Titanic Dataset

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About Dataset: On April 15, 1912, during her maiden voyage, the Titanic sank after colliding with an iceberg, killing 1502 out of 2224 passengers and crew. This tragedy shocked the international community and lead to better safety regulations for ships. One of the reasons that the shipwreck lead to such loss of life was that there were not enough lifeboats for the passengers and crew. Although there was some element of luck involved in surviving the sinking, some groups of people were more likely to survive than others, such as women, children, and the upper-class.

Description of variables in the dataset:

VARIABLE DESCRIPTIONS: survival : Survival(0 = No; 1 = Yes) pclass : Passenger Class(1 = 1st; 2 = 2nd; 3 = 3rd) name : Name sex : Sex age : Age sibsp : Number of Siblings/Spouses Aboard parch : Number of Parents/Children Aboard ticket : Ticket Number fare : Passenger Fare cabin : Cabin embarked : Port of Embarkation (C = Cherbourg; Q = Queenstown; S = Southampton)

Reading dataset from excel file ,Importing library(readxl) inorder to read excel files

```r
library(readxl)
Titanic_data<-read_excel("D:/R_CSV_folder/Semester_2_evaluation/Titanic.xls")
```

Viewing our dataset if it is imported properly

```r
head(Titanic_data)
```

```
## # A tibble: 6 x 12
##   PassengerId Survived Pclass Name  Sex     Age SibSp Parch Ticket  Fare
##         <dbl>    <dbl>  <dbl> <chr> <chr> <dbl> <dbl> <dbl> <chr>  <dbl>
## 1           1        0      3 Brau~ male     22     1     0 A/5 2~  7.25
## 2           2        1      1 Cumi~ fema~    38     1     0 PC 17~ 71.3
## 3           3        1      3 Heik~ fema~    26     0     0 STON/~  7.92
## 4           4        1      1 Futr~ fema~    35     1     0 113803 53.1
## 5           5        0      3 Alle~ male     35     0     0 373450  8.05
## 6           6        0      3 Mora~ male     NA     0     0 330877  8.46
## # ... with 2 more variables: Cabin <chr>, Embarked <chr>
```

Looking at the structure of the data

```r
str(Titanic_data)
```

```
## Classes 'tbl_df', 'tbl' and 'data.frame':    891 obs. of  12 variables:
##  $ PassengerId: num  1 2 3 4 5 6 7 8 9 10 ...
##  $ Survived   : num  0 1 1 1 0 0 0 0 1 1 ...
```

```
##  $ Pclass     : num  3 1 3 1 3 3 1 3 3 2 ...
##  $ Name       : chr  "Braund, Mr. Owen Harris" "Cumings, Mrs. John Bradley
(Florence Briggs Thayer)" "Heikkinen, Miss. Laina" "Futrelle, Mrs. Jacques
Heath (Lily May Peel)" ...
##  $ Sex        : chr  "male" "female" "female" "female" ...
##  $ Age        : num  22 38 26 35 35 NA 54 2 27 14 ...
##  $ SibSp      : num  1 1 0 1 0 0 0 3 0 1 ...
##  $ Parch      : num  0 0 0 0 0 0 0 1 2 0 ...
##  $ Ticket     : chr  "A/5 21171" "PC 17599" "STON/O2. 3101282" "113803"
...
##  $ Fare       : num  7.25 71.28 7.92 53.1 8.05 ...
##  $ Cabin      : chr  NA "C85" NA "C123" ...
##  $ Embarked   : chr  "S" "C" "S" "S" ...
```

Dimension of the datasett

```
dim(Titanic_data)

## [1] 891  12
```

Removing columns which not useful to predict the survived class

```
Titanic_data$PassengerId<-NULL
Titanic_data$Name<-NULL
Titanic_data$Cabin<-NULL
Titanic_data$Ticket<-NULL
```

