Predicting Cervical Cancer Through Biopsy Results

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Loading the Requisite Libraries

```
library(caret)
library(dplyr)
library(ggplot2)
library(RANN)
library(kernlab)
library(corrplot)
library(pander)
library(tidyverse)
library(MASS)
library(pROC)
library(factoextra)
library(MLmetrics)
```

Reading in and Inspecting the Dataset

```
#read in the cervical cancer dataset
cervdat <- read.csv("risk_factors_cervical_cancer.csv", header=TRUE,
                    stringsAsFactors = FALSE)
cervdat <- as.data.frame(apply(cervdat, 2, as.integer))

# remove unused columns
cervdat <- subset(cervdat, select = -c(Citology, Schiller, Hinselmann))
str(cervdat) # inspect the dataset
```

```
## 'data.frame':    858 obs. of  33 variables:
##  $ Age                               : int  18 15 34 52 46 42 51 26 45 44 ...
##  $ Number.of.sexual.partners         : int  4 1 1 5 3 3 3 1 1 3 ...
##  $ First.sexual.intercourse          : int  15 14 NA 16 21 23 17 26 20 15 ...
##  $ Num.of.pregnancies                : int  1 1 1 4 4 2 6 3 5 NA ...
##  $ Smokes                            : int  0 0 0 1 0 0 1 0 0 1 ...
##  $ Smokes..years.                    : int  0 0 0 37 0 0 34 0 0 1 ...
##  $ Smokes..packs.year.               : int  0 0 0 37 0 0 3 0 0 2 ...
##  $ Hormonal.Contraceptives           : int  0 0 0 1 1 0 0 1 0 0 ...
##  $ Hormonal.Contraceptives..years.   : int  0 0 0 3 15 0 0 2 0 0 ...
```

```
##  $ IUD                                : int  0 0 0 0 0 0 1 1 0 NA ...
##  $ IUD..years.                        : int  0 0 0 0 0 0 7 7 0 NA ...
##  $ STDs                               : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ STDs..number.                      : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ STDs.condylomatosis                : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ STDs.cervical.condylomatosis       : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ STDs.vaginal.condylomatosis        : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ STDs.vulvo.perineal.condylomatosis: int  0 0 0 0 0 0 0 0 0 0 ...
##  $ STDs.syphilis                      : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ STDs.pelvic.inflammatory.disease   : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ STDs.genital.herpes                : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ STDs.molluscum.contagiosum         : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ STDs.AIDS                          : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ STDs.HIV                           : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ STDs.Hepatitis.B                   : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ STDs.HPV                           : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ STDs..Number.of.diagnosis          : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ STDs..Time.since.first.diagnosis   : int  NA NA NA NA NA NA NA NA NA NA ...
##  $ STDs..Time.since.last.diagnosis    : int  NA NA NA NA NA NA NA NA NA NA ...
##  $ Dx.Cancer                          : int  0 0 0 1 0 0 0 0 1 0 ...
##  $ Dx.CIN                             : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Dx.HPV                             : int  0 0 0 1 0 0 0 0 1 0 ...
##  $ Dx                                 : int  0 0 0 0 0 0 0 0 1 0 ...
##  $ Biopsy                             : int  0 0 0 0 0 0 1 0 0 0 ...
```

```
cat("Dimensions of dataset:", dim(cervdat)) # dimensions of dataset
```

```
## Dimensions of dataset: 858 33
```

```
# Sum up all of the NA values across the whole dataset
cat("There are", sum(is.na(cervdat)),
    "'NA' values in the entire dataset.",
    "\n \nThe following columns have 'NA' values: \n \n")
```

```
## There are 3622 'NA' values in the entire dataset.
##
## The following columns have 'NA' values:
##
```

```
# List the columns with #NA values
list_na <- colnames(cervdat)[ apply(cervdat, 2, anyNA)]
list_na
```

```
##  [1] "Number.of.sexual.partners"          "First.sexual.intercourse"
##  [3] "Num.of.pregnancies"                 "Smokes"
##  [5] "Smokes..years."                     "Smokes..packs.year."
##  [7] "Hormonal.Contraceptives"            "Hormonal.Contraceptives..years."
##  [9] "IUD"                                "IUD..years."
## [11] "STDs"                               "STDs..number."
## [13] "STDs.condylomatosis"                "STDs.cervical.condylomatosis"
## [15] "STDs.vaginal.condylomatosis"        "STDs.vulvo.perineal.condylomatosis"
## [17] "STDs.syphilis"                      "STDs.pelvic.inflammatory.disease"
```

```
## [19] "STDs.genital.herpes"                "STDs.molluscum.contagiosum"
## [21] "STDs.AIDS"                          "STDs.HIV"
## [23] "STDs.Hepatitis.B"                   "STDs.HPV"
## [25] "STDs..Time.since.first.diagnosis"   "STDs..Time.since.last.diagnosis"
```

Preprocessing the Data

Imputing Missing Values by Median

```
cerv_impute <- preProcess(cervdat[2:32], method = "medianImpute")
cerv_imputed <- predict(cerv_impute, cervdat)
cervdat <- round(cerv_imputed, 0) #reassign back to original dataframe
```

Examining Degenerate Distributions (Near Zero Variance Columns)

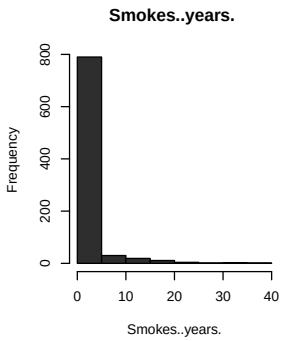
```
degen_cerv_names <- nearZeroVar(cervdat, names = TRUE); degen_cerv_names
```

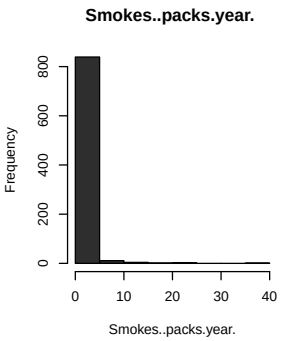
```
##  [1] "Smokes..years."                  "Smokes..packs.year."
##  [3] "IUD..years."                     "STDs..number."
##  [5] "STDs.cervical.condylomatosis"    "STDs.vaginal.condylomatosis"
##  [7] "STDs.syphilis"                   "STDs.pelvic.inflammatory.disease"
##  [9] "STDs.genital.herpes"             "STDs.molluscum.contagiosum"
## [11] "STDs.AIDS"                       "STDs.HIV"
## [13] "STDs.Hepatitis.B"                "STDs.HPV"
## [15] "STDs..Time.since.first.diagnosis" "STDs..Time.since.last.diagnosis"
## [17] "Dx.Cancer"                       "Dx.CIN"
## [19] "Dx.HPV"                          "Dx"
```

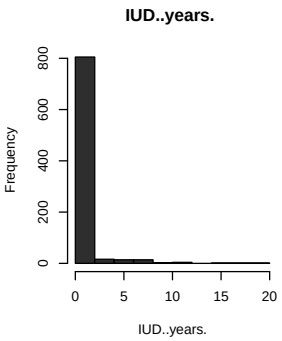
```
degen_cerv <- nearZeroVar(cervdat); degen_cerv
```

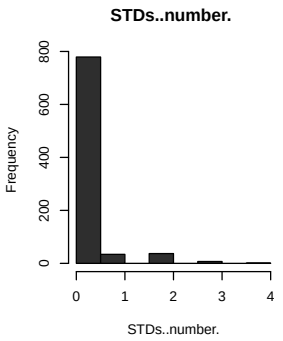
```
##  [1]  6  7 11 13 15 16 18 19 20 21 22 23 24 25 27 28 29 30 31 32
```

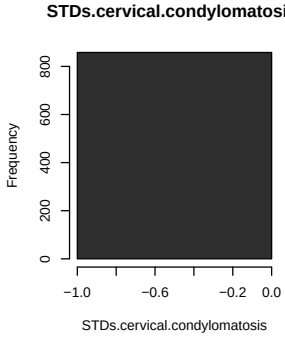
```
degen_cerv <- data.frame(cervdat[6],cervdat[7],
                         cervdat[11],cervdat[13],
                         cervdat[15],cervdat[16],
                         cervdat[18],cervdat[19],
                         cervdat[20],cervdat[21],
                         cervdat[22],cervdat[23],
                         cervdat[24],cervdat[25],
                         cervdat[26],cervdat[27],
                         cervdat[28],cervdat[29],
                         cervdat[30],cervdat[31])
par(mfrow = c(1, 4))
  for (i in 1:ncol(degen_cerv)) {
              hist(degen_cerv[,i], xlab = names(degen_cerv[i]),
                                   main = paste(names(degen_cerv[i]), ""),
                                   col="gray18")
    }
```

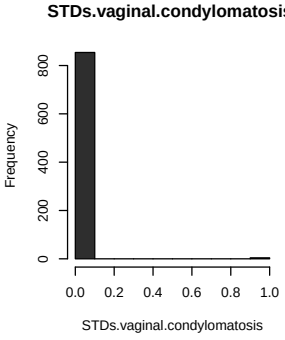

Smokes..years.
Frequency
0
200
400
600
800
0
10
20
30
40
Smokes..years.

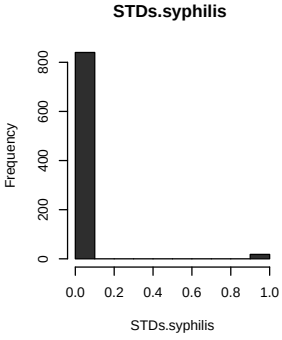

Smokes..packs.year.
Frequency
0
200
400
600
800
0
10
20
30
40
Smokes..packs.year.

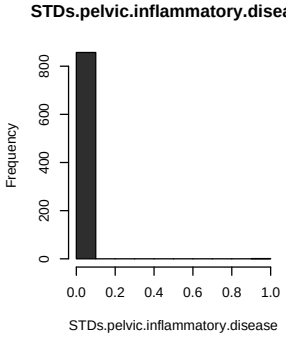

IUD..years.
Frequency
0
200
400
600
800
0
5
10
15
20
IUD..years.

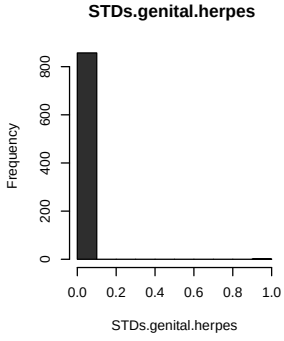

STDs..number.
Frequency
0
200
400
600
800
0
1
2
3
4
STDs..number.

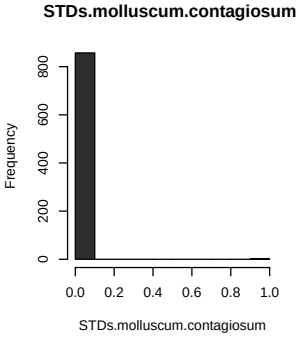

STDs.cervical.condylomatosis
Frequency
0
200
400
600
800
−1.0
−0.6
−0.2
0.0
STDs.cervical.condylomatosis

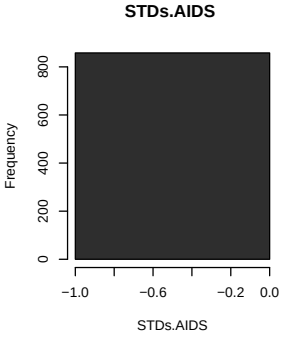

STDs.vaginal.condylomatosis
Frequency
0
200
400
600
800
0.0
0.2
0.4
0.6
0.8
1.0
STDs.vaginal.condylomatosis

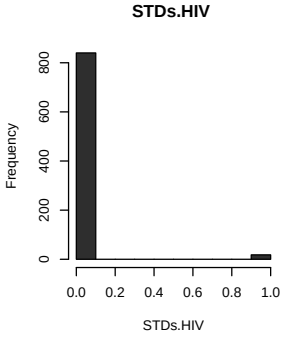

STDs.syphilis
Frequency
0
200
400
600
800
0.0
0.2
0.4
0.6
0.8
1.0
STDs.syphilis

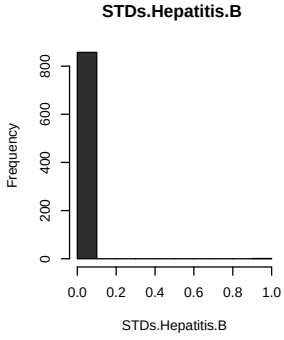

STDs.pelvic.inflammatory.disease
Frequency
0
200
400
600
800
0.0
0.2
0.4
0.6
0.8
1.0
STDs.pelvic.inflammatory.disease

