [2]. This study as requested in [3] provides initial design guidance for them.
>
> 1. Organ transplantation processes have primary steps [4]:
> 2. Referral from a primary care physician;
> 3. Determination of eligibility and placement on a waiting list;
> 4. Matching of donor organ with the patient;
> 5. Acceptance of the organ by the transplant center
> 6. Transplantation surgery and recovery." (p.1)
>
> - From D. E. Brown, "Design Improvements for the UVA Transplant Center," November 2011, SYS 4021 Assignment.

1.2 Goal

The goal of this study is to improve the quality of care given by the University of Virginia's transplant center by giving more transplants to more patients in need. This will be measured by analyzing the number of kidney and liver transplants. Then, the design will be evaluated for improvements on how to increase the number of transplants.

1.3 Data Source

This data source was taken from the Organ Procurement and Transplantation Network (OPTN) [5]. This study used the data from 1988 – 2009 only since the year 2010 had incomplete data.

2 EISE Approach to Transplant Filter Design

2.1 Design Alternatives

There were several design alternatives that were considered for this study. First, for kidney transplant, percentage of white kidney transplants and difference in the number of kidney transplants were used in designing models. For liver transplants, expected number of liver transplants for two separate time periods was used. An alternate design that was considered was the addition of a center for liver transplants.

2.2 Hypothesis

There were 5 hypothesis statements that were created for this study, each corresponding to a specific iteration in the EISE Response Surface Methodology. [6]

Kidney Transplants [7]

Iteration 1

Conjecture: There is a difference in the number of kidney transplants for UVA and MCV.

Hypothesis: There is not a statistically significant difference in the number of kidney transplants for UVA and MCV the 0.05 level of significance.

Iteration 2

Conjecture: There is a difference between UVA and MCV in the expected percentage of white kidney transplant patients.

Hypothesis: There is not a statistically significant difference between UVA and MCV percentage of white kidney transplant patients at the 0.05 level of significance.

Iteration 3

Conjecture: The percentage of kidney transplant patients who are white at UVA correlates with the number of UVA transplant patients.

Hypothesis: There is not a statistically significant correlation between the percentage of kidney transplant patients who are white at UVA and the number of UVA transplant patients at the 0.05 level of significance.

Liver Transplants [7]

Iteration 1

Conjecture: There is a difference between the expected number of liver transplants at UVA in the periods 1988-2004 and 2005-2009.

Hypothesis: There is not a statistically significant difference between the expected number of liver transplants at UVA in the 1988-2004 period and the 2005-2009 period at a 0.05 level of significance.

Iteration 2

Conjecture: Building a new center is correlated with an increasing number of liver transplant patients.

Hypothesis: There is not a statistically significant correlation between building a new center and an increasing number of liver transplant patients at the 0.05 level of significance.

2.3 Visualization and Graphical Analysis

In this study, scatter plot matrices were used to understand the correlation of transplants with other centers and Region 11 as a whole. Also a variety of scatter plots were used to observe trends for the donors and transplants by region and center for kidneys and livers.

2.4 Response Surface Models

In order to compare data set differences, statistical tests, such as the t-test and Wilcoxon Non-Parametric test were used. The response surfaces were mainly designed using a combination of multiple regression linear models with time series components. Time series models were frequently used when serial correlation in the data was detected, especially for residuals and for prediction.

Several types of plots and graphs were used with the models to assess their effectiveness. Diagnostic plots were created to assess how well hypothesized linear models fit the underlying distribution. These included the Residuals vs. Fitted, Scale-Location, Q-Q and Cook's Distance plots. ACF (Autocorrelation Function) plots and PACF (Partial Autocorrelation Function) plots were created to check for serial correlation, which complemented the time series models. The time series models were verified for accuracy using AIC bar plots.

In cases where the residuals were found to be non-Gaussian, as evidenced by the Diagnostics plots, Bootstrapping methods were used to obtain confidence intervals and predictions for response surfaces.

3 Evidence

3.1 Visualization and Graphical Analysis Results

In order to develop an understanding of the transplant center design, the data for liver and kidney transplants were analyzed in several ways. First, scatter plot matrices were obtained for liver and Kidney data (Refer to Appendix, Figures 1 and 2). Based on the result of the scatter plots, UVA and MCV have the largest correlations for kidney transplants to each other with Region 11 donors, in general. In the case of liver transplants, UVA and MCV do not have strong correlation to one another, but have strong correlations to Region 11 donors, allowing for a valid comparison [6].

Donor plots (Figures 3 and 4) and Region plots (Figures 5 -6) were obtained, which showed that there has been an increasing number of deceased donors in the years from 1988 – 2009. This closely mirrors the increasing upward trend of deceased donor transplants in the same time frame. The region plots show increasing upward trend of donors and transplants over the time period. Finally, the center plots (Figures 7 - 8) helped to understand the UVA medical center's organ transplantation center trends in the past few years, which were helpful to compare to other medical facilities, namely MCV.

3.2 Response Surface Modeling Results

The results from the models and graphs obtained are shown below in the Appendix. There were 3 iterations from the Response Surface Methodology that were tested for the kidney transplant data, and there were 2 iterations tested for the liver transplant data.

In Kidney Transplant Iteration 1, the statistical tests (Figure 9) showed that one cannot reject the hypothesis that there is no significant difference in the number of transplants for UVA and MCV. The graph for the differences is shown in Figure 10. However, there was serial correlation in the data, as seen shown by autocorrelation functions (Figure 11). A time series model was used to correct for this and an AR (1) model was obtained to more accurately model the differences between UVA and MCV (Figures 12-15). The predictions for the differences in kidney transplants are shown in Figure 16. The differences were also modeled using bootstrapping (Figures 17 – 18). Based on the confidence interval, the null hypothesis for Iteration 1 was rejected that underlying data distribution was similar.

In the Kidney Transplant Iteration 2, a difference in ethnic composition was observed (Figures 19 – 21). Initial statistical tests showed that there was a statistically significant difference between the percent white transplant patients and no serial correlation in the data (Figures 21 - 22). The null hypothesis for iteration 2 was rejected, since there was a statistically significant (p-value < 0.05) difference between the percentage of white kidney transplant patients at UVA and MCV.

Iteration 3 was first tested using two models, followed by a one-model approach. The latter uses more data points to obtain a more accurate estimate of the error variance [7]. The initial MCV model (MCV Model 1) showed serial correlation (Figures 23 – 25). The second MCV model that was developed corrected this (Figures 26 – 28). For the UVA Kidney data, the same procedures were used, with the second model correcting for serial correlation (Figures 29 – 35). From these models, the predicted number of kidney transplants was obtained from two points on the response surface (Percent white = 70 and percent white = 60), which represented the percent white population (Figure 36). The predictions were also made using the bootstrap method (Figures 37 – 38).

The residuals showed no serial correlation (Figure 39) and an F-test for equal variances was used to verify that the variances of the two samples were equal (Figure 40). The eth.rs2 model, using the "ar()" function in R, was used to obtain the optimal models, which were time series for the UVA and MCV kidney data. In the eth.rs 2 model, "the residuals from two AR models for the numbers of UVA and MCV kidney transplants was the response variable with percentage white and a categorical variable indicating the medical center as predictor variables"[7]. These models were chosen since they were superior to the MCV and UVA Model 2 that were tested. Predictions were then made using the two points (PW = 70 and PW = 60) and bootstrapping methods again. The null hypothesis for iteration 3 was not rejected at the 0.05 significance level, for the linear model, for the predictions using the response surface and the predictions using the response surface with bootstrapping (Figures 42 - 44).

For the liver transplant iteration 1, the two sets of data for the two time periods were analyzed using statistical tests and testing for serial correlation (Figures 45-46). The null hypothesis for the statistical test and therefore, iteration 1 was rejected, meaning data were found to not be similar, and there was no serial correlation that was found.

In iteration 2, the linear model for the Roanoke center was built and was shown to have serial correlation, from the autocorrelation function. (Figures 47 -49). A second linear model was developed, which corrected for the serial correlation (Figures 50 – 52). A time series model was created to estimate the number of transplants UVA would have performed without the Roanoke Center, for which the optimal model tested was an AR(1) (Figures 53 – 54). Finally, the number of liver transplants was predicted using two points (Percent white = 70 and percent white = 60) on the response surface, and again using bootstrapping methods for a 5-year projection period

(Figures 55 – 56). The bootstrap results were conclusive since the prediction results using the 2 PW points were inconclusive, since their confidence intervals overlapped [8]. The null hypothesis for iteration 2 was rejected for the final 3 years, but not for the first 2 years.

4 Recommendation

Based on the results of this study, for the kidney transplants, there was a difference in the MCV and UVA data distribution, a difference in the percent white kidney transplants for UVA and MCV, and no correlation between the percentage of kidney transplant patients who are white and the number of transplant patients at UVA. Based on the response surfaces that were obtained, I recommend that UVA focus on trying to increase number of patients in other ethnic groups. This is evidenced by the probability of 0.5, which is the chance that increasing the number of patients vs. 70 percent design [9]. The UVA medical center should also consider other variables besides race that will affect the number of kidney transplants, by possibly performing more data mining and statistical analysis.

For liver transplants, this study found that there was a significant difference in the number of liver transplants that have taken place in the period of 2005 – 2009 compared to 1988 -2004. Also, adding a center for liver transplants was shown to increase the number of liver transplants after 2 years. Thus, UVA should further evaluate whether to build a center by using projections longer than 5 years if possible and assessing costs and benefits for such a project. It should be noted if the center's construction is currently feasible and it opens after 2 years, it can expect a significantly larger number of forecasted liver transplants. One assumption that has to be made here, however, is that "the new center will not contain patients who would have gone to a currently existing UVA center" [7].

5 References

[1] B. Carveth, Transplant center," January 2009, http://www.healthsystem.virginia.edu/internet/transplant/home.cfm.

[2] R. Teaster, Operations of the University of Virginia Transplant Center,"October 2010, personal communication.

[3] D. E. Brown, "Design Improvements for the UVA Transplant Center," November 2011, SYS 4021 Assignment.

[4] U. G. A. Organ Transplant Programs: Federal agencies have acted to improve oversight, but implementation issues remain," April 2008, GAO-O8-412.

[5] OPTN: Organ Procurement and Transplantation Network. http://optn.transplant.hrsa.gov.

[6] Conversation with Friend

[7] D. E. Brown, "Lab 3.5 Quiz," November 2011, SYS 4021 weekly lab quiz.

[8] Conversation with Friend

[9] D. E. Brown, “Lab 3.4 Quiz,” November 2011, SYS 4021 weekly lab quiz.

[10] D. E. Brown, “Lab 3 Template,” November 2011, SYS 4021 Assignment.

