Project 2

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library(mlbench)

#Data

data(BreastCancer)  
ls(BreastCancer)

## [1] "Bare.nuclei" "Bl.cromatin" "Cell.shape" "Cell.size"   
## [5] "Cl.thickness" "Class" "Epith.c.size" "Id"   
## [9] "Marg.adhesion" "Mitoses" "Normal.nucleoli"

#libraries

library(e1071)  
library(klaR)

## Loading required package: MASS

library(nnet)  
library(MASS)  
library(rpart)  
library(randomForest)

## randomForest 4.7-1.1

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

library(caret)

## Loading required package: ggplot2

##   
## Attaching package: 'ggplot2'

## The following object is masked from 'package:randomForest':  
##   
## margin

## Loading required package: lattice

summary(BreastCancer)

## Id Cl.thickness Cell.size Cell.shape Marg.adhesion  
## Length:699 1 :145 1 :384 1 :353 1 :407   
## Class :character 5 :130 10 : 67 2 : 59 2 : 58   
## Mode :character 3 :108 3 : 52 10 : 58 3 : 58   
## 4 : 80 2 : 45 3 : 56 10 : 55   
## 10 : 69 4 : 40 4 : 44 4 : 33   
## 2 : 50 5 : 30 5 : 34 8 : 25   
## (Other):117 (Other): 81 (Other): 95 (Other): 63   
## Epith.c.size Bare.nuclei Bl.cromatin Normal.nucleoli Mitoses   
## 2 :386 1 :402 2 :166 1 :443 1 :579   
## 3 : 72 10 :132 3 :165 10 : 61 2 : 35   
## 4 : 48 2 : 30 1 :152 3 : 44 3 : 33   
## 1 : 47 5 : 30 7 : 73 2 : 36 10 : 14   
## 6 : 41 3 : 28 4 : 40 8 : 24 4 : 12   
## 5 : 39 (Other): 61 5 : 34 6 : 22 7 : 9   
## (Other): 66 NA's : 16 (Other): 69 (Other): 69 (Other): 17   
## Class   
## benign :458   
## malignant:241   
##   
##   
##   
##   
##

BreastCancer <- na.omit(BreastCancer)   
  
BreastCancer$Id <- NULL   
head(BreastCancer)

## Cl.thickness Cell.size Cell.shape Marg.adhesion Epith.c.size Bare.nuclei  
## 1 5 1 1 1 2 1  
## 2 5 4 4 5 7 10  
## 3 3 1 1 1 2 2  
## 4 6 8 8 1 3 4  
## 5 4 1 1 3 2 1  
## 6 8 10 10 8 7 10  
## Bl.cromatin Normal.nucleoli Mitoses Class  
## 1 3 1 1 benign  
## 2 3 2 1 benign  
## 3 3 1 1 benign  
## 4 3 7 1 benign  
## 5 3 1 1 benign  
## 6 9 7 1 malignant

str(BreastCancer)

## 'data.frame': 683 obs. of 10 variables:  
## $ Cl.thickness : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<..: 5 5 3 6 4 8 1 2 2 4 ...  
## $ Cell.size : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<..: 1 4 1 8 1 10 1 1 1 2 ...  
## $ Cell.shape : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<..: 1 4 1 8 1 10 1 2 1 1 ...  
## $ Marg.adhesion : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<..: 1 5 1 1 3 8 1 1 1 1 ...  
## $ Epith.c.size : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<..: 2 7 2 3 2 7 2 2 2 2 ...  
## $ Bare.nuclei : Factor w/ 10 levels "1","2","3","4",..: 1 10 2 4 1 10 10 1 1 1 ...  
## $ Bl.cromatin : Factor w/ 10 levels "1","2","3","4",..: 3 3 3 3 3 9 3 3 1 2 ...  
## $ Normal.nucleoli: Factor w/ 10 levels "1","2","3","4",..: 1 2 1 7 1 7 1 1 1 1 ...  
## $ Mitoses : Factor w/ 9 levels "1","2","3","4",..: 1 1 1 1 1 1 1 1 5 1 ...  
## $ Class : Factor w/ 2 levels "benign","malignant": 1 1 1 1 1 2 1 1 1 1 ...  
## - attr(\*, "na.action")= 'omit' Named int [1:16] 24 41 140 146 159 165 236 250 276 293 ...  
## ..- attr(\*, "names")= chr [1:16] "24" "41" "140" "146" ...

