DOUGLAS COLLEGE

Diabetes Dataset Analysis

CSIS4290: Special Topics in Data Analytics

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Douglas College respectfully acknowledges that our campuses are located on the unceded traditional and ancestral lands of the Coast Salish Peoples, including the territories of the q̓íc̓əy̓ (Katzie), q’ʷa:n̓ƛ’ən̓ (Kwantlen), kʷikʷəƛ̓əm (Kwikwetlem), xʷməθkʷəy̓əm (Musqueam), and qiqéyt (Qayqayt) First Nations.

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Dataset Introduction

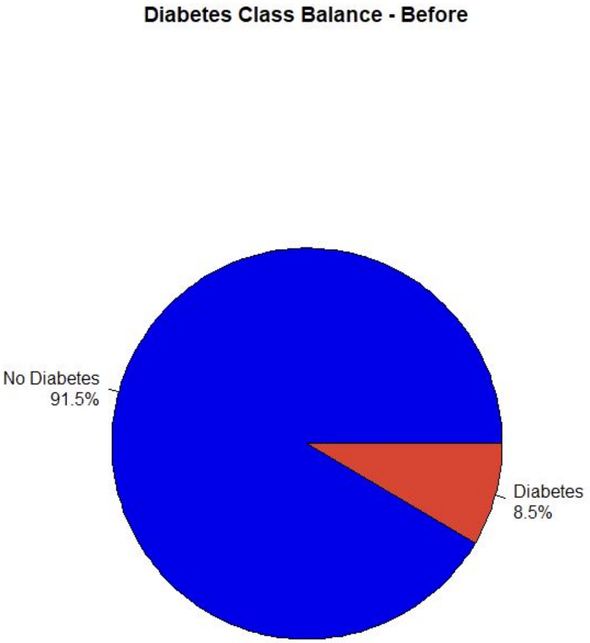
- Diabetes Dataset

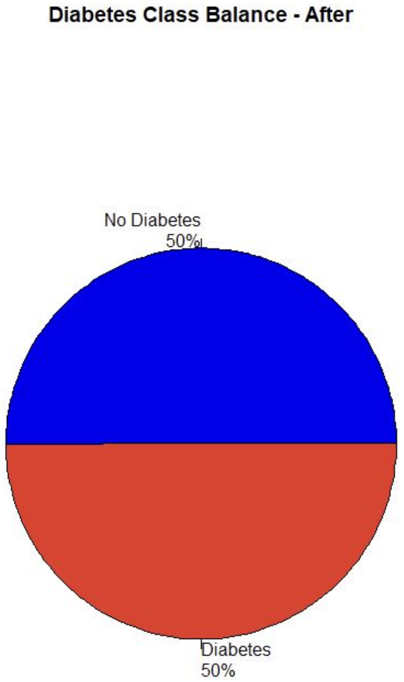
- The Diabetes dataset is a collection of medical and demographic data from patients, along with their diabetes status (positive or negative).

- The data includes features such as age, gender, body mass index (BMI), hypertension, heart disease, smoking history, HbA1c level, and blood glucose level.

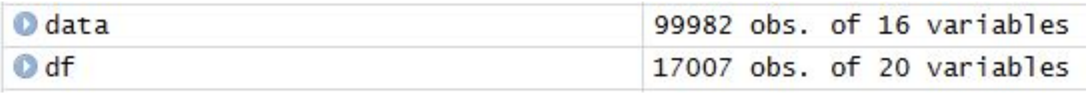
- Source: Kaggle

Data Visualization - Target Balance Comparison


Diabetes Class Balance - Before

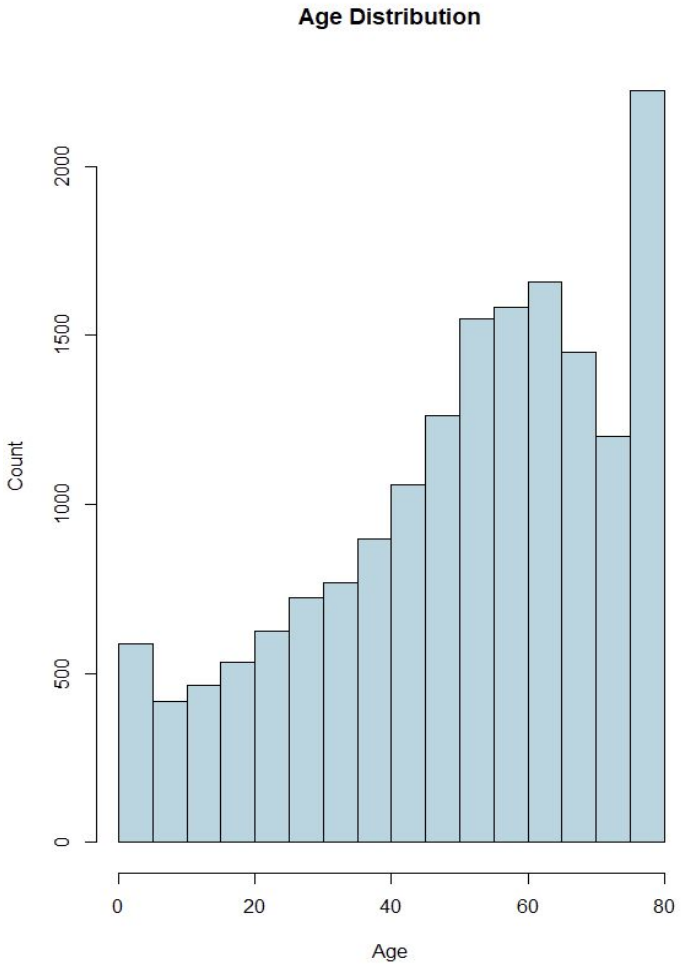

Diabetes Class Balance - After

Size of dataset was 99982 before the balancing process and 17007 after it.

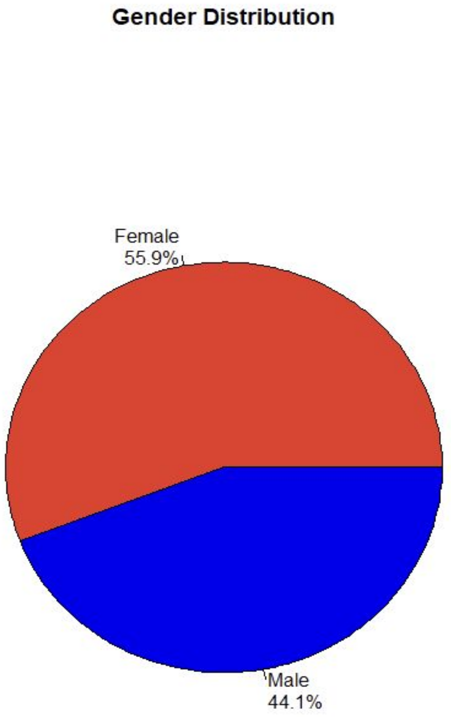


```
data    99982 obs. of 16 variables
df      17007 obs. of 20 variables
```

Data Visualization - Age and Gender Proportion

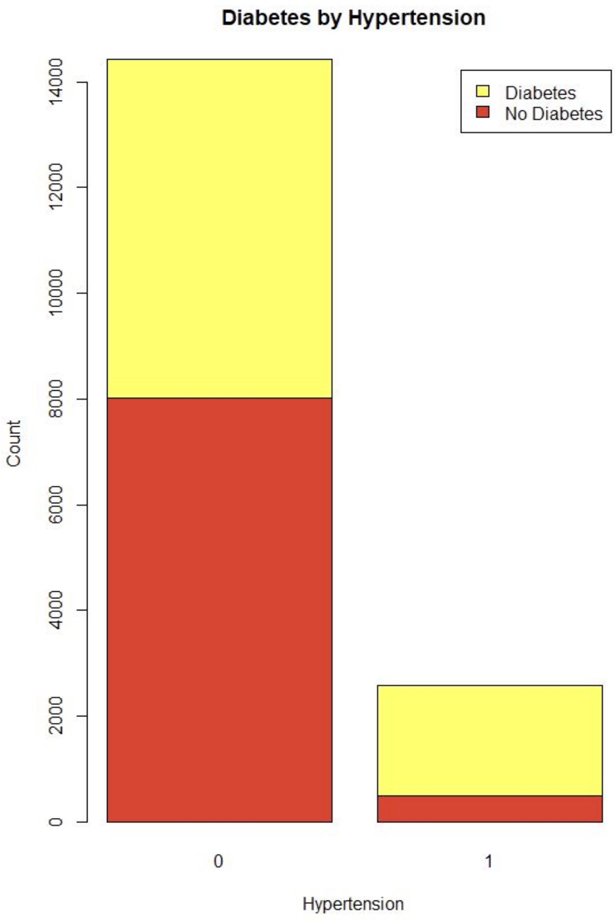


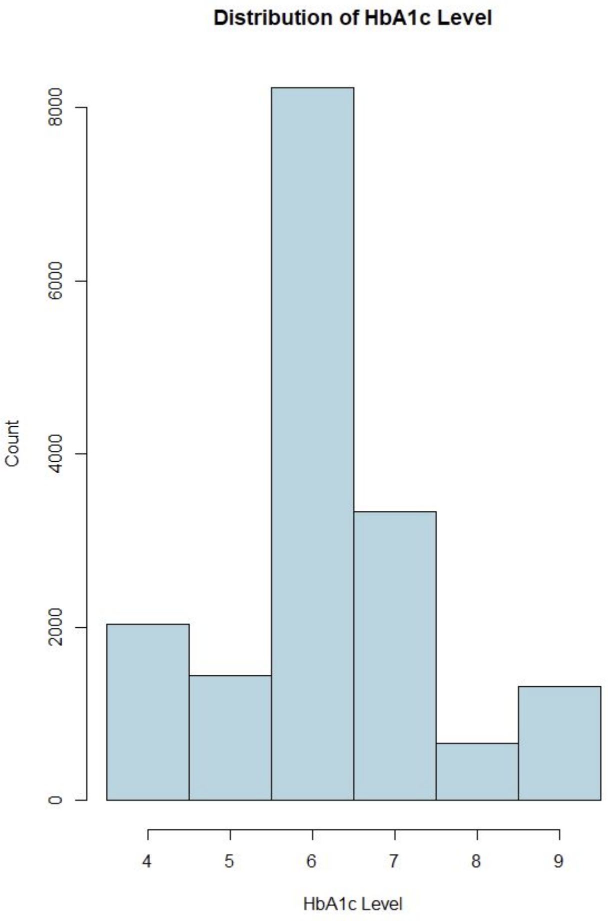
Age Distribution



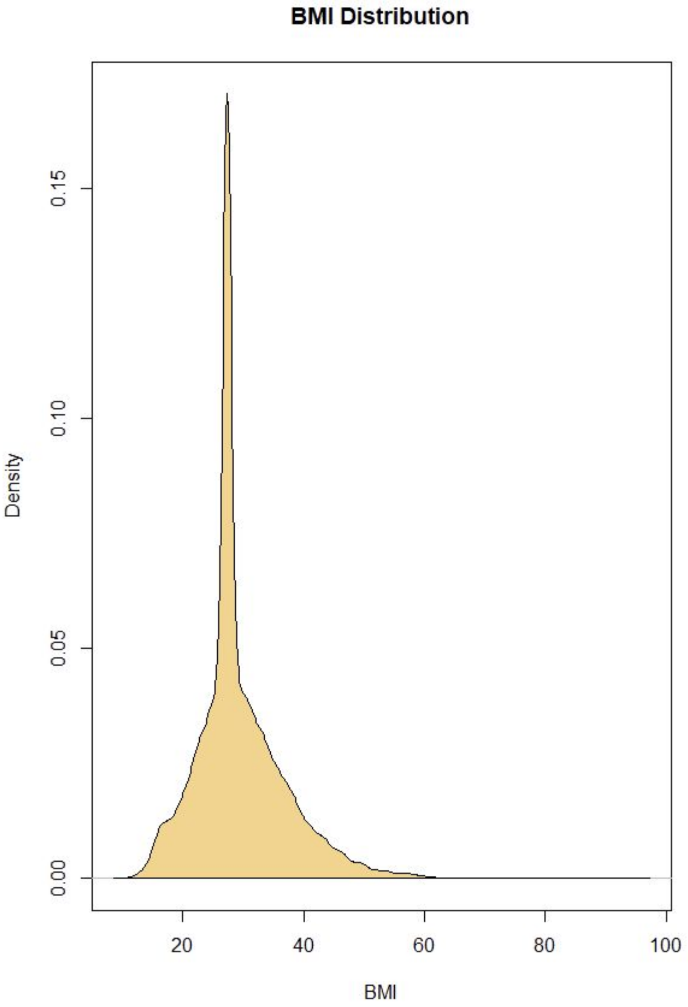
Gender Distribution

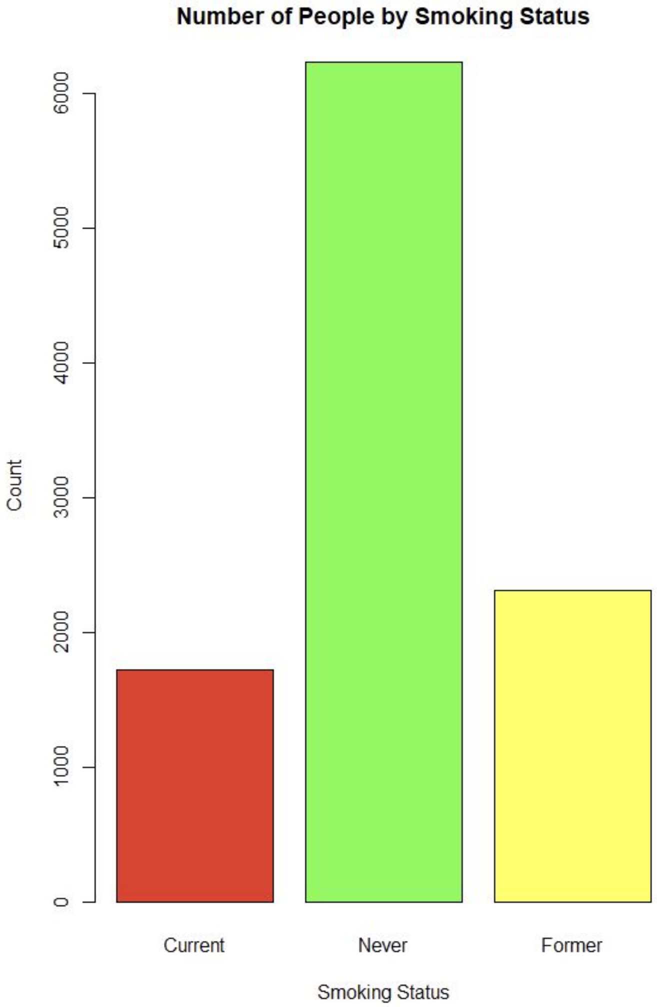
Data Visualization - Diabetes Risk Factors



