code.R

```r
#Download the data
data <- read.csv("C:/Users/Acer_302/Downloads//heart.csv")

#See the provided data
str(data)
```

```
## 'data.frame':    303 obs. of  14 variables:
##  $ п.їage  : int  63 37 41 56 57 57 56 44 52 57 ...
##  $ sex     : int  1 1 0 1 0 1 0 1 1 1 ...
##  $ cp      : int  3 2 1 1 0 0 1 1 2 2 ...
##  $ trestbps: int  145 130 130 120 120 140 140 120 172 150 ...
##  $ chol    : int  233 250 204 236 354 192 294 263 199 168 ...
##  $ fbs     : int  1 0 0 0 0 0 0 0 1 0 ...
##  $ restecg : int  0 1 0 1 1 1 0 1 1 1 ...
##  $ thalach : int  150 187 172 178 163 148 153 173 162 174 ...
##  $ exang   : int  0 0 0 0 1 0 0 0 0 0 ...
##  $ oldpeak : num  2.3 3.5 1.4 0.8 0.6 0.4 1.3 0 0.5 1.6 ...
##  $ slope   : int  0 0 2 2 2 1 1 2 2 2 ...
##  $ ca      : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ thal    : int  1 2 2 2 2 1 2 3 3 2 ...
##  $ target  : int  1 1 1 1 1 1 1 1 1 1 ...
```

```r
#Change name to more understandable
names(data)[1] <- "age"

#In my analysis I well use all 14 of provided variables
#Change the class of target variable to factor
data$target <- as.factor(data$target)

# Dealing with NAs
colSums(is.na(data))
```

```
##      age      sex       cp trestbps     chol      fbs  restecg  thalach
##        0        0        0        0        0        0        0        0
##    exang  oldpeak    slope       ca     thal   target
##        0        0        0        0        0        0
```

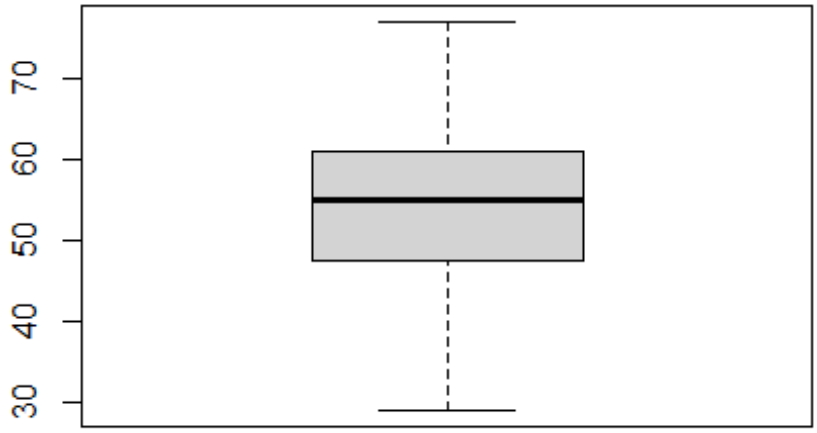
```r
#There are no NAs in the data

#Is the data imbalanced
table(data$target)
```

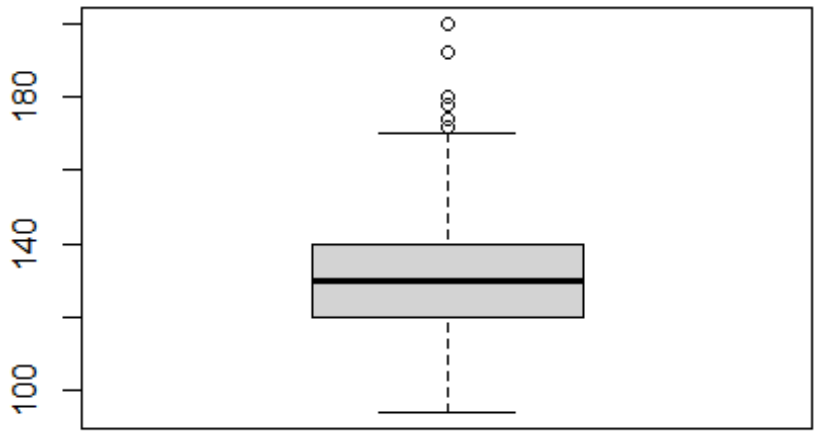
```
##
##   0   1
## 138 165
```

```r
#No, data is well balanced
```

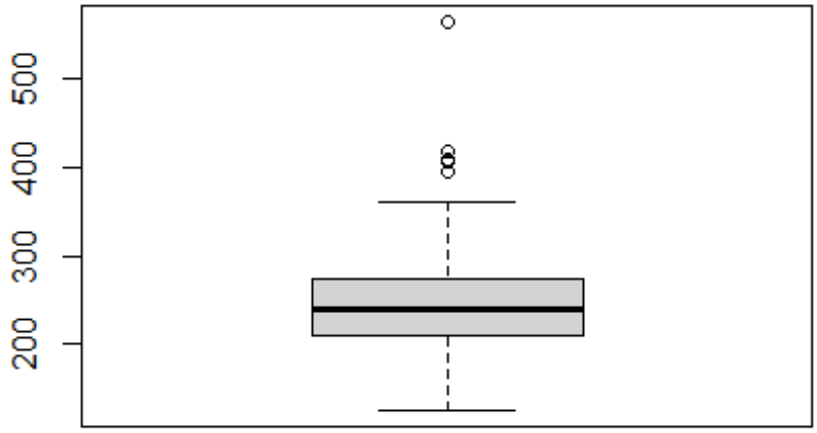
```r
#Check for outliers:
boxplot(data$age)
```



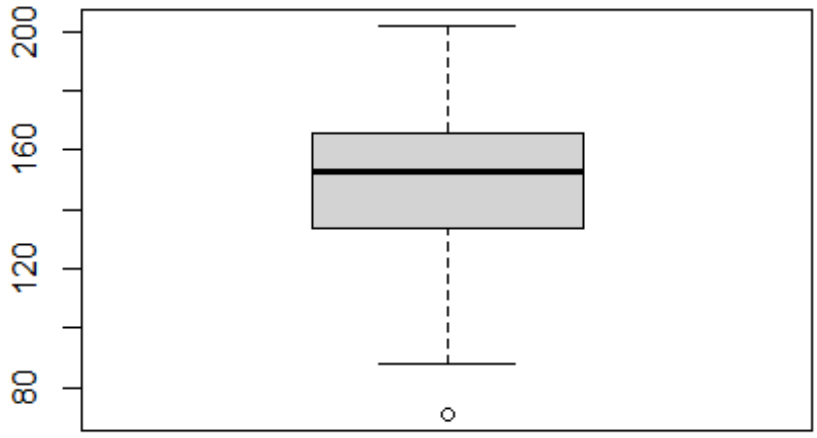

```r
boxplot(data$trestbps)
```




```r
boxplot(data$chol)
```



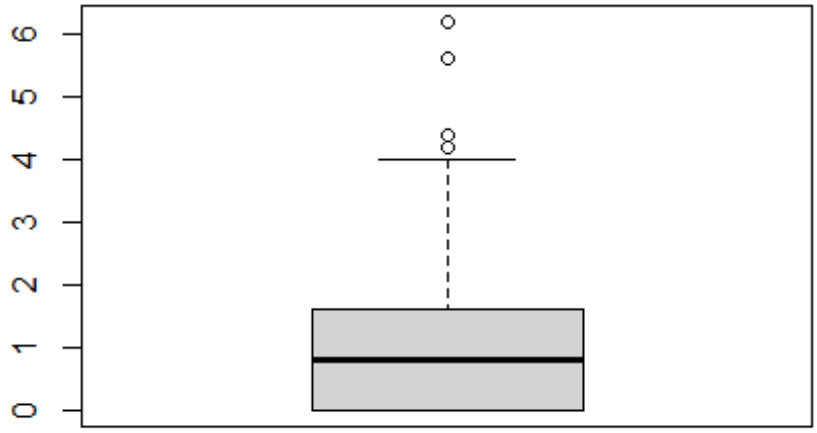

```r
boxplot(data$thalach)
```




```r
boxplot(data$oldpeak)

#There some outliers in these variables: trestbps, chol, thalach, oldpeak
```

```r
#Handling the outliers
library("DescTools")
```




```r
data$trestbps <- Winsorize(data$trestbps)
data$chol <- Winsorize(data$chol)
data$thalach <- Winsorize(data$thalach)
data$oldpeak <- Winsorize(data$oldpeak)

#Splitting the data into training and tasting sets
set.seed(111)
index_train = sample(1:nrow(data), 2 / 3 * nrow(data))
training_set = data[index_train, ]
test_set = data[-index_train, ]

#Estimating the logistic model
logmodel <-  glm(target ~ ., family = binomial(link = "logit"), data =
training_set)
summary(logmodel)

##
## Call:
## glm(formula = target ~ ., family = binomial(link = "logit"),
##     data = training_set)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.7578  -0.2917   0.1533   0.5644   2.6138
##
## Coefficients:
```

```
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.293861   3.586045   0.640 0.522391
## age          0.006564   0.029331   0.224 0.822907
## sex         -1.484051   0.589986  -2.515 0.011890 *
## cp           1.033245   0.263891   3.915 9.02e-05 ***
## trestbps    -0.022559   0.015832  -1.425 0.154189
## chol        -0.002585   0.005918  -0.437 0.662291
## fbs         -0.454689   0.666443  -0.682 0.495072
## restecg      0.239588   0.456064   0.525 0.599348
## thalach      0.028315   0.014613   1.938 0.052653 .
