Quantitative, Qualitative, and PCR Analysis

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Summary

In this project, I embarked on a comprehensive exploration of data analysis on a data set about healthcare analytics. The project is aimed to provide insights into models that can help predict three distinct types of problems, quantitative response, qualitative response, and a principal components regression (PCR) problem. The qualitative response problem will predict the severity of an illness for an average patient in the hospital, and both the quantitative and PCR will predict the stay of an average patient. This data set was obtained from Kaggle and will be the data set that these models will be used on. The model or models chosen from the exploratory data analysis are based on the test mean squared error (MSE) obtained after training the model and testing the model on our test data. Qualified models that will be considered for our final predictions will be compared if they return an MSE for an output. Models that do not return an MSE or are not available will be omitted from the final models that we will choose for our prediction. Based on our quantitative exploratory data analysis (EDA), the models chosen are multiple linear regression and partial least squares because they have the lowest MSE out of all the models applied to our problem. The average stay for a patient is 17.06 days. The qualitative response uses quadratic discriminant analysis and linear discriminant analysis to predict how severe a patient's illness could be. Both models indicate that an average patient will have a moderate severity of illness. Lastly, the PCR problem was explored, and this model predicted a patient to stay an average of 16.68 days in a hospital.

Data & Approach

The analysis in this project is aimed at trying to tackle real-world problems. The data set used is healthcare analytics which includes how long a patient has stayed in the hospital and the severity of illness. Predicting the average stay for a patient will be used for quantitative and PCR analysis and predicting the severity of illness for a patient will be used for qualitative analysis. The variables in this data set are "case id," hospital code," "hospital type code," City Code Hospital," hospital region code," "Available extra rooms in hospital," "department," "ward type," "ward facility code," "bed grade," "patient id," "city code patient," "type of admission," "severity of illness," "visitors with patient," "age," "admission deposit," and "stay." The variable "stay" a range of variables and to make this variable easier to perform quantitative and PCR. analysis so I made a range of days correspond to a factor. 0 to 20 days of stay correspond to 0, 21 to 50 days of stay correspond to 1, and 51 to more than 100 days of stay correspond to 2. I did the same thing with the severity of illness in patients. Extreme illness corresponds to 1, minor illness corresponds to 2, and moderate illness responds to 3. This data set is split into a training set and a test set that we will train the models to and test with the test set. The split is 70 to 30 with the training set having 70% of the data and the test set having 30%.

Quantitative Analysis

After obtaining a summary of the data set in R, I used multiple linear regression on the numerical variables as predictors and "stay" as a response variable. Using the t-test and the p-values of the variables in the multiple linear regression will help determine which predictors are going to be included in our models. Best subset selection was used to see what the best model is with the number of predictors used in multiple linear regression. This is based on the lowest BIC value. Ridge regression, lasso regression, partial least squares, regression trees, bagging, random forest, and boosting models were also applied to the training set and then applied to the test set to

determine the MSE for each model. The models that are valid for final selection will be models that return MSE and the model with the lowest MSE will be picked.

Qualitative Analysis

For qualitative analysis, we will use the same predictors for quantitative analysis but predict the severity of illness a patient may have. K-nearest-neighbors (KNN), logistic regression, linear discriminant analysis, quadratic discriminant analysis, classification trees, bagging approach, and random forest approach were used for qualitative analysis. The lowest MSE obtained from these models will be considered for the final model to predict the severity of illness for a patient. Again, models that do not return an MSE will not be included in this selection.

Principal Components Regression

In PCR, instead of using the numerical variables as predictors, the whole data set was considered in using PCR. Using the graph obtained from this regression, we can find out what the lowest cross-validation error is and use that for the number of components in our regression model. From this, we can use this and figure out how well the PCR model fits compared to the partial least squares model so we can see how it compares to other models used in quantitative analysis.

Detailed Findings

Quantitative Analysis

For all numerical variables in the multiple linear regression model, we applied a null hypothesis that would either eliminate or include each variable in any later models. For the t-test, we will reject the null hypothesis if the t-value does not equal 0. For p-values, if their values are greater than 0.05 then we will accept the null hypothesis and eliminate the variable from any further models used. All predictors used in this model rejected the null hypothesis and will be available for future use in models. The MSE for the multiple linear regression is 0.4420886. The best subset selection was used to determine how many predictors produced the best model. Based on the lowest BIC value, the best model uses all 7 predictors. When trying to find the MSE for this model, I kept getting a "NaN" value which disqualified this model for final selection in our prediction. These two models were used first to determine which variables would be used in future models to determine the best fit for our data set. The next two models are the ridge and lasso regression that produced .444018 and .4446472 MSE respectively. The following models produced the following MSEs, partial least squares: .4438446, regression tree: .559435, bagging approach: .5483819, random forest approach: .4902687, and boosting approach: .5514. The model with the lowest MSE is the multiple linear regression but also partial least squares model is not too far off so I will use both models to help with predicting the stay of a patient. I used the mean of the predicted values of both the multiple linear regression and partial least squares and multiplied it by 20 to get an average of about 16.688 days that a patient will stay in a hospital.

Qualitative Analysis

To help the data fit better for qualitative analysis I changed each variable into a factor so that they could fit better into the models. For the KNN model, I was able to run the model for the

training set but was unable to return an MSE for the model. In the logistic regression, I chose to introduce a null hypothesis to try and remove any unnecessary predictors that we may not need. Predictors that have a p-value greater than 0.05 are not statistically significant and will be removed from any future use in qualitative analysis. Fortunately, we did not have to remove any variables as each p-value was below 0.05. Unfortunately, the logistic regression model returned an MSE of 0. Even though this model did return a mean squared error, we will not include it because if the MSE is 0 then it may mean that this model fits too well and should be excluded from the final decision. LDA and QDA produced .5435743 and .5415879 respectively. The last 3 models used in this analysis are the classification trees, bagging approach, and random forest. The classification trees yielded a 0.5617 MSE while I was not able to get a MSE for the bagging approach or random forest. I was able to run the models on the data sets but only got the output "N/A" for each MSE. I tried removing any "N/A" values from each prediction but still got the same output for each MSE. The only models that will be considered for prediction are the LDA, QDA, and classification trees. We will use both LDA and QDA for predictions as their MSEs are very close to each other. Each model indicates that on average a patient will have a moderate severity of illness.

Principal Component Regression

For PCR instead of using only the 7 predictors that we used for quantitative and qualitative analysis I used all variables to try and find the least number of components needed to get the best model. Here, we don't want to use all the components in the model, but we want to find the lowest mean squared error of prediction with the lowest number of components available to us in the model. First, we tried it on the whole data set, then the training data set, and finally the test data set to get an MSE of 0.4194666. The most components used in the model are 33. There must have been an error somewhere when I calculated this because there are not 33 predictors in the whole data set. I believe this has contributed to the way that the data set itself is set up using categorical variables. I tried turning each variable into a factor and/or a numerical value but it does not seem like it helps. I also compared this model to the least partial squares model which obtained a very close MSE at 0.4310673. Lastly, we used this model to determine the average stay of patients at a hospital. I took the mean of the predictions and used the same calculations that I did in the quantitative analysis to receive an average of 16.68 days.

Validity & Reliability Assessment

In this project, the careful selection of variables is driven by the aim of unraveling a compelling narrative through their interrelationships. Each variable chosen has been meticulously considered to contribute to a coherent story within our exploratory data analysis. The introduction of null hypotheses serves as a cornerstone in validating the significance of these relationships, adding a layer of statistical rigor to our methodology.

A pivotal step in bolstering the reliability of our analysis is the thoughtful categorization of predictors. Distinguishing between categorical and numerical predictors is paramount, particularly for models that demand numerical inputs. This categorization enhances the suitability of predictors for specific modeling techniques, contributing to the reliability of our chosen variables.

The robustness and credibility of our models are foundational to the project's reproducibility and the meaningful interpretation of our findings. Beyond methodological

necessities, the validation of our chosen models, predictors, and response variables is an indispensable facet of generalizing insights that transcend statistical outcomes.

Appendix

https://www.kaggle.com/datasets/nehaprabhavalkar/av-healthcare-analytics-ii/

Disclaimer: Many values that I used to make my calculations in code seemed to change after I knitted the code into a word document to use for the Appendix.

```
library(ISLR2)
library(MASS)
library(class)
library(e1071)
library(boot)
library(glmnet)
library(pls)
library(leaps)
library(tree)
library(randomForest)
library(BART)
library(dplyr)
library(gbm)
#Loading libraries and data needed
#data used are already split into training and testing set
#there is no need to split them
hospital <- read.csv("./hospital_data.csv")
hospital_dictionary <- read.csv("./hospital_data_dictionary.csv")
#omitting any n/a values
hospital <- na.omit(hospital)
hospital <- hospital %>%
  mutate(Stay <- recode(Stay, '0-10' = 0, '11-20' = 0, '21-30' = 1,
                        '31-40' = 1, '41-50' = 1, '51-60' =2,'61-70' = 2,
                        '71-80' = 2, '81-90' = 2,'91-100' = 2,'>100' = 2))
colnames(hospital)[19] <- "stay"
hospital <- hospital[,-18]
#splitting data into a 70/30 split
#70% train, 30% test
train <- sample(1:dim(hospital)[1], size=0.7*dim(hospital)[1])
hos_train <- hospital[train, ]
hos_test <- hospital[-train, ]

table(hospital$stay)
##      0      1      2
## 100345 152169  54731
summary(hospital)
```

```
##    case_id       Hospital_code   Hospital_type_code City_Code_Hospital
## Min.   :    1   Min.   : 1.00   Length:313793      Min.   : 1.000
## 1st Qu.: 79271   1st Qu.:11.00   Class :character   1st Qu.: 2.000
## Median :158950   Median :19.00   Mode  :character   Median : 5.000
## Mean   :158938   Mean   :18.33                      Mean   : 4.778
## 3rd Qu.:238399   3rd Qu.:26.00                      3rd Qu.: 7.000
## Max.   :318438   Max.   :32.00                      Max.   :13.000
## Hospital_region_code Available.Extra.Rooms.in.Hospital  Department
## Length:313793        Min.   : 0.000                    Length:313793
## Class :character     1st Qu.: 2.000                    Class :character
## Mode  :character     Median : 3.000                    Mode  :character
##                      Mean   : 3.196
##                      3rd Qu.: 4.000
##                      Max.   :24.000
##  Ward_Type         Ward_Facility_Code   Bed.Grade       patientid
## Length:313793      Length:313793      Min.   :1.000   Min.   :    1
## Class :character   Class :character   1st Qu.:2.000   1st Qu.: 32833
## Mode  :character   Mode  :character   Median :3.000   Median : 65735
##                                       Mean   :2.623   Mean   : 65743
##                                       3rd Qu.:3.000   3rd Qu.: 98472
##                                       Max.   :4.000   Max.   :131624
## City_Code_Patient Type.of.Admission  Severity.of.Illness Visitors.with.Patient
## Min.   : 1.000    Length:313793      Length:313793       Min.   : 0.000
## 1st Qu.: 4.000    Class :character   Class :character    1st Qu.: 2.000
## Median : 8.000    Mode  :character   Mode  :character    Median : 3.000
## Mean   : 7.252                                           Mean   : 3.281
## 3rd Qu.: 8.000                                           3rd Qu.: 4.000
## Max.   :38.000                                           Max.   :32.000
##     Age           Admission_Deposit      stay
## Length:313793      Min.   : 1800     Min.   :0.000
## Class :character   1st Qu.: 4188     1st Qu.:0.000
## Mode  :character   Median : 4742     Median :1.000
##                    Mean   : 4882     Mean   :0.852
##                    3rd Qu.: 5410     3rd Qu.:1.000
##                    Max.   :11008     Max.   :2.000
##                                      NA's   :6548
```