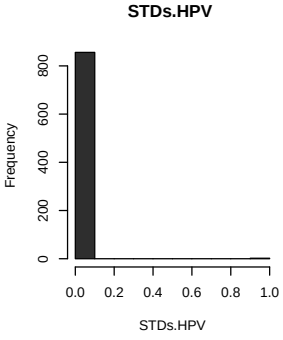

STDs.genital.herpes
Frequency
0
200
400
600
800
0.0
0.2
0.4
0.6
0.8
1.0
STDs.genital.herpes

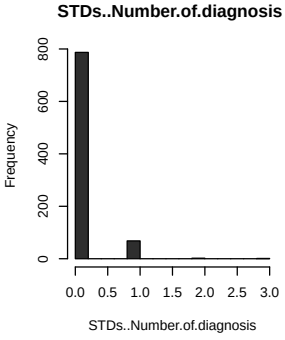

STDs.molluscum.contagiosum
Frequency
0
200
400
600
800
0.0
0.2
0.4
0.6
0.8
1.0
STDs.molluscum.contagiosum

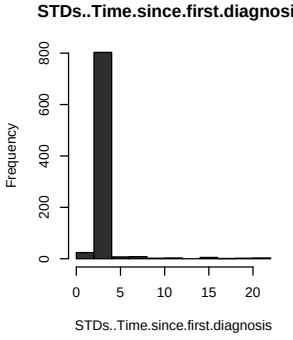

STDs.AIDS
Frequency
0
200
400
600
800
−1.0
−0.6
−0.2
0.0
STDs.AIDS

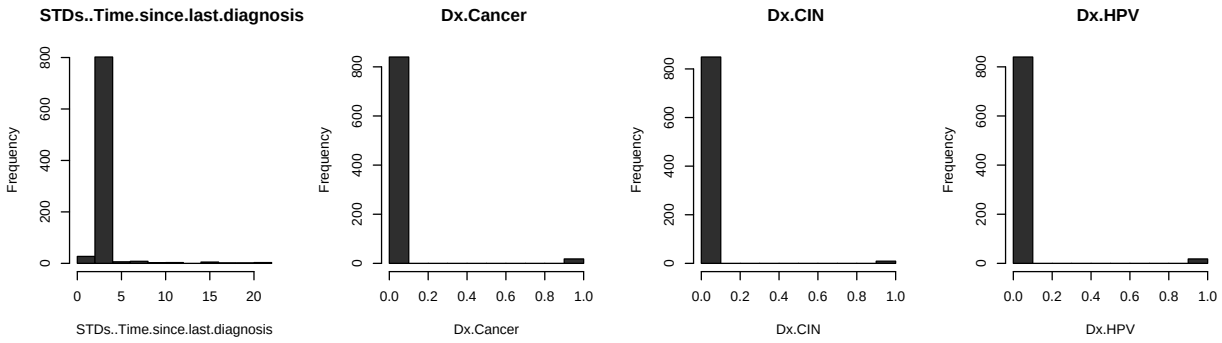

STDs.HIV
Frequency
0
200
400
600
800
0.0
0.2
0.4
0.6
0.8
1.0
STDs.HIV


STDs.Hepatitis.B
Frequency
0
200
400
600
800
0.0
0.2
0.4
0.6
0.8
1.0
STDs.Hepatitis.B


STDs.HPV
Frequency
0
200
400
600
800
0.0
0.2
0.4
0.6
0.8
1.0
STDs.HPV


STDs..Number.of.diagnosis
Frequency
0
200
400
600
800
0.0
0.5
1.0
1.5
2.0
2.5
3.0
STDs..Number.of.diagnosis


STDs..Time.since.first.diagnosis
Frequency
0
200
400
600
800
0
5
10
15
20
STDs..Time.since.first.diagnosis

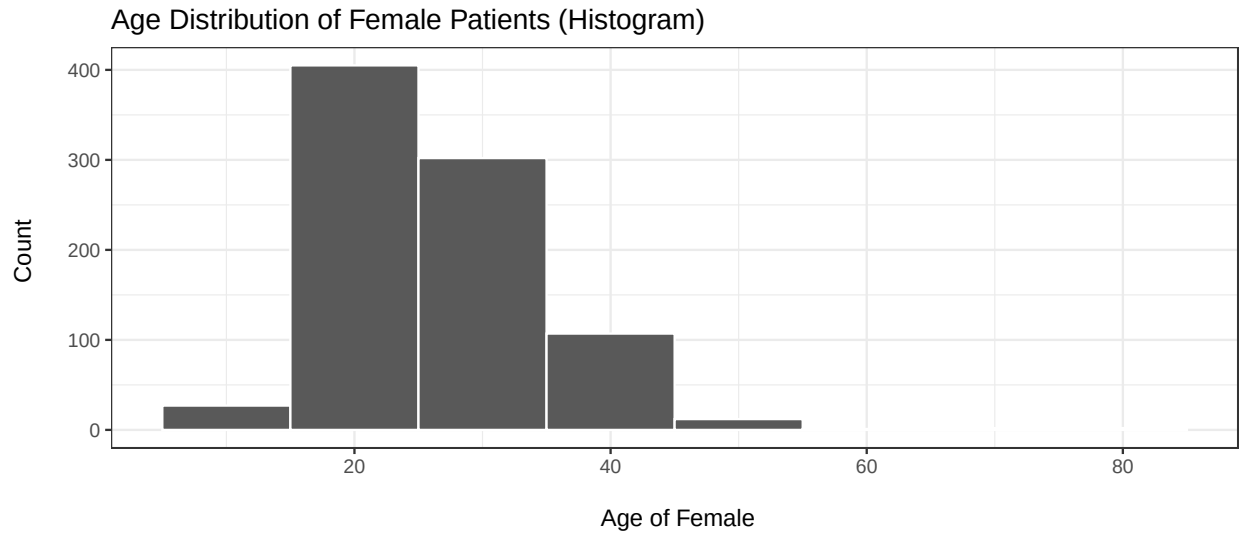



```
# Determine Near Zero Variance Columns
nearzero_cerv <- nearZeroVar(cervdat) # assign to new variable
cervdat <- cervdat[,-nearzero_cerv] # Remove Near Zero Variance Columns
# Inspect new dimensions of dataset
cat("\n There were", length(nearzero_cerv),
    "near zero variance columns.", "\n New Data Dimensions:",
    dim(cervdat))
```

```
##
##  There were 20 near zero variance columns.
##  New Data Dimensions: 858 13
```

Exploratory Data Analysis (EDA)

```
# plot the age distribution of the dataset
ggplot(cervdat, aes(Age) ) +
  geom_histogram(binwidth = 10, color="white") +
  labs(x = "\n Age of Female", y = "Count \n") +
  ggtitle("Age Distribution of Female Patients (Histogram)") +
  theme_bw()
```

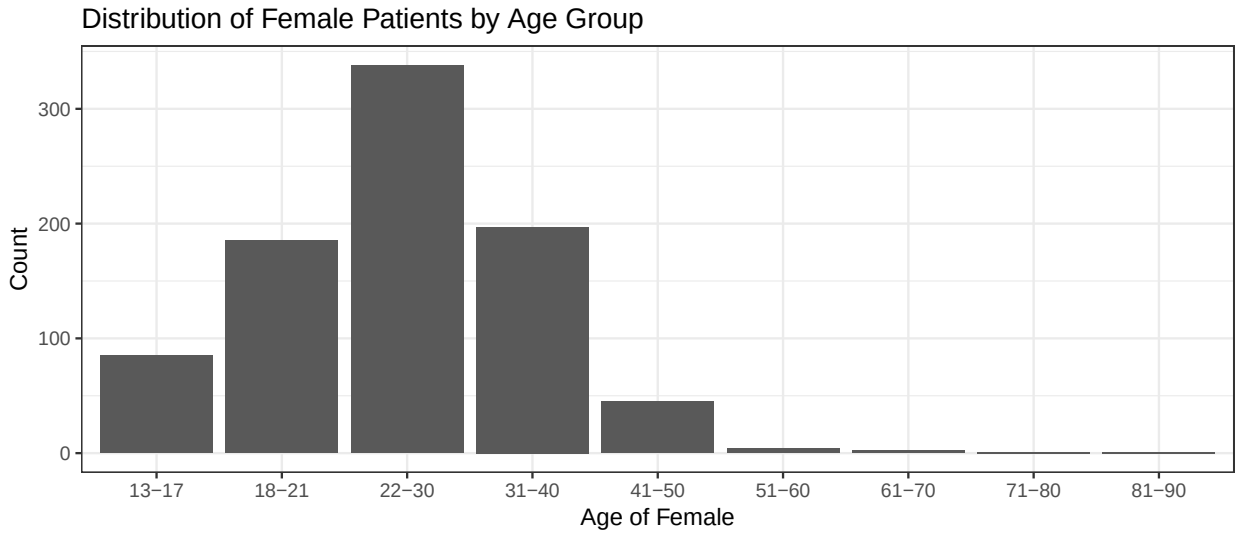


```
summary(cervdat$Age)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   13.00   20.00   25.00   26.82   32.00   84.00
```

From the positively skewed distribution (histogram) plot and summary statistics, the median age of females in this dataset is 25, whereas the mean is 26.82. The lowest age in this dataset is 13, and the maximum is 84. All ages are represented herein.

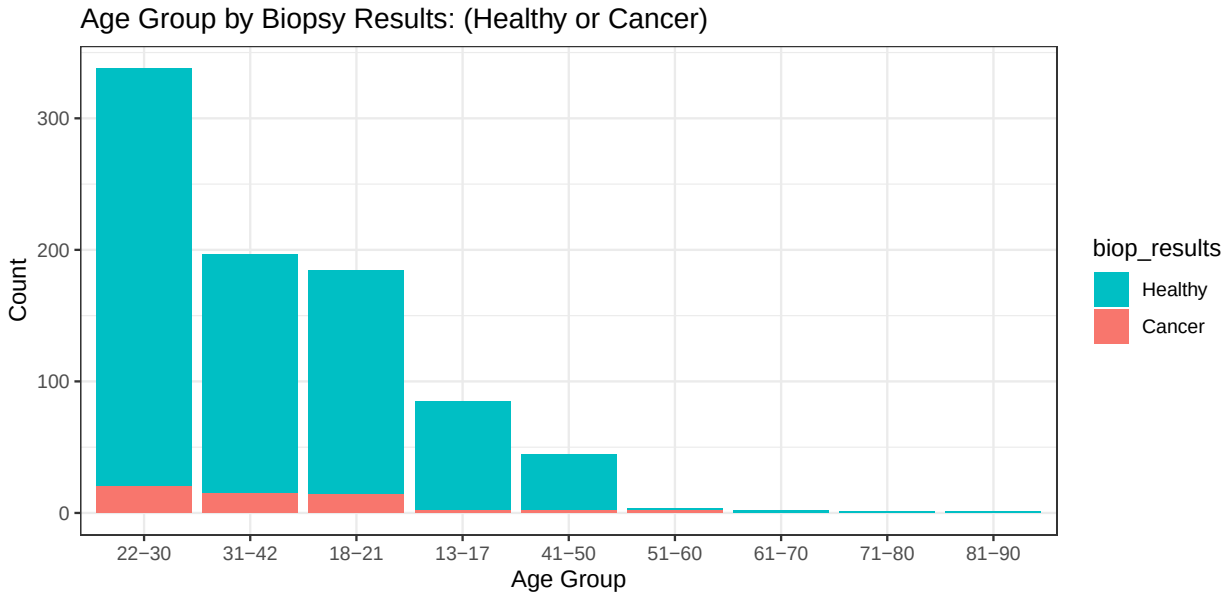
```
cervdat[cervdat$Age >= 13 & cervdat$Age <= 17, "age_group"] <- "13-17"
cervdat[cervdat$Age >= 18 & cervdat$Age <= 30, "age_group"] <- "18-21"
cervdat[cervdat$Age >= 22 & cervdat$Age <= 30, "age_group"] <- "22-30"
cervdat[cervdat$Age >= 31 & cervdat$Age <= 40, "age_group"] <- "31-40"
cervdat[cervdat$Age >= 41 & cervdat$Age <= 50, "age_group"] <- "41-50"
cervdat[cervdat$Age >= 51 & cervdat$Age <= 60, "age_group"] <- "51-60"
cervdat[cervdat$Age >= 61 & cervdat$Age <= 70, "age_group"] <- "61-70"
cervdat[cervdat$Age >= 71 & cervdat$Age <= 80, "age_group"] <- "71-80"
cervdat[cervdat$Age >= 81 & cervdat$Age <= 90, "age_group"] <- "81-90"

ggplot(cervdat) + geom_bar(aes(age_group))+ labs(x="Age of Female", y="Count") +
  ggtitle("Distribution of Female Patients by Age Group") + theme_bw()
```



