Project Portfolio Git

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# load data

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

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

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"

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.

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))

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

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

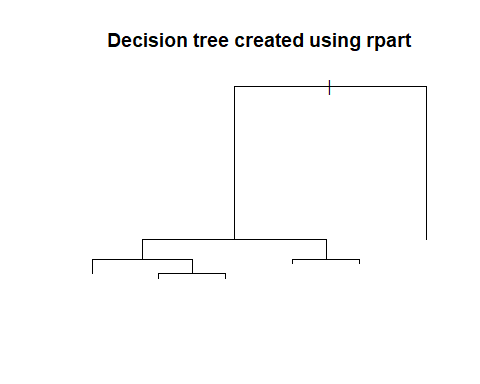
str(mysvm.pred)

## 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" ...

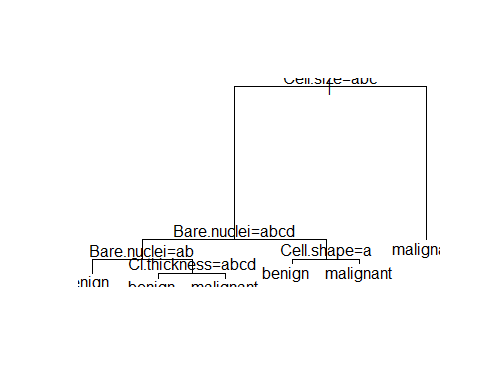
str(mynb.pred)

## 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"

x.rp <- rpart(Class ~ ., data=BreastCancer[ind == 1,])  
# predict classes for the evaluation data set  
x.rp.pred <- predict(x.rp, type="class", newdata=BreastCancer[ind == 2,])  
# score the evaluation data set (extract the probabilities)  
x.rp.prob <- predict(x.rp, type="prob", newdata=BreastCancer[ind == 2,])  
 plot(x.rp, main="Decision tree created using rpart")



library(rpart)  
mytree <- rpart(Class ~ ., BreastCancer[ind == 1,])  
plot(mytree); text(mytree)



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 0.2896175 0.03776013  
## 3 0.02185792 2 0.10928962 0.1420765 0.02717801  
## 4 0.01366120 3 0.08743169 0.1420765 0.02717801  
## 5 0.01000000 5 0.06010929 0.1366120 0.02667639  
##   
## 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