## exang       -0.857012   0.527883  -1.623 0.104485
## oldpeak     -0.835458   0.288897  -2.892 0.003829 **
## slope        0.544995   0.448186   1.216 0.223984
## ca          -0.906069   0.237254  -3.819 0.000134 ***
## thal        -0.986862   0.379433  -2.601 0.009298 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 278.05  on 201  degrees of freedom
## Residual deviance: 131.67  on 188  degrees of freedom
## AIC: 159.67
##
## Number of Fisher Scoring iterations: 6
```

```
#Prediction with the cutoff point equals 0.3
test_set$log_pred = predict(logmodel, newdata = test_set, type = 'response')
test_set$log_pred = ifelse(test_set$log_pred < 0.3, 0, 1)

#Evaluating the quality of the model (confusion matrix)
library('caret')
```

```
## Loading required package: lattice
```

```
## Loading required package: ggplot2
```

```
##
## Attaching package: 'caret'
```

```
## The following objects are masked from 'package:DescTools':
##
##     MAE, RMSE
```

```
test_set$target = factor(test_set$target)
test_set$log_pred = factor(test_set$log_pred)
mat1 <-  confusionMatrix(test_set$log_pred, test_set$target)
mat1
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  0  1
##          0 31  5
```

```
##          1 16 49
##
##                Accuracy : 0.7921
##                  95% CI : (0.6999, 0.8664)
##     No Information Rate : 0.5347
##     P-Value [Acc > NIR] : 6.755e-08
##
##                   Kappa : 0.5757
##
##  Mcnemar's Test P-Value : 0.0291
##
##             Sensitivity : 0.6596
##             Specificity : 0.9074
##          Pos Pred Value : 0.8611
##          Neg Pred Value : 0.7538
##              Prevalence : 0.4653
##          Detection Rate : 0.3069
##    Detection Prevalence : 0.3564
##       Balanced Accuracy : 0.7835
##
##        'Positive' Class : 0
##
```

```
#Evaluating the quality of the model (AUC)
library(pROC)
```

