Project Two - Breast Cancer Ensemble Classification

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

## Loading required package: mlbench

# load the data set  
data(BreastCancer)  
ls(BreastCancer)

## [1] "Bare.nuclei" "Bl.cromatin" "Cell.shape" "Cell.size"   
## [5] "Cl.thickness" "Class" "Epith.c.size" "Id"   
## [9] "Marg.adhesion" "Mitoses" "Normal.nucleoli"

# some algorithms don't like missing values, so remove rows with missing values  
# Not many NA values, so it won't impact the model prediction even if they are omitted.  
BreastCancer <- na.omit(BreastCancer)   
# remove the unique identifier, which is useless and would confuse the machine learning algorithms  
BreastCancer$Id <- NULL   
head(BreastCancer)

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

str(BreastCancer)

## 'data.frame': 683 obs. of 10 variables:  
## $ Cl.thickness : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<..: 5 5 3 6 4 8 1 2 2 4 ...  
## $ Cell.size : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<..: 1 4 1 8 1 10 1 1 1 2 ...  
## $ Cell.shape : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<..: 1 4 1 8 1 10 1 2 1 1 ...  
## $ Marg.adhesion : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<..: 1 5 1 1 3 8 1 1 1 1 ...  
## $ Epith.c.size : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<..: 2 7 2 3 2 7 2 2 2 2 ...  
## $ Bare.nuclei : Factor w/ 10 levels "1","2","3","4",..: 1 10 2 4 1 10 10 1 1 1 ...  
## $ Bl.cromatin : Factor w/ 10 levels "1","2","3","4",..: 3 3 3 3 3 9 3 3 1 2 ...  
## $ Normal.nucleoli: Factor w/ 10 levels "1","2","3","4",..: 1 2 1 7 1 7 1 1 1 1 ...  
## $ Mitoses : Factor w/ 9 levels "1","2","3","4",..: 1 1 1 1 1 1 1 1 5 1 ...  
## $ Class : Factor w/ 2 levels "benign","malignant": 1 1 1 1 1 2 1 1 1 1 ...  
## - attr(\*, "na.action")= 'omit' Named int [1:16] 24 41 140 146 159 165 236 250 276 293 ...  
## ..- attr(\*, "names")= chr [1:16] "24" "41" "140" "146" ...

df2 <- data.frame(sapply(BreastCancer[1:9], function(x) as.numeric(as.character(x))))  
z <- scale(df2[,1:9],center=TRUE,scale=TRUE)  
head(z)

## Cl.thickness Cell.size Cell.shape Marg.adhesion Epith.c.size Bare.nuclei  
## [1,] 0.1977598 -0.7016978 -0.7412304 -0.63889730 -0.5552016 -0.6983413  
## [2,] 0.1977598 0.2770488 0.2625905 0.75747664 1.6939247 1.7715689  
## [3,] -0.5112687 -0.7016978 -0.7412304 -0.63889730 -0.5552016 -0.4239068  
## [4,] 0.5522740 1.5820442 1.6010185 -0.63889730 -0.1053763 0.1249621  
## [5,] -0.1567545 -0.7016978 -0.7412304 0.05928967 -0.5552016 -0.6983413  
## [6,] 1.2613024 2.2345419 2.2702324 1.80475710 1.6939247 1.7715689  
## Bl.cromatin Normal.nucleoli Mitoses  
## [1,] -0.181694 -0.6124785 -0.3481446  
## [2,] -0.181694 -0.2848960 -0.3481446  
## [3,] -0.181694 -0.6124785 -0.3481446  
## [4,] -0.181694 1.3530163 -0.3481446  
## [5,] -0.181694 -0.6124785 -0.3481446  
## [6,] 2.267589 1.3530163 -0.3481446

#Support Vector Machine Classifier  
library(e1071)  
mysvm <- svm(Class ~ ., BreastCancer)  
mysvm.pred <- predict(mysvm, BreastCancer)  
table(mysvm.pred,BreastCancer$Class)

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

#NaiveBayes Classifier  
  
library(klaR)

## Loading required package: MASS

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

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

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

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

str(mysvm.pred)

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

str(mynb.pred)

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

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

#Neural Network Classifier  
library(nnet)  
library(neuralnet)  
str(BreastCancer)

## 'data.frame': 683 obs. of 10 variables:  
## $ Cl.thickness : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<..: 5 5 3 6 4 8 1 2 2 4 ...  
## $ Cell.size : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<..: 1 4 1 8 1 10 1 1 1 2 ...  
## $ Cell.shape : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<..: 1 4 1 8 1 10 1 2 1 1 ...  
## $ Marg.adhesion : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<..: 1 5 1 1 3 8 1 1 1 1 ...  
## $ Epith.c.size : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<..: 2 7 2 3 2 7 2 2 2 2 ...  
## $ Bare.nuclei : Factor w/ 10 levels "1","2","3","4",..: 1 10 2 4 1 10 10 1 1 1 ...  
## $ Bl.cromatin : Factor w/ 10 levels "1","2","3","4",..: 3 3 3 3 3 9 3 3 1 2 ...  
## $ Normal.nucleoli: Factor w/ 10 levels "1","2","3","4",..: 1 2 1 7 1 7 1 1 1 1 ...  
## $ Mitoses : Factor w/ 9 levels "1","2","3","4",..: 1 1 1 1 1 1 1 1 5 1 ...  
## $ Class : Factor w/ 2 levels "benign","malignant": 1 1 1 1 1 2 1 1 1 1 ...  
## - attr(\*, "na.action")= 'omit' Named int [1:16] 24 41 140 146 159 165 236 250 276 293 ...  
## ..- attr(\*, "names")= chr [1:16] "24" "41" "140" "146" ...

