Karan Khanna

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#install.packages("mlbench")

library(mlbench)

## Warning: package 'mlbench' was built under R version 4.2.3

#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(mlbench)  
library(e1071)

## Warning: package 'e1071' was built under R version 4.2.2

library(klaR)

## Warning: package 'klaR' was built under R version 4.2.2

## Loading required package: MASS

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

## Warning: package 'randomForest' was built under R version 4.2.2

## randomForest 4.7-1.1

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

library(caret)

## Warning: package 'caret' was built under R version 4.2.2

## Loading required package: ggplot2

## Warning: package 'ggplot2' was built under R version 4.2.2

##   
## 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)  
ind <- createDataPartition(BreastCancer$Class, p = 0.6, list = FALSE)  
breastCance.train <- BreastCancer[ind,]  
breastCance.test <- BreastCancer[-ind,]

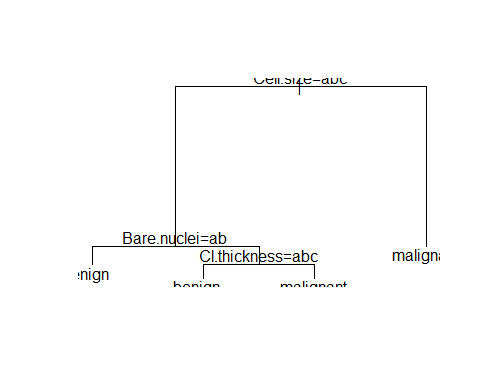
#SVM

mysvm <- svm(Class ~ ., breastCance.train)  
mysvm.pred <- predict(mysvm, breastCance.test)  
table(mysvm.pred,breastCance.test$Class)

##   
## mysvm.pred benign malignant  
## benign 174 7  
## malignant 3 88

#Decision trees

mytree <- rpart(Class ~ ., breastCance.train)  
plot(mytree); text(mytree)



summary(mytree)