df2 <- data.frame(sapply(BreastCancer[1:9], function(x) as.numeric(as.character(x))))  
z <- scale(df2[,1:9],center=TRUE,scale=TRUE)  
head(z)

## Cl.thickness Cell.size Cell.shape Marg.adhesion Epith.c.size Bare.nuclei  
## [1,] 0.1977598 -0.7016978 -0.7412304 -0.63889730 -0.5552016 -0.6983413  
## [2,] 0.1977598 0.2770488 0.2625905 0.75747664 1.6939247 1.7715689  
## [3,] -0.5112687 -0.7016978 -0.7412304 -0.63889730 -0.5552016 -0.4239068  
## [4,] 0.5522740 1.5820442 1.6010185 -0.63889730 -0.1053763 0.1249621  
## [5,] -0.1567545 -0.7016978 -0.7412304 0.05928967 -0.5552016 -0.6983413  
## [6,] 1.2613024 2.2345419 2.2702324 1.80475710 1.6939247 1.7715689  
## Bl.cromatin Normal.nucleoli Mitoses  
## [1,] -0.181694 -0.6124785 -0.3481446  
## [2,] -0.181694 -0.2848960 -0.3481446  
## [3,] -0.181694 -0.6124785 -0.3481446  
## [4,] -0.181694 1.3530163 -0.3481446  
## [5,] -0.181694 -0.6124785 -0.3481446  
## [6,] 2.267589 1.3530163 -0.3481446

set.seed(2)  
index <- createDataPartition(BreastCancer$Class, p =0.7, list = FALSE)  
bc\_train <- BreastCancer[index,]  
bc\_valid <- BreastCancer[-index,]

#Naive Bayes

mynb <- NaiveBayes(Class ~ ., bc\_train, usekernel = TRUE)  
mynb.pred <- predict(mynb,bc\_valid)

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 2

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 4

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 5

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 14

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 15

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 17

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 18

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 19

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 23

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 26

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 30

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 31

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 32

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 39

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 49

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 50

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 53

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 56

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 57

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 67

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 69

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 70

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 73

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 77

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 82

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 83

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 88

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 90

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 93

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 97

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 101

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 114

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 118

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 131

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 134

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 141

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 143

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 146

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 165

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 166

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 180

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 189

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 201

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 204

#head(mynb.pred$class)  
table(mynb.pred$class,bc\_valid$Class)

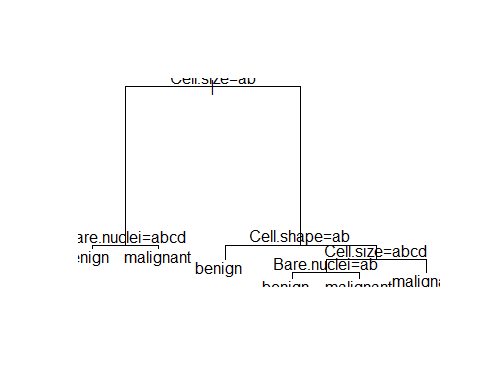
##   
## benign malignant  
## benign 132 0  
## malignant 1 71

str(mynb.pred)

## List of 2  
## $ class : Factor w/ 2 levels "benign","malignant": 1 2 1 2 2 2 1 1 1 1 ...  
## ..- attr(\*, "names")= chr [1:204] "5" "6" "11" "13" ...  
## $ posterior: num [1:204, 1:2] 1.00 4.35e-13 1.00 3.47e-02 1.61e-12 ...  
## ..- attr(\*, "dimnames")=List of 2  
## .. ..$ : chr [1:204] "5" "6" "11" "13" ...  
## .. ..$ : chr [1:2] "benign" "malignant"

#Decision trees

mytree <- rpart(Class ~ ., bc\_train)  
plot(mytree); text(mytree)



summary(mytree)