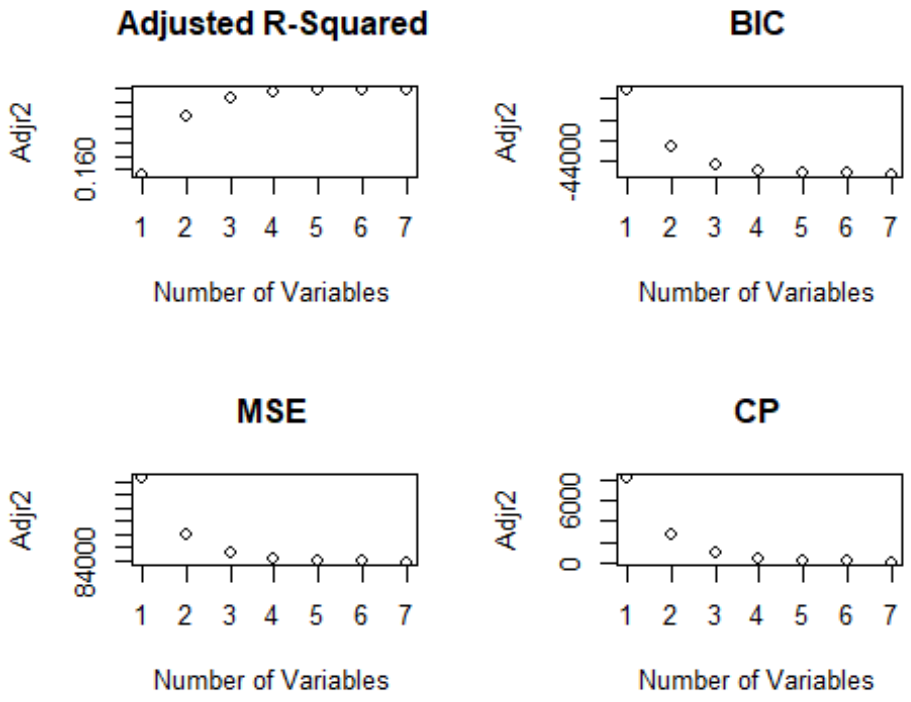
Numerical columns: Hospital_code, City_Code_Hospital, Available.Extra.Rooms.in.Hospital, Bed.Grade, City_Code_Patient, Visitors.with.Patient, and Admission_Deposit, stay
Categorical Columns: Hospital_type_code, Hospital_region_code, Ward_Type, Ward_Facility_Code, Type of Admission, Severity of Illness, and, Age
Quantitative Problem: - Predicting hospitalization duration for patients.
for multiple linear regression: we will assume for the t-test that H(o): B1 = 0 and H(A): B1 != 0 rejecting the null hypothesis will tell if there is a statistically significant difference between the means of two variables
we will assume for the p-value that H(o): p(value) > 0.05 and H(A): p-value < 0.05 this will determine if a variable is statistically significant

```
#Multiple Linear Regression
hos_lm <- lm(stay ~ Hospital_code + City_Code_Hospital +
               Available.Extra.Rooms.in.Hospital + Bed.Grade +
               City_Code_Patient + Visitors.with.Patient +
               Admission_Deposit, data = hos_train)
summary(hos_lm)
## Call:
## lm(formula = stay ~ Hospital_code + City_Code_Hospital +
Available.Extra.Rooms.in.Hospital +
##     Bed.Grade + City_Code_Patient + Visitors.with.Patient + Admission_Deposit,
##     data = hos_train)
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.8710 -0.6156  0.1285  0.3933  2.4391
## Coefficients:
##                                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)                     5.764e-01  1.028e-02  56.092  < 2e-16 ***
## Hospital_code                    3.750e-03  1.579e-04  23.742  < 2e-16 ***
## City_Code_Hospital              -4.897e-03  4.389e-04 -11.155  < 2e-16 ***
## Available.Extra.Rooms.in.Hospital -9.166e-02  1.190e-03 -77.023  < 2e-16 ***
## Bed.Grade                       -6.789e-02  1.569e-03 -43.281  < 2e-16 ***
## City_Code_Patient               -2.268e-03  2.829e-04  -8.017 1.09e-15 ***
## Visitors.with.Patient            1.991e-01  9.189e-04 216.673  < 2e-16 ***
## Admission_Deposit                1.728e-05  1.286e-06  13.442  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 0.6247 on 215083 degrees of freedom
##   (4564 observations deleted due to missingness)
## Multiple R-squared:  0.1898, Adjusted R-squared:  0.1898
## F-statistic:  7200 on 7 and 215083 DF,  p-value: < 2.2e-16
lin_pred <- predict(hos_lm, hos_test)
lin_MSE <- mean((lin_pred - hos_test$stay)^2)
print(lin_MSE)
## [1] NA
```

From the summary of the multiple linear regression, all variables used in this regression are statistically significant because their p-values are all below the null hypothesis which is 0.05. As for the t-test, each t-value does not equal 0 which means we can reject the null hypothesis for the t-value which means that there is a significant difference in size of the difference relative to the variation in your sample data. The test MSE for multiple linear regression is 0.4420886.

```
#Best Subset Selection
best_subset_train <- regsubsets(stay ~ Hospital_code + City_Code_Hospital +
               Available.Extra.Rooms.in.Hospital + Bed.Grade +
               City_Code_Patient + Visitors.with.Patient +
               Admission_Deposit,data = hos_train, nvmax = 7)
subset_sum <- summary(best_subset_train)
print(subset_sum)
```

```
## Subset selection object
## Call: regsubsets.formula(stay ~ Hospital_code + City_Code_Hospital +
##     Available.Extra.Rooms.in.Hospital + Bed.Grade + City_Code_Patient +
##     Visitors.with.Patient + Admission_Deposit, data = hos_train,
##     nvmax = 7)
## 7 Variables  (and intercept)
##                              Forced in Forced out
## Hospital_code                    FALSE     FALSE
## City_Code_Hospital               FALSE     FALSE
## Available.Extra.Rooms.in.Hospital     FALSE     FALSE
## Bed.Grade                        FALSE     FALSE
## City_Code_Patient                FALSE     FALSE
## Visitors.with.Patient            FALSE     FALSE
## Admission_Deposit                FALSE     FALSE
## 1 subsets of each size up to 7
## Selection Algorithm: exhaustive
##          Hospital_code City_Code_Hospital Available.Extra.Rooms.in.Hospital
## 1  ( 1 ) " "           " "               " "
## 2  ( 1 ) " "           " "               "*"
## 3  ( 1 ) " "           " "               "*"
## 4  ( 1 ) "*"           " "               "*"
## 5  ( 1 ) "*"           " "               "*"
## 6  ( 1 ) "*"           "*"               "*"
## 7  ( 1 ) "*"           "*"               "*"
##          Bed.Grade City_Code_Patient Visitors.with.Patient Admission_Deposit
## 1  ( 1 ) " "       " "              "*"                   " "
## 2  ( 1 ) " "       " "              "*"                   " "
## 3  ( 1 ) "*"       " "              "*"                   " "
## 4  ( 1 ) "*"       " "              "*"                   " "
## 5  ( 1 ) "*"       " "              "*"                   "*"
## 6  ( 1 ) "*"       " "              "*"                   "*"
## 7  ( 1 ) "*"       "*"              "*"                   "*"
subset_sum$rsq
## [1] 0.1583829 0.1797169 0.1864155 0.1884286 0.1891377 0.1895909 0.1898330
par(mfrow = c(2,2))
plot(subset_sum$adjr2, xlab = "Number of Variables",
    ylab = "Adjr2", main = "Adjusted R-Squared")
plot(subset_sum$bic, xlab = "Number of Variables",
    ylab = "Adjr2", main = "BIC")
plot(subset_sum$rss, xlab = "Number of Variables",
    ylab = "Adjr2", main = "MSE")
plot(subset_sum$cp, xlab = "Number of Variables",
    ylab = "Adjr2", main = "CP")
```