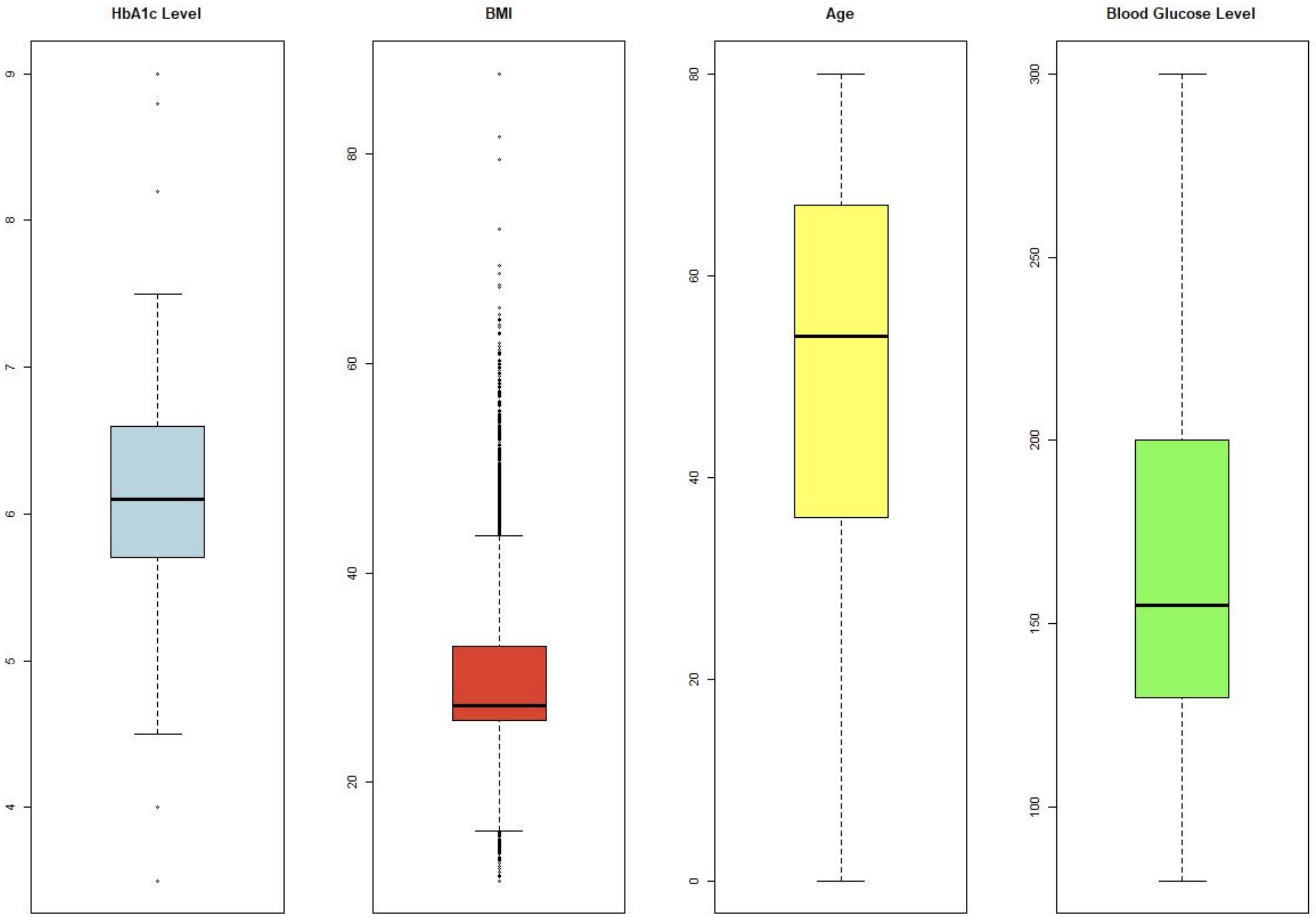


Data Visualization - BMI and Smoking Distribution

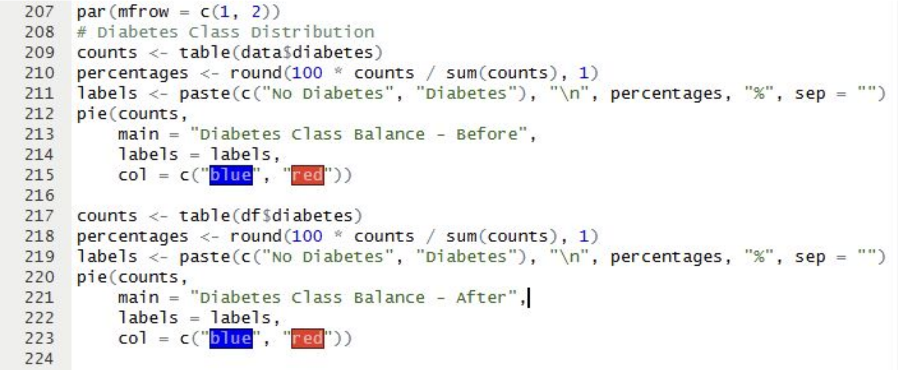

BMI Distribution


Number of People by Smoking Status

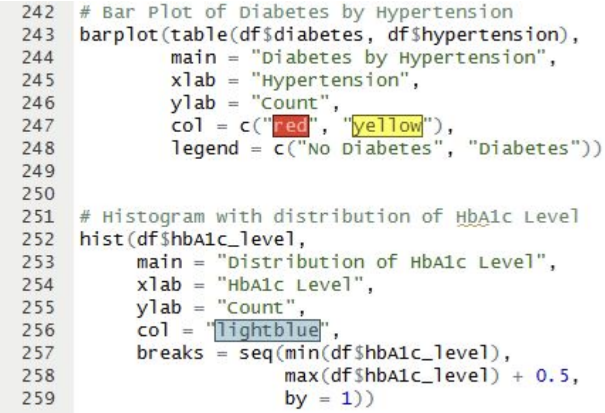
Data Visualization - Box plots



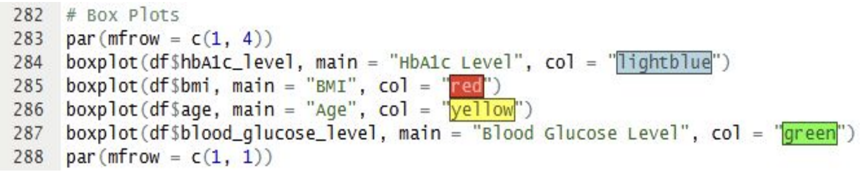
Data Visualization - Codes



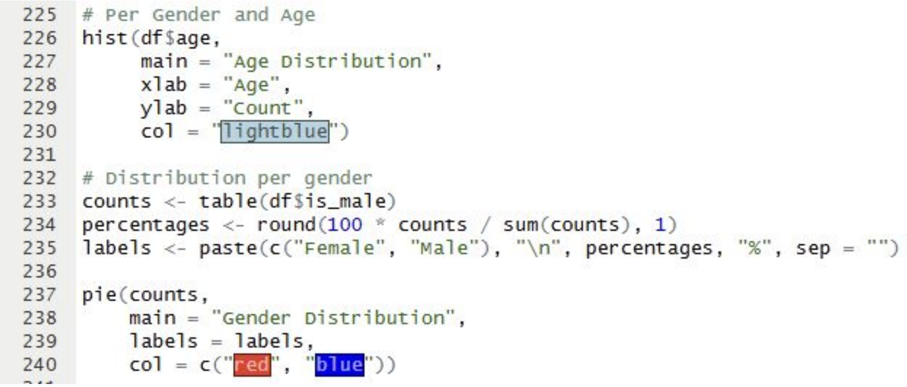
```
par(mfrow = c(1, 2))
# Diabetes Class Distribution
counts <- table(data$diabetes)
percentages <- round(100 * counts / sum(counts), 1)
labels <- paste(c("No Diabetes", "Diabetes"), "\n", percentages, "%", sep = "")
pie(counts,
    main = "Diabetes Class Balance - Before",
    labels = labels,
    col = c("blue", "red"))

counts <- table(df$diabetes)
percentages <- round(100 * counts / sum(counts), 1)
labels <- paste(c("No Diabetes", "Diabetes"), "\n", percentages, "%", sep = "")
pie(counts,
    main = "Diabetes Class Balance - After",
    labels = labels,
    col = c("blue", "red"))

```



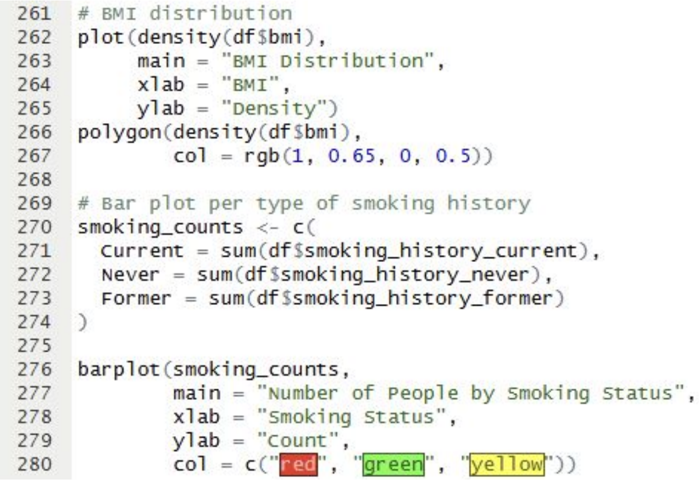
```
# Bar Plot of Diabetes by Hypertension
barplot(table(df$diabetes, df$hypertension),
        main = "Diabetes by Hypertension",
        xlab = "Hypertension",
        ylab = "Count",
        col = c("red", "yellow"),
        legend = c("No Diabetes", "Diabetes"))


# Histogram with distribution of HbA1c Level
hist(df$hbA1c_level,
     main = "Distribution of HbA1c Level",
     xlab = "HbA1c Level",
     ylab = "Count",
     col = "lightblue",
     breaks = seq(min(df$hbA1c_level),
                  max(df$hbA1c_level) + 0.5,
                  by = 1))
```



```
# Box Plots
par(mfrow = c(1, 4))
boxplot(df$hbA1c_level, main = "HbA1c Level", col = "lightblue")
boxplot(df$bmi, main = "BMI", col = "red")
boxplot(df$age, main = "Age", col = "yellow")
boxplot(df$blood_glucose_level, main = "Blood Glucose Level", col = "green")
par(mfrow = c(1, 1))
```



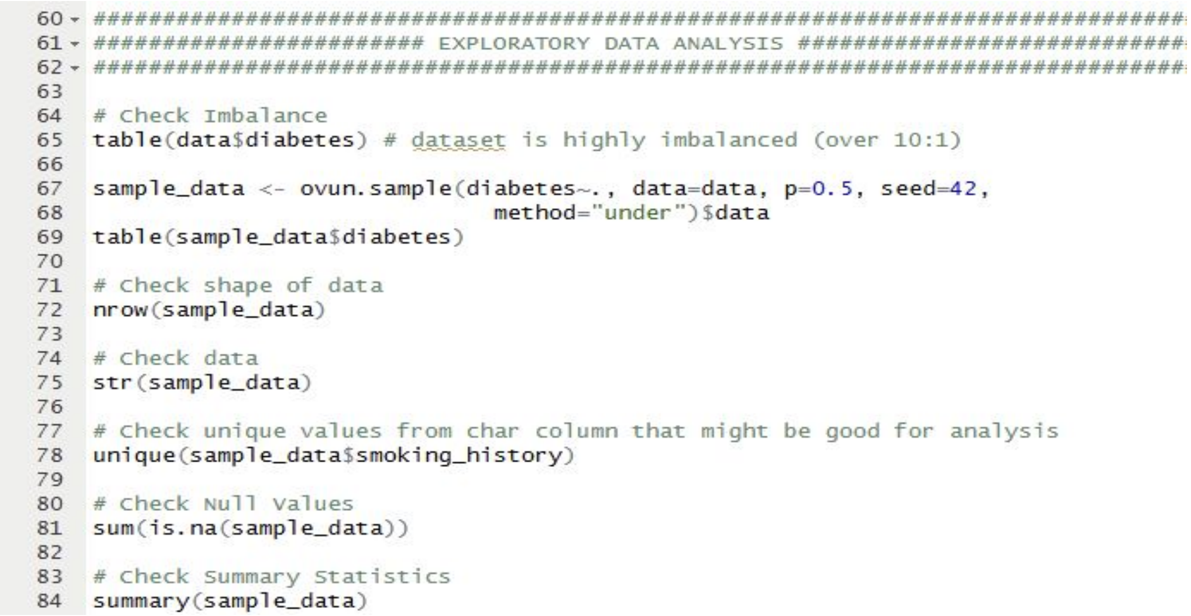
```
# Per Gender and Age
hist(df$age,
     main = "Age Distribution",
     xlab = "Age",
     ylab = "Count",
     col = "lightblue")

# Distribution per gender
counts <- table(df$is_male)
percentages <- round(100 * counts / sum(counts), 1)
labels <- paste(c("Female", "Male"), "\n", percentages, "%", sep = "")

pie(counts,
    main = "Gender Distribution",
    labels = labels,
    col = c("red", "blue"))
```



```
# BMI distribution
plot(density(df$bmi),
     main = "BMI Distribution",
     xlab = "BMI",
     ylab = "Density")
polygon(density(df$bmi),
        col = rgb(1, 0.65, 0, 0.5))

# Bar plot per type of smoking history
smoking_counts <- c(
  Current = sum(df$smoking_history_current),
  Never = sum(df$smoking_history_never),
  Former = sum(df$smoking_history_former)
)

barplot(smoking_counts,
        main = "Number of People by Smoking Status",
        xlab = "Smoking Status",
        ylab = "Count",
        col = c("red", "green", "yellow"))
```

