PROJECT 2 RCODE

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**Introduction:** This project involves generating several classification models for the same data set and then combining the output from the models in an ensemble fashion. The dataset used for this analysis is called BreastCancer.

Throughout this document I have highlighted directional text and other relevant information that would be needed to rerun or follow along.

**Table of context:**

Pg. 1 – 2 (Loading, Cleaning, Exploring)

Pg. 3 – 17 (8 classifier models)

Pg. 18 – 35 (Ensemble Process)

Install packages:

install.packages("mlbench")

Load packages:

library(e1071)

## Warning: package 'e1071' was built under R version 4.0.4

library(klaR)

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

## Loading required package: MASS

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

library(nnet)

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

library(MASS)  
library(rpart)

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

library(MASS)  
library(klaR)  
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.

library(mlbench)

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

library(caret)

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

## Loading required package: lattice

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

## Loading required package: ggplot2

## Warning: package 'ggplot2' was built under R version 4.0.4

##   
## Attaching package: 'ggplot2'

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

Load data:

data(BreastCancer)  
  
BreastCancer <- na.omit(BreastCancer)  
BreastCancer <- BreastCancer[-1] #removing the unique identifiers to not confuse the models  
  
mydata <- cbind(BreastCancer[10],BreastCancer[1:9]) #moving Class to the front so that it is easier to visualize

Data type transformation:

#Convert the variables from factors to integers  
  
mydata$Class<-as.integer(BreastCancer$Class)  
mydata$Cl.thickness<-as.integer(BreastCancer$Cl.thickness)  
mydata$Cell.size<-as.integer(BreastCancer$Cell.size)  
mydata$Cell.shape<-as.integer(BreastCancer$Cell.shape)  
mydata$Marg.adhesion<-as.integer(BreastCancer$Marg.adhesion)  
mydata$Epith.c.size<-as.integer(BreastCancer$Epith.c.size)  
mydata$Bare.nuclei<-as.integer(BreastCancer$Bare.nuclei)  
mydata$Bl.cromatin<-as.integer(BreastCancer$Bl.cromatin)  
mydata$Normal.nucleoli<-as.integer(BreastCancer$Normal.nucleoli)  
mydata$Mitoses<-as.integer(BreastCancer$Mitoses)  
  
  
sum(is.na(BreastCancer)) #check to make sure na's have been removed

## [1] 0

str(mydata$Class) #check structure to verify data types have been updated

## int [1:683] 1 1 1 1 1 2 1 1 1 1 ...

Classifier 1: SVM

mysvm <- svm(Class ~ ., BreastCancer)  
mysvm.pred <- predict(mysvm, BreastCancer)  
table(mysvm.pred,BreastCancer$Class)

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

Classifier 2: Naive Bayes

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

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## observation 683

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

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

Classifier 3: Neural Net

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

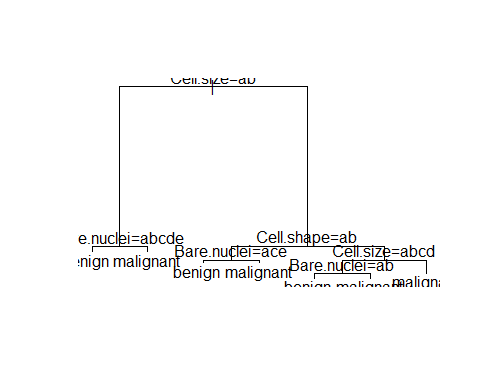
## # weights: 83  
## initial value 544.402047   
## iter 10 value 90.640040  
## iter 20 value 52.672169  
## iter 30 value 49.777460  
## iter 40 value 48.997064  
## iter 50 value 48.985988  
## iter 60 value 48.981544  
## iter 70 value 45.979657  
## iter 80 value 45.730825  
## iter 90 value 45.725910  
## iter 100 value 45.710867  
## final value 45.710867   
## stopped after 100 iterations

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

##   
## mynnet.pred benign malignant  
## benign 435 1  
## malignant 9 238

Classifier 4: Decision Tree

mytree <- rpart(Class ~ ., BreastCancer)  
plot(mytree); text(mytree) # in "Breastcancer\_tree.ps"