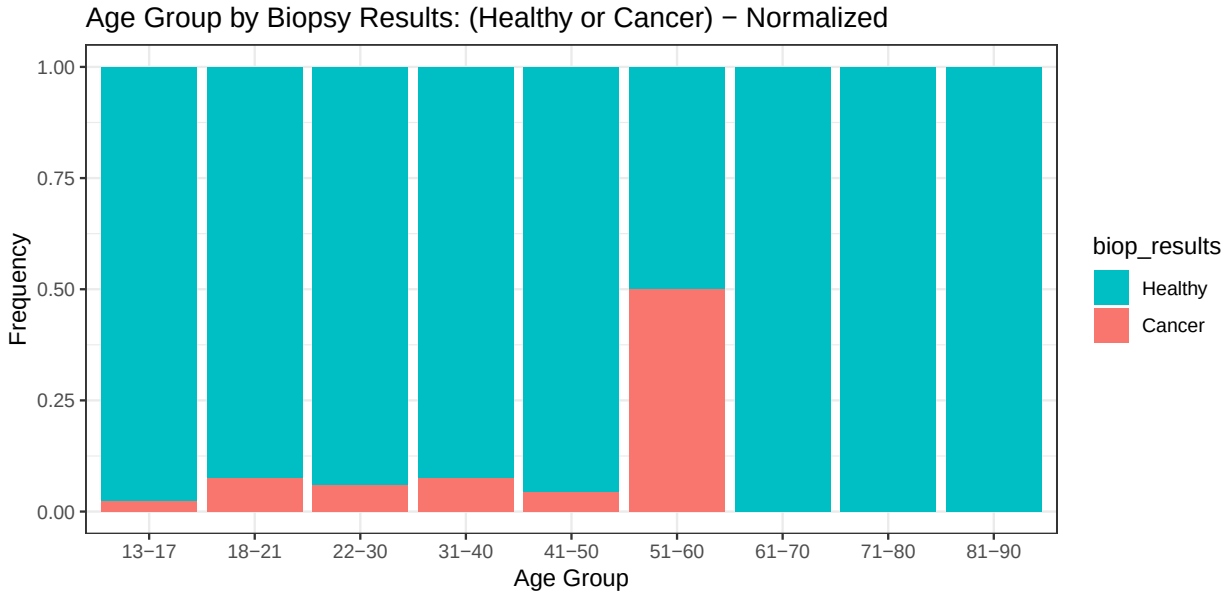

```
#Contingency Table - Age by Response Type: by Columns
biop_results <- factor(cervdat$Biopsy, levels=c(0, 1),labels=c('Healthy','Cancer'))
contingency_table <- table(biop_results, cervdat$age_group)
contingency_table_col <- addmargins(A = contingency_table, FUN = list(total = sum),
                                    quiet = TRUE); contingency_table_col
```

```
##
## biop_results 13-17 18-21 22-30 31-42 41-50 51-60 61-70 71-80 81-90 total
##      Healthy    83   171   318   182    43     2     2     1     1   803
##      Cancer      2    14    20    15     2     2     0     0     0    55
##      total      85   185   338   197    45     4     2     1     1   858
```

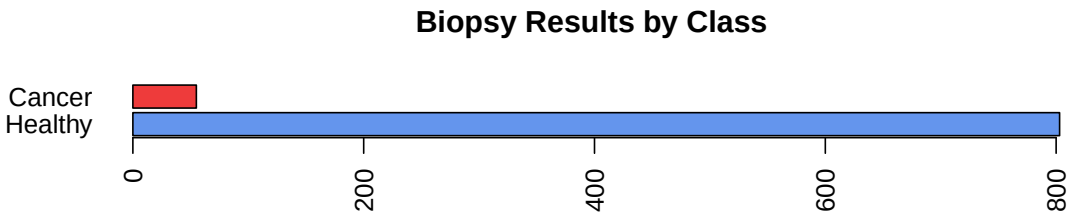
```
ggplot(cervdat,aes(fct_infreq(age_group)))+geom_bar(stat="count",aes(fill=biop_results))+
scale_fill_manual(values=c('#00BFC4','#F8766D')) + labs(x = "Age Group", y = "Count")+
ggtitle("Age Group by Biopsy Results: (Healthy or Cancer)")+theme_bw()
```




```
ggplot(cervdat, aes(age_group)) + geom_bar(aes(fill = biop_results),
       position = "fill") + labs(x = "Age Group", y = "Frequency")+
       scale_fill_manual(values=c('#00BFC4','#F8766D'))+
ggtitle("Age Group by Biopsy Results: (Healthy or Cancer) - Normalized")+theme_bw()
```




```
counts <- table(biop_results); par(las=2); par(mar=c(5,8,4,2))
barplot(counts, main = "Biopsy Results by Class", horiz = TRUE,
        names.arg = c("Healthy", "Cancer"), col=c("cornflowerblue", "brown2"))
```




```
counts
```

```
## biop_results
## Healthy  Cancer
##     803      55
```

```
corr_cerv <- cor(cervdat[c(1:12)])
corrplot(corr_cerv, method="color", col=colorRampPalette(c("yellow","white",
    "orange"))(200), addCoef.col = "black", tl.col="black", tl.srt=50)
```

```
highCorr_names <- findCorrelation(cor(cervdat[c(1:12)]), cutoff = 0.75,
                                  names = TRUE); highCorr_names
```

```
## [1] "STDs"                "STDs.condylomatosis"
```

```
highCorr <- findCorrelation(cor(cervdat[c(1:12)]), cutoff = 0.75)
cat("\n There are", length(highCorr_names), "highly correlated predictors. \n \n")
```

```
##
##  There are 2 highly correlated predictors.
##
```

```
pred_cerv <- cervdat$Biopsy
corrcerv_response <- cor(cervdat[c(1:12)], pred_cerv); corrcerv_response
```

```
##                                          [,1]
## Age                                0.0559555151
## Number.of.sexual.partners         -0.0004082348
## First.sexual.intercourse           0.0072587257
## Num.of.pregnancies                 0.0402150719
## Smokes                             0.0287237598
## Hormonal.Contraceptives           -0.0180152523
## Hormonal.Contraceptives..years.    0.0944329779
## IUD                                0.0592305229
## STDs                               0.1141480662
## STDs.condylomatosis                0.0901638872
## STDs.vulvo.perineal.condylomatosis 0.0925483178
## STDs..Number.of.diagnosis          0.0974489209
```

```
max_cerv <- max(corrcerv_response[,1]) # max
second_cerv <- Rfast::nth(corrcerv_response[,1], 2, descending = T) # 2nd max
third_cerv <- Rfast::nth(corrcerv_response[,1], 3, descending = T) # 3rd max
```

Class Imbalance and Correlation

Addressing the Class Imbalance Problem

Inspecting the biopsy target variable yielded findings commensurate with a class imbalance scenario. 803 females were found to be healthy post biopsy; whereas, only 55 had signs of cancer. Proceeding with any further analytics (i.e., model building) without addressing this critical dilemma would hamper our results. Therefore, we perform down-sampling to "randomly subset all the classes in the training set so that their class frequencies match the least prevalent class. For example, suppose that 80% of the training set samples are the first class and the remaining 20% are in the second class. Down-sampling would randomly sample the first class to be the same size as the second class (so that only 40% of the total training set is used to fit the model)" ()

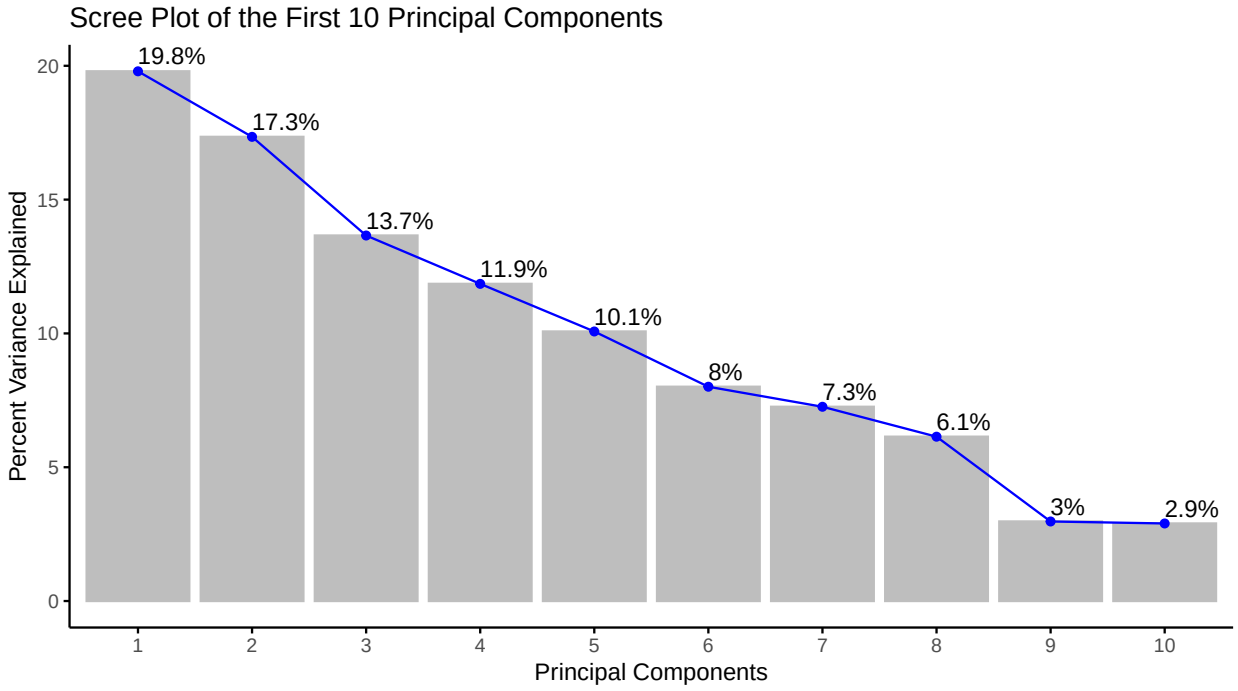
Addressing Between Predictor Relationships and Predictor vs. Response Relationships

Two highly correlated predictors were identified (STDs and STDs.condylomatosis). They were subsequently removed. Examining the relationship between the predictors and the biopsy response itself, few variables present strong correlation coefficients r. To this end, the three highest relationships are observed in STDs vs. biopsy results 0.1141481, STDs..Number.ofsiagnosis vs. biopsy results (0.0974489), and Hormonal.Contraceptives..years vs. biopsy results (0.094433).

```
# remove highly correlated predictors (predictors with predictors)
cervdat <- cervdat[,-highCorr]
```

Principal Component Analysis (PCA)

```
options(scipen=999)
cervdat_pca <- as.matrix(cervdat[1:10])
cervdat.pca <- prcomp(cervdat_pca, center = TRUE, scale. = TRUE)
var_explained <- round(cervdat.pca$sdev^2/sum((cervdat.pca$sdev)^2)*100, 4)

fviz_eig(cervdat.pca, main="Scree Plot of the First 10 Principal Components",
         xlab="Principal Components", ylab = "Percent Variance Explained",
         barcolor = "grey", barfill = "grey",  linecolor = "blue", addlabels=T,
         ggtheme=theme_classic())
```




```
pc <- 1:10
p_var <- c(var_explained[1], var_explained[2], var_explained[3], var_explained[4],
           var_explained[5], var_explained[6], var_explained[7], var_explained[8],
```

```
           var_explained[9], var_explained[10])
p_delta <- c(var_explained[1],
             var_explained[1] - var_explained[2], var_explained[2] - var_explained[3],
             var_explained[3] - var_explained[4], var_explained[4] - var_explained[5],
             var_explained[5] - var_explained[6], var_explained[6] - var_explained[7],
             var_explained[7] - var_explained[8], var_explained[8] - var_explained[9],
             var_explained[9] - var_explained[10])
table1 <- data.frame(round(pc, 2), round(p_var,2), round(p_delta,2))
colnames(table1) <- c("Principal Component","Percent Variance","Percent Change (Delta)")
table1 %>% pander(style = "simple",
                  caption = "Percent Variance and Change by Principal Component")
```

