Advanced Data Analysis (DSC424-710)

Final Project Rough Draft (Version 0.5)

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November 13, 2018

1 Executive Summary

The cost of healthcare within the United States has become a hot button issue and major burden for many individuals and families. In 2016, the most recent year in which statistics were published, the average person spent over $10,000 a year on health expenditures (CMS 2018). At the national level, that equates to $3.3 trillion, or 17.9% of the Gross Domestic Product (GDP). The Center for Medicare and Medicaid Services (CMS) projects healthcare spending to increase by an average rate of 5.5 percent – 2.5 percentage points higher than the average rate of inflation.

With healthcare costs rising at a steady rate, understanding the contributing factors that lead to high and low medical costs are extremely important. This project sought to identify contributing factors, as well as determine if a medical cost range could be predicted based on National Health Survey data collected and made publicly available by The National Center for Health Statistics (NCHS).

A number of preprocessing actions were applied to the survey data in an effort to identify variables that were missing an inordinate number of values. Once the data was determined to be in a structure conducive to analysis, a battery of statistical models were applied to the modified survey data. Methods were applied to ensure the data contained variables that

displayed semblance of predictive power towards a survey respondent's self-reported health care costs.

The original data set contained over 33,000 observations and 127 variables. Within the preprocessing phase of the project, 46 variables were determined to be sufficient and included enough data to be valuable during the modeling phase. Correspondence analysis (CA) helped identify what variables had weak to no correlation, and principal component analysis (PCA) produced components that explained a large amount of the data's variance in eight components.

Once the preprocessing steps were complete and the data was determined to be conducive to regression analysis, a number of statistical models were applied in an attempt to predict the health care cost range for survey respondents. Model results were strong and favorable as the outcomes of Logistic Regression. It was determined that one could accurately predict a respondent's health care cost range with a subset of the variables included in the survey and a year's worth of observations. The following visualization survey to underscore the in-depth analysis completed and the process developed as a product of this analysis. Figure one displays a histogram of the proportion of columns that are missing data, Figure two displays a correlation plot between a subset of the variables, and Figure three displays a scree plot of the components created as a product of PCA.

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2 Abstract

The project group decided to analyze the 2017 Health Survey data published by NCHS, in particular the family data set. There were many interesting variables to analyze, but the group decided to focus on the Cost of family medical/dental care in the past 12 months. The project group wanted to find out what are predictors of that cost, as well as interesting

dependencies.

Among the many methods of analysis available to the group, the group settled on what was perceived to be the best and the most appropriate models for our survey data set, which included mostly categorical variables, were the following:

Comparing and contrasting variables that appeared to be pertinent and provided insight into the values present within the target variable (*FHICOST*). Variables that were not correlated with another variable above the stipulated 0.3 cutoff rate were removed from the data set.

The principal components generated by another member of the project group were used as the initial inputs into the LDA model and yielded results of approximately 37% accuracy. Removing the components and using the subset of variables that were used as inputs into the PCA model only produced a model that was one percentage point more accurate than the previous model. Using a subset of variables found in the original data set, alongside generated "dummy" variables, yielded a model with 72% accuracy.

Using similar analysis to the principal component factor I reduced the variables down to 59 variables including the *FHICOST* variable. After much exploratory analysis. I was able to reduce the variables to 29 and have 5 major factors from the 29 variables, providing around 60% cumulative variance. I used the loadings coefficients to create five factors with a cutoff of at least 0.4 or above.

Using the k-means method to do clustering analysis on the 29 continuous variables that another team member generated during the preprocessing phase.

The logistic regression model for Medical Dental cost (low and high) achieved 70% accuracy on training data. The input for the model, however, included approximately 20 variables. The generated logistic regression model executed on the test data set was not as performant, as some variables because insignificant.

Completing correspondence analysis yielded a small subset of variables that exhibited strong correlation and contained insightful information when used to complete downstream phases of the analysis. Variables that did not exhibit a correlation value greater than 0.3 were removed from analysis.

Various subsets of the original data set were used as inputs and the most favorable outcome, ergo the most accurate model, was achieved by leveraging a modified data set that also contained dummy variables. Said model achieved 72% accuracy.

The five factors generated from the variables are as follows:

1. Family Demographics
2. Family Health Needs
3. Family Coverage
4. Family with Elderly
5. Family Work Status

Furthermore, the factor analysis provided around 60% of variance explained through the five factors of 29 variables extracted from the data set.

Using k-means with k equal to three is a good way to do clustering and using three principal components demonstrates clear differention between the clusters.

The implemented logistic regression model yielded 71% accuracy, 74% sensitivity, 71% precision, and 67% specificity. Overall, the implemented model produced outcomes that were extremely favorable. Cost of medical and dental costs largely depend on if family has a private insurance or not, the family's housing status, the family type, and if a family member has sought medical help or not.

Forty-six continuous variables in the dataset were analyzed using principal component analysis with the goal of reducing the variables to a smaller set of components representing the variance of the underlying variables. Exploratory analysis revealed that five variables

should be removed due to severe imbalance of missing data, and 12 variables were removed due to low correlation with other variables. The PCA analyzed 29 variables and produced eight components, representing .64 of the cumulative proportion for the data set.

Correspondence analysis provided assurance that at least a subset of the variables were correlated and could thus be used as inputs for other phases of the project without losing a lot variance. The initial data set contained 127 variables through iterations of filtering by employing analysis like correspondence analysis, the project group was able to reduce the number of variables within the data set to approximately 40.

Along with logistic regression, linear discriminant analysis produced extremely favorable results that definitely provides a solid foundation for further analysis. After three iterations of LDA with different train and test splits and different subsets of input variables or components, the final model exhibited 72% accuracy.

Common factor analysis provided evidence that many of the numeric/continuous variables were connected and could be used to run a regression analysis with *FHICOST* against the five factors mentioned, providing interesting insight into various aspects of Healthcare cost.

The project group identified three clusters with different levels of *FHICOST* and identified those families in each cluster with 29 variables.

Logistic regression proved that there are many variables, which predict if a family spends $500 or less or more than $500 per year in medical/dental costs. Income, housing, family structure, type if insurance are among those variables which influence a family medical cost in positive or negative way.

The eight principal components identified are used to reduce the number of continuous variables into a smaller set of components that would be used to build the parsimonious data models for the analyses.

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3 Introduction

The goal of the National Health Survey is to provide estimates on health status of the United States population. It was authorized by the National Health Survey Act in 1956. Our group used the family data set from the 2017 National Health Interview Survey. Most topics in the data set are concerning family structure, education, health condition, health support from the government and income. The numeric data is geared towards health and medical services as well as various economic measurements to gauge the socioeconomic status of the household. Therefore most of the metric variables are related to the number of family members within the household that have certain healthcare needs or certain incomes. Categorical variables in the data set are most interesting because they may have the most significant effect on a dependent variable, or target. The data set includes a lot of missing values, therefore extensive data cleaning had to be performed during the preprocessing phase.

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4 Literature Review

There have been numerous studies that used the previously detailed health survey data to analyze various aspects of healthcare and its effects on the population.

For example, one study analyzed the health survey data to review the effects of complementary health on children (Black et al. 2015). The data found that the highest predictor of whether a child used complementary healthcare (i.e. alternative medicine like yoga or herbalists) was the parent. Therefore, while reviewing this data it was important to understand the effects of the household and how healthcare costs are related to the household. If a parent was having health issues, the child would also be affected.

Another such study reviewed the health survey data in an attempt to find an association

between obesity and sleep (Jean-Louis et al. 2014). Again providing evidence that the cost of healthcare has various factors that can affect it. The research also presented evidence that the cost of healthcare has other factors, such as sleep apnea or a small child in the household to feed it or change it that can cause healthcare costs to increase.

A third study provided evidence that injuries and the need for rehabilitation from those injuries increased one's cost (Ma, Chan, and Carruthers 2014). The paper found that reducing back pain and spinal injuries would reduce the cost of healthcare in totality by upwards of $200 billion. This paper therefore provided one area of focus within the data for family members that needed help with routine care or personal care needs.

In any given year, a number of research projects are completed based on the previously mentioned health survey - among them the following:

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5 Methods

After coding missing values (NA) as negative one (-1), correspondence analysis was conducted on a subset of the variables in an attempt to identify correlation between different variables. The model summaries that contained the results of two variables were reviewed to determine if correlation existed between the two variables that were used as inputs. Once correspondence analysis was applied to each variable, the variables that did not exhibit 0.3 or greater correlation were removed from the data set.

Multiple iterations were executed where the input variables changed, as well as the training and testing splits. The project group employed LDA as a model and also explored the results produced from enabling the cross validation parameter to gain insight into the variables the model identified to be the most impactful.

After processing 59 numerical variables, multiple principal component and factor analyses were executed to pair down the original data set to 29 variables that provided above a 0.40 loading within a factor while also providing around 60% variance explanation for those 29 variables. This process was done by running multiple analyses of factor analysis.

After preprocessing variables, there are 29 numeric variables with the same scale (# count in each family), exhibiting signs of a data set conducive to factor analysis.

Logistic regression was performed on the modified family health survey data set. The Medical Expense Cost variable was transformed to a binary variable. The logistic regression model was executed using binned categorical variables and numerical variables on a data set containing 26,000 observations and 128 variables. A substantial amount of time was spent on preprocessing the data set. Logistic regression identified 23 significant variables as key influencers of the dependent variable.

Parsimonious variable selection is considered a best practice for building efficient and interpretable statistical models. Principal component analysis (PCA) is a common method for reducing the number of variables in a data set down to a few representative components that maximize the variance between the underlying variables. PCA was used as a preprocessing step to reduce the number of variables used in some of the statistical models for this study, while also preserving the variance of the original underlying variables in the data set.

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6 Discussion and Results

Executing correspondence analysis did not allow the project group to explicitly determine if a health spending range could be determined from the other variables in the data set. That was not the intent of this particular exercise. Correspondence analysis did however provide evidence that a subset of the variables were correlated to some extent. This analysis was

helpful and insightful and allowed the group to gain greater understanding of the relationship between different variables and the potential trends that may be present within the data set. Further analysis would almost certainly include correspondence analysis if a new data set were introduced, or if additional variables were added to the existing data set.

Executing linear discriminant analysis produced favorable results that answered the primary research directly - based on the results of the national health survey, one can predict the health spending range of a family or individual. Cross validation was applied to the subset of variables used as inputs for the lda model to identify what variables the model found to be the most impactful in determining the target variable's class.

The model did not exhibit extremely strong accuracy, and that would most likely be the main focus of future analysis that included this data set. What additional data sets exist that could be used to augment the data set analyzed by the project group to increase the accuracy of a model?

The factor analysis conducted on the data set did not directly answer or explain the research question, as it did not provide strict predictability of what exactly is the cost of healthcare. Factor analysis did however provide factors that could be used in a regression to find the factors' effects on healthcare costs.

The factor analysis did show that 29 variables within the study can be used to predict approximately 60% of the variable contribution to healthcare costs and can be broken out by the five factors and their effects. It would be interesting and insightful to augment the current data set with detailed family demographic information.

The first cluster analysis tested k with a range from two to ten to find the best k to do the analysis. From the cluster figure1(screeplot of Within-groups sum-of-squares), one can determine that setting k equal to three and five might be good candidates. Since the response variable *FHICOST* has six levels, the final analysis was run on three different k s - 3, 5, and 6. The visualizations of the cluster analysis were plotted using three significant

principal components. The clusters are split clearly, as shown in figures 16 through 19 in the *Visualization Appendix*. If one plotted assigned color to the points by the levels of *FHICOST*, the points are not easily separated, according to cluster-figure5. Refactoring *FHICOST* was a necessary step and after refactoring, one can finally start to identify patterns within the data.

Cluster 1 can be named as small size family with normal health condition and living condition. They have the most proportion of low cost in health and medical care. This kind of family might have fewer people and they are in normal health condition and without too much disabilities. Cluster 2 can be named as big size family with stable source of income and good heath condition. This kind of big family need to cover all family members' health cost so it's much more than other clusters. They also have enough health insurance to cover their cost. Cluster 3 can be named as medium size family with some family members in poor health condition or disability. This family has much more problems with living. They might have more old people who can't work but need to be taken care of. So this kind of family will spend more money in health care than cluster 1.

According to the analysis, one can identify important features in classifying different levels of *FHICOST*, which can help continue feature engineering for other models.

The binary logistic regression model was first executed on the test data set, which included 80%, or 211,184 observations. Out of this model, very few variables were determined to be significant. The confusion matrix, figure 23 in the *Visualization Appendix*, showed the the model correctly predicted 7,194 observations as false negative, and 8,304 observations as true positives (figure 24). The final model was produced using the following equation:

$$
\begin{aligned}
Final = &-0.15 * FHIMILCT + 0.19 * FHIPRVCT - 0.57 * FHIIHSCT \\
&- 0.16 * FHICADCT - 0.34 * FM\_STRCP\_12 + 0.40 * FM\_STRCP\_21 \\
&+ 0.17 * FM\_STRP\_41 - 0.22 * CURWRKN\_2 - 0.16 * TELCELN\_2 \\
&- 0.45 * FHCPHRYN\_2 - 0.57 * FHOSP2YN\_2 + 0.18 * FSBALANC\_3
\end{aligned}
$$

$$-0.50 * HOUSEOWN\_2 - 0.30 * HOUSEOWN\_3 + 0.37 * FSNAP\_2$$
$$+0.42 * INCGRP4\_2 + 0.63 * INCGRP4\_3 + 0.77 * INCGRP4\_4$$
$$+1.1 * INCGRP4\_5 - 0.42 * FINTR1YN\_2 - 1.08 * FMEDBILL\_2$$
$$-1.14 * FMEDBPAY\_2 - 0.30 * FSAF\_2$$

Families who spend more than $500 in 12 months prior to survey:

- Lower the number of family member in Military less likely the family is to spend $500 in medical cost.
- Higher the number of family members with private insurance more likely the family is to spend $500 in medical cost.
- Lower the number of family members with Indian Health Service, less likely the family is to spend $500 in medical cost.
- Lower the number of family members with Medicaid, less likely the family is to spend $500 in medical cost.
- When a person is living with a roommates, less likely the family is to spend $500 in medical cost.
- Married couples are more likely to spend $500 in medical cost.
- A parent, step parent and children are more likely to spend $500 in medical cost.
- If there is no working phone or cell phone less likely family is to spend $500 or more for health insurance.
- If any family member did not get advice or test in 2 weeks or stayed in hospital in 12 months, less likely family spent 500 in medical cost.
- If a family always was able to afford to eat balanced meal, more likely they spend $500 in medical cost.
- If a family rents house or apartment less likely they spend $500 or more in medical cost.
- If a any family member did not receive food stamps more likely the family spends $500 or more for medical care.

- If total combined family income is more then $35,000 per year then more likely the family spends $500 or more.
- If any family member received income from interest bearing account more likely the family spends $500 in medical cost
- If family does not have any problem in paying medical bills, less likely spends $500 or more.
- If family does not pay medical bills over the time less likely they spend $500 or more.
- If family does not have flexible spending account less likely spends $500 or more.

There was not significant correlations between variables (figure 25) and the variance inflation factors (VIF) were under 5.

6.0.1 Training Data Set Statistics (figure 26)

Confusion matrix summary: $TP = 8,232$, $TN = 7,021$, $FP = 3,205$, and $FN = 2,726$

$Sensitivity = 8232/(8232 + 2726) = 8232/10958 = 0.75$

$Accuracy = (8232 + 7021)/(8232 + 7021 + 3205 + 2726) = 15253/21184 = 0.72$

$Precision = 8232/(7021 + 3205) = 8232/10226 = 0.80$

$Specificity = 7021/(7021 + 3205) = 7021/10226 = 0.68$

6.0.2 Test Data Set Statistics (figure 27)

$Sensitivity = 0.74$

$Accuracy = 0.71$

$Precision = 0.71$

$Specificity = 0.67$

The above statistics show that the logistic regression model performed fairly well on test data set.

With an original dataset of well over 100 variables, exploratory analysis was conducted to determine which variables could be easily removed as either insignificant for the study, or containing a large imbalance of missing values that would make the variable unusable for analysis purposes. While categorical variables could be used for regression and other modeling approaches, it was determined that the continuous variables would be analyzed using principal components analysis to reduce the original 46 continuous variables to a few components which would be representative of the variance within the original variables. The relationships between the variables were examined using a correlation matrix and plot (figure 28 in the *Visualization Appendix*). The correlation plot in the *Visualization Appendix* clearly identifies variables with strong and weak correlations between the variables. As a result, 12 variables were removed from the PCA that had weak correlations with other variables of less than .30. After removing five more variables that had greater than 30% of observations missing, the final data set used for the PCA contained 29 variables. The PCA was run with a loading value cutoff of .3, which produced 29 total components. Of the initial 29 components, 12 components contained .792 of the cumulative variance for the variables (figure 30). The scree plot shown in PCA Figure 2 identifies eight components with an eigenvalue of greater than or equal to 1. These eight components compose .639 of the cumulative variance for the variables. A few variables were found to be cross loaded on multiple components at the .3 loading score level. It was observed that most of the cross loadings had loading scores below .5, which were then addressed by rerunning the model with a loading score cutoff of .5. The final model only contained two cross loaded variables. These variables were assigned to components according to their highest load scores.