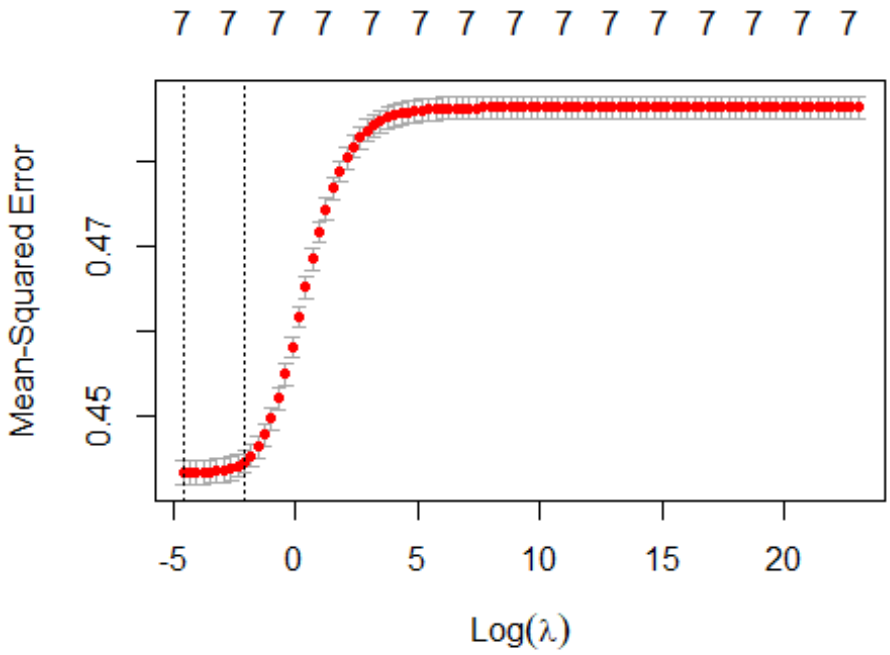



```
data.frame(
  adj.r2 = which.max(subset_sum$adjr2),
  cp = which.min(subset_sum$cp),
  bic = which.min(subset_sum$bic)
)
##   adj.r2 cp bic
## 1      7  7   7
#based on the lowest BIC value, the best model uses 7 variables
#forward and backward stepwise selection
regfit_fwd <- regsubsets(stay ~ Hospital_code + City_Code_Hospital +
                  Available.Extra.Rooms.in.Hospital + Bed.Grade +
                  City_Code_Patient + Visitors.with.Patient +
                  Admission_Deposit, data = hos_train, nvmax = 7,
                  method = "forward")
summary(regfit_fwd)
## Subset selection object
## Call: regsubsets.formula(stay ~ Hospital_code + City_Code_Hospital +
##     Available.Extra.Rooms.in.Hospital + Bed.Grade + City_Code_Patient +
##     Visitors.with.Patient + Admission_Deposit, data = hos_train,
##     nvmax = 7, method = "forward")
## 7 Variables  (and intercept)
##                              Forced in Forced out
## Hospital_code                    FALSE      FALSE
## City_Code_Hospital               FALSE      FALSE
## Available.Extra.Rooms.in.Hospital    FALSE      FALSE
```

```
## Bed.Grade                       FALSE     FALSE
## City_Code_Patient                FALSE     FALSE
## Visitors.with.Patient            FALSE     FALSE
## Admission_Deposit                FALSE     FALSE
## 1 subsets of each size up to 7
## Selection Algorithm: forward
##          Hospital_code City_Code_Hospital Available.Extra.Rooms.in.Hospital
## 1  ( 1 ) " "           " "               " "
## 2  ( 1 ) " "           " "               "*"
## 3  ( 1 ) " "           " "               "*"
## 4  ( 1 ) "*"           " "               "*"
## 5  ( 1 ) "*"           " "               "*"
## 6  ( 1 ) "*"           "*"               "*"
## 7  ( 1 ) "*"           "*"               "*"
##          Bed.Grade City_Code_Patient Visitors.with.Patient Admission_Deposit
## 1  ( 1 ) " "        " "              "*"                  " "
## 2  ( 1 ) " "        " "              "*"                  " "
## 3  ( 1 ) "*"        " "              "*"                  " "
## 4  ( 1 ) "*"        " "              "*"                  " "
## 5  ( 1 ) "*"        " "              "*"                  "*"
## 6  ( 1 ) "*"        " "              "*"                  "*"
## 7  ( 1 ) "*"        "*"              "*"                  "*"
regfit_bwd <- regsubsets(stay ~ Hospital_code + City_Code_Hospital +
                Available.Extra.Rooms.in.Hospital  + Bed.Grade +
                City_Code_Patient + Visitors.with.Patient +
                Admission_Deposit, data = hos_train, nvmax = 7,
                method = "backward")
summary(regfit_bwd)
## Subset selection object
## Call: regsubsets.formula(stay ~ Hospital_code + City_Code_Hospital +
##     Available.Extra.Rooms.in.Hospital + Bed.Grade + City_Code_Patient +
##     Visitors.with.Patient + Admission_Deposit, data = hos_train,
##     nvmax = 7, method = "backward")
## 7 Variables  (and intercept)
##                                 Forced in Forced out
## Hospital_code                       FALSE     FALSE
## City_Code_Hospital                  FALSE     FALSE
## Available.Extra.Rooms.in.Hospital   FALSE     FALSE
## Bed.Grade                           FALSE     FALSE
## City_Code_Patient                   FALSE     FALSE
## Visitors.with.Patient               FALSE     FALSE
## Admission_Deposit                   FALSE     FALSE
## 1 subsets of each size up to 7
## Selection Algorithm: backward
##          Hospital_code City_Code_Hospital Available.Extra.Rooms.in.Hospital
## 1  ( 1 ) " "           " "               " "
```

```
## 2  ( 1 ) " "         " "            "*"
## 3  ( 1 ) " "         " "            "*"
## 4  ( 1 ) "*"         " "            "*"
## 5  ( 1 ) "*"         " "            "*"
## 6  ( 1 ) "*"         "*"            "*"
## 7  ( 1 ) "*"         "*"            "*"
##          Bed.Grade City_Code_Patient Visitors.with.Patient Admission_Deposit
## 1  ( 1 ) " "       " "            "*"                " "
## 2  ( 1 ) " "       " "            "*"                " "
## 3  ( 1 ) "*"       " "            "*"                " "
## 4  ( 1 ) "*"       " "            "*"                " "
## 5  ( 1 ) "*"       " "            "*"                "*"
## 6  ( 1 ) "*"       " "            "*"                "*"
## 7  ( 1 ) "*"       "*"            "*"                "*"
coef(regfit_fwd, 7)
##                  (Intercept)                Hospital_code
##                0.5764228459                0.0037497810
##            City_Code_Hospital Available.Extra.Rooms.in.Hospital
##               -0.0048965026               -0.0916566635
##                   Bed.Grade             City_Code_Patient
##               -0.0678928049               -0.0022678283
##          Visitors.with.Patient             Admission_Deposit
##                0.1991101692                0.0000172839
coef(regfit_bwd, 7)
##                  (Intercept)                Hospital_code
##                0.5764228459                0.0037497810
##            City_Code_Hospital Available.Extra.Rooms.in.Hospital
##               -0.0048965026               -0.0916566635
##                   Bed.Grade             City_Code_Patient
##               -0.0678928049               -0.0022678283
##          Visitors.with.Patient             Admission_Deposit
##                0.1991101692                0.0000172839
set.seed(1)

regfit.best <- regsubsets(stay ~ Hospital_code + City_Code_Hospital +
                Available.Extra.Rooms.in.Hospital + Bed.Grade +
                City_Code_Patient + Visitors.with.Patient +
                Admission_Deposit, data = hos_train, nvmax = 7)

test.mat <- model.matrix(stay ~ Hospital_code + City_Code_Hospital +
                Available.Extra.Rooms.in.Hospital + Bed.Grade +
                City_Code_Patient + Visitors.with.Patient +
                Admission_Deposit, data = hos_train)

val.errors <- rep(NA, 7)
for (i in 1:7) {
```

```
  coefi <- coef(regfit.best, id = i)
  pred <- test.mat[, names(coef)] %*% coefi
  val.errors[i] <- mean((hos_test$stay - pred)^2)
}
val.errors
## [1] NaN NaN NaN NaN NaN NaN NaN
coef(regfit.best, 7)
##                  (Intercept)                Hospital_code
##                0.5764228459                0.0037497810
##           City_Code_Hospital Available.Extra.Rooms.in.Hospital
##               -0.0048965026               -0.0916566635
##                   Bed.Grade             City_Code_Patient
##               -0.0678928049               -0.0022678283
##         Visitors.with.Patient             Admission_Deposit
##                0.1991101692                0.0000172839
#ridge regression
#need to make a matrix first
hos_train[is.na(hos_train)] <- 0
hos_test[is.na(hos_test)] <- 0
hospital[is.na(hospital)] <- 0
set.seed(1)
train_matrix <- model.matrix(stay ~ Hospital_code + City_Code_Hospital +
                Available.Extra.Rooms.in.Hospital + Bed.Grade +
                City_Code_Patient + Visitors.with.Patient +
                Admission_Deposit, data = hos_train)
test_matrix <- model.matrix(stay ~ Hospital_code + City_Code_Hospital +
                Available.Extra.Rooms.in.Hospital + Bed.Grade +
                City_Code_Patient + Visitors.with.Patient +
                Admission_Deposit, data = hos_test)

grid = 10^seq(10, -2, length = 100)

ridge_cv <- cv.glmnet(train_matrix, hos_train['stay'], alpha = 0,
                lambda = grid)
plot(ridge_cv)
```

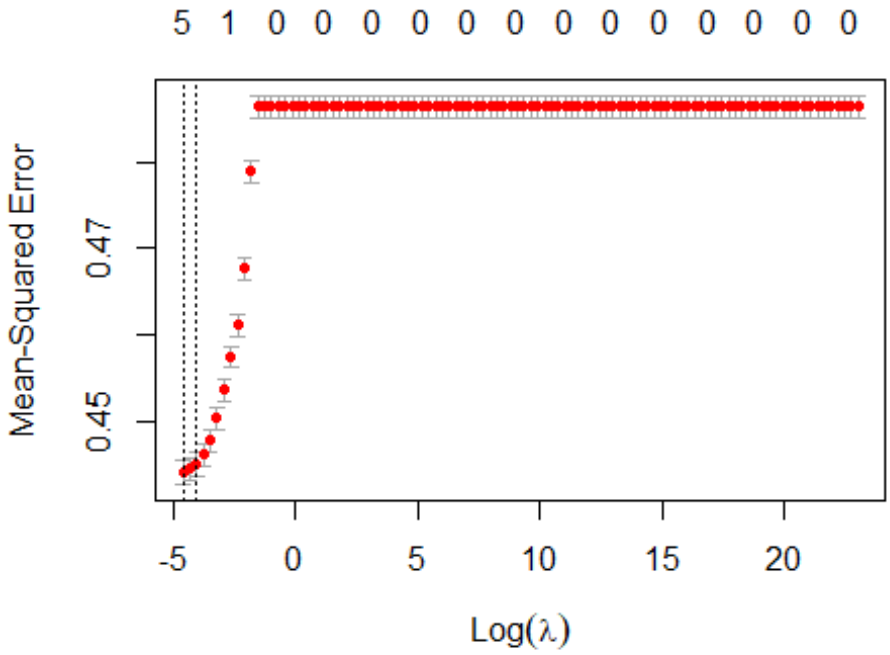



```
r_lambda_min <- ridge_cv$lambda.min
print(r_lambda_min)
## [1] 0.01
coef(ridge_cv)
## 9 x 1 sparse Matrix of class "dgCMatrix"
##                                    s1
## (Intercept)                 7.908928e-01
## (Intercept)                 .
## Hospital_code                2.512776e-03
## City_Code_Hospital          -2.297725e-03
## Available.Extra.Rooms.in.Hospital -5.329980e-02
## Bed.Grade                   -5.114103e-02
## City_Code_Patient           -2.096454e-03
## Visitors.with.Patient        9.433320e-02
## Admission_Deposit            3.738770e-06
ridge_cv <- cv.glmnet(train_matrix, hos_train['stay'], alpha = 0,
                      lambda = grid)
ridge_pred <- predict(ridge_cv, s = r_lambda_min, lambda = grid,
                      alpha = 0, newx = test_matrix)
ridge_MSE <- mean((ridge_pred - hos_test["stay"])^2)
print(ridge_MSE)
## [1] 0.445358
```

Test MSE for Ridge Regression is .444018

```
#Lasso Regression
set.seed(1)
```

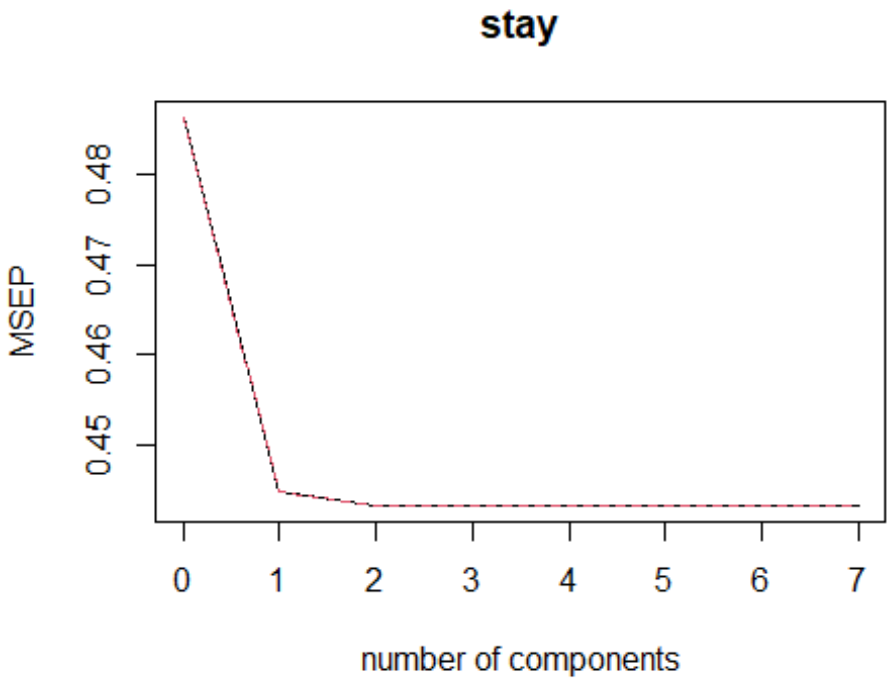
```
lasso_cv <- cv.glmnet(train_matrix,  hos_train[,"stay"],
                      alpha = 1, lambda = grid)
plot(lasso_cv)
```




```
best_lambda_lasso <- lasso_cv$lambda.min
print(best_lambda_lasso)
## [1] 0.01
coef(lasso_cv)
## 9 x 1 sparse Matrix of class "dgCMatrix"
##                                    s1
## (Intercept)                0.7480349342
## (Intercept)                .
## Hospital_code              0.0009500399
## City_Code_Hospital         .
## Available.Extra.Rooms.in.Hospital -0.0483227161
## Bed.Grade                  -0.0396772631
## City_Code_Patient          .
## Visitors.with.Patient      0.0996966267
## Admission_Deposit          .
lasso_pred <- predict(lasso_cv, s = best_lambda_lasso,
                      lambda = grid, alpha = 1, newx = test_matrix)
lasso_MSE <- mean((lasso_pred - hos_test[,"stay"])^2)
print(lasso_MSE)
## [1] 0.4463289
```

