Final Project

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3/16/2021

#In the below Chunk please find the data being uploaded into the global enivronment. I am also omitting all NA’s within the dataset and setting the Id column within BreastCancer to Null.

#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

# if you don't have any required package, use the install.packages() command  
# load the data set  
data(BreastCancer)  
# 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

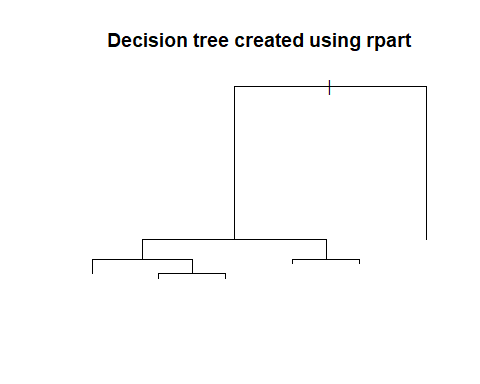
#In the chunk below I will be partitioning my data and creating a model using recursive partitioning with my training data set.

# partition the data set for 80% training and 20% evaluation  
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

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

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,])  
  
# To view the decision tree, uncomment this line.  
plot(x.rp, main="Decision tree created using rpart")



#Now i will be creating 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

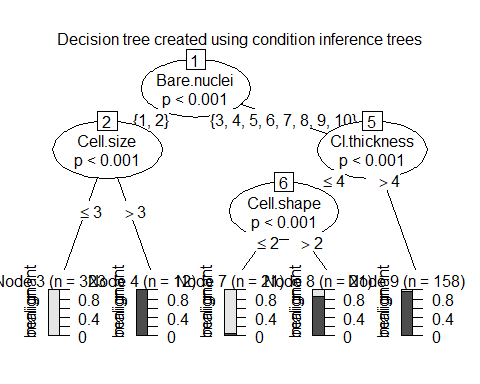
##   
## Attaching package: 'zoo'

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



#THis is the random forest model and we are using the bagging enseble for 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)]

# 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,])

# 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

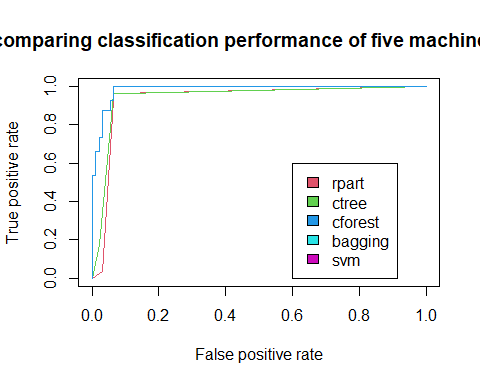
# If the tuning results are on the margin of the parameters (e.g., gamma = 2^-8),   
# then widen the parameters.  
# I manually copied the cost and gamma from console messages above to parameters below.  
x.svm <- svm(Class~., data = BreastCancer[ind == 1,], cost=4, gamma=0.0625, probability = TRUE)  
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

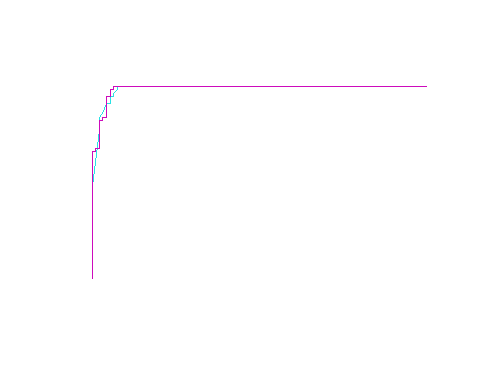
## Warning: package 'ROCR' was built under R version 4.0.3

# create an ROCR prediction object from rpart() probabilities. I will now be taking the models and comparing the performances of them in a line chart. I show this by making a legend with in the graph and labeling these as different colors.

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

Below you can see that I am importing breastcancer again, this is essentiall starting with a different/new data set from the one previously worked on. For this reason I needed to do the compile.cases process to ensure that there are no NAs in the model.