for (i in c(1:9)){  
BreastCancer[,i] <-(as.numeric(BreastCancer[,i])-min(as.numeric(BreastCancer[,i]))) /  
 (max(as.numeric(BreastCancer[,i]))-min(as.numeric(BreastCancer[,i])))  
}  
mynnet <- neuralnet(Class ~ ., BreastCancer, hidden=c(5,4))  
head(BreastCancer)

## Cl.thickness Cell.size Cell.shape Marg.adhesion Epith.c.size Bare.nuclei  
## 1 0.4444444 0.0000000 0.0000000 0.0000000 0.1111111 0.0000000  
## 2 0.4444444 0.3333333 0.3333333 0.4444444 0.6666667 1.0000000  
## 3 0.2222222 0.0000000 0.0000000 0.0000000 0.1111111 0.1111111  
## 4 0.5555556 0.7777778 0.7777778 0.0000000 0.2222222 0.3333333  
## 5 0.3333333 0.0000000 0.0000000 0.2222222 0.1111111 0.0000000  
## 6 0.7777778 1.0000000 1.0000000 0.7777778 0.6666667 1.0000000  
## Bl.cromatin Normal.nucleoli Mitoses Class  
## 1 0.2222222 0.0000000 0 benign  
## 2 0.2222222 0.1111111 0 benign  
## 3 0.2222222 0.0000000 0 benign  
## 4 0.2222222 0.6666667 0 benign  
## 5 0.2222222 0.0000000 0 benign  
## 6 0.8888889 0.6666667 0 malignant

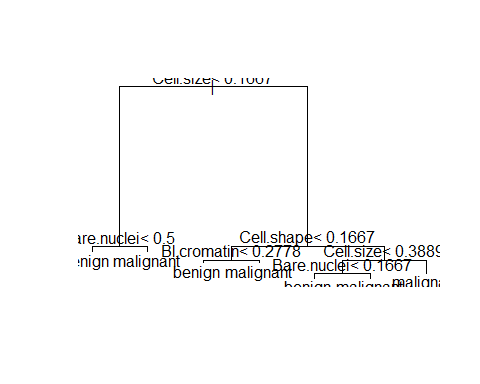
str(mynnet)

## List of 14  
## $ call : language neuralnet(formula = Class ~ ., data = BreastCancer, hidden = c(5, 4))  
## $ response : logi [1:683, 1:2] TRUE TRUE TRUE TRUE TRUE FALSE ...  
## ..- attr(\*, "dimnames")=List of 2  
## .. ..$ : chr [1:683] "1" "2" "3" "4" ...  
## .. ..$ : chr [1:2] "benign" "malignant"  
## $ covariate : num [1:683, 1:9] 0.444 0.444 0.222 0.556 0.333 ...  
## ..- attr(\*, "dimnames")=List of 2  
## .. ..$ : chr [1:683] "1" "2" "3" "4" ...  
## .. ..$ : chr [1:9] "Cl.thickness" "Cell.size" "Cell.shape" "Marg.adhesion" ...  
## $ model.list :List of 2  
## ..$ response : chr [1:2] "benign" "malignant"  
## ..$ variables: chr [1:9] "Cl.thickness" "Cell.size" "Cell.shape" "Marg.adhesion" ...  
## $ err.fct :function (x, y)   
## ..- attr(\*, "type")= chr "sse"  
## $ act.fct :function (x)   
## ..- attr(\*, "type")= chr "logistic"  
## $ linear.output : logi TRUE  
## $ data :'data.frame': 683 obs. of 10 variables:  
## ..$ Cl.thickness : num [1:683] 0.444 0.444 0.222 0.556 0.333 ...  
## ..$ Cell.size : num [1:683] 0 0.333 0 0.778 0 ...  
## ..$ Cell.shape : num [1:683] 0 0.333 0 0.778 0 ...  
## ..$ Marg.adhesion : num [1:683] 0 0.444 0 0 0.222 ...  
## ..$ Epith.c.size : num [1:683] 0.111 0.667 0.111 0.222 0.111 ...  
## ..$ Bare.nuclei : num [1:683] 0 1 0.111 0.333 0 ...  
## ..$ Bl.cromatin : num [1:683] 0.222 0.222 0.222 0.222 0.222 ...  
## ..$ Normal.nucleoli: num [1:683] 0 0.111 0 0.667 0 ...  
## ..$ Mitoses : num [1:683] 0 0 0 0 0 0 0 0 0.5 0 ...  
## ..$ Class : Factor w/ 2 levels "benign","malignant": 1 1 1 1 1 2 1 1 1 1 ...  
## ..- attr(\*, "na.action")= 'omit' Named int [1:16] 24 41 140 146 159 165 236 250 276 293 ...  
## .. ..- attr(\*, "names")= chr [1:16] "24" "41" "140" "146" ...  
## $ exclude : NULL  
## $ net.result :List of 1  
## ..$ : num [1:683, 1:2] 1 1 1 0.987 0.999 ...  
## .. ..- attr(\*, "dimnames")=List of 2  
## .. .. ..$ : chr [1:683] "1" "2" "3" "4" ...  
## .. .. ..$ : NULL  
## $ weights :List of 1  
## ..$ :List of 3  
## .. ..$ : num [1:10, 1:5] -3.435 -1.646 1.66 -0.401 4.548 ...  
## .. ..$ : num [1:6, 1:4] 0.343 11.001 -30.024 -15.68 18.562 ...  
## .. ..$ : num [1:5, 1:2] 0.313 1.387 -1.082 0.258 -0.824 ...  
## $ generalized.weights:List of 1  
## ..$ : num [1:683, 1:18] 0.528 4311.38 -306.941 -131.15 13.181 ...  
## .. ..- attr(\*, "dimnames")=List of 2  
## .. .. ..$ : chr [1:683] "1" "2" "3" "4" ...  
## .. .. ..$ : NULL  
## $ startweights :List of 1  
## ..$ :List of 3  
## .. ..$ : num [1:10, 1:5] -0.334 -0.467 -0.257 0.186 -1.384 ...  
## .. ..$ : num [1:6, 1:4] 1.284 -1.507 -1.342 -0.655 1.022 ...  
## .. ..$ : num [1:5, 1:2] 0.335 1.171 -1.113 0.261 -0.637 ...  
## $ result.matrix : num [1:87, 1] 1.87 9.86e-03 1.33e+04 -3.43 -1.65 ...  
## ..- attr(\*, "dimnames")=List of 2  
## .. ..$ : chr [1:87] "error" "reached.threshold" "steps" "Intercept.to.1layhid1" ...  
## .. ..$ : NULL  
## - attr(\*, "class")= chr "nn"