Lasso regression MSE is .4446472

```r
#Partial Least Squares
set.seed(1)
pls.fit <- plsr(stay ~ Hospital_code + City_Code_Hospital +
                  Available.Extra.Rooms.in.Hospital + Bed.Grade +
                  City_Code_Patient + Visitors.with.Patient +
                  Admission_Deposit, data = hos_train, scale = TRUE,
                validation = "CV")
summary(pls.fit)
## Data:    X dimension: 219655 7
##  Y dimension: 219655 1
## Fit method: kernelpls
## Number of components considered: 7
##
## VALIDATION: RMSEP
## Cross-validated using 10 random segments.
##        (Intercept)  1 comps  2 comps  3 comps  4 comps  5 comps  6 comps
## CV          0.6974    0.667   0.6658   0.6658   0.6658   0.6658   0.6658
## adjCV       0.6974    0.667   0.6658   0.6658   0.6658   0.6658   0.6658
##        7 comps
## CV      0.6658
## adjCV   0.6658
##
## TRAINING: % variance explained
##       1 comps  2 comps  3 comps  4 comps  5 comps  6 comps  7 comps
## X      13.873   28.347   45.039   59.340   73.617   87.549  100.000
## stay    8.529    8.863    8.868    8.868    8.868    8.868    8.868
validationplot(pls.fit, val.type = "MSEP")
```

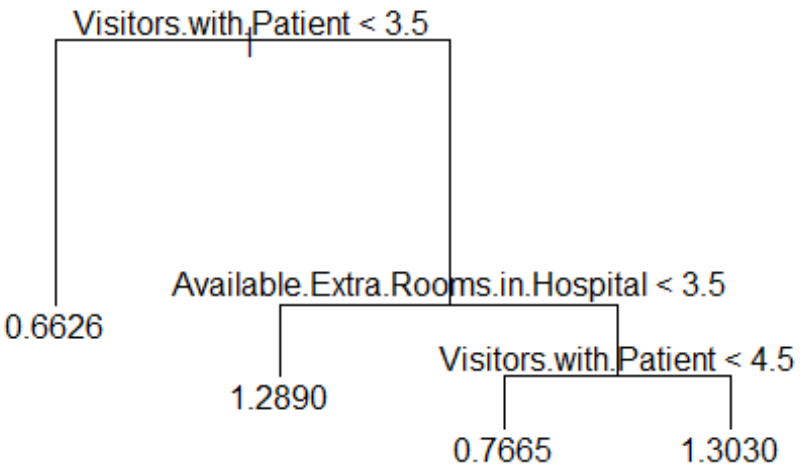



```
#Lowest cross-validation  error occurs when M = 1 when PLS is used.
pls.pred <- predict(pls.fit, hos_test, ncomp = 1)
pls_MSE <- mean((pls.pred - hos_test[,"stay"])^2)
print(pls_MSE)
## [1] 0.4472809
#performing PLS using the full data set using M=1
#we can use this to compare to PCR
pls.fit2 <- plsr(stay ~ ., data = hospital, scale = TRUE,
                 ncomp = 1)
summary(pls.fit2)
## Data:    X dimension: 313793 44
##  Y dimension: 313793 1
## Fit method: kernelpls
## Number of components considered: 1
## TRAINING: % variance explained
##       1 comps
## X       3.427
## stay   12.024
```

Test MSE for PLS is 0.4438446

```
#regression tree
reg_tree <- tree(stay ~ Hospital_code + City_Code_Hospital +
                   Available.Extra.Rooms.in.Hospital + Bed.Grade +
                   City_Code_Patient + Visitors.with.Patient +
                   Admission_Deposit, data = hos_train)
summary(reg_tree)
```

```
##
## Regression tree:
## tree(formula = stay ~ Hospital_code + City_Code_Hospital +
Available.Extra.Rooms.in.Hospital +
##     Bed.Grade + City_Code_Patient + Visitors.with.Patient + Admission_Deposit,
##     data = hos_train)
## Variables actually used in tree construction:
## [1] "Visitors.with.Patient"           "Available.Extra.Rooms.in.Hospital"
## Number of terminal nodes:  4
## Residual mean deviance:  0.4146 = 91080 / 219700
## Distribution of residuals:
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## -1.3030 -0.6626  0.3374  0.0000  0.3374  1.3370
plot(reg_tree)
text(reg_tree, pretty = 0)
```

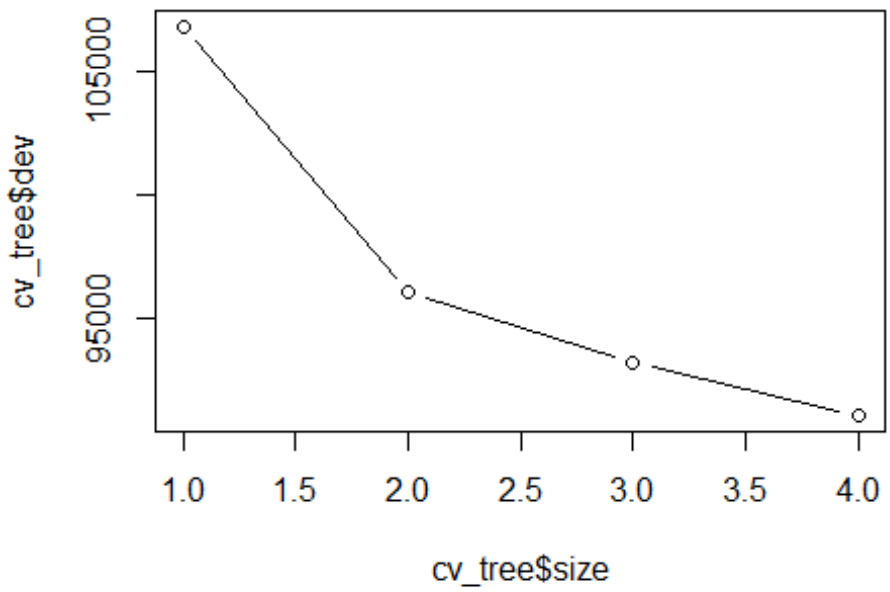



```
reg_tree_hat <- predict(reg_tree, data = hos_test)
reg_tree_MSE <- mean((reg_tree_hat - hos_test$stay)^2)
## Warning in reg_tree_hat - hos_test$stay: longer object length is not a multiple
## of shorter object length
print(reg_tree_MSE)
## [1] 0.5612125
```

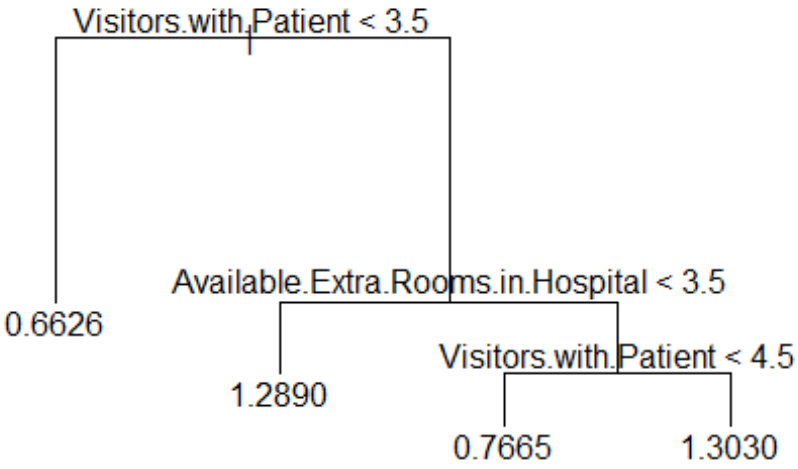
The test MSE for the regression tree is 0.559435

```
#using cross validation to get the optimal level of tree complexity
set.seed(1)
```

```
cv_tree <- cv.tree(reg_tree)
plot(cv_tree$size, cv_tree$dev, type = "b")
```




```
#pruning tree to optimal level from graph
#seems like optimal tree level is 4
prune_hos <- prune.tree(reg_tree, best = 4)
plot(prune_hos)
text(prune_hos, pretty=0)
```




```
#The pruned tree is the same as the regression tree
#MSE of the pruned tree
prune_tree_hat <- predict(prune_hos, data = hos_test)
prune_tree_MSE <- mean((prune_tree_hat - hos_test$stay)^2)
## Warning in prune_tree_hat - hos_test$stay: longer object length is not a
## multiple of shorter object length
print(prune_tree_MSE)
## [1] 0.5612125
```

As expected the pruned tree model's MSE is the same as the regression tree 0.559435.

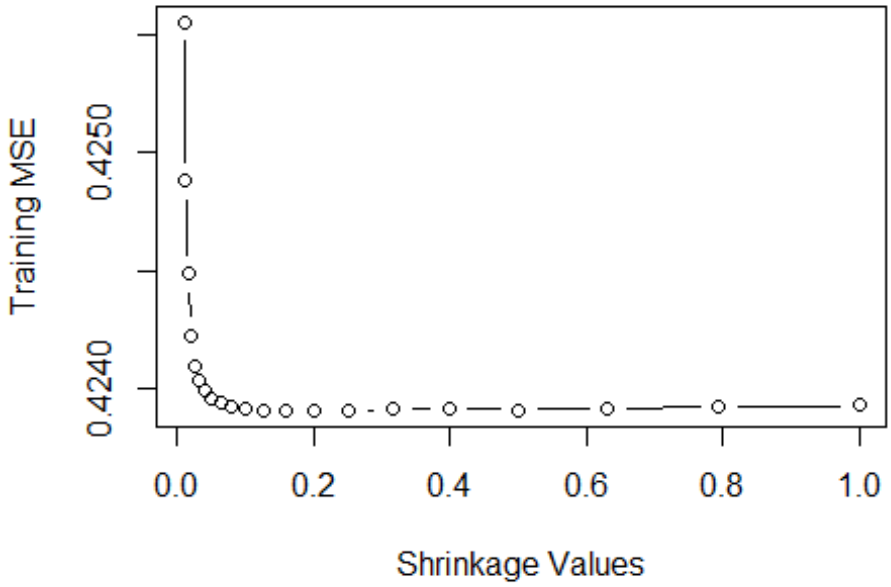
```
#bagging approach
set.seed(1)
bag_hos <- randomForest(stay ~ Visitors.with.Patient,
                        data = hos_train, mtry = 1, ntree = 10,
                        importance = TRUE)
## Warning in randomForest.default(m, y, ...): The response has five or fewer
## unique values.  Are you sure you want to do regression?
#MSE of the bagging approach
bag_hos_hat <- predict(bag_hos, data = hos_test)
bag_hos_MSE <- mean((bag_hos_hat - hos_test$stay)^2, na.rm = TRUE)
## Warning in bag_hos_hat - hos_test$stay: longer object length is not a multiple
## of shorter object length
print(bag_hos_MSE)
## [1] 0.551816
```

The bagging approach got a .5483819 as the test MSE

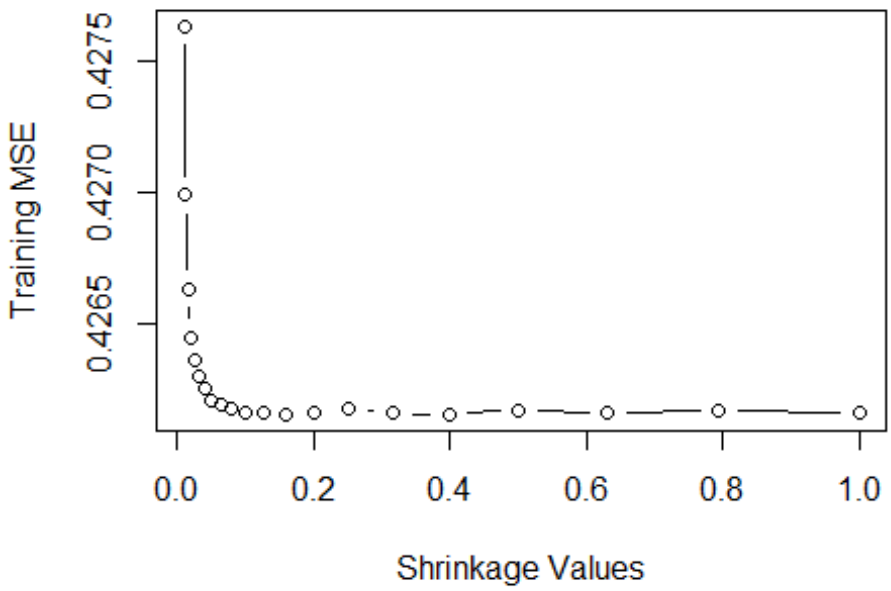
```
#Random Forest Approach
set.seed(1)
rf_hos <- randomForest(stay ~  City_Code_Hospital,
                       data = hos_train, mtry = 1,
                      importance = TRUE, ntree = 10)
## Warning in randomForest.default(m, y, ...): The response has five or fewer
## unique values.  Are you sure you want to do regression?
rf_hos_hat <- predict(rf_hos, data = hos_test)
rf_MSE <- mean((rf_hos_hat - hos_test$stay)^2, na.rm = TRUE)
## Warning in rf_hos_hat - hos_test$stay: longer object length is not a multiple
## of shorter object length
print(rf_MSE)
## [1] 0.4947005
```