The factor analysis and the principal component analysis that were done did result in similar factors/components for what the factor analysis described as Family Health Needs, therefore

showing that these two analyses did result in similar components/factors. It would then be important to run potentially a future regression with the factors and components and find how these factors/components do affect healthcare cost. The project team did find that factor analysis could explain around 60% of the data using five factors, while the principal component analysis provided 64% with eight factors so it may be important to keep reviewing and re-writing the analysis to find a happy medium to provide that needed variance percentage while also providing good factors/components to research.

In order to make our analysis simpler, the group refactored *FHICOST* from six levels to two levels. So the project team could only analyze and predict whether the family spent more than $500 in medical/dental care last year, which is a main limitation of the research. For further study in this area, one could try to predict the original six levels of *FHICOST*, but additional changes may arise, like imbalanced data since there are not many families spending a lot of money (more than $5,000) in our data set. In addition to these challenges, LDA and logistic regression models do not have a very high accuracy (around 70%) in predicting the levels. On the one hand, one can add some extra data set which may have strong correlation with *FHICOST*. Demographic data, geographic data and insurance data are examples of data sets that may allow future analysis to represent families more accurately. In addition to data set augmentation, the project group could improve implemented models by making full use of feature engineering work. One major shortcoming of the research conducted was not full implementation of PCA and FA results to represent all of the continuous variables as a part of input for logistic regression. Ideally, this could be completed in the future. Machine learning techniques like decision tree, random forest and gradient boost may aid in the development of classification models as well.

For cluster analysis, only 29 continuous variables were used as input, thus the model ignored many useful categorical and ordinal variables. The results of the cluster analysis are not very good at differentiating two levels of *FHICOST* clearly. If one were to try cluster analysis

on categorical data using Jaccard dissimilarity, interesting and insightful patterns may be discovered. In addition to the previously mentioned shortcomings, the project group did not check other categorical variables to see if the clusters might differ, which could potentially provide the group with useful insights for other research topics. The variables vary a lot in different clusters, which could also be used for future analysis.

The dataset is quite wide with 127 variables, but the project group only focused on *FHICOST* (Cost of family medical/dental care in the past 12 months) since this variable can be used for many medical related businesses. Medical services companies might want to know what kind of families spend a lot of money in medical care. The developed LDA and logistic regression models could help said companies target these kind of families more efficiently so they could develop business arrangements with them to increase their profits. For insurance companies, they could also utilize the developed cluster analysis and LDA to design corresponding insurance plans for different kinds of families to increase their profits. When they collect information from customers, they can easily see whether the customers will spend lots of money in medical care and ask the insurance company to reimburse these payments.

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7 Conclusion

In this paper, the project group analyzed the family data set for the National Health Survey Data with the goals of identifying factors that contribute to healthcare costs for families and determine predictable medical cost ranges for families. Using various statistical modeling techniques, we determined that logistic regression yielded the strongest model for predicting the health care cost range for survey respondents. The logistic regression model showed that less fortunate individuals who earn less than $35,000 per year, have Medicaid or food stamps, have private insurance, who do not have a landline or cell phone, who rent, or live with

roommates who have substandard nutrition habits, who are not married, have problems with paying medical bill make up the population who spend less than $500 for Medical/Dental cost in a year. The project group also determined that one could accurately predict a respondent's health care cost range with a subset of the variables included in the survey and a year's worth of observations. Additional statistical models were used for examining the data set. After executing correspondence analysis and linear discriminant analysis, the project group was able to determine that some of the variables did display correlation with other variables. While this was an insightful and helpful step in our project, it did not present a model yielding strong results. Linear discriminant analysis showed some semblance of accuracy, but ultimately additional data sets, information, or insight might be required to attain results that demonstrate a model is able to achieve consistently high accuracy. Cluster analysis was used to define families having different levels of *FHICOST*. Families with more members having health insurance coverage, more members in good health and more members working tend to spend more money on medical care, while families with more members having disabilities and working limitations tend to spend less. The analyses in this study could be improved through future work to bring in data sets from other sources that could be analyzed and compared with the National Health Survey Data to help determine significant factors and variables which can help predict annual health care costs for families.

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8 Appendix

Please find the code used to complete the analysis discussed throughout this paper below:

8.1 Cluster Analysis

```
## read data
setwd("~/Desktop/MSPA/advanced data analysis/final/data")
library(tidyverse)
library(corrplot)
library(plyr)
library(plotly)
library(ggplot2)
library("RColorBrewer")


data <- read.csv("family_modified_001.csv")
data <- data[-which(data$FHICOST > 5), ]


## Select numeric variables
NewSub <- data[, c("FM_SIZE", "FCHLMCT", "FSPEDCT",
    "FLAADLCT", "FLIADLCT", "FWKLIMCT", "FWALKCT",
    "FREMEMCT", "FANYLCT", "FHSTATEX", "FHSTATVG",
    "FHSTATG", "FHSTATFR", "FHSTATPR", "FHICOVCT",
    "FHIPRVCT", "FHIEXCT", "FHISINCT", "FHICARCT",
    "FHICADCT", "FHICHPCT", "FHIMILCT", "FHIIHSCT",
    "FHIPUBCT", "FHIOGVCT", "FHIEBCCT", "FHDSTCT",
    "FDGLWCT1", "FDGLWCT2", "FWRKLWCT", "FSALCT", "FSEINCCT",
```

```
    "FSSRRCT", "FPENSCT", "FOPENSCT", "FSSICT", "FTANFCT",
    "FOWBENCT", "FINTR1CT", "FDIVDCT", "FCHSPCT", "FINCOTCT",
    "FSSAPLCT", "FSDAPLCT", "FWICCT", "FM_ELDR")]

## convert to Matrix
DataMatrix <- as.matrix(as.data.frame(NewSub))

## Remove Variables with missing values coded as -1
NewSub1 <- NewSub[-c(2, 27, 3, 45, 30)]
DataMatrix <- as.matrix(as.data.frame(NewSub1))

## correlation plot
CorData <- cor(DataMatrix)
corrplot(CorData, method = "circle", tl.cex = 0.5)

## Drop Variables with correlation <.3 Final PCA Set
PCASet <- NewSub1[-c(match(c("FHIEXCT", "FHIMILCT",
    "FHIIHSCT", "FHIPUBCT", "FHIOGVCT", "FDGLWCT2",
    "FSEINCCT", "FTANFCT", "FOWBENCT", "FINTR1CT",
    "FCHSPCT", "FINCOTCT"), names(NewSub1)))]
DataMatrix <- as.matrix(as.data.frame(PCASet))

## corrplot again
CorData <- cor(DataMatrix)
corrplot(CorData, method = "circle", tl.cex = 0.5)

## Add FHICOST;Normalize data
```

```r
std <- apply(PCASet[, -30], 2, sd)  # finding standard deviations of variables
PCASet.std <- sweep(PCASet[, -30], 2, std, FUN = "/")

my.k.choices <- 3:10
n <- length(PCASet.std[, 1])
wss1 <- (n - 1) * sum(apply(PCASet.std, 2, var))
wss <- numeric(0)
for (i in my.k.choices)
{
    W <- sum(kmeans(PCASet.std, i)$withinss)
    wss <- c(wss, W)
}
wss <- c(wss1, wss)
plot(c(1, my.k.choices), wss, type = "l", xlab = "Number of clusters",
    ylab = "Within-groups sum-of-squares", lwd = 2)

## FHICOST has 6 levels so try k = 6 first
PCASet.k6 <- kmeans(PCASet.std, centers = 6, iter.max = 500,
    nstart = 25)

## According to the plot, we ccan choose k = 3,5
PCASet.k3 <- kmeans(PCASet.std, centers = 3, iter.max = 500,
    nstart = 25)

## Also want to try k = 5
PCASet.k5 <- kmeans(PCASet.std, centers = 5, iter.max = 500,
    nstart = 25)
```

```
## Run pca
health.pc <- princomp(PCASet.std, cor = T)


## 3d plot of k = 3,5,6
colors <- brewer.pal(n = 6, name = "Set2")
pc <- data_frame(health.pc$scores[, 1], health.pc$scores[,
    2], health.pc$scores[, 3], PCASet.k6$cluster)
colnames(pc) <- c("pc1", "pc2", "pc3", "cluster")
p <- plot_ly(pc,
             x = ~pc1,
             y = ~pc2,
             z = ~pc3,
             color = ~cluster,
             colors = colors) %>%
  add_markers() %>%
  layout(scene = list(xaxis = list(title = "pc1"),
                      yaxis = list(title = "pc2"),
                      zaxis = list(title = "pc3")))
p


colors <- brewer.pal(n = 5, name = "Set2")
pc <- data_frame(health.pc$scores[, 1], health.pc$scores[,
    2], health.pc$scores[, 3], PCASet.k5$cluster)
colnames(pc) <- c("pc1", "pc2", "pc3", "cluster")
p <- plot_ly(pc, x = ~pc1, y = ~pc2, z = ~pc3, color = ~cluster,
    colors = colors) %>% add_markers() %>%
```

```
    layout(scene = list(xaxis = list(title = "pc1"),
    yaxis = list(title = "pc2"), zaxis = list(title = "pc3")))
p

colors <- brewer.pal(n = 3, name = "Set2")
pc <- data_frame(health.pc$scores[, 1], health.pc$scores[,
    2], health.pc$scores[, 3], PCASet.k3$cluster)
colnames(pc) <- c("pc1", "pc2", "pc3", "cluster")
p <- plot_ly(pc, x = ~pc1, y = ~pc2, z = ~pc3, color = ~cluster,
    colors = colors) %>% add_markers() %>%
    layout(scene = list(xaxis = list(title = "pc1"),
    yaxis = list(title = "pc2"), zaxis = list(title = "pc3")))
p

## Prepare data for checking the percentage of
## diffenrent levels of FHICOST
dt6 <- data_frame(as.numeric(data$FHICOST), PCASet.k6$cluster)
colnames(dt6) <- c("FHICOST", "cluster")
dt5 <- data_frame(as.numeric(data$FHICOST), PCASet.k5$cluster)
colnames(dt5) <- c("FHICOST", "cluster")
dt3 <- data_frame(as.numeric(data$FHICOST), PCASet.k3$cluster)
colnames(dt3) <- c("FHICOST", "cluster")

## FHICOST percentage in each cluster
## tapply(dt6$FHICOST, dt6$cluster, table)
dt6 %>% group_by(cluster) %>% table() %>% prop.table(.,
    1)
```

```
dt6 %>% group_by(cluster) %>% table() %>% prop.table(.,
    2)

# tapply(dt5$FHICOST, dt5$cluster, table)
dt5 %>% group_by(cluster) %>% table() %>% prop.table(.,
    1)
dt5 %>% group_by(cluster) %>% table() %>% prop.table(.,
    2)

dt3 %>% group_by(cluster) %>% table() %>% prop.table(.,
    1)
dt3 %>% group_by(cluster) %>% table() %>% prop.table(.,
    2)

## 3d plot of FHICOST using 3 principal components
colors <- brewer.pal(n = 6, name = "Set2")
pc <- data_frame(health.pc$scores[, 1], health.pc$scores[,
    2], health.pc$scores[, 3], data$FHICOST)
colnames(pc) <- c("pc1", "pc2", "pc3", "FHICOST")
p <- plot_ly(pc, x = ~pc1, y = ~pc2, z = ~pc3, color = ~FHICOST,
    colors = colors) %>% add_markers() %>%
    layout(scene = list(xaxis = list(title = "pc1"),
    yaxis = list(title = "pc2"), zaxis = list(title = "pc3")))
p

## rescale by the size of FHICOST level
colors <- brewer.pal(n = 6, name = "Set2")
```

```r
dt <- as.numeric(data$FHICOST) + 1
pc <- data_frame(health.pc$scores[, 1], health.pc$scores[,
    2], health.pc$scores[, 3], dt)
colnames(pc) <- c("pc1", "pc2", "pc3", "FHICOST")
p <- plot_ly(pc, x = ~pc1, y = ~pc2, z = ~pc3, color = ~FHICOST,
    size = ~FHICOST, colors = colors) %>% add_markers() %>%
    layout(scene = list(xaxis = list(title = "pc1"),
        yaxis = list(title = "pc2"), zaxis = list(title = "pc3")))
p

## refactor FHICOST from six levels to three levels
data <- within(data, {
    y3 <- NA
    y3[FHICOST <= 1] <- "low"
    y3[FHICOST <= 3 & FHICOST > 1] <- "Middle"
    y3[FHICOST > 3] <- "high"
})

colors <- brewer.pal(n = 3, name = "Set2")
pc <- data_frame(health.pc$scores[, 1], health.pc$scores[,
    2], health.pc$scores[, 3], data$y3)
colnames(pc) <- c("pc1", "pc2", "pc3", "FHICOST")
p <- plot_ly(pc, x = ~pc1, y = ~pc2, z = ~pc3, color = ~FHICOST,
    colors = colors) %>% add_markers() %>%
    layout(scene = list(xaxis = list(title = "pc1"),
    yaxis = list(title = "pc2"), zaxis = list(title = "pc3")))
p
```

```r
dt6 <- data_frame(data$y3, PCASet.k6$cluster)
colnames(dt6) <- c("FHICOST", "cluster")
dt5 <- data_frame(data$y3, PCASet.k5$cluster)
colnames(dt5) <- c("FHICOST", "cluster")
dt3 <- data_frame(data$y3, PCASet.k3$cluster)
colnames(dt3) <- c("FHICOST", "cluster")

## new FHICOST percentage in each cluster
dt6 %>% group_by(FHICOST) %>% table() %>% prop.table(.,
    1)
dt6 %>% group_by(FHICOST) %>% table() %>% prop.table(.,
    2)

dt5 %>% group_by(FHICOST) %>% table() %>% prop.table(.,
    1)
dt5 %>% group_by(FHICOST) %>% table() %>% prop.table(.,
    2)

dt3 %>% group_by(FHICOST) %>% table() %>% prop.table(.,
    1)
dt3 %>% group_by(FHICOST) %>% table() %>% prop.table(.,
    2)

# According to cluster analysis above, it is quite
# difficult to cluster different FHICOST very
# clearly. After refactoring FHICOST, one cluster
```

```
# has higher FHICOST which means the people in this
# cluster spend more money in healthcare. The rest
# clusters are more mixed with low FHICOST.

## refactor based on Michal's code
data <- within(data, {
    y4 <- NA
    y4[FHICOST <= 1] <- "low"
    y4[FHICOST > 1] <- "high"
})

colors <- brewer.pal(n = 2, name = "Set2")
pc <- data_frame(health.pc$scores[, 1], health.pc$scores[,
    2], health.pc$scores[, 3], data$y4)
colnames(pc) <- c("pc1", "pc2", "pc3", "FHICOST")
p <- plot_ly(pc, x = ~pc1, y = ~pc2, z = ~pc3, color = ~FHICOST,
    colors = colors) %>% add_markers() %>%
    layout(scene = list(xaxis = list(title = "pc1"),
    yaxis = list(title = "pc2"), zaxis = list(title = "pc3")))
p

## Prepare data
dt6 <- data_frame(data$y4, PCASet.k6$cluster)
colnames(dt6) <- c("FHICOST", "cluster")
dt5 <- data_frame(data$y4, PCASet.k5$cluster)
colnames(dt5) <- c("FHICOST", "cluster")
dt3 <- data_frame(data$y4, PCASet.k3$cluster)
```

```r
colnames(dt3) <- c("FHICOST", "cluster")

dt6 %>% group_by(FHICOST) %>% table() %>% prop.table(.,
    1)
dt6 %>% group_by(FHICOST) %>% table() %>% prop.table(.,
    2)

dt5 %>% group_by(FHICOST) %>% table() %>% prop.table(.,
    1)
dt5 %>% group_by(FHICOST) %>% table() %>% prop.table(.,
    2)

table(data$y4)
dt3 %>% group_by(FHICOST) %>% table() %>% prop.table(.,
    1)
dt3 %>% group_by(FHICOST) %>% table() %>% prop.table(.,
    2)

# If we refacor FHICOST again to just tow category,
# then it is clear that one cluster has high FHICOST
# or low FHICOST dominating inside them. So this
# can help some companies to target those people
# who pay more in healthcare.

PCASet.k3$centers

# If we look at the centers of three clusters by
```

```
# kmeans using k = 3.


# In the cluster that has highest percentage of
# high FHICOST, variable FHSTATEX(# fam mem in
# excellent health) and FHSTATVG(# fam mem in very
# good health) is higher then other clusters, which
# means families in this cluster are willing to pay
# more money to keep the family healthy.


# In cluster that has highest percetage of low
# FHICOST, it has much more family in pooe health
# but there are more people not pay much in health
# care. In this cluster, there are more people
# receiving money from sources other than wages and
# salary. It has much higher FSSICT(# fam mem
# receive income from SSI (Supplemental Security
# Income)) and FSSRRCT(# fam mem receive income
# from Social Security or Railroad retirement
# inc),FSSAPLCT(# fam mem ever apply for SSI
# (Supplemental Security Income)), FSDAPLCT(# fam
# mem ever apply for SSDI (Social Security
# Disability)) which indicates they try to find
# other sources to help cover their healthcare
# cost. These families might have more difficulty
# living than other families which can also be
# found in higher FPENSCT(# fam mem receive
# disability pensions),lower FDGLWCT1(# of fam mem
```

```
# working last week) and higher FM_ELDR(# of family
# members over 65).
```