Exploratory Data Analysis

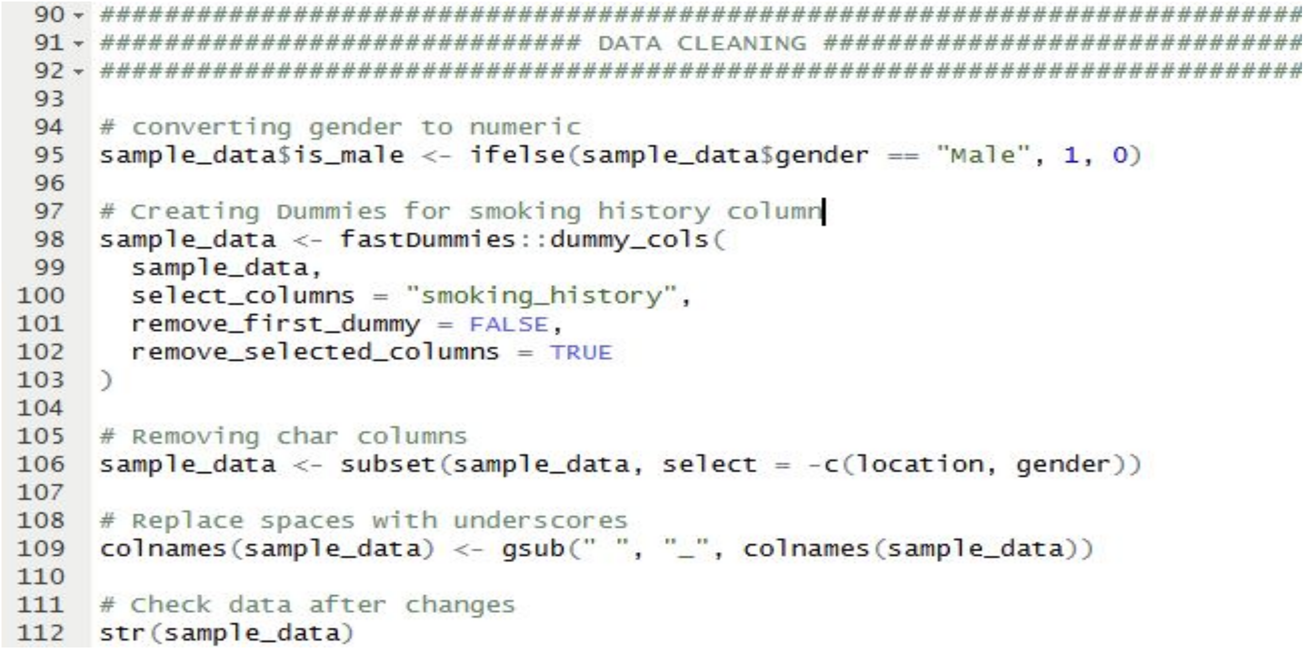
- Check Imbalance in dataset, shape, values from attributes, statistics, and missing values.



```
###############################################################################
######################## EXPLORATORY DATA ANALYSIS ############################
###############################################################################

# Check Imbalance
table(data$diabetes) # dataset is highly imbalanced (over 10:1)

sample_data <- ovun.sample(diabetes~., data=data, p=0.5, seed=42,
                              method="under")$data
table(sample_data$diabetes)

# Check shape of data
nrow(sample_data)

# Check data
str(sample_data)

# Check unique values from char column that might be good for analysis
unique(sample_data$smoking_history)

# Check Null Values
sum(is.na(sample_data))

# Check Summary Statistics
summary(sample_data)
```

Data Cleaning

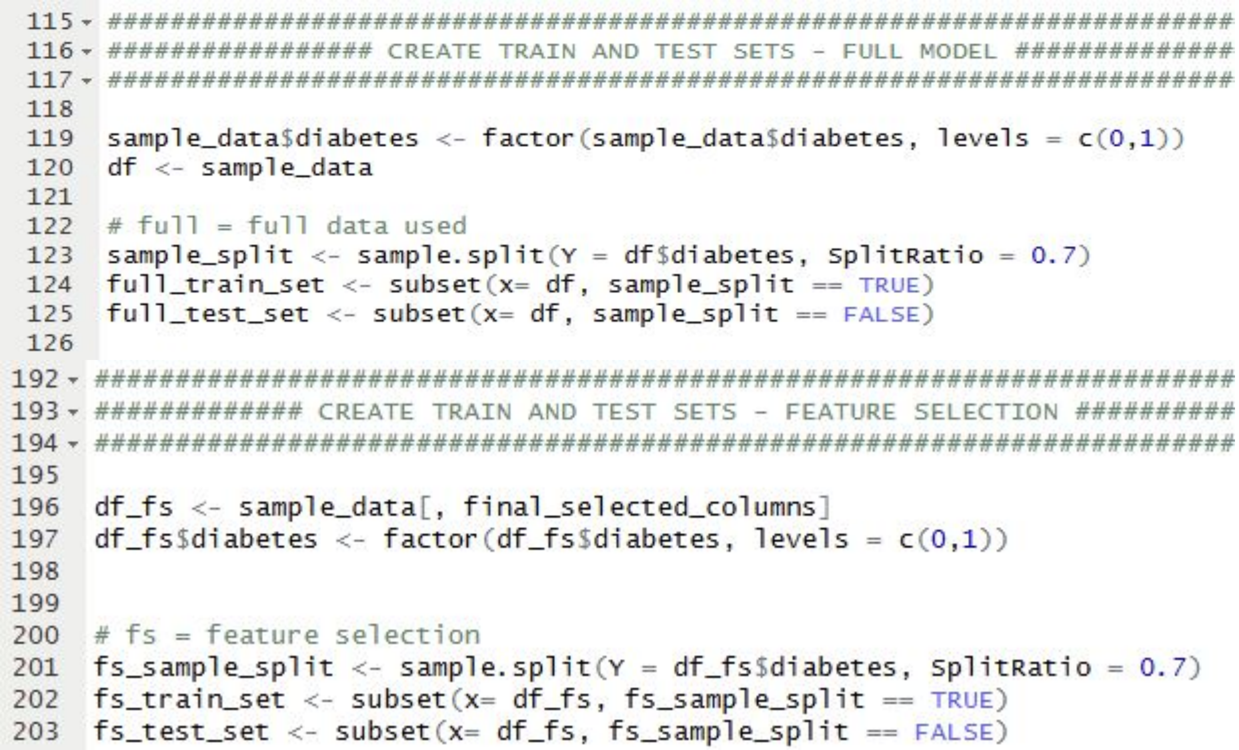
- Converted gender to numeric, created dummies for smoking history, remove char columns, and fixed naming convention from attributes.



```r
###########################################################################
############################## DATA CLEANING ##############################
###########################################################################

# converting gender to numeric
sample_data$is_male <- ifelse(sample_data$gender == "Male", 1, 0)

# Creating Dummies for smoking history column
sample_data <- fastDummies::dummy_cols(
  sample_data,
  select_columns = "smoking_history",
  remove_first_dummy = FALSE,
  remove_selected_columns = TRUE
)

# Removing char columns
sample_data <- subset(sample_data, select = -c(location, gender))

# Replace spaces with underscores
colnames(sample_data) <- gsub(" ", "_", colnames(sample_data))

# Check data after changes
str(sample_data)
```

Creating Train, Test datasets

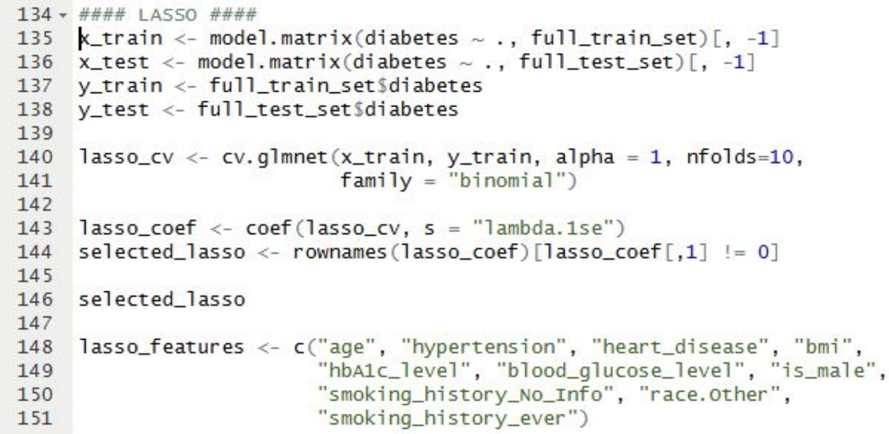
- We used two sets in our project, one with all attributes named ‘full’ and one with the selected features named ‘fs’. Both with ratio 70:30.



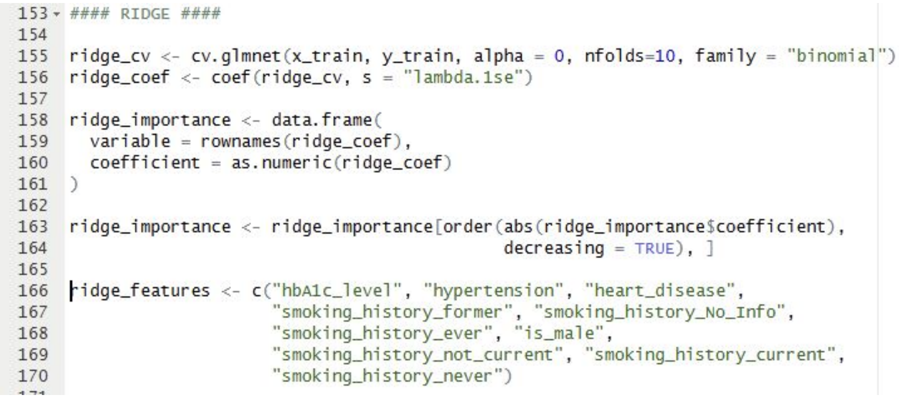
```
########################################################################
################# CREATE TRAIN AND TEST SETS - FULL MODEL ##############
########################################################################

sample_data$diabetes <- factor(sample_data$diabetes, levels = c(0,1))
df <- sample_data

# full = full data used
sample_split <- sample.split(Y = df$diabetes, SplitRatio = 0.7)
full_train_set <- subset(x= df, sample_split == TRUE)
full_test_set <- subset(x= df, sample_split == FALSE)

########################################################################
############# CREATE TRAIN AND TEST SETS - FEATURE SELECTION ##########
########################################################################

df_fs <- sample_data[, final_selected_columns]
df_fs$diabetes <- factor(df_fs$diabetes, levels = c(0,1))


# fs = feature selection
fs_sample_split <- sample.split(Y = df_fs$diabetes, SplitRatio = 0.7)
fs_train_set <- subset(x= df_fs, fs_sample_split == TRUE)
fs_test_set <- subset(x= df_fs, fs_sample_split == FALSE)
```

Feature Selection

- Used to reduce overfitting, and handle multicollinearity
- Used Correlation, LASSO and RIDGE Techniques to decide the better attributes to keep in our model.



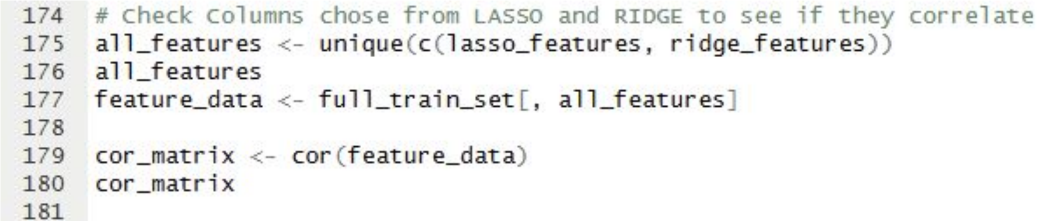
```r
#### LASSO ####
x_train <- model.matrix(diabetes ~ ., full_train_set)[, -1]
x_test <- model.matrix(diabetes ~ ., full_test_set)[, -1]
y_train <- full_train_set$diabetes
y_test <- full_test_set$diabetes

lasso_cv <- cv.glmnet(x_train, y_train, alpha = 1, nfolds=10,
                      family = "binomial")

lasso_coef <- coef(lasso_cv, s = "lambda.1se")
selected_lasso <- rownames(lasso_coef)[lasso_coef[,1] != 0]

selected_lasso

lasso_features <- c("age", "hypertension", "heart_disease", "bmi",
                    "hbA1c_level", "blood_glucose_level", "is_male",
                    "smoking_history_No_Info", "race.Other",
                    "smoking_history_ever")
```



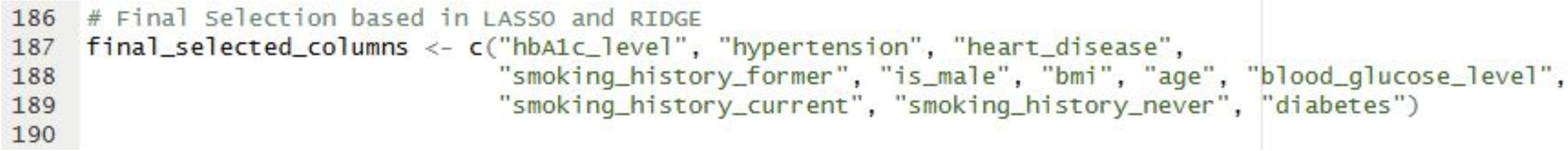
```r
#### RIDGE ####

ridge_cv <- cv.glmnet(x_train, y_train, alpha = 0, nfolds=10, family = "binomial")
ridge_coef <- coef(ridge_cv, s = "lambda.1se")

ridge_importance <- data.frame(
  variable = rownames(ridge_coef),
  coefficient = as.numeric(ridge_coef)
)

ridge_importance <- ridge_importance[order(abs(ridge_importance$coefficient),
                                           decreasing = TRUE), ]

ridge_features <- c("hbA1c_level", "hypertension", "heart_disease",
                    "smoking_history_former", "smoking_history_No_Info",
                    "smoking_history_ever", "is_male",
                    "smoking_history_not_current", "smoking_history_current",
                    "smoking_history_never")
```

Feature Selection

- We did the correlation between attributes selected from LASSO and RIDGE.
- None of the attributes presented correlation higher than 47%, hence all of them could be added.
- but for our study doesn't make sense consider some of the columns even though they could be added.