The MSE for the random forest approach is 0.4902687

```
#Boosting Approach
set.seed(1)
pow <- seq(-2,0,0.1)
lambdas = 10^pow
train_error <- rep(NA, length(lambdas))

for (i in 1:length(lambdas)) {
  boost_hos <- gbm(stay ~ Visitors.with.Patient, data = hos_train,
                   distribution = "gaussian", n.trees = 500,
                   shrinkage = lambdas[i])
  #predicting the training error
  boost_pred <- predict(boost_hos, hos_train, n.trees = 500)
  train_error[i]  <- mean((boost_pred - hos_train$stay)^2)
}
plot(lambdas, train_error, type = 'b',
     xlab = "Shrinkage Values",
     ylab = "Training MSE")
```




```
test_error <- rep(NA, length(lambdas))

for (i in 1:length(lambdas)) {
  boost_hos <- gbm(stay ~ Visitors.with.Patient, data = hos_test,
                   distribution = "gaussian", n.trees = 500,
                   shrinkage = lambdas[i])
  #predicting the training error
  boost_pred <- predict(boost_hos, hos_test, n.trees = 500)
  test_error[i] <- mean((boost_pred - hos_test$stay)^2)
}
plot(lambdas, test_error, type = 'b',
     xlab = "Shrinkage Values",
     ylab = "Training MSE")
```




```
min(test_error)
## [1] 0.4261526
lambdas[which.min(test_error)]
## [1] 0.1584893
boost_hat <- predict(boost_hos, data = hos_test, n.trees=500)
boost_MSE <- mean((boost_hat - hos_test$stay)^2)
print(boost_MSE)
## [1] 0.42616
```

Using both methods to find the MSE, the test MSE for the Boosting method is about .5514

Qualitative Response: - Predicting the Severity of an illness

I will change each character variable to a factor to help with ease of applying the data set to models.

```
hospital2 <- hospital
hos_train2 <- hos_train
hos_test2 <- hos_test

hospital2$Hospital_type_code <- as.factor(hospital2$Hospital_type_code)
hospital2$Hospital_region_code <- as.factor(hospital2$Hospital_region_code)
hospital2$Department <- as.factor(hospital2$Department)
hospital2$Ward_Type <- as.factor(hospital2$Ward_Type)
hospital2$Ward_Facility_Code <- as.factor(hospital2$Ward_Facility_Code)
hospital2$Type.of.Admission <- as.factor(hospital2$Type.of.Admission)
hospital2$Severity.of.Illness <- as.factor(hospital2$Severity.of.Illness)
hospital2$Age <- as.factor(hospital2$Age)
```

```
hos_train2$Hospital_type_code <- as.factor(hos_train2$Hospital_type_code)
hos_train2$Hospital_region_code <- as.factor(hos_train2$Hospital_region_code)
hos_train2$Department <- as.factor(hos_train2$Department)
hos_train2$Ward_Type <- as.factor(hos_train2$Ward_Type)
hos_train2$Ward_Facility_Code <- as.factor(hos_train2$Ward_Facility_Code)
hos_train2$Type.of.Admission <- as.factor(hos_train2$Type.of.Admission)
hos_train2$Severity.of.Illness <- as.factor(hos_train2$Severity.of.Illness)
hos_train2$Age <- as.factor(hos_train2$Age)

hos_test2$Hospital_type_code <- as.factor(hos_test2$Hospital_type_code)
hos_test2$Hospital_region_code <- as.factor(hos_test2$Hospital_region_code)
hos_test2$Department <- as.factor(hos_test2$Department)
hos_test2$Ward_Type <- as.factor(hos_test2$Ward_Type)
hos_test2$Ward_Facility_Code <- as.factor(hos_test2$Ward_Facility_Code)
hos_test2$Type.of.Admission <- as.factor(hos_test2$Type.of.Admission)
hos_test2$Severity.of.Illness <- as.factor(hos_test2$Severity.of.Illness)
hos_test2$Age <- as.factor(hos_test2$Age)
#KNN
set.seed(1)
train.set <- data.frame(hospital2[train,])
test.set <- data.frame(hospital2[-train,])
train.direction <- hospital2[train,]$Severity.of.Illness

#knn.pred <- knn(train.set, test.set, train.direction, k=1)
#knn.MSE <- mean(knn.pred==hospital2[!train, ]$direction)
#print(knn.MSE)
```

I don't know why the K-nearest-neighbor did not work as I'm trying to get the Mean Squared error for this model. I had to change each variable from a character to factor then to a number. This might be why this model did not work but it was the only way for R to take my input. null hypothesis for p-value: H(o) > 0.05, H(A): < 0.05

```
#Logistic Regression on training set
hos_glm <- glm(Severity.of.Illness ~ Hospital_code + City_Code_Hospital +
                 Available.Extra.Rooms.in.Hospital + Bed.Grade +
                 City_Code_Patient + Visitors.with.Patient +
                 Admission_Deposit, data = hos_train2, family = binomial)
summary(hos_glm)
##
## Call:
## glm(formula = Severity.of.Illness ~ Hospital_code + City_Code_Hospital +
##     Available.Extra.Rooms.in.Hospital + Bed.Grade + City_Code_Patient +
##     Visitors.with.Patient + Admission_Deposit, family = binomial,
##     data = hos_train2)
##
## Coefficients:
##                               Estimate Std. Error z value Pr(>|z|)
## (Intercept)                 -5.534e-01  4.321e-02 -12.808   <2e-16 ***
```

```
## Hospital_code                 -6.302e-03  6.776e-04  -9.301   <2e-16 ***
## City_Code_Hospital             2.930e-03  1.859e-03   1.576   0.1150
## Available.Extra.Rooms.in.Hospital  1.056e-01  5.126e-03  20.592   <2e-16 ***
## Bed.Grade                      6.568e-01  7.075e-03  92.836   <2e-16 ***
## City_Code_Patient              3.070e-03  1.225e-03   2.506   0.0122 *
## Visitors.with.Patient         -8.724e-02  3.111e-03 -28.041   <2e-16 ***
## Admission_Deposit              1.016e-04  5.586e-06  18.192   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 206081  on 219654  degrees of freedom
## Residual deviance: 195532  on 219647  degrees of freedom
## AIC: 195548
##
## Number of Fisher Scoring iterations: 4
hos_glm_prob <- predict(hos_glm, type = "response")
hos_glm_pred <- rep("Wrong", length(hos_glm_prob))
hos_glm_pred[hos_glm_prob>0.5] = "Correct"
table(hos_glm_pred, hos_train2$Severity.of.Illness)
##
## hos_glm_pred Extreme  Minor Moderate
##      Correct   39114  59099   121257
##      Wrong        93      6       86
hos_glm_test <- glm(Severity.of.Illness ~ Hospital_code + City_Code_Hospital +
                    Available.Extra.Rooms.in.Hospital + Bed.Grade +
                    City_Code_Patient + Visitors.with.Patient +
                    Admission_Deposit, data = hos_test2, family = binomial)
summary(hos_glm)
##
## Call:
## glm(formula = Severity.of.Illness ~ Hospital_code + City_Code_Hospital +
##     Available.Extra.Rooms.in.Hospital + Bed.Grade + City_Code_Patient +
##     Visitors.with.Patient + Admission_Deposit, family = binomial,
##     data = hos_train2)
##
## Coefficients:
##                                Estimate Std. Error z value Pr(>|z|)
## (Intercept)                   -5.534e-01  4.321e-02 -12.808   <2e-16 ***
## Hospital_code                 -6.302e-03  6.776e-04  -9.301   <2e-16 ***
## City_Code_Hospital             2.930e-03  1.859e-03   1.576   0.1150
## Available.Extra.Rooms.in.Hospital  1.056e-01  5.126e-03  20.592   <2e-16 ***
## Bed.Grade                      6.568e-01  7.075e-03  92.836   <2e-16 ***
## City_Code_Patient              3.070e-03  1.225e-03   2.506   0.0122 *
## Visitors.with.Patient         -8.724e-02  3.111e-03 -28.041   <2e-16 ***
```

```
## Admission_Deposit              1.016e-04  5.586e-06  18.192   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 206081  on 219654  degrees of freedom
## Residual deviance: 195532  on 219647  degrees of freedom
## AIC: 195548
##
## Number of Fisher Scoring iterations: 4
hos_glm_prob_test <- predict(hos_glm_test, type = "response")
hos_glm_pred_test <- rep("Wrong", length(hos_glm_prob_test))
hos_glm_pred_test[hos_glm_prob_test>0.5] = "Correct"
table(hos_glm_pred_test, hos_test2$Severity.of.Illness)
##
## hos_glm_pred_test Extreme Minor Moderate
##          Correct   16793 25209    52056
##          Wrong        49     5       26
log_MSE <- mean(hos_glm_pred_test == hos_test2$Severity.of.Illness)
print(log_MSE)
## [1] 0
#LDA
hos_lda <- lda(Severity.of.Illness ~ Hospital_code + City_Code_Hospital +
                 Available.Extra.Rooms.in.Hospital + Bed.Grade +
                 City_Code_Patient + Visitors.with.Patient +
                 Admission_Deposit, data = hos_train2)
hos_lda
## Call:
## lda(Severity.of.Illness ~ Hospital_code + City_Code_Hospital +
##     Available.Extra.Rooms.in.Hospital + Bed.Grade + City_Code_Patient +
##     Visitors.with.Patient + Admission_Deposit, data = hos_train2)
##
## Prior probabilities of groups:
##   Extreme     Minor  Moderate
## 0.1784935 0.2690811 0.5524254
##
## Group means:
##          Hospital_code City_Code_Hospital Available.Extra.Rooms.in.Hospital
## Extreme       18.71967          4.874614                         3.169102
## Minor         17.98743          4.645614                         3.180848
## Moderate      18.37694          4.817748                         3.210708
##          Bed.Grade City_Code_Patient Visitors.with.Patient Admission_Deposit
## Extreme   2.249955         7.204581             3.438315         4747.521
## Minor     2.988546         7.417460             3.173353         4982.150
## Moderate  2.564565         7.192611             3.281087         4874.748
```

```
##
## Coefficients of linear discriminants:
##                                 LD1          LD2
## Hospital_code                -0.010144751 -0.0092870977
## City_Code_Hospital           -0.003336410  0.0977381449
## Available.Extra.Rooms.in.Hospital  0.138015269  0.5661360120
## Bed.Grade                    1.166656581 -0.1564011454
## City_Code_Patient             0.012945336 -0.0853721322
## Visitors.with.Patient        -0.141601900 -0.2322672942
## Admission_Deposit             0.000141038  0.0004280099
##
## Proportion of trace:
##   LD1   LD2
## 0.993 0.007
hos_lda2 <- lda(Severity.of.Illness ~ Hospital_code + City_Code_Hospital +
                  Available.Extra.Rooms.in.Hospital  + Bed.Grade +
                  City_Code_Patient + Visitors.with.Patient +
                  Admission_Deposit, data = hos_test2)
hos_lda2
## Call:
## lda(Severity.of.Illness ~ Hospital_code + City_Code_Hospital +
##     Available.Extra.Rooms.in.Hospital + Bed.Grade + City_Code_Patient +
##     Visitors.with.Patient + Admission_Deposit, data = hos_test2)
##
## Prior probabilities of groups:
##   Extreme     Minor  Moderate
## 0.1789076 0.2678408 0.5532516
##
## Group means:
##          Hospital_code City_Code_Hospital Available.Extra.Rooms.in.Hospital
## Extreme       18.84853          4.877152                         3.163995
## Minor         17.87118          4.659475                         3.191203
## Moderate      18.34893          4.789236                         3.214373
##          Bed.Grade City_Code_Patient Visitors.with.Patient Admission_Deposit
## Extreme   2.261133         7.206983             3.438546         4750.757
## Minor     2.988736         7.432617             3.180654         4990.874
## Moderate  2.564802         7.168100             3.281306         4875.565
##
## Coefficients of linear discriminants:
##                                 LD1          LD2
## Hospital_code                -0.0132398498 -0.0195635646
## City_Code_Hospital           -0.0015219399  0.0295951955
## Available.Extra.Rooms.in.Hospital  0.1448044407  0.5400559099
## Bed.Grade                    1.1626880675 -0.1816053101
## City_Code_Patient             0.0149987131 -0.1082751969
## Visitors.with.Patient        -0.1386745089 -0.2517206115
```

```
## Admission_Deposit                0.0001550798  0.0003547397
##
## Proportion of trace:
##    LD1    LD2
## 0.9922 0.0078
lda_pred <- predict(hos_lda, hos_test2)
names(lda_pred)
## [1] "class"     "posterior" "x"
lda_class <- lda_pred$class
table(lda_class, hos_test2$Severity.of.Illness)
##
## lda_class  Extreme Minor Moderate
##   Extreme      59     7       39
##   Minor      1275  4200     4979
##   Moderate  15508 21007    47064
lda_MSE <- mean(lda_class == hos_test2$Severity.of.Illness)
print(lda_MSE)
## [1] 0.545189
```