```
## Type 'citation("pROC")' for a citation.
```

```
##
## Attaching package: 'pROC'
```

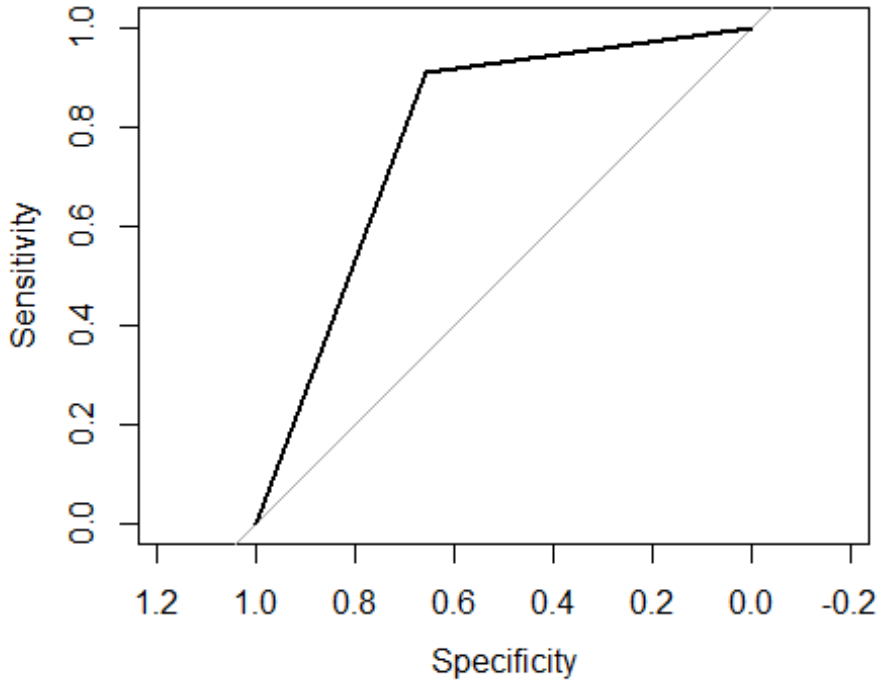
```
## The following objects are masked from 'package:stats':
##
##     cov, smooth, var
```

```
ROC_log1 = roc(as.numeric(test_set$target), as.numeric(test_set$log_pred))
```

```
## Setting levels: control = 1, case = 2
```

```
## Setting direction: controls < cases
```

```
plot(ROC_log1)
```




```
auc(ROC_log1)
```

```
## Area under the curve: 0.7835
```

```
#choice of the cutoff
library(e1071)
library(tidyr)
cutoffs_vec = c()
accur_vec = c()
sens_vec = c()
spec_vec = c()

test_set$log_pred = predict(logmodel, newdata = test_set, type = 'response')
for (i in seq(0, 1, by = 0.05)) {
  print(i)
  cutoffs_vec = c(cutoffs_vec, i)
  test_set$cutoff2 = ifelse(test_set$log_pred < i, 0, 1)
  test_set$cutoff2 = factor(test_set$cutoff2)
  mat1 = confusionMatrix(test_set$cutoff2, test_set$target)
  accur_vec = c(accur_vec, mat1$overall[3])
  sens_vec = c(sens_vec, mat1$byClass[1])
  spec_vec = c(spec_vec, mat1$byClass[2])

}
```

```
## [1] 0
```

```
## Warning in confusionMatrix.default(test_set$cutoff2, test_set$target): Levels
## are not in the same order for reference and data. Refactoring data to match.
```

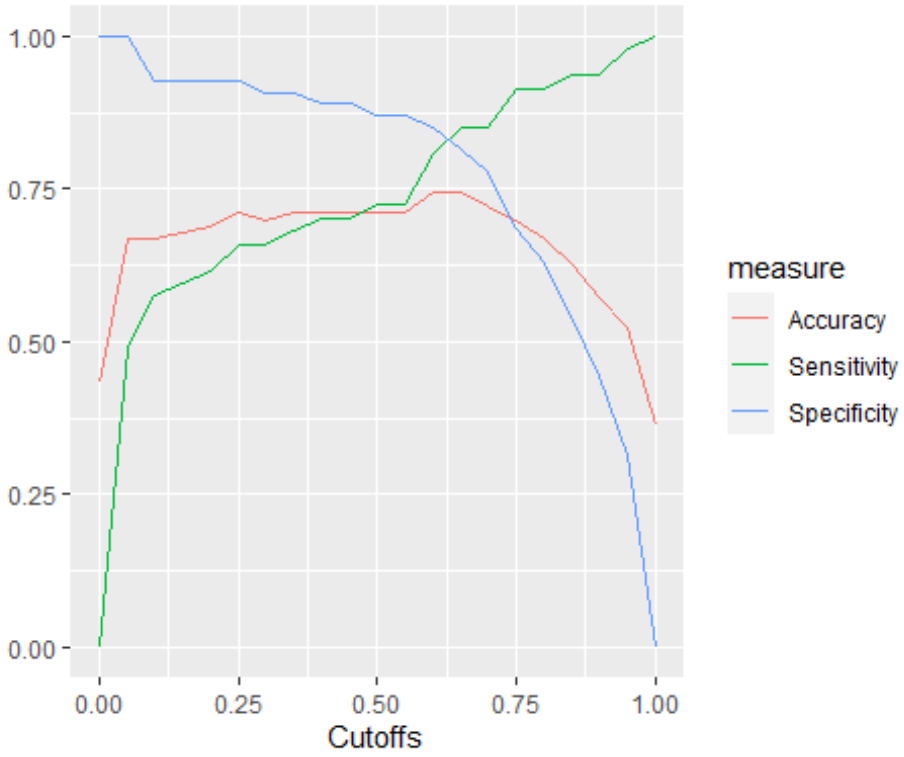
```
## [1] 0.05
## [1] 0.1
## [1] 0.15
## [1] 0.2
## [1] 0.25
## [1] 0.3
## [1] 0.35
## [1] 0.4
## [1] 0.45
## [1] 0.5
## [1] 0.55
## [1] 0.6
## [1] 0.65
## [1] 0.7
## [1] 0.75
## [1] 0.8
## [1] 0.85
## [1] 0.9
## [1] 0.95
## [1] 1

## Warning in confusionMatrix.default(test_set$cutoff2, test_set$target): Levels
## are not in the same order for reference and data. Refactoring data to match.
```