I am also binding the rows/columns that we are working with.

data("BreastCancer")  
BreastCancer <- BreastCancer[complete.cases(BreastCancer), ]  
  
mydata <- cbind(BreastCancer[10],BreastCancer[1:9])

Below I run my first model on the breastcancer dataset. This Model is the Support Vector Machine. SVM is primarily used for pattern recognition, regression and distribution estimation.

library(e1071)  
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

#install.packages("klaR")

I began running into some issues regarding my data, so I broke all of my columns up and counted the NA’s within the data set. I found that there was one column that showed NA’s.I then solved this in the first chunk, which we review already.

#View(BreastCancer)  
  
sum(complete.cases(BreastCancer))

## [1] 683

sum(!complete.cases(BreastCancer))

## [1] 0

sum(is.na(BreastCancer$Class))

## [1] 0

sum(is.na(BreastCancer$Id))

## [1] 0

sum(is.na(BreastCancer$Cl.thickness))

## [1] 0

sum(is.na(BreastCancer$Cell.size))

## [1] 0

sum(is.na(BreastCancer$Marg.adhesion))

## [1] 0

sum(is.na(BreastCancer$Epith.c.size))

## [1] 0

sum(is.na(BreastCancer$Bare.nuclei))

## [1] 0

sum(is.na(BreastCancer$Bl.cromatin))

## [1] 0

sum(is.na(BreastCancer$Mitoses))

## [1] 0

Find the NaiveBayes Model ran on the BreastCancer data set. This is primarily used to predict the probability of different class based on various attributes.

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  
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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 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

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

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

Below you can find the neural net model ran on the BreastCancer data set. The neural net model is used to help cluster and classify data. THey also help to group unlabeled data according to similarities of inputs.

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

library(MASS)  
str(mynnet.pred)

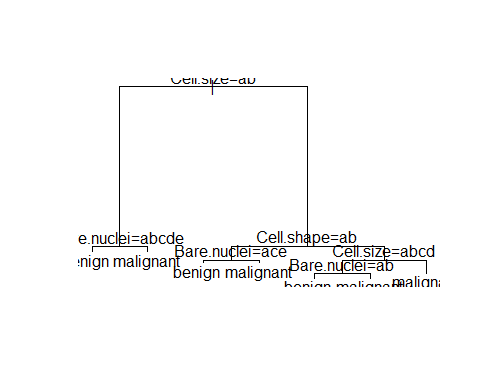
## chr [1:683] "benign" "benign" "benign" "benign" "benign" "malignant" ...

head(BreastCancer)

## Id Cl.thickness Cell.size Cell.shape Marg.adhesion Epith.c.size  
## 1 1000025 5 1 1 1 2  
## 2 1002945 5 4 4 5 7  
## 3 1015425 3 1 1 1 2  
## 4 1016277 6 8 8 1 3  
## 5 1017023 4 1 1 3 2  
## 6 1017122 8 10 10 8 7  
## Bare.nuclei Bl.cromatin Normal.nucleoli Mitoses Class  
## 1 1 3 1 1 benign  
## 2 10 3 2 1 benign  
## 3 2 3 1 1 benign  
## 4 4 3 7 1 benign  
## 5 1 3 1 1 benign  
## 6 10 9 7 1 malignant

#Below is the Decision tree model #below find the decision tree with all variables except for the ID variable as it will not add very much value to the model and it also took away from the visuals.

library(rpart)  
mytree <- rpart(Class ~ Cell.size+Cell.shape+Bare.nuclei  
+Cl.thickness+Normal.nucleoli+Epith.c.size+Bl.cromatin  
+Mitoses  
, BreastCancer)  
plot(mytree); text(mytree) # in "iris\_tree.ps"



summary(mytree)