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 0.2384937 0.03024241  
## 3 0.02510460 2 0.15481172 0.1841004 0.02684532  
## 4 0.01255230 3 0.12970711 0.1422594 0.02378228  
## 5 0.01000000 6 0.09205021 0.1464435 0.02411089  
##   
## Variable importance  
## Cell.size Cell.shape Bare.nuclei Epith.c.size Bl.cromatin   
## 21 18 16 15 14   
## 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=20.58158, (0 missing)  
## Cell.size splits as LLLRRRRRRR, improve=18.27650, (0 missing)  
## Bare.nuclei splits as LRRRRRRRRR, improve=16.81493, (0 missing)  
## Bl.cromatin splits as LLRRRRRRRR, improve=13.91034, (0 missing)  
## Marg.adhesion splits as LLRRRRRRRR, improve=11.17148, (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)  
## Marg.adhesion splits as LLLLLLLRRR, agree=0.826, adj=0.429, (0 split)  
## Normal.nucleoli splits as LLRRLL-L--, agree=0.826, adj=0.429, (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)  
## Marg.adhesion splits as LLLLLRRRRR, improve=2.754821, (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)  
## Marg.adhesion splits as LRRRRRRRRR, agree=0.744, adj=0.088, (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)  
## Marg.adhesion splits as LLLLLRRRRR, improve=2.615385, (0 missing)  
## Bl.cromatin splits as LLLLRLLR-R, improve=1.640351, (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

Classifier 5: 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 430 20  
## malignant 14 219

# The same as above in this case

Classifier 6: Quadratic Discriminant Analysis

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

##   
## 1 2  
## 1 422 6  
## 2 22 233

Classifier 7: Regularized Discriminant Analysis

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

##   
## benign malignant  
## benign 433 2  
## malignant 11 237

Classifier 8: Random Forests

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

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

Combining models:

#combining all the models into a new dataframe so that ensemble can take place.   
  
combine.classes <- data.frame(myrf.pred, myrda.pred$class, #myqda.pred,   
 mytree.pred, mynnet.pred, mysvm.pred, mynb.pred$class)  
  
head(combine.classes) #view the dataframe to verify the structure and values the new datafram contains

