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(caret)

## Loading required package: ggplot2

## Loading required package: lattice

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

confusionMatrix(mysvm.pred,BreastCancer$Class)

## Confusion Matrix and Statistics  
##   
## Reference  
## Prediction benign malignant  
## benign 431 8  
## malignant 13 231  
##   
## Accuracy : 0.9693   
## 95% CI : (0.9534, 0.9809)  
## No Information Rate : 0.6501   
## P-Value [Acc > NIR] : <2e-16   
##   
## Kappa : 0.9327   
##   
## Mcnemar's Test P-Value : 0.3827   
##   
## Sensitivity : 0.9707   
## Specificity : 0.9665   
## Pos Pred Value : 0.9818   
## Neg Pred Value : 0.9467   
## Prevalence : 0.6501   
## Detection Rate : 0.6310   
## Detection Prevalence : 0.6428   
## Balanced Accuracy : 0.9686   
##   
## 'Positive' Class : benign   
##

#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

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

## Confusion Matrix and Statistics  
##   
## Reference  
## Prediction benign malignant  
## benign 431 3  
## malignant 13 236  
##   
## Accuracy : 0.9766   
## 95% CI : (0.9622, 0.9866)  
## No Information Rate : 0.6501   
## P-Value [Acc > NIR] : < 2e-16   
##   
## Kappa : 0.949   
##   
## Mcnemar's Test P-Value : 0.02445   
##   
## Sensitivity : 0.9707   
## Specificity : 0.9874   
## Pos Pred Value : 0.9931   
## Neg Pred Value : 0.9478   
## Prevalence : 0.6501   
## Detection Rate : 0.6310   
## Detection Prevalence : 0.6354   
## Balanced Accuracy : 0.9791   
##   
## 'Positive' Class : benign   
##

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

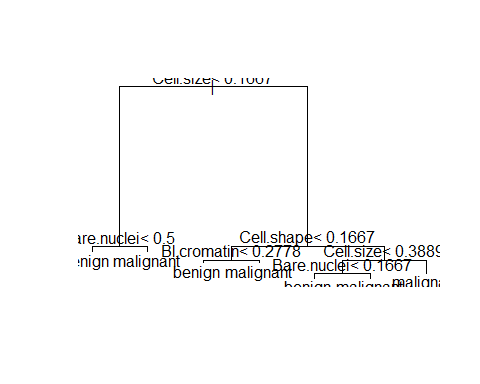
str(mynnet)

## 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 0.998 1 0.997 1 ...  
## .. ..- 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] 0.74 -0.19 -10.56 2.31 -2.76 ...  
## .. ..$ : num [1:6, 1:4] -22.7 -54.7 -38.5 90.9 72.8 ...  
## .. ..$ : num [1:5, 1:2] -0.303 0.997 0.306 -0.542 31.528 ...  
## $ generalized.weights:List of 1  
## ..$ : num [1:683, 1:18] 2.65e-03 -6.96e+01 1.73e-38 -1.03e+02 1.94e-04 ...  
## .. ..- 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] 0.451 -0.764 0.109 1.139 -0.712 ...  
## .. ..$ : num [1:6, 1:4] -0.0112 1.24666 -0.21042 1.58628 -0.00742 ...  
## .. ..$ : num [1:5, 1:2] -0.797 0.511 -0.295 -0.597 -0.786 ...  
## $ result.matrix : num [1:87, 1] 6.51e-03 9.44e-03 4.91e+03 7.40e-01 -1.90e-01 ...  
## ..- 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')  
  
confusionMatrix(table(mynnet.pred2,BreastCancer$Class))

## Confusion Matrix and Statistics  
##   
##   
## mynnet.pred2 benign malignant  
## benign 444 0  
## malignant 0 239  
##   
## Accuracy : 1   
## 95% CI : (0.9946, 1)  
## No Information Rate : 0.6501   
## P-Value [Acc > NIR] : < 2.2e-16   
##   
## Kappa : 1   
##   
## Mcnemar's Test P-Value : NA   
##   
## Sensitivity : 1.0000   
## Specificity : 1.0000   
## Pos Pred Value : 1.0000   
## Neg Pred Value : 1.0000   
## Prevalence : 0.6501   
## Detection Rate : 0.6501   
## Detection Prevalence : 0.6501   
## Balanced Accuracy : 1.0000   
##   
## 'Positive' Class : benign   
##