mynnet.pred <- predict(mynnet,BreastCancer,type="class")  
  
#mynnet.pred doesn't convert to confusion matrix table because it now has two values 'v1' and 'v2'.  
#They need to be merged into 1 column so that it has same length as the validation set.  
#Put a data frame and then find better accuracy out of two and then merge it with better value.  
  
mynnet.df <- as.data.frame(mynnet.pred)  
mynnet.pred2 <- ifelse(mynnet.df$V1 > mynnet.df$V2, 'benign', 'malignant')  
  
table(mynnet.pred2,BreastCancer$Class)

##   
## mynnet.pred2 benign malignant  
## benign 442 0  
## malignant 2 239

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



summary(mytree)

## Call:  
## rpart(formula = Class ~ ., data = BreastCancer)  
## n= 683   
##   
## CP nsplit rel error xerror xstd  
## 1 0.79079498 0 1.00000000 1.0000000 0.05215335  
## 2 0.05439331 1 0.20920502 0.2677824 0.03186596  
## 3 0.02510460 2 0.15481172 0.1548117 0.02475192  
## 4 0.01255230 3 0.12970711 0.1506276 0.02443403  
## 5 0.01000000 6 0.09205021 0.1380753 0.02344798  
##   
## Variable importance  
## Cell.size Cell.shape Bare.nuclei Epith.c.size Bl.cromatin   
## 21 18 16 15 15   
## Normal.nucleoli Cl.thickness   
## 14 1   
##   
## Node number 1: 683 observations, complexity param=0.790795  
## predicted class=benign expected loss=0.3499268 P(node) =1  
## class counts: 444 239  
## probabilities: 0.650 0.350   
## left son=2 (418 obs) right son=3 (265 obs)  
## Primary splits:  
## Cell.size < 0.1666667 to the left, improve=222.3221, (0 missing)  
## Cell.shape < 0.2777778 to the left, improve=216.4111, (0 missing)  
## Bare.nuclei < 0.1666667 to the left, improve=203.7284, (0 missing)  
## Bl.cromatin < 0.2777778 to the left, improve=196.3903, (0 missing)  
## Epith.c.size < 0.1666667 to the left, improve=193.1310, (0 missing)  
## Surrogate splits:  
## Cell.shape < 0.2777778 to the left, agree=0.917, adj=0.785, (0 split)  
## Epith.c.size < 0.1666667 to the left, agree=0.900, adj=0.743, (0 split)  
## Bare.nuclei < 0.1666667 to the left, agree=0.880, adj=0.691, (0 split)  
## Normal.nucleoli < 0.1666667 to the left, agree=0.877, adj=0.683, (0 split)  
## Bl.cromatin < 0.2777778 to the left, agree=0.876, adj=0.679, (0 split)  
##   
## Node number 2: 418 observations, complexity param=0.0251046  
## predicted class=benign expected loss=0.02870813 P(node) =0.6120059  
## class counts: 406 12  
## probabilities: 0.971 0.029   
## left son=4 (410 obs) right son=5 (8 obs)  
## Primary splits:  
## Bare.nuclei < 0.5 to the left, improve=11.68296, (0 missing)  
## Cl.thickness < 0.6111111 to the left, improve=10.32214, (0 missing)  
## Normal.nucleoli < 0.2777778 to the left, improve=10.32214, (0 missing)  
## Bl.cromatin < 0.3888889 to the left, improve= 8.53307, (0 missing)  
## Epith.c.size < 0.2777778 to the left, improve= 4.63208, (0 missing)  
## Surrogate splits:  
## Cl.thickness < 0.8333333 to the left, agree=0.988, adj=0.375, (0 split)  
## Normal.nucleoli < 0.2777778 to the left, agree=0.983, adj=0.125, (0 split)  
##   
## Node number 3: 265 observations, complexity param=0.05439331  
## predicted class=malignant expected loss=0.1433962 P(node) =0.3879941  
## class counts: 38 227  
## probabilities: 0.143 0.857   
## left son=6 (23 obs) right son=7 (242 obs)  
## Primary splits:  
## Cell.shape < 0.1666667 to the left, improve=20.58158, (0 missing)  
## Cell.size < 0.2777778 to the left, improve=18.27650, (0 missing)  
## Bare.nuclei < 0.05555556 to the left, improve=16.81493, (0 missing)  
## Bl.cromatin < 0.1666667 to the left, improve=13.91034, (0 missing)  
## Marg.adhesion < 0.1666667 to the left, improve=11.17148, (0 missing)  
## Surrogate splits:  
## Bl.cromatin < 0.05555556 to the left, agree=0.932, adj=0.217, (0 split)  
##   
## Node