## Call:  
## rpart(formula = Class ~ ., data = bc\_train)  
## n= 479   
##   
## CP nsplit rel error xerror xstd  
## 1 0.77380952 0 1.0000000 1.0000000 0.06216670  
## 2 0.04761905 1 0.2261905 0.2559524 0.03723921  
## 3 0.01488095 2 0.1785714 0.2023810 0.03345357  
## 4 0.01190476 4 0.1488095 0.2083333 0.03390381  
## 5 0.01000000 5 0.1369048 0.2023810 0.03345357  
##   
## Variable importance  
## Cell.size Cell.shape Bare.nuclei Epith.c.size Bl.cromatin   
## 21 18 16 16 15   
## Normal.nucleoli   
## 14   
##   
## Node number 1: 479 observations, complexity param=0.7738095  
## predicted class=benign expected loss=0.3507307 P(node) =1  
## class counts: 311 168  
## probabilities: 0.649 0.351   
## left son=2 (289 obs) right son=3 (190 obs)  
## Primary splits:  
## Cell.size splits as LLRRRRRRRR, improve=152.0711, (0 missing)  
## Cell.shape splits as LLLRRRRRRR, improve=144.9658, (0 missing)  
## Bare.nuclei splits as LLRRRRRRRR, improve=142.8998, (0 missing)  
## Epith.c.size splits as LLRRRRRRRR, improve=133.1530, (0 missing)  
## Bl.cromatin splits as LLLRRRRRRR, improve=130.1807, (0 missing)  
## Surrogate splits:  
## Cell.shape splits as LLRRRRRRRR, agree=0.912, adj=0.779, (0 split)  
## Epith.c.size splits as LLRRRRRRRR, agree=0.908, adj=0.768, (0 split)  
## Bare.nuclei splits as LLRRRRRRRR, agree=0.879, adj=0.695, (0 split)  
## Bl.cromatin splits as LLLRRRRRRR, agree=0.868, adj=0.668, (0 split)  
## Normal.nucleoli splits as LLRRRRRRRR, agree=0.862, adj=0.653, (0 split)  
##   
## Node number 2: 289 observations, complexity param=0.01190476  
## predicted class=benign expected loss=0.02768166 P(node) =0.6033403  
## class counts: 281 8  
## probabilities: 0.972 0.028   
## left son=4 (277 obs) right son=5 (12 obs)  
## Primary splits:  
## Bare.nuclei splits as LLLLRRR--R, improve=7.730980, (0 missing)  
## Normal.nucleoli splits as LLRR-RRL-R, improve=4.167296, (0 missing)  
## Cl.thickness splits as LLLLLRRRRR, improve=3.193977, (0 missing)  
## Bl.cromatin splits as LLLLR-R---, improve=2.871789, (0 missing)  
## Epith.c.size splits as LLLRRRRRRR, improve=2.581292, (0 missing)  
## Surrogate splits:  
## Bl.cromatin splits as LLLLR-L---, agree=0.972, adj=0.333, (0 split)  
## Normal.nucleoli splits as LLLR-LRL-R, agree=0.969, adj=0.250, (0 split)  
## Cl.thickness splits as LLLLLLLLRR, agree=0.965, adj=0.167, (0 split)  
## Mitoses splits as LLR-L-L--, agree=0.962, adj=0.083, (0 split)  
##   
## Node number 3: 190 observations, complexity param=0.04761905  
## predicted class=malignant expected loss=0.1578947 P(node) =0.3966597  
## class counts: 30 160  
## probabilities: 0.158 0.842   
## left son=6 (18 obs) right son=7 (172 obs)  
## Primary splits:  
## Cell.shape splits as LLRRRRRRRR, improve=12.664560, (0 missing)  
## Cell.size splits as LLLRRRRRRR, improve=12.363640, (0 missing)  
## Bl.cromatin splits as LLRRRRRRRR, improve=12.250450, (0 missing)  
## Bare.nuclei splits as LLRRRRRRRR, improve=11.621530, (0 missing)  
## Cl.thickness splits as LLLLLLRRRR, improve= 9.268454, (0 missing)  
## Surrogate splits:  
## Bl.cromatin splits as LRRRRRRRRR, agree=0.932, adj=0.278, (0 split)  
##   
## Node number 4: 277 observations  
## predicted class=benign expected loss=0.003610108 P(node) =0.5782881  
## class counts: 276 1  
## probabilities: 0.996 0.004   
##   
## Node number 5: 12 observations  
## predicted class=malignant expected loss=0.4166667 P(node) =0.02505219  
## class counts: 5 7  
## probabilities: 0.417 0.583   
##   
## Node number 6: 18 observations  
## predicted class=benign expected loss=0.2777778 P(node) =0.03757829  
## class counts: 13 5  
## probabilities: 0.722 0.278   
##   
## Node number 7: 172 observations, complexity param=0.01488095  
## predicted class=malignant expected loss=0.09883721 P(node) =0.3590814  
## class counts: 17 155  
## probabilities: 0.099 0.901   
## left son=14 (51 obs) right son=15 (121 obs)  
## Primary splits:  
## Cell.size splits as LLLLRRRRRR, improve=4.474570, (0 missing)  
## Bl.cromatin splits as RLLLRLRRRR, improve=3.432143, (0 missing)  
## Cl.thickness splits as LLLLLLRRRR, improve=3.334105, (0 missing)  
## Bare.nuclei splits as LLRRRRRRRR, improve=3.067463, (0 missing)  
## Cell.shape splits as LLLLRRRRRR, improve=2.955286, (0 missing)  
## Surrogate splits:  
## Cell.shape splits as LLLLRRRRRR, agree=0.785, adj=0.275, (0 split)  
## Epith.c.size splits as LLLRRRRRRR, agree=0.756, adj=0.176, (0 split)  
## Bl.cromatin splits as LLLLRLRRRR, agree=0.738, adj=0.118, (0 split)  
## Marg.adhesion splits as LRRRRRRRRR, agree=0.733, adj=0.098, (0 split)  
## Normal.nucleoli splits as RRLRRRRRRR, agree=0.715, adj=0.039, (0 split)  
##   
## Node number 14: 51 observations, complexity param=0.01488095  
## predicted class=malignant expected loss=0.2745098 P(node) =0.1064718  
## class counts: 14 37  
## probabilities: 0.275 0.725   
## left son=28 (11 obs) right son=29 (40 obs)  
## Primary splits:  
## Bare.nuclei splits as LLRRR-RRRR, improve=5.750089, (0 missing)  
## Cl.thickness splits as LLLLLLRRRR, improve=4.610022, (0 missing)  
## Normal.nucleoli splits as LLRRRLLRRR, improve=3.063725, (0 missing)  
## Marg.adhesion splits as LLLRRRRRRR, improve=2.026688, (0 missing)  
## Cell.shape splits as LLLLRRRRRR, improve=1.739191, (0 missing)  
##   
## Node number 15: 121 observations  
## predicted class=malignant expected loss=0.02479339 P(node) =0.2526096  
## class counts: 3 118  
## probabilities: 0.025 0.975   
##   
## Node number 28: 11 observations  
## predicted class=benign expected loss=0.2727273 P(node) =0.02296451  
## class counts: 8 3  
## probabilities: 0.727 0.273   
##   
## Node number 29: 40 observations  
## predicted class=malignant expected loss=0.15 P(node) =0.08350731  
## class counts: 6 34  
## probabilities: 0.150 0.850