6 Appendix

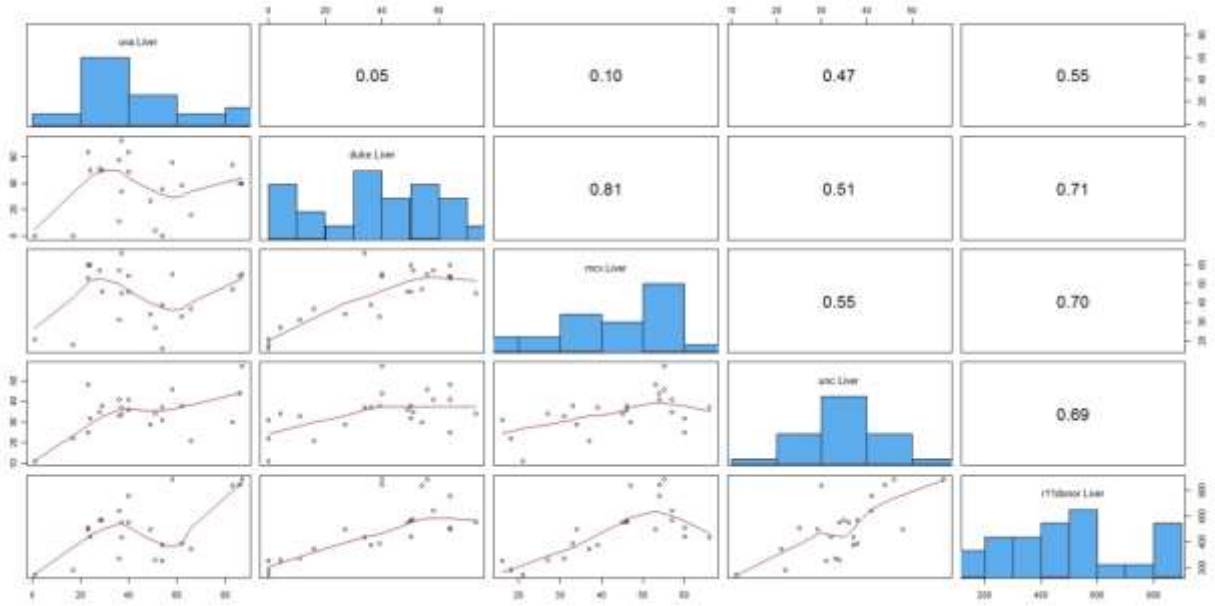

Figure 1 - Scatter Plot Matrix for Liver Transplants

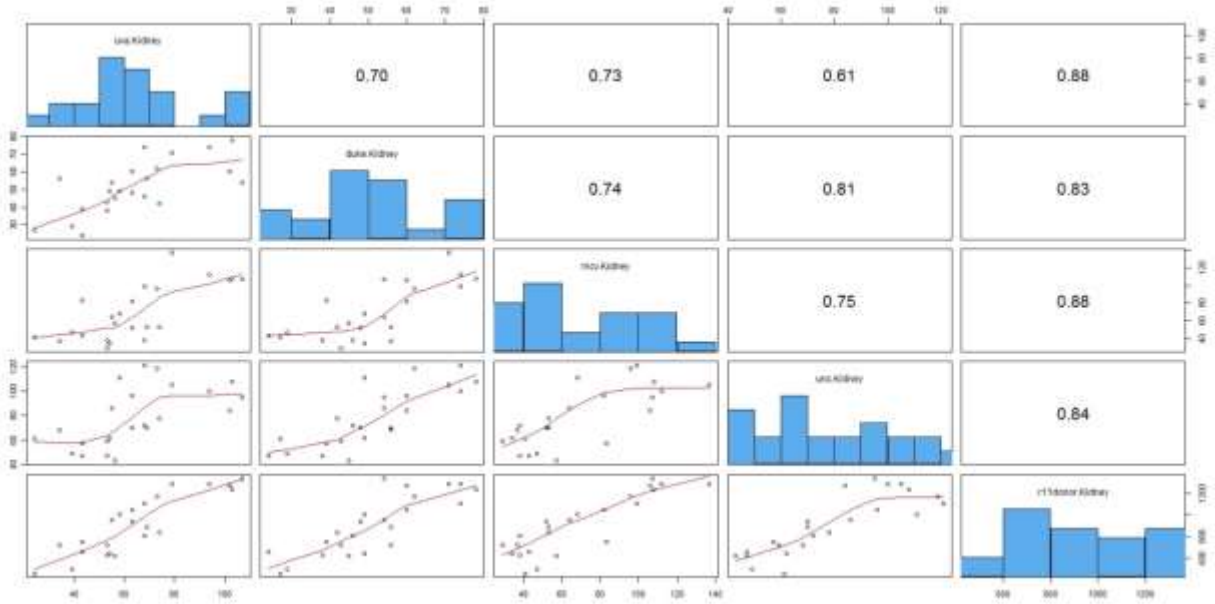

Figure 2 - Scatter Plot Matrix for Kidney Data

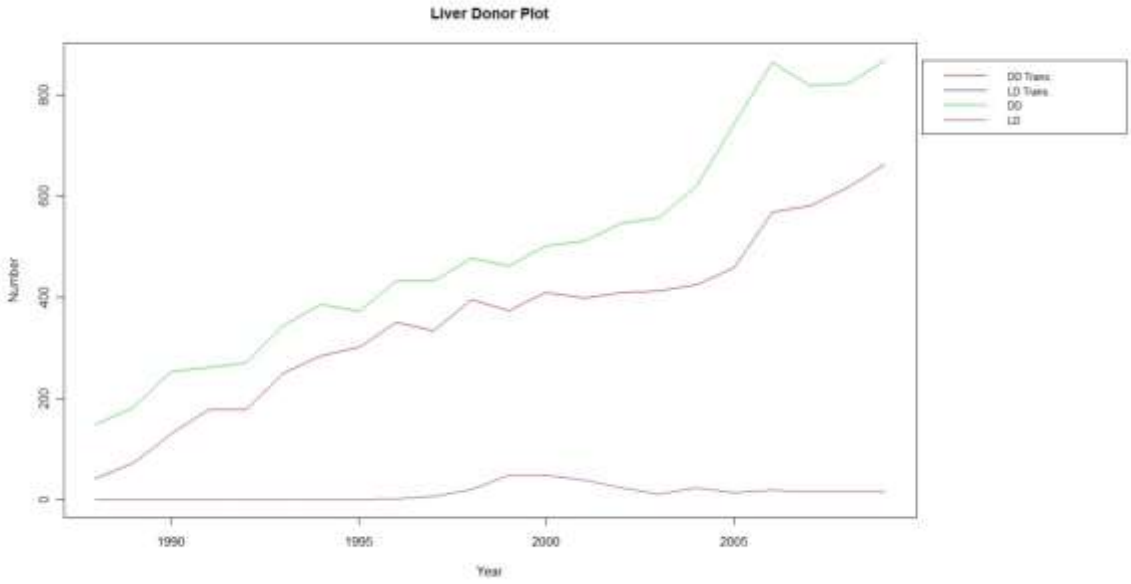

Figure 3 - Liver Donor Plot

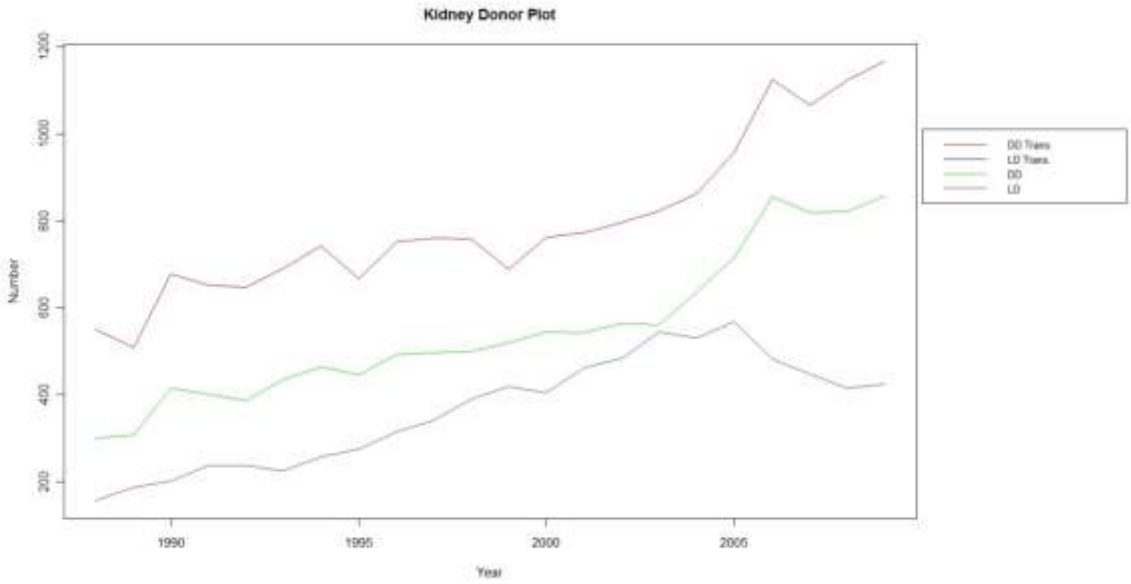

Figure 4 - Kidney Donor Plot

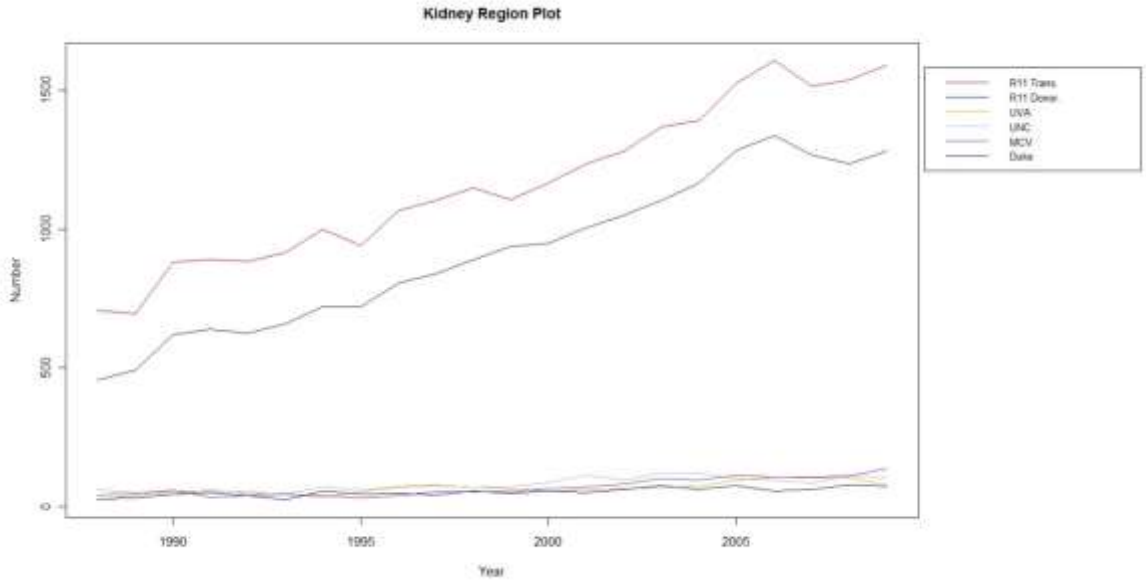

Figure 5 - Kidney Region Plot

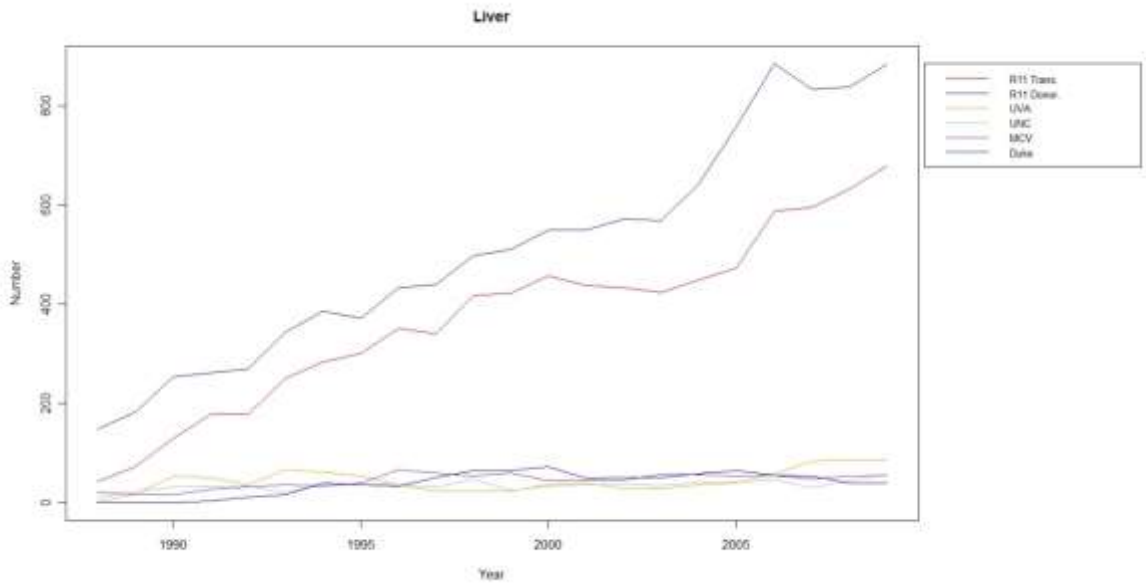

Figure 6 - Liver Region Plot

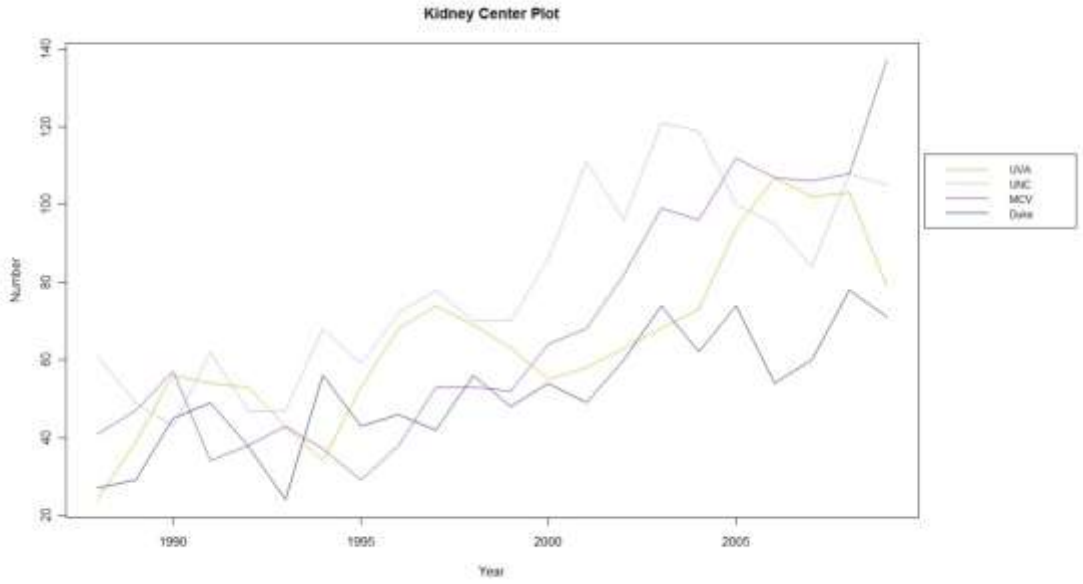

Figure 7 - Kidney Center Plot

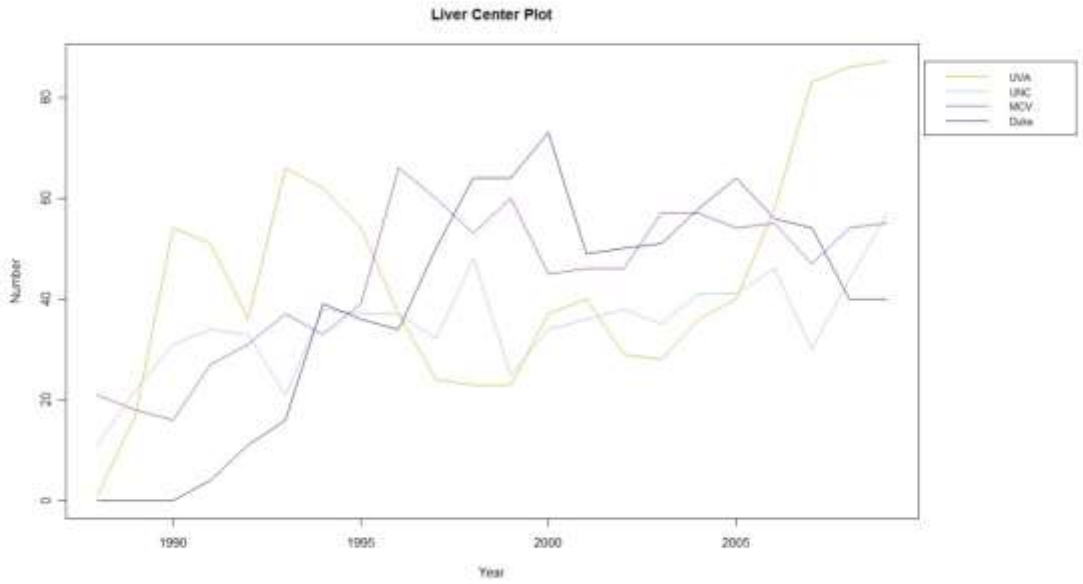

Figure 8 - Liver Center Plot

```
> kid.diff <- ts((uva.donors - mcv.donors), 1988, 2009)
> mean(kid.diff)
[1] -3.136364
> sd(kid.diff)
[1] 20.50156
> var(kid.diff)
[1] 420.3139
> t.test(uva.donors, mcv.donors)

        Welch Two Sample t-test

data:  uva.donors and mcv.donors
t = -0.5941, df = 39.566, p-value = 0.5558
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -20.86605  11.38779
sample estimates:
mean of x mean of y
 64.13043  68.86957

> wilcox.test(uva.donors, mcv.donors)

        Wilcoxon rank sum test with continuity correction

data:  uva.donors and mcv.donors
W = 263, p-value = 0.9825
alternative hypothesis: true location shift is not equal to 0

Warning message:
In wilcox.test.default(uva.donors, mcv.donors) :
  cannot compute exact p-value with ties
```