8.2 Factor Analysis

```
# libraries

library(foreign)
library(corrplot)
library(car)
library(QuantPsyc)
library(leaps)
library(RColorBrewer)
library(Hmisc)
library(psych)
library(dplyr)

# Set the working directory
setwd("C:/Users/User/Documents/DSC 424/Final Dataset")

# import final file#
a1 <- read.csv("family_modified_001.csv")

# read first files
head(a1, 10)

# create obs based upon values from 18 to 127
```

```r
b1 <- a1[, c(7, 18:127)]


# reduce variables
z1 <- a1[, c(7, 18, 19, 21, 23, 25, 27, 29, 31, 33,
    39, 44:48, 57:69, 73, 93:119, 124, 127)]


pc.z1 <- prcomp(z1, scale = T)
pc.z1


screeplot(pc.z1, npcs = 58, type = "barplot", main = "Scree Plot")
title(ylab = "Variances", xlab = "PCA Number")
abline(h = 1, lwd = 4, col = "black")
summary(pc.z1)


xy1 <- psych::principal(z1, rotate = "varimax", nfactors = 8,
    score = TRUE)
print(xy1$loadings, sort = T)
print(xy1$loadings, cutoff = 0.559, sort = T)
print(xy1$loadings, cutoff = 0.3, sort = T)
print(xy1$loadings, cutoff = 0.5, sort = T)
print(xy1$loadings, cutoff = 0.54, sort = T)


xy2 <- psych::principal(z1, rotate = "varimax", nfactors = 16,
    score = TRUE)
print(xy2$loadings, sort = T)
print(xy2$loadings, cutoff = 0.559, sort = T)
print(xy2$loadings, cutoff = 0.3, sort = T)
```

```r
print(xy2$loadings, cutoff = 0.5, sort = T)


# Remove non good variables
z1$FHIPUBCT <- NULL
z1$FHIOGVCT <- NULL
z1$FHIIHSCT <- NULL
z1$FINCOTCT <- NULL
z1$FHICHPCT <- NULL
z1$FPENSCT <- NULL
z1$FTANFCT <- NULL
z1$FOWBENCT <- NULL
z1$FDGLWCT2 <- NULL
z1$FHSTATVG <- NULL
z1$FHCDVCT <- NULL
z1$FHCPHRCT <- NULL


# run some more
xy1 <- psych::principal(z1, rotate = "varimax", nfactors = 8,
    score = TRUE)
print(xy1$loadings, sort = T)
print(xy1$loadings, cutoff = 0.559, sort = T)
print(xy1$loadings, cutoff = 0.3, sort = T)
print(xy1$loadings, cutoff = 0.5, sort = T)
print(xy1$loadings, cutoff = 0.54, sort = T)


# Remove additional variables
z1$FINTR1CT <- NULL
```

```
z1$F10DVCT <- NULL
z1$FHOSP2CT <- NULL
z1$FHSTATG <- NULL
z1$FHSTATFR <- NULL
z1$FSNAPMYR <- NULL
z1$FCHSPCT <- NULL
z1$FHIMILCT <- NULL
z1$FHIEXCT <- NULL

# run some more
xy1 <- psych::principal(z1, rotate = "varimax", nfactors = 8,
    score = TRUE)
print(xy1$loadings, sort = T)
print(xy1$loadings, cutoff = 0.559, sort = T)
print(xy1$loadings, cutoff = 0.3, sort = T)
print(xy1$loadings, cutoff = 0.5, sort = T)
print(xy1$loadings, cutoff = 0.54, sort = T)
print(xy1$loadings, cutoff = 0.351, sort = T)

# run some more
xy3 <- psych::principal(z1, rotate = "varimax", nfactors = 5,
    score = TRUE)
print(xy3$loadings, sort = T)
print(xy3$loadings, cutoff = 0.559, sort = T)
print(xy3$loadings, cutoff = 0.3, sort = T)

# drop some more variables
```

```
z1$FSSKDAYS <- NULL
z1$FSNEDAYS <- NULL
z1$FNMEDCT <- NULL
z1$FDMEDCT <- NULL

# run some more
xy1 <- psych::principal(z1, rotate = "varimax", nfactors = 8,
    score = TRUE)
print(xy1$loadings, sort = T)
print(xy1$loadings, cutoff = 0.559, sort = T)
print(xy1$loadings, cutoff = 0.3, sort = T)
print(xy1$loadings, cutoff = 0.5, sort = T)

xy3 <- psych::principal(z1, rotate = "varimax", nfactors = 5,
    score = TRUE)
print(xy3$loadings, sort = T)
print(xy3$loadings, cutoff = 0.559, sort = T)
print(xy3$loadings, cutoff = 0.3, sort = T)

# Factoral Analysis

fz1 <- factanal(z1, 8)
print(fz1$loadings, cutoff = 0.4, sort = T)

fz2 <- factanal(z1, 5)
print(fz2$loadings, cutoff = 0.4, sort = T)
```

```r
# drop additional variables
z1$FSSICT <- NULL
z1$FDIVDCT <- NULL
z1$FHCHMCT <- NULL
z1$FSEINCCT <- NULL
z1$FHCHMCT <- NULL

# factor analysis
fz3 <- factanal(z1, 5)
print(fz3$loadings, cutoff = 0.44, sort = T)

# drop cost variables
z1$FHICOST <- NULL

# run factor analysis
fz4 <- factanal(z1, 5)
print(fz4$loadings, cutoff = 0.44, sort = T)
```

8.3 Logistic Regression

8.3.1 Preprocessing

```r
# import libraries
library(foreign)
library(corrplot)
library(car)
library(QuantPsyc)
```

```
library(leaps)
library(RColorBrewer)
library(Hmisc)
library(psych)
library(ggplot2)
library(MASS)
library(reshape2)
library(RCurl)
library(tidyverse)
library(plyr)
library(caTools)
# family_data <-
# getURL('https://raw.githubusercontent.com/stfox13/
#         DSC424FinalProject/master/family_modified_001.csv')
# family_df <- read.csv(text = family_data) View(family_df)
# Set the working directory
setwd("C:/Depaul_Win7/DSC 424 Advanced Data Analysis/Project/family")
# Read data
fam <- read.csv("familyxx.csv", sep = ",", header = T)
dim(fam)
str(fam)
head(fam)
# FHICOST Cost of family medical/dental care in the past 12 months
# put FHICOST in first column
fam <- fam[, c(119, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15,
    16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32,
    33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49,
```

```
    50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66,
    67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83,
    84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100,
    101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114,
    115, 116, 117, 118, 120, 121, 122, 123, 124, 125, 126, 127)]
str(fam)
# clean NAs check na after cleaning
sum(is.na(fam))
# #recode missing values -1 to NA fam[fam==-1] <-NA
# recode missing values 99 to NA
fam[fam == 99] <- NA
# recode missing values 98 to NA
fam[fam == 98] <- NA
# recode missing values 97 to NA
fam[fam == 97] <- NA
# recode missing values 96 to NA
fam[fam == 96] <- NA
# recode missing values 7 to NA
fam[fam == 7] <- NA
# recode missing values 8 to NA
fam[fam == 8] <- NA
# recode missing values 9 to NA
fam[fam == 9] <- NA
# check for missing values
sum(is.na(fam))
# check which columns have the most NAs
map(fam, ~sum(is.na(.)))
```

```
# drop variables which have too many NAs sum(is.na(fam$WRKCELN))
fam$WRKCELN <- NULL  #
fam$PHONEUSE <- NULL  #
fam$FM_EDUC1 <- NULL  #
fam$FSSKIP <- NULL  #
fam$FSSKDAYS <- NULL  #
fam$FSLESS <- NULL  #
fam$FSHUNGRY <- NULL  #
fam$FSWEIGHT <- NULL  #
fam$FSNOTEAT <- NULL  #
fam$FSNEDAYS <- NULL  #
fam$FHDSTCT <- NULL  #
fam$FWRKLWCT <- NULL  #
fam$FCHLMYN <- NULL  #
fam$FSPEDYN <- NULL  #
fam$FCHLMCT <- NULL  #
fam$FSPEDCT <- NULL  #
fam$FGAH <- NULL  #
fam$FSNAPMYR <- NULL  #
fam$RAT_CAT4 <- NULL  #
fam$RAT_CAT5 <- NULL  #
fam$FWICYN <- NULL  #
fam$FWICCT <- NULL  #
fam$COVCONF <- NULL  #
fam$FMEDBNOP <- NULL  #
fam$FPRCOOH <- NULL  #
fam$FHIEBCCT <- NULL  #
```

```r
# drop not importand variables
fam$RECTYPE <- NULL  #
fam$WTFA_FAM <- NULL  #
fam$FINT_Y_P <- NULL  #
fam$SRVY_YR <- NULL  #
fam$FMX <- NULL  #
fam$HHX <- NULL  #
fam$FINT_M_P <- NULL  #
fam$FINT_Y_P <- NULL  #
map(fam, ~sum(is.na(.)))
# check NA by rows
fam[!complete.cases(fam), ]
# remove rows which include NAs
famcleaned <- na.omit(fam)
head(famcleaned)
dim(fam)
dim(famcleaned)
# check na after cleaning
sum(is.na(famcleaned))
# no NAs, 19800 rows, 101 columns
# not recognized as catergorical variable
is.factor(famcleaned$FHICOST)
# no dummy variables contrasts(famcleaned$FHICOST)
# bin FHICOST to low and high to use it in logistic regression low=0 -
# less then $500 per year, high=1 - more than $500 per year 0 and 1
# will be 0 2, 3, 4, 5, will be 1
famcleaned$FHICOST[famcleaned$FHICOST == 1] <- 0
```

```r
famcleaned$FHICOST[famcleaned$FHICOST == 0] <- 0
famcleaned$FHICOST[famcleaned$FHICOST == 2] <- 1
famcleaned$FHICOST[famcleaned$FHICOST == 3] <- 1
famcleaned$FHICOST[famcleaned$FHICOST == 4] <- 1
famcleaned$FHICOST[famcleaned$FHICOST == 5] <- 1
head(famcleaned)
plot(famcleaned$FHICOST)
hist(famcleaned$FHICOST, col = "green")
sum(is.na(famcleaned))
# #create dataset with categorical variables only drop
# <-c('FM_SIZE','FM_KIDS','FM_ELDR','F10DVCT',
# 'FDMEDCT','FHCDVCT','FHCHMCT','FHCPHRCT',
# 'FHOSP2CT','FNMEDCT','FDGLWCT1','FDGLWCT2', 'FLIADLCT','FWKLIMCT',
# 'FWALKCT','FREMEMCT','FANYLCT','FHSTATEX',
# 'FHSTATVG','FHSTATG','FHSTATFR','FHSTATPR',
# 'FLAADLCT','FSALCT','FSEINCCT',
# 'FSSRRCT','FPENSCT','FOPENSCT','FSSICT',
# 'FTANFCT','FOWBENCT','FINTR1CT','FDIVDCT',
# 'FCHSPCT','FINCOTCT','FSSAPLCT','FSDAPLCT',
# 'FHIPRVCT','FHISINCT','FHICARCT',
# 'FHICADCT','FHICHPCT','FHIMILCT','FHIPUBCT',
# 'FHIOGVCT','FHIIHSCT','FHIEXCT','FHICOVCT')
# fam_cat=famcleaned[,!(names(famcleaned)%in%drop)]
head(fam_cat)
dim(fam_cat)
# 46 variables left, 19800 rows
famnum <- famcleaned[c("FHICOST", "F10DVCT", "FHCPHRCT", "FDGLWCT2", "FWKLIMCT",
```

```
    "FHSTATEX", "FHSTATPR", "FSEINCCT", "FSSICT", "FDIVDCT", "FSDAPLCT",
    "FHICARCT", "FHIPUBCT", "FHICOVCT", "FM_ELDR", "FHCHMCT", "FDGLWCT1",
    "FLIADLCT", "FANYLCT", "FHSTATFR", "FSALCT", "FOPENSCT", "FINTR1CT",
    "FSSAPLCT", "FHISINCT", "FHIMILCT", "FHIEXCT", "FM_KIDS", "FHCDVCT",
    "FNMEDCT", "FREMEMCT", "FHSTATG", "FLAADLCT", "FPENSCT", "FOWBENCT",
    "FINCOTCT", "FHIPRVCT", "FHICHPCT", "FHIIHSCT", "FM_SIZE", "FDMEDCT",
    "FHOSP2CT", "FWALKCT", "FHSTATVG", "FSSRRCT", "FTANFCT", "FCHSPCT",
    "FHICADCT", "FHIOGVCT")]
head(famnum)
# save famnum to csv
write.csv(famnum, "famnum.csv")
# categorical
famcat <- famcleaned[c("FM_STRCP", "FM_TYPE", "FM_STRP", "TELN_FLG", "CURWRKN",
    "TELCELN", "FLNGINTV", "F10DVYN", "FDMEDYN", "FHCDVYN", "FHCHMYN",
    "FHCPHRYN", "FHOSP2YN", "FNMEDYN", "FSRUNOUT", "FSLAST", "FSBALANC",
    "FLAADLYN", "FLIADLYN", "FWKLIMYN", "FWALKYN", "FREMEMYN", "FANYLYN",
    "HOUSEOWN", "FSNAP", "INCGRP4", "INCGRP5", "FSALYN", "FSEINCYN", "FSSRRYN",
    "FPENSYN", "FOPENSYN", "FSSIYN", "FTANFYN", "FOWBENYN", "FINTR1YN",
    "FDIVDYN", "FCHSPYN", "FINCOTYN", "FSSAPLYN", "FSDAPLYN", "FMEDBILL",
    "FMEDBPAY", "FSAF", "FHICOVYN")]
# save famcleaned to csv to create dummy variables using Python
write.csv(famcat, "famcat.csv")
```