## 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 malignant malignant malignant  
## 3 benign benign malignant benign benign benign  
## 4 benign malignant malignant malignant 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 malignant 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] malignant 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 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 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 malignant  
## [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 malignant  
## [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 benign 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 8.541419e-32  
## [2,] 1.232231e-03 9.987678e-01  
## [3,] 1.000000e+00 6.817689e-34  
## [4,] 8.924916e-12 1.000000e+00  
## [5,] 1.000000e+00 2.172848e-31  
## [6,] 4.733106e-73 1.000000e+00  
## [7,] 1.000000e+00 1.801776e-26  
## [8,] 1.000000e+00 4.928862e-36  
## [9,] 1.000000e+00 4.942351e-23  
## [10,] 1.000000e+00 3.490073e-34  
## [11,] 1.000000e+00 3.894818e-38  
## [12,] 1.000000e+00 1.779063e-36  
## [13,] 2.439686e-10 1.000000e+00  
## [14,] 1.000000e+00 1.613296e-32  
## [15,] 1.256117e-97 1.000000e+00  
## [16,] 2.131537e-40 1.000000e+00  
## [17,] 1.000000e+00 1.553974e-34  
## [18,] 1.000000e+00 1.539802e-33  
## [19,] 1.255714e-60 1.000000e+00  
## [20,] 1.000000e+00 1.197110e-28  
## [21,] 2.059807e-58 1.000000e+00  
## [22,] 1.022283e-67 1.000000e+00  
## [23,] 1.000000e+00 7.641046e-36  
## [24,] 1.000000e+00 7.354229e-36  
## [25,] 8.861825e-17 1.000000e+00  
## [26,] 1.000000e+00 1.388541e-38  
## [27,] 1.000000e+00 1.503910e-33  
## [28,] 1.000000e+00 1.779063e-36  
## [29,] 1.000000e+00 2.045749e-32  
## [30,] 1.000000e+00 6.300714e-38  
## [31,] 1.000000e+00 1.322438e-35  
## [32,] 1.409000e-66 1.000000e+00  
## [33,] 1.000000e+00 7.044824e-36  
## [34,] 1.000000e+00 2.245713e-36  
## [35,] 1.000000e+00 1.779063e-36  
## [36,] 2.195133e-71 1.000000e+00  
## [37,] 1.000000e+00 7.301439e-26  
## [38,] 1.781425e-38 1.000000e+00  
## [39,] 2.863227e-45 1.000000e+00  
## [40,] 1.325234e-39 1.000000e+00  
## [41,] 7.037603e-46 1.000000e+00  
## [42,] 2.985030e-38 1.000000e+00  
## [43,] 2.045404e-56 1.000000e+00  
## [44,] 1.000000e+00 4.449393e-31  
## [45,] 4.789881e-55 1.000000e+00  
## [46,] 1.000000e+00 2.154796e-37  
## [47,] 1.000000e+00 2.172848e-31  
## [48,] 5.285967e-53 1.000000e+00  
## [49,] 3.558810e-47 1.000000e+00  
## [50,] 1.061065e-13 1.000000e+00  
## [51,] 1.686772e-40 1.000000e+00  
## [52,] 6.151702e-73 1.000000e+00  
## [53,] 1.482387e-62 1.000000e+00  
## [54,] 1.115736e-46 1.000000e+00  
## [55,] 1.605407e-50 1.000000e+00  
## [56,] 2.419192e-41 1.000000e+00  
## [57,] 2.729733e-16 1.000000e+00  
## [58,] 2.935679e-41 1.000000e+00  
## [59,] 1.352562e-31 1.000000e+00  
## [60,] 1.000000e+00 9.470969e-37  
## [61,] 3.117293e-47 1.000000e+00  
## [62,] 3.240275e-18 1.000000e+00  
## [63,] 1.000000e+00 2.154796e-37  
## [64,] 9.949548e-28 1.000000e+00  
## [65,] 1.000000e+00 1.539802e-33  
## [66,] 3.942784e-35 1.000000e+00  
## [67,] 2.726186e-76 1.000000e+00  
## [68,] 1.000000e+00 1.979582e-38  
## [69,] 1.000000e+00 3.322925e-30  
## [70,] 