## Call:  
## rpart(formula = Class ~ ., data = breastCance.train)  
## n= 411   
##   
## CP nsplit rel error xerror xstd  
## 1 0.80555556 0 1.00000000 1.0000000 0.06716662  
## 2 0.05555556 1 0.19444444 0.2638889 0.04078146  
## 3 0.01000000 3 0.08333333 0.1875000 0.03487901  
##   
## Variable importance  
## Cell.size Cell.shape Bare.nuclei Bl.cromatin Normal.nucleoli   
## 20 17 17 15 14   
## Marg.adhesion Cl.thickness Epith.c.size Mitoses   
## 13 2 1 1   
##   
## Node number 1: 411 observations, complexity param=0.8055556  
## predicted class=benign expected loss=0.350365 P(node) =1  
## class counts: 267 144  
## probabilities: 0.650 0.350   
## left son=2 (277 obs) right son=3 (134 obs)  
## Primary splits:  
## Cell.size splits as LLLRRRRRRR, improve=134.9103, (0 missing)  
## Bare.nuclei splits as LLRRRRRRRR, improve=131.2616, (0 missing)  
## Cell.shape splits as LLRRRRRRRR, improve=129.3126, (0 missing)  
## Bl.cromatin splits as LLLRRRRRRR, improve=119.7576, (0 missing)  
## Normal.nucleoli splits as LLRRRRRRRR, improve=118.1358, (0 missing)  
## Surrogate splits:  
## Cell.shape splits as LLLRRRRRRR, agree=0.942, adj=0.821, (0 split)  
## Bare.nuclei splits as LLLRRRRRRR, agree=0.905, adj=0.709, (0 split)  
## Bl.cromatin splits as LLLRRRRRRR, agree=0.895, adj=0.679, (0 split)  
## Normal.nucleoli splits as LLRRRRRRRR, agree=0.888, adj=0.657, (0 split)  
## Marg.adhesion splits as LLLRRRRRRR, agree=0.881, adj=0.634, (0 split)  
##   
## Node number 2: 277 observations, complexity param=0.05555556  
## predicted class=benign expected loss=0.06859206 P(node) =0.6739659  
## class counts: 258 19  
## probabilities: 0.931 0.069   
## left son=4 (247 obs) right son=5 (30 obs)  
## Primary splits:  
## Bare.nuclei splits as LLRRRR-RRR, improve=19.00160, (0 missing)  
## Normal.nucleoli splits as LLRRLR-LRR, improve=18.21888, (0 missing)  
## Cl.thickness splits as LLLLLLRRRR, improve=15.16591, (0 missing)  
## Cell.shape splits as LLRRRRRRRR, improve=11.30634, (0 missing)  
## Epith.c.size splits as LLLRRRRRRR, improve=10.62647, (0 missing)  
## Surrogate splits:  
## Normal.nucleoli splits as LLRRRL-LLR, agree=0.924, adj=0.300, (0 split)  
## Cl.thickness splits as LLLLLLRRRR, agree=0.921, adj=0.267, (0 split)  
## Bl.cromatin splits as LLLLRLLR--, agree=0.921, adj=0.267, (0 split)  
## Mitoses splits as LLRRL-RR-, agree=0.917, adj=0.233, (0 split)  
## Marg.adhesion splits as LLLRRRRRRR, agree=0.910, adj=0.167, (0 split)  
##   
## Node number 3: 134 observations  
## predicted class=malignant expected loss=0.06716418 P(node) =0.3260341  
## class counts: 9 125  
## probabilities: 0.067 0.933   
##   
## Node number 4: 247 observations  
## predicted class=benign expected loss=0.004048583 P(node) =0.6009732  
## class counts: 246 1  
## probabilities: 0.996 0.004   
##   
## Node number 5: 30 observations, complexity param=0.05555556  
## predicted class=malignant expected loss=0.4 P(node) =0.0729927  
## class counts: 12 18  
## probabilities: 0.400 0.600   
## left son=10 (12 obs) right son=11 (18 obs)  
## Primary splits:  
## Cl.thickness splits as LLLRRRRRRR, improve=10.677780, (0 missing)  
## Normal.nucleoli splits as LRRRLR--RR, improve= 8.400000, (0 missing)  
## Cell.shape splits as LLRRRRRRRR, improve= 7.810714, (0 missing)  
## Cell.size splits as LRRRRRRRRR, improve= 6.074641, (0 missing)  
## Bl.cromatin splits as LLRRR-RR--, improve= 3.816149, (0 missing)  
## Surrogate splits:  
## Cell.shape splits as LRRRRRRRRR, agree=0.867, adj=0.667, (0 split)  
## Cell.size splits as LRRRRRRRRR, agree=0.833, adj=0.583, (0 split)  
## Bl.cromatin splits as LLRLR-RR--, agree=0.800, adj=0.500, (0 split)  
## Normal.nucleoli splits as LRRRRR--RR, agree=0.800, adj=0.500, (0 split)  
## Epith.c.size splits as LLRRRRRRRR, agree=0.767, adj=0.417, (0 split)  
##   
## Node number 10: 12 observations  
## predicted class=benign expected loss=0.08333333 P(node) =0.02919708  
## class counts: 11 1  
## probabilities: 0.917 0.083   
##   
## Node number 11: 18 observations  
## predicted class=malignant expected loss=0.05555556 P(node) =0.04379562  
## class counts: 1 17  
## probabilities: 0.056 0.944

mytree.pred <- predict(mytree,breastCance.test,type="class")  
table(mytree.pred,breastCance.test$Class)

##   
## mytree.pred benign malignant  
## benign 170 5  
## malignant 7 90

# 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 ~ ., breastCance.train)  
myrda.pred <- predict(myrda, breastCance.test)  
table(myrda.pred$class,breastCance.test$Class)

##   
## benign malignant  
## benign 174 3  
## malignant 3 92

#Naive Bayes  
  
library(klaR)  
mynb <- NaiveBayes(Class ~ ., breastCance.train, usekernel = TRUE)  
mynb.pred <- predict(mynb,breastCance.test)