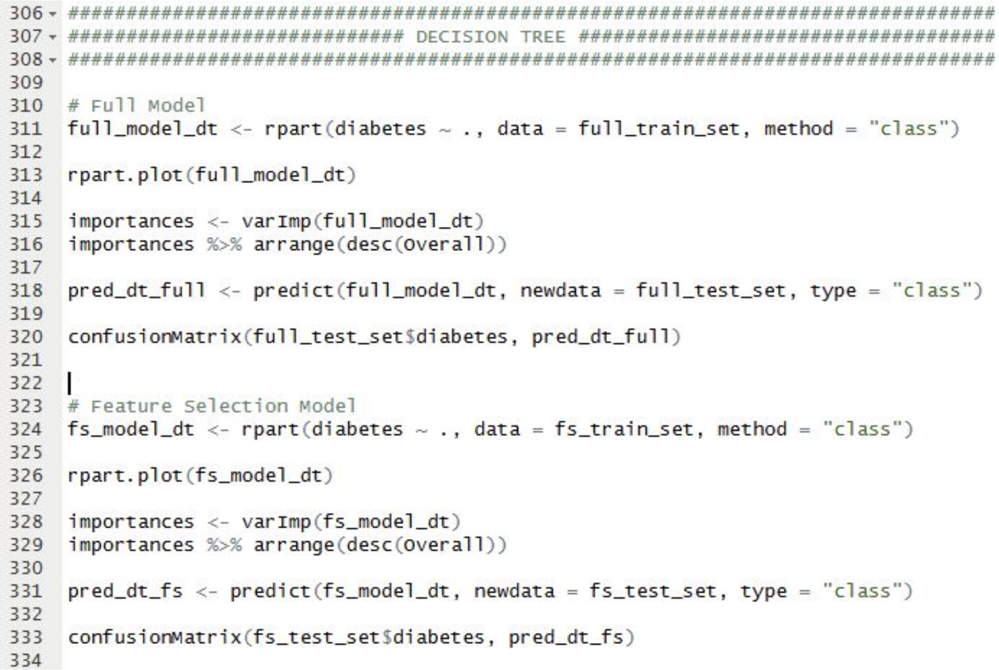


```
# Check Columns chose from LASSO and RIDGE to see if they correlate
all_features <- unique(c(lasso_features, ridge_features))
all_features
feature_data <- full_train_set[, all_features]

cor_matrix <- cor(feature_data)
cor_matrix

```

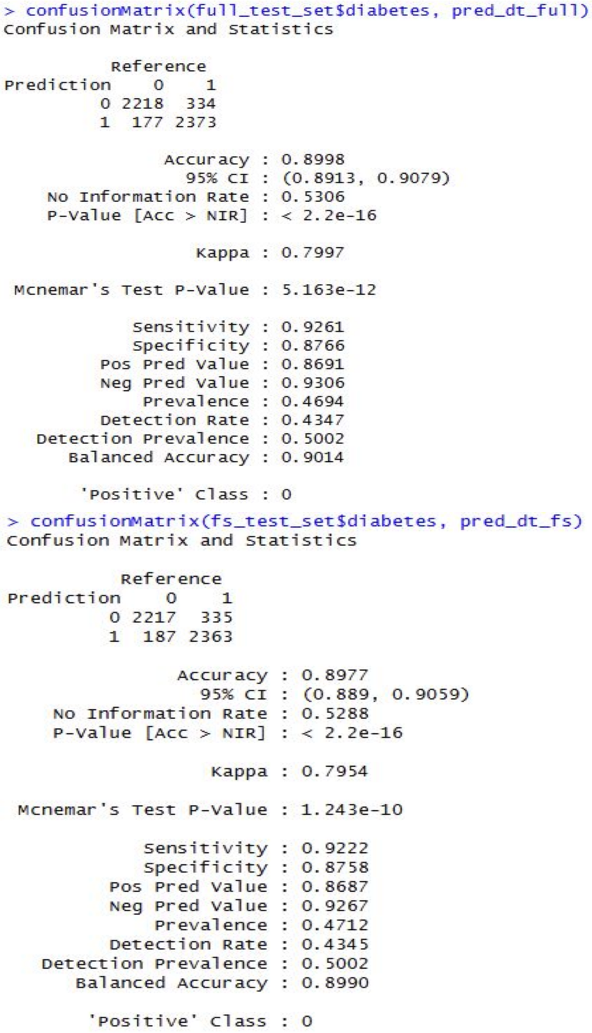


```
# Final Selection based in LASSO and RIDGE
final_selected_columns <- c("hbA1c_level", "hypertension", "heart_disease",
                            "smoking_history_former", "is_male", "bmi", "age", "blood_glucose_level",
                            "smoking_history_current", "smoking_history_never", "diabetes")

```

Models Analysis - Decision Tree



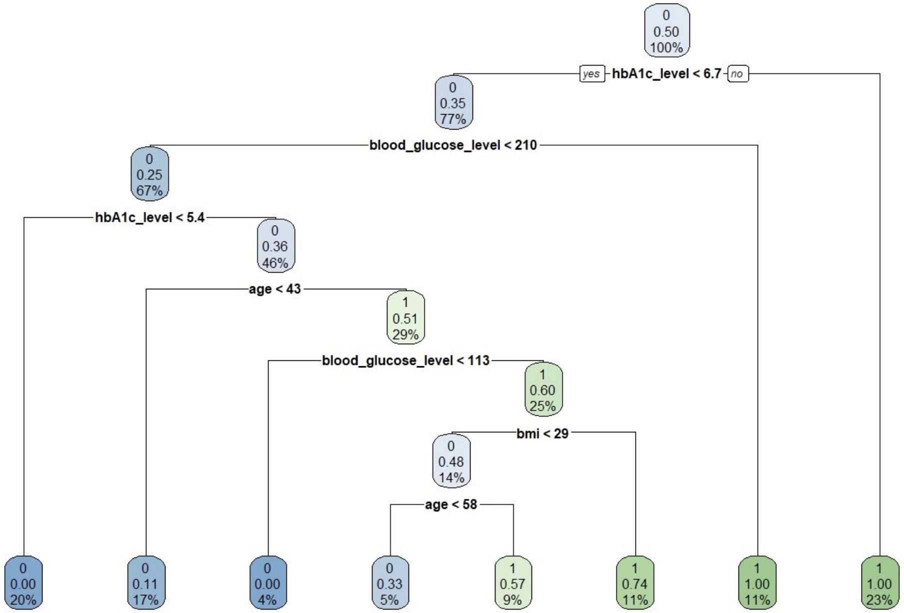
```
##########################################################################
############################ DECISION TREE ###############################
##########################################################################

# Full Model
full_model_dt <- rpart(diabetes ~ ., data = full_train_set, method = "class")

rpart.plot(full_model_dt)

importances <- varImp(full_model_dt)
importances %>% arrange(desc(Overall))

pred_dt_full <- predict(full_model_dt, newdata = full_test_set, type = "class")

confusionMatrix(full_test_set$diabetes, pred_dt_full)


# Feature Selection Model
fs_model_dt <- rpart(diabetes ~ ., data = fs_train_set, method = "class")

rpart.plot(fs_model_dt)

importances <- varImp(fs_model_dt)
importances %>% arrange(desc(Overall))

pred_dt_fs <- predict(fs_model_dt, newdata = fs_test_set, type = "class")

confusionMatrix(fs_test_set$diabetes, pred_dt_fs)

```



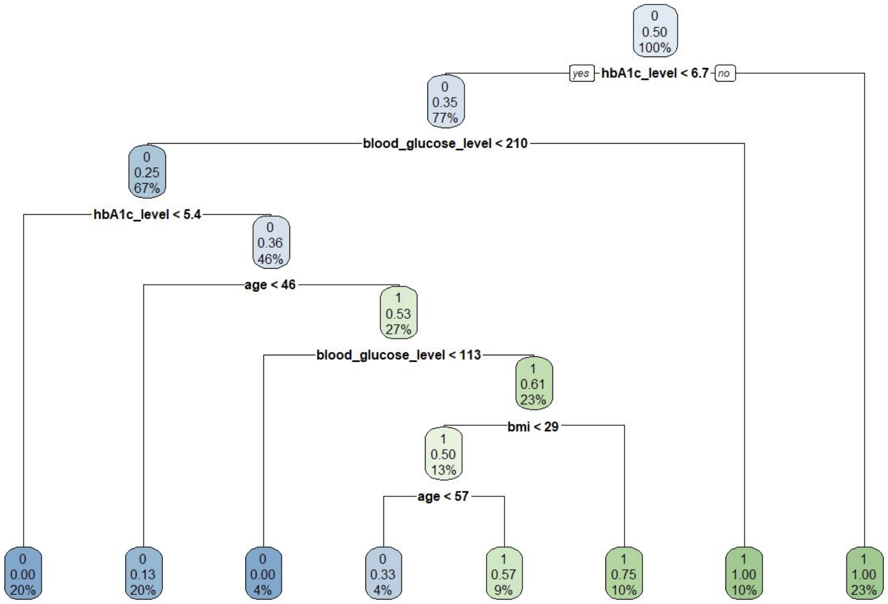
```
> confusionMatrix(full_test_set$diabetes, pred_dt_full)
Confusion Matrix and Statistics

          Reference
Prediction    0    1
         0 2218  334
         1  177 2373

               Accuracy : 0.8998
                 95% CI : (0.8913, 0.9079)
    No Information Rate : 0.5306
    P-Value [Acc > NIR] : < 2.2e-16

                  Kappa : 0.7997

 Mcnemar's Test P-Value : 5.163e-12

            Sensitivity : 0.9261
            Specificity : 0.8766
         Pos Pred Value : 0.8691
         Neg Pred Value : 0.9306
             Prevalence : 0.4694
         Detection Rate : 0.4347
   Detection Prevalence : 0.5002
      Balanced Accuracy : 0.9014

       'Positive' Class : 0
> confusionMatrix(fs_test_set$diabetes, pred_dt_fs)
Confusion Matrix and Statistics

          Reference
Prediction    0    1
         0 2217  335
         1  187 2363

               Accuracy : 0.8977
                 95% CI : (0.889, 0.9059)
    No Information Rate : 0.5288
    P-Value [Acc > NIR] : < 2.2e-16

                  Kappa : 0.7954

 Mcnemar's Test P-Value : 1.243e-10

            Sensitivity : 0.9222
            Specificity : 0.8758
         Pos Pred Value : 0.8687
         Neg Pred Value : 0.9267
             Prevalence : 0.4712
         Detection Rate : 0.4345
   Detection Prevalence : 0.5002
      Balanced Accuracy : 0.8990

       'Positive' Class : 0
```

Models Analysis - Decision Tree

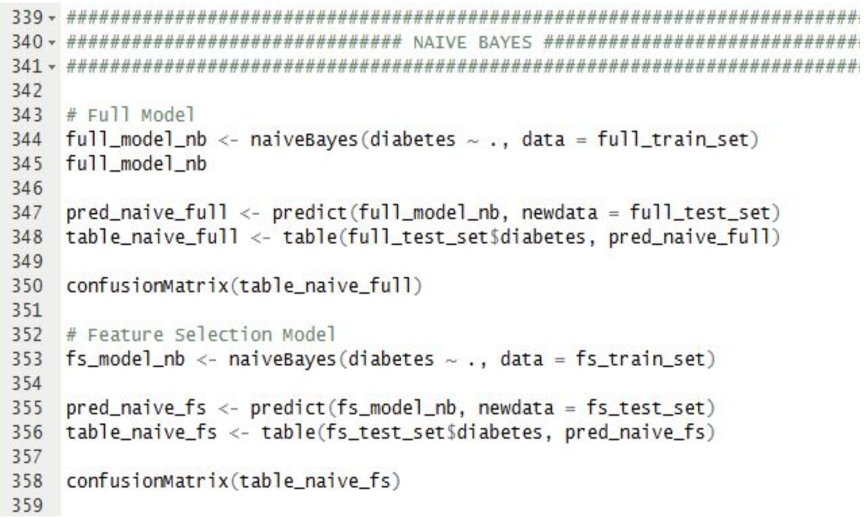
Decision Tree Full Model



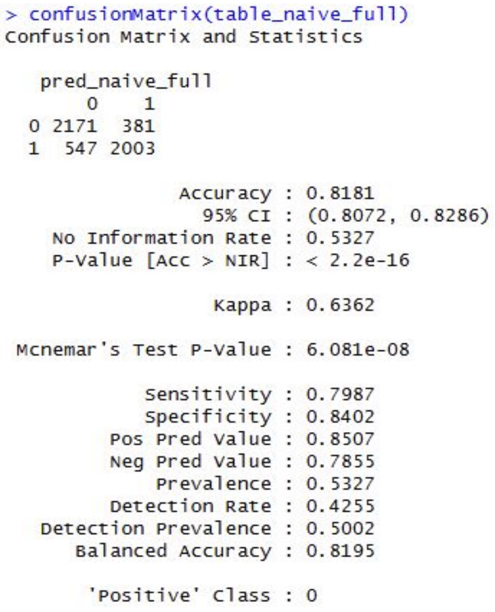
Decision Tree Feature Selection Model



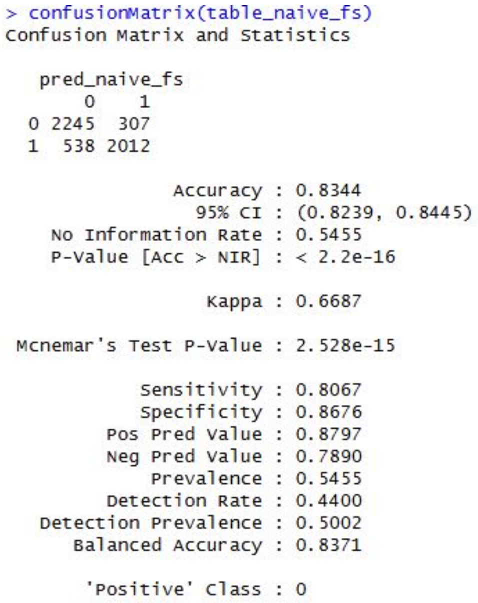
Models Analysis - Naive Bayes



```r
##########################################################################
############################### NAIVE BAYES ##############################
##########################################################################

# Full Model
full_model_nb <- naiveBayes(diabetes ~ ., data = full_train_set)
full_model_nb

pred_naive_full <- predict(full_model_nb, newdata = full_test_set)
table_naive_full <- table(full_test_set$diabetes, pred_naive_full)

confusionMatrix(table_naive_full)

# Feature Selection Model
fs_model_nb <- naiveBayes(diabetes ~ ., data = fs_train_set)

pred_naive_fs <- predict(fs_model_nb, newdata = fs_test_set)
table_naive_fs <- table(fs_test_set$diabetes, pred_naive_fs)

confusionMatrix(table_naive_fs)