## Call:  
## rpart(formula = Class ~ Cell.size + Cell.shape + Bare.nuclei +   
## Cl.thickness + Normal.nucleoli + Epith.c.size + Bl.cromatin +   
## Mitoses, 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 0.2468619 0.03071921  
## 3 0.02510460 2 0.15481172 0.1799163 0.02655926  
## 4 0.01255230 3 0.12970711 0.1673640 0.02567599  
## 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 splits as LLRRRRRRRR, improve=222.3221, (0 missing)  
## Cell.shape splits as LLLRRRRRRR, improve=216.4111, (0 missing)  
## Bare.nuclei splits as LLRRRRRRRR, improve=203.7284, (0 missing)  
## Bl.cromatin splits as LLLRRRRRRR, improve=196.3903, (0 missing)  
## Epith.c.size splits as LLRRRRRRRR, improve=193.1310, (0 missing)  
## Surrogate splits:  
## Cell.shape splits as LLLRRRRRRR, agree=0.917, adj=0.785, (0 split)  
## Epith.c.size splits as LLRRRRRRRR, agree=0.900, adj=0.743, (0 split)  
## Bare.nuclei splits as LLRRRRRRRR, agree=0.880, adj=0.691, (0 split)  
## Normal.nucleoli splits as LLRRRRRRRR, agree=0.877, adj=0.683, (0 split)  
## Bl.cromatin splits as LLLRRRRRRR, 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 splits as LLLLLRRR-R, improve=11.68296, (0 missing)  
## Normal.nucleoli splits as LLLR-RRL-R, improve=11.68296, (0 missing)  
## Cl.thickness splits as LLLLLLRRRR, improve=10.32214, (0 missing)  
## Bl.cromatin splits as LLLLR-R---, improve= 8.53307, (0 missing)  
## Epith.c.size splits as LLLRRRRRRR, improve= 4.63208, (0 missing)  
## Surrogate splits:  
## Cl.thickness splits as LLLLLLLLRR, agree=0.988, adj=0.375, (0 split)  
## Normal.nucleoli splits as LLLR-RRL-L, agree=0.988, adj=0.375, (0 split)  
## Mitoses splits as LLRLL-LL-, 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 splits as LLRRRRRRRR, improve=20.581580, (0 missing)  
## Cell.size splits as LLLRRRRRRR, improve=18.276500, (0 missing)  
## Bare.nuclei splits as LRRRRRRRRR, improve=16.814930, (0 missing)  
## Bl.cromatin splits as LLRRRRRRRR, improve=13.910340, (0 missing)  
## Epith.c.size splits as LLRRRRRRRR, improve= 9.450955, (0 missing)  
## Surrogate splits:  
## Bl.cromatin splits as LRRRRRRRRR, 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:  
## Bare.nuclei splits as LRLRL----R, improve=4.968944, (0 missing)  
## Bl.cromatin splits as LLLRR-RR--, improve=4.968944, (0 missing)  
## Cl.thickness splits as LLLLRRRRRR, improve=3.381643, (0 missing)  
## Epith.c.size splits as LLRRRRRRRR, improve=1.992754, (0 missing)  
## Cell.shape splits as LRRRRRRRRR, improve=1.397516, (0 missing)  
## Surrogate splits:  
## Bl.cromatin splits as LLLRR-RR--, agree=0.913, adj=0.714, (0 split)  
## 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)  
## Normal.nucleoli splits as LLRRLL-L--, agree=0.826, adj=0.429, (0 split)  
## Epith.c.size splits as LLLLRRRRRR, 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 splits as LLLLRRRRRR, improve=5.297663, (0 missing)  
## Bare.nuclei splits as LLRRRRRRRR, improve=4.093695, (0 missing)  
## Cell.shape splits as LLLLRRRRRR, improve=2.958548, (0 missing)  
## Bl.cromatin splits as LLLLRLRRRR, improve=2.838336, (0 missing)  
## Cl.thickness splits as LLLLLLRRRR, improve=2.435362, (0 missing)  
## Surrogate splits:  
## Cell.shape splits as LLLLRRRRRR, agree=0.789, adj=0.250, (0 split)  
## Epith.c.size splits as LLRRRRRRRR, agree=0.777, adj=0.206, (0 split)  
## Bl.cromatin splits as LLRRRRRRRR, agree=0.736, adj=0.059, (0 split)  
## Bare.nuclei splits as RRRRRRLRRR, agree=0.723, adj=0.015, (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 splits as LLRRR-RRRR, improve=7.600529, (0 missing)  
## Cl.thickness splits as LLLLLLRRRR, improve=3.558824, (0 missing)  
## Normal.nucleoli splits as LLRRRLLLRR, improve=2.951389, (0 missing)  
## Bl.cromatin splits as LLLLRLLR-R, improve=1.640351, (0 missing)  
## Cell.shape splits as LLLLRRRRRR, improve=1.461404, (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)

#When I was running this I kept running into this error-Error in model.frame.default(Terms, newdata, na.action = na.action, xlev = attr(object, : factor Id has new level 1000025.

