TBANLT 560 Project 2 Towards a Data Mining Portfolio

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3/17/2021

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

## Loading required package: mlbench

## Warning: package 'mlbench' was built under R version 4.0.4

#### Upload Data Set. Omit missing data.

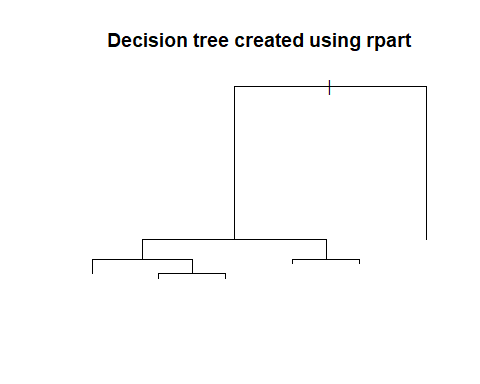
data(BreastCancer)  
BreastCancer <- na.omit(BreastCancer)

### Partition the data set for 80% training and 20% evaluation. The method used is recursive (or iterative) partitioning

BreastCancer$Id <- NULL   
# 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))  
# create model using recursive partitioning on the training data set  
require(rpart)

## Loading required package: rpart

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")



### The above decision tree shows the probabilities of the evaluation dataset

### Next I will create a model using conditional inference trees

# create model using conditional inference trees  
require(party)

## Loading required package: party

## Warning: package 'party' was built under R version 4.0.4

## Loading required package: grid

## Loading required package: mvtnorm

## Warning: package 'mvtnorm' was built under R version 4.0.3

## Loading required package: modeltools

## Warning: package 'modeltools' was built under R version 4.0.3

## Loading required package: stats4

## Loading required package: strucchange

## Warning: package 'strucchange' was built under R version 4.0.4

## Loading required package: zoo

##   
## Attaching package: 'zoo'

## The following objects are masked from 'package:base':  
##   
## as.Date, as.Date.numeric

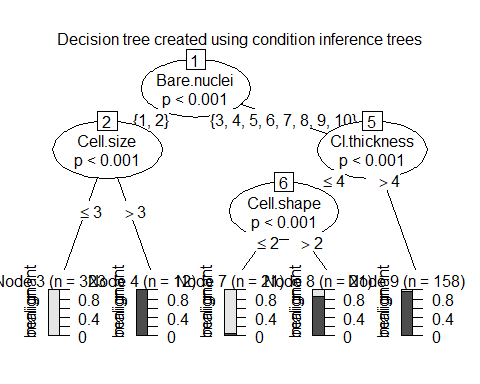
## Loading required package: sandwich

## Warning: package 'sandwich' was built under R version 4.0.4

x.ct <- ctree(Class ~ ., data=BreastCancer[ind == 1,])  
x.ct.pred <- predict(x.ct, newdata=BreastCancer[ind == 2,])  
x.ct.prob <- 1- unlist(treeresponse(x.ct, BreastCancer[ind == 2,]), use.names=F)[seq(1,nrow(BreastCancer[ind == 2,])\*2,2)]

### Next, we plot the Decision tree created using condition inference trees and bagging ensemble

# To view the decision tree, uncomment this line.  
plot(x.ct, main="Decision tree created using condition inference trees")



# create model using random forest and bagging ensemble using conditional inference trees  
x.cf <- cforest(Class ~ ., data=BreastCancer[ind == 1,], control = cforest\_unbiased(mtry = ncol(BreastCancer)-2))  
x.cf.pred <- predict(x.cf, newdata=BreastCancer[ind == 2,])  
x.cf.prob <- 1- unlist(treeresponse(x.cf, BreastCancer[ind == 2,]), use.names=F)[seq(1,nrow(BreastCancer[ind == 2,])\*2,2)]

### Now I will experiment with bootstrap aggregating / bagging

# create model using bagging (bootstrap aggregating)  
require(ipred)

## Loading required package: ipred

## Warning: package 'ipred' was built under R version 4.0.3

x.ip <- bagging(Class ~ ., data=BreastCancer[ind == 1,])  
x.ip.prob <- predict(x.ip, type="prob", newdata=BreastCancer[ind == 2,])