```

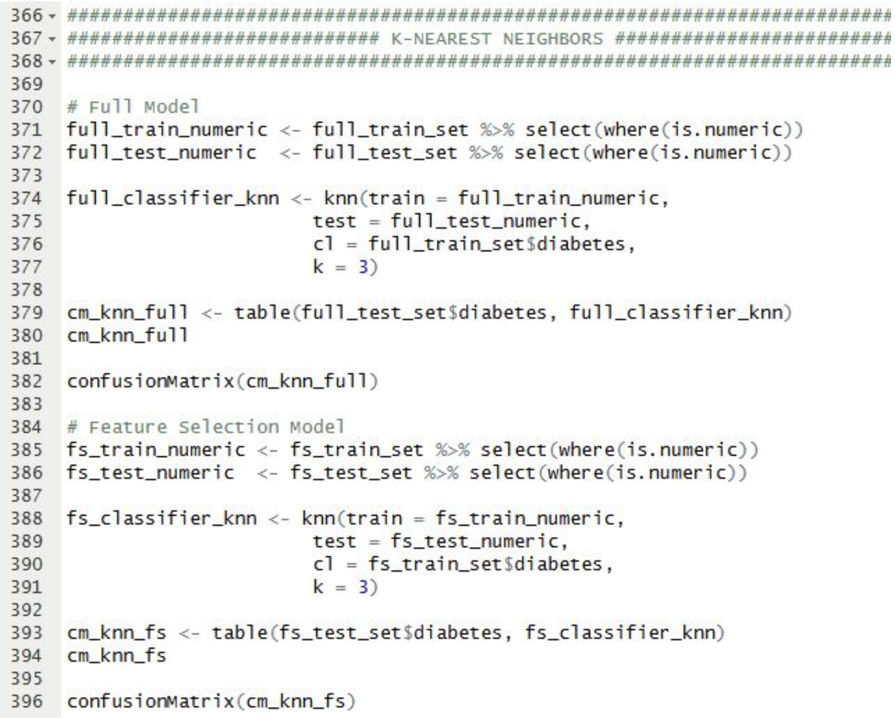


```
> confusionMatrix(table_naive_full)
Confusion Matrix and Statistics

   pred_naive_full
       0    1
  0 2171  381
  1  547 2003

               Accuracy : 0.8181
                 95% CI : (0.8072, 0.8286)
    No Information Rate : 0.5327
    P-Value [Acc > NIR] : < 2.2e-16

                  Kappa : 0.6362

 Mcnemar's Test P-Value : 6.081e-08

            Sensitivity : 0.7987
            Specificity : 0.8402
         Pos Pred Value : 0.8507
         Neg Pred Value : 0.7855
             Prevalence : 0.5327
         Detection Rate : 0.4255
   Detection Prevalence : 0.5002
      Balanced Accuracy : 0.8195

       'Positive' Class : 0
```

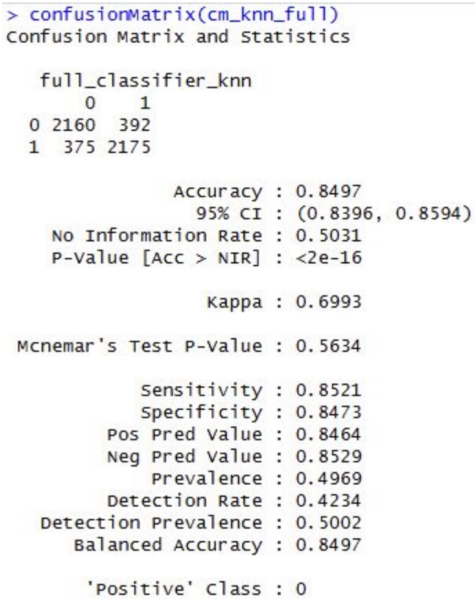


```
> confusionMatrix(table_naive_fs)
Confusion Matrix and Statistics

   pred_naive_fs
       0    1
  0 2245  307
  1  538 2012

               Accuracy : 0.8344
                 95% CI : (0.8239, 0.8445)
    No Information Rate : 0.5455
    P-Value [Acc > NIR] : < 2.2e-16

                  Kappa : 0.6687

 Mcnemar's Test P-Value : 2.528e-15

            Sensitivity : 0.8067
            Specificity : 0.8676
         Pos Pred Value : 0.8797
         Neg Pred Value : 0.7890
             Prevalence : 0.5455
         Detection Rate : 0.4400
   Detection Prevalence : 0.5002
      Balanced Accuracy : 0.8371

       'Positive' Class : 0
```

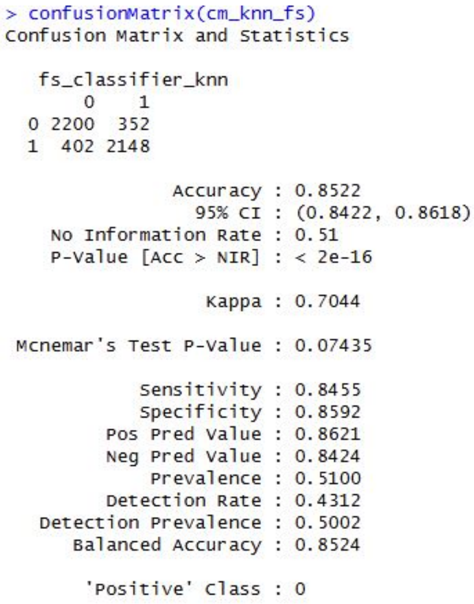
Models Analysis - K-Nearest Neighbors



```
##########################################################################
############################ K-NEAREST NEIGHBORS #########################
##########################################################################

# Full Model
full_train_numeric <- full_train_set %>% select(where(is.numeric))
full_test_numeric  <- full_test_set %>% select(where(is.numeric))

full_classifier_knn <- knn(train = full_train_numeric,
                      test = full_test_numeric,
                      cl = full_train_set$diabetes,
                      k = 3)

cm_knn_full <- table(full_test_set$diabetes, full_classifier_knn)
cm_knn_full

confusionMatrix(cm_knn_full)

# Feature Selection Model
fs_train_numeric <- fs_train_set %>% select(where(is.numeric))
fs_test_numeric  <- fs_test_set %>% select(where(is.numeric))

fs_classifier_knn <- knn(train = fs_train_numeric,
                      test = fs_test_numeric,
                      cl = fs_train_set$diabetes,
                      k = 3)

cm_knn_fs <- table(fs_test_set$diabetes, fs_classifier_knn)
cm_knn_fs

confusionMatrix(cm_knn_fs)
```

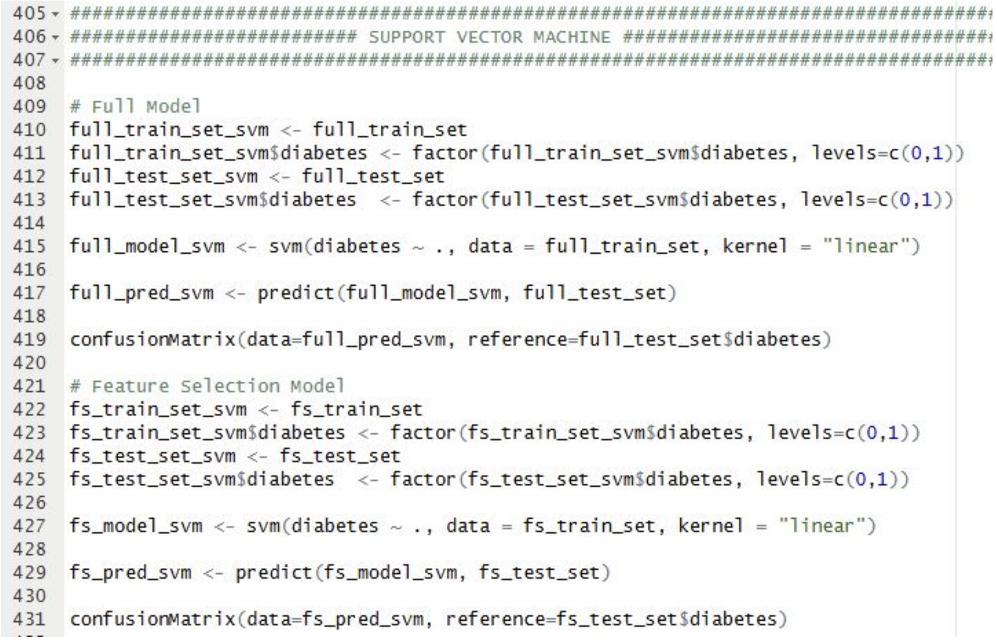


```
> confusionMatrix(cm_knn_full)
Confusion Matrix and Statistics

   full_classifier_knn
        0    1
  0  2160  392
  1   375 2175

               Accuracy : 0.8497
                 95% CI : (0.8396, 0.8594)
    No Information Rate : 0.5031
    P-Value [Acc > NIR] : <2e-16

                  Kappa : 0.6993

 Mcnemar's Test P-Value : 0.5634

            Sensitivity : 0.8521
            Specificity : 0.8473
         Pos Pred Value : 0.8464
         Neg Pred Value : 0.8529
             Prevalence : 0.4969
         Detection Rate : 0.4234
   Detection Prevalence : 0.5002
      Balanced Accuracy : 0.8497

       'Positive' Class : 0
```

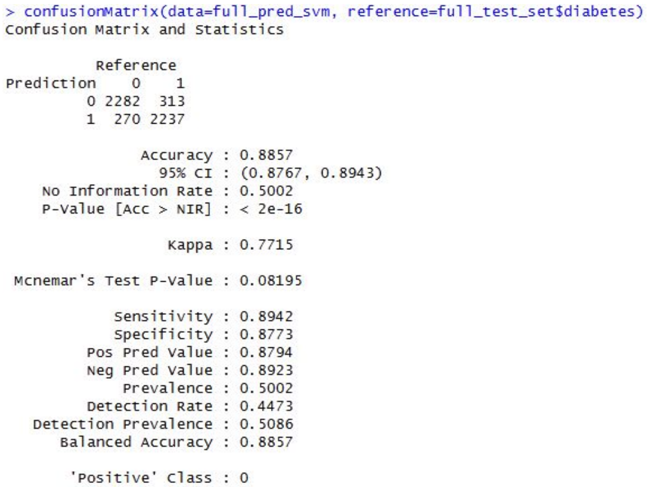


```
> confusionMatrix(cm_knn_fs)
Confusion Matrix and Statistics

   fs_classifier_knn
        0    1
  0  2200  352
  1   402 2148

               Accuracy : 0.8522
                 95% CI : (0.8422, 0.8618)
    No Information Rate : 0.51
    P-Value [Acc > NIR] : < 2e-16

                  Kappa : 0.7044

 Mcnemar's Test P-Value : 0.07435

            Sensitivity : 0.8455
            Specificity : 0.8592
         Pos Pred Value : 0.8621
         Neg Pred Value : 0.8424
             Prevalence : 0.5100
         Detection Rate : 0.4312
   Detection Prevalence : 0.5002
      Balanced Accuracy : 0.8524

       'Positive' Class : 0
```

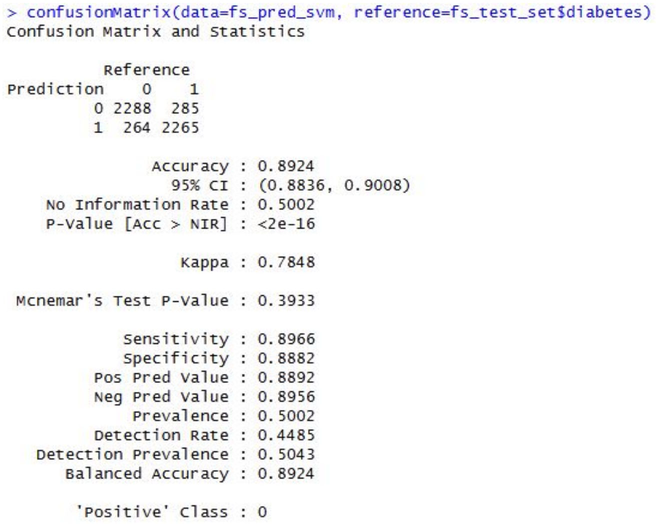
Models Analysis - Support Vector Machine



```
###############################################################################
######################### SUPPORT VECTOR MACHINE ##############################
###############################################################################

# Full Model
full_train_set_svm <- full_train_set
full_train_set_svm$diabetes <- factor(full_train_set_svm$diabetes, levels=c(0,1))
full_test_set_svm <- full_test_set
full_test_set_svm$diabetes  <- factor(full_test_set_svm$diabetes, levels=c(0,1))

full_model_svm <- svm(diabetes ~ ., data = full_train_set, kernel = "linear")

full_pred_svm <- predict(full_model_svm, full_test_set)

confusionMatrix(data=full_pred_svm, reference=full_test_set$diabetes)

# Feature Selection Model
fs_train_set_svm <- fs_train_set
fs_train_set_svm$diabetes <- factor(fs_train_set_svm$diabetes, levels=c(0,1))
fs_test_set_svm <- fs_test_set
fs_test_set_svm$diabetes  <- factor(fs_test_set_svm$diabetes, levels=c(0,1))

fs_model_svm <- svm(diabetes ~ ., data = fs_train_set, kernel = "linear")

fs_pred_svm <- predict(fs_model_svm, fs_test_set)

confusionMatrix(data=fs_pred_svm, reference=fs_test_set$diabetes)
```

