560\_ProjectTwo

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GITHUB LINK :

BreastCancer\_Ensemble

KNIT FILE

#load the mlbench package which has the BreastCancer data set  
library(mlbench)  
  
# load the data set  
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"

# some algorithms don't like missing values, so remove rows with missing values  
BreastCancer <- na.omit(BreastCancer)   
# remove the unique identifier, which is useless and would confuse the machine learning algorithms  
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

#SVM  
  
library(e1071)  
  
mysvm <- svm(Class ~ ., BreastCancer)  
mysvm.pred <- predict(mysvm, BreastCancer)  
  
table(mysvm.pred,BreastCancer$Class)

##   
## mysvm.pred benign malignant  
## benign 431 8  
## malignant 13 231

#Naive Bayes  
  
#install.packages("klaR")  
library(klaR)

## Loading required package: MASS

mynb <- NaiveBayes(Class ~ ., BreastCancer)  
mynb.pred <- predict(mynb,BreastCancer)

## 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  
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 683

head(mynb.pred$class)

## 1 2 3 4 5 6   
## benign malignant benign malignant benign malignant   
## Levels: benign malignant

table(mynb.pred$class,BreastCancer$Class)

##   
## benign malignant  
## benign 431 3  
## malignant 13 236

str(mysvm.pred)

## Factor w/ 2 levels "benign","malignant": 1 2 1 2 1 2 1 1 1 1 ...  
## - attr(\*, "names")= chr [1:683] "1" "2" "3" "4" ...

str(mynb.pred)

## List of 2  
## $ class : Factor w/ 2 levels "benign","malignant": 1 2 1 2 1 2 1 1 1 1 ...  
## ..- attr(\*, "names")= chr [1:683] "1" "2" "3" "4" ...  
## $ posterior: num [1:683, 1:2] 1.00 8.28e-05 1.00 4.93e-05 1.00 ...  
## ..- attr(\*, "dimnames")=List of 2  
## .. ..$ : chr [1:683] "1" "2" "3" "4" ...  
## .. ..$ : chr [1:2] "benign" "malignant"

# setosa versicolor virginica  
# setosa 50 0 0  
# versicolor 0 47 3  
# virginica 0 3 47

#Neural Network  
  
library(nnet)  
library(neuralnet)  
  
  
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" ...

for (i in c(1:9)){  
BreastCancer[,i] <-(as.numeric(BreastCancer[,i])-min(as.numeric(BreastCancer[,i]))) /  
 (max(as.numeric(BreastCancer[,i]))-min(as.numeric(BreastCancer[,i])))  
}  
  
  
library(caret)

## Loading required package: ggplot2

## Loading required package: lattice

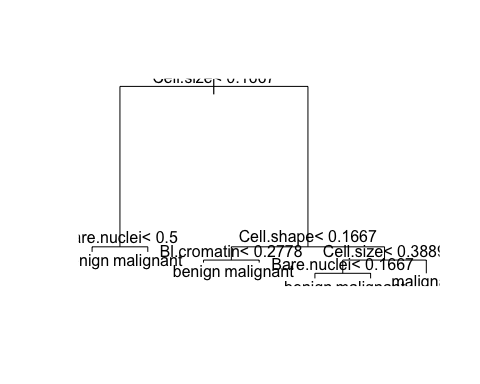
# convert categorical variables to dummy variables  
dummy\_transform <- dummyVars(Class ~ ., data = BreastCancer)  
BC\_transformed <- data.frame(predict(dummy\_transform, newdata = BreastCancer))

## Warning in model.frame.default(Terms, newdata, na.action = na.action, xlev =  
## object$lvls): variable 'Class' is not a factor

BC\_transformed$Class <- BreastCancer$Class  
  
  
mynnet <- neuralnet(Class ~ ., BC\_transformed, hidden=c(5,4))  
mynnet.pred <- predict(mynnet,BC\_transformed)  
mynnet.class <- ifelse(mynnet.pred > 0.5, "malignant", "benign")  
mynnet.class <- factor(mynnet.class[, 1], levels = c("benign", "malignant"))  
  
  
table(mynnet.class,BC\_transformed$Class)

##   
## mynnet.class benign malignant  
## benign 1 239  
## malignant 443 0

#Decision trees  
library(MASS)  
library(rpart)  
  
mytree <- rpart(Class ~ ., BreastCancer)  
plot(mytree); text(mytree)



summary(mytree)