#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 0.2301255 0.02975452  
## 3 0.02510460 2 0.15481172 0.1757322 0.02626911  
## 4 0.01255230 3 0.12970711 0.1799163 0.02655926  
## 5 0.01000000 6 0.09205021 0.1548117 0.02475192  
##   
## 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")  
confusionMatrix(mytree.pred,BreastCancer$Class)

## Confusion Matrix and Statistics  
##   
## Reference  
## Prediction benign malignant  
## benign 431 9  
## malignant 13 230  
##   
## Accuracy : 0.9678   
## 95% CI : (0.9516, 0.9797)  
## No Information Rate : 0.6501   
## P-Value [Acc > NIR] : <2e-16   
##   
## Kappa : 0.9295   
##   
## Mcnemar's Test P-Value : 0.5224   
##   
## Sensitivity : 0.9707   
## Specificity : 0.9623   
## Pos Pred Value : 0.9795   
## Neg Pred Value : 0.9465   
## Prevalence : 0.6501   
## Detection Rate : 0.6310   
## Detection Prevalence : 0.6442   
## Balanced Accuracy : 0.9665   
##   
## 'Positive' Class : benign   
##

# 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$Class))  
confusionMatrix(ans,BreastCancer$Class)

## Confusion Matrix and Statistics  
##   
## Reference  
## Prediction benign malignant  
## benign 431 24  
## malignant 13 215  
##   
## Accuracy : 0.9458   
## 95% CI : (0.9261, 0.9616)  
## No Information Rate : 0.6501   
## P-Value [Acc > NIR] : <2e-16   
##   
## Kappa : 0.8796   
##   
## Mcnemar's Test P-Value : 0.1002   
##   
## Sensitivity : 0.9707   
## Specificity : 0.8996   
## Pos Pred Value : 0.9473   
## Neg Pred Value : 0.9430   
## Prevalence : 0.6501   
## Detection Rate : 0.6310   
## Detection Prevalence : 0.6662   
## Balanced Accuracy : 0.9352   
##   
## 'Positive' Class : benign   
##

# 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

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

## Confusion Matrix and Statistics  
##   
## Reference  
## Prediction benign malignant  
## benign 422 6  
## malignant 22 233  
##   
## Accuracy : 0.959   
## 95% CI : (0.9413, 0.9726)  
## No Information Rate : 0.6501   
## P-Value [Acc > NIR] : < 2.2e-16   
##   
## Kappa : 0.9113   
##   
## Mcnemar's Test P-Value : 0.004586   
##   
## Sensitivity : 0.9505   
## Specificity : 0.9749   
## Pos Pred Value : 0.9860   
## Neg Pred Value : 0.9137   
## Prevalence : 0.6501   
## Detection Rate : 0.6179   
## Detection Prevalence : 0.6266   
## Balanced Accuracy : 0.9627   
##   
## 'Positive' Class : benign   
##

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

##   
## benign malignant  
## benign 431 7  
## malignant 13 232

#Random Forests  
library(randomForest)

## randomForest 4.7-1.1

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

##   
## Attaching package: 'randomForest'

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

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

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

table(myrf.pred, BreastCancer$Class)

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

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

#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 1.000140547 -0.0001683587 benign  
## 2 benign malignant malignant 0.998259983 0.0017137353 malignant  
## 3 benign benign malignant 1.000140551 -0.0001683621 benign  
## 4 benign malignant malignant 0.997143480 0.0028311173 malignant  
## 5 benign benign malignant 1.000140550 -0.0001683614 benign  
## 6 malignant malignant malignant -0.001102232 1.0008396095 malignant  
## mynb.pred.class  
## 1 benign  
## 2 malignant  
## 3 benign  
## 4 malignant  
## 5 benign  
## 6 malignant

head(myrf.pred)

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

head(myrda.pred)