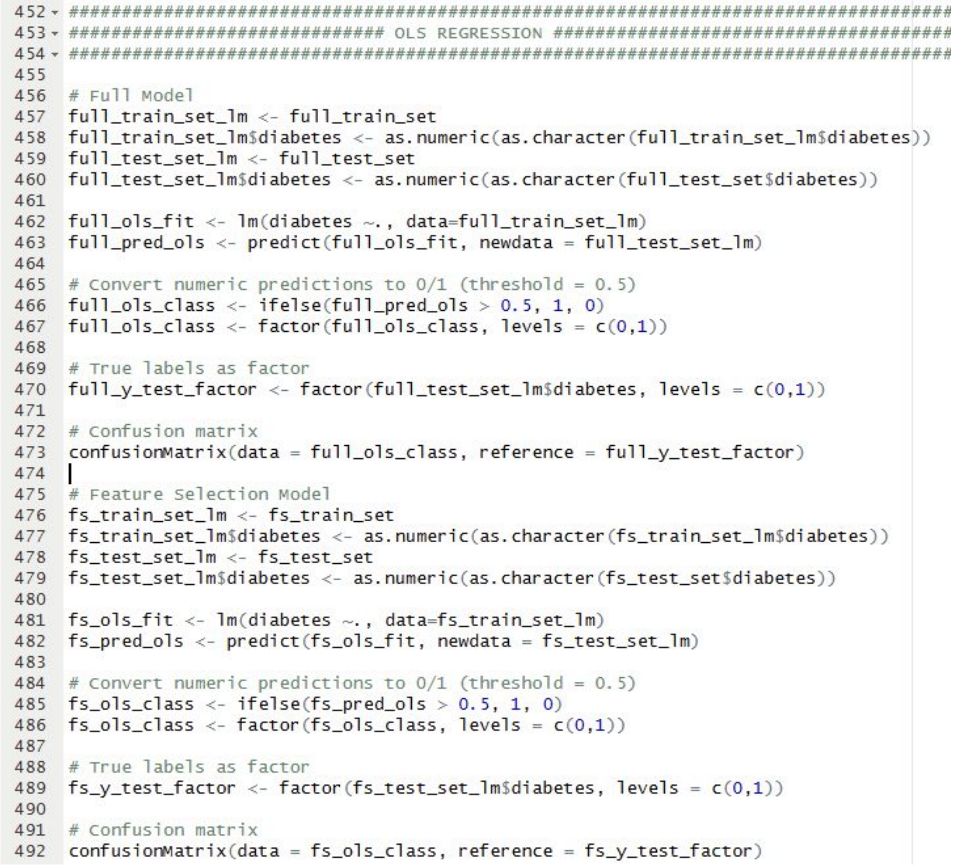


```
> confusionMatrix(data=full_pred_svm, reference=full_test_set$diabetes)
Confusion Matrix and Statistics

          Reference
Prediction    0    1
         0 2282  313
         1  270 2237

               Accuracy : 0.8857
                 95% CI : (0.8767, 0.8943)
    No Information Rate : 0.5002
    P-Value [Acc > NIR] : < 2e-16

                  Kappa : 0.7715

 Mcnemar's Test P-Value : 0.08195

            Sensitivity : 0.8942
            Specificity : 0.8773
         Pos Pred Value : 0.8794
         Neg Pred Value : 0.8923
             Prevalence : 0.5002
         Detection Rate : 0.4473
   Detection Prevalence : 0.5086
      Balanced Accuracy : 0.8857

       'Positive' Class : 0
```

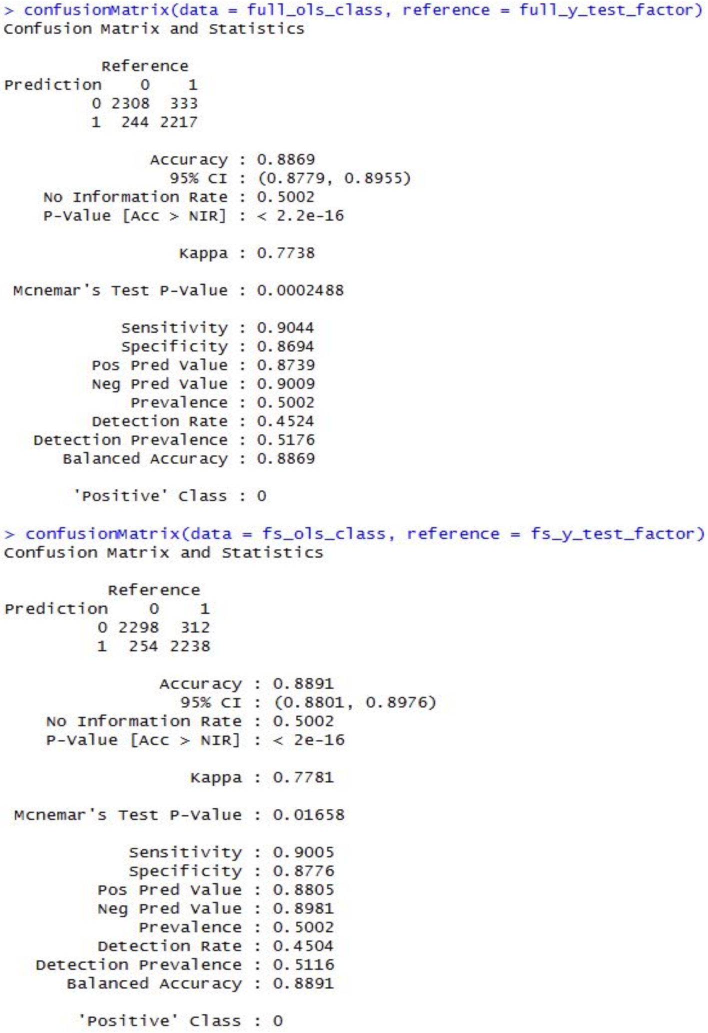


```
> confusionMatrix(data=fs_pred_svm, reference=fs_test_set$diabetes)
Confusion Matrix and Statistics

          Reference
Prediction    0    1
         0 2288  285
         1  264 2265

               Accuracy : 0.8924
                 95% CI : (0.8836, 0.9008)
    No Information Rate : 0.5002
    P-Value [Acc > NIR] : <2e-16

                  Kappa : 0.7848

 Mcnemar's Test P-Value : 0.3933

            Sensitivity : 0.8966
            Specificity : 0.8882
         Pos Pred Value : 0.8892
         Neg Pred Value : 0.8956
             Prevalence : 0.5002
         Detection Rate : 0.4485
   Detection Prevalence : 0.5043
      Balanced Accuracy : 0.8924

       'Positive' Class : 0
```

Models Analysis - OLS Regression

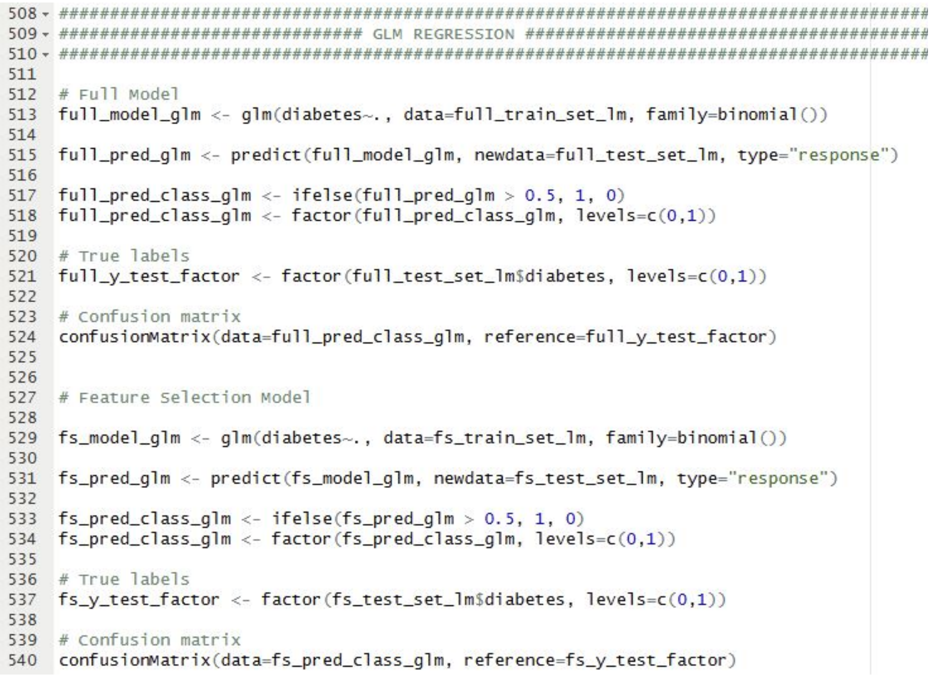


```
################################################################################
############################## OLS REGRESSION ##################################
################################################################################

# Full Model
full_train_set_lm <- full_train_set
full_train_set_lm$diabetes <- as.numeric(as.character(full_train_set_lm$diabetes))
full_test_set_lm <- full_test_set
full_test_set_lm$diabetes <- as.numeric(as.character(full_test_set$diabetes))

full_ols_fit <- lm(diabetes ~., data=full_train_set_lm)
full_pred_ols <- predict(full_ols_fit, newdata = full_test_set_lm)

# Convert numeric predictions to 0/1 (threshold = 0.5)
full_ols_class <- ifelse(full_pred_ols > 0.5, 1, 0)
full_ols_class <- factor(full_ols_class, levels = c(0,1))

# True labels as factor
full_y_test_factor <- factor(full_test_set_lm$diabetes, levels = c(0,1))

# Confusion matrix
confusionMatrix(data = full_ols_class, reference = full_y_test_factor)

# Feature Selection Model
fs_train_set_lm <- fs_train_set
fs_train_set_lm$diabetes <- as.numeric(as.character(fs_train_set_lm$diabetes))
fs_test_set_lm <- fs_test_set
fs_test_set_lm$diabetes <- as.numeric(as.character(fs_test_set$diabetes))

fs_ols_fit <- lm(diabetes ~., data=fs_train_set_lm)
fs_pred_ols <- predict(fs_ols_fit, newdata = fs_test_set_lm)

# Convert numeric predictions to 0/1 (threshold = 0.5)
fs_ols_class <- ifelse(fs_pred_ols > 0.5, 1, 0)
fs_ols_class <- factor(fs_ols_class, levels = c(0,1))

# True labels as factor
fs_y_test_factor <- factor(fs_test_set_lm$diabetes, levels = c(0,1))

# Confusion matrix
confusionMatrix(data = fs_ols_class, reference = fs_y_test_factor)
```

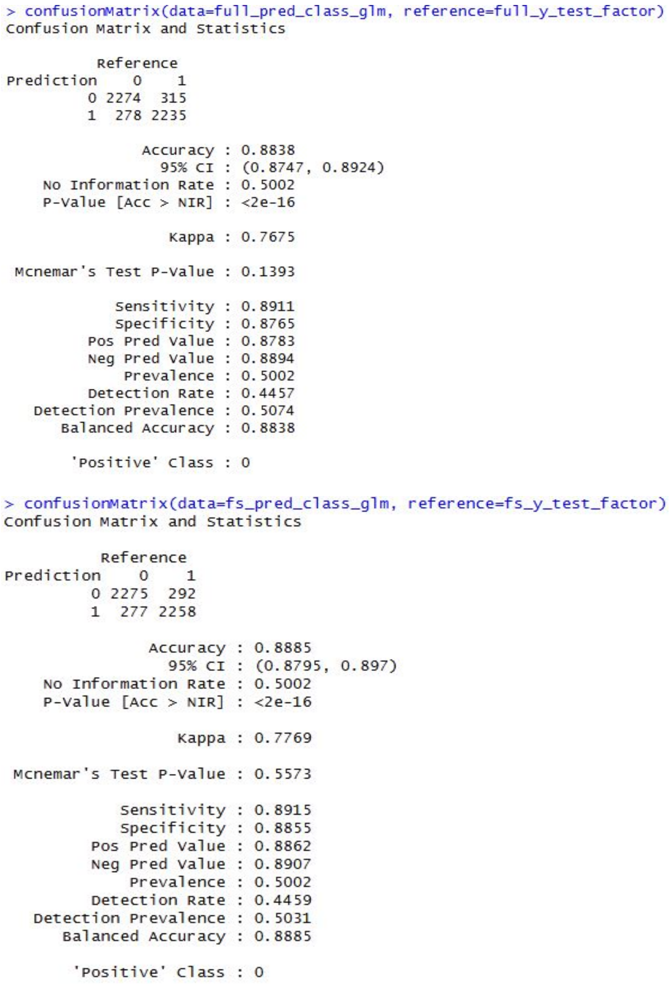


```
> confusionMatrix(data = full_ols_class, reference = full_y_test_factor)
Confusion Matrix and Statistics

          Reference
Prediction    0    1
         0 2308  333
         1  244 2217

               Accuracy : 0.8869
                 95% CI : (0.8779, 0.8955)
    No Information Rate : 0.5002
    P-Value [Acc > NIR] : < 2.2e-16

                  Kappa : 0.7738

 Mcnemar's Test P-Value : 0.0002488

            Sensitivity : 0.9044
            Specificity : 0.8694
         Pos Pred Value : 0.8739
         Neg Pred Value : 0.9009
             Prevalence : 0.5002
         Detection Rate : 0.4524
   Detection Prevalence : 0.5176
      Balanced Accuracy : 0.8869

       'Positive' Class : 0

> confusionMatrix(data = fs_ols_class, reference = fs_y_test_factor)
Confusion Matrix and Statistics

          Reference
Prediction    0    1
         0 2298  312
         1  254 2238

               Accuracy : 0.8891
                 95% CI : (0.8801, 0.8976)
    No Information Rate : 0.5002
    P-Value [Acc > NIR] : < 2e-16

                  Kappa : 0.7781

 Mcnemar's Test P-Value : 0.01658

            Sensitivity : 0.9005
            Specificity : 0.8776
         Pos Pred Value : 0.8805
         Neg Pred Value : 0.8981
             Prevalence : 0.5002
         Detection Rate : 0.4504
   Detection Prevalence : 0.5116
      Balanced Accuracy : 0.8891

       'Positive' Class : 0
```