mytree.pred <- predict(mytree,bc\_valid,type="class")  
table(mytree.pred,bc\_valid$Class)

##   
## mytree.pred benign malignant  
## benign 129 4  
## malignant 4 67

#Random Forests

myrf <- randomForest(Class ~ ., bc\_train)  
myrf.pred <- predict(myrf, bc\_valid)  
head(myrf.pred)

## 5 6 11 13 15 19   
## benign malignant benign malignant malignant malignant   
## Levels: benign malignant

table(myrf.pred, bc\_valid$Class)

##   
## myrf.pred benign malignant  
## benign 132 1  
## malignant 1 70

#SVM

mysvm <- svm(Class ~ ., bc\_train)  
mysvm.pred <- predict(mysvm, bc\_valid)  
table(mysvm.pred,bc\_valid$Class)

##   
## mysvm.pred benign malignant  
## benign 132 4  
## malignant 1 67

# Leave-1-Out Cross Validation (LOOCV)

ans <- numeric(length(BreastCancer[,1]))  
for (i in 1:length(BreastCancer[,1])) {  
 mytree <- rpart(Class ~ ., BreastCancer[-i,])  
 mytree.pred <- predict(mytree,BreastCancer[i,],type="class")  
 ans[i] <- mytree.pred  
}  
ans <- factor(ans,labels=levels(BreastCancer$Class))  
table(ans,BreastCancer$Class)

##   
## ans benign malignant  
## benign 430 20  
## malignant 14 219

#Regularised Discriminant Analysis

myrda <- rda(Class ~ ., bc\_train)  
myrda.pred <- predict(myrda, bc\_valid)  
table(myrda.pred$class,bc\_valid$Class)

##   
## benign malignant  
## benign 132 1  
## malignant 1 70

combine.classes<-data.frame(myrf.pred, myrda.pred$class,#myqda.pred,   
 mytree.pred,mysvm.pred, mynb.pred$class)  
#,mynnet.pred  
head(combine.classes)

## myrf.pred myrda.pred.class mytree.pred mysvm.pred mynb.pred.class  
## 5 benign benign malignant benign benign  
## 6 malignant malignant malignant malignant malignant  
## 11 benign benign malignant benign benign  
## 13 malignant malignant malignant benign malignant  
## 15 malignant malignant malignant malignant malignant  
## 19 malignant malignant malignant malignant malignant

head(myrf.pred)

## 5 6 11 13 15 19   
## benign malignant benign malignant malignant malignant   
## Levels: benign malignant

head(myrda.pred)