```
d_loop = data.frame(cutoffs_vec, accur_vec, sens_vec, spec_vec)
d_loop_long = gather(d_loop, key = measure, value = value, -cutoffs_vec)
d_loop_long$measure = factor(d_loop_long$measure, levels=c("accur_vec",
"sens_vec", "spec_vec"),

                             labels=c("Accuracy", "Sensitivity", "Specificity"))

ggplot(data = d_loop_long, aes(x = cutoffs_vec, y = value, col = measure)) +
  geom_line() +
  xlab("Cutoffs") +
  ylab("")
```




```r
#According to the graph, the best cutoff point is equal 0.625
test_set$log_pred2 = predict(logmodel, newdata = test_set, type = 'response')
test_set$log_pred2 = ifelse(test_set$log_pred2 < 0.625, 0, 1)


#Evaluating the quality of the model with new cutoff point (confusion matrix)
test_set$target = factor(test_set$target)
test_set$log_pred2 = factor(test_set$log_pred2)
mat2 <-  confusionMatrix(test_set$log_pred2, test_set$target)
mat2
```

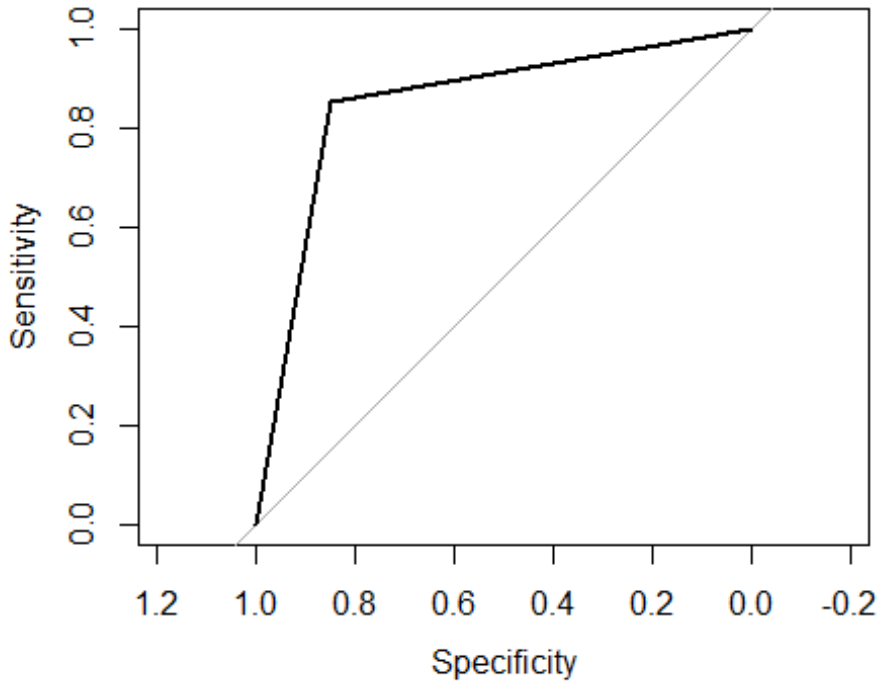
```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  0  1
##          0 40  8
##          1  7 46
##
##                Accuracy : 0.8515
##                  95% CI : (0.7669, 0.9144)
##     No Information Rate : 0.5347
##     P-Value [Acc > NIR] : 1.579e-11
##
##                   Kappa : 0.7019
##
##  Mcnemar's Test P-Value : 1
##
##             Sensitivity : 0.8511
##             Specificity : 0.8519
```

```
##          Pos Pred Value : 0.8333
##          Neg Pred Value : 0.8679
##              Prevalence : 0.4653
##          Detection Rate : 0.3960
##    Detection Prevalence : 0.4752
##       Balanced Accuracy : 0.8515
##
##        'Positive' Class : 0
##
```