Models Analysis - GLM Regression

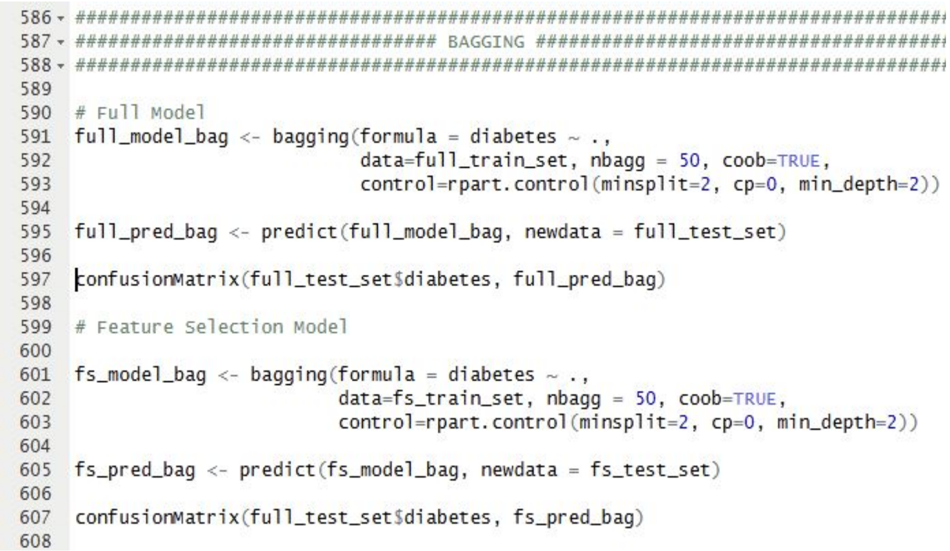


```
######################################################################################
############################## GLM REGRESSION ########################################
######################################################################################

# Full Model
full_model_glm <- glm(diabetes~., data=full_train_set_lm, family=binomial())

full_pred_glm <- predict(full_model_glm, newdata=full_test_set_lm, type="response")

full_pred_class_glm <- ifelse(full_pred_glm > 0.5, 1, 0)
full_pred_class_glm <- factor(full_pred_class_glm, levels=c(0,1))

# True labels
full_y_test_factor <- factor(full_test_set_lm$diabetes, levels=c(0,1))

# Confusion matrix
confusionMatrix(data=full_pred_class_glm, reference=full_y_test_factor)


# Feature Selection Model

fs_model_glm <- glm(diabetes~., data=fs_train_set_lm, family=binomial())

fs_pred_glm <- predict(fs_model_glm, newdata=fs_test_set_lm, type="response")

fs_pred_class_glm <- ifelse(fs_pred_glm > 0.5, 1, 0)
fs_pred_class_glm <- factor(fs_pred_class_glm, levels=c(0,1))

# True labels
fs_y_test_factor <- factor(fs_test_set_lm$diabetes, levels=c(0,1))

# Confusion matrix
confusionMatrix(data=fs_pred_class_glm, reference=fs_y_test_factor)
```

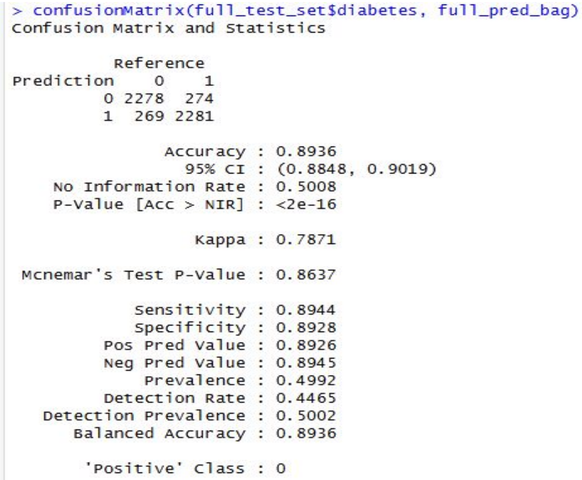


```
> confusionMatrix(data=full_pred_class_glm, reference=full_y_test_factor)
Confusion Matrix and Statistics

          Reference
Prediction    0    1
         0 2274  315
         1  278 2235

               Accuracy : 0.8838
                 95% CI : (0.8747, 0.8924)
    No Information Rate : 0.5002
    P-Value [Acc > NIR] : <2e-16

                  Kappa : 0.7675

 Mcnemar's Test P-Value : 0.1393

            Sensitivity : 0.8911
            Specificity : 0.8765
         Pos Pred Value : 0.8783
         Neg Pred Value : 0.8894
             Prevalence : 0.5002
         Detection Rate : 0.4457
   Detection Prevalence : 0.5074
      Balanced Accuracy : 0.8838

       'Positive' Class : 0

> confusionMatrix(data=fs_pred_class_glm, reference=fs_y_test_factor)
Confusion Matrix and Statistics

          Reference
Prediction    0    1
         0 2275  292
         1  277 2258

               Accuracy : 0.8885
                 95% CI : (0.8795, 0.897)
    No Information Rate : 0.5002
    P-Value [Acc > NIR] : <2e-16

                  Kappa : 0.7769

 Mcnemar's Test P-Value : 0.5573

            Sensitivity : 0.8915
            Specificity : 0.8855
         Pos Pred Value : 0.8862
         Neg Pred Value : 0.8907
             Prevalence : 0.5002
         Detection Rate : 0.4459
   Detection Prevalence : 0.5031
      Balanced Accuracy : 0.8885

       'Positive' Class : 0
```

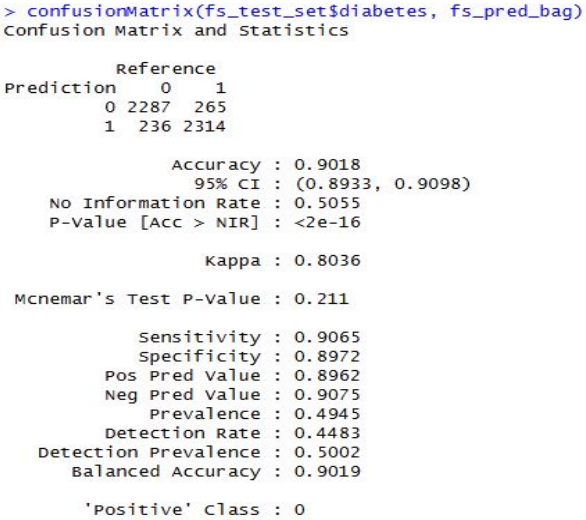
Models Analysis - Bagging



```
################################################################################
################################## BAGGING ####################################
################################################################################

# Full Model
full_model_bag <- bagging(formula = diabetes ~ .,
                          data=full_train_set, nbagg = 50, coob=TRUE,
                          control=rpart.control(minsplit=2, cp=0, min_depth=2))

full_pred_bag <- predict(full_model_bag, newdata = full_test_set)

confusionMatrix(full_test_set$diabetes, full_pred_bag)

# Feature Selection Model

fs_model_bag <- bagging(formula = diabetes ~ .,
                        data=fs_train_set, nbagg = 50, coob=TRUE,
                        control=rpart.control(minsplit=2, cp=0, min_depth=2))

fs_pred_bag <- predict(fs_model_bag, newdata = fs_test_set)

confusionMatrix(full_test_set$diabetes, fs_pred_bag)
```

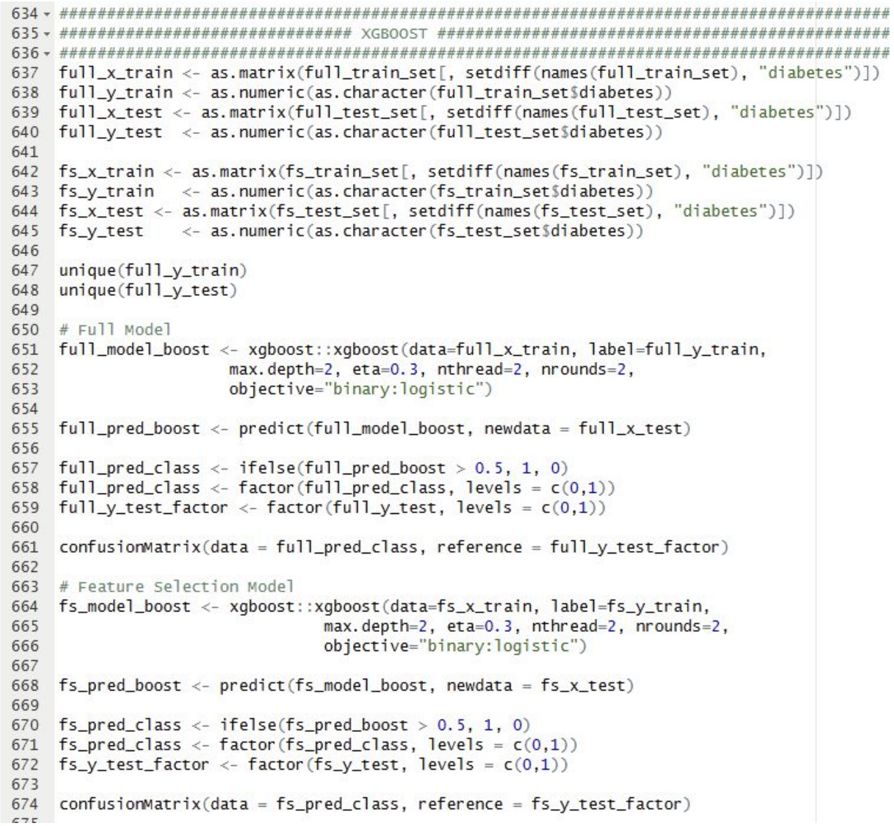


```
> confusionMatrix(full_test_set$diabetes, full_pred_bag)
Confusion Matrix and Statistics

          Reference
Prediction    0    1
         0 2278  274
         1  269 2281

               Accuracy : 0.8936
                 95% CI : (0.8848, 0.9019)
    No Information Rate : 0.5008
    P-Value [Acc > NIR] : <2e-16

                  Kappa : 0.7871

 Mcnemar's Test P-Value : 0.8637

            Sensitivity : 0.8944
            Specificity : 0.8928
         Pos Pred Value : 0.8926
         Neg Pred Value : 0.8945
             Prevalence : 0.4992
         Detection Rate : 0.4465
   Detection Prevalence : 0.5002
      Balanced Accuracy : 0.8936

       'Positive' Class : 0
```

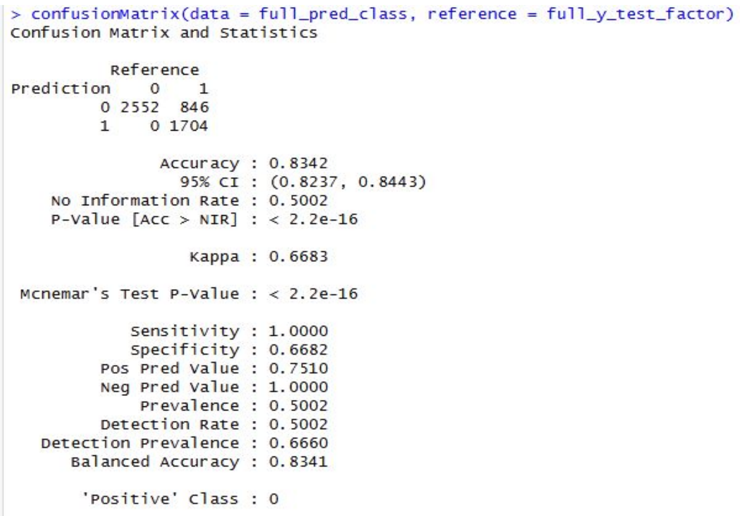


```
> confusionMatrix(fs_test_set$diabetes, fs_pred_bag)
Confusion Matrix and Statistics

          Reference
Prediction    0    1
         0 2287  265
         1  236 2314

               Accuracy : 0.9018
                 95% CI : (0.8933, 0.9098)
    No Information Rate : 0.5055
    P-Value [Acc > NIR] : <2e-16

                  Kappa : 0.8036

 Mcnemar's Test P-Value : 0.211

            Sensitivity : 0.9065
            Specificity : 0.8972
         Pos Pred Value : 0.8962
         Neg Pred Value : 0.9075
             Prevalence : 0.4945
         Detection Rate : 0.4483
   Detection Prevalence : 0.5002
      Balanced Accuracy : 0.9019

       'Positive' Class : 0
```

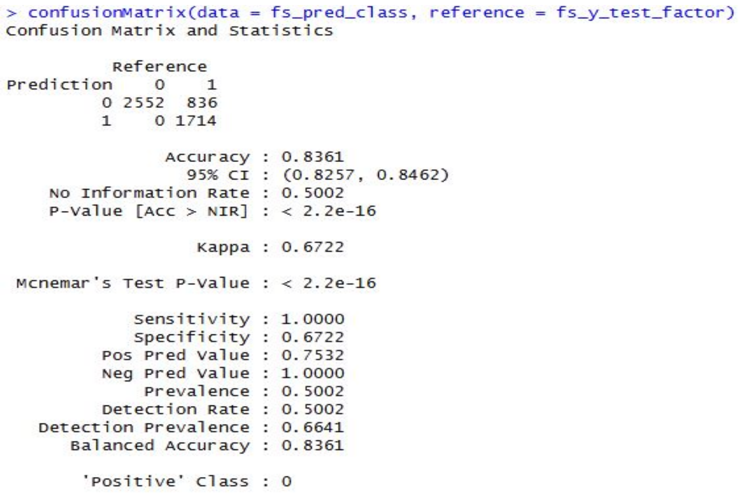
Models Analysis - XGBoost



```
####################################################################################
############################## XGBOOST #############################################
####################################################################################
full_x_train <- as.matrix(full_train_set[, setdiff(names(full_train_set), "diabetes")])
full_y_train <- as.numeric(as.character(full_train_set$diabetes))
full_x_test <- as.matrix(full_test_set[, setdiff(names(full_test_set), "diabetes")])
full_y_test  <- as.numeric(as.character(full_test_set$diabetes))

fs_x_train <- as.matrix(fs_train_set[, setdiff(names(fs_train_set), "diabetes")])
fs_y_train   <- as.numeric(as.character(fs_train_set$diabetes))
fs_x_test <- as.matrix(fs_test_set[, setdiff(names(fs_test_set), "diabetes")])
fs_y_test    <- as.numeric(as.character(fs_test_set$diabetes))

unique(full_y_train)
unique(full_y_test)

# Full Model
full_model_boost <- xgboost::xgboost(data=full_x_train, label=full_y_train,
                  max.depth=2, eta=0.3, nthread=2, nrounds=2,
                  objective="binary:logistic")

full_pred_boost <- predict(full_model_boost, newdata = full_x_test)

full_pred_class <- ifelse(full_pred_boost > 0.5, 1, 0)
full_pred_class <- factor(full_pred_class, levels = c(0,1))
full_y_test_factor <- factor(full_y_test, levels = c(0,1))

confusionMatrix(data = full_pred_class, reference = full_y_test_factor)

# Feature Selection Model
fs_model_boost <- xgboost::xgboost(data=fs_x_train, label=fs_y_train,
                            max.depth=2, eta=0.3, nthread=2, nrounds=2,
                            objective="binary:logistic")

fs_pred_boost <- predict(fs_model_boost, newdata = fs_x_test)

fs_pred_class <- ifelse(fs_pred_boost > 0.5, 1, 0)
fs_pred_class <- factor(fs_pred_class, levels = c(0,1))
fs_y_test_factor <- factor(fs_y_test, levels = c(0,1))

confusionMatrix(data = fs_pred_class, reference = fs_y_test_factor)
```

