Project Portfolio Git

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# Package for loading breast cancer data

#install.packages("mlbench")  
library(mlbench)

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

# Read 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)

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

## Loading required package: MASS

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

library(nnet)

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

library(MASS)  
library(rpart)

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

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.

# Partitioning the data and cleaning the missing values

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" ...

# partition the data set for 80% training and 20% evaluation (adapted from ?randomForest)  
set.seed(2)  
  
ind <- sample(2, nrow(BreastCancer), replace = TRUE, prob=c(0.8, 0.2))

# Support Vector Machine

mysvm <- svm(Class ~ ., BreastCancer[ind == 1,])  
mysvm.pred <- predict(mysvm, BreastCancer[ind == 2,])  
table(mysvm.pred,BreastCancer[ind == 2,]$Class)

##   
## mysvm.pred benign malignant  
## benign 87 1  
## malignant 5 55

# Naive bayes

mynb <- NaiveBayes(Class ~ ., BreastCancer[ind == 1,])  
mynb.pred <- predict(mynb,BreastCancer[ind == 2,])

## 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 12

## 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 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 18

## 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 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 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 31

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 38

## 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 40

## 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 44

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 47

## 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 51

## 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 54

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 55

## 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 59

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 60

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 64

## 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 75

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 76

## 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 86

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 96

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 103

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 121

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 127

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 128

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 129

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 130

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 136

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 137

## 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 140

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

head(mynb.pred$class)

## 5 6 8 16 17 23   
## benign malignant benign malignant benign benign   
## Levels: benign malignant

table(mynb.pred$class,BreastCancer[ind == 2,]$Class)

##   
## benign malignant  
## benign 87 0  
## malignant 5 56

str(mysvm.pred)

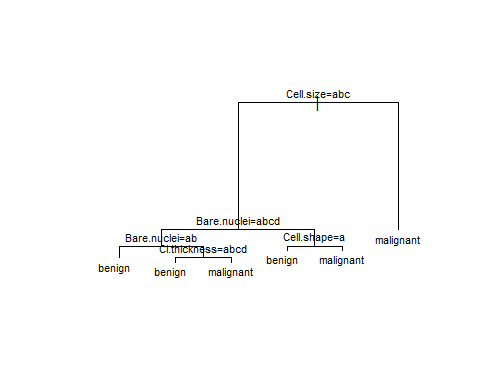
## Factor w/ 2 levels "benign","malignant": 1 2 1 2 1 1 1 1 1 1 ...  
## - attr(\*, "names")= chr [1:148] "5" "6" "8" "16" ...

str(mynb.pred)

## List of 2  
## $ class : Factor w/ 2 levels "benign","malignant": 1 2 1 2 1 1 1 1 1 1 ...  
## ..- attr(\*, "names")= chr [1:148] "5" "6" "8" "16" ...  
## $ posterior: num [1:148, 1:2] 1.00 1.86e-14 1.00 1.78e-07 1.00 ...  
## ..- attr(\*, "dimnames")=List of 2  
## .. ..$ : chr [1:148] "5" "6" "8" "16" ...  
## .. ..$ : chr [1:2] "benign" "malignant"

# Decision tree using rpart

library(rpart)  
mytree <- rpart(Class ~ ., BreastCancer[ind == 1,])  
plot(mytree, cex = 0.7, margin = 0.1)  
text(mytree, cex = 0.7, xpd = TRUE)



summary(mytree)