Figure 9 - Statistical Test Results

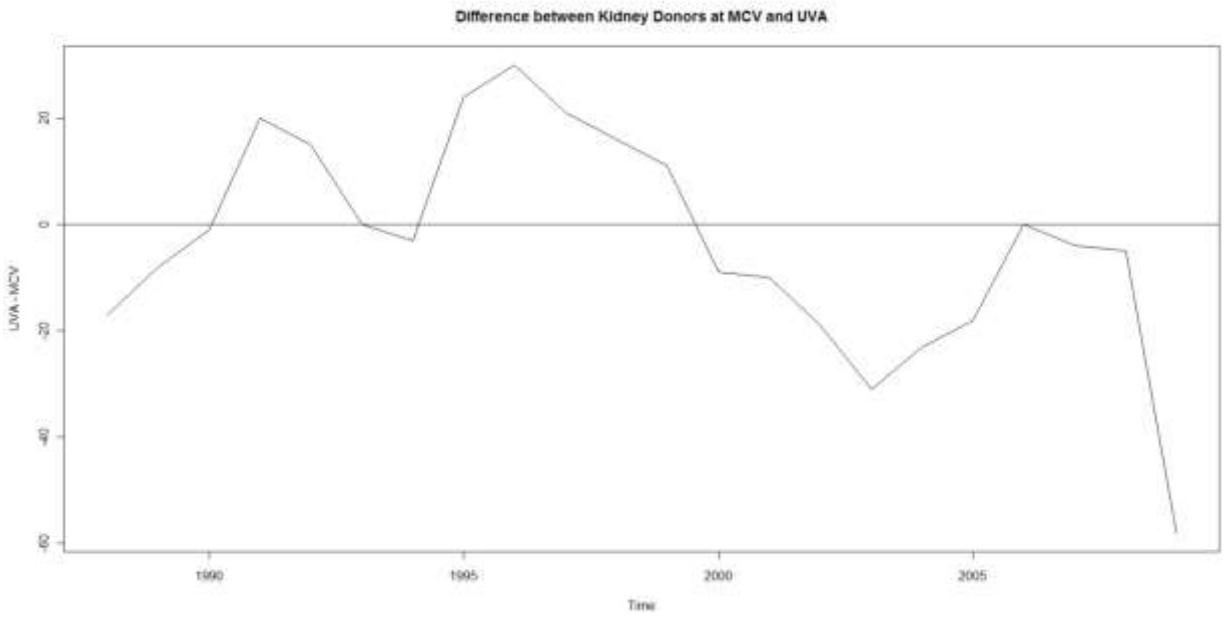

Figure 10 - Time Series for Difference in UVA and MCV Kidney Donors

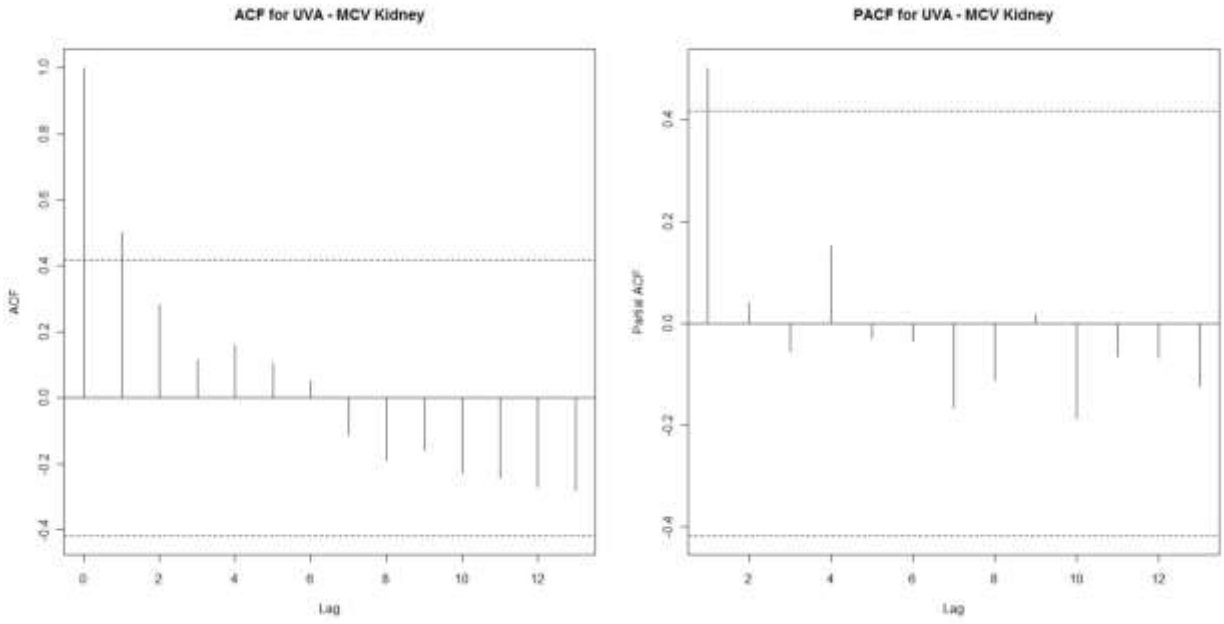

Figure 11 - ACF & PACF for UVA - MCV

```
> diff.ar

Call:
ar(x = kid.diff[1:22], method = "mle")

Coefficients:
     1
0.7336

Order selected 1  sigma^2 estimated as  239.2
```

Figure 12 - AR Model Results

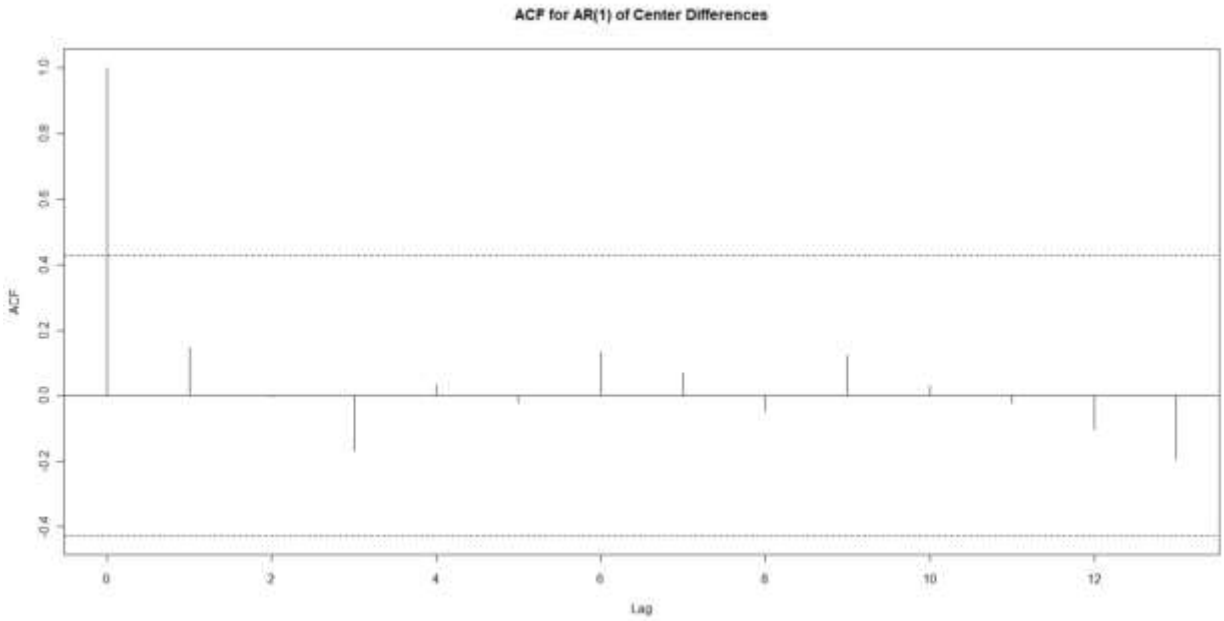

Figure 13 - ACF for the AR(1) Model

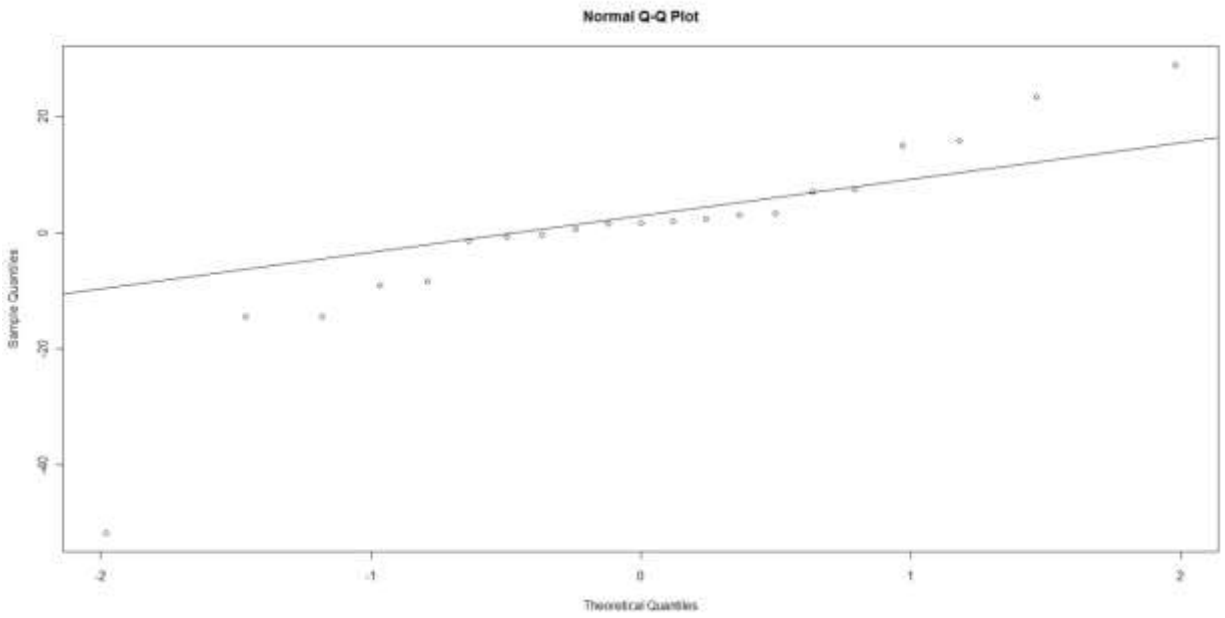

Figure 14 - Normal Q-Q Plot

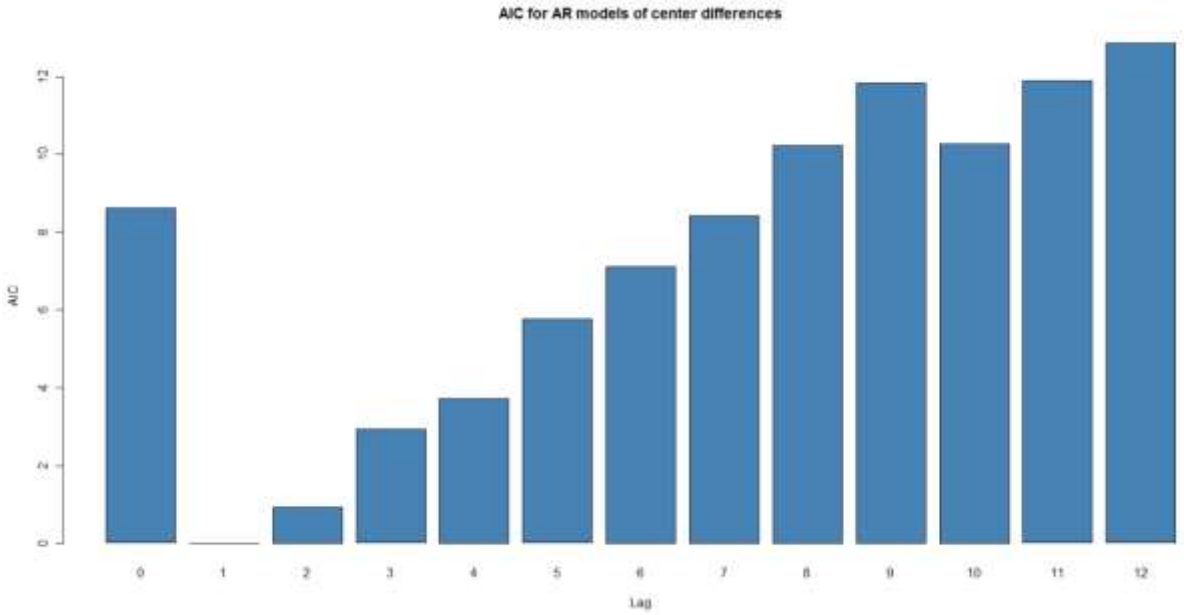

Figure 15 - AIC for AR Models of Center Differences

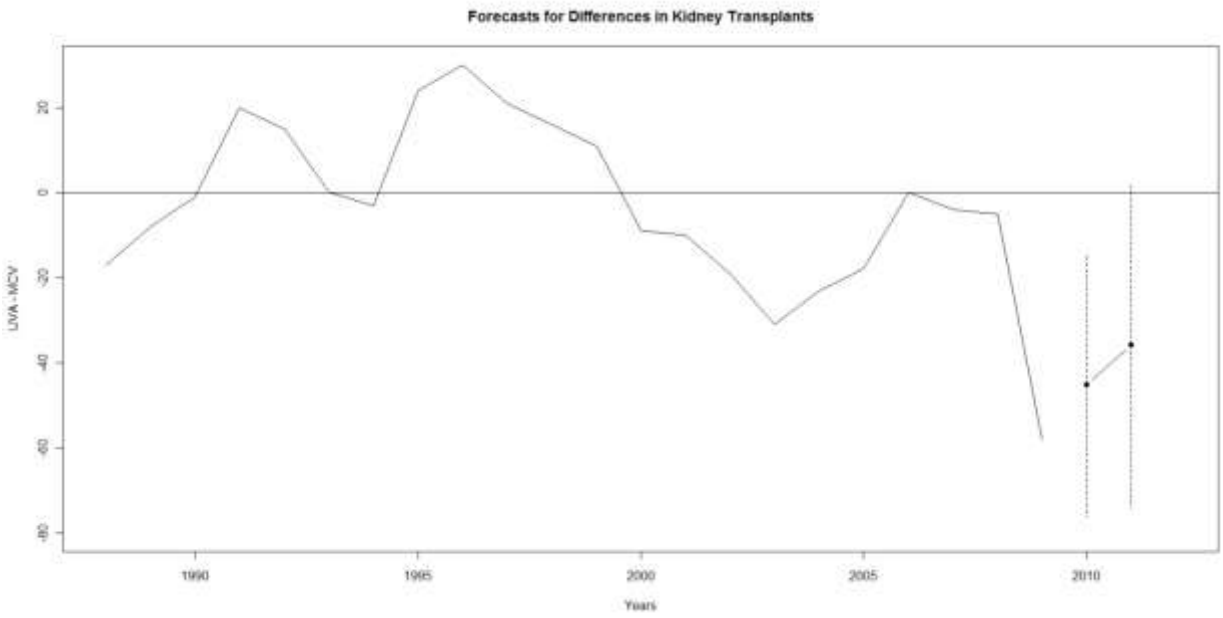

Figure 16 - Forecasts for Differences in Kidney Transplants

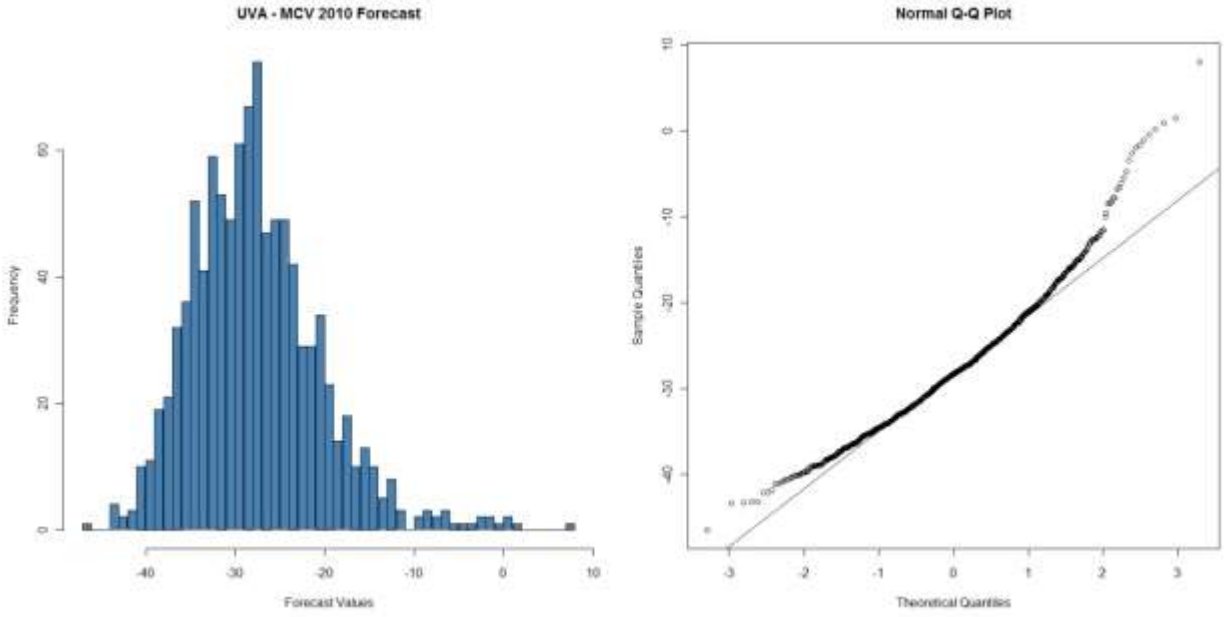

Figure 17 - Bootstrap Diagnostic Plots

```
> tsboot.ci(diff.boot)
       5%        95%
-37.97149 -15.07787
```