Table 1: Percent Variance and Change by Principal Component

Principal Component	Percent Variance	Percent Change (Delta)
1	19.79	19.79
2	17.34	2.45
3	13.66	3.69
4	11.85	1.81
5	10.07	1.78
6	8.01	2.06
7	7.26	0.75
8	6.14	1.12
9	2.97	3.17
10	2.9	0.07

Create a Data Partition and Address Class Imbalance Problem

```
# Set up (binarize) the response (dependent variable: Biopsy)
cervdat$Biopsy <- factor(cervdat$Biopsy, levels = c(0, 1),
                         labels=c('Healthy', 'Cancer'))

cerv_predictors <- cervdat[c(-11, -12)]
cerv_response <- cervdat$Biopsy

set.seed(222)
# Being mindful of class imbalances, dataset is partitioned as follows:
cerv_part <- createDataPartition(cerv_response, p = 0.8, list = FALSE)

train_cerv <- cerv_predictors[cerv_part,]
test_cerv <- cerv_predictors[-cerv_part,]

train_biopsy <- cerv_response[cerv_part]
test_biopsy <- cerv_response[-cerv_part]

cat("\n Training Dimensions:",dim(train_cerv),
    "\n Testing Dimensions:", dim(test_cerv), "\n",
    "\n Confirming Train_Test Split Percentages:", "\n",
    "\n Training Dimensions Percentage:", round(length(train_cerv[,1])/
```

```
      (length(cervdat[,1])),2),
    "\n Testing Dimensions Percentage:", round(length(test_cerv[,1])/
      (length(cervdat[,1])),2))
```

```
##
##  Training Dimensions: 687 10
##  Testing Dimensions: 171 10
##
##  Confirming Train_Test Split Percentages:
##
##  Training Dimensions Percentage: 0.8
##  Testing Dimensions Percentage: 0.2
```

```
#ctrl params
ctrl_cerv <- trainControl(method="LGOCV", summaryFunction = twoClassSummary,
                          classProbs = TRUE, savePredictions = TRUE, sampling = "down")
```

Models

Generalized Linear Model (GLM)

```
set.seed(222)
cerv_glm <- caret::train(train_cerv, train_biopsy, method = "glm", trControl = ctrl_cerv,
                  preProcess=c("center", "scale"), metric="ROC")
cerv_glm
```

```
## Generalized Linear Model
##
## 687 samples
##  10 predictor
##   2 classes: 'Healthy', 'Cancer'
##
## Pre-processing: centered (10), scaled (10)
## Resampling: Repeated Train/Test Splits Estimated (25 reps, 75%)
## Summary of sample sizes: 516, 516, 516, 516, 516, 516, ...
## Addtional sampling using down-sampling prior to pre-processing
##
## Resampling results:
##
##   ROC        Sens   Spec
##   0.6142273  0.638  0.5272727
```

```
cerv_glm.predictions <- predict(cerv_glm, cerv_predictors, type = "prob")
cerv_glm.rocCurve <- pROC::roc(response = cerv_response,
                               predictor = cerv_glm.predictions[,1])
cerv_glm.auc = cerv_glm.rocCurve$auc[1]
cat('cerv_predictors glm AUC:', cerv_glm.auc, "\n", "\n")
```

```
## cerv_predictors glm AUC: 0.6360806
##
```

```r
# Predict on testing set
cerv_pred_glm <- predict(cerv_glm, test_cerv)
confusionMatrix(cerv_pred_glm, test_biopsy)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction Healthy Cancer
##    Healthy     102      8
##    Cancer       58      3
##
##                Accuracy : 0.614
##                  95% CI : (0.5367, 0.6874)
##     No Information Rate : 0.9357
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : -0.0288
##
##  Mcnemar's Test P-Value : 0.000000001625
##
##             Sensitivity : 0.63750
##             Specificity : 0.27273
##          Pos Pred Value : 0.92727
##          Neg Pred Value : 0.04918
##              Prevalence : 0.93567
##          Detection Rate : 0.59649
##    Detection Prevalence : 0.64327
##       Balanced Accuracy : 0.45511
##
##        'Positive' Class : Healthy
##
```

Linear Discriminant Analysis (LDA)

```r
set.seed(222)
cerv_lda <- caret::train(train_cerv, train_biopsy, method = "lda", trControl = ctrl_cerv,
                  preProcess=c("center", "scale"), metric="ROC")
cerv_lda
```

```
## Linear Discriminant Analysis
##
## 687 samples
##  10 predictor
##   2 classes: 'Healthy', 'Cancer'
##
## Pre-processing: centered (10), scaled (10)
## Resampling: Repeated Train/Test Splits Estimated (25 reps, 75%)
## Summary of sample sizes: 516, 516, 516, 516, 516, 516, ...
## Addtional sampling using down-sampling prior to pre-processing
##
## Resampling results:
```

```
##
##   ROC        Sens    Spec
##   0.6194318  0.6545  0.5236364
```

```
cerv_lda.predictions <- predict(cerv_lda, cerv_predictors, type = "prob")
cerv_lda.rocCurve <- pROC::roc(response = cerv_response,
                               predictor = cerv_lda.predictions[,1])
cerv_lda.auc = cerv_lda.rocCurve$auc[1]
cat('cerv_predictors lda AUC:', cerv_lda.auc, "\n", "\n")
```

```
## cerv_predictors lda AUC: 0.638526
##
```

```
# Predict on testing set
cerv_pred_lda <- predict(cerv_lda, test_cerv)
confusionMatrix(cerv_pred_lda, test_biopsy)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction Healthy Cancer
##    Healthy     105      8
##    Cancer       55      3
##
##                Accuracy : 0.6316
##                  95% CI : (0.5546, 0.7039)
##     No Information Rate : 0.9357
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : -0.0238
##
##  Mcnemar's Test P-Value : 0.000000006814
##
##             Sensitivity : 0.65625
##             Specificity : 0.27273
##          Pos Pred Value : 0.92920
##          Neg Pred Value : 0.05172
##              Prevalence : 0.93567
##          Detection Rate : 0.61404
##    Detection Prevalence : 0.66082
##       Balanced Accuracy : 0.46449
##
##        'Positive' Class : Healthy
##
```

Mixture Discriminant Analysis (MDA)

```
set.seed(222)
mdaGrid <- expand.grid(.subclasses = 1:8)
cerv_mda <- train(train_cerv, train_biopsy, method = "mda",
```

```
                  preProc = c("center", "scale"), tuneGrid = mdaGrid,
                  metric = "ROC", trControl = ctrl_cerv)
cerv_mda
```

```
## Mixture Discriminant Analysis
##
## 687 samples
##  10 predictor
##   2 classes: 'Healthy', 'Cancer'
##
## Pre-processing: centered (10), scaled (10)
## Resampling: Repeated Train/Test Splits Estimated (25 reps, 75%)
## Summary of sample sizes: 516, 516, 516, 516, 516, 516, ...
## Addtional sampling using down-sampling prior to pre-processing
##
## Resampling results across tuning parameters:
##
##   subclasses  ROC        Sens     Spec
##   1           0.5872500  0.65075  0.4872727
##   2           0.6133295  0.61850  0.5200000
##   3           0.6296136  0.60125  0.5563636
##   4           0.6186477  0.57575  0.5781818
##   5           0.5919545  0.56250  0.5745455
##   6           0.5952955  0.57825  0.5563636
##   7           0.5670341  0.57925  0.5090909
##   8           0.5548864  0.55625  0.5381818
##
## ROC was used to select the optimal model using the largest value.
## The final value used for the model was subclasses = 3.
```

```
cerv_mda.predictions <- predict(cerv_mda, cerv_predictors, type = "prob")
cerv_mda.rocCurve <- pROC::roc(response = cerv_response,
                               predictor = cerv_mda.predictions[,1])
cerv_mda.auc = cerv_mda.rocCurve$auc[1]
cat('cerv_predictors mda AUC:', cerv_mda.auc, "\n", "\n")
```

```
## cerv_predictors mda AUC: 0.6963546
##
```

```
# Predict on testing set
cerv_pred_mda <- predict(cerv_mda, test_cerv)
confusionMatrix(cerv_pred_mda, test_biopsy)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction Healthy Cancer
##    Healthy     101      9
##    Cancer       59      2
##
##                Accuracy : 0.6023
##                  95% CI : (0.5248, 0.6763)
```

```
##     No Information Rate : 0.9357
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : -0.06
##
##  Mcnemar's Test P-Value : 0.000000002814
##
##             Sensitivity : 0.63125
##             Specificity : 0.18182
##          Pos Pred Value : 0.91818
##          Neg Pred Value : 0.03279
##              Prevalence : 0.93567
##          Detection Rate : 0.59064
##    Detection Prevalence : 0.64327
##       Balanced Accuracy : 0.40653
##
##        'Positive' Class : Healthy
##
```

Partial Least Squares Discriminant Analysis (PLSDA)

```
set.seed(222)
plsGrid = expand.grid(.ncomp = 1:10)
# Train a PLSDA - Partial Least Squares Discriminant Analysis Model
cerv_plsda <- train(train_cerv, train_biopsy, method = "pls", tuneGrid = plsGrid,
                    preProc = c("center","scale"), metric = "ROC", trControl = ctrl_cerv)
cerv_plsda
```

```
## Partial Least Squares
##
## 687 samples
##  10 predictor
##   2 classes: 'Healthy', 'Cancer'
##
## Pre-processing: centered (10), scaled (10)
## Resampling: Repeated Train/Test Splits Estimated (25 reps, 75%)
## Summary of sample sizes: 516, 516, 516, 516, 516, 516, ...
## Addtional sampling using down-sampling prior to pre-processing
##
## Resampling results across tuning parameters:
##
##   ncomp  ROC        Sens     Spec
##    1     0.6603636  0.67400  0.5418182
##    2     0.6410909  0.67525  0.5345455
##    3     0.6244091  0.65125  0.5309091
##    4     0.6247045  0.65750  0.5309091
##    5     0.6208864  0.65500  0.5236364
##    6     0.6198636  0.65500  0.5236364
##    7     0.6194773  0.65450  0.5200000
##    8     0.6195000  0.65425  0.5272727
##    9     0.6194318  0.65450  0.5236364
##   10     0.6194318  0.65450  0.5236364
```

```
##
## ROC was used to select the optimal model using the largest value.
## The final value used for the model was ncomp = 1.
```

```
cerv_plsda.predictions <- predict(cerv_plsda, cerv_predictors, type = "prob")
cerv_plsda.rocCurve <- pROC::roc(response = cerv_response,
                                 predictor = cerv_plsda.predictions[,1])
cerv_plsda.auc = cerv_plsda.rocCurve$auc[1]
cat('cerv_predictors plsda AUC:', cerv_plsda.auc, "\n", "\n")
```

```
## cerv_predictors plsda AUC: 0.63479
##
```

```
# Predict on testing set
cerv_pred_plsda <- predict(cerv_plsda, test_cerv)
confusionMatrix(cerv_pred_plsda, test_biopsy)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction Healthy Cancer
##    Healthy     101      6
##    Cancer       59      5
##
##                Accuracy : 0.6199
##                  95% CI : (0.5426, 0.6929)
##     No Information Rate : 0.9357
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : 0.0265
##
##  Mcnemar's Test P-Value : 0.000000000112
##
##             Sensitivity : 0.63125
##             Specificity : 0.45455
##          Pos Pred Value : 0.94393
##          Neg Pred Value : 0.07813
##              Prevalence : 0.93567
##          Detection Rate : 0.59064
##    Detection Prevalence : 0.62573
##       Balanced Accuracy : 0.54290
##
##        'Positive' Class : Healthy
##
```