## Call:  
## rpart(formula = Class ~ ., data = BreastCancer[ind == 1, ])  
## n= 535   
##   
## CP nsplit rel error xerror xstd  
## 1 0.78688525 0 1.00000000 1.0000000 0.05996100  
## 2 0.10382514 1 0.21311475 0.3005464 0.03838610  
## 3 0.02185792 2 0.10928962 0.1092896 0.02397677  
## 4 0.01366120 3 0.08743169 0.1147541 0.02454501  
## 5 0.01000000 5 0.06010929 0.1147541 0.02454501  
##   
## Variable importance  
## Cell.size Cell.shape Bare.nuclei Bl.cromatin Epith.c.size   
## 21 18 17 14 13   
## Marg.adhesion Cl.thickness Normal.nucleoli   
## 12 3 2   
##   
## Node number 1: 535 observations, complexity param=0.7868852  
## predicted class=benign expected loss=0.3420561 P(node) =1  
## class counts: 352 183  
## probabilities: 0.658 0.342   
## left son=2 (375 obs) right son=3 (160 obs)  
## Primary splits:  
## Cell.size splits as LLLRRRRRRR, improve=168.7328, (0 missing)  
## Bare.nuclei splits as LLRRRRRRRR, improve=168.0772, (0 missing)  
## Cell.shape splits as LLRRRRRRRR, improve=163.6488, (0 missing)  
## Bl.cromatin splits as LLLRRRRRRR, improve=153.4274, (0 missing)  
## Epith.c.size splits as LLRRRRRRRR, improve=147.2678, (0 missing)  
## Surrogate splits:  
## Cell.shape splits as LLLRRRRRRR, agree=0.935, adj=0.781, (0 split)  
## Epith.c.size splits as LLLRRRRRRR, agree=0.890, adj=0.631, (0 split)  
## Bare.nuclei splits as LLLRRRRRRR, agree=0.890, adj=0.631, (0 split)  
## Bl.cromatin splits as LLLRRRRRRR, agree=0.886, adj=0.619, (0 split)  
## Marg.adhesion splits as LLLRRRRRRR, agree=0.875, adj=0.581, (0 split)  
##   
## Node number 2: 375 observations, complexity param=0.1038251  
## predicted class=benign expected loss=0.08266667 P(node) =0.7009346  
## class counts: 344 31  
## probabilities: 0.917 0.083   
## left son=4 (344 obs) right son=5 (31 obs)  
## Primary splits:  
## Bare.nuclei splits as LLLLRRRRRR, improve=35.40655, (0 missing)  
## Normal.nucleoli splits as LLRRRRRLRR, improve=28.31034, (0 missing)  
## Cl.thickness splits as LLLLLLRRRR, improve=24.57962, (0 missing)  
## Bl.cromatin splits as LLLRRLRR--, improve=23.90767, (0 missing)  
## Cell.shape splits as LLRRRRRRRR, improve=16.91486, (0 missing)  
## Surrogate splits:  
## Normal.nucleoli splits as LLLRRRRLRR, agree=0.947, adj=0.355, (0 split)  
## Cl.thickness splits as LLLLLLRRRR, agree=0.944, adj=0.323, (0 split)  
## Bl.cromatin splits as LLLLRLRR--, agree=0.941, adj=0.290, (0 split)  
## Cell.shape splits as LLLLRRRRRR, agree=0.933, adj=0.194, (0 split)  
## Marg.adhesion splits as LLLRRRRRRR, agree=0.928, adj=0.129, (0 split)  
##   
## Node number 3: 160 observations  
## predicted class=malignant expected loss=0.05 P(node) =0.2990654  
## class counts: 8 152  
## probabilities: 0.050 0.950   
##   
## Node number 4: 344 observations, complexity param=0.0136612  
## predicted class=benign expected loss=0.01744186 P(node) =0.6429907  
## class counts: 338 6  
## probabilities: 0.983 0.017   
## left son=8 (323 obs) right son=9 (21 obs)  
## Primary splits:  
## Bare.nuclei splits as LLRR------, improve=3.219269, (0 missing)  
## Bl.cromatin splits as LLLRLLR---, improve=3.014650, (0 missing)  
## Normal.nucleoli splits as LLRRLL-L-R, improve=3.014650, (0 missing)  
## Cell.shape splits as LLRRRRRRRR, improve=1.267738, (0 missing)  
## Epith.c.size splits as LLRRRRRRRR, improve=1.267738, (0 missing)  
## Surrogate splits:  
## Normal.nucleoli splits as LLLRRL-L-R, agree=0.948, adj=0.143, (0 split)  
## Mitoses splits as LLL-L-RL-, agree=0.942, adj=0.048, (0 split)  
##   
## Node number 5: 31 observations, complexity param=0.02185792  
## predicted class=malignant expected loss=0.1935484 P(node) =0.05794393  
## class counts: 6 25  
## probabilities: 0.194 0.806   
## left son=10 (8 obs) right son=11 (23 obs)  
## Primary splits:  
## Cell.shape splits as LRRRRRRRRR, improve=6.677419, (0 missing)  
## Cl.thickness splits as LLLRRRRRRR, improve=5.677419, (0 missing)  
## Cell.size splits as LRRRRRRRRR, improve=4.877419, (0 missing)  
## Normal.nucleoli splits as L-RRRRR-RR, improve=3.677419, (0 missing)  
## Epith.c.size splits as LLRRRRRRRR, improve=3.215881, (0 missing)  
## Surrogate splits:  
## Cell.size splits as LRRRRRRRRR, agree=0.935, adj=0.750, (0 split)  
## Cl.thickness splits as LRRRRRRRRR, agree=0.871, adj=0.500, (0 split)  
## Epith.c.size splits as LLRRRRRRRR, agree=0.839, adj=0.375, (0 split)  
## Bare.nuclei splits as ----LRRRRR, agree=0.806, adj=0.250, (0 split)  
## Normal.nucleoli splits as L-RRRRR-RR, agree=0.806, adj=0.250, (0 split)  
##   
## Node number 8: 323 observations  
## predicted class=benign expected loss=0 P(node) =0.6037383  
## class counts: 323 0  
## probabilities: 1.000 0.000   
##   
## Node number 9: 21 observations, complexity param=0.0136612  
## predicted class=benign expected loss=0.2857143 P(node) =0.03925234  
## class counts: 15 6  
## probabilities: 0.714 0.286   
## left son=18 (14 obs) right son=19 (7 obs)  
## Primary splits:  
## Cl.thickness splits as LLLLRRRRRR, improve=6.857143, (0 missing)  
## Cell.size splits as LRRRRRRRRR, improve=3.771429, (0 missing)  
## Bl.cromatin splits as LLRR--R---, improve=3.771429, (0 missing)  
## Cell.shape splits as LRRRRRRRRR, improve=3.116883, (0 missing)  
## Epith.c.size splits as LLRRRRRRRR, improve=2.293651, (0 missing)  
## Surrogate splits:  
## Cell.size splits as LRRRRRRRRR, agree=0.857, adj=0.571, (0 split)  
## Cell.shape splits as LLRRRRRRRR, agree=0.857, adj=0.571, (0 split)  
## Bl.cromatin splits as LLLR--R---, agree=0.857, adj=0.571, (0 split)  
## Normal.nucleoli splits as L-RRL----R, agree=0.857, adj=0.571, (0 split)  
## Marg.adhesion splits as LLLRRRRRRR, agree=0.714, adj=0.143, (0 split)  
##   
## Node number 10: 8 observations  
## predicted class=benign expected loss=0.25 P(node) =0.01495327  
## class counts: 6 2  
## probabilities: 0.750 0.250   
##   
## Node number 11: 23 observations  
## predicted class=malignant expected loss=0 P(node) =0.04299065  
## class counts: 0 23  
## probabilities: 0.000 1.000   
##   
## Node number 18: 14 observations  
## predicted class=benign expected loss=0 P(node) =0.02616822  
## class counts: 14 0  
## probabilities: 1.000 0.000   
##   
## Node number 19: 7 observations  
## predicted class=malignant expected loss=0.1428571 P(node) =0.01308411  
## class counts: 1 6  
## probabilities: 0.143 0.857