number 4: 410 observations  
## predicted class=benign expected loss=0.01219512 P(node) =0.6002928  
## class counts: 405 5  
## probabilities: 0.988 0.012   
##   
## Node number 5: 8 observations  
## predicted class=malignant expected loss=0.125 P(node) =0.01171303  
## class counts: 1 7  
## probabilities: 0.125 0.875   
##   
## Node number 6: 23 observations, complexity param=0.0125523  
## predicted class=benign expected loss=0.2173913 P(node) =0.03367496  
## class counts: 18 5  
## probabilities: 0.783 0.217   
## left son=12 (16 obs) right son=13 (7 obs)  
## Primary splits:  
## Bl.cromatin < 0.2777778 to the left, improve=4.968944, (0 missing)  
## Cl.thickness < 0.3888889 to the left, improve=3.381643, (0 missing)  
## Bare.nuclei < 0.05555556 to the left, improve=2.826087, (0 missing)  
## Mitoses < 0.0625 to the left, improve=2.522516, (0 missing)  
## Epith.c.size < 0.1666667 to the left, improve=1.992754, (0 missing)  
## Surrogate splits:  
## Cl.thickness < 0.5 to the left, agree=0.870, adj=0.571, (0 split)  
## Marg.adhesion < 0.6666667 to the left, agree=0.826, adj=0.429, (0 split)  
## Normal.nucleoli < 0.1666667 to the left, agree=0.826, adj=0.429, (0 split)  
## Mitoses < 0.0625 to the left, agree=0.826, adj=0.429, (0 split)  
## Epith.c.size < 0.3333333 to the left, agree=0.783, adj=0.286, (0 split)  
##   
## Node number 7: 242 observations, complexity param=0.0125523  
## predicted class=malignant expected loss=0.08264463 P(node) =0.3543192  
## class counts: 20 222  
## probabilities: 0.083 0.917   
## left son=14 (68 obs) right son=15 (174 obs)  
## Primary splits:  
## Cell.size < 0.3888889 to the left, improve=5.297663, (0 missing)  
## Bare.nuclei < 0.1666667 to the left, improve=4.093695, (0 missing)  
## Cell.shape < 0.3888889 to the left, improve=2.958548, (0 missing)  
## Bl.cromatin < 0.2777778 to the left, improve=2.805426, (0 missing)  
## Marg.adhesion < 0.5 to the left, improve=2.754821, (0 missing)  
## Surrogate splits:  
## Cell.shape < 0.3888889 to the left, agree=0.789, adj=0.250, (0 split)  
## Epith.c.size < 0.1666667 to the left, agree=0.777, adj=0.206, (0 split)  
## Marg.adhesion < 0.05555556 to the left, agree=0.744, adj=0.088, (0 split)  
## Bl.cromatin < 0.1666667 to the left, agree=0.736, adj=0.059, (0 split)  
##   
## Node number 12: 16 observations  
## predicted class=benign expected loss=0 P(node) =0.02342606  
## class counts: 16 0  
## probabilities: 1.000 0.000   
##   
## Node number 13: 7 observations  
## predicted class=malignant expected loss=0.2857143 P(node) =0.0102489  
## class counts: 2 5  
## probabilities: 0.286 0.714   
##   
## Node number 14: 68 observations, complexity param=0.0125523  
## predicted class=malignant expected loss=0.25 P(node) =0.09956076  
## class counts: 17 51  
## probabilities: 0.250 0.750   
## left son=28 (14 obs) right son=29 (54 obs)  
## Primary splits:  
## Bare.nuclei < 0.1666667 to the left, improve=7.600529, (0 missing)  
## Cl.thickness < 0.6111111 to the left, improve=3.558824, (0 missing)  
## Marg.adhesion < 0.5 to the left, improve=2.615385, (0 missing)  
## Normal.nucleoli < 0.1666667 to the left, improve=1.937690, (0 missing)  
## Bl.cromatin < 0.2777778 to the left, improve=1.525641, (0 missing)  
##   
## Node number 15: 174 observations  
## predicted class=malignant expected loss=0.01724138 P(node) =0.2547584  
## class counts: 3 171  
## probabilities: 0.017 0.983   
##   
## Node number 28: 14 observations  
## predicted class=benign expected loss=0.2857143 P(node) =0.0204978  
## class counts: 10 4  
## probabilities: 0.714 0.286   
##   
## Node number 29: 54 observations  
## predicted class=malignant expected loss=0.1296296 P(node) =0.07906296  
## class counts: 7 47  
## probabilities: 0.130 0.870