Figure 18 - Bootstrap Confidence Intervals

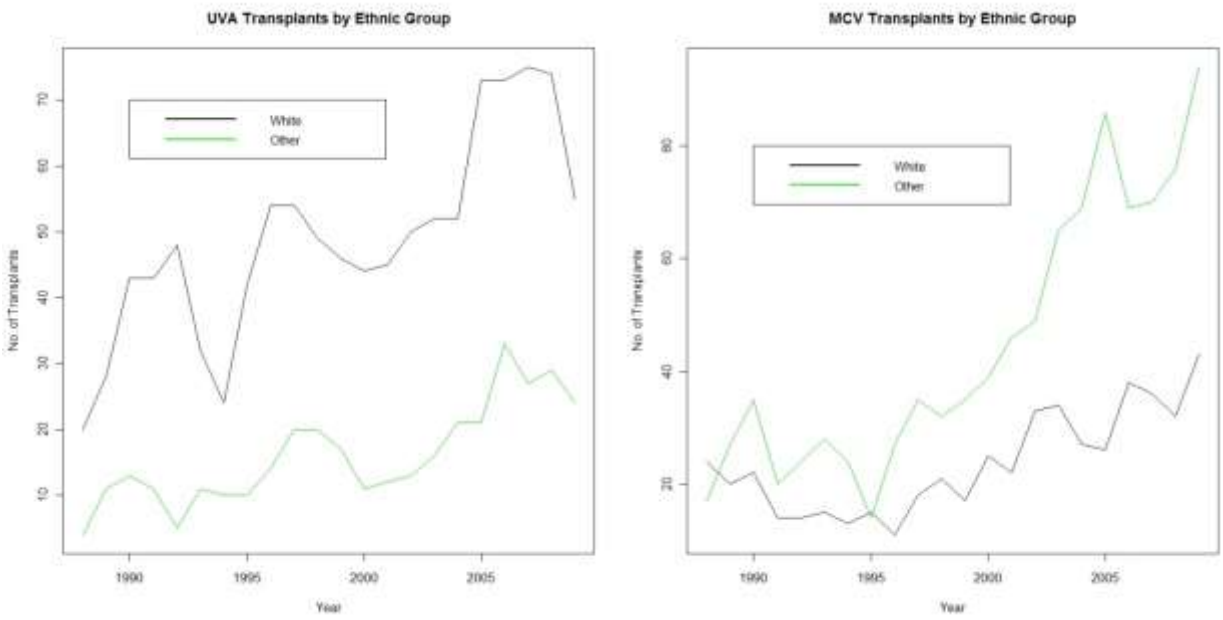

Figure 19 - MCV & UVA Transplants by Ethnic Group

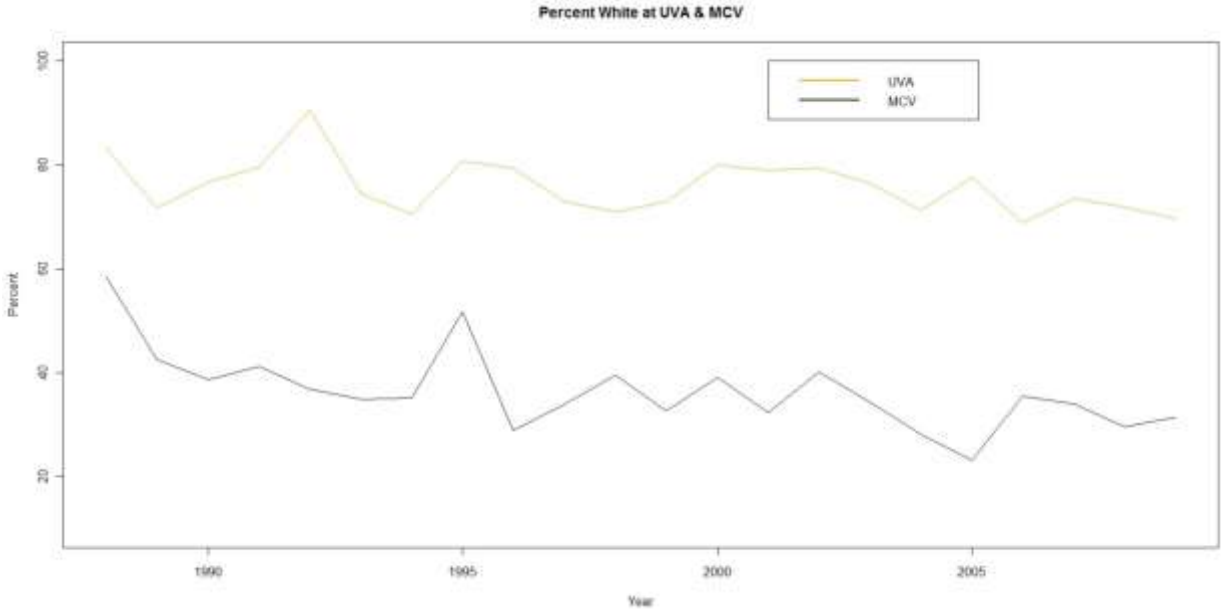

Figure 20 - Percent White MCV & UVA

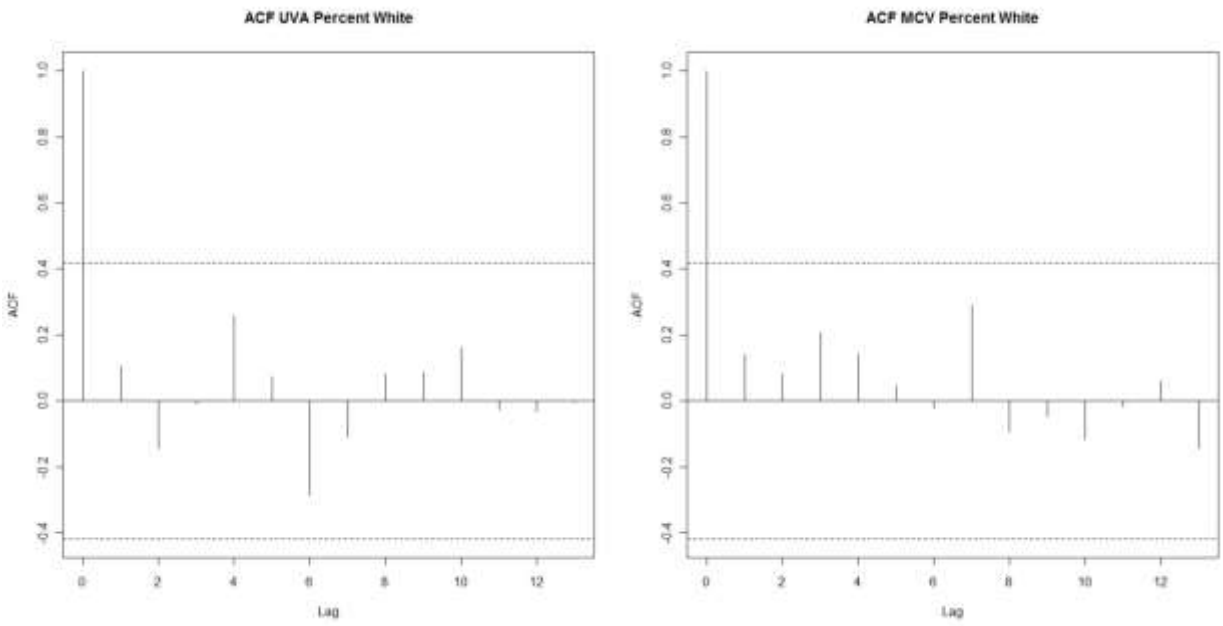

Figure 21 - ACF & PACF Percent White

```
> t.test(uvapw, mcvpw)

        Welch Two Sample t-test

data:  uvapw and mcvpw
t = 19.8783, df = 37.155, p-value < 2.2e-16
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 35.48786 43.54226
sample estimates:
mean of x mean of y
 75.99266  36.47760

> wilcox.test(uvapw, mcvpw)

        Wilcoxon rank sum test with continuity correction

data:  uvapw and mcvpw
W = 484, p-value = 1.438e-08
alternative hypothesis: true location shift is not equal to 0

Warning message:
In wilcox.test.default(uvapw, mcvpw) :
  cannot compute exact p-value with ties
```

Figure 22 - Statistical Test Results for UVA & MCV Percent White

```
> mcv.rs <- lm(mcv$Kidney[-23]~mcvpw)
> summary(mcv.rs)

Call:
lm(formula = mcv$Kidney[-23] ~ mcvpw)

Residuals:
    Min      1Q  Median      3Q     Max
-46.912 -23.062  -5.989  22.000  57.493

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 149.0505    29.1079   5.121 5.21e-05 ***
mcvpw        -2.2157     0.7816  -2.835   0.0102 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 27.55 on 20 degrees of freedom
Multiple R-squared: 0.2867,     Adjusted R-squared: 0.251
F-statistic: 8.037 on 1 and 20 DF,  p-value: 0.01023
```