mytree.pred <- predict(mytree,BreastCancer[ind == 2,],type="class")  
table(mytree.pred,BreastCancer[ind == 2,]$Class)

##   
## mytree.pred benign malignant  
## benign 86 2  
## malignant 6 54

# Regularised Discriminant Analysis

myrda <- rda(Class ~ ., BreastCancer[ind == 1,])  
myrda.pred <- predict(myrda, BreastCancer[ind == 2,])  
table(myrda.pred$class,BreastCancer[ind == 2,]$Class)

##   
## benign malignant  
## benign 87 0  
## malignant 5 56

# Random Forests

myrf <- randomForest(Class ~ ., BreastCancer[ind == 1,])  
myrf.pred <- predict(myrf, BreastCancer[ind == 2,])  
head(myrf.pred)

## 5 6 8 16 17 23   
## benign malignant benign malignant benign benign   
## Levels: benign malignant

table(myrf.pred, BreastCancer[ind == 2,]$Class)

##   
## myrf.pred benign malignant  
## benign 87 0  
## malignant 5 56

# Combining the 5 classifiers results

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

## myrf.pred mytree.pred mysvm.pred mynb.pred.class myrda.pred.class  
## 5 benign benign benign benign benign  
## 6 malignant malignant malignant malignant malignant  
## 8 benign benign benign benign benign  
## 16 malignant malignant malignant malignant malignant  
## 17 benign benign benign benign benign  
## 23 benign benign benign benign benign

head(myrf.pred)

## 5 6 8 16 17 23   
## benign malignant benign malignant benign benign   
## Levels: benign malignant

head(myrda.pred)