Nearest Shrunken Centroids (NSC)

```
nscGrid <- data.frame(.threshold = 0:10)
set.seed(222)
cerv_nsc <- train(train_cerv, train_biopsy, method = "pam",
                  preProc = c("center", "scale"), tuneGrid = nscGrid,
                  metric = "ROC", trControl = ctrl_cerv)
```

```
## 1111111111111111111111111
```

```
cerv_nsc
```

```
## Nearest Shrunken Centroids
##
## 687 samples
##  10 predictor
##   2 classes: 'Healthy', 'Cancer'
##
## Pre-processing: centered (10), scaled (10)
## Resampling: Repeated Train/Test Splits Estimated (25 reps, 75%)
## Summary of sample sizes: 516, 516, 516, 516, 516, 516, ...
## Addtional sampling using down-sampling prior to pre-processing
##
## Resampling results across tuning parameters:
##
##   threshold  ROC        Sens     Spec
##    0         0.6607045  0.67700  0.5418182
##    1         0.5638636  0.84275  0.2654545
##    2         0.5000000  1.00000  0.0000000
##    3         0.5000000  1.00000  0.0000000
##    4         0.5000000  1.00000  0.0000000
##    5         0.5000000  1.00000  0.0000000
##    6         0.5000000  1.00000  0.0000000
##    7         0.5000000  1.00000  0.0000000
##    8         0.5000000  1.00000  0.0000000
##    9         0.5000000  1.00000  0.0000000
##   10         0.5000000  1.00000  0.0000000
##
## ROC was used to select the optimal model using the largest value.
## The final value used for the model was threshold = 0.
```

```
cerv_nsc.predictions <- predict(cerv_nsc, cerv_predictors, type = "prob")
cerv_nsc.rocCurve <- pROC::roc(response = cerv_response,
                               predictor = cerv_nsc.predictions[,1])
cerv_nsc.auc = cerv_nsc.rocCurve$auc[1]
cat('cerv_predictors NSC AUC:', cerv_nsc.auc, "\n", "\n")
```

```
## cerv_predictors NSC AUC: 0.6347447
##
```

```
# Predict on testing set
cerv_pred_nsc <- predict(cerv_nsc, test_cerv)
confusionMatrix(cerv_pred_nsc, test_biopsy)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction Healthy Cancer
##    Healthy     101      6
##    Cancer       59      5
```

```
##
##                Accuracy : 0.6199
##                  95% CI : (0.5426, 0.6929)
##     No Information Rate : 0.9357
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : 0.0265
##
##  Mcnemar's Test P-Value : 0.000000000112
##
##             Sensitivity : 0.63125
##             Specificity : 0.45455
##          Pos Pred Value : 0.94393
##          Neg Pred Value : 0.07813
##              Prevalence : 0.93567
##          Detection Rate : 0.59064
##    Detection Prevalence : 0.62573
##       Balanced Accuracy : 0.54290
##
##        'Positive' Class : Healthy
##
```

Neural Network

```
set.seed(222)
nnetGrid <- expand.grid(size=1:3, decay=c(0,0.1,1,2))
cerv_nnet <- train(train_cerv, train_biopsy, method = "nnet",
                   preProc = c("center", "scale", "spatialSign"), tuneGrid = nnetGrid,
                   metric = "ROC", trace = FALSE,
                   maxit = 2000, trControl = ctrl_cerv)
cerv_nnet
```

```
## Neural Network
##
## 687 samples
##  10 predictor
##   2 classes: 'Healthy', 'Cancer'
##
## Pre-processing: centered (10), scaled (10), spatial sign transformation (10)
## Resampling: Repeated Train/Test Splits Estimated (25 reps, 75%)
## Summary of sample sizes: 516, 516, 516, 516, 516, 516, ...
## Addtional sampling using down-sampling prior to pre-processing
##
## Resampling results across tuning parameters:
##
##   size  decay  ROC        Sens     Spec
##   1     0.0    0.5895568  0.62750  0.5418182
##   1     0.1    0.5756818  0.60650  0.5200000
##   1     1.0    0.5446364  0.48000  0.5200000
##   1     2.0    0.5307386  0.52000  0.4800000
##   2     0.0    0.5778295  0.69100  0.4872727
##   2     0.1    0.6149318  0.61475  0.5709091
```

```
##   2     1.0    0.5645227  0.68000  0.3200000
##   2     2.0    0.5344545  0.68000  0.3200000
##   3     0.0    0.5443182  0.55575  0.4909091
##   3     0.1    0.5951818  0.59450  0.5490909
##   3     1.0    0.5821705  0.52000  0.4800000
##   3     2.0    0.5989318  0.36000  0.6400000
##
## ROC was used to select the optimal model using the largest value.
## The final values used for the model were size = 2 and decay = 0.1.
```

```
cerv_nnet.predictions <- predict(cerv_nnet, cerv_predictors, type = "prob")
cerv_nnet.rocCurve <- pROC::roc(response = cerv_response,
                                predictor = cerv_nnet.predictions[,1])
cerv_nnet.auc = cerv_nnet.rocCurve$auc[1]
cat('cerv_predictors mda AUC:', cerv_nnet.auc, "\n", "\n")
```

```
## cerv_predictors mda AUC: 0.6066682
##
```

```
# Predict on testing set
cerv_pred_nnet <- predict(cerv_nnet, test_cerv)
confusionMatrix(cerv_pred_nnet, test_biopsy)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction Healthy Cancer
##    Healthy      97      9
##    Cancer       63      2
##
##                Accuracy : 0.5789
##                  95% CI : (0.5012, 0.6539)
##     No Information Rate : 0.9357
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : -0.0645
##
##  Mcnemar's Test P-Value : 0.0000000004208
##
##             Sensitivity : 0.60625
##             Specificity : 0.18182
##          Pos Pred Value : 0.91509
##          Neg Pred Value : 0.03077
##              Prevalence : 0.93567
##          Detection Rate : 0.56725
##    Detection Prevalence : 0.61988
##       Balanced Accuracy : 0.39403
##
##        'Positive' Class : Healthy
##
```

GLMNET

```
set.seed(222)
cerv_glmnet.grid <- expand.grid(.alpha = c(0, .1, .2, .4, .6, .8, 1),
                                .lambda = seq(.01, .2, length = 40))
cerv_glmnet <- caret::train(train_cerv, y = train_biopsy, method = "glmnet",
                            tuneGrid = cerv_glmnet.grid, trControl = ctrl_cerv,
                            preProc = c("center", "scale"), metric = "ROC")

cerv_glmnet.predictions <- predict(cerv_glmnet, cerv_predictors, type = "prob")
cerv_glmnet.rocCurve <- pROC::roc(response = cerv_response,
                                  predictor = cerv_glmnet.predictions[,1])
cerv_glmnet.auc = cerv_glmnet.rocCurve$auc[1]
cat('cerv_predictors GLMNET AUC:', cerv_glmnet.auc, "\n", "\n")
```

```
## cerv_predictors GLMNET AUC: 0.6587683
##
```

```
# Predict on testing set
cerv_pred_glmnet <- predict(cerv_glmnet, test_cerv)
confusionMatrix(cerv_pred_glmnet, test_biopsy)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction Healthy Cancer
##    Healthy     114      9
##    Cancer       46      2
##
##                Accuracy : 0.6784
##                  95% CI : (0.6028, 0.7476)
##     No Information Rate : 0.9357
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : -0.0412
##
##  Mcnemar's Test P-Value : 0.000001208
##
##             Sensitivity : 0.71250
##             Specificity : 0.18182
##          Pos Pred Value : 0.92683
##          Neg Pred Value : 0.04167
##              Prevalence : 0.93567
##          Detection Rate : 0.66667
##    Detection Prevalence : 0.71930
##       Balanced Accuracy : 0.44716
##
##        'Positive' Class : Healthy
##
```

Random Forest

```
set.seed(222)
cerv_rf <- caret::train(train_cerv, y = train_biopsy, method = "rf",
trControl = ctrl_cerv, preProc = c("center", "scale"), metric = "ROC")
cerv_rf
```

```
## Random Forest
##
## 687 samples
##  10 predictor
##   2 classes: 'Healthy', 'Cancer'
##
## Pre-processing: centered (10), scaled (10)
## Resampling: Repeated Train/Test Splits Estimated (25 reps, 75%)
## Summary of sample sizes: 516, 516, 516, 516, 516, 516, ...
## Addtional sampling using down-sampling prior to pre-processing
##
## Resampling results across tuning parameters:
##
##   mtry  ROC        Sens     Spec
##    2    0.6621477  0.61325  0.6327273
##    6    0.6222500  0.58350  0.5709091
##   10    0.6383182  0.57925  0.6181818
##
## ROC was used to select the optimal model using the largest value.
## The final value used for the model was mtry = 2.
```

```
cerv_rf.predictions <- predict(cerv_rf, cerv_predictors, type = "prob")
cerv_rf.rocCurve <- pROC::roc(response = cerv_response,
                              predictor = cerv_rf.predictions[,1])
cerv_rf.auc = cerv_rf.rocCurve$auc[1]
cat('cerv_predictors Random Forest AUC:', cerv_rf.auc, "\n", "\n")
```

```
## cerv_predictors Random Forest AUC: 0.8032492
##
```

```
# Predict on testing set
cerv_pred_rf <- predict(cerv_rf, test_cerv)
confusionMatrix(cerv_pred_rf, test_biopsy)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction Healthy Cancer
##    Healthy     101     10
##    Cancer       59      1
##
##                Accuracy : 0.5965
##                  95% CI : (0.5189, 0.6707)
##     No Information Rate : 0.9357
```

```
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : -0.0904
##
##  Mcnemar's Test P-Value : 0.000000007536
##
##             Sensitivity : 0.63125
##             Specificity : 0.09091
##          Pos Pred Value : 0.90991
##          Neg Pred Value : 0.01667
##              Prevalence : 0.93567
##          Detection Rate : 0.59064
##    Detection Prevalence : 0.64912
##       Balanced Accuracy : 0.36108
##
##        'Positive' Class : Healthy
##
```

K - Nearest Neighbors (KNN)

```
set.seed(222)
cerv_knn <- train(train_cerv, train_biopsy, method = "knn", trControl = ctrl_cerv,
                  preProcess=c("center", "scale"), metric="ROC")
cerv_knn
```

```
## k-Nearest Neighbors
##
## 687 samples
##  10 predictor
##   2 classes: 'Healthy', 'Cancer'
##
## Pre-processing: centered (10), scaled (10)
## Resampling: Repeated Train/Test Splits Estimated (25 reps, 75%)
## Summary of sample sizes: 516, 516, 516, 516, 516, 516, ...
## Addtional sampling using down-sampling prior to pre-processing
##
## Resampling results across tuning parameters:
##
##   k  ROC        Sens     Spec
##   5  0.5852273  0.58725  0.5490909
##   7  0.5875000  0.59100  0.5054545
##   9  0.5799886  0.59625  0.5200000
##
## ROC was used to select the optimal model using the largest value.
## The final value used for the model was k = 7.
```

```
cerv_knn.predictions <- predict(cerv_knn, cerv_predictors, type = "prob")
cerv_knn.rocCurve <- pROC::roc(response = cerv_response,
                               predictor = cerv_knn.predictions[,1])
cerv_knn.auc = cerv_knn.rocCurve$auc[1]
cat('cerv_predictors KNN AUC:', cerv_knn.auc, "\n", "\n")
```

```
## cerv_predictors KNN AUC: 0.6443224
##
```

```
# Predict on testing set
cerv_pred_knn <- predict(cerv_knn, test_cerv)
confusionMatrix(cerv_pred_knn, test_biopsy)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction Healthy Cancer
##    Healthy      95      8
##    Cancer       65      3
##
##                Accuracy : 0.5731
##                  95% CI : (0.4953, 0.6483)
##     No Information Rate : 0.9357
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : -0.0391
##
##  Mcnemar's Test P-Value : 0.0000000000559
##
##             Sensitivity : 0.59375
##             Specificity : 0.27273
##          Pos Pred Value : 0.92233
##          Neg Pred Value : 0.04412
##              Prevalence : 0.93567
##          Detection Rate : 0.55556
##    Detection Prevalence : 0.60234
##       Balanced Accuracy : 0.43324
##
##        'Positive' Class : Healthy
##
```