Figure 23 - MCV Model 1 Results

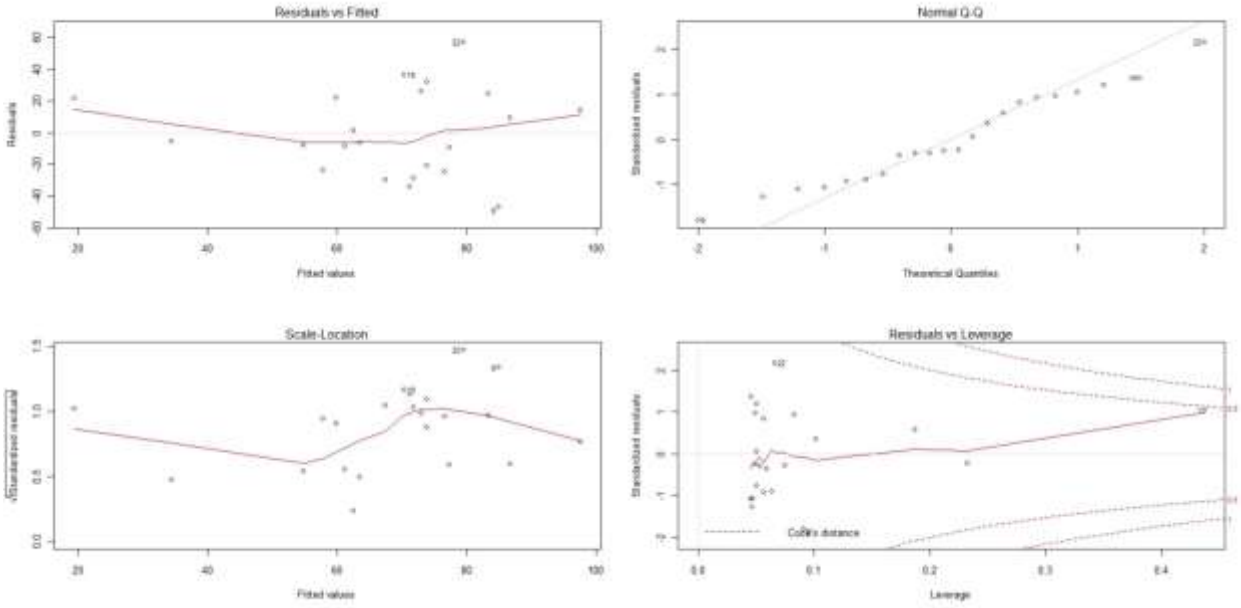

Figure 24 - Diagnostic Plots for MCV Model 1

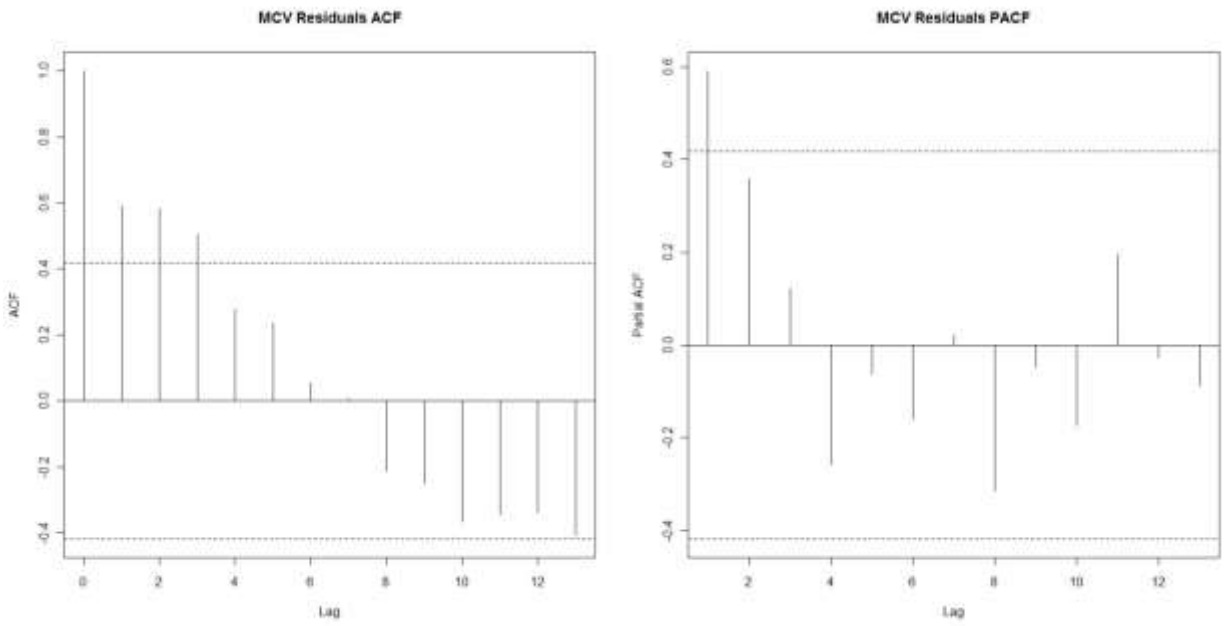

Figure 25 - ACF & PACF for MCV Model 1

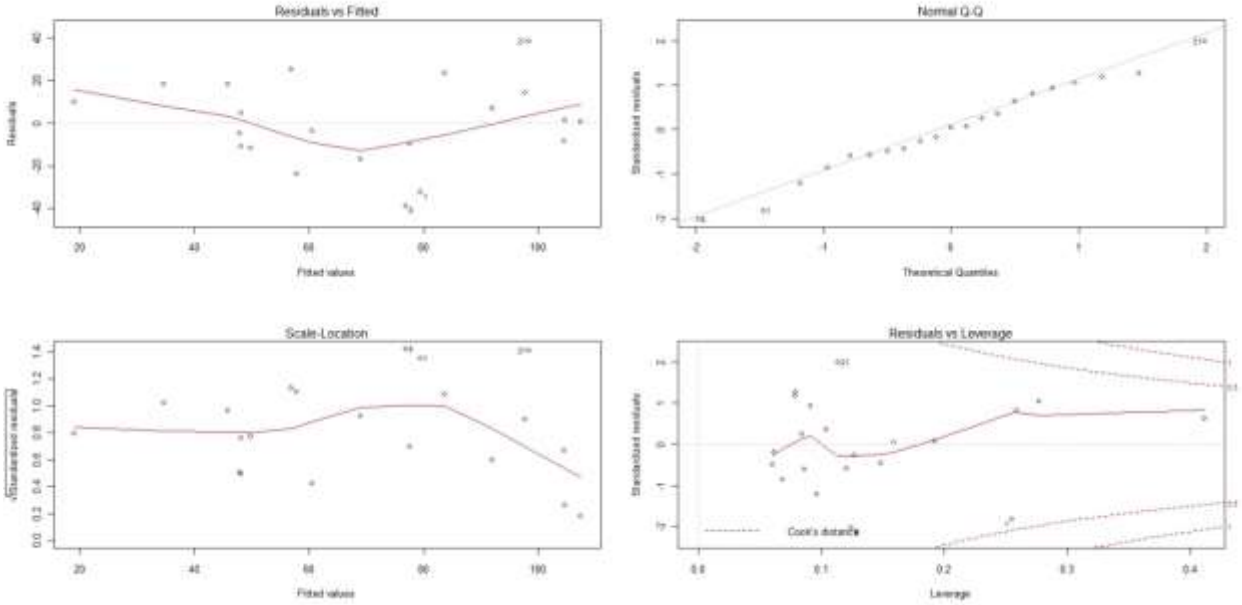

Figure 26 - Diagnostic Plots for MCV Model 2

```
> summary(mcv.rs2)

Call:
lm(formula = mcv$Kidney[-c(1, 23)] ~ mcvpw[-1] + mcv.rs$resid[1:21])

Residuals:
    Min      1Q  Median      3Q     Max
-38.841 -11.143   0.612  14.345  38.583

Coefficients:
                   Estimate Std. Error t value Pr(>|t|)
(Intercept)        124.2335    29.7641   4.174 0.000570 ***
mcvpw[-1]           -1.4795     0.8373  -1.767 0.094178 .
mcv.rs$resid[1:21]   0.8383     0.2094   4.003 0.000834 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 20.53 on 18 degrees of freedom
Multiple R-squared: 0.6298,     Adjusted R-squared: 0.5887
F-statistic: 15.31 on 2 and 18 DF,  p-value: 0.0001305
```

Figure 27 - MCV Model 2 Results

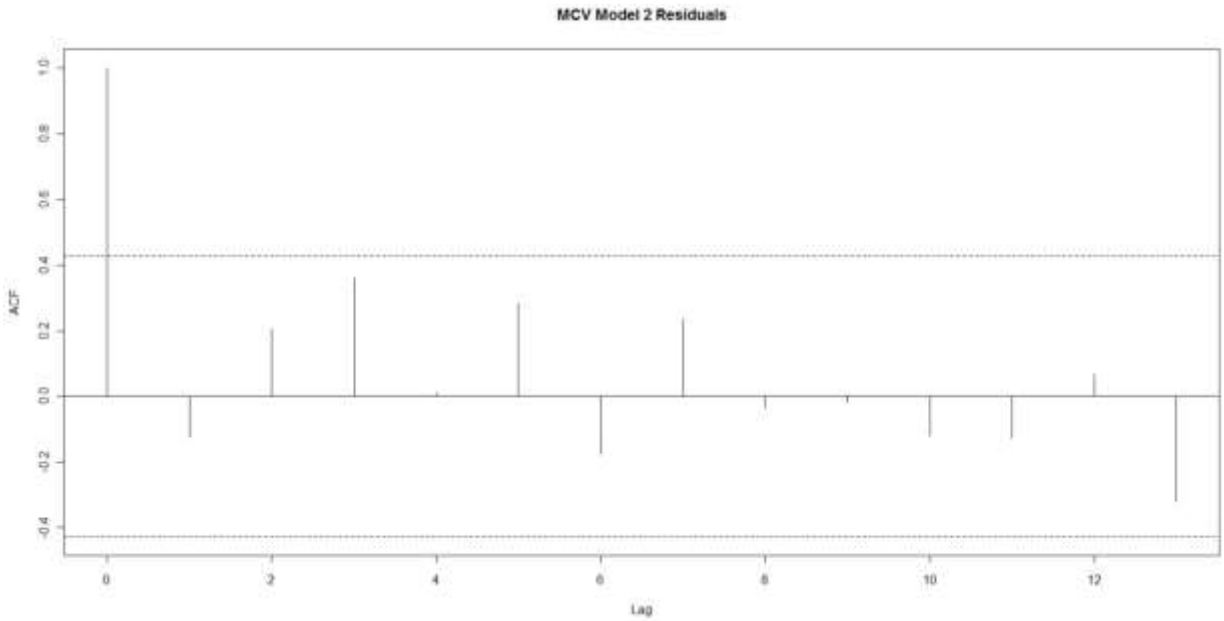

Figure 28 - MCV Model 2 Residuals

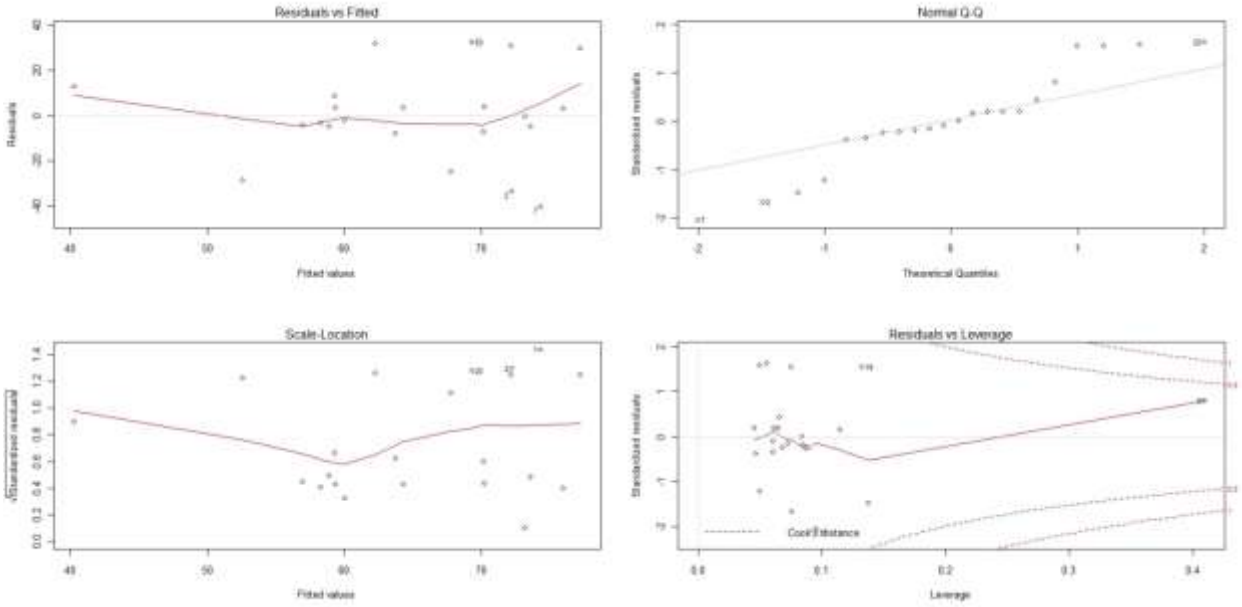

Figure 29 - Diagnostic Plot for UVA Model 1

```
> summary(uva.rs)

Call:
lm(formula = uva$Kidney[-23] ~ uvapw)

Residuals:
    Min      1Q  Median      3Q     Max
-40.292  -6.594  -1.128   7.490  32.715

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 194.4762    65.2184   2.982  0.00737 **
uvapw        -1.7026     0.8563  -1.988  0.06062 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 20.68 on 20 degrees of freedom
Multiple R-squared: 0.1651,     Adjusted R-squared: 0.1233
F-statistic: 3.954 on 1 and 20 DF,  p-value: 0.06062
```

Figure 30 - UVA Model 1 Results

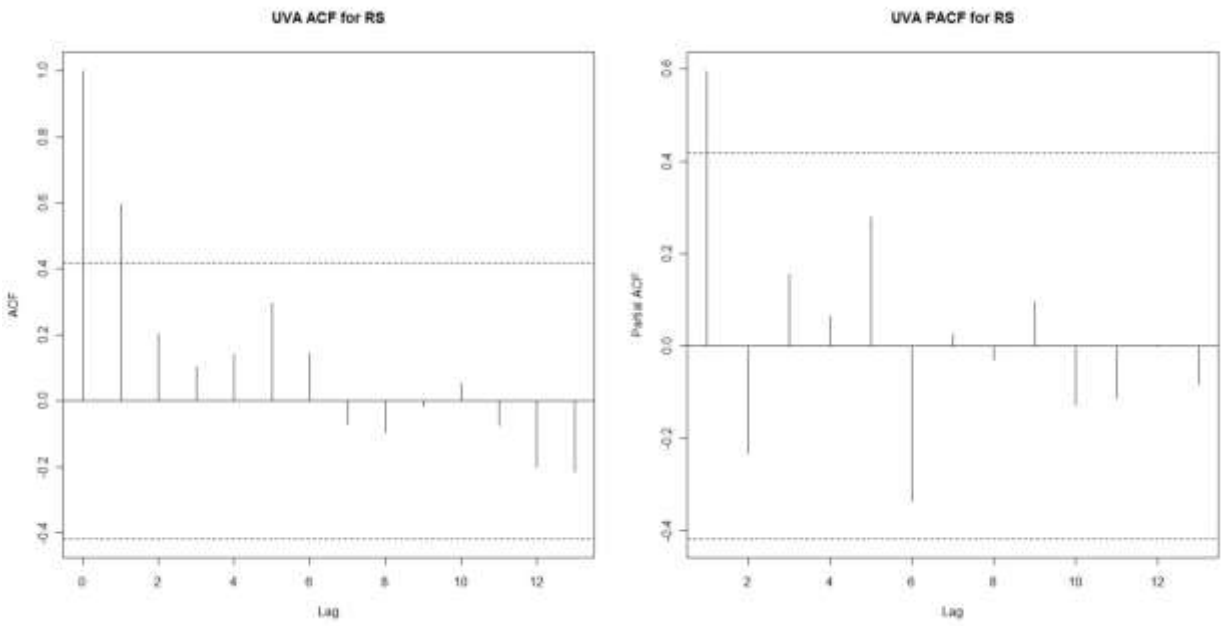

Figure 31 - ACF & PACF for UVA Model 1

```
> ar(uva.rs$resid)

Call:
ar(x = uva.rs$resid)

Coefficients:
     1
0.5955

Order selected 1  sigma^2 estimated as  276
```

Figure 32 - Time Series Model Result for UVA

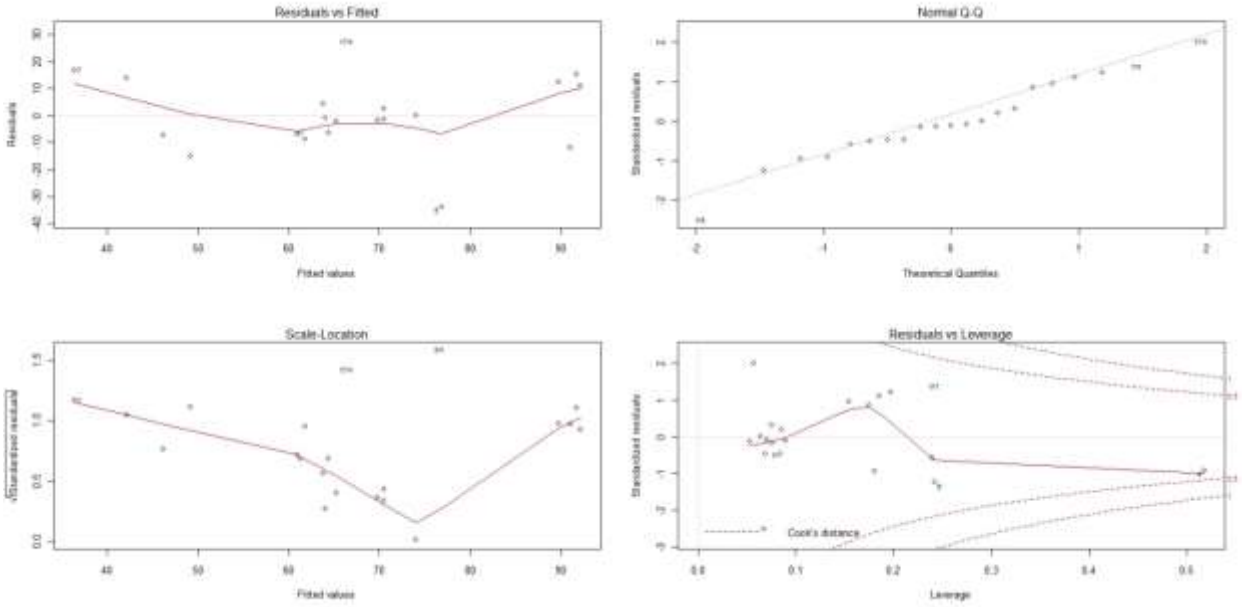

Figure 33 - Diagnostic Plots for UVA Model 2

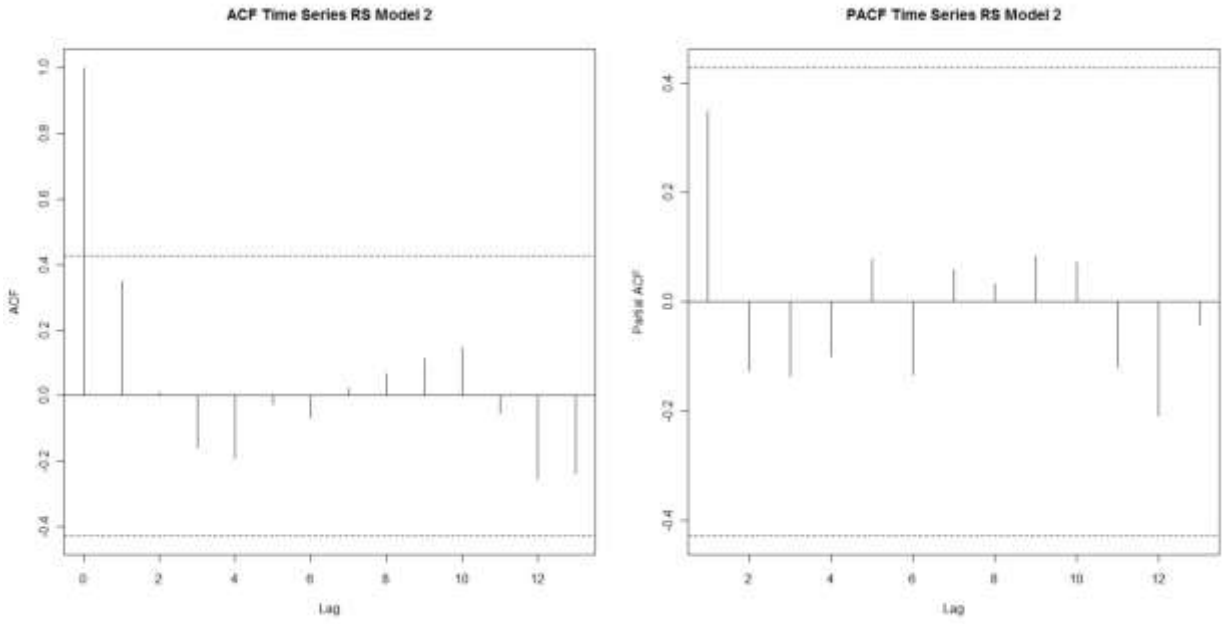

Figure 34 - ACF and PACF for UVA Model 2

```
> summary(uva.rs2)

Call:
lm(formula = uva$Kidney[-c(1, 23)] ~ uvapw[-1] + uva.rs$resid[1:21])

Residuals:
    Min      1Q  Median      3Q     Max
-33.836  -6.906  -1.500  10.879  27.214

Coefficients:
                   Estimate Std. Error t value Pr(>|t|)
(Intercept)         75.6006    50.1205   1.508 0.148810
uvapw[-1]           -0.1116     0.6615  -0.169 0.867874
uva.rs$resid[1:21]   0.7501     0.1643   4.567 0.000239 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 13.99 on 18 degrees of freedom
Multiple R-squared: 0.5843,     Adjusted R-squared: 0.5381
F-statistic: 12.65 on 2 and 18 DF,  p-value: 0.0003708
```