## 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 7

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 8

## 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 16

## 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 19

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 21

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 22

## 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 24

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 25

## 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 27

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 28

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 29

## 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 35

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 41

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 42

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 43

## 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 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 61

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 63

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 68

## 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 74

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 79

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 94

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 95

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 98

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 102

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 106

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 112

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 113

## 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 120

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 138

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 139

## 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 158

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 160

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 161

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 168

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 172

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 185

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 194

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 195

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 197

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 222

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 223

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 238

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 239

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 243

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 249

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 250

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 257

#head(mynb.pred$class)  
table(mynb.pred$class,breastCance.test$Class)

##   
## benign malignant  
## benign 174 2  
## malignant 3 93

#Random Forests

myrf <- randomForest(Class ~ ., breastCance.train)  
myrf.pred <- predict(myrf, breastCance.test)  
head(myrf.pred)

## 5 11 12 13 15 20   
## benign benign benign malignant malignant benign   
## Levels: benign malignant

table(myrf.pred, breastCance.test$Class)

##   
## myrf.pred benign malignant  
## benign 174 3  
## malignant 3 92

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

## myrf.pred myrda.pred.class mytree.pred mynb.pred.class  
## 5 benign benign malignant benign  
## 11 benign benign malignant benign  
## 12 benign benign malignant benign  
## 13 malignant malignant malignant malignant  
## 15 malignant malignant malignant malignant  
## 20 benign benign malignant benign

head(myrf.pred)

## 5 11 12 13 15 20   
## benign benign benign malignant malignant benign   
## Levels: benign malignant

head(myrda.pred)