#similarly to the model above, I am going to remove ID from the model.

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

# The same as above in this case

#Quadratic Discriminant Analysis Below you will find the quadratic Discriminant analysis, this is used to determine which variables in the model discriminate between two or more naturally.

library(MASS)  
BreastCancer$Cl.thickness <- as.numeric(BreastCancer$Cl.thickness)  
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$Bare.nuclei <- as.numeric(BreastCancer$Bare.nuclei)  
BreastCancer$Bl.cromatin <- as.numeric(BreastCancer$Bl.cromatin)  
BreastCancer$Normal.nucleoli <- as.numeric(BreastCancer$Normal.nucleoli)  
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

# in the below chunk you will find the Regularised Discriminant Analysis Similar to the model above this, this is made to discover variables that discriminate between each other.

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

##   
## benign malignant  
## benign 433 9  
## malignant 11 230

#Here is the Random Forests model below

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

below you will find a list of taking the findings/outputs from all of the models and turning them into classifiers. This was very wrong and should be ignored.

#  
  
# Classifier 1 output  
#benign 427 11  
#malignant 17 228  
  
classifier1<- c(427,11,17,228)  
  
# benign malignant  
# benign 431 2  
# malignant 13 237  
  
classifier2<-c(431,2,13,237)  
  
#mynnet.pred benign malignant  
 # benign 437 2  
 # malignant 7 237  
   
classifier3<-c(437,2,7,237)  
  
#mytree.pred benign malignant  
 # benign 431 9  
 # malignant 13 230  
   
classifier4<-c(431,9,13,230)  
  
#ans benign malignant  
# benign 430 20  
# malignant 14 219  
  
classifier5<-c(430,20,14,219)  
  
# benign malignant  
# benign 422 6  
# malignant 22 233  
classifier6<-c(422,6,22,233)  
  
  
 #benign malignant  
 #benign 433 9  
 #malignant 11 230  
  
classifier7<-c(433,9,11,230)  
  
#myrf.pred benign malignant  
 # benign 444 0  
 #malignant 0 239  
  
classifier8<-c(444,0,0,239)  
  
#combine.df

This chunk shows the diferent types of data within the data.

#str(combine.classes)

This chunk will outline the right approach and answer associated with the combination of all the models. This is useing the ensemble method.