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

## myrf.pred mytree.pred mysvm.pred mynb.pred.class x.rp.pred  
## 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 4.814108e-27  
## [2,] 3.323523e-66 1.000000e+00  
## [3,] 1.000000e+00 7.935574e-32  
## [4,] 8.887013e-42 1.000000e+00  
## [5,] 1.000000e+00 3.044962e-30  
## [6,] 1.000000e+00 2.030715e-31  
## [7,] 1.000000e+00 2.713529e-28  
## [8,] 1.000000e+00 1.017491e-31  
## [9,] 1.000000e+00 1.034993e-31  
## [10,] 1.000000e+00 5.762716e-20  
## [11,] 1.077424e-43 1.000000e+00  
## [12,] 1.796440e-45 1.000000e+00  
## [13,] 1.000000e+00 4.814108e-27  
## [14,] 1.910586e-07 9.999998e-01  
## [15,] 9.831328e-44 1.000000e+00  
## [16,] 2.401558e-31 1.000000e+00  
## [17,] 2.717982e-32 1.000000e+00  
## [18,] 1.052128e-11 1.000000e+00  
## [19,] 1.000000e+00 8.040924e-30  
## [20,] 1.000000e+00 1.169826e-29  
## [21,] 1.075804e-61 1.000000e+00  
## [22,] 1.000000e+00 8.040924e-30  
## [23,] 1.000000e+00 8.040924e-30  
## [24,] 8.230360e-53 1.000000e+00  
## [25,] 1.242134e-18 1.000000e+00  
## [26,] 1.000000e+00 8.069162e-27  
## [27,] 1.000000e+00 1.715185e-11  
## [28,] 2.975258e-60 1.000000e+00  
## [29,] 1.000000e+00 2.821855e-18  
## [30,] 1.000000e+00 1.890825e-32  
## [31,] 4.656019e-69 1.000000e+00  
## [32,] 1.000000e+00 1.633948e-32  
## [33,] 1.000000e+00 3.630065e-34  
## [34,] 1.000000e+00 1.416988e-23  
## [35,] 1.000000e+00 1.265550e-30  
## [36,] 1.000000e+00 4.122642e-31  
## [37,] 1.000000e+00 1.400518e-32  
## [38,] 2.289865e-61 1.000000e+00  
## [39,] 3.264505e-53 1.000000e+00  
## [40,] 7.652035e-52 1.000000e+00  
## [41,] 1.000000e+00 1.341713e-31  
## [42,] 7.132737e-06 9.999929e-01  
## [43,] 6.434850e-47 1.000000e+00  
## [44,] 2.176908e-53 1.000000e+00  
## [45,] 2.289607e-78 1.000000e+00  
## [46,] 1.000000e+00 1.481841e-31  
## [47,] 3.619269e-54 1.000000e+00  
## [48,] 1.000000e+00 8.143797e-30  
## [49,] 1.145784e-63 1.000000e+00  
## [50,] 1.000000e+00 1.633948e-32  
## [51,] 9.062806e-59 1.000000e+00  
## [52,] 1.000000e+00 8.551978e-32  
## [53,] 1.884271e-51 1.000000e+00  
## [54,] 2.191617e-57 1.000000e+00  
## [55,] 1.361613e-29 1.000000e+00  
## [56,] 8.854472e-66 1.000000e+00  
## [57,] 1.536022e-23 1.000000e+00  
## [58,] 1.000000e+00 5.786262e-29  
## [59,] 1.058696e-19 1.000000e+00  
## [60,] 1.532250e-24 1.000000e+00  
## [61,] 1.077424e-43 1.000000e+00  
## [62,] 4.126566e-13 1.000000e+00  
## [63,] 1.000000e+00 1.633948e-32  
## [64,] 1.138883e-51 1.000000e+00  
## [65,] 1.000000e+00 1.429225e-30  
## [66,] 1.000000e+00 1.017491e-31  
## [67,] 7.155047e-68 1.000000e+00  
## [68,] 1.000000e+00 1.481841e-31  
## [69,] 1.459226e-22 1.000000e+00  
## [70,] 3.675709e-45 1.000000e+00  
## [71,] 1.402318e-37 1.000000e+00  
## [72,] 1.000000e+00 1.429225e-30  
## [73,] 1.000000e+00 1.481841e-31  
## [74,] 1.000000e+00 6.992122e-16  
## [75,] 2.099368e-37 1.000000e+00  
## [76,] 9.960562e-68 1.000000e+00  
## [77,] 1.000000e+00 1.633948e-32  
## [78,] 1.000000e+00 1.017954e-29  
## [79,] 6.607282e-41 1.000000e+00  
## [80,] 4.952865e-64 1.000000e+00  
## [81,] 1.000000e+00 3.710543e-31  
## [82,] 1.000000e+00 1.276287e-31  