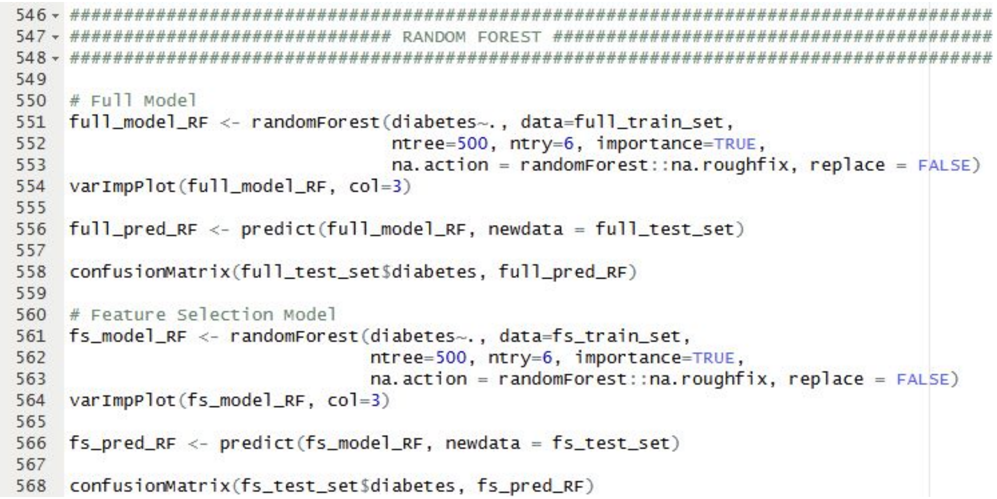


```
> confusionMatrix(data = full_pred_class, reference = full_y_test_factor)
Confusion Matrix and Statistics

          Reference
Prediction    0    1
         0 2552  846
         1    0 1704

               Accuracy : 0.8342
                 95% CI : (0.8237, 0.8443)
    No Information Rate : 0.5002
    P-Value [Acc > NIR] : < 2.2e-16

                  Kappa : 0.6683

 Mcnemar's Test P-Value : < 2.2e-16

            Sensitivity : 1.0000
            Specificity : 0.6682
         Pos Pred Value : 0.7510
         Neg Pred Value : 1.0000
             Prevalence : 0.5002
         Detection Rate : 0.5002
   Detection Prevalence : 0.6660
      Balanced Accuracy : 0.8341

       'Positive' Class : 0
```

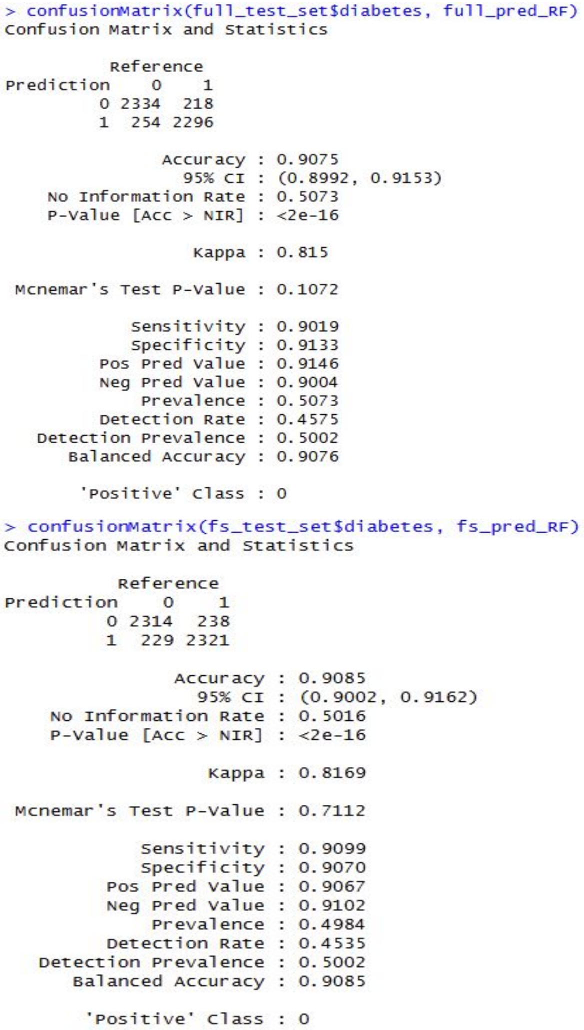


```
> confusionMatrix(data = fs_pred_class, reference = fs_y_test_factor)
Confusion Matrix and Statistics

          Reference
Prediction    0    1
         0 2552  836
         1    0 1714

               Accuracy : 0.8361
                 95% CI : (0.8257, 0.8462)
    No Information Rate : 0.5002
    P-Value [Acc > NIR] : < 2.2e-16

                  Kappa : 0.6722

 Mcnemar's Test P-Value : < 2.2e-16

            Sensitivity : 1.0000
            Specificity : 0.6722
         Pos Pred Value : 0.7532
         Neg Pred Value : 1.0000
             Prevalence : 0.5002
         Detection Rate : 0.5002
   Detection Prevalence : 0.6641
      Balanced Accuracy : 0.8361

       'Positive' Class : 0
```

Models Analysis - Random Forest

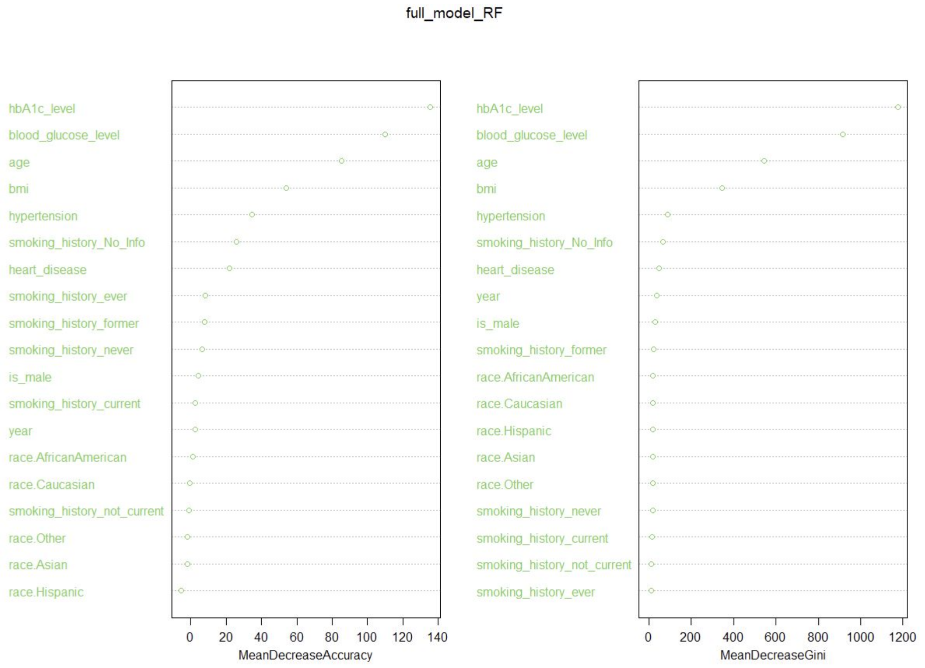


```
###################################################################################
############################## RANDOM FOREST ######################################
###################################################################################

# Full Model
full_model_RF <- randomForest(diabetes~., data=full_train_set,
                              ntree=500, ntry=6, importance=TRUE,
                              na.action = randomForest::na.roughfix, replace = FALSE)
varImpPlot(full_model_RF, col=3)

full_pred_RF <- predict(full_model_RF, newdata = full_test_set)

confusionMatrix(full_test_set$diabetes, full_pred_RF)

# Feature Selection Model
fs_model_RF <- randomForest(diabetes~., data=fs_train_set,
                            ntree=500, ntry=6, importance=TRUE,
                            na.action = randomForest::na.roughfix, replace = FALSE)
varImpPlot(fs_model_RF, col=3)

fs_pred_RF <- predict(fs_model_RF, newdata = fs_test_set)

confusionMatrix(fs_test_set$diabetes, fs_pred_RF)
```

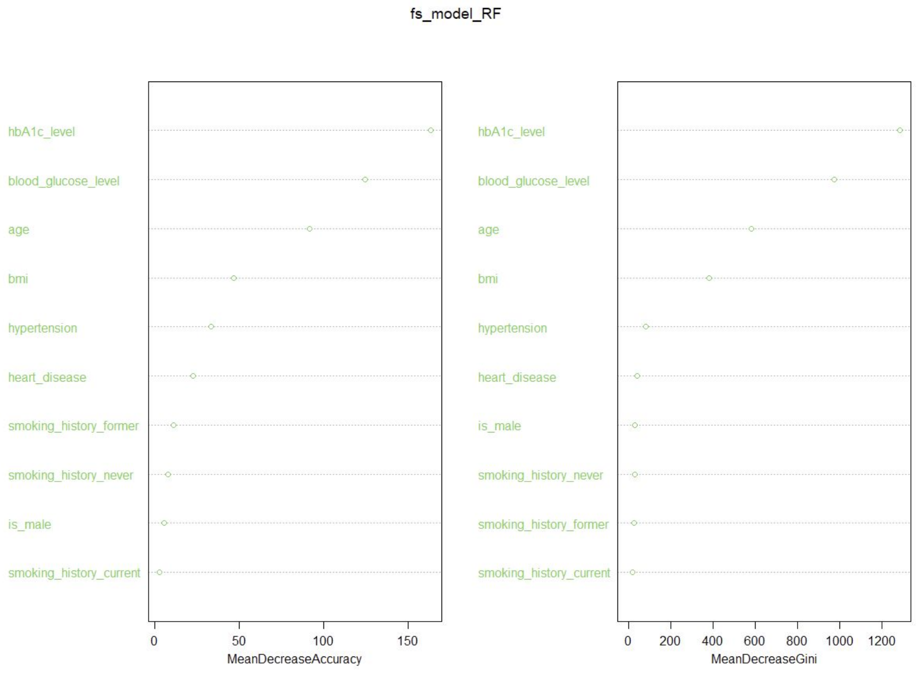


```
> confusionMatrix(full_test_set$diabetes, full_pred_RF)
Confusion Matrix and Statistics

          Reference
Prediction    0    1
         0 2334  218
         1  254 2296

               Accuracy : 0.9075
                 95% CI : (0.8992, 0.9153)
    No Information Rate : 0.5073
    P-Value [Acc > NIR] : <2e-16

                  Kappa : 0.815

 Mcnemar's Test P-Value : 0.1072

            Sensitivity : 0.9019
            Specificity : 0.9133
         Pos Pred Value : 0.9146
         Neg Pred Value : 0.9004
             Prevalence : 0.5073
         Detection Rate : 0.4575
   Detection Prevalence : 0.5002
      Balanced Accuracy : 0.9076

       'Positive' Class : 0

> confusionMatrix(fs_test_set$diabetes, fs_pred_RF)
Confusion Matrix and Statistics

          Reference
Prediction    0    1
         0 2314  238
         1  229 2321

               Accuracy : 0.9085
                 95% CI : (0.9002, 0.9162)
    No Information Rate : 0.5016
    P-Value [Acc > NIR] : <2e-16

                  Kappa : 0.8169

 Mcnemar's Test P-Value : 0.7112

            Sensitivity : 0.9099
            Specificity : 0.9070
         Pos Pred Value : 0.9067
         Neg Pred Value : 0.9102
             Prevalence : 0.4984
         Detection Rate : 0.4535
   Detection Prevalence : 0.5002
      Balanced Accuracy : 0.9085

       'Positive' Class : 0
```

Models Analysis - Random Forest



full_model_RF



fs_model_RF

Model Comparison

Model	Accuracy	Kappa
Decision Tree - Full	89.98%	0.7997
Decision Tree - FS	89.77%	0.7954
Naive Bayes - Full	81.81%	0.6362
Naive Bayes - FS	83.44%	0.6687
KNN - Full	84.97%	0.6993
KNN - FS	85.22%	0.7044
SVM - Full	88.57%	0.7715
SVM - FS	89.24%	0.7848
Linear Regression - Full	88.69%	0.7738
Linear Regression - FS	88.91%	0.7781

Model	Accuracy	Kappa
Logistic Regression - Full	88.38%	0.7675
GLM - FS	88.85%	0.7769
RF - Full	90.75%	0.815
RF - FS	90.85%	0.8169
Bagging - Full	89.36%	0.7871
Bagging - FS	90.18%	0.8036
XGBoost - Full	83.42%	0.6683
XGBoost - FS	83.61%	0.6722

Research Findings

- Random Forest was the model with best accuracy (~91%)
- The model describes correctly 82% of the data according to the kappa metric
- Accordingly to the feature importance plot, hemoglobin A1c and Blood glucose level heavy indicates if the patience has diabetes or not, followed by age and bmi
- It provides a good balance for between catching disease cases while minimizing unnecessary follow-up tests

Research Findings

- The model performance is statistically significant as it has extremely low p-value

- The model has a good recall value which is important for this study case where we want to avoid false negatives as much as possible

- Random Forest was the best one due to its capacity to handling complex non-linear relationships, less hyperparameter sensitivity, and robust to overfitting

Bibliography

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THANK YOU.

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