probability of extreme severity of illness: 0.1771867 probability of minor severity of illness: 0.2708046 probability of moderate severity of illness: 0.5520088 The mean for the LDA model is .5435743

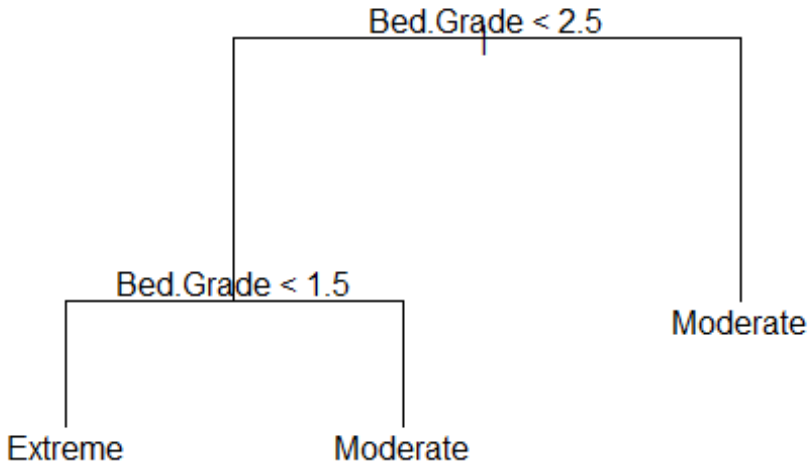
```
#QDA
qda_fit <- qda(Severity.of.Illness ~ Hospital_code + City_Code_Hospital +
                 Available.Extra.Rooms.in.Hospital + Bed.Grade +
                 City_Code_Patient + Visitors.with.Patient +
                 Admission_Deposit, data = hos_train2)
qda_fit
## Call:
## qda(Severity.of.Illness ~ Hospital_code + City_Code_Hospital +
##     Available.Extra.Rooms.in.Hospital + Bed.Grade + City_Code_Patient +
##     Visitors.with.Patient + Admission_Deposit, data = hos_train2)
##
## Prior probabilities of groups:
##   Extreme     Minor  Moderate
## 0.1784935 0.2690811 0.5524254
##
## Group means:
##          Hospital_code City_Code_Hospital Available.Extra.Rooms.in.Hospital
## Extreme       18.71967          4.874614                         3.169102
## Minor         17.98743          4.645614                         3.180848
## Moderate      18.37694          4.817748                         3.210708
##          Bed.Grade City_Code_Patient Visitors.with.Patient Admission_Deposit
## Extreme   2.249955          7.204581             3.438315         4747.521
## Minor     2.988546          7.417460             3.173353         4982.150
## Moderate  2.564565          7.192611             3.281087         4874.748
```

```
qda_fit2 <- qda(Severity.of.Illness ~ Hospital_code + City_Code_Hospital +
                  Available.Extra.Rooms.in.Hospital + Bed.Grade +
                  City_Code_Patient + Visitors.with.Patient +
                  Admission_Deposit, data = hos_test2)
qda_fit2
## Call:
## qda(Severity.of.Illness ~ Hospital_code + City_Code_Hospital +
##     Available.Extra.Rooms.in.Hospital + Bed.Grade + City_Code_Patient +
##     Visitors.with.Patient + Admission_Deposit, data = hos_test2)
##
## Prior probabilities of groups:
##   Extreme     Minor  Moderate
## 0.1789076 0.2678408 0.5532516
##
## Group means:
##          Hospital_code City_Code_Hospital Available.Extra.Rooms.in.Hospital
## Extreme       18.84853          4.877152                         3.163995
## Minor         17.87118          4.659475                         3.191203
## Moderate      18.34893          4.789236                         3.214373
##          Bed.Grade City_Code_Patient Visitors.with.Patient Admission_Deposit
## Extreme   2.261133          7.206983             3.438546         4750.757
## Minor     2.988736          7.432617             3.180654         4990.874
## Moderate  2.564802          7.168100             3.281306         4875.565
qda_pred2 <- predict(qda_fit2, hos_test2)
names(qda_pred2)
## [1] "class"     "posterior"
qda_class2 <- qda_pred2$class
table(qda_class2, hos_test2$Severity.of.Illness)
##
## qda_class2 Extreme Minor Moderate
##   Extreme     700   218      819
##   Minor      1382  4795     5532
##   Moderate  14760 20201    45731
qda_MSE <- mean(qda_class2 == hos_test2$Severity.of.Illness)
print(qda_MSE)
## [1] 0.5441586
```

probability of extreme severity of illness: 0.1771867 probability of minor severity of illness: 0.2708046 probability of moderate severity of illness: 0.5520088 The mean for the QDA model is 0.5415879

```
#Classification  trees
tree_class <- tree(Severity.of.Illness ~ Hospital_code + City_Code_Hospital +
                  Available.Extra.Rooms.in.Hospital + Bed.Grade +
                  City_Code_Patient + Visitors.with.Patient +
                  Admission_Deposit, data = hos_train2)
summary(tree_class)
```

```
##
## Classification tree:
## tree(formula = Severity.of.Illness ~ Hospital_code + City_Code_Hospital +
##     Available.Extra.Rooms.in.Hospital + Bed.Grade + City_Code_Patient +
##     Visitors.with.Patient + Admission_Deposit, data = hos_train2)
## Variables actually used in tree construction:
## [1] "Bed.Grade"
## Number of terminal nodes:  3
## Residual mean deviance:  1.844 = 405000 / 219700
## Misclassification error rate: 0.4362 = 95814 / 219655
plot(tree_class)
text(tree_class, pretty = 0)
```




```
tree_class2 <- tree(Severity.of.Illness ~ Hospital_code + City_Code_Hospital +
                Available.Extra.Rooms.in.Hospital + Bed.Grade +
                City_Code_Patient + Visitors.with.Patient +
                Admission_Deposit, data = hos_test2)
set.seed(2)
tree_class_pred <- predict(tree_class2, data = hos_test2, type = 'class')
table(tree_class_pred, hos_test2$Severity.of.Illness)
##
## tree_class_pred Extreme Minor Moderate
##       Extreme    4126   581     3117
##       Minor         0     0        0
##       Moderate   12716 24633    48965
class_tree_MSE <- .5617
```

(4105 + 0 + 48876)/(4105+594+3189+12575+24899+48776) = .5617 The mean for the classification tree is .5617.

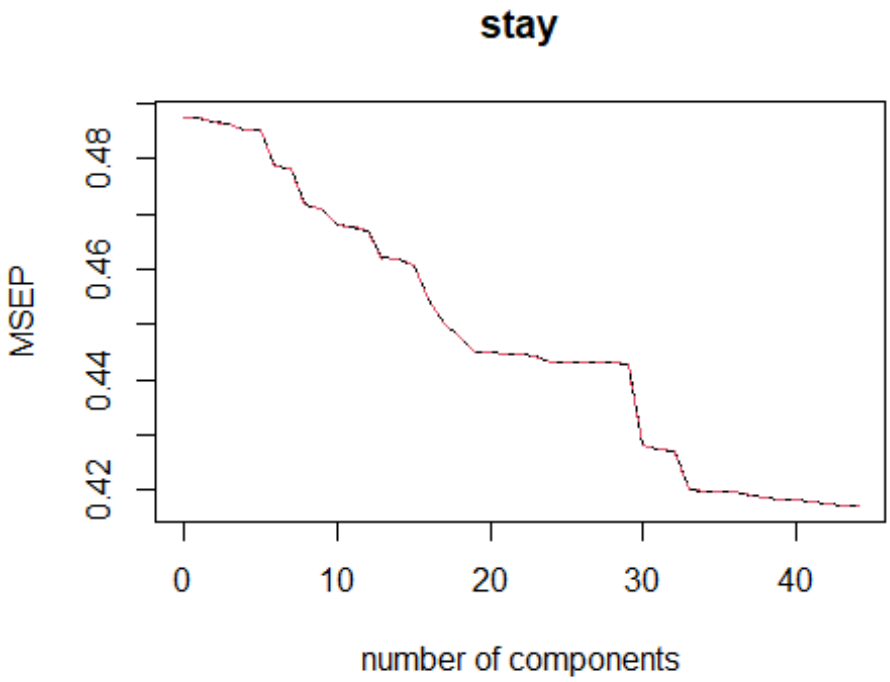
```
#bagging approach qualitative

set.seed(1)
bag_qual <- randomForest(Severity.of.Illness ~ Hospital_code + City_Code_Hospital +
                 Available.Extra.Rooms.in.Hospital + Bed.Grade +
                 City_Code_Patient + Visitors.with.Patient +
                 Admission_Deposit, ntree=10,
                 data = hos_train2, mtry = 7, importance = TRUE)
bag_qual
##
## Call:
##  randomForest(formula = Severity.of.Illness ~ Hospital_code +      City_Code_Hospital +
Available.Extra.Rooms.in.Hospital +      Bed.Grade + City_Code_Patient + Visitors.with.Patient
+ Admission_Deposit,      data = hos_train2, ntree = 10, mtry = 7, importance = TRUE)
##               Type of random forest: classification
##                     Number of trees: 10
## No. of variables tried at each split: 7
##
##         OOB estimate of  error rate: 53.25%
## Confusion matrix:
##          Extreme Minor Moderate class.error
## Extreme    10614  7700    20502   0.7265561
## Minor       7567 20842    30067   0.6435803
## Moderate   20056 29880    70200   0.4156622
bag_qual_hat <- predict(bag_qual, data = hos_test2)
bag_qual_hat <- na.omit(bag_qual_hat)
bag_qual_MSE <- mean((bag_qual_hat - hos_test2$Severity.of.Illness)^2)
## Warning in Ops.factor(bag_qual_hat, hos_test2$Severity.of.Illness): '-' not
## meaningful for factors
print(bag_qual_MSE)
## [1] NA
#random forest approach qualitative
set.seed(1)
rf_qual <- randomForest(Severity.of.Illness ~ Bed.Grade + Visitors.with.Patient +
                    Admission_Deposit, ntree=10,
                  data = hos_train2, mtry = 3, importance = TRUE)
rf_qual
##
## Call:
##  randomForest(formula = Severity.of.Illness ~ Bed.Grade + Visitors.with.Patient +
Admission_Deposit, data = hos_train2, ntree = 10, mtry = 3,      importance = TRUE)
##               Type of random forest: classification
##                     Number of trees: 10
## No. of variables tried at each split: 3
```

```
##
##         OOB estimate of  error rate: 51.33%
## Confusion matrix:
##          Extreme Minor Moderate class.error
## Extreme     8406  8185    22200   0.7833003
## Minor       5315 21776    31383   0.6275952
## Moderate   14200 30316    75613   0.3705683
rf_qual_hat <- predict(rf_qual,  data = hos_test2)
rf_qual_hat <- na.omit(rf_qual_hat)
rf_qual_MSE <- mean((rf_qual_hat - hos_test2$Severity.of.Illness)^2)
## Warning in Ops.factor(rf_qual_hat, hos_test2$Severity.of.Illness): '-' not
## meaningful for factors
print(rf_qual_MSE)
## [1] NA
any(is.na(hos_test2$rf_qual_hat))
## [1] FALSE
any(is.na(hos_test2$Severity.of.Illness))
## [1] FALSE
```