### Next I will create my SVM model

# create model using svm (support vector machine)  
require(e1071)

## Loading required package: e1071

## Warning: package 'e1071' was built under R version 4.0.3

# svm requires tuning  
x.svm.tune <- tune(svm, Class~., data = BreastCancer[ind == 1,],  
 ranges = list(gamma = 2^(-8:1), cost = 2^(0:4)),  
 tunecontrol = tune.control(sampling = "fix"))  
# display the tuning results (in text format)  
x.svm.tune

##   
## Parameter tuning of 'svm':  
##   
## - sampling method: fixed training/validation set   
##   
## - best parameters:  
## gamma cost  
## 0.0625 1  
##   
## - best performance: 0.02234637

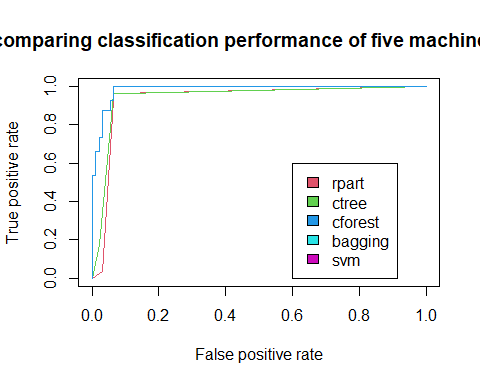
# If the tuning results are on the margin of the parameters (e.g., gamma = 2^-8),   
# then widen the parameters.  
# I manually copied the cost and gamma from console messages above to parameters below.  
x.svm <- svm(Class~., data = BreastCancer[ind == 1,], cost=4, gamma=0.0625, probability = TRUE)  
x.svm.prob <- predict(x.svm, type="prob", newdata=BreastCancer[ind == 2,], probability = TRUE)  
  
  
##  
## plot ROC curves to compare the performance of the individual classifiers  
##  
  
# Output the plot to a PNG file for display on web. To draw to the screen,   
# comment this line out.  
png(filename="roc\_curve\_5\_models.png", width=700, height=700)  
  
# load the ROCR package which draws the ROC curves  
require(ROCR)

## Loading required package: ROCR

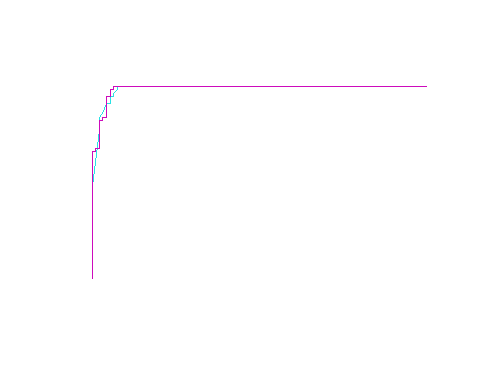
## Warning: package 'ROCR' was built under R version 4.0.4

### The next block of code shows how to create an ROCR prediction object. The best part is being able to see the models’ performance depicted in a chart.

x.rp.prob.rocr <- prediction(x.rp.prob[,2], BreastCancer[ind == 2,'Class'])  
# prepare an ROCR performance object for ROC curve (tpr=true positive rate, fpr=false positive rate)  
x.rp.perf <- performance(x.rp.prob.rocr, "tpr","fpr")  
# plot it  
plot(x.rp.perf, col=2, main="ROC curves comparing classification performance of five machine learning models")  
  
# Draw a legend.  
legend(0.6, 0.6, c('rpart', 'ctree', 'cforest','bagging','svm'), 2:6)  
  
# ctree  
x.ct.prob.rocr <- prediction(x.ct.prob, BreastCancer[ind == 2,'Class'])  
x.ct.perf <- performance(x.ct.prob.rocr, "tpr","fpr")  
# add=TRUE draws on the existing chart   
plot(x.ct.perf, col=3, add=TRUE)  
  
  
# cforest  
x.cf.prob.rocr <- prediction(x.cf.prob, BreastCancer[ind == 2,'Class'])  
x.cf.perf <- performance(x.cf.prob.rocr, "tpr","fpr")  
plot(x.cf.perf, col=4, add=TRUE)