## $class  
## [1] benign benign benign malignant malignant benign malignant  
## [8] malignant benign benign benign benign benign malignant  
## [15] malignant malignant malignant malignant malignant benign malignant  
## [22] malignant malignant malignant malignant malignant malignant malignant  
## [29] malignant benign benign malignant benign benign malignant  
## [36] benign benign benign benign benign benign malignant  
## [43] benign benign benign benign benign malignant benign   
## [50] malignant benign benign malignant benign benign malignant  
## [57] malignant benign benign benign malignant benign malignant  
## [64] benign benign benign benign malignant malignant malignant  
## [71] malignant benign malignant malignant malignant benign benign   
## [78] malignant malignant benign benign benign malignant malignant  
## [85] benign benign benign malignant benign benign malignant  
## [92] benign malignant malignant malignant malignant benign malignant  
## [99] benign benign malignant malignant malignant benign malignant  
## [106] malignant benign malignant malignant benign malignant malignant  
## [113] malignant malignant benign malignant benign benign benign   
## [120] malignant benign benign malignant malignant benign benign   
## [127] malignant malignant benign benign malignant benign benign   
## [134] benign benign benign malignant malignant malignant benign   
## [141] malignant benign benign benign benign malignant benign   
## [148] benign benign benign benign benign benign benign   
## [155] benign benign benign malignant benign malignant malignant  
## [162] benign benign malignant benign benign benign malignant  
## [169] benign benign malignant malignant benign benign benign   
## [176] benign benign benign benign malignant malignant benign   
## [183] benign benign malignant benign benign benign malignant  
## [190] benign benign benign benign malignant benign benign   
## [197] benign benign benign benign benign benign malignant  
## [204] benign benign benign benign benign benign benign   
## [211] benign benign benign benign benign benign benign   
## [218] benign benign benign benign malignant malignant benign   
## [225] benign benign benign benign malignant benign malignant  
## [232] benign benign benign benign benign benign malignant  
## [239] malignant benign benign malignant malignant benign benign   
## [246] benign benign benign malignant malignant benign benign   
## [253] benign benign benign benign malignant benign benign   
## [260] benign benign benign benign benign benign benign   
## [267] benign benign benign malignant benign benign   
## Levels: benign malignant  
##   
## $posterior  
## benign malignant  
## [1,] 1.000000e+00 2.069910e-21  
## [2,] 1.000000e+00 1.912583e-25  
## [3,] 1.000000e+00 4.538182e-25  
## [4,] 1.254500e-03 9.987455e-01  
## [5,] 1.697945e-48 1.000000e+00  
## [6,] 1.000000e+00 3.301561e-19  
## [7,] 1.394585e-36 1.000000e+00  
## [8,] 7.297273e-04 9.992703e-01  
## [9,] 1.000000e+00 5.996522e-26  
## [10,] 1.000000e+00 3.132285e-23  
## [11,] 1.000000e+00 2.417459e-20  
## [12,] 1.000000e+00 1.402530e-26  
## [13,] 1.000000e+00 4.538182e-25  
## [14,] 7.681518e-38 1.000000e+00  
## [15,] 4.167971e-20 1.000000e+00  
## [16,] 7.641824e-19 1.000000e+00  
## [17,] 6.336212e-18 1.000000e+00  
## [18,] 4.413075e-27 1.000000e+00  
## [19,] 1.044515e-28 1.000000e+00  
## [20,] 1.000000e+00 2.069910e-21  
## [21,] 