## Call:  
## rpart(formula = Class ~ ., data = BreastCancer)  
## n= 683   
##   
## CP nsplit rel error xerror xstd  
## 1 0.79079498 0 1.00000000 1.0000000 0.05215335  
## 2 0.05439331 1 0.20920502 0.2510460 0.03095362  
## 3 0.02510460 2 0.15481172 0.1589958 0.02506475  
## 4 0.01255230 3 0.12970711 0.1631799 0.02537272  
## 5 0.01000000 6 0.09205021 0.1589958 0.02506475  
##   
## Variable importance  
## Cell.size Cell.shape Bare.nuclei Epith.c.size Bl.cromatin   
## 21 18 16 15 15   
## Normal.nucleoli Cl.thickness   
## 14 1   
##   
## Node number 1: 683 observations, complexity param=0.790795  
## predicted class=benign expected loss=0.3499268 P(node) =1  
## class counts: 444 239  
## probabilities: 0.650 0.350   
## left son=2 (418 obs) right son=3 (265 obs)  
## Primary splits:  
## Cell.size < 0.1666667 to the left, improve=222.3221, (0 missing)  
## Cell.shape < 0.2777778 to the left, improve=216.4111, (0 missing)  
## Bare.nuclei < 0.1666667 to the left, improve=203.7284, (0 missing)  
## Bl.cromatin < 0.2777778 to the left, improve=196.3903, (0 missing)  
## Epith.c.size < 0.1666667 to the left, improve=193.1310, (0 missing)  
## Surrogate splits:  
## Cell.shape < 0.2777778 to the left, agree=0.917, adj=0.785, (0 split)  
## Epith.c.size < 0.1666667 to the left, agree=0.900, adj=0.743, (0 split)  
## Bare.nuclei < 0.1666667 to the left, agree=0.880, adj=0.691, (0 split)  
## Normal.nucleoli < 0.1666667 to the left, agree=0.877, adj=0.683, (0 split)  
## Bl.cromatin < 0.2777778 to the left, agree=0.876, adj=0.679, (0 split)  
##   
## Node number 2: 418 observations, complexity param=0.0251046  
## predicted class=benign expected loss=0.02870813 P(node) =0.6120059  
## class counts: 406 12  
## probabilities: 0.971 0.029   
## left son=4 (410 obs) right son=5 (8 obs)  
## Primary splits:  
## Bare.nuclei < 0.5 to the left, improve=11.68296, (0 missing)  
## Cl.thickness < 0.6111111 to the left, improve=10.32214, (0 missing)  
## Normal.nucleoli < 0.2777778 to the left, improve=10.32214, (0 missing)  
## Bl.cromatin < 0.3888889 to the left, improve= 8.53307, (0 missing)  
## Epith.c.size < 0.2777778 to the left, improve= 4.63208, (0 missing)  
## Surrogate splits:  
## Cl.thickness < 0.8333333 to the left, agree=0.988, adj=0.375, (0 split)  
## Normal.nucleoli < 0.2777778 to the left, agree=0.983, adj=0.125, (0 split)  
##   
## Node number 3: 265 observations, complexity param=0.05439331  
## predicted class=malignant expected loss=0.1433962 P(node) =0.3879941  
## class counts: 38 227  
## probabilities: 0.143 0.857   
## left son=6 (23 obs) right son=7 (242 obs)  
## Primary splits:  
## Cell.shape < 0.1666667 to the left, improve=20.58158, (0 missing)  
## Cell.size < 0.2777778 to the left, improve=18.27650, (0 missing)  
## Bare.nuclei < 0.05555556 to the left, improve=16.81493, (0 missing)  
## Bl.cromatin < 0.1666667 to the left, improve=13.91034, (0 missing)  
## Marg.adhesion < 0.1666667 to the left, improve=11.17148, (0 missing)  
## Surrogate splits:  
## Bl.cromatin < 0.05555556 to the left, agree=0.932, adj=0.217, (0 split)  
##   
## Node number 4: 410 observations  
## predicted class=benign expected loss=0.01219512 P(node) =0.6002928  
## class counts: 405 5  
## probabilities: 0.988 0.012   
##   
## Node number 5: 8 observations  
## predicted class=malignant expected loss=0.125 P(node) =0.01171303  
## class counts: 1 7  
## probabilities: 0.125 0.875   
##   
## Node number 6: 23 observations, complexity param=0.0125523  
## predicted class=benign expected loss=0.2173913 P(node) =0.03367496  
## class counts: 18 5  
## probabilities: 0.783 0.217   
## left son=12 (16 obs) right son=13 (7 obs)  
## Primary splits:  
## Bl.cromatin < 0.2777778 to the left, improve=4.968944, (0 missing)  
## Cl.thickness < 0.3888889 to the left, improve=3.381643, (0 missing)  
## Bare.nuclei < 0.05555556 to the left, improve=2.826087, (0 missing)  
## Mitoses < 0.0625 to the left, improve=2.522516, (0 missing)  
## Epith.c.size < 0.1666667 to the left, improve=1.992754, (0 missing)  
## Surrogate splits:  
## Cl.thickness < 0.5 to the left, agree=0.870, adj=0.571, (0 split)  
## Marg.adhesion < 0.6666667 to the left, agree=0.826, adj=0.429, (0 split)  
## Normal.nucleoli < 0.1666667 to the left, agree=0.826, adj=0.429, (0 split)  
## Mitoses < 0.0625 to the left, agree=0.826, adj=0.429, (0 split)  
## Epith.c.size < 0.3333333 to the left, agree=0.783, adj=0.286, (0 split)  
##   
## Node number 7: 242 observations, complexity param=0.0125523  
## predicted class=malignant expected loss=0.08264463 P(node) =0.3543192  
## class counts: 20 222  
## probabilities: 0.083 0.917   
## left son=14 (68 obs) right son=15 (174 obs)  
## Primary splits:  
## Cell.size < 0.3888889 to the left, improve=5.297663, (0 missing)  
## Bare.nuclei < 0.1666667 to the left, improve=4.093695, (0 missing)  
## Cell.shape < 0.3888889 to the left, improve=2.958548, (0 missing)  
## Bl.cromatin < 0.2777778 to the left, improve=2.805426, (0 missing)  
## Marg.adhesion < 0.5 to the left, improve=2.754821, (0 missing)  
## Surrogate splits:  
## Cell.shape < 0.3888889 to the left, agree=0.789, adj=0.250, (0 split)  
## Epith.c.size < 0.1666667 to the left, agree=0.777, adj=0.206, (0 split)  
## Marg.adhesion < 0.05555556 to the left, agree=0.744, adj=0.088, (0 split)  
## Bl.cromatin < 0.1666667 to the left, agree=0.736, adj=0.059, (0 split)  
##   
## Node number 12: 16 observations  
## predicted class=benign expected loss=0 P(node) =0.02342606  
## class counts: 16 0  
## probabilities: 1.000 0.000   
##   
## Node number 13: 7 observations  
## predicted class=malignant expected loss=0.2857143 P(node) =0.0102489  
## class counts: 2 5  
## probabilities: 0.286 0.714   
##   
## Node number 14: 68 observations, complexity param=0.0125523  
## predicted class=malignant expected loss=0.25 P(node) =0.09956076  
## class counts: 17 51  
## probabilities: 0.250 0.750   
## left son=28 (14 obs) right son=29 (54 obs)  
## Primary splits:  
## Bare.nuclei < 0.1666667 to the left, improve=7.600529, (0 missing)  
## Cl.thickness < 0.6111111 to the left, improve=3.558824, (0 missing)  
## Marg.adhesion < 0.5 to the left, improve=2.615385, (0 missing)  
## Normal.nucleoli < 0.1666667 to the left, improve=1.937690, (0 missing)  
## Bl.cromatin < 0.2777778 to the left, improve=1.525641, (0 missing)  
##   
## Node number 15: 174 observations  
## predicted class=malignant expected loss=0.01724138 P(node) =0.2547584  
## class counts: 3 171  
## probabilities: 0.017 0.983   
##   
## Node number 28: 14 observations  
## predicted class=benign expected loss=0.2857143 P(node) =0.0204978  
## class counts: 10 4  
## probabilities: 0.714 0.286   
##   
## Node number 29: 54 observations  
## predicted class=malignant expected loss=0.1296296 P(node) =0.07906296  
## class counts: 7 47  
## probabilities: 0.130 0.870