Converting Sex column to factor as it is in characrer.

```
Titanic_data$Sex<-as.factor(Titanic_data$Sex)
str(Titanic_data)

## Classes 'tbl_df', 'tbl' and 'data.frame':    891 obs. of  8 variables:
##  $ Survived: num  0 1 1 1 0 0 0 0 1 1 ...
##  $ Pclass  : num  3 1 3 1 3 3 1 3 3 2 ...
##  $ Sex     : Factor w/ 2 levels "female","male": 2 1 1 1 2 2 2 2 1 1 ...
##  $ Age     : num  22 38 26 35 35 NA 54 2 27 14 ...
##  $ SibSp   : num  1 1 0 1 0 0 0 3 0 1 ...
##  $ Parch   : num  0 0 0 0 0 0 0 1 2 0 ...
##  $ Fare    : num  7.25 71.28 7.92 53.1 8.05 ...
##  $ Embarked: chr  "S" "C" "S" "S" ...

colSums(is.na(Titanic_data))

## Survived   Pclass      Sex      Age    SibSp    Parch     Fare Embarked
##        0        0        0      177        0        0        0        2
```

Replacing "NA" values in Age column with median value of age as we know that usually age variable is normally distributed variable

```
median(Titanic_data$Age,na.rm = T)

## [1] 28
```

Median value is 28 from above result

```
Titanic_data$Age[is.na(Titanic_data$Age)]<-28
```

Converting continuous variable to categorical

```
Titanic_data$Age<-cut(Titanic_data$Age,breaks = c(0,20,28,40,Inf),labels =
c("c1","c2","c3","c4"))
str(Titanic_data)
```

```
## Classes 'tbl_df', 'tbl' and 'data.frame':    891 obs. of  8 variables:
##  $ Survived: num  0 1 1 1 0 0 0 0 1 1 ...
##  $ Pclass  : num  3 1 3 1 3 3 1 3 3 2 ...
##  $ Sex     : Factor w/ 2 levels "female","male": 2 1 1 1 2 2 2 2 1 1 ...
##  $ Age     : Factor w/ 4 levels "c1","c2","c3",..: 2 3 2 3 3 2 4 1 2 1 ...
##  $ SibSp   : num  1 1 0 1 0 0 0 3 0 1 ...
##  $ Parch   : num  0 0 0 0 0 0 0 1 2 0 ...
##  $ Fare    : num  7.25 71.28 7.92 53.1 8.05 ...
##  $ Embarked: chr  "S" "C" "S" "S" ...
```

```
summary(Titanic_data)
```

```
##     Survived          Pclass          Sex        Age          SibSp      
##  Min.   :0.0000   Min.   :1.000   female:314   c1:179   Min.   :0.000  
##  1st Qu.:0.0000   1st Qu.:2.000   male  :577   c2:360   1st Qu.:0.000  
##  Median :0.0000   Median :3.000                c3:202   Median :0.000  
##  Mean   :0.3838   Mean   :2.309                c4:150   Mean   :0.523  
##  3rd Qu.:1.0000   3rd Qu.:3.000                         3rd Qu.:1.000  
##  Max.   :1.0000   Max.   :3.000                         Max.   :8.000  
##      Parch             Fare          Embarked        
##  Min.   :0.0000   Min.   :  0.00   Length:891        
##  1st Qu.:0.0000   1st Qu.:  7.91   Class :character  
##  Median :0.0000   Median : 14.45   Mode  :character  
##  Mean   :0.3816   Mean   : 32.20                     
##  3rd Qu.:0.0000   3rd Qu.: 31.00                     
##  Max.   :6.0000   Max.   :512.33                     
```

we need to convert numerical and characrter variables to factor

```
names<-c("Survived","Pclass","Embarked")
Titanic_data[,names]<-lapply(Titanic_data[,names],as.factor)
str(Titanic_data)
```

```
## Classes 'tbl_df', 'tbl' and 'data.frame':    891 obs. of  8 variables:
##  $ Survived: Factor w/ 2 levels "0","1": 1 2 2 2 1 1 1 1 2 2 ...
##  $ Pclass  : Factor w/ 3 levels "1","2","3": 3 1 3 1 3 3 1 3 3 2 ...
##  $ Sex     : Factor w/ 2 levels "female","male": 2 1 1 1 2 2 2 2 1 1 ...
##  $ Age     : Factor w/ 4 levels "c1","c2","c3",..: 2 3 2 3 3 2 4 1 2 1 ...
##  $ SibSp   : num  1 1 0 1 0 0 0 3 0 1 ...
##  $ Parch   : num  0 0 0 0 0 0 0 1 2 0 ...
##  $ Fare    : num  7.25 71.28 7.92 53.1 8.05 ...
##  $ Embarked: Factor w/ 3 levels "C","Q","S": 3 1 3 3 3 2 3 3 3 1 ...
```

```
head(Titanic_data)

## # A tibble: 6 x 8
##   Survived Pclass Sex    Age   SibSp Parch  Fare Embarked
##   <fct>    <fct>  <fct>  <fct> <dbl> <dbl> <dbl> <fct>
## 1 0        3      male   c2        1     0  7.25 S
## 2 1        1      female c3        1     0 71.3  C
## 3 1        3      female c2        0     0  7.92 S
## 4 1        1      female c3        1     0 53.1  S
## 5 0        3      male   c3        0     0  8.05 S
## 6 0        3      male   c2        0     0  8.46 Q
```