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

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

# Leave-1-Out Cross Validation (LOOCV)  
ans <- numeric(length(BreastCancer[,1]))  
for (i in 1:length(BreastCancer[,1])) {  
 mytree <- rpart(Class ~ ., BreastCancer[-i,])  
 mytree.pred <- predict(mytree,BreastCancer[i,],type="class")  
 ans[i] <- mytree.pred  
}  
ans <- factor(ans,labels=levels(BreastCancer$Class))  
table(ans,BreastCancer$Class)

##   
## ans benign malignant  
## benign 431 24  
## malignant 13 215

# The same as above in this case

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

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

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

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

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

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

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

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

#Random Forests  
library(randomForest)

## randomForest 4.7-1.1

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

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

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

table(myrf.pred, BreastCancer$Class)

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

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

#heterogeneous ensemble method by majority vote with multiple classifiers   
head(combine.classes)

## myrf.pred myrda.pred.class mytree.pred X1 X2 mysvm.pred  
## 1 benign benign malignant 1.000065085 -0.0001056472 benign  
## 2 benign malignant malignant 1.000397086 0.0003618166 malignant  
## 3 benign benign malignant 0.999996459 -0.0001233653 benign  
## 4 benign malignant malignant 0.987336409 0.0134766650 malignant  
## 5 benign benign malignant 0.999253746 0.0012530376 benign  
## 6 malignant malignant malignant -0.008800041 1.0089039883 malignant  
## mynb.pred.class  
## 1 benign  
## 2 malignant  
## 3 benign  
## 4 malignant  
## 5 benign  
## 6 malignant

head(myrf.pred)

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

head(myrda.pred)