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

##   
## mytree.pred benign malignant  
## benign 431 9  
## malignant 13 230

# 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 431 24  
## malignant 13 215

# The same positives as above in this case

#Quadratic Discriminant Analysis  
library(MASS)  
library(MASS)  
myqda <- qda(Species ~ ., iris)  
myqda.pred <- predict(myqda, iris)  
table(myqda.pred$class,iris$Species)

##   
## setosa versicolor virginica  
## setosa 50 0 0  
## versicolor 0 48 1  
## virginica 0 2 49

myqda <- qda(Class ~ ., BreastCancer)  
myqda.pred <- predict(myqda, BreastCancer)  
head(myqda.pred$class)

## [1] benign malignant benign malignant benign malignant  
## Levels: benign malignant

table(myqda.pred$class,BreastCancer$Class)

##   
## benign malignant  
## benign 422 6  
## malignant 22 233

#Regularised Discriminant Analysis  
library(klaR)  
myrda <- rda(Class ~ ., BreastCancer)  
myrda.pred <- predict(myrda, BreastCancer)  
  
table(myrda.pred$class,BreastCancer$Class)

##   
## benign malignant  
## benign 430 6  
## malignant 14 233

#Random Forests  
library(randomForest)

## randomForest 4.7-1.1

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

##   
## Attaching package: 'randomForest'

## The following object is masked from 'package:ggplot2':  
##   
## margin

myrf <- randomForest(Class ~ ., BreastCancer)  
myrf.pred <- predict(myrf, BreastCancer)  
head(myrf.pred)

## 1 2 3 4 5 6   
## benign benign benign benign benign malignant   
## Levels: benign malignant

table(myrf.pred, BreastCancer$Class)

##   
## myrf.pred benign malignant  
## benign 444 0  
## malignant 0 239

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

## myrf.pred myrda.pred.class mytree.pred X1 X2 mysvm.pred  
## 1 benign benign malignant 0.999986900 5.642474e-05 benign  
## 2 benign malignant malignant 0.998219477 2.197725e-03 malignant  
## 3 benign benign malignant 0.999986900 5.642474e-05 benign  
## 4 benign malignant malignant 0.999986900 5.642480e-05 malignant  
## 5 benign benign malignant 0.999986900 5.642474e-05 benign  
## 6 malignant malignant malignant 0.003040013 9.969352e-01 malignant  
## mynb.pred.class  
## 1 benign  
## 2 malignant  
## 3 benign  
## 4 malignant  
## 5 benign  
## 6 malignant

head(myrf.pred)