Replacing NA values present in the Embarked column with mode of Embarked col.

```
summary(Titanic_data$Embarked)

##    C    Q    S NA's
##  168   77  644    2
```

Replacing NA values with "S"

```
Titanic_data$Embarked[is.na(Titanic_data$Embarked)]<-"S"
summary(Titanic_data$Embarked)

##   C   Q   S
## 168  77 646
```

Checking if there are any NA values

```
colSums(is.na(Titanic_data))

## Survived   Pclass      Sex      Age    SibSp    Parch     Fare Embarked
##        0        0        0        0        0        0        0        0
```

Scaling numeric data

```
names1<-c("Parch", "SibSp", "Fare")
Titanic_data[,names1]<-lapply(Titanic_data[,names1], scale)
summary(Titanic_data)

##  Survived Pclass      Sex       Age             SibSp.V1
##  0:549    1:216   female:314   c1:179   Min.   :-0.474279
##  1:342    2:184   male  :577   c2:360   1st Qu.:-0.474279
##           3:491                c3:202   Median :-0.474279
##                                c4:150   Mean   : 0.000000
##                                         3rd Qu.: 0.432550
##                                         Max.   : 6.780355
##       Parch.V1            Fare.V1         Embarked
##  Min.   :-0.473408   Min.   :-0.648058   C:168
##  1st Qu.:-0.473408   1st Qu.:-0.488874   Q: 77
##  Median :-0.473408   Median :-0.357190   S:646
##  Mean   : 0.000000   Mean   : 0.000000
```

```
##   3rd Qu.:-0.473408   3rd Qu.:-0.024233
##   Max.   : 6.970233   Max.   : 9.661740
```

using set.seed to get same results

```r
set.seed(100)
```

importing caret library for spliting the dataset into training and testing Dividing dataset into 70:30 ratio (70:training)

```r
library(caret)

## Loading required package: lattice

## Loading required package: ggplot2

index<-createDataPartition(Titanic_data$Survived,p=0.70,list = F)
training_set<-Titanic_data[index,]
testing_set<-Titanic_data[-index,]
dim(training_set)

## [1] 625   8

dim(testing_set)

## [1] 266   8
```

####Applying logistic regression Model

```r
titanic_model<-glm(Survived~.,data = training_set,family = "binomial")
summary(titanic_model)

##
## Call:
## glm(formula = Survived ~ ., family = "binomial", data = training_set)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.1027  -0.6974  -0.4105   0.6058   2.4715
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  3.27716    0.46282   7.081 1.43e-12 ***
## Pclass2     -0.82501    0.35749  -2.308  0.02101 *
## Pclass3     -2.03914    0.36186  -5.635 1.75e-08 ***
## Sexmale     -2.57536    0.23293 -11.057  < 2e-16 ***
## Agec2       -0.99272    0.30350  -3.271  0.00107 **
## Agec3       -0.71172    0.33401  -2.131  0.03310 *
## Agec4       -1.56704    0.37676  -4.159 3.19e-05 ***
## SibSp       -0.36164    0.13925  -2.597  0.00940 **
## Parch       -0.06057    0.12712  -0.476  0.63374
## Fare         0.13488    0.16149   0.835  0.40360
## EmbarkedQ    0.46524    0.44861   1.037  0.29970
```

```
## EmbarkedS   -0.23584    0.28594  -0.825  0.40949
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 832.49  on 624  degrees of freedom
## Residual deviance: 569.16  on 613  degrees of freedom
## AIC: 593.16
##
## Number of Fisher Scoring iterations: 5
```