Figure 35 - UVA Model 2 Results

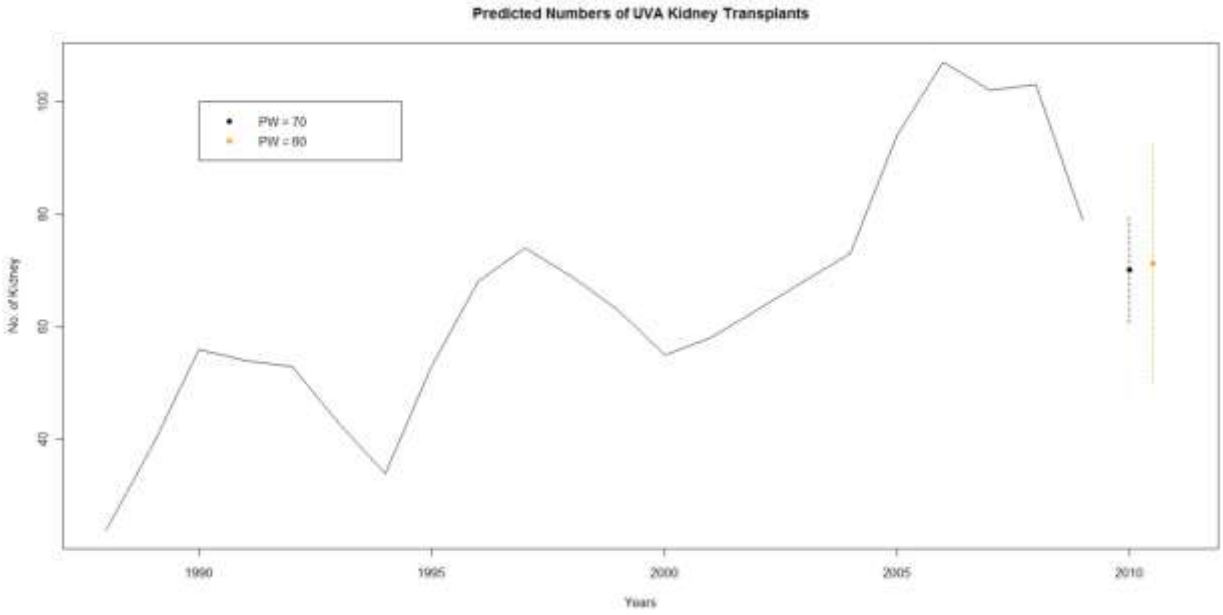

Figure 36 - Predicted Numbers of Kidney Transplants Iteration 2

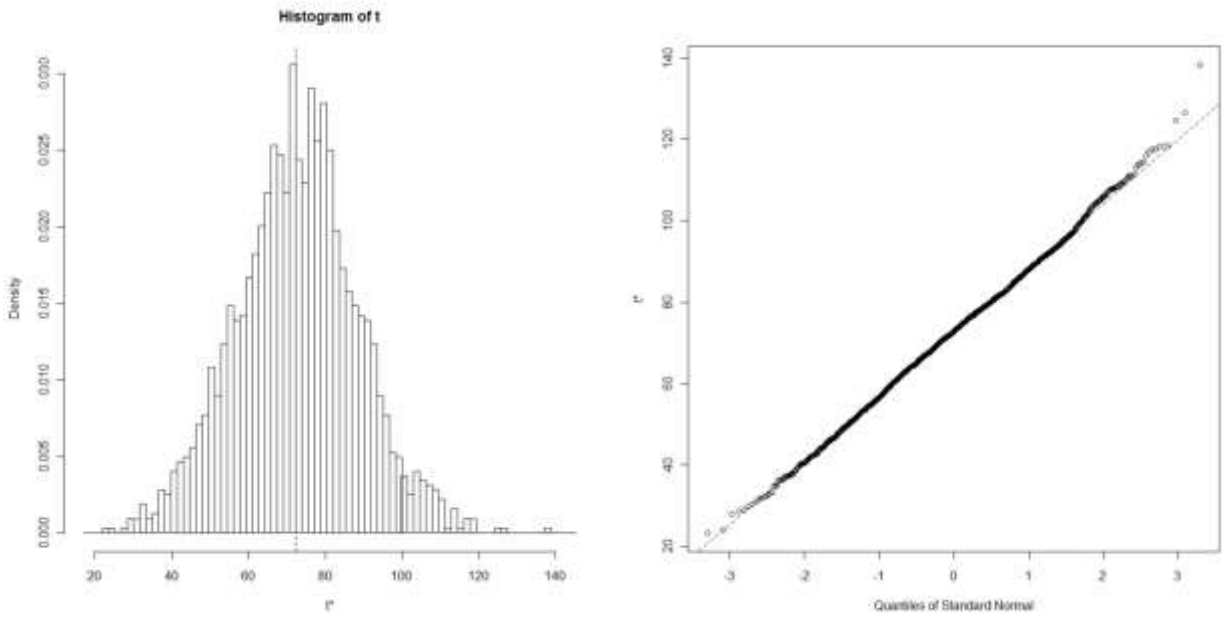

Figure 37 - Bootstrap Plot

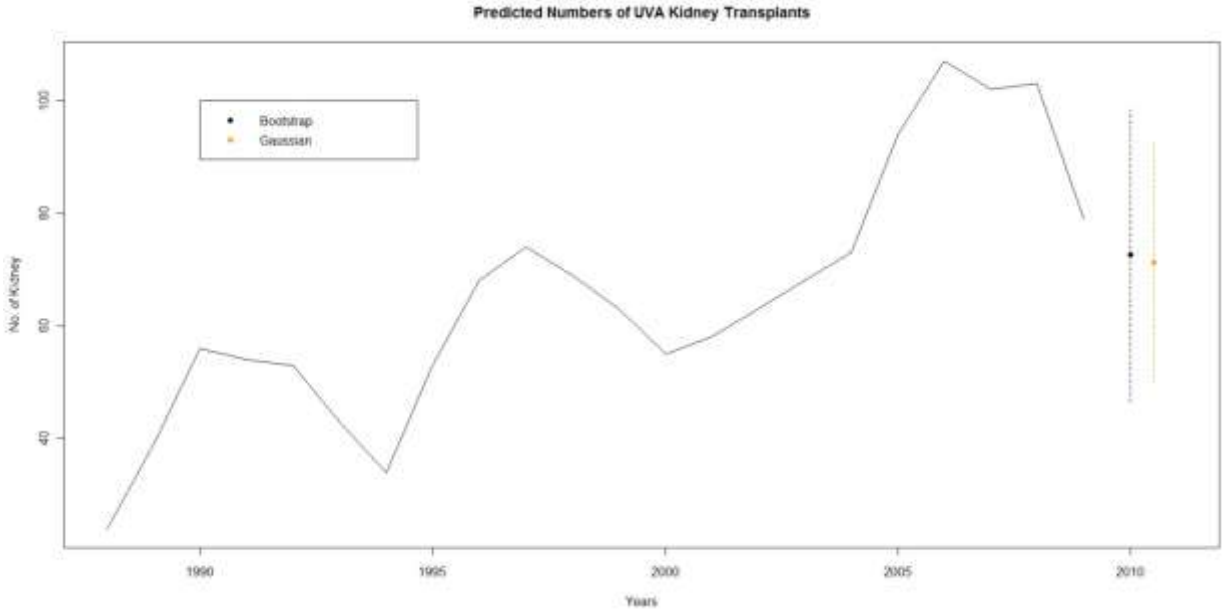

Figure 38 - Predicted Numbers of UVA Transplants using Bootstrapping Iteration 2

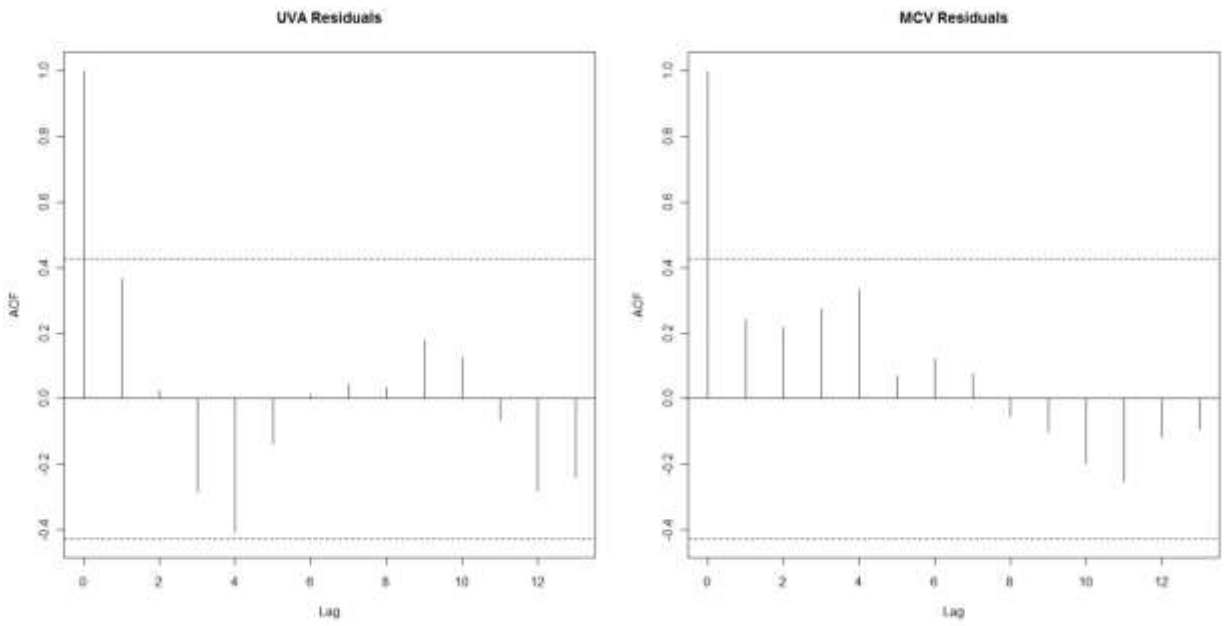

Figure 39 - UVA & MCV Residuals Iteration 3 Model

```
> var.test(uva.ar$resid[-1], mcv.ar$resid[-1])

        F test to compare two variances

data:  uva.ar$resid[-1] and mcv.ar$resid[-1]
F = 0.6338, num df = 20, denom df = 20, p-value = 0.3159
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
 0.2571538 1.5618708
sample estimates:
ratio of variances
         0.6337516
```

Figure 40 - F-Test Results for UVA & MCV Residuals

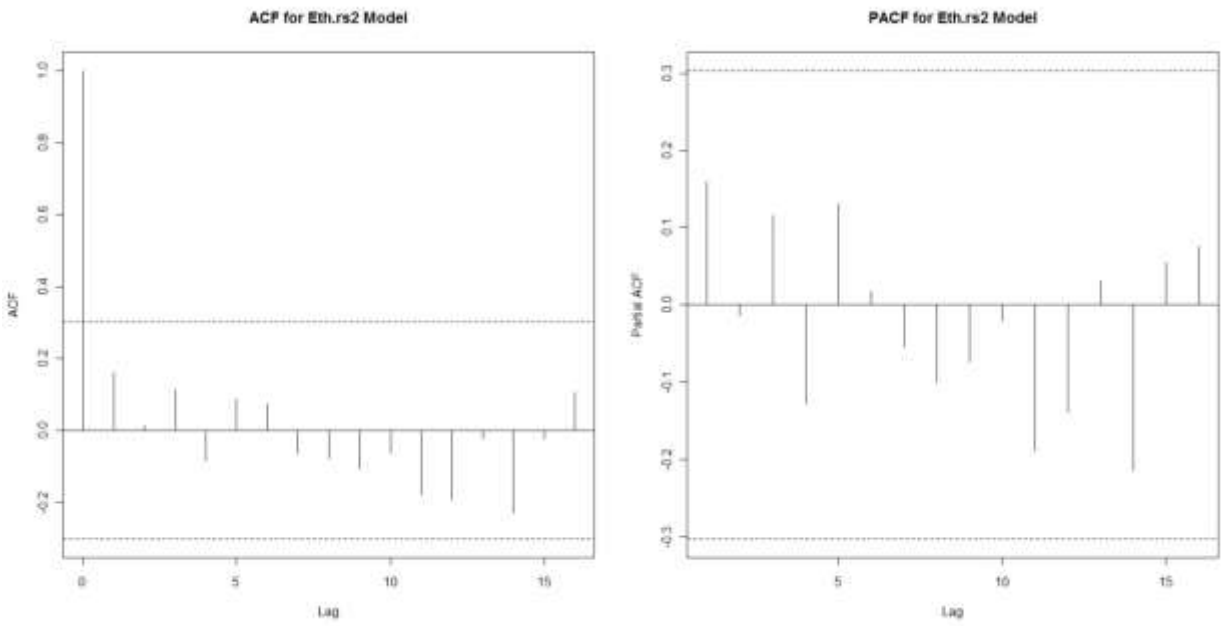

Figure 41 - ACF & PACF Plot for Eth.rs2

```
> summary(eth.rs2)

Call:
lm(formula = res ~ pw + UVA, data = eth)

Residuals:
     Min       1Q   Median       3Q      Max
-25.6638  -6.3630   0.8233   4.4898  30.4512

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  25.3146    11.7265   2.159   0.0371 *
pw           -0.6037     0.3234  -1.867   0.0694 .
UVA          22.8196    13.4781   1.693   0.0984 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 11.48 on 39 degrees of freedom
  (2 observations deleted due to missingness)
Multiple R-squared: 0.08568,    Adjusted R-squared: 0.03879
F-statistic: 1.827 on 2 and 39 DF,  p-value: 0.1743
```