## $class  
## [1] benign malignant benign malignant malignant malignant benign   
## [8] benign benign benign benign benign malignant malignant  
## [15] malignant benign malignant malignant malignant benign benign   
## [22] malignant malignant malignant benign malignant benign benign   
## [29] benign benign malignant malignant malignant benign benign   
## [36] benign benign malignant malignant benign benign malignant  
## [43] benign benign benign malignant benign benign malignant  
## [50] malignant benign benign malignant malignant benign malignant  
## [57] malignant benign benign benign malignant benign benign   
## [64] benign malignant benign malignant benign malignant malignant  
## [71] benign malignant malignant malignant benign malignant malignant  
## [78] benign malignant benign malignant malignant malignant malignant  
## [85] benign benign benign malignant benign malignant malignant  
## [92] benign malignant benign benign benign malignant benign   
## [99] benign benign malignant benign malignant benign benign   
## [106] benign benign benign benign benign benign benign   
## [113] benign malignant benign benign benign malignant benign   
## [120] benign benign malignant benign benign benign malignant  
## [127] benign benign benign benign malignant benign benign   
## [134] malignant benign benign benign benign benign benign   
## [141] benign benign malignant benign malignant malignant benign   
## [148] benign benign benign benign benign benign benign   
## [155] benign benign benign benign malignant benign benign   
## [162] benign benign benign malignant malignant benign benign   
## [169] benign benign malignant malignant benign malignant benign   
## [176] benign benign benign benign malignant benign malignant  
## [183] benign benign benign benign benign benign malignant  
## [190] benign benign benign benign benign benign malignant  
## [197] benign benign malignant benign malignant benign benign   
## [204] malignant  
## Levels: benign malignant  
##   
## $posterior  
## benign malignant  
## [1,] 1.000000e+00 6.745613e-23  
## [2,] 7.769408e-48 1.000000e+00  
## [3,] 1.000000e+00 7.774775e-26  
## [4,] 4.233732e-07 9.999996e-01  
## [5,] 3.575310e-72 1.000000e+00  
## [6,] 7.927987e-40 1.000000e+00  
## [7,] 1.000000e+00 8.387964e-21  
## [8,] 1.000000e+00 4.588244e-28  
## [9,] 1.000000e+00 8.821611e-25  
## [10,] 1.000000e+00 2.731057e-23  
## [11,] 1.000000e+00 1.392686e-26  
## [12,] 1.000000e+00 3.230274e-27  
## [13,] 9.163116e-45 1.000000e+00  
## [14,] 4.600660e-27 1.000000e+00  
## [15,] 3.916899e-31 1.000000e+00  
## [16,] 1.000000e+00 6.745613e-23  
## [17,] 1.005228e-36 1.000000e+00  
## [18,] 7.884243e-34 1.000000e+00  
## [19,] 1.116285e-26 1.000000e+00  
## [20,] 1.000000e+00 3.666036e-26  
## [21,] 1.000000e+00 7.244588e-24  
## [22,] 2.238771e-21 1.000000e+00  
## [23,] 6.185560e-65 1.000000e+00  
## [24,] 4.388199e-48 1.000000e+00  
## [25,] 1.000000e+00 7.039225e-21  
## [26,] 5.279551e-40 1.000000e+00  
## [27,] 1.000000e+00 3.607941e-25  
## [28,] 1.000000e+00 7.244588e-24  
## [29,] 1.000000e+00 9.141657e-26  
## [30,] 9.927651e-01 7.234935e-03  
## [31,] 1.996536e-07 9.999998e-01  
## [32,] 8.677154e-44 1.000000e+00  