8.3.2 Model Development

```
#DSC 424 project
#logistic regression
```

```r
#Michal Chowaniak


#import libraries
library(foreign)
library(corrplot)
library(car)
library(QuantPsyc)
library(leaps)
library(RColorBrewer)
library(Hmisc)
library(psych)
library(ggplot2)
library(MASS)
library(reshape2)
library(RCurl)
library(tidyverse)
library(plyr)
library(caTools)
library(ROCR)
library(caret)
library(glmnet)
install.packages('e1071', dependencies=TRUE)
library(Amelia)
library(pscl)
```

```r
# Set the working directory
setwd("C:/Depaul_Win7/DSC 424 Advanced Data Analysis/Project/family")



#Read data
famreg <- read.csv("fam_all_dummies.csv", sep=",", header=T)




famreg$FHICOST <- as.factor(famreg$FHICOST)
famreg$X = NULL
dim(famreg)
str(famreg)
head(famreg)

# Bar Plot
counts <- table(famreg$FHICOST)
barplot(counts, main="Cost of family medical/dental care in the past 12 months low (0) c
        xlab="0-less then $500, 1- more than $500")
# per above bar plot Y is balanced




#create a list of names for barplots
names <- c("FHICOST",   "F10DVCT",  "FHCPHRCT", "FDGLWCT2", "FWKLIMCT", "FHSTATEX",
           "FHSTATPR",  "FSEINCCT", "FSSICT",   "FDIVDCT",  "FSDAPLCT", "FHICARCT",
```

```
          "FHIPUBCT",  "FHICOVCT", "FM_ELDR",  "FHCHMCT",  "FDGLWCT1", "FLIADLCT",
          "FANYLCT",   "FHSTATFR", "FSALCT",   "FOPENSCT", "FINTR1CT", "FSSAPLCT",
          "FHISINCT",  "FHIMILCT", "FHIEXCT",  "FM_KIDS",  "FHCDVCT",  "FNMEDCT",
          "FREMEMCT",  "FHSTATG",  "FLAADLCT", "FPENSCT",  "FOWBENCT", "FINCOTCT",
          "FHIPRVCT",  "FHICHPCT", "FHIIHSCT", "FM_SIZE",  "FDMEDCT",  "FHOSP2CT",
          "FWALKCT",   "FHSTATVG", "FSSRRCT",  "FTANFCT",  "FCHSPCT",  "FHICADCT",
          "FHIOGVCT",  "FM_STRCP_12",  "FM_STRCP_21",  "FM_STRCP_22",  "FM_STRCP_23",
          "FM_STRCP_31",   "FM_STRCP_32",  "FM_STRCP_33",  "FM_STRCP_41",  "FM_STRCP_42
          "FM_STRCP_43",   "FM_STRCP_44",  "FM_STRCP_45",  "FM_TYPE_2",    "FM_TYPE_3",
          "FM_TYPE_4", "FM_STRP_12",   "FM_STRP_21",   "FM_STRP_22",   "FM_STRP_23",
          "FM_STRP_31",    "FM_STRP_32",   "FM_STRP_33",   "FM_STRP_41",   "FM_STRP_42"
          "FM_STRP_43",    "FM_STRP_44",   "FM_STRP_45",   "CURWRKN_2",    "TELCELN_2",
          "FLNGINTV_2",    "FLNGINTV_3",   "FLNGINTV_4",   "F10DVYN_2",    "FDMEDYN_2",
          "FHCDVYN_2", "FHCHMYN_2",    "FHCPHRYN_2",   "FHOSP2YN_2",   "FNMEDYN_2",
          "FSRUNOUT_2",    "FSRUNOUT_3",   "FSLAST_2", "FSLAST_3", "FSBALANC_2",
          "FSBALANC_3",    "FLAADLYN_2",   "FLIADLYN_2",   "FWKLIMYN_2",   "FWALKYN_2",
          "FREMEMYN_2",    "FANYLYN_2",    "HOUSEOWN_2",   "HOUSEOWN_3",   "FSNAP_2",
          "INCGRP4_2", "INCGRP4_3",    "INCGRP4_4",    "INCGRP4_5",    "INCGRP5_2",
          "INCGRP5_3", "INCGRP5_4",    "FSALYN_2", "FSEINCYN_2",   "FSSRRYN_2",
          "FPENSYN_2", "FOPENSYN_2",   "FSSIYN_2", "FTANFYN_2",    "FOWBENYN_2",
          "FINTR1YN_2",    "FDIVDYN_2",    "FCHSPYN_2",    "FINCOTYN_2",   "FSSAPLYN_2"
          "FSDAPLYN_2",    "FMEDBILL_2",   "FMEDBPAY_2",   "FSAF_2",   "FHICOVYN_2")


names[1]
```

```
#Create barpots for all variables
for ( i in 1:length(famreg)){
  count <- table(famreg[[i]])
  name <- names[i]
  barplot(count, main = name)
}
#barplots show x variables are imbalanced




#check for correlation on numerical variables
famnum <- famreg[c('F10DVCT','FHCPHRCT','FDGLWCT2','FWKLIMCT','FHSTATEX',
                   'FHSTATPR','FSEINCCT','FSSICT','FDIVDCT','FSDAPLCT',
                   'FHICARCT','FHIPUBCT','FHICOVCT','FM_ELDR','FHCHMCT',
                   'FDGLWCT1','FLIADLCT','FANYLCT','FHSTATFR','FSALCT',
                   'FOPENSCT','FINTR1CT','FSSAPLCT','FHISINCT','FHIMILCT',
                   'FHIEXCT','FM_KIDS','FHCDVCT','FNMEDCT','FREMEMCT',
                   'FHSTATG','FLAADLCT','FPENSCT','FOWBENCT','FINCOTCT',
                   'FHIPRVCT','FHICHPCT','FHIIHSCT','FM_SIZE','FDMEDCT',
                   'FHOSP2CT','FWALKCT','FHSTATVG','FSSRRCT','FTANFCT',
                   'FCHSPCT','FHICADCT','FHIOGVCT')]



#check for correlation
cor.famnum = cor(famnum)
```

```
cor.famnum
corrplot(cor.famnum, method = "number")
corrplot(cor.famnum, method = "ellipse")



#drop correlated variables
famreg$FM_ELDR = NULL #
famreg$FANYLCT = NULL #
famreg$FSALCT = NULL #
famreg$FHICOVCT = NULL #
famreg$FSSRRCT = NULL #
famreg$FM_SIZE = NULL #
famreg$FSSAPLCT = NULL #
famreg$FDMEDCT = NULL #
famreg$FDGLWCT1 = NULL #



#check for correclation on numerical
famnum <- famreg[c('F10DVCT','FHCPHRCT','FDGLWCT2','FWKLIMCT','FHSTATEX',
                   'FHSTATPR','FSEINCCT','FSSICT','FDIVDCT','FSDAPLCT',
                   'FHICARCT','FHIPUBCT','FHCHMCT',
                   'FLIADLCT','FHSTATFR',
                   'FOPENSCT','FINTR1CT','FHISINCT','FHIMILCT',
                   'FHIEXCT','FM_KIDS','FHCDVCT','FNMEDCT','FREMEMCT',
                   'FHSTATG','FLAADLCT','FPENSCT','FOWBENCT','FINCOTCT',
                   'FHIPRVCT','FHICHPCT','FHIIHSCT',
                   'FHOSP2CT','FWALKCT','FHSTATVG','FTANFCT',
```

```
                    'FCHSPCT','FHICADCT','FHIOGVCT')]


#check for correlation
cor.famnum = cor(famnum)
cor.famnum
corrplot(cor.famnum, method = "ellipse")
corrplot(cor.famnum, method = "number")









#split data set to training and test
set.seed(314)
split <- sample.split(famreg$FHICOST, SplitRatio = 0.80)
fam_train = subset(famreg, split == TRUE)
fam_test = subset(famreg, split == FALSE)
head(fam_train)
dim(fam_train)
dim(fam_test)



#check for missing
#missmap(fam_train, main = "Missing values vs observed")
```

```r
#check for categorical status
is.factor(fam_train$FHICOST)




######################
#automatic logistic regression model, forward selection on test


model.null = glm(FHICOST ~ 1, data=fam_train, family = binomial(link="logit"))

model.full = glm(FHICOST ~ ., data=fam_train, family = binomial(link="logit"))

#step(model.null, scope = list(upper=model.full), direction="forward", test="Chisq", d




#result of above
#56 variables
model6 <- glm(formula = FHICOST ~ FHIPRVCT + FMEDBPAY_2 + HOUSEOWN_2 +
                F10DVYN_2 + FINTR1CT + INCGRP4_5 + FMEDBILL_2 + FSNAP_2 +
                FM_TYPE_2 + FHCDVCT + FHICADCT + INCGRP4_4 + INCGRP5_2 +
                FDMEDYN_2 + FHICARCT + FSEINCYN_2 + FSAF_2 + FHOSP2YN_2 +
                FSRUNOUT_3 + FHIIHSCT + FDIVDYN_2 + FSSICT + FANYLYN_2 +
                FHIMILCT + FM_TYPE_4 + INCGRP4_2 + CURWRKN_2 + FHSTATEX +
```

```
                FM_KIDS + FHCPHRYN_2 + FM_STRP_42 + HOUSEOWN_3 + FHSTATFR +
                FSBALANC_3 + FM_STRCP_21 + FINTR1YN_2 + F10DVCT + FTANFCT +
                TELCELN_2 + FM_STRCP_12 + FLNGINTV_4 + FHSTATPR + FLIADLCT +
                FM_TYPE_3 + FREMEMCT + FHCHMYN_2 + FM_STRCP_23 + FHIEXCT +
                FHIOGVCT + FDIVDCT + FWKLIMYN_2 + FWKLIMCT + FLIADLYN_2,
              family = binomial(link = "logit"), data = fam_train)


summary(model6) #not all variable under 0.05
vif(model6) #vif under 5


anova(model6,test="Chisq")


famfit <- predict(model6, type = 'response')


#confusion matrix
table(fam_train$FHICOST, famfit > 0.5)

prop.table(table(fam_train$FHICOST, famfit > 0.5))


tp = 8304
tn = 7193
fp = 3033
```

```
fn = 2654


sensitivity = tp/(tp+fn)

sensitivity

accuracy = (tp+tn)/(tp+tn+fp+fn)

accuracy

precision = tp/(tp+fp)

precision

specificity = tn/(tn+fp)

specificity









# model is too complicated, too many variables


#End of automatic model selection forward on test

#####################################################







#########################################################

#logistic regression model - manual variable selection


model <- glm (FHICOST ~ ., data = fam_train, family = binomial)
```

```r
summary(model)



predict <- predict(model, type = 'response')


#confusion matrix
table(fam_train$FHICOST, predict > 0.5)



ROCRpred <- prediction(predict, fam_train$FHICOST)
ROCRperf <- performance(ROCRpred, 'tpr','fpr')
plot(ROCRperf, colorize = TRUE, text.adj = c(-0.2,1.7))




#drop non significant variables
fam_train_sig <- fam_train[c('FHICOST','F10DVCT','FHIMILCT','FHIPRVCT','FHIIHSCT',
                             'FHICADCT','FM_STRCP_12','FM_STRCP_21','FM_STRP_41',
                             'CURWRKN_2','TELCELN_2','F10DVYN_2','FHCPHRYN_2',
                             'FHOSP2YN_2','FSRUNOUT_2','FSBALANC_3','HOUSEOWN_2',
                             'HOUSEOWN_3','FSNAP_2','INCGRP4_2','INCGRP4_3',
                             'INCGRP4_4','INCGRP4_5','FSALYN_2','FINTR1YN_2',
                             'FMEDBILL_2','FMEDBPAY_2','FSAF_2')]


model2 <- glm (FHICOST ~ ., data = fam_train_sig, family = binomial)
summary(model2)
```

```
#drop more non significant variables
fam_train_sig2 <- fam_train[c('FHICOST','F10DVCT','FHIMILCT','FHIPRVCT','FHIIHSCT',
                             'FHICADCT','FM_STRCP_12','FM_STRCP_21','FM_STRP_41',
                             'CURWRKN_2','TELCELN_2','F10DVYN_2','FHCPHRYN_2',
                             'FHOSP2YN_2','FSBALANC_3','HOUSEOWN_2',
                             'HOUSEOWN_3','FSNAP_2','INCGRP4_2','INCGRP4_3',
                             'INCGRP4_4','INCGRP4_5','FINTR1YN_2',
                             'FMEDBILL_2','FMEDBPAY_2','FSAF_2')]



model3 <- glm (FHICOST ~ ., data = fam_train_sig2, family = binomial)
summary(model3)

vif(model3) #vif normal, under 5

#drop variables vif over 5, F10DVCT,F10DVYN_2
fam_train_sig3 <- fam_train[c('FHICOST','FHIMILCT','FHIPRVCT','FHIIHSCT',
                             'FHICADCT','FM_STRCP_12','FM_STRCP_21','FM_STRP_41',
                             'CURWRKN_2','TELCELN_2','FHCPHRYN_2',
                             'FHOSP2YN_2','FSBALANC_3','HOUSEOWN_2',
                             'HOUSEOWN_3','FSNAP_2','INCGRP4_2','INCGRP4_3',
                             'INCGRP4_4','INCGRP4_5','FINTR1YN_2',
```

```
                              'FMEDBILL_2','FMEDBPAY_2','FSAF_2')]

model4 <- glm (FHICOST ~ ., data = fam_train_sig3, family = binomial)
summary(model4) #all variable under 0.05
vif(model4) #vif under 5



predict2 <- predict(model4, type = 'response')



#confusion matrix
table(fam_train_sig3$FHICOST, predict2 > 0.5)



ROCRpred <- prediction(predict2, fam_train_sig3$FHICOST)
ROCRperf <- performance(ROCRpred, 'tpr','fpr')
plot(ROCRperf, colorize = TRUE, text.adj = c(-0.2,1.7))



##################################################
#run model on  test data
```

```
fam_test2 <- fam_test[c('FHICOST','FHIMILCT','FHIPRVCT','FHIIHSCT',
                        'FHICADCT','FM_STRCP_12','FM_STRCP_21','FM_STRP_41',
                        'CURWRKN_2','TELCELN_2','FHCPHRYN_2',
                        'FHOSP2YN_2','FSBALANC_3','HOUSEOWN_2',
                        'HOUSEOWN_3','FSNAP_2','INCGRP4_2','INCGRP4_3',
                        'INCGRP4_4','INCGRP4_5','FINTR1YN_2',
                        'FMEDBILL_2','FMEDBPAY_2','FSAF_2')]


model5 <- glm (FHICOST ~ ., data = fam_test2, family = binomial)
summary(model5) #not all variable under 0.05
vif(model5) #vif under 5


anova(model5,test="Chisq")


pR2(model5)


famfit <- predict(model5, type = 'response')


#confusion matrix
table(fam_test2$FHICOST, famfit > 0.5)

prop.table(table(fam_test2$FHICOST, famfit > 0.5))
```

```
tp = 2051

tn = 1729

fp = 828

fn = 689


sensitivity = tp/(tp+fn)

sensitivity

accuracy = (tp+tn)/(tp+tn+fp+fn)

accuracy

precision = tp/(tp+fp)

precision

specificity = tn/(tn+fp)

specificity




ROCRpred <- prediction(famfit, fam_test2$FHICOST)

ROCRperf <- performance(ROCRpred, 'tpr','fpr')

plot(ROCRperf, colorize = TRUE, text.adj = c(-0.2,1.7))


# AUC- the probability that the model will rank a randomly chosen positive example

#higher than a randomly chosen negative example

auc <- performance(ROCRpred, measure = "auc")

auc <- auc@y.values[[1]]

auc
```

```
#the end
##############################################
```

8.4 Principle Component Analysis

```
setwd("C:/Users/izl7729/Desktop/DePaul/Project")
getwd()
data <- read.csv("family_modified_001.csv")
library(tidyverse)
library(corrplot)
library(plyr)
library(ggplot2)
library(psych)
# Subset continuous variables
NewSub <- data[, c("FM_SIZE", "FCHLMCT", "FSPEDCT", "FLAADLCT", "FLIADLCT",
    "FWKLIMCT", "FWALKCT", "FREMEMCT", "FANYLCT", "FHSTATEX", "FHSTATVG",
    "FHSTATG", "FHSTATFR", "FHSTATPR", "FHICOVCT", "FHIPRVCT", "FHIEXCT",
    "FHISINCT", "FHICARCT", "FHICADCT", "FHICHPCT", "FHIMILCT", "FHIIHSCT",
    "FHIPUBCT", "FHIOGVCT", "FHIEBCCT", "FHDSTCT", "FDGLWCT1", "FDGLWCT2",
    "FWRKLWCT", "FSALCT", "FSEINCCT", "FSSRRCT", "FPENSCT", "FOPENSCT",
    "FSSICT", "FTANFCT", "FOWBENCT", "FINTR1CT", "FDIVDCT", "FCHSPCT",
    "FINCOTCT", "FSSAPLCT", "FSDAPLCT", "FWICCT", "FM_ELDR")]
# convert to Matrix
DataMatrix <- as.matrix(as.data.frame(NewSub))
# Reveiw Missing data
colSums(is.na(DataMatrix))
```

```r
# HIstograms
ggplot(gather(NewSub), aes(value)) + geom_histogram(bins = 20) + facet_wrap(~key,
    scales = "free_x")
# Correlation Matrices
CorData <- cor(DataMatrix)
corrplot(CorData, method = "circle")
# Remove Variables with missing values coded as -1
NewSub1 <- NewSub[-c(2, 27, 3, 45, 30)]
DataMatrix <- as.matrix(as.data.frame(NewSub1))
# Drop Variables with correlation <.3 Final PCA Set
PCASet <- NewSub1[-c(match(c("FHIEXCT", "FHIMILCT", "FHIIHSCT", "FHIPUBCT",
    "FHIOGVCT", "FDGLWCT2", "FSEINCCT", "FTANFCT", "FOWBENCT", "FINTR1CT",
    "FCHSPCT", "FINCOTCT"), names(NewSub1)))]
DataMatrix <- as.matrix(as.data.frame(PCASet))
describe(DataMatrix)
options(scipen = 100, digits = 5)
round(cor(DataMatrix), 2)
MCorrTest <- corr.test(DataMatrix, adjust = "none")
MCorrTest
M <- MCorrTest$p
M
MTest <- ifelse(M < 0.01, T, F)
MTest
colSums(MTest) - 1
# PCA Analysis
p2 <- psych::principal(DataMatrix, rotate = "varimax", nfactors = 12, scores = TRUE,
    oblique.scores = TRUE)
```

```
p2
plot(p2$values)
abline(1, 0, col = "red")
# Validation Statistics
print(p2$loadings, cutoff = 0.5, sort = T)
p2$loadings
p2$values
p2$communality
p2$rot.mat
```