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 benign   
## [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 4.719915e-08  
## [2,] 1.187953e-06 9.999988e-01  
## [3,] 1.000000e+00 2.079593e-08  
## [4,] 1.619699e-06 9.999984e-01  
## [5,] 9.999999e-01 6.673678e-08  
## [6,] 3.321296e-23 1.000000e+00  
## [7,] 9.577178e-01 4.228220e-02  
## [8,] 1.000000e+00 6.342236e-09  
## [9,] 1.000000e+00 7.612478e-09  
## [10,] 1.000000e+00 1.805739e-08  
## [11,] 1.000000e+00 9.879094e-10  
## [12,] 1.000000e+00 1.338407e-09  
## [13,] 9.973840e-01 2.615998e-03  
## [14,] 1.000000e+00 2.018229e-08  
## [15,] 3.860554e-15 1.000000e+00  
## [16,] 1.387034e-01 8.612966e-01  
## [17,] 1.000000e+00 7.654674e-09  
## [18,] 1.000000e+00 1.573935e-08  
## [19,] 1.054112e-12 1.000000e+00  
## [20,] 9.999998e-01 1.647847e-07  
## [21,] 6.083003e-11 1.000000e+00  
## [22,] 5.242289e-13 1.000000e+00  
## [23,] 1.000000e+00 2.966469e-09  
## [24,] 1.000000e+00 1.453303e-09  
## [25,] 5.300288e-02 9.469971e-01  
## [26,] 1.000000e+00 4.851013e-09  
## [27,] 1.000000e+00 2.299582e-08  
## [28,] 1.000000e+00 1.338407e-09  
## [29,] 1.000000e+00 2.713000e-09  
## [30,] 1.000000e+00 2.021670e-09  
## [31,] 1.000000e+00 2.761835e-09  
## [32,] 3.368230e-11 1.000000e+00  
## [33,] 1.000000e+00 5.235495e-09  
## [34,] 1.000000e+00 6.795770e-09  
## [35,] 1.000000e+00 1.338407e-09  
## [36,] 2.274904e-18 1.000000e+00  
## [37,] 9.999708e-01 2.923902e-05  
## [38,] 5.227608e-10 1.000000e+00  
## [39,] 2.273162e-04 9.997727e-01  
## [40,] 4.255358e-03 9.957446e-01  
## [41,] 2.560699e-17 1.000000e+00  
## [42,] 1.119527e-03 9.988805e-01  
## [43,] 4.478729e-18 1.000000e+00  
## [44,] 1.000000e+00 9.190112e-10  
## [45,] 4.315497e-10 1.000000e+00  
## [46,] 1.000000e+00 7.030265e-10  
## [47,] 9.999999e-01 6.673678e-08  
## [48,] 8.279371e-11 1.000000e+00  
## [49,] 1.827114e-03 9.981729e-01  
## [50,] 9.872185e-01 1.278149e-02  
## [51,] 1.632457e-08 1.000000e+00  
## [52,] 2.898881e-13 1.000000e+00  
## [53,] 2.146931e-11 1.000000e+00  
## [54,] 4.480476e-07 9.999996e-01  
## [55,] 4.728069e-14 1.000000e+00  
## [56,] 7.584969e-01 2.415031e-01  
## [57,] 4.675434e-04 9.995325e-01  
## [58,] 2.819638e-01 7.180362e-01  
## [59,] 1.928675e-04 9.998071e-01  
## [60,] 1.000000e+00 2.417974e-09  
## [61,] 2.376443e-16 1.000000e+00  
## [62,] 6.604121e-02 9.339588e-01  
## [63,] 1.000000e+00 7.030265e-10  
## [64,] 1.863622e-03 9.981364e-01  
## [65,] 1.000000e+00 1.573935e-08  
## [66,] 6.810860e-10 1.000000e+00  
## [67,] 4.423069e-16 1.000000e+00  
## [68,] 1.000000e+00 3.106989e-09  
## [69,] 9.999999e-01 1.411701e-07  
## [70,] 6.739782e-16 1.000000e+00  
## [71,] 9.999778e-01 2.215515e-05  
## [72,] 1.098691e-15 1.000000e+00  
## [73,] 5.491088e-03 9.945089e-01  
## [74,] 9.999999e-01 5.886918e-08  
## [75,] 1.000000e+00 1.567903e-08  
## [76,] 9.999997e-01 2.841194e-07  
## [77,] 9.999999e-01 8.398334e-08  
## [78,] 1.000000e+00 2.385795e-09  
## [79,] 9.999989e-01 