## $class  
## [1] benign malignant benign malignant benign malignant 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   
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## [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  
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## [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   
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## [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,] 9.999992e-01 7.955116e-07  
## [2,] 1.516272e-05 9.999848e-01  
## [3,] 9.999996e-01 3.501076e-07  
## [4,] 3.764422e-05 9.999624e-01  
## [5,] 9.999992e-01 8.074771e-07  
## [6,] 1.121831e-17 1.000000e+00  
## [7,] 8.492541e-01 1.507459e-01  
## [8,] 9.999999e-01 9.731424e-08  
## [9,] 9.999998e-01 1.973630e-07  
## [10,] 9.999997e-01 3.039857e-07  
## [11,] 1.000000e+00 1.940432e-08  
## [12,] 1.000000e+00 2.740868e-08  
## [13,] 9.956658e-01 4.334161e-03  
## [14,] 9.999997e-01 2.897717e-07  
## [15,] 1.013788e-11 1.000000e+00  
## [16,] 3.939078e-01 6.060922e-01  
## [17,] 9.999998e-01 1.535159e-07  
## [18,] 9.999997e-01 2.828485e-07  
## [19,] 2.685988e-10 1.000000e+00  
## [20,] 9.999975e-01 2.512828e-06  
## [21,] 5.082405e-09 1.000000e+00  
## [22,] 2.254067e-10 1.000000e+00  
## [23,] 9.999999e-01 6.120807e-08  
## [24,] 1.000000e+00 2.551642e-08  
## [25,] 8.529303e-02 9.147070e-01  
## [26,] 9.999999e-01 9.538892e-08  
## [27,] 9.999996e-01 4.324361e-07  
## [28,] 1.000000e+00 2.740868e-08  
## [29,] 1.000000e+00 4.288083e-08  
## [30,] 1.000000e+00 4.671192e-08  
## [31,] 9.999999e-01 5.065711e-08  
## [32,] 1.012803e-08 1.000000e+00  
## [33,] 9.999999e-01 7.944484e-08  
## [34,] 9.999999e-01 1.170458e-07  
## [35,] 1.000000e+00 2.740868e-08  
## [36,] 1.186893e-13 1.000000e+00  
## [37,] 9.997422e-01 2.577602e-04  
## [38,] 4.279679e-08 1.000000e+00  
## [39,] 2.232829e-03 9.977672e-01  
## [40,] 1.258246e-02 9.874175e-01  
## [41,] 6.761887e-14 1.000000e+00  
## [42,] 7.696366e-03 9.923036e-01  
## [43,] 1.511836e-13 1.000000e+00  
## [44,] 1.000000e+00 1.706915e-08  
## [45,] 6.895643e-08 9.999999e-01  
## [46,] 1.000000e+00 1.378452e-08  
## [47,] 9.999992e-01 8.074771e-07  
## [48,] 1.134467e-08 1.000000e+00  
## [49,] 3.071999e-03 9.969280e-01  
## [50,] 9.835206e-01 1.647936e-02  
## [51,] 4.934668e-07 9.999995e-01  
## [52,] 7.429468e-11 1.000000e+00  
## [53,] 2.776485e-09 1.000000e+00  
## [54,] 1.537977e-05 9.999846e-01  
## [55,] 2.345494e-11 1.000000e+00  
## [56,] 7.428283e-01 2.571717e-01  
## [57,] 6.298886e-04 9.993701e-01  
## [58,] 3.650801e-01 6.349199e-01  
## [59,] 2.191627e-03 9.978084e-01  
## [60,] 1.000000e+00 4.341555e-08  
## [61,] 2.423961e-13 1.000000e+00  
## [62,] 1.521752e-01 8.478248e-01  
## [63,] 1.000000e+00 1.378452e-08  
## [64,] 4.645941e-04 9.995354e-01  
## [65,] 9.999997e-01 2.828485e-07  
## [66,] 1.678514e-08 1.000000e+00  
## [67,] 7.178007e-14 1.000000e+00  
## [68,] 1.000000e+00 4.666499e-08  
## [69,] 9.999982e-01 1.831478e-06  
## [70,] 3.781365e-13 1.000000e+00  
## [71,] 9.999333e-01 6.673202e-05  
## [72,] 1.911076e-12 1.000000e+00  
## [73,] 1.240937e-02 9.875906e-01  
## [74,] 9.999994e-01 5.913406e-07  
## [75,] 9.999998e-01 1.908400e-07  
## [76,] 9.999969e-01 3.103662e-06  
## [77,] 9.999987e-01 1.264702e-06  
## [78,] 1.000000e+00 4.401824e-08  
## [79,] 9.999902e-01 9.760102e-06  
## [80,] 9.999998e-01 2.402417e-07  
## [81,] 9.999985e-01 1.538570e-06  
## [82,] 9.999759e-01 2.410473e-05  
## [83,] 1.210331e-13 1.000000e+00  
## [84,] 6.974248e-13 1.000000e+00  
## [85,] 2.906721e-03 9.970933e-01  
## [86,] 2.305993e-09 1.000000e+00  
## [87,] 9.999997e-01 2.828485e-07  
## [88,] 9.999999e-01 6.898311e-08  
## [89,] 1.000000e+00 2.551642e-08  
## [90,] 9.999999e-01 6.323729e-08  
## [91,] 9.999997e-01 2.828485e-07  
## [92,] 1.000000e+00 1.378452e-08  
## [93,] 9.999999e-01 5.065711e-08  
## [94,] 1.000000e+00 2.551642e-08  
## [95,] 1.000000e+00 2.844238e-08  
## [96,] 9.999992e-01 7.955116e-07  
## [97,] 2.165944e-14 1.000000e+00  
## [98,] 1.030037e-13 1.000000e+00  
## [99,] 3.966631e-09 1.000000e+00  
## [100,] 9.751818e-01 2.481822e-02  
## [101,] 9.999995e-01 5.289227e-07  
## [102,] 3.505105e-01 6.494895e-01  
## [103,] 4.790127e-18 1.000000e+00  
## [104,] 2.083002e-01 7.916998e-01  
## [105,] 7.211657e-15 1.000000e+00  
## [106,] 5.181203e-12 1.000000e+00  