8.5 Correspondence Analysis

```
setwd("/Users/sidneyfox/Documents/DePaul/Fall2018/DSC424/FinalProject/")
family_csv2 <- read.csv("familyxx.csv", header = T, sep = ",")
family_csv <- read.csv("familyxx.csv", header = T, sep = ",")
family_csv[is.na(family_csv)] <- -1
write.csv(family_csv, "family_modified_001.csv", row.names = F)
# read in data from GitHub
library(RCurl)
family_data <- getURL("https://raw.githubusercontent.com/stfox13/
                      DSC424FinalProject/master/family_modified_001.csv")
family_df <- read.csv(text = family_data)
View(family_df)
#### Correspondence Analysis ####
library(ca)
# compare variables for family type and highest eduction of family
# attained:
```

```r
family_type_education <- with(family_df, table(FM_TYPE, FM_EDUC1))
prop.table(family_type_education, 1)  # row percentages
prop.table(family_type_education, 2)  # column percentages
fit <- ca(family_type_education)
print(fit)
print(summary(fit))
plot(fit, main = "Correspondence Analysis (symetric map)\n
     1. family type 2. highest education level")
plot(fit, mass = TRUE, contrib = "absolute", map = "rowgreen", arrows = c(F,
    T), main = "Correspondence Analysis (assymetric map)\n
    1. family type 2. highest education level")
# compare variables for language of interview and family structure:
int_lang_fam_struct <- with(family_df, table(FLNGINTV, FM_STRCP))
prop.table(int_lang_fam_struct, 1)  # row percentages
prop.table(int_lang_fam_struct, 2)  # column percentages
fit <- ca(int_lang_fam_struct)
print(fit)
print(summary(fit))
plot(fit, main = "Correspondence Analysis (symetric map)\n
     1. language of interview 2. family structure")
plot(fit, mass = TRUE, contrib = "absolute", map = "rowgreen", arrows = c(F,
    T), main = "Correspondence Analysis (assymetric map)\n
    1. language of interview 2. family structure")
# compare variables for language of interview and family structure:
cov_inc_grp <- with(family_df, table(COVCONF, INCGRP4))
prop.table(cov_inc_grp, 1)  # row percentages
prop.table(cov_inc_grp, 2)  # column percentages
```

```r
fit <- ca(cov_inc_grp)
print(fit)
print(summary(fit))
plot(fit, main = "Correspondence Analysis (symetric map)\n
     1. coverage confidence 2. income group")
plot(fit, mass = TRUE, contrib = "absolute", map = "rowgreen", arrows = c(F,
    T), main = "Correspondence Analysis (assymetric map)\n
    1. coverage confidence 2. income group")
# compare variables for language of interview and family structure:
phone_house <- with(family_df, table(PHONEUSE, HOUSEOWN))
prop.table(phone_house, 1)  # row percentages
prop.table(phone_house, 2)  # column percentages
fit <- ca(phone_house)
print(fit)
print(summary(fit))
plot(fit, main = "Correspondence Analysis (symetric map)\n
     1. working cell phone / landline 2. home ownership status")
plot(fit, mass = TRUE, contrib = "absolute", map = "rowgreen", arrows = c(F,
    T), main = "Correspondence Analysis (assymetric map)\n
    1. working cell phone / landline 2. home ownership status")
# count the number of NAs
family_na_summary <- data.frame(colSums_vals = colSums(is.na(family_csv)))
family_na_per <- data.frame(per_na = colMeans(is.na(family_csv)))
# visualize: histogram:
hist(family_na_per$per_na,
     main = "Percentage of missing values within data set \n
     total number of variables = 127",
```

```
    xlab = "Percentage of missing values")
```

8.6 Linear Discriminant Analysis

```
library(tidyverse)
library(corrplot)
library(plyr)
library(ggplot2)
library(RCurl)
library(psych)
require(MASS)
family_data <- getURL("https://raw.githubusercontent.com/stfox13/
                      DSC424FinalProject/master/family_modified_001.csv")
data <- read.csv(text = family_data)
setwd("/Users/sidneyfox/Documents/DePaul/Fall2018/DSC424/FinalProject/")
data_w_dummy_vars <- read.csv("fam_all_dummies.csv")[,
    -1]  # drop row_names
# data = read.csv('family_modified_001.csv') data2
# = read.csv('familyxx.csv')
data <- family_df
data2
head(SubData, 2)
NewSub <- data[, c("FM_SIZE", "FCHLMCT", "FSPEDCT",
    "FLAADLCT", "FLIADLCT", "FWKLIMCT", "FWALKCT",
    "FREMEMCT", "FANYLCT", "FHSTATEX", "FHSTATVG",
    "FHSTATG", "FHSTATFR", "FHSTATPR", "FHICOVCT",
```

```
    "FHIPRVCT", "FHIEXCT", "FHISINCT", "FHICARCT",
    "FHICADCT", "FHICHPCT", "FHIMILCT", "FHIIHSCT",
    "FHIPUBCT", "FHIOGVCT", "FHIEBCCT", "FHDSTCT",
    "FDGLWCT1", "FDGLWCT2", "FWRKLWCT", "FSALCT", "FSEINCCT",
    "FSSRRCT", "FPENSCT", "FOPENSCT", "FSSICT", "FTANFCT",
    "FOWBENCT", "FINTR1CT", "FDIVDCT", "FCHSPCT", "FINCOTCT",
    "FSSAPLCT", "FSDAPLCT", "FWICCT", "FM_ELDR")]
# convert to Matrix
DataMatrix <- as.matrix(as.data.frame(NewSub))
# Missing data
colSums(is.na(DataMatrix))
# HIstograms
ggplot(gather(NewSub), aes(value)) + geom_histogram(bins = 20) +
    facet_wrap(~key, scales = "free_x")
# Correlation Matrices
CorData <- cor(DataMatrix)
corrplot(CorData, method = "circle")
# Remove Variables with missing values coded as -1
NewSub1 <- NewSub[-c(2, 27, 3, 45, 30)]
DataMatrix <- as.matrix(as.data.frame(NewSub1))
# Drop Variables with correlation <.3 Final PCA Set
PCASet <- NewSub1[-c(match(c("FHIEXCT", "FHIMILCT",
    "FHIIHSCT", "FHIPUBCT", "FHIOGVCT", "FDGLWCT2",
    "FSEINCCT", "FTANFCT", "FOWBENCT", "FINTR1CT",
    "FCHSPCT", "FINCOTCT"), names(NewSub1)))]
DataMatrix <- as.matrix(as.data.frame(PCASet))
CorData <- cor(DataMatrix)
```

```r
corrplot(CorData, method = "circle")
library(psych)
describe(DataMatrix)
options(scipen = 100, digits = 5)
round(cor(DataMatrix), 2)
MCorrTest <- corr.test(DataMatrix, adjust = "none")
MCorrTest
M <- MCorrTest$p
# M
MTest <- ifelse(M < 0.01, T, F)
MT
colSums(MTest) - 1
p2 <- psych::principal(DataMatrix, rotate = "varimax",
    nfactors = 12, scores = TRUE, oblique.scores = TRUE)
p2
# plot(p2$values) abline(1, 0,col = 'red')
# combine principal component scores with target
# variable
pc_data <- merge(p2$scores[, 0:8], data$FHICOST, by = "row.names",
    all = T)[, -1]
cleaned_data <- merge(PCASet, data$FHICOST, by = "row.names",
    all = T)[, -1]
#### linear discriminant analysis ####
# break data into test and train (80 / 20 split):
set.seed(101)
sample_pcdata <- sample.int(n = nrow(pc_data), size = floor(0.8 *
    nrow(pc_data)), replace = F)
```

```
pc_data_train <- as.data.frame(pc_data[sample_pcdata,
    ])
pc_data_test <- as.data.frame(pc_data[-sample_pcdata,
    ])
familyLDA <- lda(y ~ ., data = pc_data_train)
# plot(familyLDA)
# predict
familyLDA.values <- predict(familyLDA, pc_data_test)
p <- predict(familyLDA, newdata = pc_data_test)
mean(p$class == pc_data_test$y)
# 37% - not great :(
# cleaned data # break data into test and train (80
# / 20 split):
set.seed(101)
sample_cleaneddata <- sample.int(n = nrow(cleaned_data),
    size = floor(0.8 * nrow(cleaned_data)), replace = F)
cleaned_data_train <- as.data.frame(cleaned_data[sample_cleaneddata,
    ])
cleaned_data_test <- as.data.frame(cleaned_data[-sample_cleaneddata,
    ])
familyLDA2 <- lda(y ~ ., data = cleaned_data_train)
# plot(familyLDA)
# predict
familyLDA2.values <- predict(familyLDA2, cleaned_data_test)
p2 <- predict(familyLDA2, newdata = cleaned_data_test)
mean(p2$class == cleaned_data_test$y)
# 38% - not great :(
```

```r
# data with dummy vars # break data into test and
# train (80 / 20 split):
set.seed(101)
sample_dummyvardata <- sample.int(n = nrow(data_w_dummy_vars2),
    size = floor(0.8 * nrow(data_w_dummy_vars2)), replace = F)
dummy_var_data_train <- as.data.frame(data_w_dummy_vars2[sample_dummyvardata,
    ])
dummy_var_data_test <- as.data.frame(data_w_dummy_vars2[-sample_dummyvardata,
    ])
familyLDA3 <- lda(FHICOST ~ ., data = dummy_var_data_train)
# plot(familyLDA)
# predict
familyLDA3.values <- predict(familyLDA3, dummy_var_data_test)
ldahist(data = familyLDA3.values$x[, 2], g = FHICOST)
plot(familyLDA3.values$x[, 1], familyLDA3.values$x[,
    2])
p3 <- predict(familyLDA3, newdata = dummy_var_data_test)
# accuracy: 72% - pretty good! :)
mean(p3$class == dummy_var_data_test$FHICOST)
p3_df <- data.frame(LD1 = p3$x, class = p3$class)
# display density plot of linear discriminants and
# predicted values
ggplot(p3_df) + geom_density(aes(LD1, fill = class),
    alpha = 0.2) + ggtitle("Density plot displaying the density of LD1\n
                           color coded by the class variable.")
reg_formula <- paste("FHICOST ~", paste(names(data_w_dummy_vars2)[-1],
    collapse = " + "))
```

```r
# observation: aliased coefficients:
alias(lm(reg_formula, data = data_w_dummy_vars2))
fit <- lm(reg_formula, data = data_w_dummy_vars2)
vif_results <- car::vif(fit)
# observation: rampant multicollinearity (vif > 10)
vif_results
remove_factors <- c(FM_STRCP_12, FM_STRCP_21, FM_STRCP_22,
    FM_STRCP_23, FM_STRCP_31, FM_STRCP_32, FM_STRCP_33,
    FM_STRCP_41, FM_STRCP_42, FM_STRCP_43, FM_STRCP_44,
    FM_STRCP_45)
data_w_dummy_vars2 <- subset(data_w_dummy_vars, select = -c(FM_STRCP_12,
    FM_STRCP_21, FM_STRCP_22, FM_STRCP_23, FM_STRCP_31,
    FM_STRCP_32, FM_STRCP_33, FM_STRCP_41, FM_STRCP_42,
    FM_STRCP_43, FM_STRCP_44, FM_STRCP_45, FM_TYPE_2,
    FM_TYPE_3, FM_TYPE_4, INCGRP4_2, INCGRP4_3, INCGRP4_4,
    INCGRP4_5, FHCPHRCT, FWKLIMCT, FHSTATEX, FHSTATPR,
    FSSICT, FSDAPLCT, FHICOVCT, FLIADLCT, FANYLCT,
    FHSTATFR, FOPENSCT, FSSAPLCT, FM_KIDS, FREMEMCT,
    FHSTATG, FLAADLCT, FPENSCT, FHIPRVCT, FM_SIZE,
    FWALKCT, FHSTATVG, FSSRRCT, FHCHMYN_2, FHCPHRYN_2,
    FLAADLYN_2, FLIADLYN_2, FWKLIMYN_2, FLIADLYN_2,
    FWKLIMYN_2, FWALKYN_2, FREMEMYN_2, FANYLYN_2, FPENSYN_2,
    FOPENSYN_2, FSSIYN_2, FSSAPLYN_2, FSDAPLYN_2))
```

---

9 Visualization Appendix

Please find the figures referenced throughout this paper below:

9.1 Executive Summary

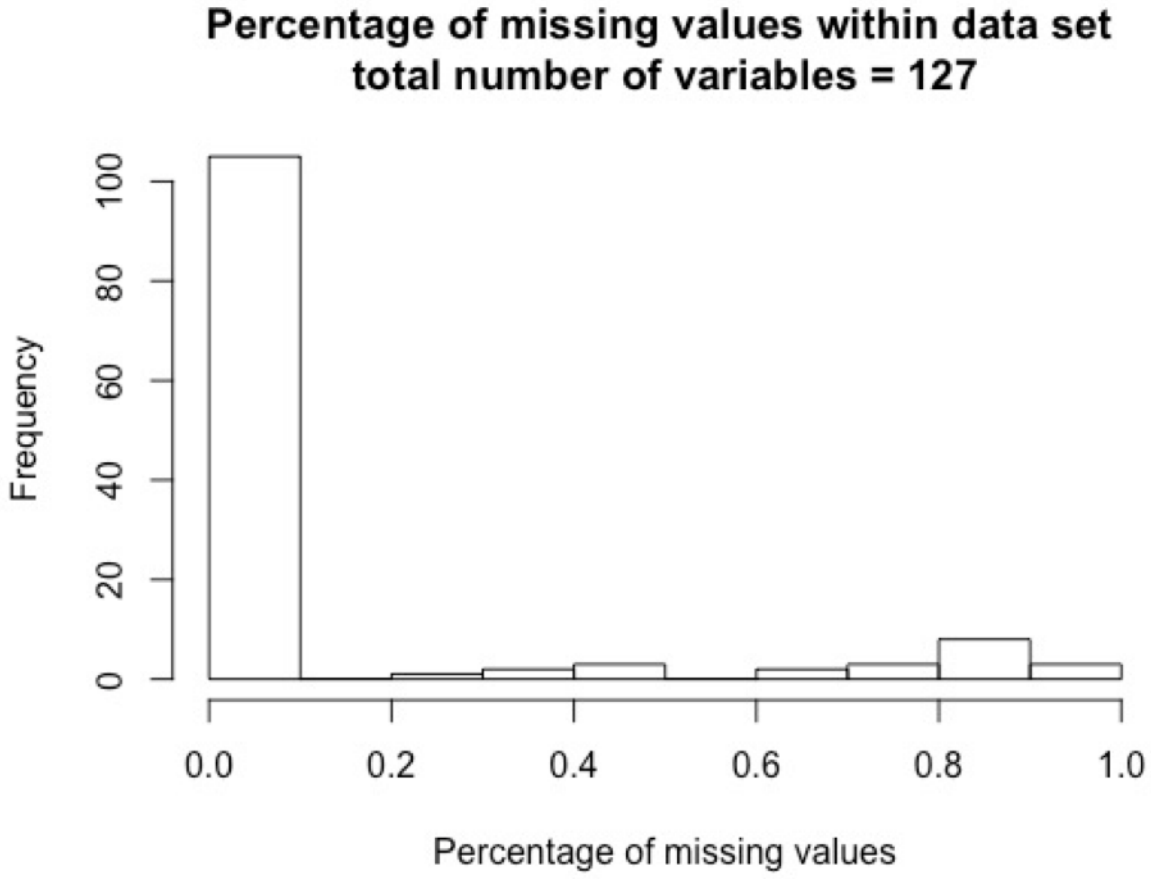

Figure 1: Histogram of Missing Values

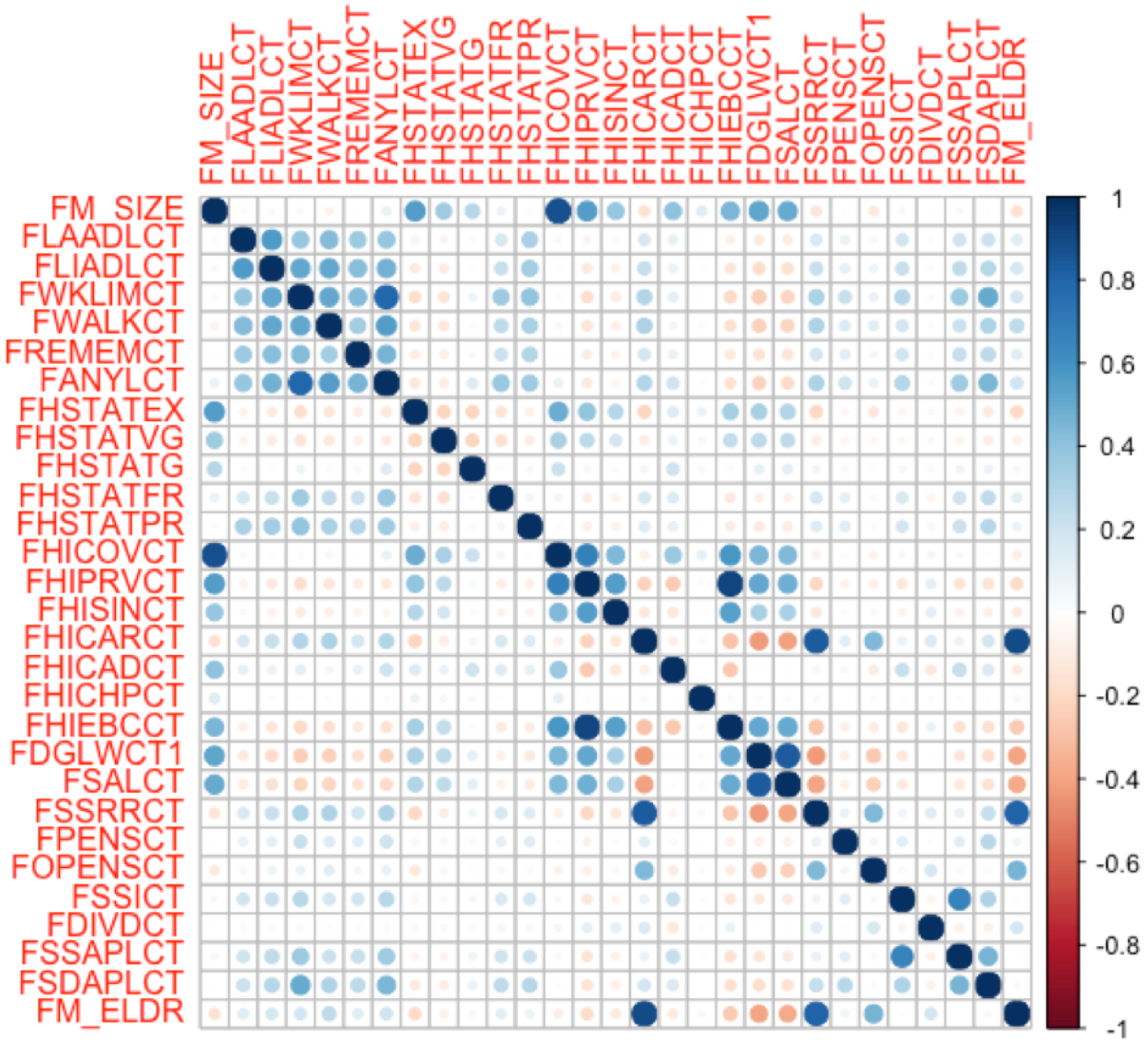

Figure 2: Correlation Plot Displaying a Subset of Variables

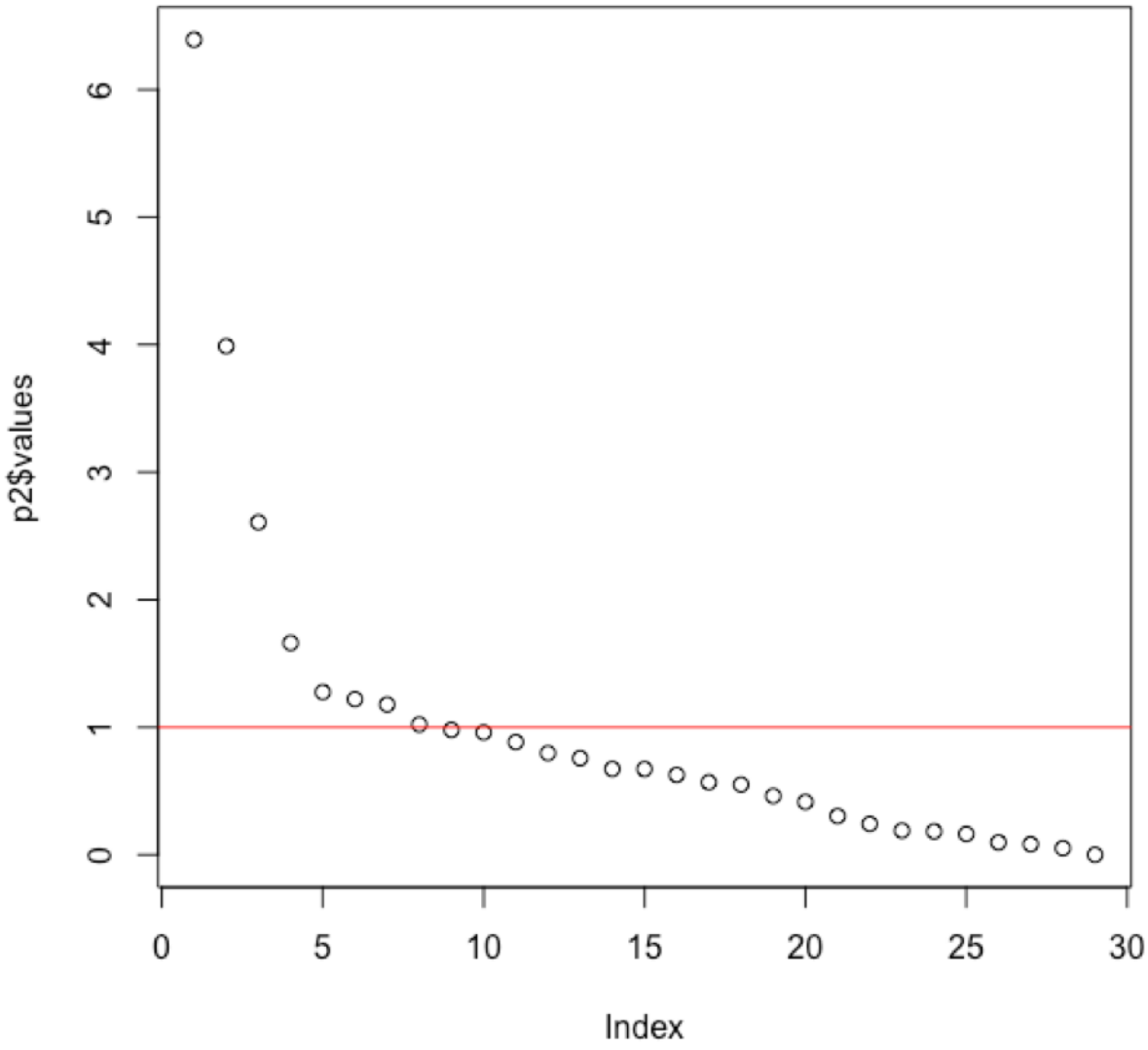

Figure 3: PCA Scree Plot

9.2 Correspondence Analysis

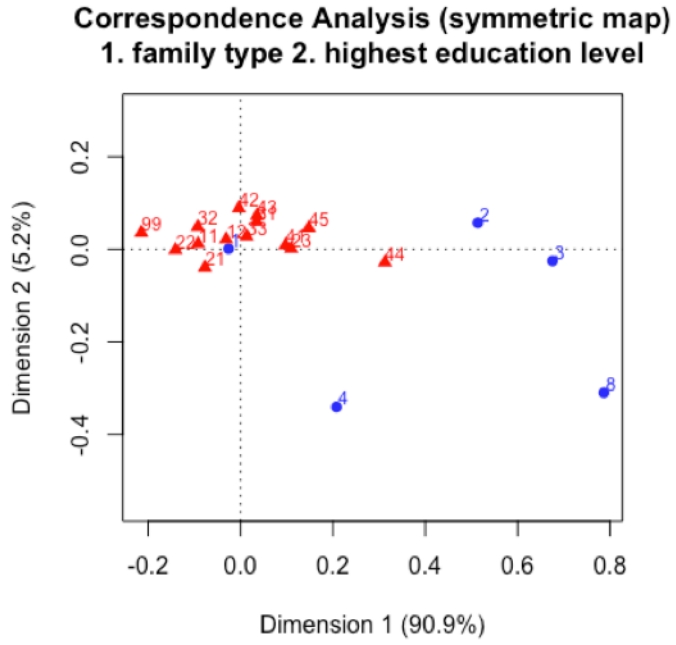

Figure 4: Correspondence Analysis Plot 1

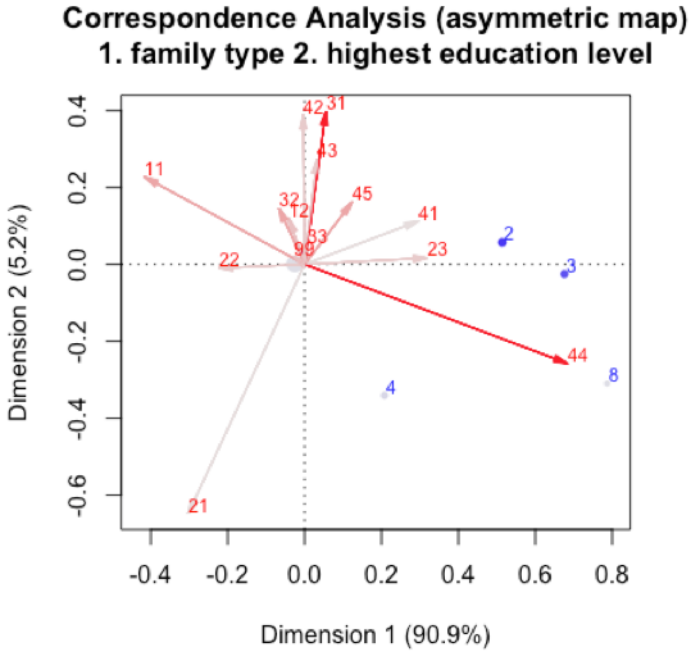

Figure 5: Correspondence Analysis Plot 2

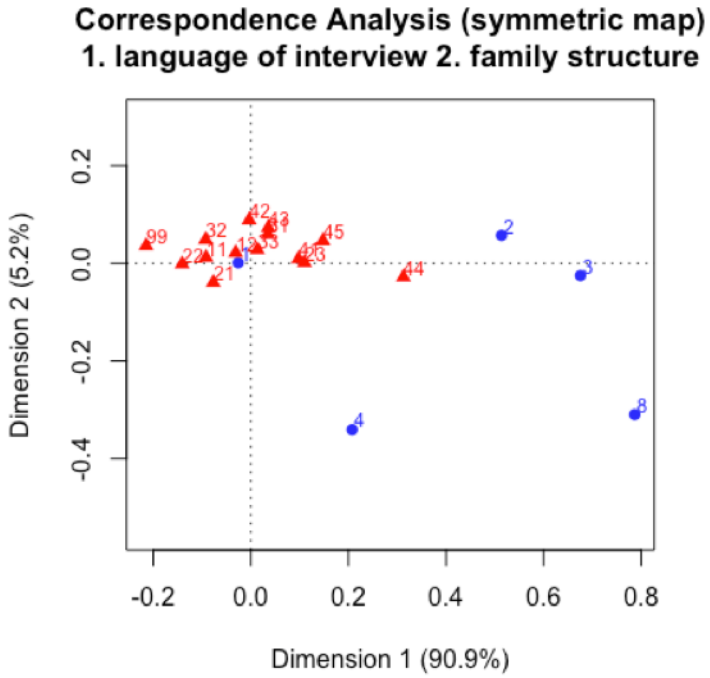

Figure 6: Correspondence Analysis Plot 3

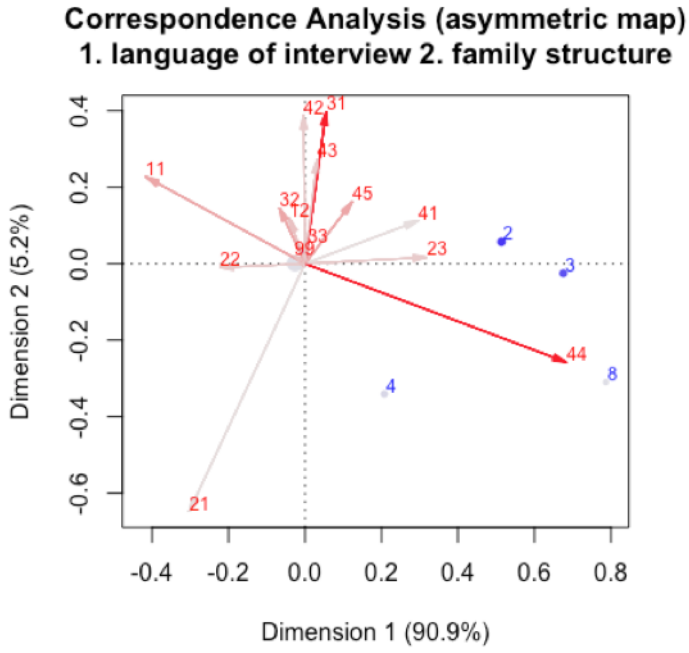

Figure 7: Correspondence Analysis Plot 4

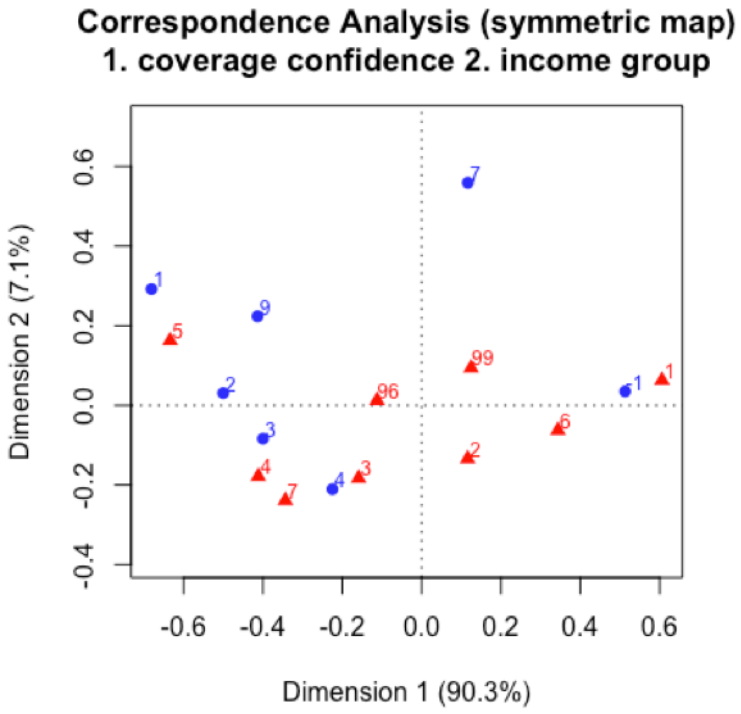

Figure 8: Correspondence Analysis Plot 5

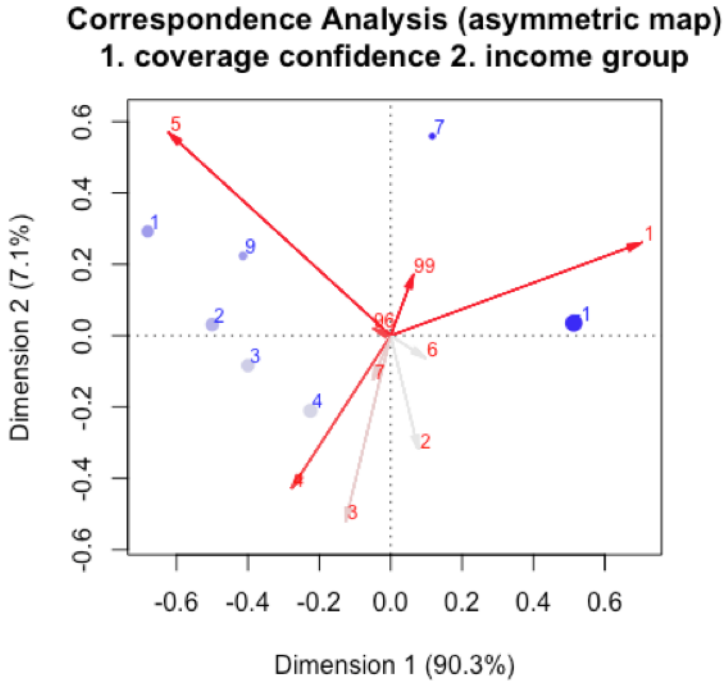

Figure 9: Correspondence Analysis Plot 6

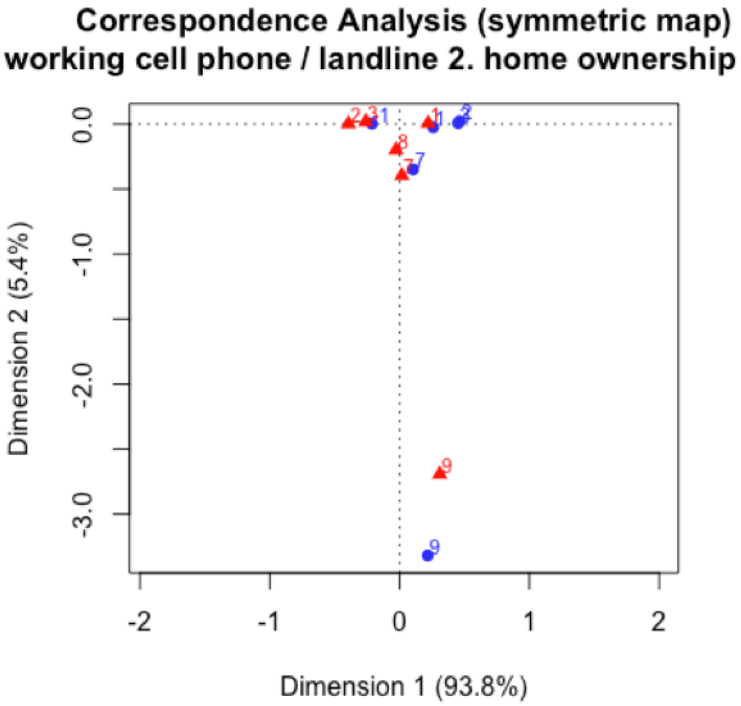

Figure 10: Correspondence Analysis Plot 7

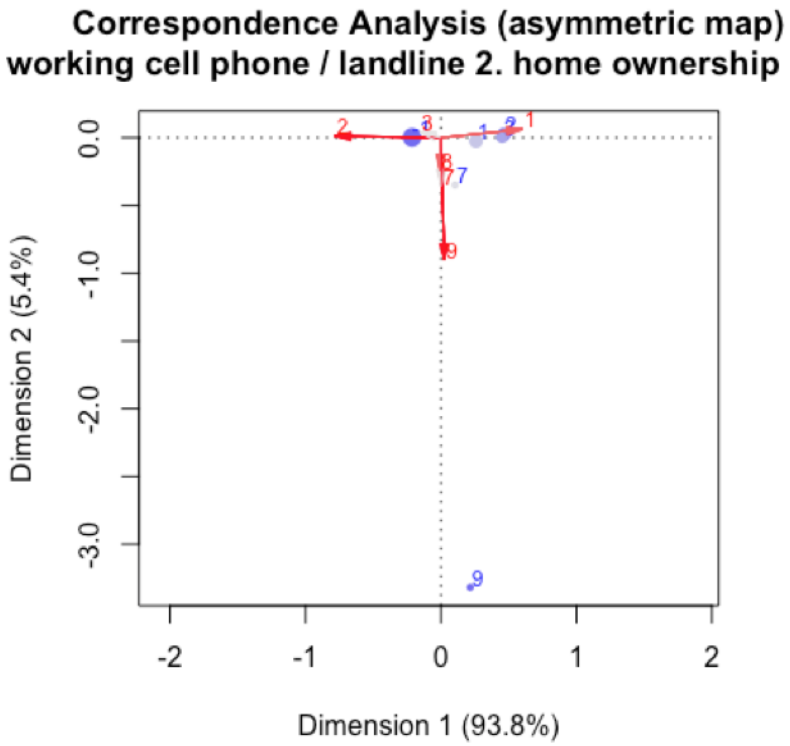

Figure 11: Correspondence Analysis Plot 8

9.3 Linear Discriminant Analysis

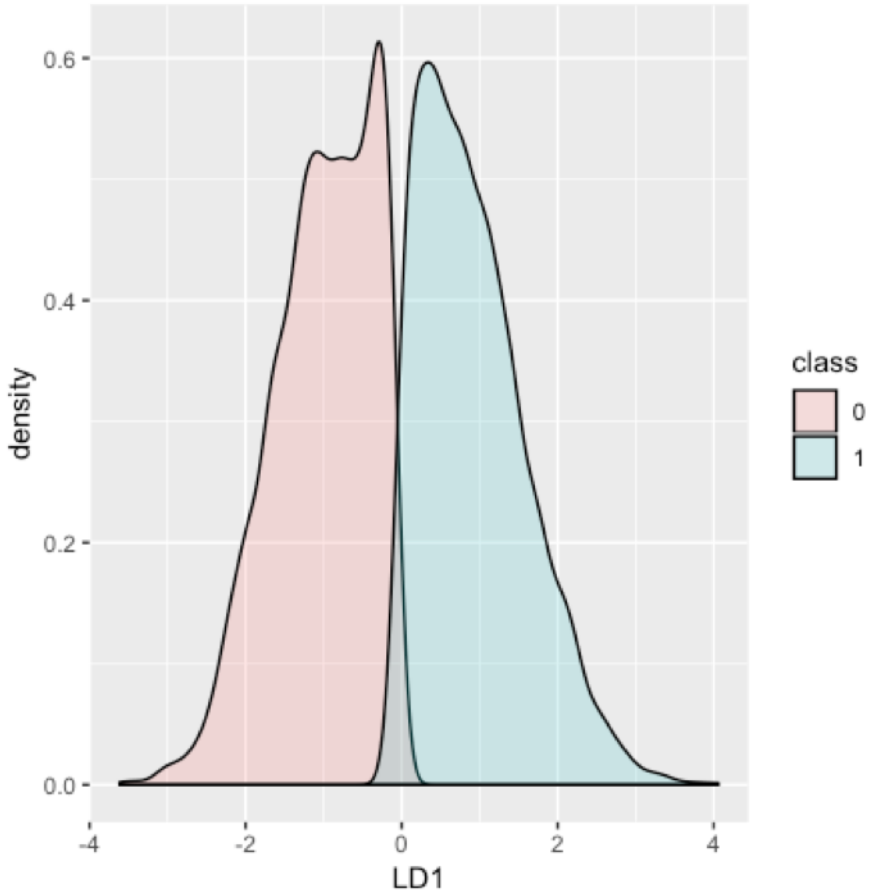

Figure 12: Density Plot Comparing Outcomes of LDA

9.4 Common Factor Analysis

Var Char	Variable Description	Loadings	Factor Name
FDGLWCT1	Family Working Last Week	0.659	Likelihood of Insured
FHSTATEX	Family in Excellent Health	0.501	
FSALCT	Family Receiving Income from Wages	0.642	
FHIPRVCT	Family on Private Insurance	0.798	
FHICOVCT	Family with Insurance	0.814	
FHISINCT	Family on Single Plan Health Insurance	0.571	