```
#Evaluating the quality of the model with new cutoff point (AUC)
ROC_log2 = roc(as.numeric(test_set$target), as.numeric(test_set$log_pred2))
```

```
## Setting levels: control = 1, case = 2
## Setting direction: controls < cases
```

```
plot(ROC_log2)
```




```
auc(ROC_log2)
```

```
## Area under the curve: 0.8515
```

```
#Random forest without cross validation
rf_tt = train(target ~ ., method= "rf", ntree = 100, data = training_set)
test_set$rf_tt <- predict(rf_tt, test_set)

#Evaluating the quality of the model (confusion matrix)
test_set$target = factor(test_set$target)
test_set$rf_tt = factor(test_set$rf_tt)
```

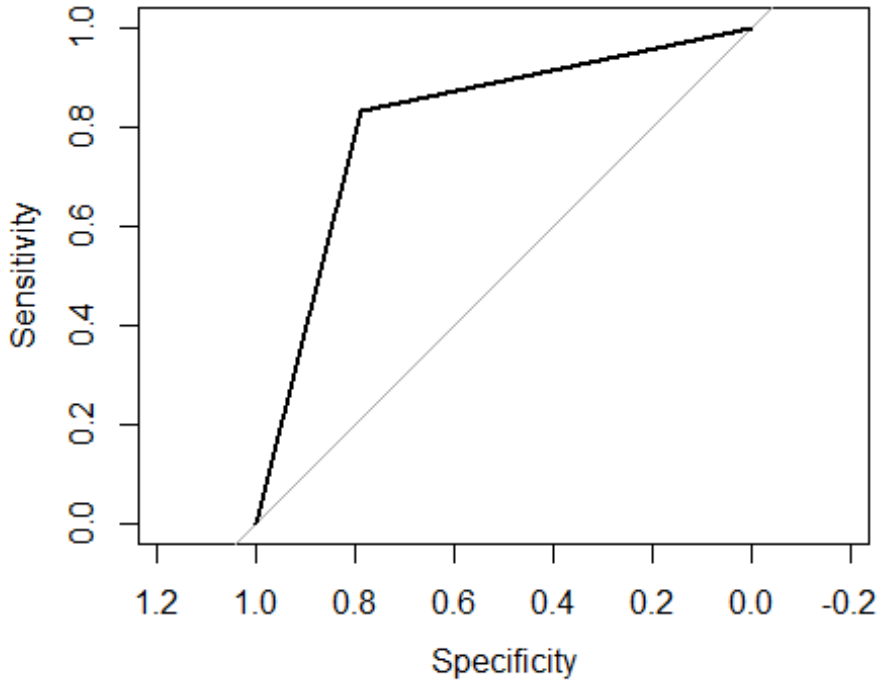
```r
mat3 <-  confusionMatrix(test_set$rf_tt, test_set$target)
mat3
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  0  1
##          0 37  9
##          1 10 45
##
##                Accuracy : 0.8119
##                  95% CI : (0.7219, 0.8828)
##     No Information Rate : 0.5347
##     P-Value [Acc > NIR] : 5.384e-09
##
##                   Kappa : 0.6214
##
##  Mcnemar's Test P-Value : 1
##
##             Sensitivity : 0.7872
##             Specificity : 0.8333
##          Pos Pred Value : 0.8043
##          Neg Pred Value : 0.8182
##              Prevalence : 0.4653
##          Detection Rate : 0.3663
##    Detection Prevalence : 0.4554
##       Balanced Accuracy : 0.8103
##
##        'Positive' Class : 0
##
```

```r
#Evaluating the quality of the model (AUC)
ROC_rf_tt = roc(test_set$target, as.numeric(test_set$rf_tt))
```

```