7.253797e-58 1.000000e+00  
## [71,] 1.000000e+00 6.772139e-21  
## [72,] 5.922712e-63 1.000000e+00  
## [73,] 1.063474e-35 1.000000e+00  
## [74,] 1.000000e+00 1.385586e-30  
## [75,] 1.000000e+00 8.991298e-29  
## [76,] 1.000000e+00 5.936243e-29  
## [77,] 1.000000e+00 4.103607e-31  
## [78,] 1.000000e+00 3.959953e-34  
## [79,] 1.000000e+00 3.395726e-30  
## [80,] 1.000000e+00 2.524141e-34  
## [81,] 1.000000e+00 1.365222e-30  
## [82,] 1.000000e+00 6.356750e-26  
## [83,] 2.225271e-85 1.000000e+00  
## [84,] 3.548242e-57 1.000000e+00  
## [85,] 9.444338e-40 1.000000e+00  
## [86,] 4.470706e-75 1.000000e+00  
## [87,] 1.000000e+00 1.539802e-33  
## [88,] 1.000000e+00 1.975652e-34  
## [89,] 1.000000e+00 7.354229e-36  
## [90,] 1.000000e+00 1.609845e-33  
## [91,] 1.000000e+00 1.539802e-33  
## [92,] 1.000000e+00 2.154796e-37  
## [93,] 1.000000e+00 1.322438e-35  
## [94,] 1.000000e+00 7.354229e-36  
## [95,] 1.000000e+00 2.035135e-35  
## [96,] 1.000000e+00 8.541419e-32  
## [97,] 2.980680e-99 1.000000e+00  
## [98,] 9.119810e-90 1.000000e+00  
## [99,] 7.272244e-49 1.000000e+00  
## [100,] 8.883520e-09 1.000000e+00  
## [101,] 1.000000e+00 3.762187e-34  
## [102,] 5.126094e-16 1.000000e+00  
## [103,] 8.052465e-69 1.000000e+00  
## [104,] 1.107830e-29 1.000000e+00  
## [105,] 4.885082e-49 1.000000e+00  
## [106,] 6.102312e-60 1.000000e+00  
## [107,] 1.000000e+00 4.001670e-32  
## [108,] 1.447677e-58 1.000000e+00  
## [109,] 1.000000e+00 1.711214e-16  
## [110,] 4.978537e-40 1.000000e+00  
## [111,] 8.020056e-37 1.000000e+00  
## [112,] 3.078737e-50 1.000000e+00  
## [113,] 1.000000e+00 7.824142e-25  
## [114,] 1.000000e+00 4.716601e-30  
## [115,] 1.000000e+00 8.299336e-15  
## [116,] 4.974054e-66 1.000000e+00  
## [117,] 1.000000e+00 5.180696e-24  
## [118,] 1.000000e+00 1.372640e-33  
## [119,] 1.000000e+00 2.236285e-37  
## [120,] 1.000000e+00 2.151946e-32  
## [121,] 9.055790e-59 1.000000e+00  
## [122,] 1.343145e-27 1.000000e+00  
## [123,] 1.899566e-76 1.000000e+00  
## [124,] 1.000000e+00 2.154796e-37  
## [125,] 5.434463e-78 1.000000e+00  
## [126,] 1.000000e+00 1.948740e-34  
## [127,] 2.263889e-46 1.000000e+00  
## [128,] 1.000000e+00 2.040097e-19  
## [129,] 1.000000e+00 3.322925e-30  
## [130,] 1.000000e+00 1.322438e-35  
## [131,] 3.252729e-56 1.000000e+00  
## [132,] 1.000000e+00 1.074246e-38  
## [133,] 1.000000e+00 1.767634e-32  
## [134,] 1.000000e+00 1.696617e-26  
## [135,] 1.000000e+00 1.553974e-34  
## [136,] 1.000000e+00 1.943599e-34  
## [137,] 1.000000e+00 3.711184e-35  
## [138,] 1.000000e+00 1.943599e-34  
## [139,] 1.000000e+00 1.912030e-35  
## [140,] 1.564763e-69 1.000000e+00  
## [141,] 1.000000e+00 4.716601e-30  
## [142,] 1.000000e+00 1.779063e-36  
## [143,] 2.898995e-28 1.000000e+00  
## [144,] 1.000000e+00 3.254339e-34  
## [145,] 9.999948e-01 5.244761e-06  
## [146,] 4.282972e-76 1.000000e+00  
## [147,] 1.000000e+00 3.894818e-38  
## [148,] 4.147429e-59 1.000000e+00  
## [149,] 2.977695e-68 1.000000e+00  
## [150,] 1.000000e+00 1.251139e-29  
## [151,] 1.000000e+00 6.467840e-36  
## [152,] 4.535258e-30 1.000000e+00  
## [153,] 1.000000e+00 4.046487e-36  
## [154,] 1.000000e+00 1.322438e-35  
## [155,] 