2.862313e-27 1.000000e+00  
## [22,] 1.043477e-19 1.000000e+00  
## [23,] 1.155374e-04 9.998845e-01  
## [24,] 6.312105e-24 1.000000e+00  
## [25,] 5.974662e-40 1.000000e+00  
## [26,] 1.244024e-31 1.000000e+00  
## [27,] 5.173332e-20 1.000000e+00  
## [28,] 2.018090e-13 1.000000e+00  
## [29,] 5.405858e-25 1.000000e+00  
## [30,] 1.000000e+00 6.372937e-25  
## [31,] 1.000000e+00 1.275220e-22  
## [32,] 9.836704e-17 1.000000e+00  
## [33,] 1.000000e+00 3.040426e-21  
## [34,] 1.000000e+00 4.360477e-20  
## [35,] 1.470725e-40 1.000000e+00  
## [36,] 1.000000e+00 1.275220e-22  
## [37,] 1.000000e+00 2.045929e-23  
## [38,] 1.000000e+00 1.017427e-23  
## [39,] 1.000000e+00 1.275220e-22  
## [40,] 1.000000e+00 1.158583e-23  
## [41,] 9.955844e-01 4.415629e-03  
## [42,] 4.665165e-31 1.000000e+00  
## [43,] 9.994271e-01 5.728958e-04  
## [44,] 1.000000e+00 7.688979e-17  
## [45,] 1.000000e+00 4.703151e-20  
## [46,] 1.000000e+00 5.170035e-26  
## [47,] 1.000000e+00 2.387117e-21  
## [48,] 1.723225e-35 1.000000e+00  
## [49,] 1.000000e+00 6.372937e-25  
## [50,] 1.868107e-23 1.000000e+00  
## [51,] 1.000000e+00 1.419111e-12  
## [52,] 1.000000e+00 5.187455e-20  
## [53,] 5.688760e-25 1.000000e+00  
## [54,] 1.000000e+00 3.774956e-17  
## [55,] 1.000000e+00 6.514945e-24  
## [56,] 4.275205e-39 1.000000e+00  
## [57,] 1.675223e-11 1.000000e+00  
## [58,] 1.000000e+00 5.359708e-19  
## [59,] 1.000000e+00 6.673251e-24  
## [60,] 1.000000e+00 1.158583e-23  
## [61,] 2.896361e-30 1.000000e+00  
## [62,] 1.000000e+00 3.465485e-23  
## [63,] 5.809937e-36 1.000000e+00  
## [64,] 1.000000e+00 1.158583e-23  
## [65,] 1.000000e+00 1.275220e-22  
## [66,] 1.000000e+00 1.912583e-25  
## [67,] 1.000000e+00 3.301561e-19  
## [68,] 5.285927e-29 1.000000e+00  
## [69,] 8.643465e-48 1.000000e+00  
## [70,] 1.213927e-29 1.000000e+00  
## [71,] 7.741498e-36 1.000000e+00  
## [72,] 1.000000e+00 1.806688e-23  
## [73,] 3.712598e-33 1.000000e+00  
## [74,] 6.439907e-35 1.000000e+00  
## [75,] 1.621683e-34 1.000000e+00  
## [76,] 1.000000e+00 9.137178e-22  
## [77,] 1.000000e+00 1.806688e-23  
## [78,] 2.869970e-33 1.000000e+00  
## [79,] 3.883039e-28 1.000000e+00  
## [80,] 1.000000e+00 1.912583e-25  
## [81,] 1.000000e+00 1.912583e-25  
## [82,] 1.000000e+00 8.640519e-24  
## [83,] 2.728345e-38 1.000000e+00  
## [84,] 3.599815e-26 1.000000e+00  
## [85,] 1.000000e+00 6.372937e-25  
## [86,] 1.000000e+00 1.806688e-23  
## [87,] 1.000000e+00 1.063279e-16  
## [88,] 1.562192e-34 1.000000e+00  
## [89,] 1.000000e+00 3.129487e-21  
## [90,] 1.000000e+00 6.372937e-25  
## [91,] 5.420652e-39 1.000000e+00  
## [92,] 1.000000e+00 1.912583e-25  
## [93,] 1.844178e-30 1.000000e+00  
## [94,] 1.578640e-34 1.000000e+00  
## [95,] 2.972849e-17 1.000000e+00  
## [96,] 3.605807e-18 1.000000e+00  
## [97,] 1.000000e+00 7.079097e-13  
## [98,] 3.245462e-39 1.000000e+00  
## [99,] 1.000000e+00 5.048833e-24  
## [100,] 1.000000e+00 5.564836e-23  
## [101,] 1.536641e-26 1.000000e+00  
## [102,] 5.405858e-25 1.000000e+00  
## [103,] 3.315154e-18 1.000000e+00  
## [104,] 1.000000e+00 3.465485e-23  
## [105,] 1.412253e-35 1.000000e+00  
## [106,] 5.447191e-40 1.000000e+00  
## [107,] 1.000000e+00 1.474167e-17  
## [108,] 2.933774e-36 1.000000e+00  
## [109,] 1.148413e-02 9.885159e-01  
## [110,] 1.000000e+00 1.806688e-23  
## [111,] 1.148413e-02 9.885159e-01  
## [112,] 9.702074e-45 1.000000e+00  
## [113,] 5.350205e-12 1.000000e+00  