# bagging  
x.ip.prob.rocr <- prediction(x.ip.prob[,2], BreastCancer[ind == 2,'Class'])  
x.ip.perf <- performance(x.ip.prob.rocr, "tpr","fpr")  
plot.new()  
plot(x.ip.perf, col=5, add=TRUE)  
# svm  
x.svm.prob.rocr <- prediction(attr(x.svm.prob, "probabilities")[,2], BreastCancer[ind == 2,'Class'])  
x.svm.perf <- performance(x.svm.prob.rocr, "tpr","fpr")  
  
plot(x.svm.perf, col=6, add=TRUE)



# Close and save the PNG file.  
dev.off()

## png   
## 3

### I’m starting my analysis with the Breast Cancer set again and choosing to only utilize rows / records with all the data.

data("BreastCancer")  
#import only complete cases  
BreastCancer <- BreastCancer[complete.cases(BreastCancer), ]  
mydata <- cbind(BreastCancer[10],BreastCancer[1:9])  
  
mysvm <- svm(BreastCancer$Class ~ ., BreastCancer)  
mysvm.pred <- predict(mysvm, BreastCancer)  
table(mysvm.pred,BreastCancer$Class)

##   
## mysvm.pred benign malignant  
## benign 427 11  
## malignant 17 228

### Next I will use the Naive Bayes model to predict Class.

library(klaR)

## Warning: package 'klaR' was built under R version 4.0.3

## Loading required package: MASS

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

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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 374

## 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  
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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  
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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  
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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  
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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  
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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  
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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  
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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  
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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  
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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  
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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  
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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  
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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  
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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  
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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  
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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  
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
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## observation 622

## 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  
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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 666

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 676

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 681

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 682

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

### This table shows the confusion matrix for benign and malignant

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

##   
## benign malignant  
## benign 431 2  
## malignant 13 237

### This block of code shows the weights of the neural net and assists in grouping data.

library(nnet)  
mynnet <- nnet(Class ~ ., BreastCancer, size=1)

## # weights: 712  
## initial value 446.123857   
## iter 10 value 77.055111  
## iter 20 value 51.424192  
## iter 30 value 51.385450  
## iter 40 value 51.379012  
## iter 50 value 51.376510  
## iter 60 value 51.376139  
## iter 70 value 51.375536  
## iter 80 value 48.022943  
## iter 90 value 47.997184  
## iter 100 value 44.541877  
## final value 44.541877   
## stopped after 100 iterations

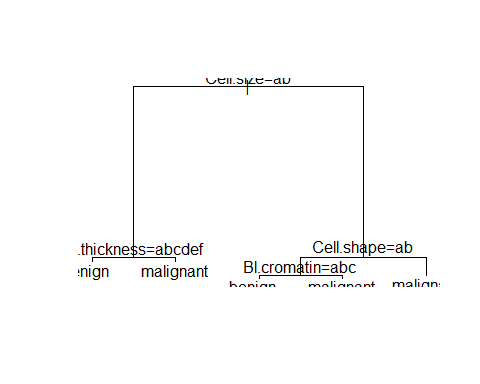
mynnet.pred <- predict(mynnet,BreastCancer,type="class")  
table(mynnet.pred,BreastCancer$Class)

##   
## mynnet.pred benign malignant  
## benign 437 2  
## malignant 7 237

### Next is the Decision Tree model. I iterated and experimented with the tree.

mytree <- rpart(Class ~ Cell.size+Cell.shape+Marg.adhesion+Cl.thickness+Mitoses+Bl.cromatin+Mitoses,BreastCancer)

plot(mytree); text(mytree)



summary(mytree)