## 1 2 3 4 5 6   
## benign benign benign benign benign malignant   
## Levels: benign malignant

head(myrda.pred)

## $class  
## [1] benign malignant benign malignant benign malignant malignant  
## [8] benign benign benign benign benign benign benign   
## [15] malignant malignant benign benign malignant benign malignant  
## [22] malignant benign benign malignant benign benign benign   
## [29] benign benign benign malignant benign benign benign   
## [36] malignant benign malignant malignant malignant malignant malignant  
## [43] malignant benign malignant benign benign malignant malignant  
## [50] benign malignant malignant malignant malignant malignant malignant  
## [57] malignant malignant malignant benign malignant malignant benign   
## [64] malignant benign malignant malignant benign benign malignant  
## [71] benign malignant malignant benign benign benign benign   
## [78] benign benign benign benign benign malignant malignant  
## [85] malignant malignant benign benign benign benign benign   
## [92] benign benign benign benign benign malignant malignant  
## [99] malignant malignant benign malignant malignant malignant malignant  
## [106] malignant benign malignant benign malignant malignant malignant  
## [113] benign benign benign malignant benign benign benign   
## [120] benign malignant malignant malignant benign malignant benign   
## [127] malignant benign benign benign malignant benign benign   
## [134] benign benign benign benign benign benign malignant  
## [141] benign benign malignant benign malignant malignant benign   
## [148] malignant malignant benign benign malignant benign benign   
## [155] malignant malignant benign benign benign benign malignant  
## [162] malignant benign benign benign benign benign malignant  
## [169] malignant malignant benign malignant benign malignant benign   
## [176] benign benign malignant malignant benign malignant malignant  
## [183] malignant benign malignant malignant benign benign benign   
## [190] benign malignant benign benign benign malignant malignant  
## [197] benign benign benign malignant malignant benign benign   
## [204] benign malignant malignant benign malignant malignant malignant  
## [211] benign benign malignant benign benign malignant benign   
## [218] malignant malignant benign malignant malignant benign malignant  
## [225] malignant malignant malignant malignant benign malignant malignant  
## [232] malignant malignant benign benign benign benign benign   
## [239] benign malignant malignant benign benign malignant malignant  
## [246] malignant malignant malignant benign benign benign malignant  
## [253] malignant malignant malignant malignant malignant benign malignant  
## [260] malignant malignant benign malignant benign malignant benign   
## [267] benign benign benign benign malignant benign benign   
## [274] malignant malignant malignant malignant malignant benign malignant  
## [281] malignant benign benign malignant malignant malignant benign   
## [288] malignant malignant benign malignant benign malignant malignant  
## [295] benign benign malignant benign benign benign malignant  
## [302] benign benign malignant malignant benign malignant malignant  
## [309] benign malignant benign benign malignant benign malignant  
## [316] malignant malignant benign benign malignant malignant benign   
## [323] malignant benign benign malignant malignant benign benign   
## [330] benign malignant benign benign benign malignant malignant  
## [337] benign benign malignant malignant benign benign benign   
## [344] malignant malignant malignant malignant malignant benign benign   
## [351] benign benign malignant malignant benign benign benign   
## [358] benign benign benign benign benign benign benign   
## [365] benign benign benign malignant benign benign benign   
## [372] benign malignant benign benign benign benign malignant  
## [379] benign benign benign benign benign benign benign   
## [386] benign malignant benign