From above model we can say that Columns “Parch” and “Fare” are insignificant variables as they have quite high p-values

```
training_set$Parch<-NULL
training_set$Fare<-NULL
testing_set$Parch<-NULL
testing_set$Fare<-NULL
```

Running model again as we have now removed both “Parch” & “Fare” variables

```
titanic_model<-glm(Survived~.,data = training_set,family = "binomial")
summary(titanic_model)

##
## Call:
## glm(formula = Survived ~ ., family = "binomial", data = training_set)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.0683  -0.7102  -0.4074   0.6652   2.4943
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   3.4057     0.4304   7.914 2.50e-15 ***
## Pclass2      -0.9715     0.3136  -3.098  0.00195 **
## Pclass3      -2.2169     0.2971  -7.462 8.53e-14 ***
## Sexmale      -2.5675     0.2285 -11.237  < 2e-16 ***
## Agec2        -0.9744     0.3002  -3.246  0.00117 **
## Agec3        -0.6977     0.3333  -2.093  0.03632 *
## Agec4        -1.5921     0.3757  -4.238 2.25e-05 ***
## SibSp        -0.3566     0.1285  -2.776  0.00550 **
## EmbarkedQ     0.4650     0.4452   1.045  0.29620
## EmbarkedS    -0.2634     0.2832  -0.930  0.35240
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 832.49  on 624  degrees of freedom
```

```
## Residual deviance: 569.99  on 615  degrees of freedom
## AIC: 589.99
##
## Number of Fisher Scoring iterations: 5
```

Fitting logistic model on training set

```
training_set$predicted_prob<-fitted(titanic_model)
head(training_set)
```

```
## # A tibble: 6 x 7
##   Survived Pclass Sex    Age   SibSp[,1] Embarked predicted_prob
##   <fct>    <fct>  <fct>  <fct>     <dbl> <fct>             <dbl>
## 1 0        3      male   c2        0.433 S                0.0589
## 2 1        3      female c2       -0.474 S                0.530
## 3 1        1      female c3        0.433 S                0.908
## 4 0        3      male   c3       -0.474 S                0.102
## 5 0        3      male   c2       -0.474 Q                0.152
## 6 0        1      male   c4       -0.474 S                0.300
```

Creating and AUC-ROC curve as bydefault threshold is 0.5(probability),So to find best threshold value we use AUC ROC curve, which will not only tell us about accuracy but will also tell us about sensitivity and apecificity

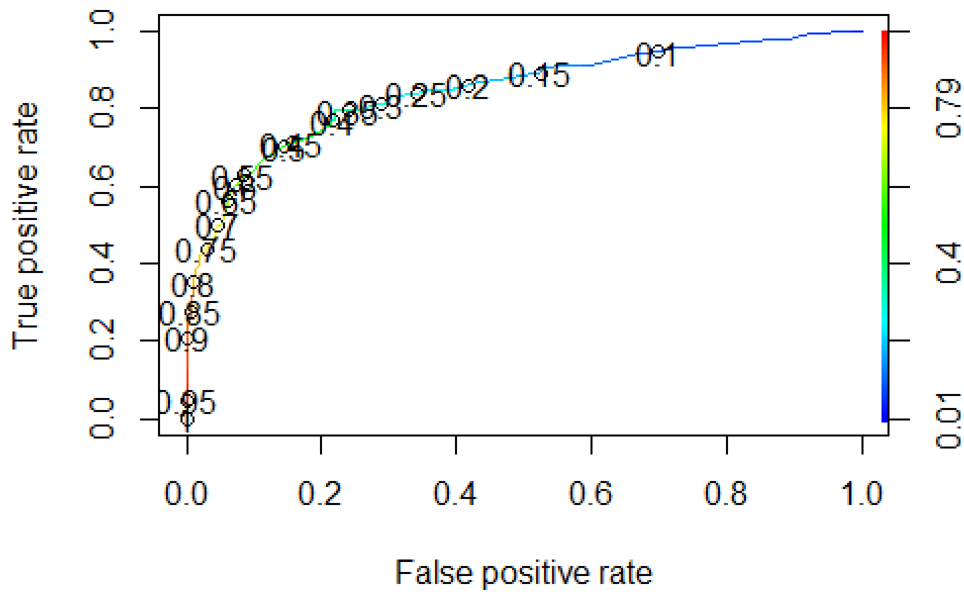
```
library(ROCR)

## Loading required package: gplots

##
## Attaching package: 'gplots'

## The following object is masked from 'package:stats':
##
##     lowess

pred<-prediction(training_set$predicted_prob,training_set$Survived)
perf<-performance(pred,"tpr","fpr")
plot(perf,colorize=T,print.cutoffs.at=seq(0.1,by=0.05))
```