## Call:  
## rpart(formula = Class ~ Cell.size + Cell.shape + Marg.adhesion +   
## Cl.thickness + Mitoses + Bl.cromatin + Mitoses, data = BreastCancer)  
## n= 683   
##   
## CP nsplit rel error xerror xstd  
## 1 0.79079498 0 1.0000000 1.0000000 0.05215335  
## 2 0.05439331 1 0.2092050 0.2468619 0.03071921  
## 3 0.02092050 2 0.1548117 0.1841004 0.02684532  
## 4 0.01255230 3 0.1338912 0.1799163 0.02655926  
## 5 0.01000000 4 0.1213389 0.1589958 0.02506475  
##   
## Variable importance  
## Cell.size Cell.shape Bl.cromatin Marg.adhesion Cl.thickness   
## 24 21 17 14 14   
## Mitoses   
## 9   
##   
## 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 splits as LLRRRRRRRR, improve=222.3221, (0 missing)  
## Cell.shape splits as LLLRRRRRRR, improve=216.4111, (0 missing)  
## Bl.cromatin splits as LLLRRRRRRR, improve=196.3903, (0 missing)  
## Marg.adhesion splits as LLLRRRRRRR, improve=154.5832, (0 missing)  
## Cl.thickness splits as LLLLLLRRRR, improve=146.2240, (0 missing)  
## Surrogate splits:  
## Cell.shape splits as LLLRRRRRRR, agree=0.917, adj=0.785, (0 split)  
## Bl.cromatin splits as LLLRRRRRRR, agree=0.876, adj=0.679, (0 split)  
## Marg.adhesion splits as LLRRRRRRRR, agree=0.843, adj=0.596, (0 split)  
## Cl.thickness splits as LLLLLRRRRR, agree=0.818, adj=0.532, (0 split)  
## Mitoses splits as LRRRRRRRR, agree=0.753, adj=0.362, (0 split)  
##   
## Node number 2: 418 observations, complexity param=0.0209205  
## predicted class=benign expected loss=0.02870813 P(node) =0.6120059  
## class counts: 406 12  
## probabilities: 0.971 0.029   
## left son=4 (409 obs) right son=5 (9 obs)  
## Primary splits:  
## Cl.thickness splits as LLLLLLRRRR, improve=10.322140, (0 missing)  
## Bl.cromatin splits as LLLLR-R---, improve= 8.533070, (0 missing)  
## Mitoses splits as LRRRL-LL-, improve= 3.179519, (0 missing)  
## Cell.shape splits as LLRRRRRRRR, improve= 2.854454, (0 missing)  
## Cell.size splits as LRRRRRRRRR, improve= 2.241240, (0 missing)  
## Surrogate splits:  
## Mitoses splits as LLRRL-LL-, agree=0.983, adj=0.222, (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 splits as LLRRRRRRRR, improve=20.581580, (0 missing)  
## Cell.size splits as LLLRRRRRRR, improve=18.276500, (0 missing)  
## Bl.cromatin splits as LLRRRRRRRR, improve=13.910340, (0 missing)  
## Marg.adhesion splits as LLRRRRRRRR, improve=11.171480, (0 missing)  
## Cl.thickness splits as LLLLLLRRRR, improve= 8.987611, (0 missing)  
## Surrogate splits:  
## Bl.cromatin splits as LRRRRRRRRR, agree=0.932, adj=0.217, (0 split)  
##   
## Node number 4: 409 observations  
## predicted class=benign expected loss=0.01222494 P(node) =0.5988287  
## class counts: 404 5  
## probabilities: 0.988 0.012   
##   
## Node number 5: 9 observations  
## predicted class=malignant expected loss=0.2222222 P(node) =0.01317716  
## class counts: 2 7  
## probabilities: 0.222 0.778   
##   
## 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 splits as LLLRR-RR--, improve=4.9689440, (0 missing)  
## Cl.thickness splits as LLLLRRRRRR, improve=3.3816430, (0 missing)  
## Cell.shape splits as LRRRRRRRRR, improve=1.3975160, (0 missing)  
## Marg.adhesion splits as LRRRRRRRRR, improve=0.3975155, (0 missing)  
## Surrogate splits:  
## Cl.thickness splits as LLLLLRRRRR, agree=0.870, adj=0.571, (0 split)  
## Mitoses splits as LRLR----R, agree=0.870, adj=0.571, (0 split)  
## Marg.adhesion splits as LLLLLLLRRR, agree=0.826, adj=0.429, (0 split)  
## Cell.size splits as LLLRRRRRRR, agree=0.739, adj=0.143, (0 split)  
##   
## Node number 7: 242 observations  
## predicted class=malignant expected loss=0.08264463 P(node) =0.3543192  
## class counts: 20 222  
## probabilities: 0.083 0.917   
##   
## 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

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

##   
## mytree.pred benign malignant  
## benign 420 5  
## malignant 24 234

### Breast Cancer subset of variables and a loop to generate the confusion matrix

BreastCancer <- subset(BreastCancer, select = -c(1))  
  