## [83,] 2.834003e-51 1.000000e+00  
## [84,] 1.000000e+00 1.383643e-20  
## [85,] 1.000000e+00 1.633948e-32  
## [86,] 3.901061e-56 1.000000e+00  
## [87,] 1.000000e+00 1.576408e-18  
## [88,] 1.000000e+00 5.028190e-25  
## [89,] 1.000000e+00 1.265550e-30  
## [90,] 2.275099e-38 1.000000e+00  
## [91,] 1.000000e+00 1.295481e-28  
## [92,] 1.000000e+00 1.481841e-31  
## [93,] 1.000000e+00 1.295481e-28  
## [94,] 1.000000e+00 2.855793e-27  
## [95,] 1.000000e+00 1.027137e-28  
## [96,] 2.569187e-62 1.000000e+00  
## [97,] 1.000000e+00 7.552357e-25  
## [98,] 1.000000e+00 4.369145e-33  
## [99,] 1.000000e+00 2.056227e-32  
## [100,] 1.000000e+00 2.723075e-26  
## [101,] 1.000000e+00 9.919388e-30  
## [102,] 1.000000e+00 1.265550e-30  
## [103,] 8.437487e-01 1.562513e-01  
## [104,] 1.000000e+00 9.119108e-29  
## [105,] 1.000000e+00 3.044962e-30  
## [106,] 1.000000e+00 1.481841e-31  
## [107,] 1.000000e+00 1.295481e-28  
## [108,] 1.000000e+00 1.295481e-28  
## [109,] 8.471966e-57 1.000000e+00  
## [110,] 1.000000e+00 3.619352e-28  
## [111,] 1.000000e+00 4.436916e-32  
## [112,] 1.000000e+00 4.166678e-28  
## [113,] 1.000000e+00 2.040793e-28  
## [114,] 2.994827e-37 1.000000e+00  
## [115,] 1.000000e+00 1.911453e-33  
## [116,] 1.000000e+00 1.265550e-30  
## [117,] 1.000000e+00 3.000772e-30  
## [118,] 1.000000e+00 4.436916e-32  
## [119,] 4.927947e-45 1.000000e+00  
## [120,] 6.472880e-57 1.000000e+00  
## [121,] 7.262192e-38 1.000000e+00  
## [122,] 1.000000e+00 1.443499e-28  
## [123,] 1.000000e+00 1.625499e-31  
## [124,] 1.000000e+00 1.265550e-30  
## [125,] 1.000000e+00 1.481841e-31  
## [126,] 1.000000e+00 1.467249e-32  
## [127,] 9.617946e-62 1.000000e+00  
## [128,] 3.031922e-35 1.000000e+00  
## [129,] 1.055493e-40 1.000000e+00  
## [130,] 2.033403e-46 1.000000e+00  
## [131,] 1.000000e+00 2.030715e-31  
## [132,] 1.000000e+00 1.308883e-18  
## [133,] 1.000000e+00 1.481841e-31  
## [134,] 1.000000e+00 2.621663e-23  
## [135,] 1.000000e+00 1.481841e-31  
## [136,] 1.715461e-37 1.000000e+00  
## [137,] 2.044126e-27 1.000000e+00  
## [138,] 1.148448e-54 1.000000e+00  
## [139,] 1.000000e+00 1.633948e-32  
## [140,] 1.302182e-30 1.000000e+00  
## [141,] 2.125630e-38 1.000000e+00  
## [142,] 1.000000e+00 1.341713e-31  
## [143,] 1.000000e+00 4.369145e-33  
## [144,] 1.000000e+00 1.276287e-31  
## [145,] 1.000000e+00 1.481841e-31  
## [146,] 1.294163e-44 1.000000e+00  
## [147,] 1.000000e+00 1.265550e-30  
## [148,] 1.000000e+00 1.239002e-25

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 ...  
## $ x.rp.pred : 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 2  
## malignant 5 54

# 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 confusion matrix  
cm <- table(combine.classes[, 7], BreastCancer[ind == 2, ]$Class)  
  
# Calculate accuracy, precision, and recall  
accuracy <- confusionMatrix(cm)$overall[1]  
precision <- confusionMatrix(cm)$byClass[1]  
recall <- confusionMatrix(cm)$byClass[2]  
  
# Print the results  
cat("Accuracy:", round(accuracy, 3), "\n")

## Accuracy: 0.953

cat("Precision:", round(precision, 3), "\n")

## Precision: 0.946

cat("Recall:", round(recall, 3), "\n")

## Recall: 0.964