Figure 42 - Linear Model Summary

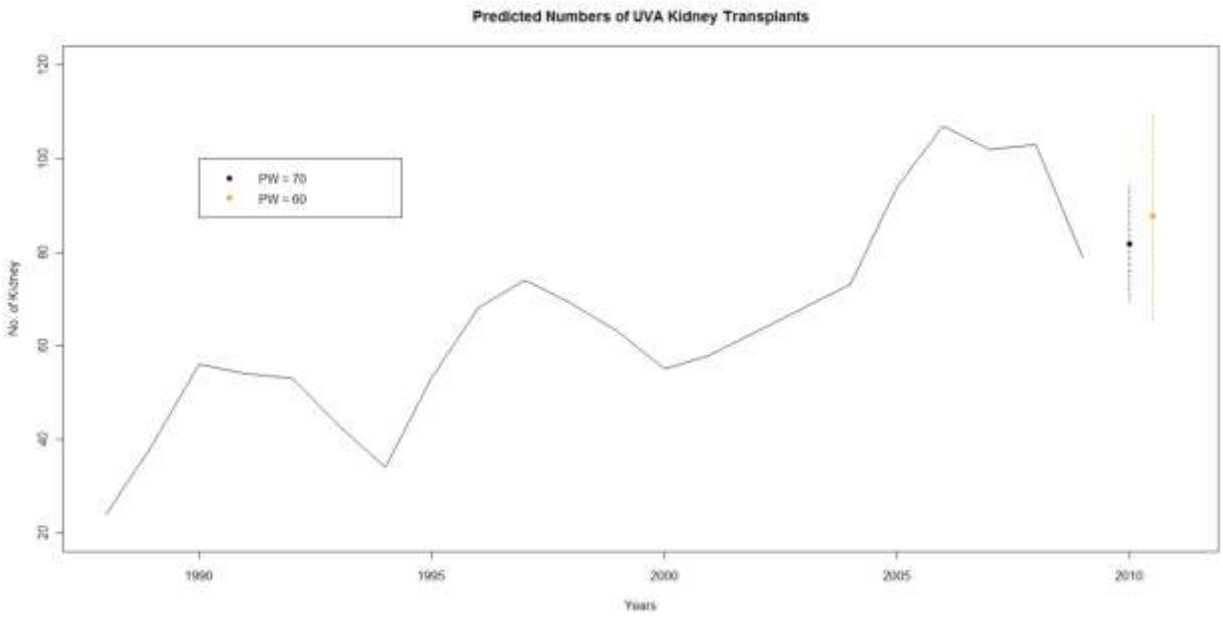

Figure 43 - Predicted Number of UVA Kidney Transplants Iteration 3

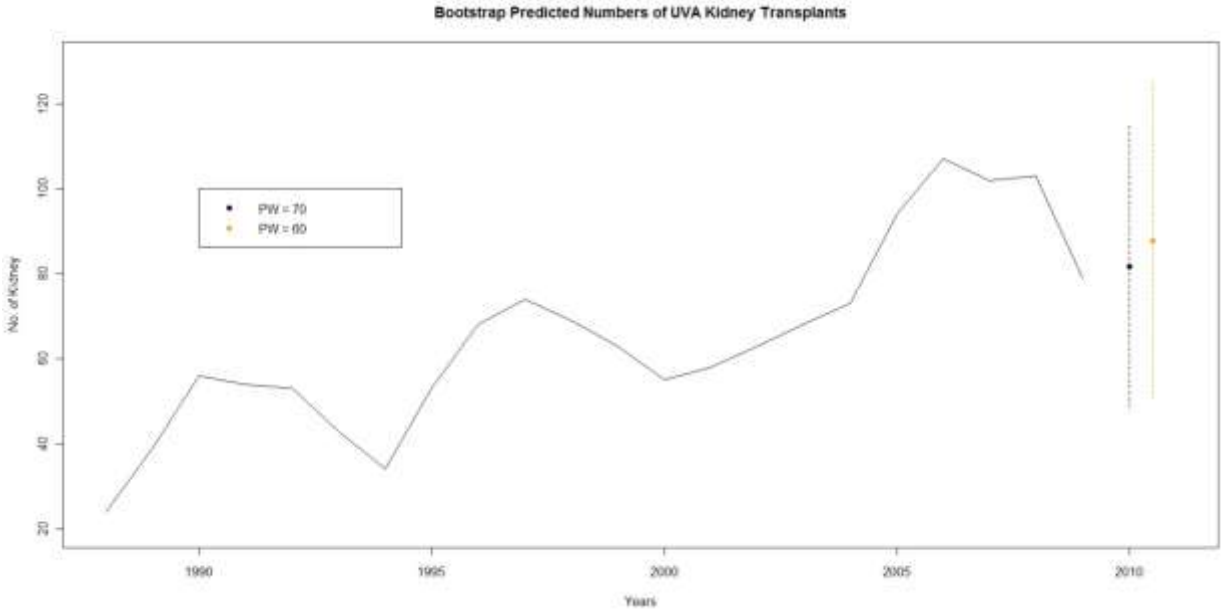

Figure 44 - Bootstrap Predicted Number of Kidney Transplants Iteration 3

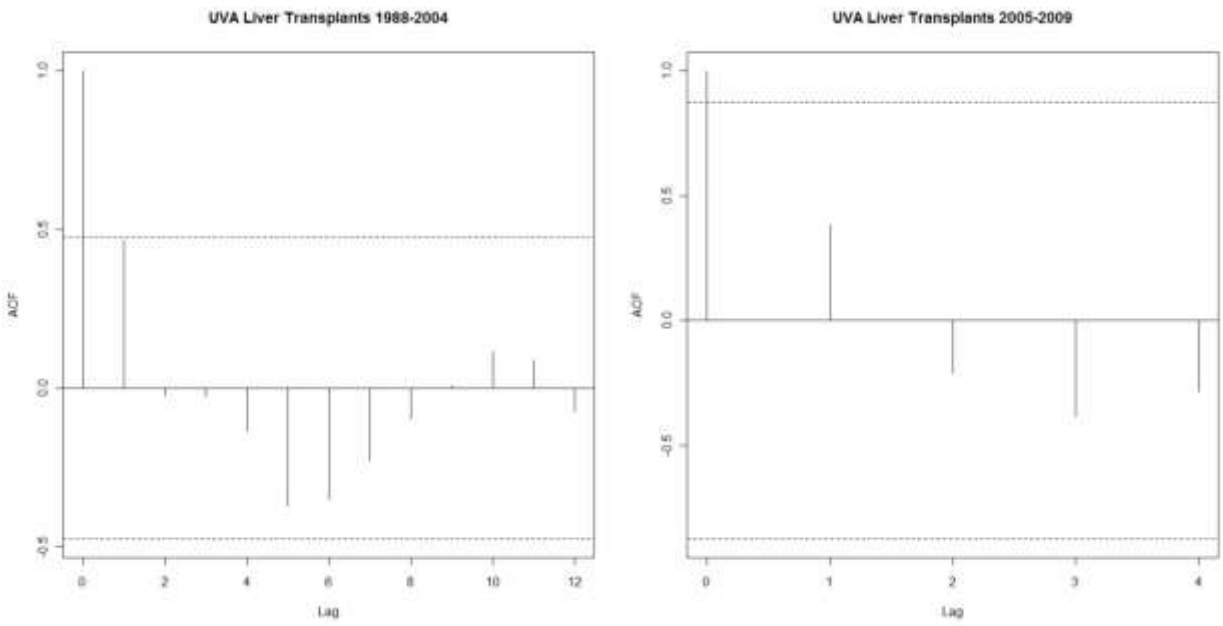

Figure 45 - Liver Transplants Data ACF

```
> t.test(uva$Liver[1:17], uva$Liver[18:22])

        Welch Two Sample t-test

data:  uva$Liver[1:17] and uva$Liver[18:22]
t = -3.3646, df = 5.655, p-value = 0.01657
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -59.873743  -9.020374
sample estimates:
mean of x mean of y
 36.35294  70.80000

> wilcox.test(uva$Liver[1:17], uva$Liver[18:22])

        Wilcoxon rank sum test with continuity correction

data:  uva$Liver[1:17] and uva$Liver[18:22]
W = 7.5, p-value = 0.006794
alternative hypothesis: true location shift is not equal to 0

Warning message:
In wilcox.test.default(uva$Liver[1:17], uva$Liver[18:22]) :
  cannot compute exact p-value with ties
```

Figure 46 - Liver Transplants Data Statistical Tests

```
> Roan <- c(rep(0, 17), rep(1, 5))
> uva.rs1 <- lm(uva$Liver[1:22] ~ Roan[1:22])
> summary(uva.rs1)

Call:
lm(formula = uva$Liver[1:22] ~ Roan[1:22])

Residuals:
    Min      1Q  Median      3Q     Max
-35.353 -12.688   0.147  15.062  29.647

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   36.353      4.339   8.378 5.67e-08 ***
Roan[1:22]    34.447      9.101   3.785  0.00116 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 17.89 on 20 degrees of freedom
Multiple R-squared: 0.4173,     Adjusted R-squared: 0.3882
F-statistic: 14.33 on 1 and 20 DF,  p-value: 0.001163
```

Figure 47 - UVA Roanoke Center Model Results

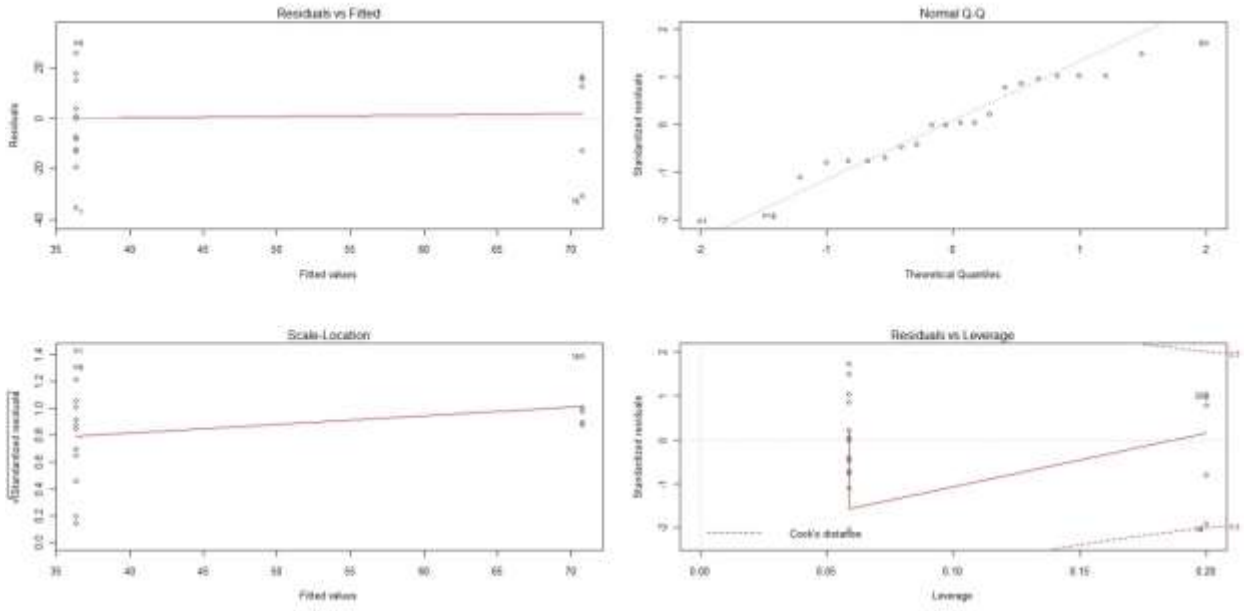

Figure 48 - Diagnostics Plot for the UVA Liver Roanoke Center Model 1

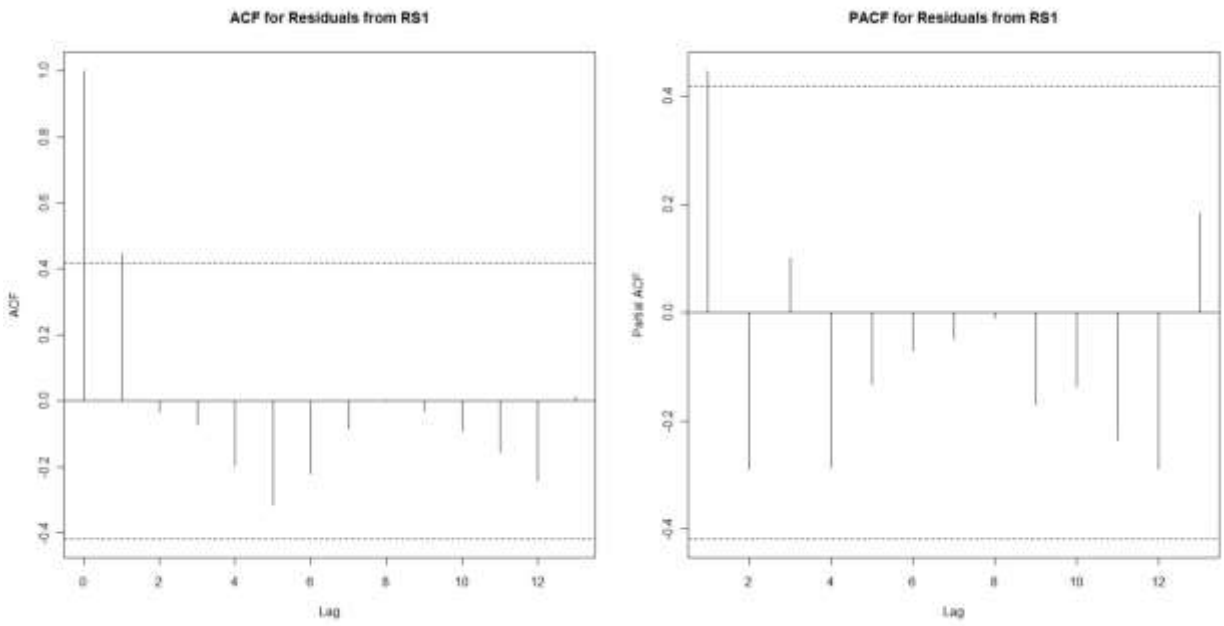

Figure 49 - UVA Roanoke Center Model 1 ACF & PACF

```
> uva.rs2 <- lm(uva$Liver[2:22]~Roan[2:22] + uva.rs1$resid[1:21])
> summary(uva.rs2)

Call:
lm(formula = uva$Liver[2:22] ~ Roan[2:22] + uva.rs1$resid[1:21])

Residuals:
    Min      1Q  Median      3Q     Max
-32.189  -9.429   1.144   7.509  27.614

Coefficients:
                   Estimate Std. Error t value Pr(>|t|)
(Intercept)         38.5521     3.5996  10.710 3.08e-09 ***
Roan[2:22]          33.8022     7.4026   4.566 0.000239 ***
uva.rs1$resid[1:21]  0.4695     0.1846   2.543 0.020381 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 14.4 on 18 degrees of freedom
Multiple R-squared: 0.5868,     Adjusted R-squared: 0.5409
F-statistic: 12.78 on 2 and 18 DF,  p-value: 0.0003509
```