Naive Bayes

```
set.seed(222)
cerv_nb <- caret::train(train_cerv, train_biopsy, method = "nb", trControl = ctrl_cerv,
                  preProcess=c("center", "scale"), metric="ROC")
cerv_nb
```

```
## Naive Bayes
##
## 687 samples
##  10 predictor
##   2 classes: 'Healthy', 'Cancer'
##
## Pre-processing: centered (10), scaled (10)
## Resampling: Repeated Train/Test Splits Estimated (25 reps, 75%)
## Summary of sample sizes: 516, 516, 516, 516, 516, 516, ...
```

```
## Addtional sampling using down-sampling prior to pre-processing
##
## Resampling results across tuning parameters:
##
##   usekernel  ROC        Sens       Spec
##   FALSE      0.6711230  0.7632353  0.5080214
##    TRUE      0.6181136  0.8165000  0.3054545
##
## Tuning parameter 'fL' was held constant at a value of 0
## Tuning
##  parameter 'adjust' was held constant at a value of 1
## ROC was used to select the optimal model using the largest value.
## The final values used for the model were fL = 0, usekernel = FALSE and adjust
##  = 1.
```

```
cerv_nb.predictions <- predict(cerv_nb, cerv_predictors, type = "prob")
cerv_nb.rocCurve <- pROC::roc(response = cerv_response,
                              predictor = cerv_nb.predictions[,1])
cerv_nb.auc = cerv_nb.rocCurve$auc[1]
cat('cerv_predictors lda AUC:', cerv_nb.auc, "\n", "\n")
```

```
## cerv_predictors lda AUC: 0.6542171
##
```

```
# Predict on testing set
cerv_pred_nb <- predict(cerv_nb, test_cerv)
confusionMatrix(cerv_pred_nb, test_biopsy)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction Healthy Cancer
##    Healthy     131      8
##    Cancer       29      3
##
##                Accuracy : 0.7836
##                  95% CI : (0.7143, 0.8428)
##     No Information Rate : 0.9357
##     P-Value [Acc > NIR] : 1.000000
##
##                   Kappa : 0.0484
##
##  Mcnemar's Test P-Value : 0.001009
##
##             Sensitivity : 0.81875
##             Specificity : 0.27273
##          Pos Pred Value : 0.94245
##          Neg Pred Value : 0.09375
##              Prevalence : 0.93567
##          Detection Rate : 0.76608
##    Detection Prevalence : 0.81287
##       Balanced Accuracy : 0.54574
##
```

```
##        'Positive' Class : Healthy
##
```

Support Vector Machines

```
set.seed(222)
sigmaEst <- kernlab::sigest(as.matrix(cerv_predictors))
svmGrid <- expand.grid(sigma=sigmaEst[1], C=2^seq(-4, 4))

cerv_svm <- train(train_cerv, train_biopsy, method = "svmRadial",
                  tuneGrid = svmGrid, preProcess = c("center", "scale"),
                  metric="ROC", fit = FALSE, trControl = ctrl_cerv)
cerv_svm
```

```
## Support Vector Machines with Radial Basis Function Kernel
##
## 687 samples
##  10 predictor
##   2 classes: 'Healthy', 'Cancer'
##
## Pre-processing: centered (10), scaled (10)
## Resampling: Repeated Train/Test Splits Estimated (25 reps, 75%)
## Summary of sample sizes: 516, 516, 516, 516, 516, 516, ...
## Addtional sampling using down-sampling prior to pre-processing
##
## Resampling results across tuning parameters:
##
##   C        ROC        Sens     Spec
##    0.0625  0.5999773  0.62425  0.5018182
##    0.1250  0.6273636  0.63775  0.5090909
##    0.2500  0.6176364  0.62775  0.5236364
##    0.5000  0.5985455  0.61300  0.5200000
##    1.0000  0.5855909  0.63425  0.5054545
##    2.0000  0.5988636  0.67200  0.4763636
##    4.0000  0.5665682  0.61525  0.4945455
##    8.0000  0.5486818  0.60150  0.4727273
##   16.0000  0.5241818  0.55825  0.5018182
##
## Tuning parameter 'sigma' was held constant at a value of 0.02371243
## ROC was used to select the optimal model using the largest value.
## The final values used for the model were sigma = 0.02371243 and C = 0.125.
```

```
cerv_svm.predictions <- predict(cerv_svm, cerv_predictors, type = "prob")
cerv_svm.rocCurve <- pROC::roc(response = cerv_response,
                               predictor = cerv_svm.predictions[,1])
cerv_svm.auc = cerv_svm.rocCurve$auc[1]
cat('cerv_predictors SVM AUC:', cerv_svm.auc, "\n", "\n")
```

```
## cerv_predictors SVM AUC: 0.6479226
##
```

```r
# Predict on testing set
cerv_pred_svm <- predict(cerv_svm, test_cerv)
confusionMatrix(cerv_pred_svm, test_biopsy)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction Healthy Cancer
##    Healthy     109      8
##    Cancer       51      3
##
##                Accuracy : 0.655
##                  95% CI : (0.5786, 0.7259)
##     No Information Rate : 0.9357
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : -0.0163
##
##  Mcnemar's Test P-Value : 0.00000004553
##
##             Sensitivity : 0.68125
##             Specificity : 0.27273
##          Pos Pred Value : 0.93162
##          Neg Pred Value : 0.05556
##              Prevalence : 0.93567
##          Detection Rate : 0.63743
##    Detection Prevalence : 0.68421
##       Balanced Accuracy : 0.47699
##
##        'Positive' Class : Healthy
##
```

```r
# Model Train and Test Variables
cerv_glm_opt <- which.max(cerv_glm$results[,"ROC"])
cerv_glm_roc_train <- cerv_glm$results[cerv_glm_opt,"ROC"]
cerv_glm_sens_train <- cerv_glm$results[cerv_glm_opt,"Sens"]
cerv_glm_spec_train <- cerv_glm$results[cerv_glm_opt,"Spec"]
cerv_glm_accur <- Accuracy(cerv_pred_glm, test_biopsy)
cerv_glm_sens <- sensitivity(cerv_pred_glm, test_biopsy)
cerv_glm_spec <- specificity(cerv_pred_glm, test_biopsy)

cerv_lda_opt <- which.max(cerv_lda$results[,"ROC"])
cerv_lda_roc_train <- cerv_lda$results[cerv_lda_opt,"ROC"]
cerv_lda_sens_train <- cerv_lda$results[cerv_lda_opt,"Sens"]
cerv_lda_spec_train <- cerv_lda$results[cerv_lda_opt,"Spec"]
cerv_lda_accur <- Accuracy(cerv_pred_lda, test_biopsy)
cerv_lda_sens <- sensitivity(cerv_pred_lda, test_biopsy)
cerv_lda_spec <- specificity(cerv_pred_lda, test_biopsy)

cerv_mda_opt <- which.max(cerv_mda$results[,"ROC"])
cerv_mda_roc_train <- cerv_mda$results[cerv_mda_opt,"ROC"]
cerv_mda_sens_train <- cerv_mda$results[cerv_mda_opt,"Sens"]
cerv_mda_spec_train <- cerv_mda$results[cerv_mda_opt,"Spec"]
```

```
cerv_mda_accur <- Accuracy(cerv_pred_mda, test_biopsy)
cerv_mda_sens <- sensitivity(cerv_pred_mda, test_biopsy)
cerv_mda_spec <- specificity(cerv_pred_mda, test_biopsy)

cerv_plsda_opt <- which.max(cerv_plsda$results[,"ROC"])
cerv_plsda_roc_train <- cerv_plsda$results[cerv_plsda_opt,"ROC"]
cerv_plsda_sens_train <- cerv_plsda$results[cerv_plsda_opt,"Sens"]
cerv_plsda_spec_train <- cerv_plsda$results[cerv_plsda_opt,"Spec"]
cerv_plsda_accur <- Accuracy(cerv_pred_plsda, test_biopsy)
cerv_plsda_sens <- sensitivity(cerv_pred_plsda, test_biopsy)
cerv_plsda_spec <- specificity(cerv_pred_plsda, test_biopsy)

cerv_nsc_opt <- which.max(cerv_nsc$results[,"ROC"])
cerv_nsc_roc_train <- cerv_nsc$results[cerv_nsc_opt,"ROC"]
cerv_nsc_sens_train <- cerv_nsc$results[cerv_nsc_opt,"Sens"]
cerv_nsc_spec_train <- cerv_nsc$results[cerv_nsc_opt,"Spec"]
cerv_nsc_accur <- Accuracy(cerv_pred_nsc, test_biopsy)
cerv_nsc_sens <- sensitivity(cerv_pred_nsc, test_biopsy)
cerv_nsc_spec <- specificity(cerv_pred_nsc, test_biopsy)

cerv_glmnet_opt <- which.max(cerv_glmnet$results[,"ROC"])
cerv_glmnet_roc_train <- cerv_glmnet$results[cerv_glmnet_opt,"ROC"]
cerv_glmnet_sens_train <- cerv_glmnet$results[cerv_glmnet_opt,"Sens"]
cerv_glmnet_spec_train <- cerv_glmnet$results[cerv_glmnet_opt,"Spec"]
cerv_glmnet_accur <- Accuracy(cerv_pred_glmnet, test_biopsy)
cerv_glmnet_sens <- sensitivity(cerv_pred_glmnet, test_biopsy)
cerv_glmnet_spec <- specificity(cerv_pred_glmnet, test_biopsy)

cerv_rf_opt <- which.max(cerv_rf$results[,"ROC"])
cerv_rf_roc_train <- cerv_rf$results[cerv_rf_opt,"ROC"]
cerv_rf_sens_train <- cerv_rf$results[cerv_rf_opt,"Sens"]
cerv_rf_spec_train <- cerv_rf$results[cerv_rf_opt,"Spec"]
cerv_rf_accur <- Accuracy(cerv_pred_rf, test_biopsy)
cerv_rf_sens <- sensitivity(cerv_pred_rf, test_biopsy)
cerv_rf_spec <- specificity(cerv_pred_rf, test_biopsy)

cerv_nnet_opt <- which.max(cerv_nnet$results[,"ROC"])
cerv_nnet_roc_train <- cerv_nnet$results[cerv_nnet_opt,"ROC"]
cerv_nnet_sens_train <- cerv_nnet$results[cerv_nnet_opt,"Sens"]
cerv_nnet_spec_train <- cerv_nnet$results[cerv_nnet_opt,"Spec"]
cerv_nnet_accur <- Accuracy(cerv_pred_nnet, test_biopsy)
cerv_nnet_sens <- sensitivity(cerv_pred_nnet, test_biopsy)
cerv_nnet_spec <- specificity(cerv_pred_nnet, test_biopsy)

cerv_knn_opt <- which.max(cerv_knn$results[,"ROC"])
cerv_knn_roc_train <- cerv_knn$results[cerv_knn_opt,"ROC"]
cerv_knn_sens_train <- cerv_knn$results[cerv_knn_opt,"Sens"]
cerv_knn_spec_train <- cerv_knn$results[cerv_knn_opt,"Spec"]
cerv_knn_accur <- Accuracy(cerv_pred_knn, test_biopsy)
cerv_knn_sens <- sensitivity(cerv_pred_knn, test_biopsy)
cerv_knn_spec <- specificity(cerv_pred_knn, test_biopsy)

cerv_nb_opt <- which.max(cerv_nb$results[,"ROC"])
```

```
cerv_nb_roc_train <- cerv_nb$results[cerv_nb_opt,"ROC"]
cerv_nb_sens_train <- cerv_nb$results[cerv_nb_opt,"Sens"]
cerv_nb_spec_train <- cerv_nb$results[cerv_nb_opt,"Spec"]
cerv_nb_accur <- Accuracy(cerv_pred_nb, test_biopsy)
cerv_nb_sens <- sensitivity(cerv_pred_nb, test_biopsy)
cerv_nb_spec <- specificity(cerv_pred_nb, test_biopsy)

cerv_svm_opt <- which.max(cerv_svm$results[,"ROC"])
cerv_svm_roc_train <- cerv_svm$results[cerv_svm_opt,"ROC"]
cerv_svm_sens_train <- cerv_svm$results[cerv_svm_opt,"Sens"]
cerv_svm_spec_train <- cerv_svm$results[cerv_svm_opt,"Spec"]
cerv_svm_accur <- Accuracy(cerv_pred_svm, test_biopsy)
cerv_svm_sens <- sensitivity(cerv_pred_svm, test_biopsy)
cerv_svm_spec <- specificity(cerv_pred_svm, test_biopsy)
```

```
cerv_models <- c("Generalized Linear Model","Linear Discriminant Analysis",
                 "Mixture Discriminant Analysis",
                 "PLSDA",
                 "Nearest Shrunken Centroids","GLMNET","Random Forest","Neural Network",
                 "K-Nearest Neighbors",
                 "Naive Bayes", "Support Vector Machines")
# Create Columns for Training Data
roc <- c(cerv_glm_roc_train,cerv_lda_roc_train,cerv_mda_roc_train,cerv_plsda_roc_train,
         cerv_nsc_roc_train,cerv_glmnet_roc_train,cerv_rf_roc_train,cerv_nnet_roc_train,
         cerv_knn_roc_train,cerv_nb_roc_train,cerv_svm_roc_train)
auc <- c(cerv_glm.auc,cerv_lda.auc,cerv_mda.auc,cerv_plsda.auc,cerv_nsc.auc,
         cerv_glmnet.auc,cerv_rf.auc,cerv_nnet.auc,cerv_knn.auc,cerv_nb.auc,cerv_svm.auc)
senstr <- c(cerv_glm_sens_train,cerv_lda_sens_train,cerv_mda_sens_train,
            cerv_plsda_sens_train,cerv_nsc_sens_train,cerv_glmnet_sens_train,
            cerv_rf_sens_train,cerv_nnet_sens_train,cerv_knn_sens_train,
            cerv_nb_sens_train,cerv_svm_sens_train)
spectr <- c(cerv_glm_spec_train,cerv_lda_spec_train,cerv_mda_spec_train,
            cerv_plsda_spec_train,cerv_nsc_spec_train,cerv_glmnet_spec_train,
            cerv_rf_spec_train, cerv_nnet_spec_train,cerv_knn_spec_train,
            cerv_nb_spec_train,cerv_svm_spec_train)
# Create Columns for Testing Data
accutest <- c(cerv_glm_accur,cerv_lda_accur,cerv_mda_accur,cerv_plsda_accur,
              cerv_nsc_accur,cerv_glmnet_accur,cerv_rf_accur,cerv_nnet_accur,
              cerv_knn_accur,cerv_nb_accur,cerv_svm_accur)
senstest <- c(cerv_glm_sens,cerv_lda_sens,cerv_mda_sens,cerv_plsda_sens,cerv_nsc_sens,
              cerv_glmnet_sens,cerv_rf_sens,cerv_nnet_sens,cerv_knn_sens,cerv_nb_sens,
              cerv_svm_sens)
spectest <- c(cerv_glm_spec,cerv_lda_spec,cerv_mda_spec,cerv_plsda_spec,cerv_nsc_spec,
              cerv_glmnet_spec,cerv_rf_spec,cerv_nnet_spec,cerv_knn_spec,cerv_nb_spec,cerv_svm_spec)
# Parse Training and Testing data into pander table columns
table2 <- data.frame(cerv_models,roc,auc,senstr,spectr)
table3 <- data.frame(cerv_models,accutest,senstest,spectest)
colnames(table2) <- c("Model","ROC","AUC","Sensitivity Train","Specificity Train")
colnames(table3) <- c("Model","Accuracy Test","Sensitivity Test","Specificity Test")
table2 %>% pander(style = "simple", split.table = Inf, justify = "left",
                  caption="Model Comparison For Train and Test")
```