## $class  
## [1] benign malignant benign malignant benign benign benign   
## [8] benign benign benign malignant malignant benign malignant  
## [15] malignant malignant malignant malignant benign benign malignant  
## [22] benign benign malignant malignant benign benign malignant  
## [29] benign benign malignant benign benign benign benign   
## [36] benign benign malignant malignant malignant benign malignant  
## [43] malignant malignant malignant benign malignant benign malignant  
## [50] benign malignant benign malignant malignant malignant malignant  
## [57] malignant benign malignant malignant malignant malignant benign   
## [64] malignant benign benign malignant benign malignant malignant  
## [71] malignant benign benign benign malignant malignant benign   
## [78] benign malignant malignant benign benign malignant benign   
## [85] benign malignant benign benign benign malignant benign   
## [92] benign benign benign benign malignant benign benign   
## [99] benign benign benign benign benign benign benign   
## [106] benign benign benign malignant benign benign benign   
## [113] benign malignant benign benign benign benign malignant  
## [120] malignant malignant benign benign benign benign benign   
## [127] malignant malignant malignant malignant benign benign benign   
## [134] benign benign malignant malignant malignant benign malignant  
## [141] malignant benign benign benign benign malignant benign   
## [148] benign   
## Levels: benign malignant  
##   
## $posterior  
## benign malignant  
## [1,] 1.000000e+00 9.739902e-20  
## [2,] 2.271646e-33 1.000000e+00  
## [3,] 1.000000e+00 2.806157e-20  
## [4,] 6.425245e-24 1.000000e+00  
## [5,] 1.000000e+00 4.124024e-26  
## [6,] 1.000000e+00 4.267615e-27  
## [7,] 1.000000e+00 5.323090e-20  
## [8,] 1.000000e+00 5.162651e-21  
## [9,] 1.000000e+00 3.874646e-23  
## [10,] 1.000000e+00 2.192914e-08  
## [11,] 3.740832e-30 1.000000e+00  
## [12,] 2.924215e-22 1.000000e+00  
## [13,] 1.000000e+00 9.739902e-20  
## [14,] 2.447853e-03 9.975521e-01  
## [15,] 1.256508e-24 1.000000e+00  
## [16,] 5.621550e-16 1.000000e+00  
## [17,] 3.323123e-12 1.000000e+00  
## [18,] 7.927962e-07 9.999992e-01  
## [19,] 1.000000e+00 4.739090e-25  
## [20,] 1.000000e+00 2.567660e-20  
## [21,] 6.171612e-30 1.000000e+00  
## [22,] 1.000000e+00 4.739090e-25  
## [23,] 1.000000e+00 4.739090e-25  
## [24,] 3.334922e-34 1.000000e+00  
## [25,] 1.379372e-13 1.000000e+00  
## [26,] 1.000000e+00 1.245887e-23  
## [27,] 9.999615e-01 3.850254e-05  
## [28,] 2.779180e-33 1.000000e+00  
## [29,] 1.000000e+00 1.179675e-14  
## [30,] 1.000000e+00 3.354480e-19  
## [31,] 3.720816e-25 1.000000e+00  
## [32,] 1.000000e+00 6.975198e-28  
## [33,] 1.000000e+00 3.505035e-26  
## [34,] 1.000000e+00 1.371343e-18  
## [35,] 1.000000e+00 3.969392e-25  
## [36,] 1.000000e+00 4.135211e-20  
## [37,] 1.000000e+00 3.552082e-24  
## [38,] 1.023172e-29 1.000000e+00  
## [39,] 1.342557e-24 1.000000e+00  
## [40,] 4.227251e-37 1.000000e+00  
## [41,] 1.000000e+00 8.637056e-25  
## [42,] 3.255753e-07 9.999997e-01  
## [43,] 8.718837e-24 1.000000e+00  
## [44,] 3.051332e-23 1.000000e+00  
## [45,] 1.392444e-40 1.000000e+00  
## [46,] 1.000000e+00 1.762647e-26  
## [47,] 2.328097e-23 1.000000e+00  
## [48,] 1.000000e+00 2.072323e-21  
## [49,] 4.729435e-30 1.000000e+00  
## [50,] 1.000000e+00 6.975198e-28  
## [51,] 3.248484e-33 1.000000e+00  
## [52,] 1.000000e+00 3.494841e-23  
## [53,] 2.566021e-23 1.000000e+00  
## [54,] 1.816638e-30 1.000000e+00  