## [33,] 2.594901e-25 1.000000e+00  
## [34,] 1.000000e+00 6.300401e-17  
## [35,] 1.000000e+00 9.382109e-21  
## [36,] 1.000000e+00 6.584551e-27  
## [37,] 1.000000e+00 2.839967e-24  
## [38,] 9.782672e-35 1.000000e+00  
## [39,] 3.469387e-67 1.000000e+00  
## [40,] 1.000000e+00 3.666036e-26  
## [41,] 1.000000e+00 2.777451e-22  
## [42,] 7.446110e-36 1.000000e+00  
## [43,] 1.000000e+00 1.415039e-18  
## [44,] 1.000000e+00 8.991208e-25  
## [45,] 1.000000e+00 1.258785e-20  
## [46,] 1.346904e-13 1.000000e+00  
## [47,] 1.000000e+00 2.229113e-26  
## [48,] 1.000000e+00 9.141657e-26  
## [49,] 5.142864e-70 1.000000e+00  
## [50,] 2.372395e-43 1.000000e+00  
## [51,] 1.000000e+00 9.141657e-26  
## [52,] 1.000000e+00 7.244588e-24  
## [53,] 1.100451e-47 1.000000e+00  
## [54,] 2.113051e-56 1.000000e+00  
## [55,] 1.000000e+00 1.157579e-24  
## [56,] 6.468334e-45 1.000000e+00  
## [57,] 6.639050e-51 1.000000e+00  
## [58,] 1.000000e+00 3.111527e-23  
## [59,] 1.000000e+00 1.157579e-24  
## [60,] 1.000000e+00 6.416866e-25  
## [61,] 1.439269e-47 1.000000e+00  
## [62,] 1.000000e+00 3.666036e-26  
## [63,] 1.000000e+00 1.157579e-24  
## [64,] 1.000000e+00 1.276108e-18  
## [65,] 3.637210e-43 1.000000e+00  
## [66,] 1.000000e+00 3.666036e-26  
## [67,] 5.984758e-47 1.000000e+00  
## [68,] 1.000000e+00 1.037274e-10  
## [69,] 3.222397e-57 1.000000e+00  
## [70,] 5.985151e-55 1.000000e+00  
## [71,] 1.000000e+00 6.354900e-23  
## [72,] 5.524128e-30 1.000000e+00  
## [73,] 1.096163e-29 1.000000e+00  
## [74,] 1.284144e-19 1.000000e+00  
## [75,] 1.000000e+00 4.285012e-24  
## [76,] 3.554091e-44 1.000000e+00  
## [77,] 2.659919e-44 1.000000e+00  
## [78,] 1.000000e+00 5.092665e-20  
## [79,] 1.096369e-33 1.000000e+00  
## [80,] 1.000000e+00 1.157579e-24  
## [81,] 4.470728e-08 1.000000e+00  
## [82,] 1.945986e-50 1.000000e+00  
## [83,] 8.671745e-56 1.000000e+00  
## [84,] 9.926237e-38 1.000000e+00  
## [85,] 1.000000e+00 1.157579e-24  
## [86,] 1.000000e+00 1.157579e-24  
## [87,] 1.000000e+00 6.220035e-25  
## [88,] 1.365291e-33 1.000000e+00  
## [89,] 1.000000e+00 7.066921e-27  
## [90,] 1.207863e-52 1.000000e+00  
## [91,] 6.378501e-14 1.000000e+00  
## [92,] 1.000000e+00 8.063299e-21  
## [93,] 1.405795e-12 1.000000e+00  
## [94,] 1.000000e+00 7.591429e-17  
## [95,] 1.000000e+00 8.169822e-28  
## [96,] 1.000000e+00 1.157579e-24  
## [97,] 3.375190e-16 1.000000e+00  
## [98,] 1.000000e+00 9.141657e-26  
## [99,] 1.000000e+00 3.666036e-26  
## [100,] 1.000000e+00 2.437130e-24  
## [101,] 3.009505e-39 1.000000e+00  
## [102,] 1.000000e+00 3.230274e-27  
## [103,] 3.465978e-47 1.000000e+00  
## [104,] 1.000000e+00 6.757099e-26  
## [105,] 1.000000e+00 6.439589e-25  
## [106,] 1.000000e+00 2.116164e-17  
## [107,] 1.000000e+00 4.311175e-25  
## [108,] 1.000000e+00 3.151542e-26  
## [109,] 1.000000e+00 1.780947e-29  
## [110,] 1.000000e+00 2.383276e-26  
## [111,] 1.000000e+00 3.339715e-26  
## [112,] 1.000000e+00 2.014193e-25  
## [113,] 1.000000e+00 3.341360e-24  
## [114,] 9.734913e-80 1.000000e+00  
## [115,] 1.000000e+00 1.464825e-24  
## [116,] 1.000000e+00 1.827146e-24  
## [117,] 1.000000e+00 1.368454e-23  
## [118,] 2.329678e-37 1.000000e+00  
## [119,] 1.000000e+00 2.559610e-21  