## Setting levels: control = 0, case = 1
## Setting direction: controls < cases
```

```r
plot(ROC_rf_tt)
```




```
auc(ROC_rf_tt)
```

```
## Area under the curve: 0.8103
```

```
#Random forest with cross validation
train.control = trainControl(method = "cv", number = 5)
rf_cv = train(target ~ ., method= "rf", ntree = 50, data = data, trControl =
train.control)
data$rf_cv_pred <- predict(rf_cv, data)

#Evaluating the quality of the model (confusion matrix)
data$target = factor(data$target)
data$rf_cv_pred = factor(data$rf_cv_pred)
mat4 <-  confusionMatrix(data$rf_cv_pred, data$target)
mat4
```

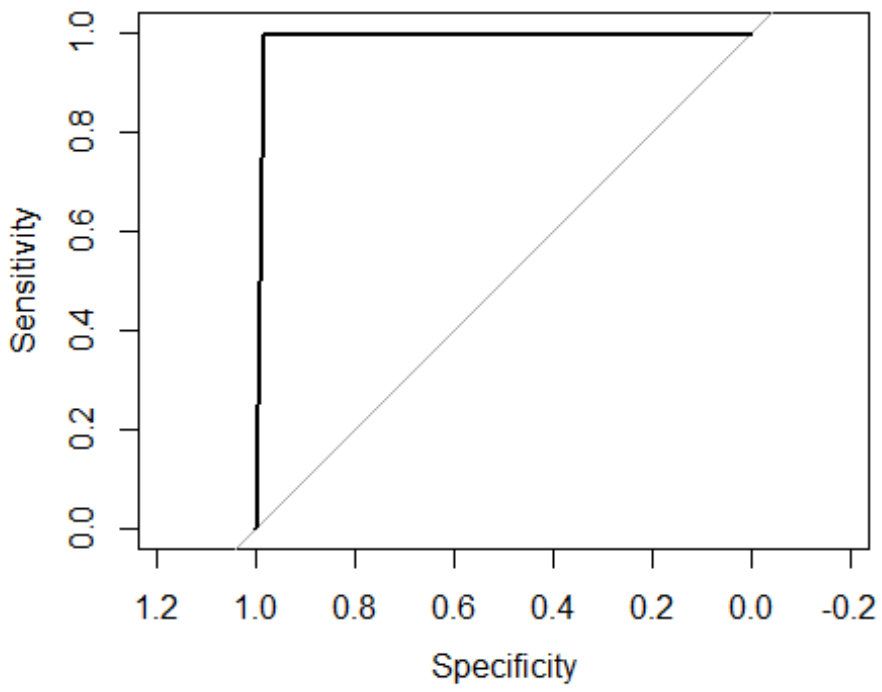
```
## Confusion Matrix and Statistics
##
##            Reference
## Prediction   0   1
##          0 136   1
##          1   2 164
##
##                Accuracy : 0.9901
##                  95% CI : (0.9713, 0.998)
##     No Information Rate : 0.5446
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.98
```

```
##
##  Mcnemar's Test P-Value : 1
##
##             Sensitivity : 0.9855
##             Specificity : 0.9939
##          Pos Pred Value : 0.9927
##          Neg Pred Value : 0.9880
##              Prevalence : 0.4554
##          Detection Rate : 0.4488
##    Detection Prevalence : 0.4521
##       Balanced Accuracy : 0.9897
##
##        'Positive' Class : 0
##
```

```
#Evaluating the quality of the model (AUC)
ROC_rf_cv_pred = roc(data$target, as.numeric(data$rf_cv_pred))
```

```
## Setting levels: control = 0, case = 1
## Setting direction: controls < cases
```

```
plot(ROC_rf_cv_pred)
```




```
auc(ROC_rf_cv_pred)
```

```
## Area under the curve: 0.9897
```