## [114,] 1.018100e-25 1.000000e+00  
## [115,] 1.000000e+00 1.806688e-23  
## [116,] 9.806358e-36 1.000000e+00  
## [117,] 1.000000e+00 1.806688e-23  
## [118,] 1.000000e+00 3.049622e-22  
## [119,] 1.000000e+00 3.396620e-23  
## [120,] 7.993099e-27 1.000000e+00  
## [121,] 1.000000e+00 3.396620e-23  
## [122,] 1.000000e+00 6.224173e-27  
## [123,] 1.911420e-18 1.000000e+00  
## [124,] 3.022114e-14 1.000000e+00  
## [125,] 1.000000e+00 3.004862e-18  
## [126,] 1.000000e+00 6.372937e-25  
## [127,] 7.411091e-19 1.000000e+00  
## [128,] 3.892704e-24 1.000000e+00  
## [129,] 1.000000e+00 1.355633e-16  
## [130,] 1.000000e+00 4.398597e-26  
## [131,] 2.064256e-09 1.000000e+00  
## [132,] 1.000000e+00 1.806688e-23  
## [133,] 1.000000e+00 3.990879e-20  
## [134,] 1.000000e+00 1.158583e-23  
## [135,] 1.000000e+00 6.372937e-25  
## [136,] 1.000000e+00 8.725781e-23  
## [137,] 1.070170e-43 1.000000e+00  
## [138,] 8.776718e-33 1.000000e+00  
## [139,] 1.194929e-25 1.000000e+00  
## [140,] 1.000000e+00 4.538182e-25  
## [141,] 1.084252e-34 1.000000e+00  
## [142,] 1.000000e+00 1.408827e-23  
## [143,] 1.000000e+00 3.716853e-24  
## [144,] 1.000000e+00 6.232551e-17  
## [145,] 1.000000e+00 3.396620e-23  
## [146,] 1.198915e-39 1.000000e+00  
## [147,] 1.000000e+00 2.482552e-23  
## [148,] 1.000000e+00 3.014140e-27  
## [149,] 1.000000e+00 7.713033e-26  
## [150,] 1.000000e+00 3.022874e-25  
## [151,] 1.000000e+00 1.525213e-24  
## [152,] 1.000000e+00 3.465485e-23  
## [153,] 1.000000e+00 3.031737e-22  
## [154,] 1.000000e+00 6.092072e-23  
## [155,] 1.000000e+00 9.164428e-17  
## [156,] 1.000000e+00 1.835587e-16  
## [157,] 1.000000e+00 3.050626e-22  
## [158,] 1.153176e-34 1.000000e+00  
## [159,] 1.000000e+00 1.902952e-22  
## [160,] 1.833070e-31 1.000000e+00  
## [161,] 4.908878e-30 1.000000e+00  
## [162,] 1.000000e+00 6.372937e-25  
## [163,] 1.000000e+00 4.182337e-18  
## [164,] 2.444308e-32 1.000000e+00  
## [165,] 1.000000e+00 3.548499e-10  
## [166,] 1.000000e+00 5.187455e-20  
## [167,] 9.999893e-01 1.071147e-05  
## [168,] 8.025982e-26 1.000000e+00  
## [169,] 1.000000e+00 7.726702e-25  
## [170,] 1.000000e+00 1.906838e-20  
## [171,] 2.603994e-23 1.000000e+00  
## [172,] 8.856542e-19 1.000000e+00  
## [173,] 1.000000e+00 3.031737e-22  
## [174,] 1.000000e+00 9.716388e-09  
## [175,] 1.000000e+00 1.165426e-19  
## [176,] 1.000000e+00 6.992839e-15  
## [177,] 1.000000e+00 2.482552e-23  
## [178,] 1.000000e+00 3.396620e-23  
## [179,] 1.000000e+00 3.022874e-25  
## [180,] 2.687559e-39 1.000000e+00  
## [181,] 3.621675e-40 1.000000e+00  
## [182,] 1.000000e+00 2.920836e-18  
## [183,] 1.000000e+00 9.164496e-19  
## [184,] 1.000000e+00 3.031737e-22  
## [185,] 3.628400e-35 1.000000e+00  
## [186,] 1.000000e+00 9.985076e-26  
## [187,] 1.000000e+00 9.164496e-19  
## [188,] 1.000000e+00 1.206195e-20  
## [189,] 6.293559e-26 1.000000e+00  
## [190,] 1.000000e+00 1.236380e-23  
## [191,] 1.000000e+00 5.676474e-22  
## [192,] 1.000000e+00 1.126228e-21  
## [193,] 1.000000e+00 1.402530e-26  
## [194,] 2.478480e-18 1.000000e+00  
## [195,] 9.997252e-01 2.748045e-04  
## [196,] 1.000000e+00 4.761523e-26  
## [197,] 9.999997e-01 3.096824e-07  
## [198,] 1.000000e+00 6.514945e-24  
## [199,] 1.000000e+00 1.622938e-20  
## [200,] 1.000000e+00 2.482552e-23  
## [201,] 1.000000e+00 1.402530e-26  
## [202,] 1.000000e+00 6.991577e-19  
## [203,] 1.687566e-39 1.000000e+00  
## [204,] 1.000000e+00 