## [55,] 6.435249e-19 1.000000e+00  
## [56,] 7.888179e-33 1.000000e+00  
## [57,] 5.314120e-23 1.000000e+00  
## [58,] 1.000000e+00 1.186081e-17  
## [59,] 9.555424e-08 9.999999e-01  
## [60,] 5.206952e-16 1.000000e+00  
## [61,] 3.740832e-30 1.000000e+00  
## [62,] 9.929000e-10 1.000000e+00  
## [63,] 1.000000e+00 6.975198e-28  
## [64,] 4.690715e-25 1.000000e+00  
## [65,] 1.000000e+00 8.399559e-26  
## [66,] 1.000000e+00 5.162651e-21  
## [67,] 2.397772e-39 1.000000e+00  
## [68,] 1.000000e+00 1.762647e-26  
## [69,] 6.930117e-14 1.000000e+00  
## [70,] 4.907995e-22 1.000000e+00  
## [71,] 1.069898e-22 1.000000e+00  
## [72,] 1.000000e+00 8.399559e-26  
## [73,] 1.000000e+00 1.762647e-26  
## [74,] 9.999937e-01 6.260407e-06  
## [75,] 1.130444e-18 1.000000e+00  
## [76,] 9.623455e-33 1.000000e+00  
## [77,] 1.000000e+00 6.975198e-28  
## [78,] 1.000000e+00 3.253725e-19  
## [79,] 3.830656e-25 1.000000e+00  
## [80,] 6.565725e-34 1.000000e+00  
## [81,] 1.000000e+00 2.662058e-19  
## [82,] 1.000000e+00 3.989280e-24  
## [83,] 3.318364e-30 1.000000e+00  
## [84,] 1.000000e+00 1.680233e-13  
## [85,] 1.000000e+00 6.975198e-28  
## [86,] 3.169672e-32 1.000000e+00  
## [87,] 1.000000e+00 7.468990e-10  
## [88,] 1.000000e+00 1.507540e-12  
## [89,] 1.000000e+00 3.969392e-25  
## [90,] 6.534890e-20 1.000000e+00  
## [91,] 1.000000e+00 1.267487e-23  
## [92,] 1.000000e+00 1.762647e-26  
## [93,] 1.000000e+00 1.267487e-23  
## [94,] 1.000000e+00 1.034370e-17  
## [95,] 1.000000e+00 1.292192e-20  
## [96,] 1.320845e-29 1.000000e+00  
## [97,] 1.000000e+00 2.882595e-21  
## [98,] 1.000000e+00 2.410375e-23  
## [99,] 1.000000e+00 1.409433e-24  
## [100,] 1.000000e+00 5.523093e-18  
## [101,] 1.000000e+00 2.218955e-24  
## [102,] 1.000000e+00 3.969392e-25  
## [103,] 6.796381e-01 3.203619e-01  
## [104,] 1.000000e+00 6.496576e-19  
## [105,] 1.000000e+00 4.124024e-26  
## [106,] 1.000000e+00 1.762647e-26  
## [107,] 1.000000e+00 1.267487e-23  
## [108,] 1.000000e+00 1.267487e-23  
## [109,] 5.772320e-34 1.000000e+00  
## [110,] 1.000000e+00 4.321789e-19  
## [111,] 1.000000e+00 1.265502e-25  
## [112,] 1.000000e+00 6.007333e-17  
## [113,] 1.000000e+00 1.469286e-15  
## [114,] 2.983035e-32 1.000000e+00  
## [115,] 1.000000e+00 1.668477e-21  
## [116,] 1.000000e+00 3.969392e-25  
## [117,] 1.000000e+00 1.915922e-14  
## [118,] 1.000000e+00 1.265502e-25  
## [119,] 2.173834e-28 1.000000e+00  
## [120,] 3.440286e-32 1.000000e+00  
## [121,] 8.053273e-23 1.000000e+00  
## [122,] 1.000000e+00 1.245196e-20  
## [123,] 1.000000e+00 3.629161e-27  
## [124,] 1.000000e+00 3.969392e-25  
## [125,] 1.000000e+00 1.762647e-26  
## [126,] 1.000000e+00 9.713951e-25  
## [127,] 1.138125e-25 1.000000e+00  
## [128,] 6.773833e-17 1.000000e+00  
## [129,] 2.626614e-27 1.000000e+00  
## [130,] 4.956894e-22 1.000000e+00  
## [131,] 1.000000e+00 4.267615e-27  
## [132,] 1.000000e+00 1.850455e-10  
## [133,] 1.000000e+00 1.762647e-26  
## [134,] 1.000000e+00 4.043363e-16  
## [135,] 1.000000e+00 1.762647e-26  
## [136,] 1.473608e-30 1.000000e+00  
## [137,] 1.114167e-09 1.000000e+00  
## [138,] 7.952632e-30 1.000000e+00  
## [139,] 1.000000e+00 6.975198e-28  
## [140,] 3.835527e-17 1.000000e+00  
## [141,] 2.989799e-23 1.000000e+00  
## [142,] 1.000000e+00 8.637056e-25  
## [143,] 1.000000e+00 2.410375e-23  
## [144,] 1.000000e+00 3.989280e-24  
## [145,] 1.000000e+00 1.762647e-26  
## [146,] 9.720231e-25 1.000000e+00  
## [147,] 1.000000e+00 3.969392e-25  
## [148,] 1.000000e+00 7.120427e-23