Figure 50 - UVA Roanoke Center Model 2 Results

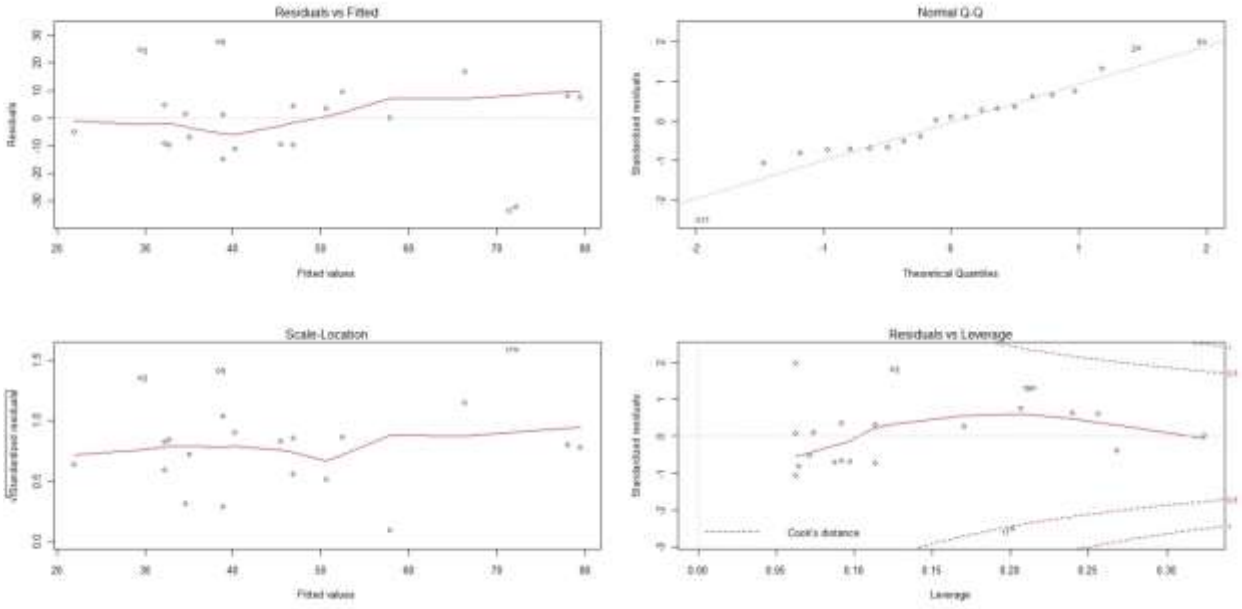

Figure 51 - Diagnostics Plot for UVA Roanoke Center Model 2

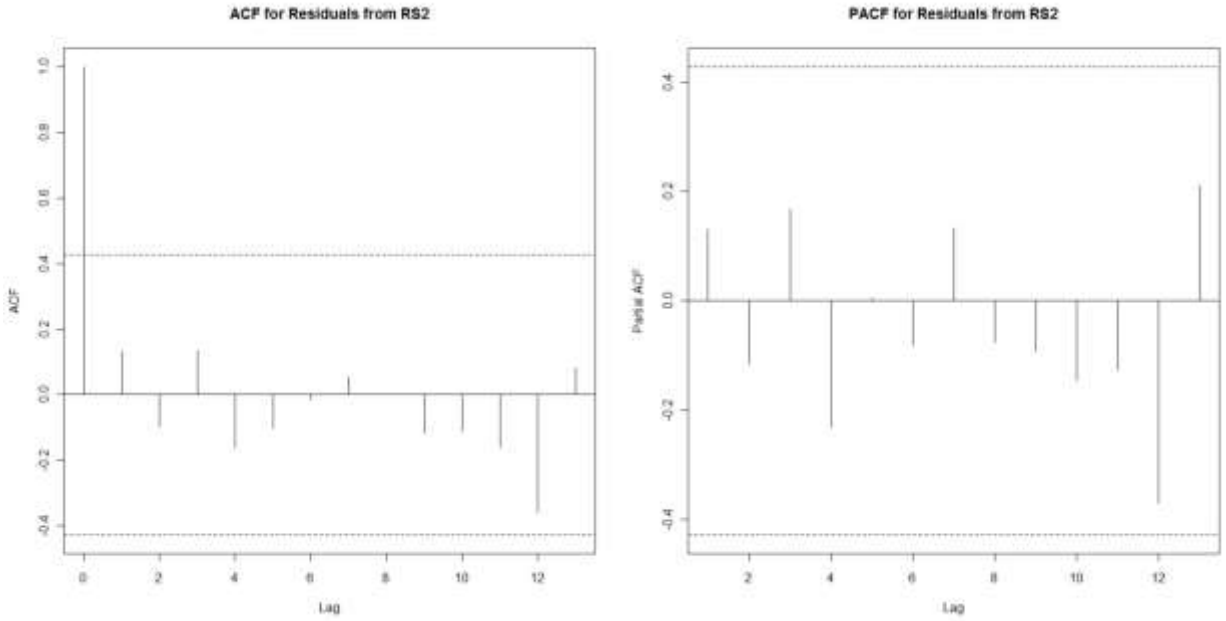

Figure 52 - UVA Roanoke Center Model 2 ACF & PACF

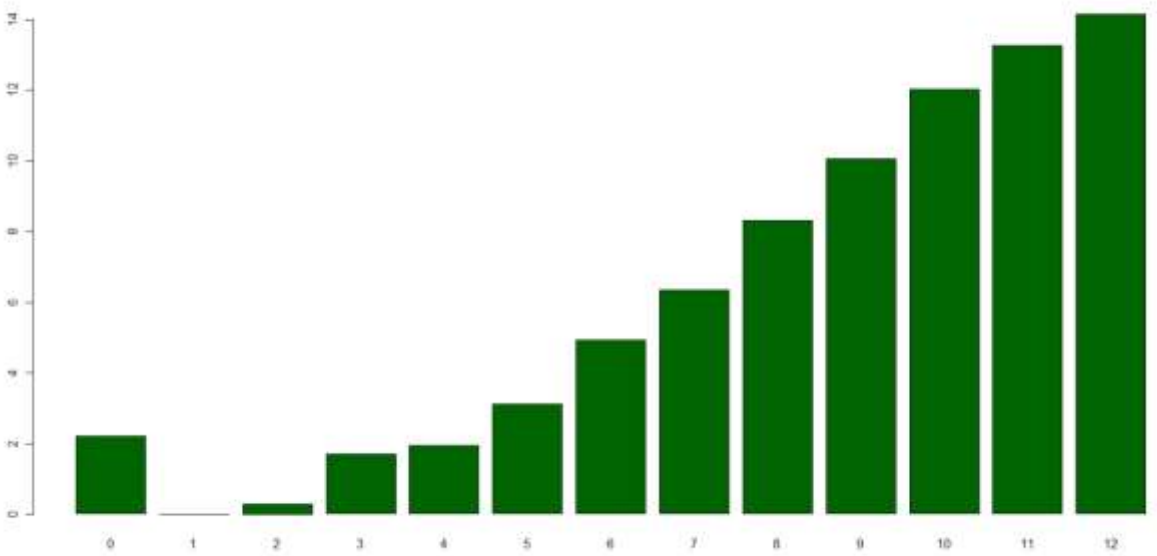

Figure 53 - AIC for AR Model for Roanoke Center

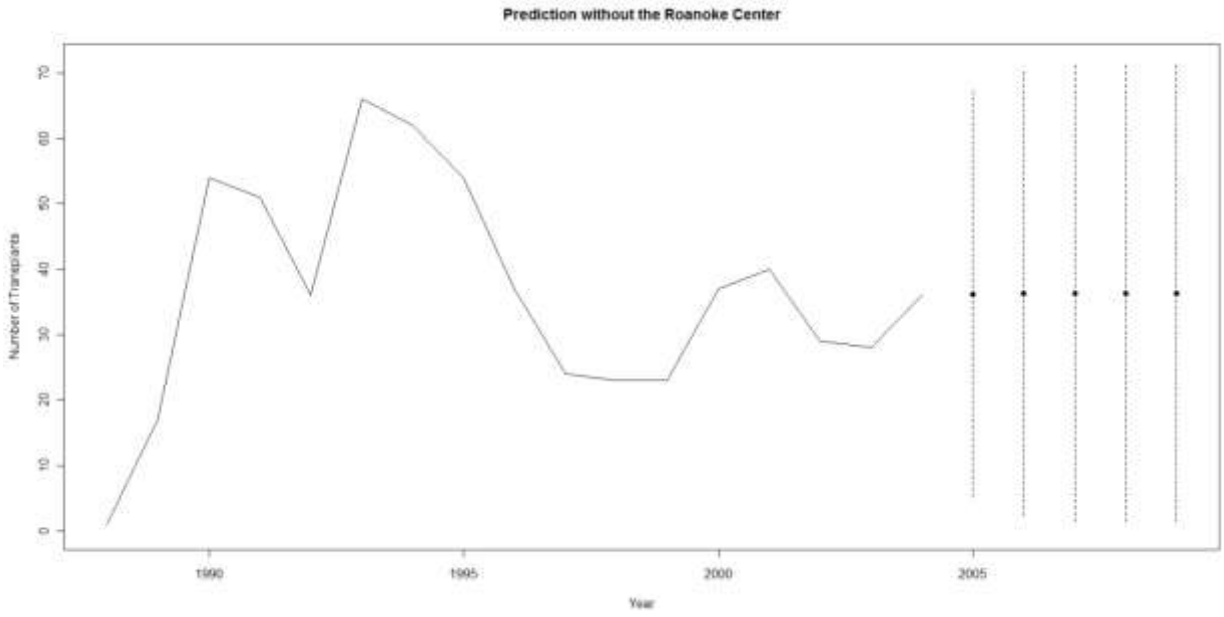

Figure 54 - Prediction without the Roanoke Center

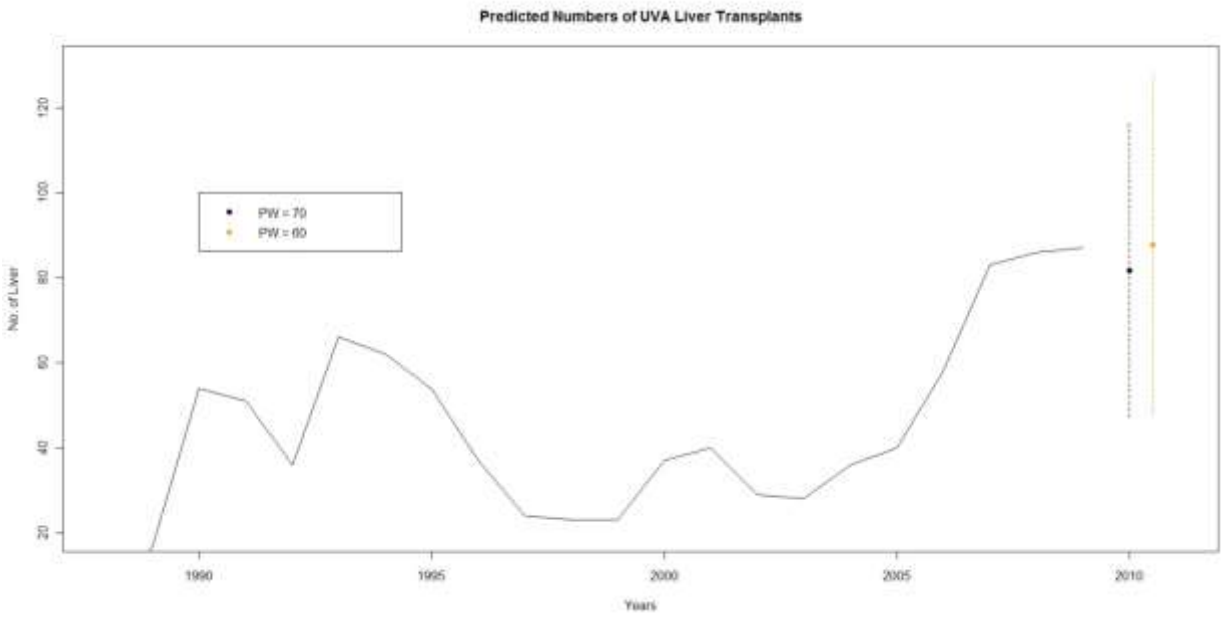

Figure 55 - Predicted of UVA Transplants Roanoke Center (PW)

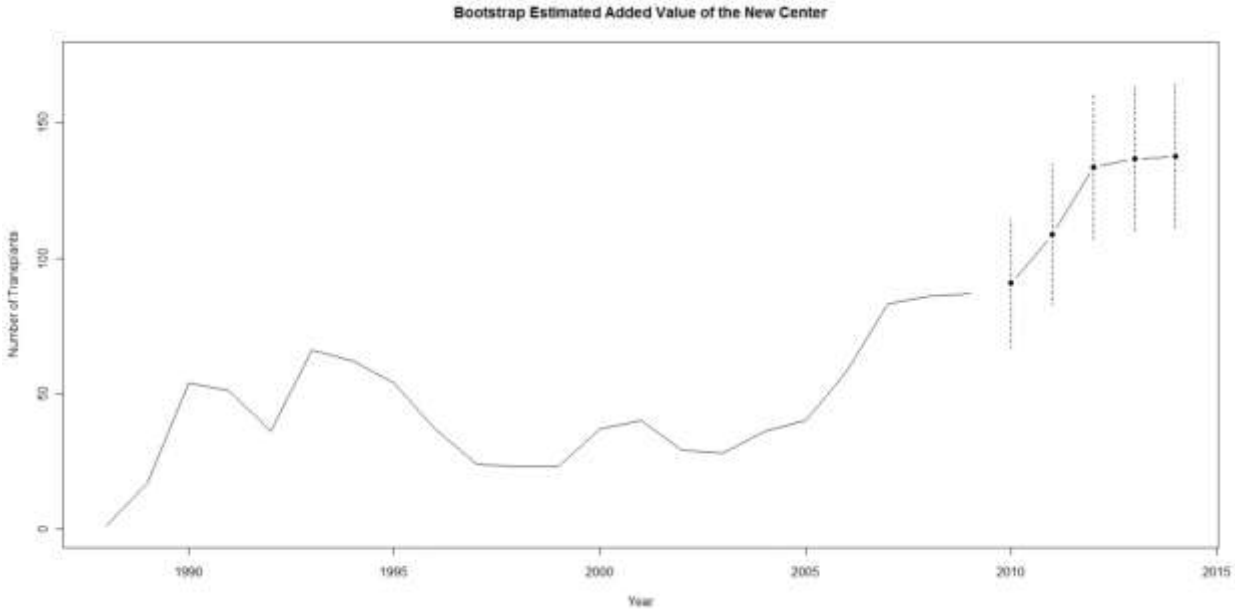

Figure 56 -Bootstrap Predicted Number of Transplants from the New Center