## [120,] 1.000000e+00 1.740459e-12  
## [121,] 1.000000e+00 2.777451e-22  
## [122,] 3.408605e-44 1.000000e+00  
## [123,] 9.999941e-01 5.928362e-06  
## [124,] 1.000000e+00 1.875568e-26  
## [125,] 1.000000e+00 9.306542e-24  
## [126,] 1.150822e-30 1.000000e+00  
## [127,] 9.999998e-01 1.869001e-07  
## [128,] 1.000000e+00 5.462499e-22  
## [129,] 1.000000e+00 3.151542e-26  
## [130,] 1.000000e+00 4.311175e-25  
## [131,] 1.432899e-59 1.000000e+00  
## [132,] 1.000000e+00 2.750783e-21  
## [133,] 1.000000e+00 9.479575e-22  
## [134,] 6.224970e-67 1.000000e+00  
## [135,] 1.000000e+00 5.541779e-27  
## [136,] 1.000000e+00 2.504040e-24  
## [137,] 1.000000e+00 1.555987e-25  
## [138,] 1.000000e+00 5.564544e-24  
## [139,] 1.000000e+00 1.392686e-26  
## [140,] 1.000000e+00 1.665876e-25  
## [141,] 9.996403e-01 3.596978e-04  
## [142,] 1.000000e+00 2.332793e-22  
## [143,] 1.471314e-46 1.000000e+00  
## [144,] 1.000000e+00 1.392686e-26  
## [145,] 3.646125e-46 1.000000e+00  
## [146,] 2.247651e-41 1.000000e+00  
## [147,] 1.000000e+00 1.321294e-21  
## [148,] 1.000000e+00 2.014193e-25  
## [149,] 1.000000e+00 2.534435e-24  
## [150,] 1.000000e+00 8.846808e-19  
## [151,] 1.000000e+00 1.827146e-24  
## [152,] 1.000000e+00 7.774775e-26  
## [153,] 1.000000e+00 2.014193e-25  
## [154,] 1.000000e+00 8.253227e-23  
## [155,] 1.000000e+00 3.111527e-23  
## [156,] 1.000000e+00 1.368454e-23  
## [157,] 1.000000e+00 8.991208e-25  
## [158,] 1.000000e+00 4.698138e-24  
## [159,] 2.708312e-24 1.000000e+00  
## [160,] 1.000000e+00 1.615123e-20  
## [161,] 9.999980e-01 1.995966e-06  
## [162,] 1.000000e+00 1.157579e-24  
## [163,] 1.000000e+00 4.291787e-26  
## [164,] 1.000000e+00 2.156797e-21  
## [165,] 2.064051e-21 1.000000e+00  
## [166,] 2.242125e-61 1.000000e+00  
## [167,] 1.000000e+00 8.821611e-25  
## [168,] 1.000000e+00 3.666036e-26  
## [169,] 1.000000e+00 3.666036e-26  
## [170,] 1.000000e+00 1.157579e-24  
## [171,] 9.710495e-44 1.000000e+00  
## [172,] 5.863162e-31 1.000000e+00  
## [173,] 1.000000e+00 5.564544e-24  
## [174,] 9.705861e-20 1.000000e+00  
## [175,] 1.000000e+00 8.821611e-25  
## [176,] 1.000000e+00 3.905771e-25  
## [177,] 1.000000e+00 2.014193e-25  
## [178,] 1.000000e+00 2.014193e-25  
## [179,] 1.000000e+00 8.991208e-25  
## [180,] 9.239209e-36 1.000000e+00  
## [181,] 1.000000e+00 4.311175e-25  
## [182,] 1.493391e-22 1.000000e+00  
## [183,] 1.000000e+00 8.991208e-25  
## [184,] 1.000000e+00 4.311175e-25  
## [185,] 1.000000e+00 7.843316e-26  
## [186,] 1.000000e+00 1.737368e-21  
## [187,] 1.000000e+00 1.587443e-23  
## [188,] 1.000000e+00 1.077522e-24  
## [189,] 2.371555e-28 1.000000e+00  
## [190,] 1.000000e+00 2.014193e-25  
## [191,] 1.000000e+00 3.965749e-15  
## [192,] 1.000000e+00 8.821611e-25  
## [193,] 1.000000e+00 1.738819e-24  
## [194,] 1.000000e+00 8.598938e-18  
## [195,] 1.000000e+00 4.285012e-24  
## [196,] 1.040451e-26 1.000000e+00  
## [197,] 1.000000e+00 5.541779e-27  
## [198,] 1.000000e+00 6.541544e-24  
## [199,] 7.200295e-45 1.000000e+00  
## [200,] 1.000000e+00 3.974427e-09  
## [201,] 1.860172e-33 1.000000e+00  
## [202,] 1.000000e+00 1.808873e-19  
## [203,] 1.000000e+00 1.107658e-21  
## [204,] 8.299192e-27 1.000000e+00