Table 2: Model Comparison For Train and Test

Model	ROC	AUC	Sensitivity Train	Specificity Train
Generalized Linear Model	0.6142	0.6361	0.638	0.5273
Linear Discriminant Analysis	0.6194	0.6385	0.6545	0.5236
Mixture Discriminant Analysis	0.6296	0.6964	0.6012	0.5564
PLSDA	0.6604	0.6348	0.674	0.5418
Nearest Shrunken Centroids	0.6607	0.6347	0.677	0.5418
GLMNET	0.6523	0.6588	0.6673	0.5564
Random Forest	0.6621	0.8032	0.6132	0.6327
Neural Network	0.6149	0.6067	0.6148	0.5709
K-Nearest Neighbors	0.5875	0.6443	0.591	0.5055
Naive Bayes	0.6711	0.6542	0.7632	0.508
Support Vector Machines	0.6274	0.6479	0.6378	0.5091

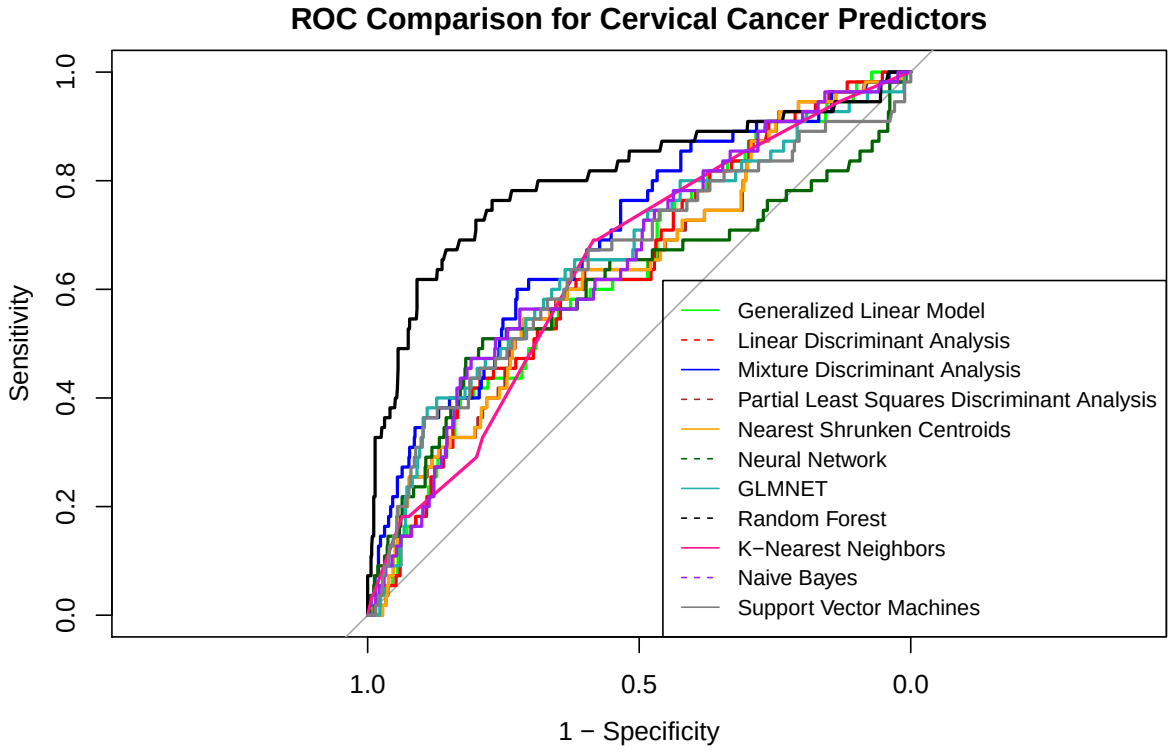
```
table3 %>% pander(style = "simple", split.table = Inf, justify = "left",
                  caption="Model Comparison For Train and Test")
```

Table 3: Model Comparison For Train and Test

Model	Accuracy Test	Sensitivity Test	Specificity Test
Generalized Linear Model	0.614	0.6375	0.2727
Linear Discriminant Analysis	0.6316	0.6562	0.2727
Mixture Discriminant Analysis	0.6023	0.6312	0.1818
PLSDA	0.6199	0.6312	0.4545
Nearest Shrunken Centroids	0.6199	0.6312	0.4545
GLMNET	0.6784	0.7125	0.1818
Random Forest	0.5965	0.6312	0.09091
Neural Network	0.5789	0.6062	0.1818
K-Nearest Neighbors	0.5731	0.5938	0.2727
Naive Bayes	0.7836	0.8187	0.2727
Support Vector Machines	0.655	0.6813	0.2727

```
plot(cerv_glm.rocCurve, col = "green",
     main = "ROC Comparison for Cervical Cancer Predictors",
     xlab= "1 - Specificity", ylab="Sensitivity")
legend("bottomright", legend=c("Generalized Linear Model","Linear Discriminant Analysis",
                  "Mixture Discriminant Analysis",
                  "Partial Least Squares Discriminant Analysis",
                  "Nearest Shrunken Centroids","Neural Network","GLMNET","Random Forest",
                  "K-Nearest Neighbors", "Naive Bayes", "Support Vector Machines"),
     col=c("green","red","blue","brown","orange","darkgreen","lightseagreen","black",
           "deeppink", "purple","grey50"),
     lty=1:2, cex=0.8)
plot(cerv_lda.rocCurve, col = "red", add = TRUE)
plot(cerv_mda.rocCurve, col = "blue", add = TRUE)
plot(cerv_plsda.rocCurve, col = "brown", add = TRUE)
plot(cerv_nsc.rocCurve, col = "orange", add = TRUE)
plot(cerv_nnet.rocCurve, col = "darkgreen", add = TRUE)
plot(cerv_glmnet.rocCurve, col = "lightseagreen", add = TRUE)
plot(cerv_rf.rocCurve, col = "black", add = TRUE)
```

```
plot(cerv_knn.rocCurve, col = "deeppink", add = TRUE)
plot(cerv_nb.rocCurve, col = "purple", add = TRUE)
plot(cerv_svm.rocCurve, col = "grey50", add = TRUE)
```




```
model_metrics_train <- c("ROC", "AUC", "Sensitivity", "Specificity")
model_metrics_test <- c("Accuracy", "Sensitivity", "Specificity")

# Minimums and Maximums (Trained Models)
min_roc <- min(roc); max_roc <- max(roc)
min_auc <- min(auc); max_auc <- max(auc)
min_sens_train <- min(senstr); max_sens_train <- max(senstr)
min_spec_train <- min(spectr); max_spec_train <- max(spectr)

mean_roc <- mean(roc)
mean_auc <- mean(auc)
mean_sens_train <- mean(senstr)
mean_spec_train <- mean(spectr)

min_roc_name <- table2[which.min(table2$ROC),1]
min_auc_name <- table2[which.min(table2$AUC),1]
min_sens_train_name <- table2[which.min(table2$`Sensitivity Train`),1]
min_spec_train_name <- table2[which.min(table2$`Specificity Train`),1]

max_roc_name <- table2[which.max(table2$ROC),1]
max_auc_name <- table2[which.max(table2$AUC),1]
max_sens_train_name <- table2[which.max(table2$`Sensitivity Train`),1]
max_spec_train_name <- table2[which.max(table2$`Specificity Train`),1]
```

```
# Minimums and Maximums (Tested Models)
min_accutest <- min(accutest); max_accutest <- max(accutest)
min_senstest <- min(senstest); max_senstest <- max(senstest)
min_spectest <- min(spectest); max_spectest <- max(spectest)

mean_accutest <- mean(accutest)
mean_senstest <- mean(senstest)
mean_spectest <- mean(spectest)

min_accutest_name <- table3[which.min(table3$`Accuracy Test`),1]
min_sens_test_name <- table2[which.min(table3$`Sensitivity Test`),1]
min_spec_test_name <- table2[which.min(table3$`Specificity Test`),1]

max_accutest_name <- table3[which.max(table3$`Accuracy Test`),1]
max_sens_test_name <- table2[which.max(table3$`Sensitivity Test`),1]
max_spec_test_name <- table2[which.max(table3$`Specificity Test`),1]

#Parse Columns into table
min_train <- c(min_roc,min_auc,min_sens_train,min_spec_train)
mean_train <- c(mean_roc,mean_auc,mean_sens_train,mean_spec_train)
max_train <- c(max_roc,max_auc,max_sens_train,max_spec_train)
min_train_names <- c(min_roc_name,min_auc_name,min_sens_train_name,min_spec_train_name)
max_train_names <- c(max_roc_name,max_auc_name,max_sens_train_name,max_spec_train_name)

min_test <- c(min_accutest,min_senstest,min_spectest)
mean_test <- c(mean_accutest,mean_senstest,mean_spectest)
max_test <- c(max_accutest,max_senstest,max_spectest)
min_test_names <- c(min_sens_test_name,min_sens_test_name,min_spec_test_name)
max_test_names <- c(max_accutest_name,max_sens_test_name,max_spec_test_name)

table4 <- data.frame(model_metrics_train,min_train,mean_train,max_train,
                     min_train_names,max_train_names)
table5 <- data.frame(model_metrics_test,min_test,mean_test,max_test,
                     min_test_names,max_test_names)
colnames(table4) <- c("Model Metrics","Minimum","Mean","Maximum", "Model with Min.",
                      "Model with Max")
colnames(table5) <- c("Model Metrics","Minimum","Mean","Maximum", "Model with Min",
                      "Model with Max")
table4 %>% pander(style = "simple", split.table = Inf, justify = "left",
                  caption = "Model Comparison Summary - Train")
```