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

library(MASS)  
BreastCancer$Cl.thickness <- as.numeric(BreastCancer$Cl.thickness)  
BreastCancer$Bare.nuclei <- as.numeric(BreastCancer$Bare.nuclei)  
BreastCancer$Bl.cromatin <- as.numeric(BreastCancer$Bl.cromatin)  
BreastCancer$Normal.nucleoli <- as.numeric(BreastCancer$Normal.nucleoli)  
BreastCancer$Cell.size <- as.numeric(BreastCancer$Cell.size)  
BreastCancer$Cell.shape <- as.numeric(BreastCancer$Cell.shape)  
BreastCancer$Marg.adhesion <- as.numeric(BreastCancer$Marg.adhesion)  
BreastCancer$Epith.c.size <- as.numeric(BreastCancer$Epith.c.size)  
BreastCancer$Mitoses <- as.numeric(BreastCancer$Mitoses)  
BreastCancer$Class <- as.factor(BreastCancer$Class)  
str(BreastCancer)

## 'data.frame': 683 obs. of 10 variables:  
## $ Cl.thickness : num 5 5 3 6 4 8 1 2 2 4 ...  
## $ Cell.size : num 1 4 1 8 1 10 1 1 1 2 ...  
## $ Cell.shape : num 1 4 1 8 1 10 1 2 1 1 ...  
## $ Marg.adhesion : num 1 5 1 1 3 8 1 1 1 1 ...  
## $ Epith.c.size : num 2 7 2 3 2 7 2 2 2 2 ...  
## $ Bare.nuclei : num 1 10 2 4 1 10 10 1 1 1 ...  
## $ Bl.cromatin : num 3 3 3 3 3 9 3 3 1 2 ...  
## $ Normal.nucleoli: num 1 2 1 7 1 7 1 1 1 1 ...  
## $ Mitoses : num 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 ...

summary(BreastCancer)

## Cl.thickness Cell.size Cell.shape Marg.adhesion   
## Min. : 1.000 Min. : 1.000 Min. : 1.000 Min. : 1.00   
## 1st Qu.: 2.000 1st Qu.: 1.000 1st Qu.: 1.000 1st Qu.: 1.00   
## Median : 4.000 Median : 1.000 Median : 1.000 Median : 1.00   
## Mean : 4.442 Mean : 3.151 Mean : 3.215 Mean : 2.83   
## 3rd Qu.: 6.000 3rd Qu.: 5.000 3rd Qu.: 5.000 3rd Qu.: 4.00   
## Max. :10.000 Max. :10.000 Max. :10.000 Max. :10.00   
## Epith.c.size Bare.nuclei Bl.cromatin Normal.nucleoli  
## Min. : 1.000 Min. : 1.000 Min. : 1.000 Min. : 1.00   
## 1st Qu.: 2.000 1st Qu.: 1.000 1st Qu.: 2.000 1st Qu.: 1.00   
## Median : 2.000 Median : 1.000 Median : 3.000 Median : 1.00   
## Mean : 3.234 Mean : 3.545 Mean : 3.445 Mean : 2.87   
## 3rd Qu.: 4.000 3rd Qu.: 6.000 3rd Qu.: 5.000 3rd Qu.: 4.00   
## Max. :10.000 Max. :10.000 Max. :10.000 Max. :10.00   
## Mitoses Class   
## Min. :1.000 benign :444   
## 1st Qu.:1.000 malignant:239   
## Median :1.000   
## Mean :1.583   
## 3rd Qu.:1.000   
## Max. :9.000

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

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

library(randomForest)