benign benign benign benign   
## [393] benign benign benign benign benign malignant benign   
## [400] malignant benign malignant benign benign benign benign   
## [407] malignant benign benign benign malignant benign malignant  
## [414] benign benign benign benign benign benign malignant  
## [421] malignant malignant benign benign benign malignant benign   
## [428] benign benign benign benign benign benign benign   
## [435] malignant benign benign benign malignant benign malignant  
## [442] malignant malignant benign benign benign benign benign   
## [449] benign benign malignant malignant malignant benign benign   
## [456] benign benign benign benign benign benign benign   
## [463] benign benign malignant benign benign malignant malignant  
## [470] benign benign benign malignant malignant benign benign   
## [477] malignant benign malignant malignant benign benign benign   
## [484] benign benign benign benign benign benign benign   
## [491] benign malignant benign benign benign benign benign   
## [498] benign benign malignant malignant benign benign benign   
## [505] malignant benign benign malignant malignant benign benign   
## [512] benign benign benign benign malignant benign benign   
## [519] benign benign benign benign benign benign benign   
## [526] benign benign benign benign benign benign malignant  
## [533] benign benign malignant benign benign benign benign   
## [540] benign benign benign benign benign benign benign   
## [547] benign benign benign benign malignant benign benign   
## [554] malignant malignant malignant malignant benign benign malignant  
## [561] benign benign benign benign benign benign malignant  
## [568] malignant benign benign benign malignant benign malignant  
## [575] benign malignant malignant malignant benign malignant benign   
## [582] benign benign benign benign benign benign benign   
## [589] malignant malignant malignant benign benign malignant benign   
## [596] malignant malignant malignant benign benign benign benign   
## [603] benign benign benign benign benign benign benign   
## [610] benign malignant benign benign benign benign benign   
## [617] benign malignant benign benign malignant benign benign   
## [624] benign benign benign benign benign benign benign   
## [631] benign benign malignant benign benign benign benign   
## [638] benign benign benign benign malignant malignant benign   
## [645] benign benign benign benign benign benign benign   
## [652] benign malignant malignant malignant benign benign benign   
## [659] benign benign benign benign benign benign malignant  
## [666] malignant benign benign benign benign benign benign   
## [673] benign benign benign malignant benign benign benign   
## [680] benign malignant malignant malignant  
## Levels: benign malignant  
##   
## $posterior  
## benign malignant  
## [1,] 1.000000e+00 2.172367e-08  
## [2,] 4.077881e-13 1.000000e+00  
## [3,] 1.000000e+00 6.344410e-09  
## [4,] 8.170866e-14 1.000000e+00  
## [5,] 1.000000e+00 3.300192e-08  
## [6,] 2.136895e-46 1.000000e+00  
## [7,] 2.393613e-03 9.976064e-01  
## [8,] 1.000000e+00 3.317407e-09  
## [9,] 9.999998e-01 2.049413e-07  
## [10,] 1.000000e+00 6.124881e-09  
## [11,] 1.000000e+00 1.413624e-09  
## [12,] 1.000000e+00 7.434080e-10  
## [13,] 9.933263e-01 6.673709e-03  
## [14,] 1.000000e+00 1.903791e-08  
## [15,] 6.361284e-30 1.000000e+00  
## [16,] 6.369976e-05 9.999363e-01  
## [17,] 1.000000e+00 2.729318e-09  
## [18,] 1.000000e+00 5.720058e-09  
## [19,] 3.193738e-24 1.000000e+00  
## [20,] 9.999999e-01 1.304370e-07  
## [21,] 3.120078e-22 1.000000e+00  
## [22,] 3.897423e-25 1.000000e+00  
## [23,] 1.000000e+00 1.132852e-09  
## [24,] 1.000000e+00 1.630836e-09  
## [25,] 9.105414e-05 9.999089e-01  
## [26,] 1.000000e+00 2.247784e-09  
## [27,] 1.000000e+00 1.039608e-08  
## [28,] 1.000000e+00 7.434080e-10  
## [29,] 1.000000e+00 4.538207e-09  
## [30,] 1.000000e+00 9.868158e-10  
## [31,] 1.000000e+00 1.567252e-09  
## [32,] 5.690220e-22 