## [107,] 9.999999e-01 5.645919e-08  
## [108,] 5.536343e-08 9.999999e-01  
## [109,] 9.999873e-01 1.266572e-05  
## [110,] 1.674299e-05 9.999833e-01  
## [111,] 7.827632e-11 1.000000e+00  
## [112,] 1.339336e-15 1.000000e+00  
## [113,] 9.999901e-01 9.886934e-06  
## [114,] 9.999977e-01 2.281359e-06  
## [115,] 9.976262e-01 2.373815e-03  
## [116,] 3.818436e-12 1.000000e+00  
## [117,] 9.999997e-01 3.276209e-07  
## [118,] 9.999993e-01 6.838107e-07  
## [119,] 9.999999e-01 7.765839e-08  
## [120,] 9.999983e-01 1.691085e-06  
## [121,] 3.049446e-16 1.000000e+00  
## [122,] 2.688902e-06 9.999973e-01  
## [123,] 6.491195e-11 1.000000e+00  
## [124,] 1.000000e+00 1.378452e-08  
## [125,] 1.854346e-09 1.000000e+00  
## [126,] 9.999999e-01 1.129497e-07  
## [127,] 3.224856e-07 9.999997e-01  
## [128,] 9.998875e-01 1.125081e-04  
## [129,] 9.999982e-01 1.831478e-06  
## [130,] 9.999999e-01 5.065711e-08  
## [131,] 1.890734e-14 1.000000e+00  
## [132,] 9.999999e-01 1.126011e-07  
## [133,] 9.999999e-01 9.787906e-08  
## [134,] 9.999908e-01 9.248840e-06  
## [135,] 9.999998e-01 1.535159e-07  
## [136,] 1.000000e+00 3.977783e-08  
## [137,] 9.999997e-01 2.896354e-07  
## [138,] 1.000000e+00 3.977783e-08  
## [139,] 1.000000e+00 1.778462e-08  
## [140,] 1.289299e-03 9.987107e-01  
## [141,] 9.999977e-01 2.281359e-06  
## [142,] 1.000000e+00 2.740868e-08  
## [143,] 2.390096e-02 9.760990e-01  
## [144,] 9.999999e-01 6.953058e-08  
## [145,] 7.307575e-01 2.692425e-01  
## [146,] 2.610275e-16 1.000000e+00  
## [147,] 1.000000e+00 1.940432e-08  
## [148,] 3.268435e-06 9.999967e-01  
## [149,] 1.091652e-13 1.000000e+00  
## [150,] 9.999988e-01 1.151282e-06  
## [151,] 1.000000e+00 8.930429e-09  
## [152,] 2.605563e-05 9.999739e-01  
## [153,] 9.999999e-01 5.259048e-08  
## [154,] 9.999999e-01 5.065711e-08  
## [155,] 8.206518e-18 1.000000e+00  
## [156,] 6.951151e-12 1.000000e+00  
## [157,] 9.999995e-01 5.088908e-07  
## [158,] 9.999999e-01 1.129497e-07  
## [159,] 9.999777e-01 2.233244e-05  
## [160,] 9.999984e-01 1.568906e-06  
## [161,] 7.775579e-13 1.000000e+00  
## [162,] 8.434273e-13 1.000000e+00  
## [163,] 9.999999e-01 1.129497e-07  
## [164,] 1.000000e+00 1.093079e-08  
## [165,] 1.000000e+00 3.977783e-08  
## [166,] 1.000000e+00 2.551642e-08  
## [167,] 1.000000e+00 1.378452e-08  
## [168,] 8.828942e-22 1.000000e+00  
## [169,] 1.453311e-07 9.999999e-01  
## [170,] 5.978102e-13 1.000000e+00  
## [171,] 9.999999e-01 5.065711e-08  
## [172,] 6.515052e-10 1.000000e+00  
## [173,] 9.999997e-01 2.828485e-07  
## [174,] 8.824912e-04 9.991175e-01  
## [175,] 1.000000e+00 1.940432e-08  
## [176,] 1.000000e+00 8.930429e-09  
## [177,] 9.999975e-01 2.512828e-06  
## [178,] 4.992433e-13 1.000000e+00  
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## [183,] 2.751770e-13 1.000000e+00  
## [184,] 9.999998e-01 2.160586e-07  
## [185,] 1.976042e-17 1.000000e+00  
## [186,] 2.047727e-17 1.000000e+00  
## [187,] 9.999996e-01 4.324361e-07  
## [188,] 1.000000e+00 2.551642e-08  
## [189,] 9.999999e-01 1.129497e-07  
## [190,] 9.999997e-01 2.828485e-07  
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## [192,] 9.999951e-01 4.885015e-06  
## [193,] 1.000000e+00 8.930429e-09  
## [194,] 9.999999e-01 6.120807e-08  
## [195,] 6.510276e-13 1.000000e+00  
## [196,] 6.034113e-15 1.000000e+00  
## [197,] 1.000000e+00 2.551642e-08  
## [198,] 9.999992e-01 7.955116e-07  
## [199,] 1.000000e+00 2.551642e-08  
## [200,] 6.891935e-18 1.000000e+00  
## [201,] 4.046274e-10 1.000000e+00  
## [202,] 1.000000e+00 1.940432e-08  
## [203,] 1.000000e+00 1.940432e-08  
## [204,] 9.999994e-01 6.154306e-07  
## [205,] 2.459301e-20 1.000000e+00  
## [206,] 2.787174e-13 1.000000e+00  
## [207,] 1.000000e+00 2.551642e-08  
## [208,] 1.377786e-20 1.000000e+00  
## [209,] 1.900163e-19 1.000000e+00  
## [210,] 4.040269e-10 1.000000e+00  
## [211,] 1.000000e+00 1.378452e-08  
## [212,] 1.000000e+00 2.551642e-08  
## [213,] 2.212496e-11 1.000000e+00  
## [214,] 9.999898e-01 1.017706e-05  
## [215,] 1.000000e+00 4.025633e-08  
## [216,] 4.421351e-16 1.000000e+00  
## [217,] 9.999261e-01 7.394122e-05  
## [218,] 4.475882e-06 9.999955e-01  
## [219,] 1.922536e-12 1.000000e+00  
## [220,] 1.000000e+00 1.378452e-08  
## [221,] 2.815122e-13 1.000000e+00  
## [222,] 6.975876e-10 1.000000e+00  
## [223,] 1.000000e+00 1.940432e-08  
## [224,] 2.009524e-20 1.000000e+00  
## [225,] 1.925727e-06 9.999981e-01  
## [226,] 2.170384e-11 1.000000e+00  
## [227,] 6.997999e-01 3.002001e-01  
## [228,] 6.685152e-08 9.999999e-01  
## [229,] 9.998962e-01 1.037761e-04  
## [230,] 2.967392e-17 1.000000e+00  
## [231,] 2.917616e-09 1.000000e+00  
## [232,] 3.325459e-19 1.000000e+00  
## [233,] 5.366773e-07 9.999995e-01  
## [234,] 9.999474e-01 5.260944e-05  
## [235,] 9.999997e-01 2.556064e-07  
## [236,] 9.999999e-01 5.065711e-08  
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## [238,] 1.000000e+00 2.551642e-08  