1.132614e-06  
## [80,] 1.000000e+00 1.448145e-08  
## [81,] 9.999999e-01 1.097823e-07  
## [82,] 9.999977e-01 2.326493e-06  
## [83,] 1.937493e-17 1.000000e+00  
## [84,] 1.781807e-15 1.000000e+00  
## [85,] 3.816599e-04 9.996183e-01  
## [86,] 3.664042e-12 1.000000e+00  
## [87,] 1.000000e+00 1.573935e-08  
## [88,] 1.000000e+00 4.520581e-09  
## [89,] 1.000000e+00 1.453303e-09  
## [90,] 1.000000e+00 3.308737e-09  
## [91,] 1.000000e+00 1.573935e-08  
## [92,] 1.000000e+00 7.030265e-10  
## [93,] 1.000000e+00 2.761835e-09  
## [94,] 1.000000e+00 1.453303e-09  
## [95,] 1.000000e+00 1.495873e-09  
## [96,] 1.000000e+00 4.719915e-08  
## [97,] 4.187553e-17 1.000000e+00  
## [98,] 1.254958e-17 1.000000e+00  
## [99,] 6.507007e-11 1.000000e+00  
## [100,] 9.742683e-01 2.573168e-02  
## [101,] 1.000000e+00 3.555604e-08  
## [102,] 4.544720e-01 5.455280e-01  
## [103,] 1.173146e-23 1.000000e+00  
## [104,] 3.042851e-01 6.957149e-01  
## [105,] 2.641179e-18 1.000000e+00  
## [106,] 8.681192e-16 1.000000e+00  
## [107,] 1.000000e+00 3.910224e-09  
## [108,] 7.693954e-10 1.000000e+00  
## [109,] 9.999972e-01 2.829279e-06  
## [110,] 2.058128e-06 9.999979e-01  
## [111,] 5.364120e-13 1.000000e+00  
## [112,] 2.555829e-19 1.000000e+00  
## [113,] 9.999988e-01 1.190610e-06  
## [114,] 9.999998e-01 1.632888e-07  
## [115,] 9.993050e-01 6.949522e-04  
## [116,] 1.095481e-14 1.000000e+00  
## [117,] 1.000000e+00 2.223201e-08  
## [118,] 1.000000e+00 4.869700e-08  
## [119,] 1.000000e+00 6.363531e-09  
## [120,] 9.999999e-01 1.243254e-07  
## [121,] 3.639910e-20 1.000000e+00  
## [122,] 3.654923e-07 9.999996e-01  
## [123,] 4.038938e-14 1.000000e+00  
## [124,] 1.000000e+00 7.030265e-10  
## [125,] 1.609750e-11 1.000000e+00  
## [126,] 1.000000e+00 6.110471e-09  
## [127,] 1.514453e-08 1.000000e+00  
## [128,] 9.999906e-01 9.384244e-06  
## [129,] 9.999999e-01 1.411701e-07  
## [130,] 1.000000e+00 2.761835e-09  
## [131,] 6.541613e-19 1.000000e+00  
## [132,] 1.000000e+00 6.348338e-09  
## [133,] 1.000000e+00 5.271590e-09  
## [134,] 9.999992e-01 8.409046e-07  
## [135,] 1.000000e+00 7.654674e-09  
## [136,] 1.000000e+00 1.732506e-09  
## [137,] 1.000000e+00 1.739268e-08  
## [138,] 1.000000e+00 1.732506e-09  
## [139,] 1.000000e+00 7.802760e-10  
## [140,] 1.211102e-04 9.998789e-01  
## [141,] 9.999998e-01 1.632888e-07  
## [142,] 1.000000e+00 1.338407e-09  
## [143,] 9.744205e-03 9.902558e-01  
## [144,] 1.000000e+00 4.303906e-09  
## [145,] 7.097695e-01 2.902305e-01  
## [146,] 2.246798e-20 1.000000e+00  
## [147,] 1.000000e+00 9.879094e-10  
## [148,] 6.155682e-07 9.999994e-01  
## [149,] 6.136026e-18 1.000000e+00  
## [150,] 9.999999e-01 6.256333e-08  
## [151,] 1.000000e+00 4.091260e-10  
## [152,] 2.168618e-06 9.999978e-01  
## [153,] 1.000000e+00 3.856193e-09  
## [154,] 1.000000e+00 2.761835e-09  
## [155,] 1.664879e-22 1.000000e+00  
## [156,] 5.186902e-15 1.000000e+00  
## [157,] 1.000000e+00 3.324603e-08  
## [158,] 1.000000e+00 6.110471e-09  
## [159,] 