1.000000e+00  
## [33,] 1.000000e+00 2.980201e-09  
## [34,] 1.000000e+00 2.387522e-09  
## [35,] 1.000000e+00 7.434080e-10  
## [36,] 1.340938e-39 1.000000e+00  
## [37,] 9.993585e-01 6.414634e-04  
## [38,] 9.057379e-20 1.000000e+00  
## [39,] 1.515141e-09 1.000000e+00  
## [40,] 2.581854e-07 9.999997e-01  
## [41,] 1.931741e-34 1.000000e+00  
## [42,] 1.157628e-10 1.000000e+00  
## [43,] 3.433575e-39 1.000000e+00  
## [44,] 1.000000e+00 1.283958e-09  
## [45,] 6.864709e-20 1.000000e+00  
## [46,] 1.000000e+00 7.712868e-10  
## [47,] 1.000000e+00 3.300192e-08  
## [48,] 1.028965e-20 1.000000e+00  
## [49,] 1.229739e-09 1.000000e+00  
## [50,] 9.399113e-01 6.008867e-02  
## [51,] 2.309372e-17 1.000000e+00  
## [52,] 2.276367e-28 1.000000e+00  
## [53,] 6.617484e-22 1.000000e+00  
## [54,] 1.199056e-13 1.000000e+00  
## [55,] 1.360694e-28 1.000000e+00  
## [56,] 1.803510e-03 9.981965e-01  
## [57,] 5.876514e-09 1.000000e+00  
## [58,] 3.116004e-04 9.996884e-01  
## [59,] 1.230444e-10 1.000000e+00  
## [60,] 1.000000e+00 2.080901e-09  
## [61,] 4.207914e-33 1.000000e+00  
## [62,] 2.642178e-06 9.999974e-01  
## [63,] 1.000000e+00 7.712868e-10  
## [64,] 2.625743e-12 1.000000e+00  
## [65,] 1.000000e+00 5.720058e-09  
## [66,] 8.329033e-20 1.000000e+00  
## [67,] 2.775025e-33 1.000000e+00  
## [68,] 1.000000e+00 3.439865e-09  
## [69,] 9.999999e-01 7.303834e-08  
## [70,] 7.261856e-38 1.000000e+00  
## [71,] 9.991134e-01 8.866327e-04  
## [72,] 1.139371e-30 1.000000e+00  
## [73,] 3.547615e-07 9.999996e-01  
## [74,] 9.999999e-01 6.546982e-08  
## [75,] 1.000000e+00 3.358735e-08  
## [76,] 9.999998e-01 1.570498e-07  
## [77,] 1.000000e+00 2.739456e-08  
## [78,] 1.000000e+00 1.409018e-09  
## [79,] 9.999831e-01 1.689535e-05  
## [80,] 1.000000e+00 5.140347e-09  
## [81,] 1.000000e+00 4.811402e-08  
## [82,] 9.999837e-01 1.633523e-05  
## [83,] 1.825506e-37 1.000000e+00  
## [84,] 1.763251e-36 1.000000e+00  
## [85,] 1.634684e-08 1.000000e+00  
## [86,] 4.890132e-24 1.000000e+00  
## [87,] 1.000000e+00 5.720058e-09  
## [88,] 1.000000e+00 2.674192e-09  
## [89,] 1.000000e+00 1.630836e-09  
## [90,] 1.000000e+00 1.673780e-09  
## [91,] 1.000000e+00 5.720058e-09  
## [92,] 1.000000e+00 7.712868e-10  
## [93,] 1.000000e+00 1.567252e-09  
## [94,] 1.000000e+00 1.630836e-09  
## [95,] 1.000000e+00 1.102268e-09  
## [96,] 1.000000e+00 2.172367e-08  
## [97,] 4.604720e-38 1.000000e+00  
## [98,] 3.758746e-35 1.000000e+00  
## [99,] 4.728436e-23 1.000000e+00  
## [100,] 4.170285e-01 5.829715e-01  
## [101,] 1.000000e+00 1.189203e-08  
## [102,] 8.608806e-04 9.991391e-01  
## [103,] 4.558370e-54 1.000000e+00  
## [104,] 1.322777e-05 9.999868e-01  
## [105,] 1.623832e-36 1.000000e+00  
## [106,] 2.979573e-33 1.000000e+00  
## [107,] 1.000000e+00 5.697112e-09  
## [108,] 1.101286e-18 1.000000e+00  
## [109,] 9.999858e-01 1.416561e-05  
## [110,] 3.248074e-12 1.000000e+00  
## [111,] 5.759736e-26 1.000000e+00  
## [112,] 5.929801e-39 1.000000e+00  
## [113,] 9.999996e-01 4.421489e-07  
## [114,] 9.999994e-01 5.838388e-07  
## [115,] 9.956032e-01 4.396756e-03  
## [116,] 1.107921e-31 1.000000e+00  
## [117,] 1.000000e+00 4.150746e-08  
## [118,] 1.000000e+00 1.413969e-08  
## [119,] 1.000000e+00 6.633311e-09  
## [120,] 1.000000e+00 3.359514e-08  
## [121,] 2.535256e-40 1.000000e+00  
## [122,] 3.904537e-14 1.000000e+00  
## [123,] 1.070429e-28 1.000000e+00  
## [124,] 1.000000e+00 7.712868e-10  
## [125,] 1.958019e-22 1.000000e+00  
## [126,] 1.000000e+00 2.381235e-09  
## [127,] 2.644093e-16 1.000000e+00  
## [128,] 8.949999e-01 1.050001e-01  
## [129,] 9.999999e-01 7.303834e-08  
## [130,] 1.000000e+00 1.567252e-09  
## [131,] 1.124429e-38 1.000000e+00  
## [132,] 1.000000e+00 2.381023e-09  
## [133,] 1.000000e+00 2.138460e-09  
## [134,] 9.999996e-01 3.948878e-07  
## [135,] 1.000000e+00 2.729318e-09  
## [136,] 1.000000e+00 8.799864e-10  
## [137,] 1.000000e+00 5.700672e-09  
## [138,] 1.000000e+00 8.799864e-10  
## [139,] 1.000000e+00 