combine.classes$myrf.pred<-ifelse(combine.classes$myrf.pred=="benign", 0, 1)  
combine.classes[,2]<-ifelse(combine.classes[,2]=="benign", 0, 1)  
combine.classes[,3]<-ifelse(combine.classes[,3]=="benign", 0, 1)  
combine.classes[,4]<-ifelse(combine.classes[,4]=="benign", 0, 1)  
combine.classes[,5]<-ifelse(combine.classes[,5]=="benign", 0, 1)  
#combine.classes[,6]<-ifelse(combine.classes[,6]=="benign", 0, 1)  
  
str(combine.classes)

## 'data.frame': 204 obs. of 5 variables:  
## $ myrf.pred : num 0 1 0 1 1 1 0 0 0 0 ...  
## $ myrda.pred.class: num 0 1 0 1 1 1 0 0 0 0 ...  
## $ mytree.pred : num 1 1 1 1 1 1 1 1 1 1 ...  
## $ mysvm.pred : num 0 1 0 0 1 1 0 0 0 0 ...  
## $ mynb.pred.class : num 0 1 0 1 1 1 0 0 0 0 ...

combine.cl<-combine.classes[, -c(6,7)]  
majority.vote=rowSums(combine.classes[,-c(6,7)])  
head(majority.vote)

## 5 6 11 13 15 19   
## 1 5 1 4 5 5

combine.classes[,6]<-rowSums(combine.classes[,-c(6,7)])  
combine.classes[,7]<-ifelse(combine.classes[,6]>=4, "malignant", "benign")  
Confusion\_B <-table(combine.classes[,7], bc\_valid$Class)  
accuracy <- sum(diag(Confusion\_B))/sum(Confusion\_B)  
accuracy

## [1] 0.9901961