2.103726e-86 1.000000e+00  
## [156,] 1.103198e-68 1.000000e+00  
## [157,] 1.000000e+00 2.740575e-36  
## [158,] 1.000000e+00 1.948740e-34  
## [159,] 1.000000e+00 1.130917e-24  
## [160,] 1.000000e+00 2.483967e-36  
## [161,] 1.713792e-68 1.000000e+00  
## [162,] 2.780957e-62 1.000000e+00  
## [163,] 1.000000e+00 1.948740e-34  
## [164,] 1.000000e+00 6.432982e-38  
## [165,] 1.000000e+00 1.943599e-34  
## [166,] 1.000000e+00 7.354229e-36  
## [167,] 1.000000e+00 2.154796e-37  
## [168,] 5.482899e-61 1.000000e+00  
## [169,] 4.846947e-58 1.000000e+00  
## [170,] 2.476061e-68 1.000000e+00  
## [171,] 1.000000e+00 1.322438e-35  
## [172,] 5.242554e-42 1.000000e+00  
## [173,] 1.000000e+00 1.539802e-33  
## [174,] 8.316836e-09 1.000000e+00  
## [175,] 1.000000e+00 3.894818e-38  
## [176,] 1.000000e+00 6.467840e-36  
## [177,] 1.000000e+00 1.197110e-28  
## [178,] 1.428367e-56 1.000000e+00  
## [179,] 1.471916e-53 1.000000e+00  
## [180,] 1.000000e+00 1.555073e-38  
## [181,] 1.068459e-57 1.000000e+00  
## [182,] 3.986604e-88 1.000000e+00  
## [183,] 3.382431e-62 1.000000e+00  
## [184,] 1.000000e+00 7.184758e-28  
## [185,] 1.803528e-67 1.000000e+00  
## [186,] 1.259587e-83 1.000000e+00  
## [187,] 1.000000e+00 1.503910e-33  
## [188,] 1.000000e+00 7.354229e-36  
## [189,] 1.000000e+00 1.948740e-34  
## [190,] 1.000000e+00 1.539802e-33  
## [191,] 6.942019e-16 1.000000e+00  
## [192,] 1.000000e+00 9.493724e-23  
## [193,] 1.000000e+00 6.467840e-36  
## [194,] 1.000000e+00 7.641046e-36  
## [195,] 7.060611e-68 1.000000e+00  
## [196,] 7.036131e-66 1.000000e+00  
## [197,] 1.000000e+00 7.354229e-36  
## [198,] 1.000000e+00 8.541419e-32  
## [199,] 1.000000e+00 7.354229e-36  
## [200,] 2.280470e-70 1.000000e+00  
## [201,] 1.160055e-61 1.000000e+00  
## [202,] 1.000000e+00 3.894818e-38  
## [203,] 1.000000e+00 3.894818e-38  
## [204,] 1.000000e+00 1.627176e-34  
## [205,] 3.701444e-70 1.000000e+00  
## [206,] 2.100691e-68 1.000000e+00  
## [207,] 1.000000e+00 7.354229e-36  
## [208,] 7.351871e-73 1.000000e+00  
## [209,] 6.565206e-55 1.000000e+00  
## [210,] 2.316707e-70 1.000000e+00  
## [211,] 1.000000e+00 2.154796e-37  
## [212,] 1.000000e+00 7.354229e-36  
## [213,] 1.574819e-73 1.000000e+00  
## [214,] 1.000000e+00 6.448089e-26  
## [215,] 1.000000e+00 3.846810e-36  
## [216,] 2.153130e-67 1.000000e+00  
## [217,] 1.000000e+00 1.129665e-25  
## [218,] 5.220274e-57 1.000000e+00  
## [219,] 3.521403e-73 1.000000e+00  
## [220,] 1.000000e+00 2.154796e-37  
## [221,] 1.784625e-77 1.000000e+00  
## [222,] 1.459078e-59 1.000000e+00  
## [223,] 1.000000e+00 3.894818e-38  
## [224,] 2.056960e-60 1.000000e+00  
## [225,] 1.497638e-52 1.000000e+00  
## [226,] 3.631117e-69 1.000000e+00  
## [227,] 2.260476e-11 1.000000e+00  
## [228,] 5.954211e-39 1.000000e+00  
## [229,] 1.000000e+00 4.198873e-16  
## [230,] 1.893372e-74 1.000000e+00  
## [231,] 1.480965e-81 1.000000e+00  
## [232,] 6.288170e-76 1.000000e+00  
## [233,] 5.904235e-28 1.000000e+00  
## [234,] 1.000000e+00 8.525274e-26  
## [235,] 1.000000e+00 1.480388e-34  
## [236,] 1.000000e+00 1.322438e-35  
## [237,] 1.000000e+00 4.186601e-21  
## [238,] 1.000000e+00 7.354229e-36  
## [239,] 1.000000e+00 