1.525213e-24  
## [205,] 1.000000e+00 1.017427e-23  
## [206,] 1.000000e+00 3.029352e-16  
## [207,] 1.000000e+00 3.050626e-22  
## [208,] 1.000000e+00 1.912583e-25  
## [209,] 1.000000e+00 1.525213e-24  
## [210,] 1.000000e+00 2.387251e-21  
## [211,] 1.000000e+00 9.137178e-22  
## [212,] 1.000000e+00 1.902952e-22  
## [213,] 1.000000e+00 6.514945e-24  
## [214,] 1.000000e+00 5.928091e-23  
## [215,] 1.000000e+00 1.820877e-25  
## [216,] 1.000000e+00 1.525213e-24  
## [217,] 1.000000e+00 7.731597e-21  
## [218,] 9.999999e-01 8.249265e-08  
## [219,] 1.000000e+00 1.806688e-23  
## [220,] 1.000000e+00 5.484198e-25  
## [221,] 1.000000e+00 8.962067e-21  
## [222,] 8.284526e-27 1.000000e+00  
## [223,] 4.579860e-23 1.000000e+00  
## [224,] 1.000000e+00 3.132285e-23  
## [225,] 1.000000e+00 6.372937e-25  
## [226,] 1.000000e+00 6.372937e-25  
## [227,] 1.000000e+00 1.806688e-23  
## [228,] 1.000000e+00 3.396620e-23  
## [229,] 1.582117e-13 1.000000e+00  
## [230,] 1.000000e+00 5.676474e-22  
## [231,] 6.894915e-20 1.000000e+00  
## [232,] 1.000000e+00 3.132285e-23  
## [233,] 1.000000e+00 1.926408e-24  
## [234,] 1.000000e+00 2.695115e-18  
## [235,] 1.000000e+00 1.525213e-24  
## [236,] 1.000000e+00 1.525213e-24  
## [237,] 1.000000e+00 6.514945e-24  
## [238,] 2.139869e-17 1.000000e+00  
## [239,] 6.569851e-38 1.000000e+00  
## [240,] 1.000000e+00 3.396620e-23  
## [241,] 1.000000e+00 1.555208e-21  
## [242,] 1.720560e-21 1.000000e+00  
## [243,] 3.141121e-19 1.000000e+00  
## [244,] 1.000000e+00 6.514945e-24  
## [245,] 1.000000e+00 3.396620e-23  
## [246,] 1.000000e+00 2.456949e-26  
## [247,] 1.000000e+00 1.527782e-09  
## [248,] 1.000000e+00 7.241723e-20  
## [249,] 7.095887e-27 1.000000e+00  
## [250,] 8.507013e-41 1.000000e+00  
## [251,] 1.000000e+00 4.011361e-14  
## [252,] 1.000000e+00 3.031737e-22  
## [253,] 1.000000e+00 1.994313e-21  
## [254,] 1.000000e+00 1.525213e-24  
## [255,] 1.000000e+00 8.113331e-22  
## [256,] 1.000000e+00 1.729309e-22  
## [257,] 2.601533e-19 1.000000e+00  
## [258,] 1.000000e+00 1.525213e-24  
## [259,] 1.000000e+00 1.382710e-14  
## [260,] 1.000000e+00 3.132285e-23  
## [261,] 1.000000e+00 3.999686e-22  
## [262,] 1.000000e+00 3.999686e-22  
## [263,] 1.000000e+00 1.169265e-16  
## [264,] 1.000000e+00 3.465485e-23  
## [265,] 1.000000e+00 9.985076e-26  
## [266,] 1.000000e+00 1.555208e-21  
## [267,] 1.000000e+00 3.396620e-23  
## [268,] 1.000000e+00 8.402364e-15  
## [269,] 1.000000e+00 1.729309e-22  
## [270,] 1.600151e-25 1.000000e+00  
## [271,] 1.000000e+00 4.273856e-19  
## [272,] 1.000000e+00 5.511113e-20

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': 272 obs. of 4 variables:  
## $ myrf.pred : num 0 0 0 1 1 0 1 1 0 0 ...  
## $ myrda.pred.class: num 0 0 0 1 1 0 1 1 0 0 ...  
## $ mytree.pred : num 1 1 1 1 1 1 1 1 1 1 ...  
## $ mynb.pred.class : num 0 0 0 1 1 0 1 1 0 0 ...

combine.cl<-combine.classes[, -c(5,6)]  
majority.vote=rowSums(combine.classes[,-c(5,6)])  
head(majority.vote)

## 5 11 12 13 15 20   
## 1 1 1 4 4 1

combine.classes[,5]<-rowSums(combine.classes[,-c(5,6)])  
combine.classes[,6]<-ifelse(combine.classes[,5]>=4, "malignant", "benign")  
table(combine.classes[,6], breastCance.test$Class)

##   
## benign malignant  
## benign 174 3  
## malignant 3 92

Confusion\_combine <-table(combine.classes[,6], breastCance.test$Class)  
accuracy <- sum(diag(Confusion\_combine))/sum(Confusion\_combine)  
accuracy

## [1] 0.9779412