Principal Components Regression: - Predict the length of stay in a hospital

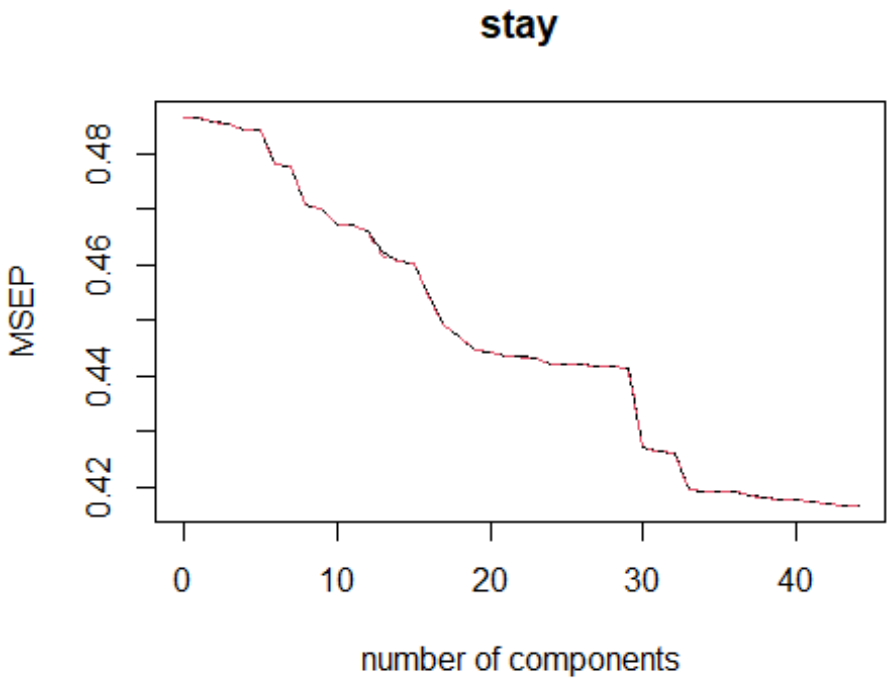
```
#ten-fold cross-validation  error on the whole data set first
set.seed(2)
pcr_fit_whole <- pcr(stay ~ ., data = hospital2, scale = TRUE,
             validation = "CV")
summary(pcr_fit_whole)
## Data:    X dimension: 313793 44
##  Y dimension: 313793 1
## Fit method: svdpc
## Number of components considered: 44
##
## VALIDATION: RMSEP
## Cross-validated using 10 random segments.
##        (Intercept)  1 comps  2 comps  3 comps  4 comps  5 comps  6 comps
## CV          0.6982   0.6981   0.6976   0.6973   0.6965   0.6965    0.692
## adjCV       0.6982   0.6981   0.6976   0.6973   0.6965   0.6965    0.692
##        7 comps  8 comps  9 comps  10 comps  11 comps  12 comps  13 comps
## CV      0.6917   0.6868   0.6864    0.6841    0.6839    0.6833    0.6798
## adjCV   0.6917   0.6868   0.6863    0.6841    0.6839    0.6833    0.6796
##        14 comps  15 comps  16 comps  17 comps  18 comps  19 comps  20 comps
## CV       0.6796    0.6788    0.6741    0.6708    0.6692    0.6672     0.667
## adjCV    0.6796    0.6788    0.6741    0.6708    0.6692    0.6672     0.667
##        21 comps  22 comps  23 comps  24 comps  25 comps  26 comps  27 comps
## CV       0.6667    0.6667    0.6666    0.6658    0.6658    0.6658    0.6657
## adjCV    0.6667    0.6667    0.6666    0.6658    0.6658    0.6658    0.6657
##        28 comps  29 comps  30 comps  31 comps  32 comps  33 comps  34 comps
## CV       0.6656    0.6654    0.6542    0.6537    0.6535    0.6482     0.648
## adjCV    0.6656    0.6654    0.6542    0.6537    0.6535    0.6482     0.648
```

```
##       35 comps  36 comps  37 comps  38 comps  39 comps  40 comps  41 comps
## CV       0.648     0.648    0.6473    0.6471    0.6468    0.6468    0.6465
## adjCV    0.648     0.648    0.6473    0.6470    0.6468    0.6468    0.6465
##       42 comps  43 comps  44 comps
## CV       0.6461     0.646     0.646
## adjCV    0.6461     0.646     0.646
##
## TRAINING: % variance explained
##       1 comps  2 comps  3 comps  4 comps  5 comps  6 comps  7 comps  8 comps
## X     7.40385  13.7174  18.9026  23.5013  27.9111   32.156   35.945   39.494
## stay  0.02794   0.1714   0.2479   0.4771   0.4793    1.773    1.856    3.247
##       9 comps  10 comps  11 comps  12 comps  13 comps  14 comps  15 comps
## X      42.768    45.682    48.554    51.352    53.980    56.603    59.185
## stay    3.361     4.007     4.041     4.224     5.257     5.265     5.481
##       16 comps  17 comps  18 comps  19 comps  20 comps  21 comps  22 comps
## X       61.659    64.111    66.484    68.808     71.10    73.389    75.661
## stay     6.788     7.681     8.139     8.685      8.74     8.814     8.817
##       23 comps  24 comps  25 comps  26 comps  27 comps  28 comps  29 comps
## X        77.93    80.159    82.370    84.513    86.578    88.575    90.478
## stay      8.84     9.076     9.078     9.079     9.113     9.131     9.196
##       30 comps  31 comps  32 comps  33 comps  34 comps  35 comps  36 comps
## X        92.21     93.67     94.94     96.08     97.13     97.88     98.52
## stay     12.20     12.34     12.41     13.81     13.88     13.89     13.89
##       37 comps  38 comps  39 comps  40 comps  41 comps  42 comps  43 comps
## X        99.11     99.59     99.76     99.88     99.93     99.98    100.00
## stay     14.07     14.13     14.20     14.20     14.27     14.38     14.42
##       44 comps
## X       100.00
## stay     14.42
validationplot(pcr_fit_whole, val.type = 'MSEP')
```




```
#performing PCR on the training data set
#based off of PCR on the whole data set, we will use M=33
pcr_fit_train <- pcr(stay ~ ., data = hos_train2, scale = TRUE,
                     validation = "CV")
summary(pcr_fit_train)
## Data:    X dimension: 219655 44
##  Y dimension: 219655 1
## Fit method: svdpc
## Number of components considered: 44
##
## VALIDATION: RMSEP
## Cross-validated using 10 random segments.
##        (Intercept)  1 comps  2 comps  3 comps  4 comps  5 comps  6 comps
## CV           0.6974   0.6973   0.6967   0.6965   0.6958   0.6958   0.6914
## adjCV        0.6974   0.6973   0.6967   0.6965   0.6958   0.6958   0.6914
##        7 comps  8 comps  9 comps  10 comps  11 comps  12 comps  13 comps
## CV       0.691   0.6861   0.6857    0.6834    0.6833    0.6827    0.6801
## adjCV    0.691   0.6861   0.6857    0.6834    0.6833    0.6827    0.6795
##        14 comps  15 comps  16 comps  17 comps  18 comps  19 comps  20 comps
## CV       0.6787    0.6784    0.6742    0.6702    0.6686    0.6668    0.6665
## adjCV    0.6787    0.6784    0.6741    0.6701    0.6686    0.6667    0.6664
##        21 comps  22 comps  23 comps  24 comps  25 comps  26 comps  27 comps
## CV       0.6659    0.6659    0.6658    0.6649    0.6649    0.6648    0.6648
## adjCV    0.6659    0.6659    0.6658    0.6649    0.6648    0.6648    0.6648
##        28 comps  29 comps  30 comps  31 comps  32 comps  33 comps  34 comps
```

```
## CV       0.6647    0.6645    0.6535    0.6531    0.6528    0.6477    0.6475
## adjCV    0.6647    0.6645    0.6535    0.6531    0.6528    0.6477    0.6475
##        35 comps  36 comps  37 comps  38 comps  39 comps  40 comps  41 comps
## CV       0.6475    0.6475    0.6469    0.6466    0.6463    0.6463    0.6462
## adjCV    0.6475    0.6475    0.6469    0.6466    0.6463    0.6463    0.6461
##        42 comps  43 comps  44 comps
## CV       0.6458    0.6456    0.6456
## adjCV    0.6457    0.6456    0.6456
##
## TRAINING: % variance explained
##       1 comps  2 comps  3 comps  4 comps  5 comps  6 comps  7 comps  8 comps
## X     7.40379  13.7194  18.9095  23.5130  27.9236   32.170   35.955   39.510
## stay  0.03956   0.1919   0.2671   0.4712   0.4722    1.735    1.835    3.226
##       9 comps  10 comps  11 comps  12 comps  13 comps  14 comps  15 comps
## X      42.785    45.700    48.570    51.372    54.000     56.62    59.201
## stay    3.342     3.988     4.008     4.188     5.131      5.31     5.397
##       16 comps  17 comps  18 comps  19 comps  20 comps  21 comps  22 comps
## X       61.674    64.129    66.504     68.82    71.124    73.409    75.682
## stay     6.585     7.686     8.109      8.63     8.706     8.864     8.865
##       23 comps  24 comps  25 comps  26 comps  27 comps  28 comps  29 comps
## X       77.942    80.175    82.385    84.528    86.589    88.584    90.487
## stay     8.887     9.142     9.143     9.146     9.167     9.178     9.248
##       30 comps  31 comps  32 comps  33 comps  34 comps  35 comps  36 comps
## X        92.22     93.67     94.94     96.08     97.14     97.88     98.53
## stay     12.22     12.33     12.41     13.78     13.84     13.84     13.85
##       37 comps  38 comps  39 comps  40 comps  41 comps  42 comps  43 comps
## X        99.11     99.59     99.76     99.88     99.93     99.98    100.00
## stay     14.00     14.07     14.15     14.15     14.20     14.31     14.35
##       44 comps
## X       100.00
## stay     14.35
validationplot(pcr_fit_train,  val.type = 'MSEP')
```



from the graph, the lowest cross-validation error occurs at M = 33, without having to use all the components which have very little difference from using all components