selecting 0.45 threshold as it is giving ggod accuracy and also ratio of sensitivity and specificity are close

```
training_set$predicted_survived<-ifelse(training_set$predicted_prob<0.45,0,1)
head(training_set)

## # A tibble: 6 x 8
##   Survived Pclass Sex   Age   SibSp[,1] Embarked predicted_prob
##   <fct>    <fct>  <fct> <fct>     <dbl> <fct>             <dbl>
## 1 0        3      male  c2        0.433 S                0.0589
## 2 1        3      fema~ c2       -0.474 S                0.530
## 3 1        1      fema~ c3        0.433 S                0.908
## 4 0        3      male  c3       -0.474 S                0.102
## 5 0        3      male  c2       -0.474 Q                0.152
## 6 0        1      male  c4       -0.474 S                0.300
## # ... with 1 more variable: predicted_survived <dbl>
```

creeating confusion matrix Converting "training_set$predicted_survived" to factor as confusion matrix needs both to be factor

```
library(caret)
training_set$predicted_survived <- as.factor(training_set$predicted_survived)
confusionMatrix(training_set$predicted_survived,training_set$Survived)

## Confusion Matrix and Statistics
##
##             Reference
```

```
## Prediction   0   1
##          0 326  70
##          1  59 170
##
##                Accuracy : 0.7936
##                  95% CI : (0.7597, 0.8247)
##     No Information Rate : 0.616
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.5599
##
##  Mcnemar's Test P-Value : 0.3786
##
##             Sensitivity : 0.8468
##             Specificity : 0.7083
##          Pos Pred Value : 0.8232
##          Neg Pred Value : 0.7424
##              Prevalence : 0.6160
##          Detection Rate : 0.5216
##    Detection Prevalence : 0.6336
##       Balanced Accuracy : 0.7775
##
##        'Positive' Class : 0
##
```

Predicting the people survived on test data

```
testing_set$predicted_prob<-predict(titanic_model,testing_set,type =
"response")
testing_set$predicted_survived<-ifelse(testing_set$predicted_prob<0.45,0,1)
table(testing_set$Survived,testing_set$predicted_survived)
```

```
##
##       0   1
##   0 141  23
##   1  26  76
```

```
testing_set$predicted_survived<-as.factor(testing_set$predicted_survived)
confusionMatrix(testing_set$predicted_survived,testing_set$Survived)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0 141  26
##          1  23  76
##
##                Accuracy : 0.8158
##                  95% CI : (0.7639, 0.8605)
##     No Information Rate : 0.6165
##     P-Value [Acc > NIR] : 1.592e-12
```

```
##
##                   Kappa : 0.6082
##
##  Mcnemar's Test P-Value : 0.7751
##
##             Sensitivity : 0.8598
##             Specificity : 0.7451
##          Pos Pred Value : 0.8443
##          Neg Pred Value : 0.7677
##              Prevalence : 0.6165
##          Detection Rate : 0.5301
##    Detection Prevalence : 0.6278
##       Balanced Accuracy : 0.8024
##
##        'Positive' Class : 0
##
```

Preparing data for Random Forest We can use above training set but we will remove columns "Predicted prob" and "predicted_survived"

```
training_set<-training_set[,1:6]
testing_set<-testing_set[,1:6]
```

####Applying Naive Bayes model

```
library(e1071)
model_naive_bayes <-naiveBayes(Survived~.,data = training_set)
pred_naive_bayes<-predict(model_naive_bayes,testing_set)
confusionMatrix(pred_naive_bayes,testing_set$Survived)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0 135  23
##          1  29  79
##
##                Accuracy : 0.8045
##                  95% CI : (0.7517, 0.8504)
##     No Information Rate : 0.6165
##     P-Value [Acc > NIR] : 3.037e-11
##
##                   Kappa : 0.5911
##
##  Mcnemar's Test P-Value : 0.4881
##
##             Sensitivity : 0.8232
##             Specificity : 0.7745
##          Pos Pred Value : 0.8544
##          Neg Pred Value : 0.7315
##              Prevalence : 0.6165
```

```
##          Detection Rate : 0.5075
##    Detection Prevalence : 0.5940
##       Balanced Accuracy : 0.7988
##
##        'Positive' Class : 0
##
```