2.575542e-31  
## [240,] 6.693177e-56 1.000000e+00  
## [241,] 2.162920e-20 1.000000e+00  
## [242,] 1.000000e+00 9.149461e-24  
## [243,] 1.000000e+00 1.004912e-33  
## [244,] 5.739142e-45 1.000000e+00  
## [245,] 1.645720e-07 9.999998e-01  
## [246,] 7.037603e-46 1.000000e+00  
## [247,] 3.117293e-47 1.000000e+00  
## [248,] 1.076391e-35 1.000000e+00  
## [249,] 1.000000e+00 1.943599e-34  
## [250,] 1.000000e+00 7.641046e-36  
## [251,] 1.000000e+00 1.948740e-34  
## [252,] 6.023844e-16 1.000000e+00  
## [253,] 8.289002e-66 1.000000e+00  
## [254,] 1.003766e-67 1.000000e+00  
## [255,] 1.284141e-62 1.000000e+00  
## [256,] 5.697299e-53 1.000000e+00  
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## [631,] 1.000000e+00 1.004912e-33  
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## [633,] 3.615788e-51 1.000000e+00  
## [634,] 1.000000e+00 7.641046e-36  
## [635,] 1.000000e+00 3.775700e-24  
## [636,] 1.000000e+00 6.427505e-37  
## [637,] 1.000000e+00 1.241519e-36  
## [638,] 1.000000e+00 1.553974e-34  
## [639,] 1.000000e+00 1.948740e-34  
## [640,] 1.000000e+00 7.641046e-36  
## [641,] 1.000000e+00 1.503910e-33  
## [642,] 7.862236e-07 9.999992e-01  
## [643,] 2.262273e-64 1.000000e+00  
## [644,] 1.000000e+00 6.467840e-36  
## [645,] 1.000000e+00 2.154796e-37  
## [646,] 1.000000e+00 1.539802e-33  
## [647,] 1.000000e+00 1.757024e-34  
## [648,] 1.000000e+00 1.757024e-34  
## [649,] 1.000000e+00 2.009557e-34  
## [650,] 1.000000e+00 6.467840e-36  
## [651,] 1.000000e+00 5.584836e-25  
## [652,] 1.000000e+00 1.948740e-34  
## [653,] 3.528750e-41 1.000000e+00  
## [654,] 1.756875e-46 1.000000e+00  
## [655,] 1.110858e-49 1.000000e+00  
## [656,] 1.000000e+00 6.514515e-34  
## [657,] 1.000000e+00 1.322438e-35  
## [658,] 1.000000e+00 3.209229e-22  
## [659,] 1.000000e+00 2.154796e-37  
## [660,] 1.000000e+00 2.496057e-25  
## [661,] 1.000000e+00 3.633620e-38  
## [662,] 1.000000e+00 4.111994e-32  
## [663,] 1.000000e+00 6.467840e-36  
## [664,] 1.000000e+00 1.912030e-35  
## [665,] 6.695350e-71 1.000000e+00  
## [666,] 1.155181e-56 1.000000e+00  
## [667,] 1.000000e+00 1.151806e-34  
## [668,] 1.000000e+00 6.467840e-36  
## [669,] 1.000000e+00 6.467840e-36  
## [670,] 1.000000e+00 6.467840e-36  
## [671,] 1.000000e+00 6.467840e-36  
## [672,] 1.000000e+00 1.540044e-30  
## [673,] 1.000000e+00 2.291152e-33  
## [674,] 1.000000e+00 8.913638e-23  
## [675,] 1.000000e+00 1.693080e-34  
## [676,] 6.565034e-48 1.000000e+00  
## [677,] 1.000000e+00 1.943599e-34  
## [678,] 1.000000e+00 1.636819e-29  
## [679,] 1.000000e+00 5.440729e-30  
## [680,] 1.000000e+00 1.912030e-35  
## [681,] 5.690013e-45 1.000000e+00  
## [682,] 2.107193e-48 1.000000e+00  
## [683,] 1.695008e-60 1.000000e+00

Making models binary:

#Convert the values to binary (o, 1) so that the models can be summed across  
  
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:

#conduct the rowsums function and and save to a new dataframe  
  
majority.vote=rowSums(combine.classes)  
head(majority.vote)

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

Produce final table:

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 433 2  
## malignant 11 237

## R Markdown