9.999992e-01 7.637275e-07  
## [160,] 9.999999e-01 1.125592e-07  
## [161,] 1.285571e-16 1.000000e+00  
## [162,] 2.381587e-15 1.000000e+00  
## [163,] 1.000000e+00 6.110471e-09  
## [164,] 1.000000e+00 5.345785e-10  
## [165,] 1.000000e+00 1.732506e-09  
## [166,] 1.000000e+00 1.453303e-09  
## [167,] 1.000000e+00 7.030265e-10  
## [168,] 1.386745e-28 1.000000e+00  
## [169,] 5.490610e-09 1.000000e+00  
## [170,] 8.519376e-17 1.000000e+00  
## [171,] 1.000000e+00 2.761835e-09  
## [172,] 1.857046e-13 1.000000e+00  
## [173,] 1.000000e+00 1.573935e-08  
## [174,] 3.716801e-04 9.996283e-01  
## [175,] 1.000000e+00 9.879094e-10  
## [176,] 1.000000e+00 4.091260e-10  
## [177,] 9.999998e-01 1.647847e-07  
## [178,] 4.808269e-17 1.000000e+00  
## [179,] 5.186798e-10 1.000000e+00  
## [180,] 1.000000e+00 1.883224e-09  
## [181,] 2.229853e-12 1.000000e+00  
## [182,] 3.748314e-21 1.000000e+00  
## [183,] 3.483966e-17 1.000000e+00  
## [184,] 1.000000e+00 2.156334e-08  
## [185,] 4.568516e-23 1.000000e+00  
## [186,] 1.822372e-22 1.000000e+00  
## [187,] 1.000000e+00 2.299582e-08  
## [188,] 1.000000e+00 1.453303e-09  
## [189,] 1.000000e+00 6.110471e-09  
## [190,] 1.000000e+00 1.573935e-08  
## [191,] 4.362383e-09 1.000000e+00  
## [192,] 9.999995e-01 5.342768e-07  
## [193,] 1.000000e+00 4.091260e-10  
## [194,] 1.000000e+00 2.966469e-09  
## [195,] 1.650952e-16 1.000000e+00  
## [196,] 2.315981e-18 1.000000e+00  
## [197,] 1.000000e+00 1.453303e-09  
## [198,] 1.000000e+00 4.719915e-08  
## [199,] 1.000000e+00 1.453303e-09  
## [200,] 1.276525e-23 1.000000e+00  
## [201,] 5.115099e-13 1.000000e+00  
## [202,] 1.000000e+00 9.879094e-10  
## [203,] 1.000000e+00 9.879094e-10  
## [204,] 1.000000e+00 3.248390e-08  
## [205,] 1.489154e-26 1.000000e+00  
## [206,] 2.456312e-17 1.000000e+00  
## [207,] 1.000000e+00 1.453303e-09  
## [208,] 2.614960e-27 1.000000e+00  
## [209,] 5.384342e-25 1.000000e+00  
## [210,] 1.540545e-13 1.000000e+00  
## [211,] 1.000000e+00 7.030265e-10  
## [212,] 1.000000e+00 1.453303e-09  
## [213,] 2.238062e-15 1.000000e+00  
## [214,] 9.999990e-01 9.837071e-07  
## [215,] 1.000000e+00 2.765508e-09  
## [216,] 9.229470e-20 1.000000e+00  
## [217,] 9.999919e-01 8.106013e-06  
## [218,] 1.853125e-07 9.999998e-01  
## [219,] 1.741327e-15 1.000000e+00  
## [220,] 1.000000e+00 7.030265e-10  
## [221,] 1.600750e-16 1.000000e+00  
## [222,] 6.526688e-13 1.000000e+00  
## [223,] 1.000000e+00 9.879094e-10  
## [224,] 2.813357e-26 1.000000e+00  
## [225,] 4.346710e-08 1.000000e+00  
## [226,] 5.719675e-15 1.000000e+00  
## [227,] 5.206675e-01 4.793325e-01  
## [228,] 1.907908e-09 1.000000e+00  
## [229,] 9.999678e-01 3.222530e-05  
## [230,] 1.440886e-20 1.000000e+00  
## [231,] 1.778684e-12 1.000000e+00  
## [232,] 4.196932e-24 1.000000e+00  
## [233,] 5.914493e-08 9.999999e-01  
## [234,] 9.999903e-01 9.719257e-06  
## [235,] 1.000000e+00 1.807602e-08  
## [236,] 1.000000e+00 2.761835e-09  
## [237,] 9.999960e-01 3.960769e-06  
## [238,] 1.000000e+00 