## Warning: package 'randomForest' was built under R version 4.0.3

## randomForest 4.6-14

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

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

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

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

##   
## benign malignant  
## benign 433 8  
## malignant 11 231

### Now it’s time to combine the output from the different models using Majority rule ensemble approach.

library(MASS)  
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 mynnet.pred mysvm.pred mynb.pred.class  
## 1 benign benign malignant benign benign benign  
## 2 benign malignant malignant benign malignant malignant  
## 3 benign benign malignant benign benign benign  
## 4 benign malignant malignant benign malignant malignant  
## 5 benign benign malignant benign benign benign  
## 6 malignant malignant malignant malignant malignant 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 benign   
## [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 benign   
## [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 benign 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 benign 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 benign 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,] 9.999991e-01 8.646149e-07  
## [2,] 1.507228e-05 9.999849e-01  
## [3,] 9.999996e-01 3.763293e-07  
## [4,] 3.886026e-05 9.999611e-01  
## [5,] 9.999991e-01 8.584499e-07  
## [6,] 1.585868e-17 1.000000e+00  
## [7,] 8.346940e-01 1.653060e-01  
## [8,] 9.999999e-01 1.023538e-07  
## [9,] 9.999999e-01 1.466897e-07  
## [10,] 9.999997e-01 3.271337e-07  
## [11,] 1.000000e+00 2.031659e-08  
## [12,] 1.000000e+00 2.899062e-08  
## [13,] 9.955410e-01 4.459042e-03  
## [14,] 9.999997e-01 3.062079e-07  
## [15,] 1.383732e-11 1.000000e+00  
## [16,] 4.002434e-01 5.997566e-01  
## [17,] 9.999998e-01 1.656848e-07  
## [18,] 9.999997e-01 3.050771e-07  
## [19,] 2.946724e-10 1.000000e+00  
## [20,] 9.999973e-01 2.747502e-06  
## [21,] 6.181986e-09 1.000000e+00  
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## [23,] 9.999999e-01 6.545136e-08  
## [24,] 1.000000e+00 2.663089e-08  
## [25,] 8.162084e-02 9.183792e-01  
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## [27,] 9.999995e-01 4.702720e-07  
## [28,] 1.000000e+00 2.899062e-08  
## [29,] 1.000000e+00 4.471185e-08  
## [30,] 9.999999e-01 5.011456e-08  
## [31,] 9.999999e-01 5.354156e-08  
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## [34,] 9.999999e-01 1.245153e-07  
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## [37,] 9.997143e-01 2.856672e-04  
## [38,] 4.506814e-08 1.000000e+00  
## [39,] 2.298943e-03 9.977011e-01  
## [40,] 1.250044e-02 9.874996e-01  
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## [43,] 2.032297e-13 1.000000e+00  
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## [139,] 1.000000e+00 1.885737e-08  
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## [366,] 9.999154e-01 8.460502e-05  
## [367,] 1.000000e+00 9.351240e-09  
## [368,] 3.570401e-12 1.000000e+00  
## [369,] 9.999989e-01 1.107002e-06  
## [370,] 1.000000e+00 1.885737e-08  
## [371,] 1.000000e+00 1.885737e-08  
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## [373,] 1.081585e-07 9.999999e-01  
## [374,] 9.999718e-01 2.822480e-05  
## [375,] 9.999999e-01 5.351785e-08  
## [376,] 9.999959e-01 4.115619e-06  
## [377,] 1.000000e+00 2.278246e-08  
## [378,] 5.527895e-14 1.000000e+00  
## [379,] 9.999999e-01 6.545136e-08  
## [380,] 1.000000e+00 7.062008e-09  
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## [382,] 9.999999e-01 6.545136e-08  
## [383,] 9.999999e-01 1.206977e-07  
## [384,] 9.999999e-01 1.080968e-07  
## [385,] 9.999998e-01 2.349559e-07  
## [386,] 9.999999e-01 8.344624e-08  
## [387,] 5.069704e-14 1.000000e+00  
## [388,] 1.000000e+00 4.263788e-08  
## [389,] 9.999923e-01 7.667754e-06  
## [390,] 9.999978e-01 2.164274e-06  
## [391,] 9.999999e-01 1.035714e-07  
## [392,] 1.000000e+00 1.439789e-08  
## [393,] 9.999994e-01 5.840876e-07  
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## [407,] 4.659353e-18 1.000000e+00  
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## [409,] 9.999980e-01 1.975061e-06  
## [410,] 1.000000e+00 4.263788e-08  
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## [412,] 9.998397e-01 1.602844e-04  
## [413,] 4.919212e-07 9.999995e-01  
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## [415,] 1.000000e+00 2.899062e-08  
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## [417,] 9.999882e-01 1.181743e-05  