FLIADLCT	Family with IADL	0.605	Likelihood of Health Issues
FWKLIMCT	Family with work limits due to health	0.858	
FWALKCT	Family difficult walking	0.604	
FREMEMCT	Family difficult remembering	0.531	
FANYLCT	Family limited in any way	0.858	
FSDAPLCT	Family apply for SSDI	0.56	
FHSTATPR	Family in Poor Health	0.459	
FLAADLCT	Family with ADL Help	0.501	
FSSAPLCT	Family apply for SSI	0.447	
FM_ELDR	Family Members over 65	0.932	Likelihood of Being Elderly
FSSRRCT	Family receive income from R/R or Pension	0.823	
FHICARCT	Family on Medicare	0.921	
FOPENSCT	Family receive survivor/spousal benefits	0.477	

Figure 13: Factors with Loadings

	Likelihood of Insured	Likelihood of Health Issues	Likelihood of Being Elderly
SS loadings	3.661	2.943	2.842
Proportion Var	0.193	0.155	0.15
Cumulative Var	0.193	0.348	0.497

Figure 14: Overview of Variance with Factor Names

9.5 Cluster Analysis

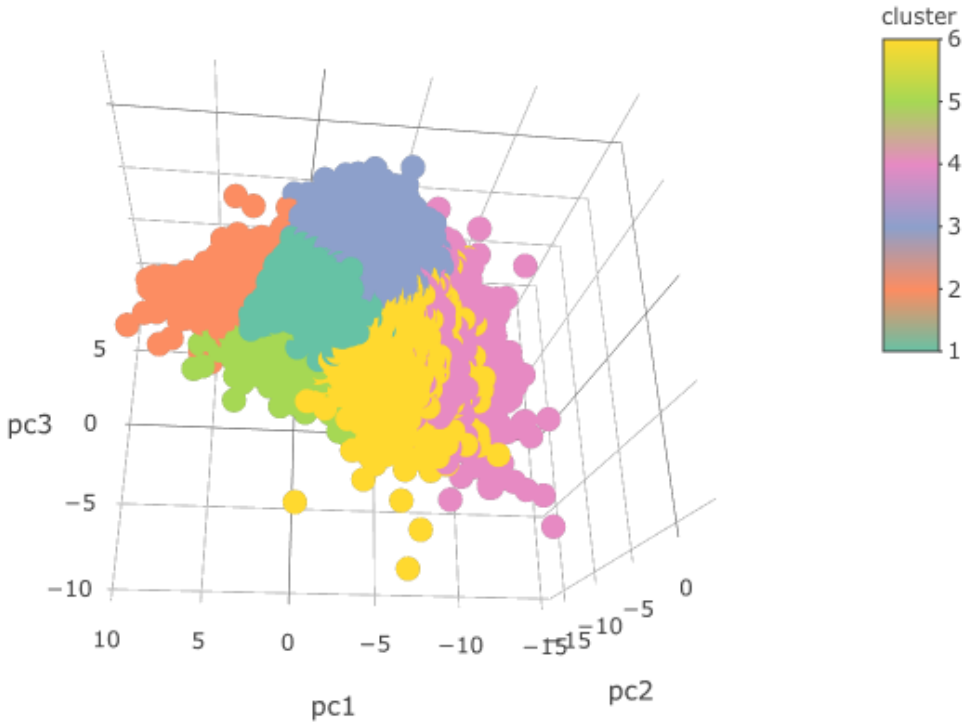

Figure 15: Cluster Representation

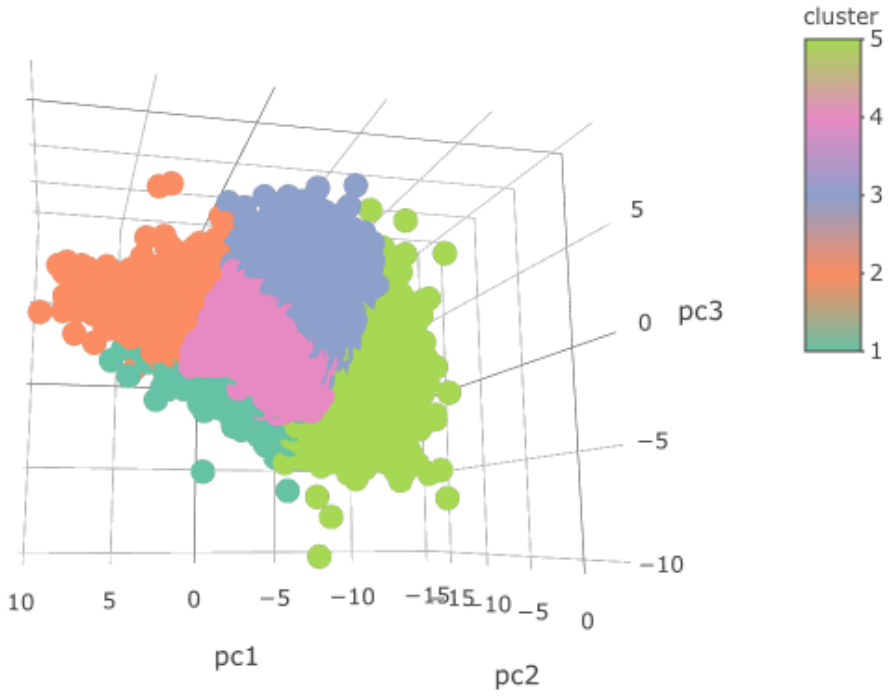

Figure 16: Cluster Representation

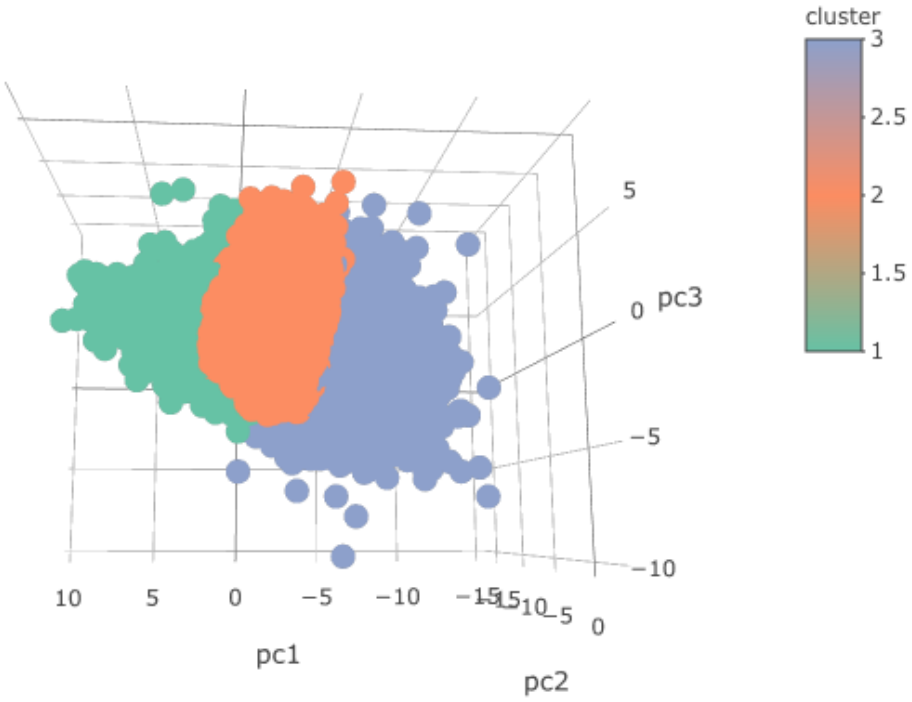

Figure 17: Cluster Representation

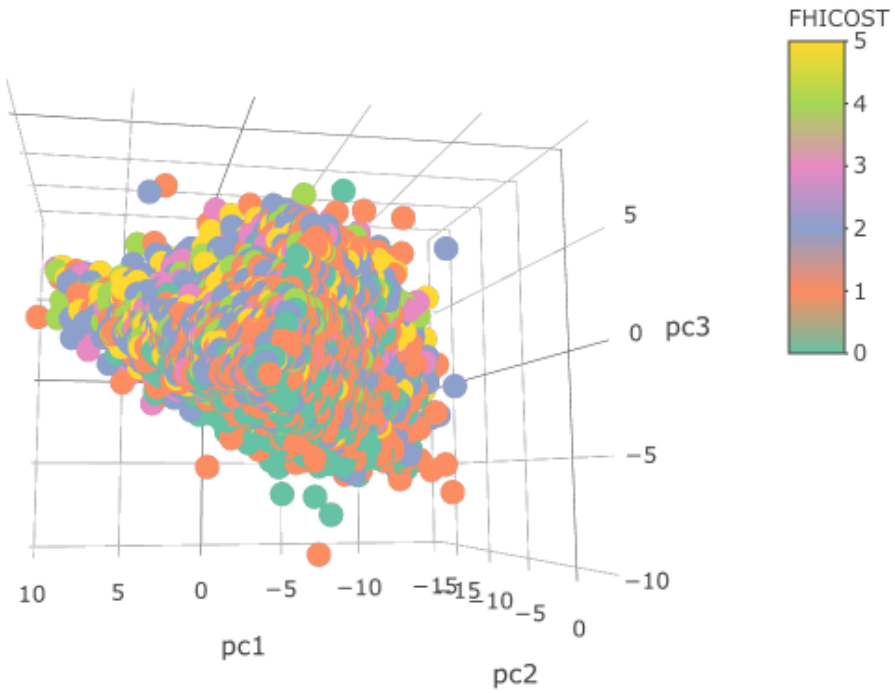

Figure 18: Cluster Representation

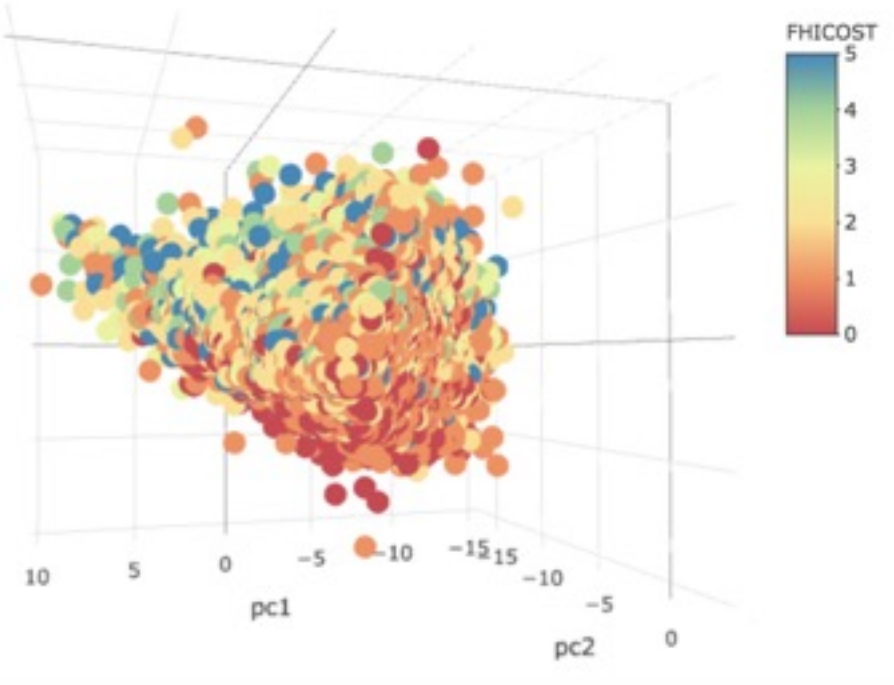

Figure 19: All Data Points Representation

```
##         cluster
## FHICOST         1         2         3
##    high 0.4238197 0.6340136 0.4970060
##    low  0.5761803 0.3659864 0.5029940
```