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)  
combine.cl<-combine.classes[, -c(6,7)]  
  
# Calculate row sums  
majority.vote <- rowSums(combine.classes[, -c(6,7)])  
  
#majority.vote=rowSums(combine.classes[,-c(7,8)])  
head(majority.vote)

## 5 6 8 16 17 23   
## 0 5 0 5 0 0

combine.classes[,6]<-rowSums(combine.classes[,-c(6,7)])  
combine.classes[,7]<-ifelse(combine.classes[,6]>=4, "malignant", "benign")  
str(combine.classes)

## 'data.frame': 148 obs. of 7 variables:  
## $ myrf.pred : num 0 1 0 1 0 0 0 0 0 0 ...  
## $ mytree.pred : num 0 1 0 1 0 0 0 0 0 0 ...  
## $ mysvm.pred : num 0 1 0 1 0 0 0 0 0 0 ...  
## $ mynb.pred.class : num 0 1 0 1 0 0 0 0 0 0 ...  
## $ myrda.pred.class: num 0 1 0 1 0 0 0 0 0 0 ...  
## $ V6 : num 0 5 0 5 0 0 0 0 0 0 ...  
## $ V7 : chr "benign" "malignant" "benign" "malignant" ...

table(combine.classes[,7], BreastCancer[ind == 2,]$Class)

##   
## benign malignant  
## benign 87 0  
## malignant 5 56

# Load the caret package  
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

# Create a sample confusion matrix  
confusion\_matrix <- table(combine.classes[,7], BreastCancer[ind == 2,]$Class)  
  
# Calculate accuracy, precision, and recall  
accuracy <- sum(diag(confusion\_matrix))/sum(confusion\_matrix)  
precision <- diag(confusion\_matrix)/colSums(confusion\_matrix)  
recall <- diag(confusion\_matrix)/rowSums(confusion\_matrix)  
  
# Print the results  
cat(paste0("Accuracy: ", round(accuracy, 2), "\n"))

## Accuracy: 0.97

cat(paste0("Precision: ", paste(round(precision, 2), collapse = ", "), "\n"))

## Precision: 0.95, 1

cat(paste0("Recall: ", paste(round(recall, 2), collapse = ", "), "\n"))

## Recall: 1, 0.92