## [418,] 9.999991e-01 8.537939e-07  
## [419,] 9.999996e-01 4.459666e-07  
## [420,] 1.376068e-07 9.999999e-01  
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## [432,] 1.000000e+00 9.351240e-09  
## [433,] 9.999997e-01 3.072788e-07  
## [434,] 1.000000e+00 7.062008e-09  
## [435,] 6.798130e-15 1.000000e+00  
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## [452,] 2.193204e-12 1.000000e+00  
## [453,] 3.755005e-09 1.000000e+00  
## [454,] 9.999999e-01 1.080968e-07  
## [455,] 1.000000e+00 2.816506e-08  
## [456,] 9.999999e-01 5.011456e-08  
## [457,] 9.999972e-01 2.799102e-06  
## [458,] 9.999992e-01 7.559131e-07  
## [459,] 9.999999e-01 1.080968e-07  
## [460,] 9.999997e-01 3.072788e-07  
## [461,] 1.000000e+00 4.263788e-08  
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## [463,] 9.999999e-01 1.080968e-07  
## [464,] 9.999994e-01 6.103898e-07  
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## [476,] 1.000000e+00 9.351240e-09  
## [477,] 6.116127e-10 1.000000e+00  
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## [487,] 9.999998e-01 1.656848e-07  
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## [498,] 9.999997e-01 3.072788e-07  
## [499,] 9.999999e-01 5.011456e-08  
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## [513,] 9.999997e-01 3.050771e-07  
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## [533,] 1.000000e+00 1.430315e-08  
## [534,] 1.000000e+00 3.248162e-08  
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## [537,] 1.000000e+00 2.663089e-08  
## [538,] 9.999977e-01 2.328153e-06  
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## [559,] 1.000000e+00 1.439789e-08  
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## [561,] 9.999984e-01 1.585162e-06  
## [562,] 9.999995e-01 4.702720e-07  
## [563,] 1.000000e+00 1.439789e-08  
## [564,] 1.000000e+00 1.439789e-08  
## [565,] 1.000000e+00 2.663089e-08  
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## [572,] 2.369141e-20 1.000000e+00  
## [573,] 9.999991e-01 8.537939e-07  
## [574,] 7.581911e-08 9.999999e-01  
## [575,] 9.999997e-01 3.072788e-07  
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## [577,] 3.264639e-08 1.000000e+00  
## [578,] 8.507520e-07 9.999991e-01  
## [579,] 9.999994e-01 5.736850e-07  
## [580,] 8.073730e-08 9.999999e-01  
## [581,] 9.999995e-01 4.702720e-07  
## [582,] 9.999997e-01 3.108369e-07  
## [583,] 9.999964e-01 3.565856e-06  
## [584,] 9.999999e-01 6.545136e-08  
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## [586,] 9.999999e-01 6.545136e-08  
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## [590,] 3.188853e-07 9.999997e-01  
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## [595,] 9.999997e-01 3.072788e-07  
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## [597,] 8.259015e-11 1.000000e+00  
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## [605,] 9.999999e-01 6.545136e-08  
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## [612,] 9.999951e-01 4.886692e-06  
## [613,] 1.000000e+00 1.885737e-08  
## [614,] 9.999999e-01 1.080968e-07  
## [615,] 9.999927e-01 7.262243e-06  
## [616,] 9.999995e-01 4.702720e-07  
## [617,] 1.000000e+00 9.351240e-09  
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## [640,] 9.999999e-01 6.545136e-08  
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## [644,] 1.000000e+00 9.351240e-09  
## [645,] 1.000000e+00 1.439789e-08  
## [646,] 9.999997e-01 3.050771e-07  
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## [655,] 6.259887e-10 1.000000e+00  
## [656,] 9.999996e-01 3.613164e-07  
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## [664,] 1.000000e+00 1.885737e-08  
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## [666,] 6.961204e-15 1.000000e+00  
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## [670,] 1.000000e+00 9.351240e-09  
## [671,] 1.000000e+00 9.351240e-09  
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## [673,] 9.999999e-01 1.080968e-07  
## [674,] 9.999965e-01 3.492637e-06  
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## [676,] 6.927183e-08 9.999999e-01  
## [677,] 1.000000e+00 4.263788e-08  
## [678,] 9.999999e-01 7.853968e-08  
## [679,] 9.999998e-01 2.160296e-07  
## [680,] 1.000000e+00 1.885737e-08  
## [681,] 2.621757e-11 1.000000e+00  
## [682,] 2.266475e-06 9.999977e-01  
## [683,] 1.133590e-07 9.999999e-01

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)  
majority.vote=rowSums(combine.classes)  
head(majority.vote)

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

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

##   
## benign malignant  
## benign 432 1  
## malignant 12 238