5.757676e-10  
## [140,] 4.482137e-09 1.000000e+00  
## [141,] 9.999994e-01 5.838388e-07  
## [142,] 1.000000e+00 7.434080e-10  
## [143,] 1.779262e-06 9.999982e-01  
## [144,] 1.000000e+00 3.935546e-09  
## [145,] 1.758867e-05 9.999824e-01  
## [146,] 1.119954e-41 1.000000e+00  
## [147,] 1.000000e+00 1.413624e-09  
## [148,] 2.011762e-13 1.000000e+00  
## [149,] 2.872139e-36 1.000000e+00  
## [150,] 1.000000e+00 2.479822e-08  
## [151,] 1.000000e+00 5.955980e-10  
## [152,] 9.862343e-13 1.000000e+00  
## [153,] 1.000000e+00 3.743199e-09  
## [154,] 1.000000e+00 1.567252e-09  
## [155,] 1.097918e-45 1.000000e+00  
## [156,] 4.076407e-28 1.000000e+00  
## [157,] 1.000000e+00 1.186223e-08  
## [158,] 1.000000e+00 2.381235e-09  
## [159,] 9.964366e-01 3.563406e-03  
## [160,] 1.000000e+00 3.131131e-08  
## [161,] 1.473621e-33 1.000000e+00  
## [162,] 5.867647e-37 1.000000e+00  
## [163,] 1.000000e+00 2.381235e-09  
## [164,] 1.000000e+00 9.937197e-10  
## [165,] 1.000000e+00 8.799864e-10  
## [166,] 1.000000e+00 1.630836e-09  
## [167,] 1.000000e+00 7.712868e-10  
## [168,] 3.269842e-61 1.000000e+00  
## [169,] 8.581604e-17 1.000000e+00  
## [170,] 2.324088e-33 1.000000e+00  
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## [545,] 1.000000e+00 1.039608e-08  
## [546,] 1.000000e+00 2.172367e-08  
## [547,] 1.000000e+00 2.172367e-08  
## [548,] 1.000000e+00 1.630836e-09  
## [549,] 1.000000e+00 1.132852e-09  
## [550,] 1.000000e+00 1.186223e-08  
## [551,] 3.047173e-47 1.000000e+00  
## [552,] 1.000000e+00 4.995282e-09  
## [553,] 1.000000e+00 3.149843e-08  
## [554,] 1.129954e-14 1.000000e+00  
## [555,] 2.093549e-38 1.000000e+00  
## [556,] 1.992019e-29 1.000000e+00  
## [557,] 8.685288e-38 1.000000e+00  
## [558,] 1.000000e+00 1.132852e-09  
## [559,] 1.000000e+00 7.712868e-10  
## [560,] 9.648084e-22 1.000000e+00  
## [561,] 1.000000e+00 4.475966e-08  
## [562,] 1.000000e+00 1.039608e-08  
## [563,] 1.000000e+00 7.712868e-10  
## [564,] 1.000000e+00 7.712868e-10  
## [565,] 1.000000e+00 1.630836e-09  
## [566,] 1.000000e+00 2.151986e-08  
## [567,] 4.274560e-29 1.000000e+00  
## [568,] 2.658854e-32 1.000000e+00  
## [569,] 1.000000e+00 8.799864e-10  
## [570,] 9.999519e-01 4.807420e-05  
## [571,] 1.000000e+00 5.955980e-10  
## [572,] 1.386748e-55 1.000000e+00  
## [573,] 1.000000e+00 2.160478e-08  
## [574,] 8.581829e-22 1.000000e+00  
## [575,] 1.000000e+00 8.123395e-09  
## [576,] 1.615284e-20 1.000000e+00  
## [577,] 3.839193e-21 1.000000e+00  
## [578,] 2.882809e-15 1.000000e+00  
## [579,] 1.000000e+00 1.689366e-08  
## [580,] 1.947207e-18 1.000000e+00  
## [581,] 1.000000e+00 1.039608e-08  
## [582,] 1.000000e+00 5.700672e-09  
## [583,] 9.999998e-01 1.512104e-07  
## [584,] 1.000000e+00 1.132852e-09  
## [585,] 9.999994e-01 6.226889e-07  
## [586,] 1.000000e+00 1.132852e-09  
## [587,] 1.000000e+00 6.664319e-10  
## [588,] 1.000000e+00 2.729318e-09  
## [589,] 7.562042e-20 1.000000e+00  
## [590,] 9.753314e-18 1.000000e+00  
## [591,] 2.195474e-30 1.000000e+00  
## [592,] 1.000000e+00 4.018320e-09  
## [593,] 1.000000e+00 5.955980e-10  
## [594,] 2.784414e-49 1.000000e+00  
## [595,] 1.000000e+00 8.123395e-09  
## [596,] 1.095945e-25 1.000000e+00  
## [597,] 6.736995e-32 1.000000e+00  
## [598,] 6.927447e-65 1.000000e+00  
## [599,] 1.000000e+00 6.341446e-09  
## [600,] 1.000000e+00 6.449537e-10  
## [601,] 1.000000e+00 1.952269e-08  
## [602,] 1.000000e+00 1.132852e-09  
## [603,] 1.000000e+00 2.729318e-09  
## [604,] 1.000000e+00 1.039608e-08  
## [605,] 1.000000e+00 1.132852e-09  
## [606,] 9.758505e-01 2.414953e-02  
## [607,] 9.999933e-01 6.703523e-06  
## [608,] 1.000000e+00 5.955980e-10  
## [609,] 1.000000e+00 1.717408e-08  
## [610,] 9.999991e-01 9.414101e-07  
## [611,] 5.897578e-18 1.000000e+00  
## [612,] 9.999994e-01 5.562116e-07  
## [613,] 1.000000e+00 5.757676e-10  
## [614,] 1.000000e+00 2.126373e-09  
## [615,] 9.999993e-01 7.390381e-07  
## [616,] 1.000000e+00 1.039608e-08  
## [617,] 