Table 4: Model Comparison Summary - Train

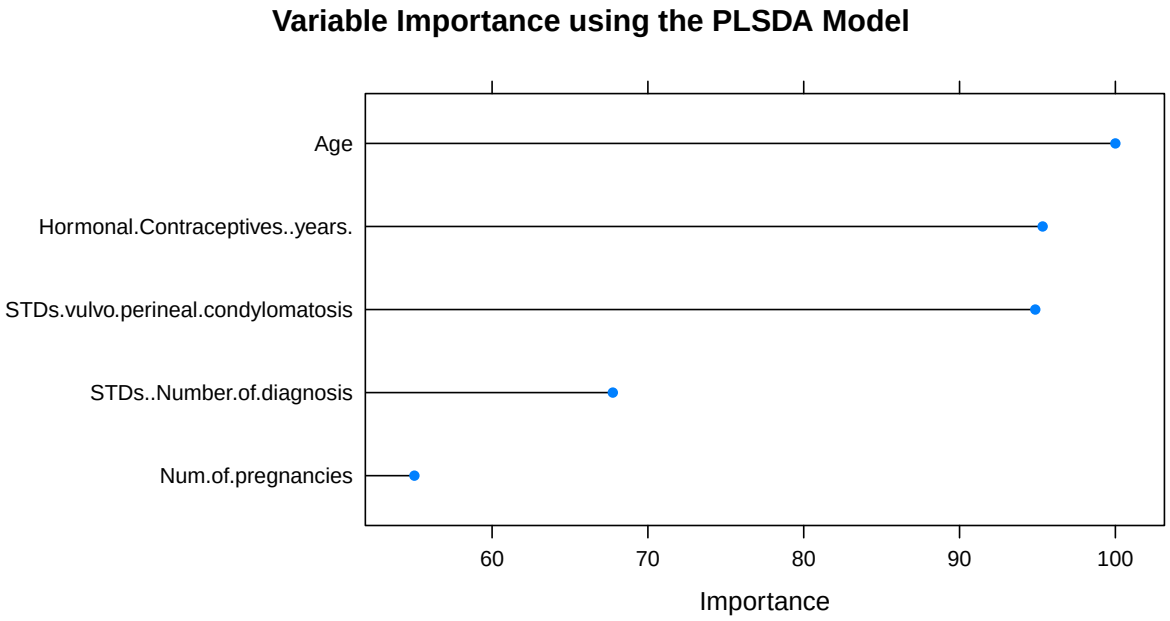
Model Metrics	Minimum	Mean	Maximum	Model with Min.	Model with Max
ROC	0.5875	0.6363	0.6711	K-Nearest Neighbors	Naive Bayes
AUC	0.6067	0.6596	0.8032	Neural Network	Random Forest
Sensitivity	0.591	0.6484	0.7632	K-Nearest Neighbors	Naive Bayes
Specificity	0.5055	0.543	0.6327	K-Nearest Neighbors	Random Forest

```
table5 %>% pander(style = "simple", split.table = Inf, justify = "left",
                  caption = "Model Comparison Summary - Test")
```

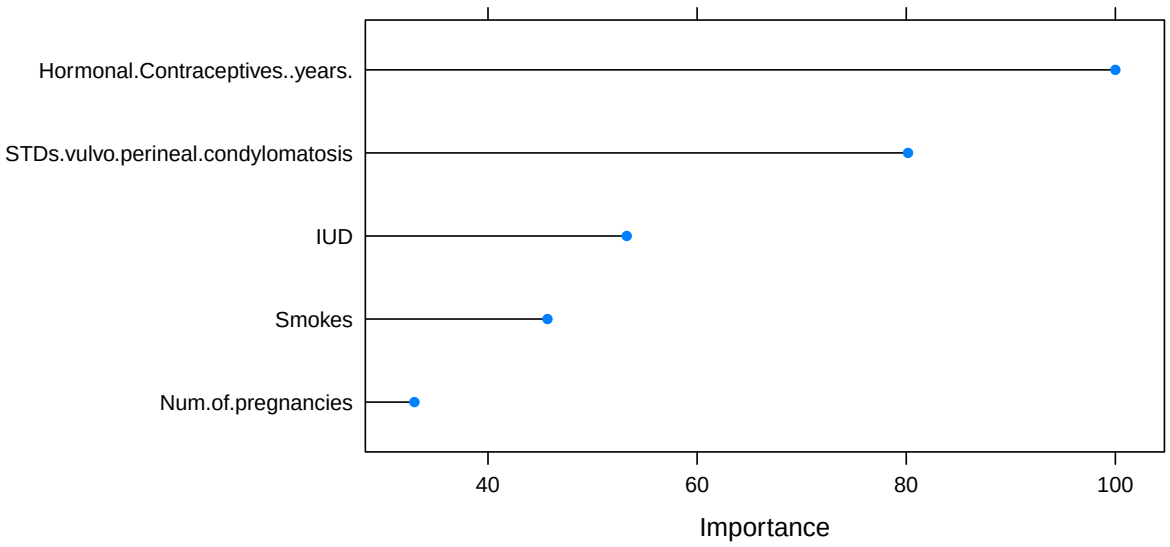
Table 5: Model Comparison Summary - Test

Model Metrics	Minimum	Mean	Maximum	Model with Min	Model with Max
Accuracy	0.5731	0.6321	0.7836	K-Nearest Neighbors	Naive Bayes
Sensitivity	0.5938	0.6574	0.8187	K-Nearest Neighbors	Naive Bayes
Specificity	0.09091	0.2645	0.4545	Random Forest	PLSDA

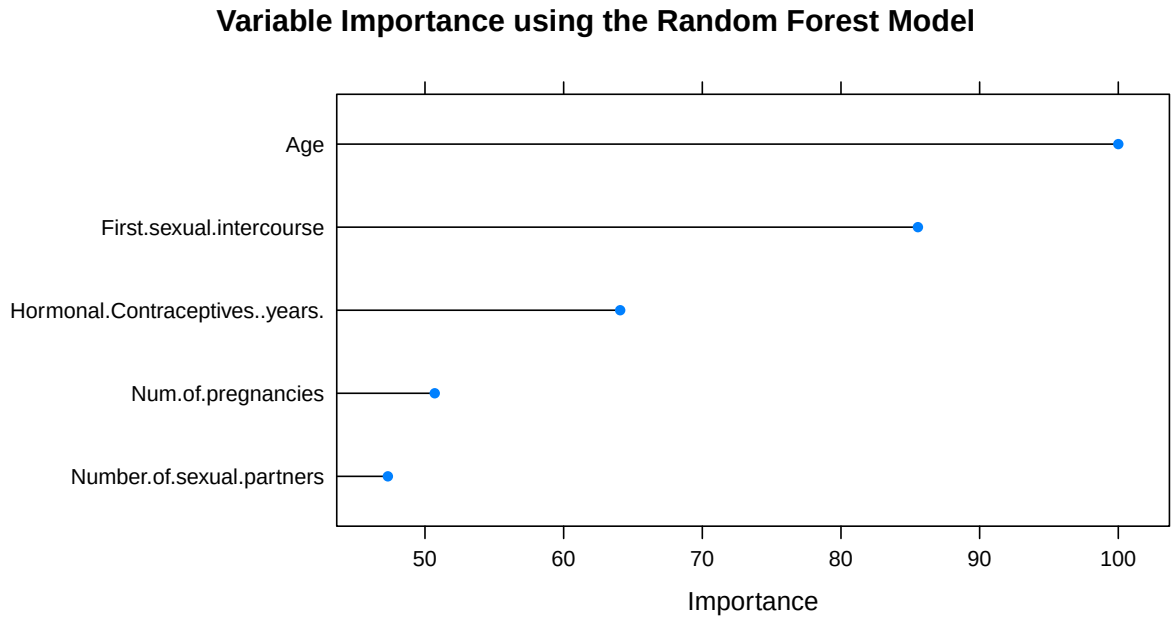
```
plot(varImp(cerv_plsda), top = 5, main = "Variable Importance using the PLSDA Model")
```



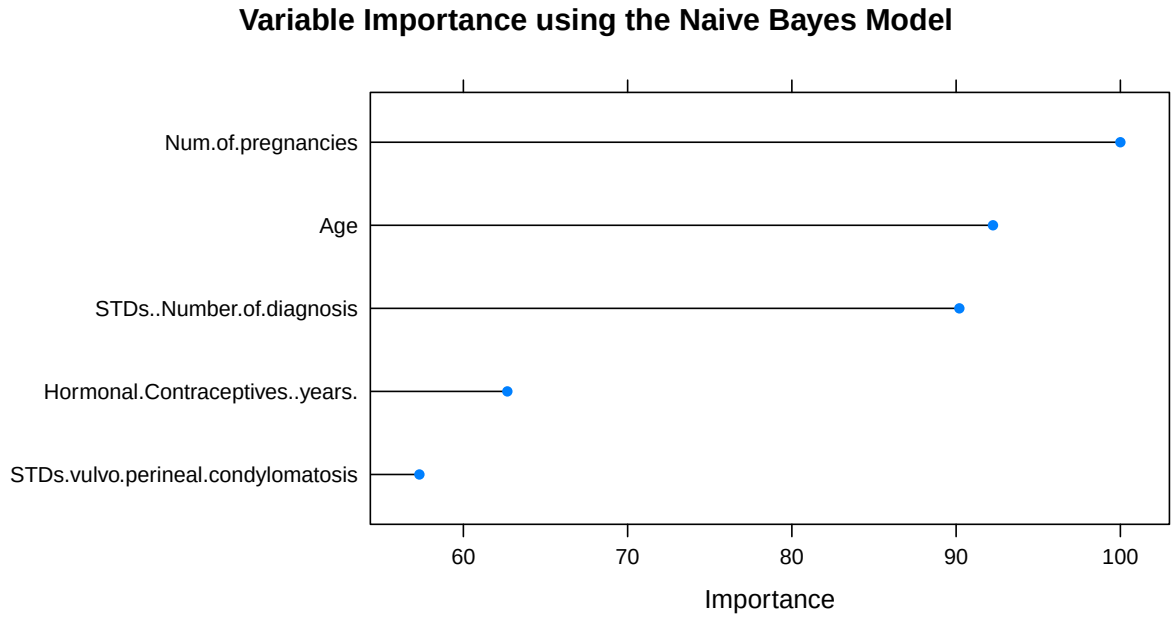

```
plot(varImp(cerv_glm), top = 5, main = "Variable Importance using the GLM Model")
```



```
plot(varImp(cerv_rf), top = 5, main = "Variable Importance using the Random Forest Model")
```




```
plot(varImp(cerv_nb), top = 5, main = "Variable Importance using the Naive Bayes Model")
```




```
cerv_log <- glm(train_biopsy ~., data = train_cerv, family = binomial)
summary(cerv_log)
```

```
##
## Call:
```

```
## glm(formula = train_biopsy ~ ., family = binomial, data = train_cerv)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.1212  -0.3532  -0.3026  -0.2751   2.6473
##
## Coefficients:
##                                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)                       -3.60416    1.15273  -3.127  0.00177 **
## Age                                0.01624    0.02487   0.653  0.51367
## Number.of.sexual.partners         -0.09318    0.12702  -0.734  0.46320
## First.sexual.intercourse           0.01179    0.06482   0.182  0.85570
## Num.of.pregnancies                 0.02620    0.13671   0.192  0.84802
## Smokes                             0.33928    0.42423   0.800  0.42385
## Hormonal.Contraceptives           -0.06879    0.39546  -0.174  0.86190
## Hormonal.Contraceptives..years.    0.08380    0.03651   2.295  0.02172 *
## IUD                                0.21502    0.49385   0.435  0.66328
## STDs.vulvo.perineal.condylomatosis  0.57742    0.67589   0.854  0.39293
## STDs..Number.of.diagnosis          0.85803    0.49288   1.741  0.08171 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 326.96  on 686  degrees of freedom
## Residual deviance: 306.48  on 676  degrees of freedom
## AIC: 328.48
##
## Number of Fisher Scoring iterations: 6
```

```
coef_log <- coef(summary(cerv_log))[,'Pr(>|z|)']
min_coef_log <- Rfast::nth(coef_log, 2, descending = F) # 2nd min (first is intercept)
```

Operating the generalized linear model (logistic regression) on the training set of the data uncovered only one statistically significant predictor (Hormonal.Contraceptives..years.) with a p-value of 0.021721.

$$\hat{p}(y) = \frac{\exp(b_0 + b_1 x_1 + \cdots + b_p x_p)}{1 + \exp(b_0 + b_1 x_1 + \cdots + b_p x_p)}$$

$$\hat{p}(y) = \frac{\exp(b_0 + b_1(Hormonal.Contraceptives..years.)}{1 + \exp(b_0 + b_1(Hormonal.Contraceptives..years.)}$$