## [239,] 9.999963e-01 3.706552e-06  
## [240,] 1.071059e-16 1.000000e+00  
## [241,] 3.371532e-04 9.996628e-01  
## [242,] 9.999711e-01 2.890469e-05  
## [243,] 1.000000e+00 3.487956e-08  
## [244,] 1.664975e-10 1.000000e+00  
## [245,] 2.530048e-05 9.999747e-01  
## [246,] 6.761887e-14 1.000000e+00  
## [247,] 2.423961e-13 1.000000e+00  
## [248,] 6.566461e-07 9.999993e-01  
## [249,] 1.000000e+00 3.977783e-08  
## [250,] 9.999999e-01 6.120807e-08  
## [251,] 9.999999e-01 1.129497e-07  
## [252,] 1.760661e-05 9.999824e-01  
## [253,] 2.063203e-12 1.000000e+00  
## [254,] 5.111657e-18 1.000000e+00  
## [255,] 1.334239e-13 1.000000e+00  
## [256,] 1.343881e-11 1.000000e+00  
## [257,] 3.223135e-09 1.000000e+00  
## [258,] 9.999844e-01 1.555805e-05  
## [259,] 2.187489e-11 1.000000e+00  
## [260,] 2.562455e-04 9.997438e-01  
## [261,] 7.778704e-12 1.000000e+00  
## [262,] 1.000000e+00 2.551642e-08  
## [263,] 9.614121e-10 1.000000e+00  
## [264,] 9.999992e-01 7.955116e-07  
## [265,] 2.562455e-04 9.997438e-01  
## [266,] 9.729185e-01 2.708149e-02  
## [267,] 9.999998e-01 2.043256e-07  
## [268,] 9.999999e-01 6.120807e-08  
## [269,] 1.000000e+00 1.378452e-08  
## [270,] 1.000000e+00 2.551642e-08  
## [271,] 1.304661e-08 1.000000e+00  
## [272,] 9.999999e-01 1.129497e-07  
## [273,] 9.999999e-01 7.944484e-08  
## [274,] 1.723886e-07 9.999998e-01  
## [275,] 6.964620e-08 9.999999e-01  
## [276,] 1.207500e-10 1.000000e+00  
## [277,] 9.997723e-20 1.000000e+00  
## [278,] 1.240418e-23 1.000000e+00  
## [279,] 9.999999e-01 9.787906e-08  
## [280,] 1.169170e-03 9.988308e-01  
## [281,] 4.799556e-12 1.000000e+00  
## [282,] 1.000000e+00 8.930429e-09  
## [283,] 1.000000e+00 2.551642e-08  
## [284,] 2.231140e-07 9.999998e-01  
## [285,] 7.933632e-10 1.000000e+00  
## [286,] 9.809176e-02 9.019082e-01  
## [287,] 9.998368e-01 1.631819e-04  
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## [653,] 6.003249e-05 9.999400e-01  
## [654,] 5.380149e-13 1.000000e+00  
## [655,] 5.247890e-10 1.000000e+00  
## [656,] 9.999997e-01 3.420783e-07  
## [657,] 9.999999e-01 5.065711e-08  
## [658,] 9.999965e-01 3.537217e-06  
## [659,] 1.000000e+00 1.378452e-08  
## [660,] 9.999987e-01 1.258577e-06  
## [661,] 1.000000e+00 2.707924e-08  
## [662,] 9.999997e-01 2.819072e-07  
## [663,] 1.000000e+00 8.930429e-09  
## [664,] 1.000000e+00 1.778462e-08  
## [665,] 5.052365e-23 1.000000e+00  
## [666,] 5.141785e-15 1.000000e+00  
## [667,] 9.999986e-01 1.423476e-06  
## [668,] 1.000000e+00 8.930429e-09  
## [669,] 1.000000e+00 8.930429e-09  
## [670,] 1.000000e+00 8.930429e-09  
## [671,] 1.000000e+00 8.930429e-09  
## [672,] 9.999998e-01 2.452924e-07  
## [673,] 9.999999e-01 9.992211e-08  
## [674,] 9.999910e-01 8.998361e-06  
## [675,] 1.000000e+00 2.747738e-08  
## [676,] 6.135092e-08 9.999999e-01  
## [677,] 1.000000e+00 3.977783e-08  
## [678,] 9.999999e-01 7.614369e-08  
## [679,] 9.999998e-01 2.003040e-07  
## [680,] 1.000000e+00 1.778462e-08  
## [681,] 2.035775e-11 1.000000e+00  
## [682,] 2.071147e-06 9.999979e-01  
## [683,] 1.003933e-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)  
str(combine.classes)

## 'data.frame': 683 obs. of 7 variables:  
## $ myrf.pred : num 0 0 0 0 0 1 0 0 0 0 ...  
## $ myrda.pred.class: num 0 1 0 1 0 1 0 0 0 0 ...  
## $ mytree.pred : num 1 1 1 1 1 1 1 1 1 1 ...  
## $ X1 : num 1 1 1 1 1 1 1 1 1 1 ...  
## $ X2 : num 1 1 1 1 1 1 1 1 1 1 ...  
## $ mysvm.pred : num 0 1 0 1 0 1 0 0 0 0 ...  
## $ mynb.pred.class : Factor w/ 2 levels "benign","malignant": 1 2 1 2 1 2 1 1 1 1 ...

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

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

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

##   
## benign malignant  
## benign 430 0  
## malignant 14 239