1.000000e+00 5.955980e-10  
## [618,] 2.017064e-17 1.000000e+00  
## [619,] 1.000000e+00 8.799864e-10  
## [620,] 1.000000e+00 3.681903e-08  
## [621,] 2.098860e-41 1.000000e+00  
## [622,] 9.999967e-01 3.341748e-06  
## [623,] 1.000000e+00 2.126373e-09  
## [624,] 1.000000e+00 4.689302e-08  
## [625,] 1.000000e+00 1.243498e-08  
## [626,] 1.000000e+00 1.132852e-09  
## [627,] 1.000000e+00 1.132852e-09  
## [628,] 1.000000e+00 5.955980e-10  
## [629,] 1.000000e+00 5.757676e-10  
## [630,] 1.000000e+00 1.132852e-09  
## [631,] 1.000000e+00 2.920970e-09  
## [632,] 1.000000e+00 3.621293e-09  
## [633,] 5.547869e-58 1.000000e+00  
## [634,] 1.000000e+00 1.132852e-09  
## [635,] 9.999997e-01 2.504785e-07  
## [636,] 1.000000e+00 1.056561e-08  
## [637,] 1.000000e+00 2.160478e-08  
## [638,] 1.000000e+00 2.729318e-09  
## [639,] 1.000000e+00 2.381235e-09  
## [640,] 1.000000e+00 1.132852e-09  
## [641,] 1.000000e+00 1.039608e-08  
## [642,] 1.998608e-05 9.999800e-01  
## [643,] 1.337826e-27 1.000000e+00  
## [644,] 1.000000e+00 5.955980e-10  
## [645,] 1.000000e+00 7.712868e-10  
## [646,] 1.000000e+00 5.720058e-09  
## [647,] 1.000000e+00 5.822563e-09  
## [648,] 1.000000e+00 5.822563e-09  
## [649,] 1.000000e+00 6.666231e-09  
## [650,] 1.000000e+00 5.955980e-10  
## [651,] 9.999999e-01 1.151208e-07  
## [652,] 1.000000e+00 2.381235e-09  
## [653,] 4.515868e-16 1.000000e+00  
## [654,] 1.552415e-36 1.000000e+00  
## [655,] 1.569675e-26 1.000000e+00  
## [656,] 1.000000e+00 1.005417e-08  
## [657,] 1.000000e+00 1.567252e-09  
## [658,] 9.999998e-01 2.492946e-07  
## [659,] 1.000000e+00 7.712868e-10  
## [660,] 9.999999e-01 8.660229e-08  
## [661,] 1.000000e+00 1.654986e-09  
## [662,] 1.000000e+00 8.123395e-09  
## [663,] 1.000000e+00 5.955980e-10  
## [664,] 1.000000e+00 5.757676e-10  
## [665,] 8.446515e-63 1.000000e+00  
## [666,] 1.047331e-39 1.000000e+00  
## [667,] 1.000000e+00 4.479651e-08  
## [668,] 1.000000e+00 5.955980e-10  
## [669,] 1.000000e+00 5.955980e-10  
## [670,] 1.000000e+00 5.955980e-10  
## [671,] 1.000000e+00 5.955980e-10  
## [672,] 1.000000e+00 8.180729e-09  
## [673,] 1.000000e+00 2.126373e-09  
## [674,] 9.859661e-01 1.403392e-02  
## [675,] 1.000000e+00 3.621293e-09  
## [676,] 3.147692e-21 1.000000e+00  
## [677,] 1.000000e+00 8.799864e-10  
## [678,] 1.000000e+00 1.887992e-09  
## [679,] 1.000000e+00 4.458878e-09  
## [680,] 1.000000e+00 5.757676e-10  
## [681,] 5.120099e-33 1.000000e+00  
## [682,] 1.531822e-17 1.000000e+00  
## [683,] 1.242753e-20 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': 683 obs. of 7 variables:  
## $ myrf.pred : num 0 0 0 0 0 1 0 0 0 0 ...  
## $ myrda.pred.class: num 0 1 0 1 0 1 1 0 0 0 ...  
## $ mytree.pred : num 1 1 1 1 1 1 1 1 1 1 ...  
## $ X1 : num 1 1 1 1 1 1 1 1 1 1 ...  
## $ X2 : num 1 1 1 1 1 1 1 1 1 1 ...  
## $ mysvm.pred : num 0 1 0 1 0 1 0 0 0 0 ...  
## $ mynb.pred.class : Factor w/ 2 levels "benign","malignant": 1 2 1 2 1 2 1 1 1 1 ...

combine.cl<-combine.classes[, -c(7,8)]  
majority.vote=rowSums(combine.classes[,-c(7,8)])  
head(majority.vote)

## 1 2 3 4 5 6   
## 3 5 3 5 3 6

combine.classes[,7]<-rowSums(combine.classes[,-c(7,8)])  
combine.classes[,8]<-ifelse(combine.classes[,7]>=4, "malignant", "benign")  
table(combine.classes[,8], BreastCancer$Class)

##   
## benign malignant  
## benign 428 0  
## malignant 16 239

confusion <- table(combine.classes[,6], BreastCancer$Class)  
  
# Calculate performance metrics  
accuracy <- sum(diag(confusion))/sum(confusion)  
precision <- diag(confusion)/colSums(confusion)  
recall <- diag(confusion)/rowSums(confusion)  
f1\_score <- 2 \* precision \* recall / (precision + recall)  
  
# Print results  
cat("Accuracy: ", accuracy, "\n")

## Accuracy: 0.9692533

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

## Precision: 0.9707207 0.9665272

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

## Recall: 0.9817768 0.9467213

cat("F1 Score: ", f1\_score, "\n")

## F1 Score: 0.9762174 0.9565217