1.453303e-09  
## [239,] 9.999997e-01 2.965939e-07  
## [240,] 8.174052e-22 1.000000e+00  
## [241,] 1.519860e-04 9.998480e-01  
## [242,] 9.999961e-01 3.934619e-06  
## [243,] 1.000000e+00 2.274872e-09  
## [244,] 8.859425e-13 1.000000e+00  
## [245,] 3.005550e-06 9.999970e-01  
## [246,] 2.560699e-17 1.000000e+00  
## [247,] 2.376443e-16 1.000000e+00  
## [248,] 2.418971e-08 1.000000e+00  
## [249,] 1.000000e+00 1.732506e-09  
## [250,] 1.000000e+00 2.966469e-09  
## [251,] 1.000000e+00 6.110471e-09  
## [252,] 1.086292e-06 9.999989e-01  
## [253,] 2.533706e-15 1.000000e+00  
## [254,] 2.333072e-23 1.000000e+00  
## [255,] 2.275641e-17 1.000000e+00  
## [256,] 1.710517e-14 1.000000e+00  
## [257,] 7.230417e-12 1.000000e+00  
## [258,] 9.999981e-01 1.916662e-06  
## [259,] 1.200415e-13 1.000000e+00  
## [260,] 7.983523e-05 9.999202e-01  
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## [632,] 1.000000e+00 1.815357e-09  
## [633,] 9.728473e-25 1.000000e+00  
## [634,] 1.000000e+00 2.966469e-09  
## [635,] 9.999996e-01 3.822513e-07  
## [636,] 1.000000e+00 7.300335e-09  
## [637,] 1.000000e+00 4.881823e-08  
## [638,] 1.000000e+00 7.654674e-09  
## [639,] 1.000000e+00 6.110471e-09  
## [640,] 1.000000e+00 2.966469e-09  
## [641,] 1.000000e+00 2.299582e-08  
## [642,] 2.503670e-01 7.496330e-01  
## [643,] 2.744223e-14 1.000000e+00  
## [644,] 1.000000e+00 4.091260e-10  
## [645,] 1.000000e+00 7.030265e-10  
## [646,] 1.000000e+00 1.573935e-08  
## [647,] 1.000000e+00 4.608269e-09  
## [648,] 1.000000e+00 4.608269e-09  
## [649,] 1.000000e+00 1.281807e-08  
## [650,] 1.000000e+00 4.091260e-10  
## [651,] 9.999998e-01 1.713802e-07  
## [652,] 1.000000e+00 6.110471e-09  
## [653,] 1.555755e-06 9.999984e-01  
## [654,] 1.876138e-17 1.000000e+00  
## [655,] 4.257141e-13 1.000000e+00  
## [656,] 1.000000e+00 2.696816e-08  
## [657,] 1.000000e+00 2.761835e-09  
## [658,] 9.999997e-01 3.412293e-07  
## [659,] 1.000000e+00 7.030265e-10  
## [660,] 9.999999e-01 9.440449e-08  
## [661,] 1.000000e+00 1.637151e-09  
## [662,] 1.000000e+00 1.347824e-08  
## [663,] 1.000000e+00 4.091260e-10  
## [664,] 1.000000e+00 7.802760e-10  
## [665,] 8.767676e-30 1.000000e+00  
## [666,] 1.527057e-19 1.000000e+00  
## [667,] 9.999999e-01 9.929872e-08  
## [668,] 1.000000e+00 4.091260e-10  
## [669,] 1.000000e+00 4.091260e-10  
## [670,] 1.000000e+00 4.091260e-10  
## [671,] 1.000000e+00 4.091260e-10  
## [672,] 1.000000e+00 1.623662e-08  
## [673,] 1.000000e+00 4.478538e-09  
## [674,] 9.999998e-01 1.818293e-07  
## [675,] 1.000000e+00 1.815357e-09  
## [676,] 2.447084e-10 1.000000e+00  
## [677,] 1.000000e+00 1.732506e-09  
## [678,] 1.000000e+00 3.879784e-09  
## [679,] 1.000000e+00 1.058124e-08  
## [680,] 1.000000e+00 7.802760e-10  
## [681,] 2.576739e-15 1.000000e+00  
## [682,] 2.399474e-08 1.000000e+00  
## [683,] 4.529519e-10 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)  
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 2  
## malignant 12 237