Figure 20: Cluster Outputs

```
##    FM_SIZE   FLAADLCT   FLIADLCT  FWKLIMCT    FWALKCT   FREMEMCT   FANYLCT
## 1 1.092025 0.01065537 0.03121684 0.2077038 0.11642761 0.06340858 0.2818646
## 2 2.495778 0.03607345 0.03139931 0.1152362 0.04542679 0.04812904 0.2892039
## 3 1.567117 1.38307279 1.76483329 2.2029402 1.86077461 1.49034298 2.2022212
##    FHSTATEX  FHSTATVG   FHSTATG  FHSTATFR   FHSTATPR FHICOVCT  FHIPRVCT
## 1 0.3142845 0.4920817 0.5014329 0.2470549 0.04535570 0.927514 0.5495737
## 2 1.2094439 1.0923727 0.6895353 0.2176955 0.03652751 2.369624 1.8628696
## 3 0.2058218 0.3020967 0.7396466 1.2912004 1.22773659 1.460852 0.5216723
##    FHISINCT   FHICARCT  FHICADCT   FHICHPCT    FHIEBCCT  FDGLWCT1
## 1 0.3194660 0.79648478 0.1922279 0.03132827  0.07747224 0.7862517
## 2 1.2439924 0.06941039 0.4979016 0.17503870  1.33046425 2.1076456
## 3 0.3412092 1.42163553 0.7899674 0.07180846 -0.05442460 0.5183454
##      FSALCT    FSSRRCT    FPENSCT   FOPENSCT     FSSICT   FDIVDCT
## 1 0.8010731 0.77836747 0.12290732 0.57603634 0.05100196 0.4256121
## 2 2.0732982 0.08198257 0.09199469 0.09147293 0.04176725 0.4568340
## 3 0.5920391 1.42759461 0.80741273 0.64481988 1.17241969 0.2935624
##     FSSAPLCT  FSDAPLCT    FM_ELDR
## 1 0.07897665 0.1591161 0.82287901
## 2 0.08575811 0.1050765 0.08296434
## 3 1.42454694 1.6990005 1.11643645
```

Figure 21: Cluster Variable Matrix

9.6 Logistic Regression

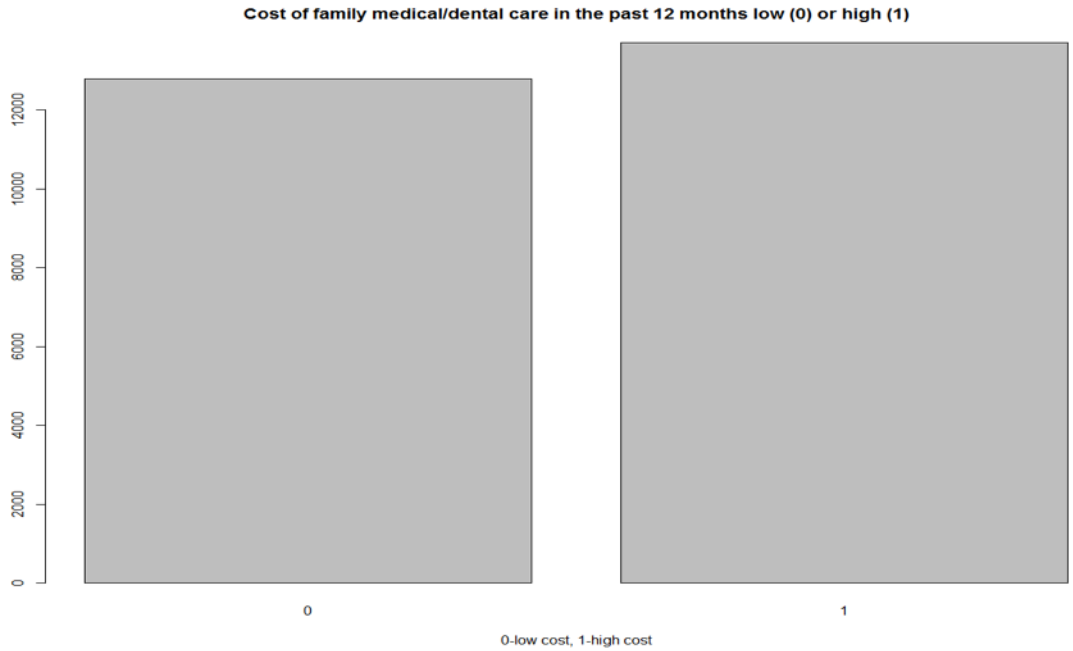

Figure 22: Logistic Regression

	FALSE	TRUE
0	7194	3032
1	2654	8304

Figure 23: Logistic Regression

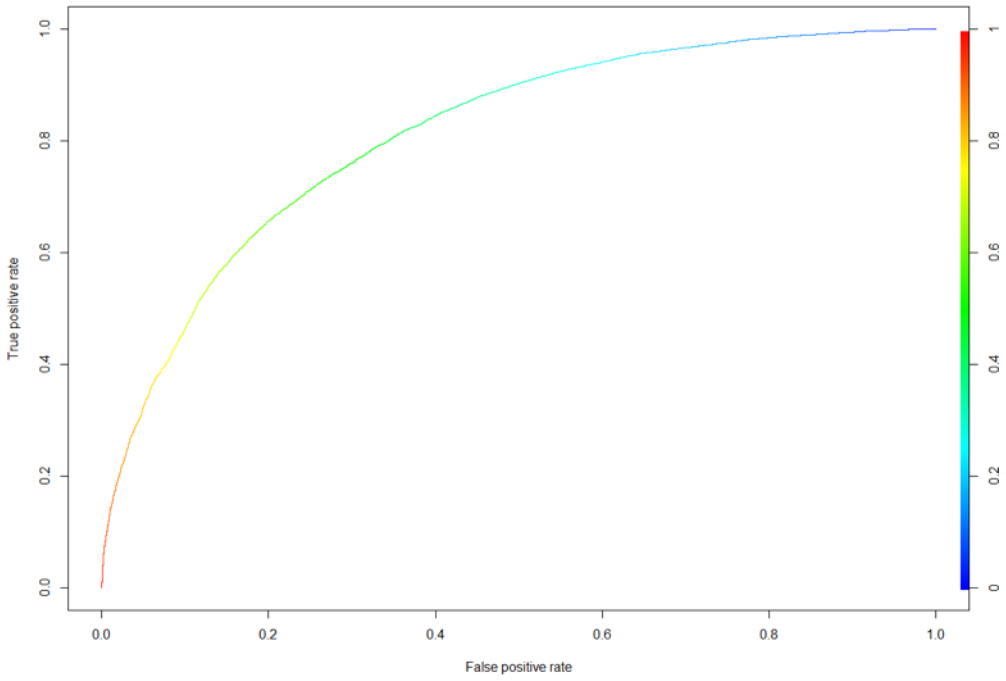

Figure 24: Logistic Regression

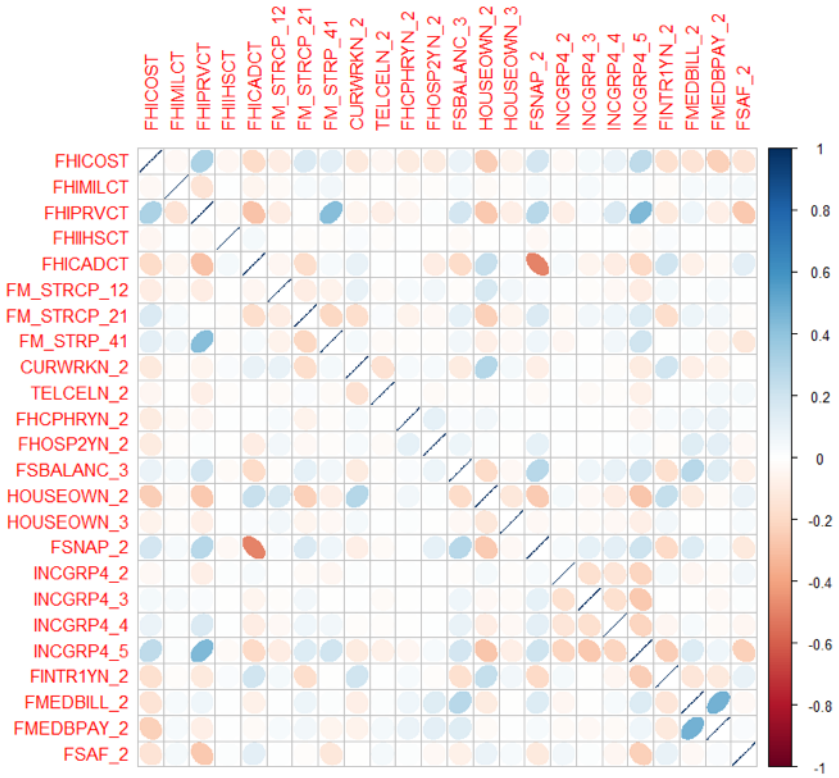

Figure 25: Logistic Regression

	FALSE	TRUE
0	7021	3205
1	2726	8232

Figure 26: Logistic Regression

	FALSE	TRUE
0	1729	828
1	689	2051

Figure 27: Logistic Regression

9.7 Principal Component Analysis

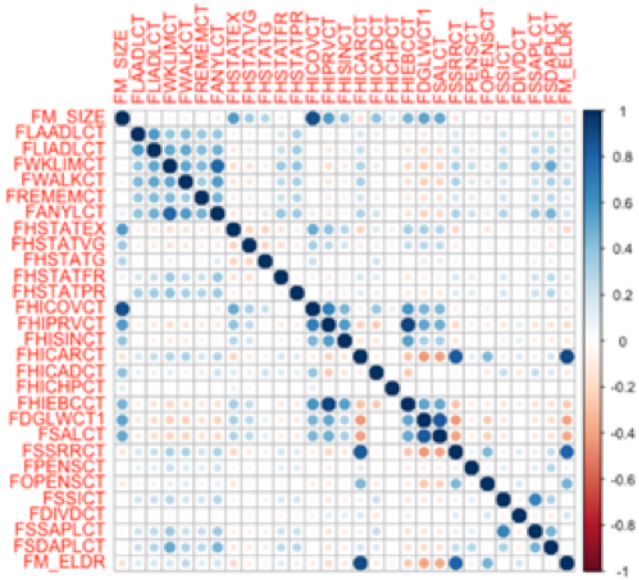

Figure 28: Principal Component Analysis

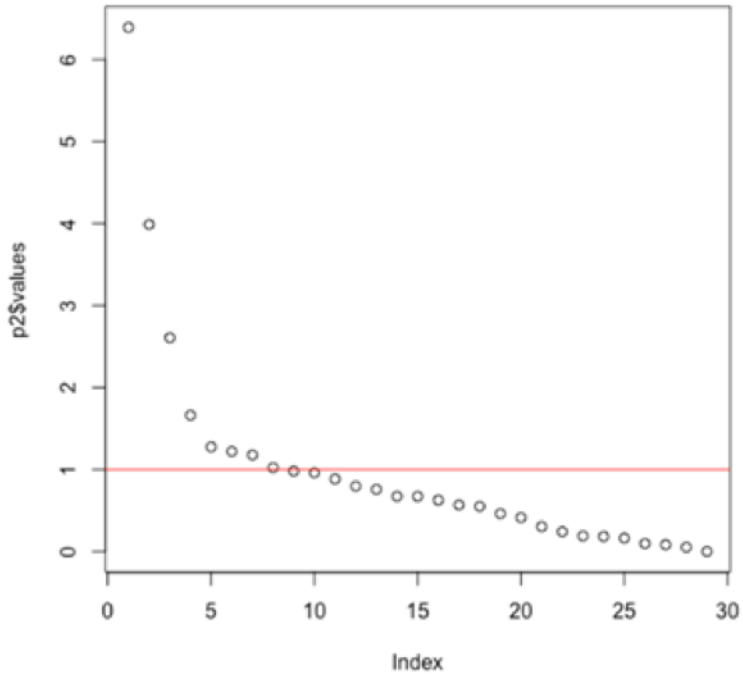

Figure 29: Principal Component Analysis

```
Loadings:
          RC1    RC2    RC3    RC4    RC5    RC12   RC8    RC7    RC6    RC10   RC9    RC11
FLAADLCT  0.754
FLIADLCT  0.793
FWKLIMCT  0.681
FWALKCT   0.695
FREMEMCT  0.636
FANYLCT   0.680
FHSTATPR  0.592
FHICOVCT         0.679         0.632
FHIPRVCT         0.913
FHISINCT         0.753
FHIEBCCT         0.879
FHICARCT                0.912
FSSRRCT                 0.868
FOPENSCT                0.608
FM_ELDR                 0.930
FM_SIZE          0.551         0.695
FHICADCT                       0.870
FSSICT                                0.879
FSSAPLCT                              0.870
FDGLWCT1                                     0.765
FSALCT                                       0.779
FPENSCT                                             0.893
FHSTATG                                                    0.963
FHSTATEX                                                          -0.601
FHSTATVG                                                           0.903
FHSTATFR                                                                  0.857
FHICHPCT                                                                         0.995
FDIVDCT                                                                                 0.963
FSDAPLCT

                 RC1   RC2   RC3   RC4   RC5   RC12   RC8   RC7   RC6   RC10   RC9   RC11
SS loadings    3.768 3.565 3.210 1.979 1.862 1.680 1.245 1.216 1.216 1.202 1.036 0.984
Proportion Var 0.130 0.123 0.111 0.068 0.064 0.058 0.043 0.042 0.042 0.041 0.036 0.034
Cumulative Var 0.130 0.253 0.364 0.432 0.496 0.554 0.597 0.639 0.681 0.722 0.758 0.792
```

Figure 30: Principal Component Analysis

References

Black, L. I., T. C. Clarke, P. M. Barnes, B. J. Stussman, and R. L. Nahin. 2015. "Use of Complementary Health Approaches Among Children Aged 4-17 Years in the United States: National Health Interview Survey, 2007-2012." *National Health Statistics Reports* 78: 1–19.

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Jean-Louis, G., N. J. Williams, D. Sarpong, A. Pandey, S. Youngstedt, F. Zizi, and G. Ogedegbe. 2014. "Associations Between Inadequate Sleep and Obesity in the Us Adult Population: Analysis of the National Health Interview Survey (1977-2009)." *BMC Public Health* 14: 290.

Ma, V. Y., L. Chan, and K. J. Carruthers. 2014. "Incidence, Prevalence, Costs, and Impact on Disability of Common Conditions Requiring Rehabilitation in the United States: Stroke, Spinal Cord Injury, Traumatic Brain Injury, Multiple Sclerosis, Osteoarthritis, Rheumatoid Arthritis, Limb Loss, and Back Pain." *Archives of Physical Medicine and Rehabilitation* 95 (5): 986–95.