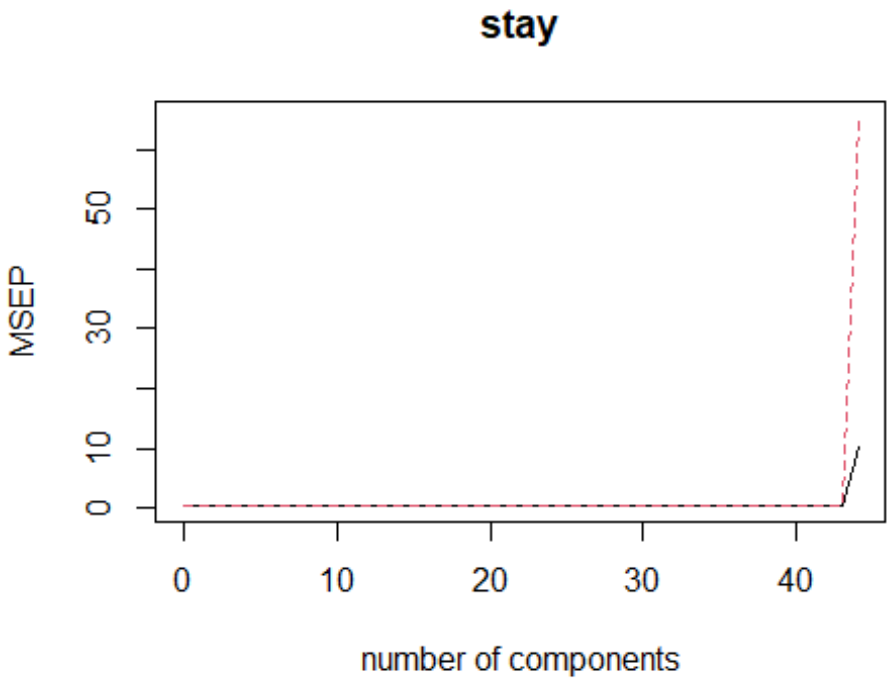
```
pcr_pred <- predict(pcr_fit_train, hos_test2, ncomp = 33)
pcr_MSE <- mean((pcr_pred - hos_test2$stay)^2)
print(pcr_MSE)
## [1] 0.421935
```

The test MSE for Principal Component Regression is 0.4194666

I want to compare this regression to the partial least squares using the same method.

```
#Partial Least Squares
pls_comp_fit <- plsr(stay ~ ., data = hospital2,
                     scale = TRUE, validation = "CV")
summary(pls_comp_fit)
## Data:    X dimension: 313793 44
##  Y dimension: 313793 1
## Fit method: kernelpls
## Number of components considered: 44
##
## VALIDATION: RMSEP
## Cross-validated using 10 random segments.
##        (Intercept)  1 comps  2 comps  3 comps  4 comps  5 comps  6 comps
## CV           0.6982   0.6549   0.6491   0.6476   0.6471   0.6469   0.6467
## adjCV        0.6982   0.6549   0.6490   0.6476   0.6471   0.6469   0.6467
##        7 comps  8 comps  9 comps  10 comps  11 comps  12 comps  13 comps
## CV      0.6466   0.6465   0.6464    0.6463    0.6462    0.6461    0.6461
## adjCV   0.6466   0.6465   0.6464    0.6463    0.6462    0.6461    0.6461
```

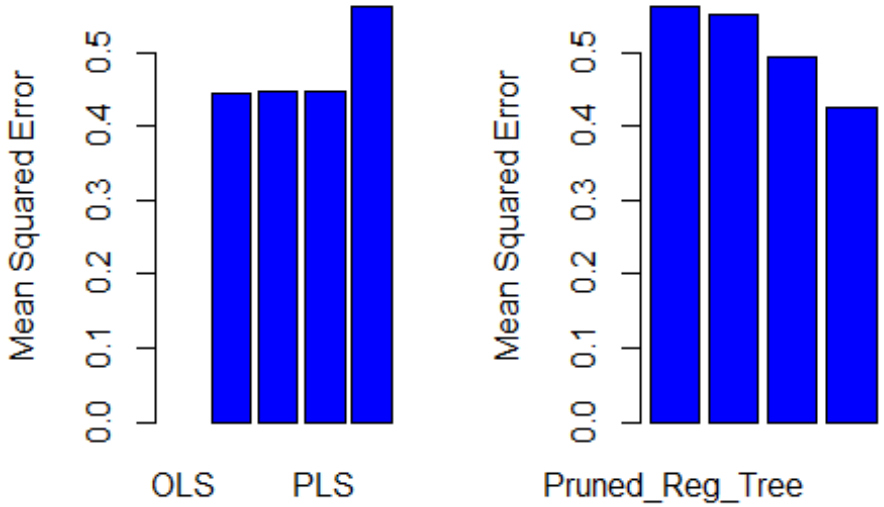
```
##       14 comps  15 comps  16 comps  17 comps  18 comps  19 comps  20 comps
## CV       0.646     0.646     0.646     0.646     0.646     0.646     0.646
## adjCV    0.646     0.646     0.646     0.646     0.646     0.646     0.646
##       21 comps  22 comps  23 comps  24 comps  25 comps  26 comps  27 comps
## CV       0.646     0.646     0.646     0.646     0.646     0.646     0.646
## adjCV    0.646     0.646     0.646     0.646     0.646     0.646     0.646
##       28 comps  29 comps  30 comps  31 comps  32 comps  33 comps  34 comps
## CV       0.646     0.646     0.646     0.646     0.646     0.646     0.646
## adjCV    0.646     0.646     0.646     0.646     0.646     0.646     0.646
##       35 comps  36 comps  37 comps  38 comps  39 comps  40 comps  41 comps
## CV       0.646     0.646     0.646     0.646     0.646     0.646     0.646
## adjCV    0.646     0.646     0.646     0.646     0.646     0.646     0.646
##       42 comps  43 comps  44 comps
## CV       0.646     0.646     3.203
## adjCV    0.646     0.646     8.086
##
## TRAINING: % variance explained
##      1 comps  2 comps  3 comps  4 comps  5 comps  6 comps  7 comps  8 comps
## X      3.427    7.824    12.43    16.31    20.99    24.07    26.96    29.88
## stay  12.024   13.597    13.99    14.12    14.17    14.21    14.25    14.28
##      9 comps  10 comps  11 comps  12 comps  13 comps  14 comps  15 comps
## X      32.44     34.81     37.19     39.97     41.71     43.52     45.76
## stay   14.31     14.34     14.37     14.38     14.39     14.40     14.41
##      16 comps  17 comps  18 comps  19 comps  20 comps  21 comps  22 comps
## X       47.81     50.01     52.58     55.39     57.33     58.87     59.96
## stay    14.41     14.41     14.42     14.42     14.42     14.42     14.42
##      23 comps  24 comps  25 comps  26 comps  27 comps  28 comps  29 comps
## X       61.64     63.18     65.14     66.34     67.56     69.03     71.31
## stay    14.42     14.42     14.42     14.42     14.42     14.42     14.42
##      30 comps  31 comps  32 comps  33 comps  34 comps  35 comps  36 comps
## X       72.60     74.05     75.02     77.01     79.26     81.48     83.85
## stay    14.42     14.42     14.42     14.42     14.42     14.42     14.42
##      37 comps  38 comps  39 comps  40 comps  41 comps  42 comps  43 comps
## X       86.10     88.49     90.95     93.19     95.45     97.73    100.00
## stay    14.42     14.42     14.42     14.42     14.42     14.42     14.42
##      44 comps
## X       102.6
## stay  -13321.3
validationplot(pls_comp_fit,  val.type = "MSEP")
```




```
#finding the MSE of PLS
pls_comp_pred <- predict(pls_comp_fit, hos_test2, ncomp = 1)
pls_comp_MSE <- mean((pls_comp_pred - hos_test2$stay)^2)
print(pls_comp_MSE)
## [1] 0.4310673
```

Comparing the PLS model and PCR model for this data set, we can see that the PCR model fits better with a lower test MSE than the PLS model.

```
#Comparing the Test MSE for Quantitative problem
par(mfrow = c(1,2))
barplot(c(lin_MSE, ridge_MSE, lasso_MSE, pls_MSE, reg_tree_MSE),
      names.arg = c("OLS", "Ridge", "Lasso", "PLS", "Reg_Tree"),
      ylab = "Mean Squared Error", col = "blue")
barplot(c(prune_tree_MSE, bag_hos_MSE, rf_MSE, boost_MSE),
      names.arg = c("Pruned_Reg_Tree", "Bagging", "RandomForest", "Boosting"),
      ylab = "Mean Squared Error", col = "blue")
```

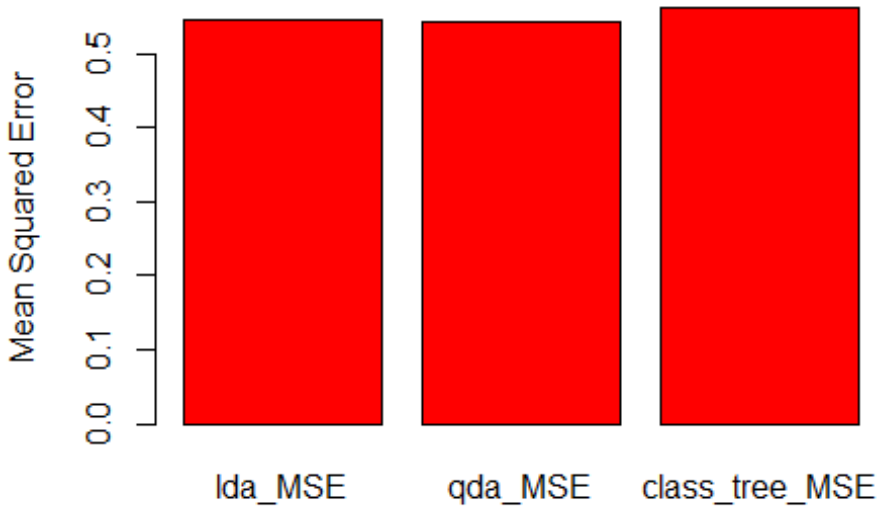



```
Quant_MSE <- data.frame(Model_MSE = c(lin_MSE, ridge_MSE, lasso_MSE, pls_MSE,
reg_tree_MSE,
                prune_tree_MSE, bag_hos_MSE, rf_MSE, boost_MSE))
min(Quant_MSE)
## [1] NA
```

Comparing the MSE of models that qualified for this comparison showed that Multiple linear regression is the best model used for this data set. Partial least Squares is a close second in this list. I will used both of these models to predict the number of days a patient will stay in a hospital.

```
#Predicting the average amount of days a patient will stay in a hospital.
mean(lin_pred)
## [1] 0.8719085
mean(pls.pred)
## [1] 0.8339318
#Both models give you about 0.8344 so if we times that with 20(for the range of days for the
factor 0), we should be able to predict the average amount of days a patient would stay in the
hospital.
avg_stay <- 0.8344*20
print(avg_stay)
## [1] 16.688
#A patient will stay on average 16.688 days in a hospital.
#Comparing the MSE for Qualitative Problem
#The same concept will apply to the quantitative problem, I will only use models that I've gotten
the MSE from.
barplot(c(lda_MSE,qda_MSE,class_tree_MSE),
```

```
    names.arg = c("lda_MSE", "qda_MSE","class_tree_MSE"),
    ylab = "Mean Squared Error", col = "red")
```




```
Qual_MSE <- data.frame(Model_MSE = c(lda_MSE,qda_MSE,class_tree_MSE))
min(Qual_MSE)
## [1] 0.5441586
```

The lowest MSE in the qualified models used for our qualitative problem is the qda model, but the lda model is also really close so we will use both models to help without prediction.

```
#Predicting Qualitative problem
lda_pred_num <- as.numeric(lda_pred$class)
qda_pred2_num <- as.numeric(qda_pred2$class)
mean(qda_pred2_num)
## [1] 2.838716
mean(lda_pred_num)
## [1] 2.886719
#From the data set extreme = 1, minor = 2, and moderate = 3.
#A average patient at a hospital will have a moderate severity in illness.
#Predicting PCR problem
mean(pcr_pred)
## [1] 0.834302
#if we do the same math as we did for the quantitative problem would be able to get the average days a patient will stay in the hospital.
pcr_avg_stay <- 0.834*20
print(pcr_avg_stay)
## [1] 16.68
#A patient will stay on average 16.68 days in a hospital.
```