####Applying Random Forest Model

```r
library(randomForest)
```

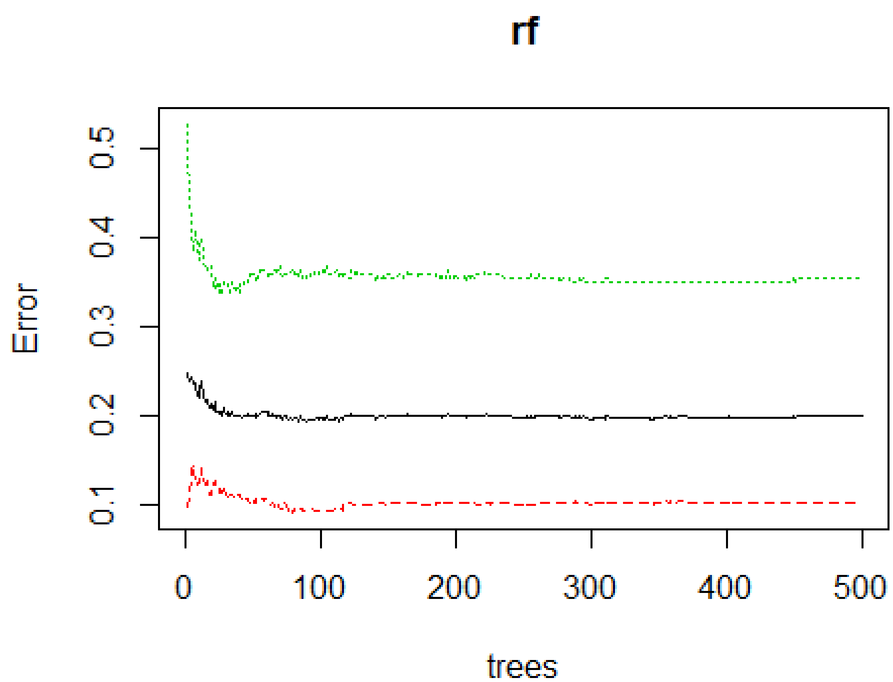
```
## randomForest 4.6-14

## Type rfNews() to see new features/changes/bug fixes.

##
## Attaching package: 'randomForest'

## The following object is masked from 'package:ggplot2':
##
##     margin
```

```r
rf<-randomForest(Survived~.,data = training_set)
plot(rf)
```




```r
pred_test_random_forest<-predict(rf,testing_set)
str(pred_test_random_forest)
```

```
##  Factor w/ 2 levels "0","1": 2 1 2 2 2 1 1 2 1 2 ...
##  - attr(*, "names")= chr [1:266] "1" "2" "3" "4" ...
```

```r
confusionMatrix(pred_test_random_forest,testing_set$Survived)
```

```
## Confusion Matrix and Statistics
## 
##           Reference
## Prediction   0   1
##          0 154  37
##          1  10  65
## 
##                Accuracy : 0.8233
##                  95% CI : (0.7721, 0.8672)
##     No Information Rate : 0.6165
##     P-Value [Acc > NIR] : 1.974e-13
## 
##                   Kappa : 0.6066
## 
##  Mcnemar's Test P-Value : 0.0001491
## 
##             Sensitivity : 0.9390
##             Specificity : 0.6373
##          Pos Pred Value : 0.8063
##          Neg Pred Value : 0.8667
##              Prevalence : 0.6165
##          Detection Rate : 0.5789
##    Detection Prevalence : 0.7180
##       Balanced Accuracy : 0.7881
## 
##        'Positive' Class : 0
## 
```

Conclusion 1. As we can we get the best accuracy from random forest model with very high sensitivity as compared to specificity. (Acc = 82.33%) 2. We also get a very good accuracy of naive bayes model which has its sensitivity very close to specificity. 3. Now it depends on us which model we want to select according to the requirement.If we want a high sensitivity model then we will go for Random forest else we will go for naive bayes model.