## $class  
## [1] benign malignant benign malignant benign malignant malignant  
## [8] benign benign benign benign benign benign benign   
## [15] malignant malignant benign benign malignant benign malignant  
## [22] malignant benign benign malignant benign benign benign   
## [29] benign benign benign malignant benign benign benign   
## [36] malignant benign malignant malignant malignant malignant malignant  
## [43] malignant benign malignant benign benign malignant malignant  
## [50] benign malignant malignant malignant malignant malignant malignant  
## [57] malignant malignant malignant benign malignant malignant benign   
## [64] malignant benign malignant malignant benign benign malignant  
## [71] benign malignant malignant benign benign benign benign   
## [78] benign benign benign benign benign malignant malignant  
## [85] malignant malignant benign benign benign benign benign   
## [92] benign benign benign benign benign malignant malignant  
## [99] malignant 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 malignant malignant benign   
## [148] malignant malignant benign benign malignant benign benign   
## [155] malignant malignant benign benign benign benign malignant  
## [162] malignant benign benign benign benign benign malignant  
## [169] malignant malignant benign malignant benign malignant benign   
## [176] benign benign malignant malignant benign malignant malignant  
## [183] malignant benign malignant malignant benign benign benign   
## [190] benign malignant benign benign benign malignant malignant  
## [197] benign benign benign malignant malignant benign benign   
## [204] benign malignant malignant benign malignant malignant malignant  
## [211] benign benign malignant benign benign malignant benign   
## [218] malignant malignant benign malignant malignant benign malignant  
## [225] malignant malignant benign malignant benign malignant malignant  
## [232] malignant malignant benign benign benign benign benign   
## [239] benign malignant malignant benign benign malignant malignant  
## [246] malignant malignant malignant benign benign benign malignant  
## [253] malignant malignant malignant malignant malignant benign malignant  
## [260] malignant malignant benign malignant benign malignant benign   
## [267] benign benign benign benign malignant benign benign   
## [274] malignant malignant malignant malignant malignant benign malignant  
## [281] malignant benign benign malignant malignant malignant benign   
## [288] malignant malignant benign malignant benign malignant malignant  
## [295] benign benign malignant benign benign benign malignant  
## [302] benign benign malignant malignant benign malignant malignant  
## [309] benign malignant benign benign malignant benign malignant  
## [316] malignant malignant benign benign malignant malignant benign   
## [323] malignant benign benign malignant malignant benign benign   
## [330] benign malignant benign benign benign malignant malignant  
## [337] benign benign malignant malignant benign benign benign   
## [344] malignant malignant malignant malignant malignant benign benign   
## [351] benign benign malignant malignant benign benign benign   
## [358] benign benign benign benign benign benign benign   
## [365] benign benign benign malignant benign benign benign   
## [372] benign malignant benign benign benign benign malignant  
## [379] benign benign benign benign benign benign benign   
## [386] benign malignant benign benign benign benign benign   
## [393] benign benign benign benign benign malignant benign   
## [400] malignant benign malignant benign benign benign benign   
## [407] malignant benign benign benign malignant benign malignant  
## [414] benign benign benign benign benign benign malignant  
## [421] malignant malignant benign benign benign malignant benign   
## [428] benign benign benign benign benign benign benign   
## [435] malignant benign benign benign malignant benign malignant  
## [442] malignant malignant benign benign benign benign benign   
## [449] benign benign malignant malignant malignant benign benign   
## [456] benign benign benign benign benign benign benign   
## [463] benign benign malignant benign benign malignant malignant  
## [470] benign benign benign malignant malignant benign benign   
## [477] malignant benign malignant malignant benign benign benign   
## [484] benign benign benign benign benign benign benign   
## [491] benign malignant benign benign benign benign benign   
## [498] benign benign malignant malignant benign benign benign   
## [505] malignant benign benign malignant malignant benign benign   
## [512] benign benign benign benign malignant benign benign   
## [519] benign benign benign benign benign benign benign   
## [526] benign benign benign benign benign benign malignant  
## [533] benign benign malignant benign benign benign benign   
## [540] benign benign benign benign benign benign benign   
## [547] benign benign benign benign malignant benign benign   
## [554] malignant malignant malignant malignant benign benign malignant  
## [561] benign benign benign benign benign benign malignant  
## [568] malignant benign benign benign malignant benign malignant  
## [575] benign malignant malignant malignant benign malignant benign   
## [582] benign benign benign benign benign benign benign   
## [589] malignant malignant malignant benign benign malignant benign   
## [596] malignant malignant malignant benign benign benign benign   
## [603] benign benign benign benign benign benign benign   
## [610] benign malignant benign benign benign benign benign   
## [617] benign malignant benign benign malignant benign benign   
## [624] benign benign benign benign benign benign benign   
## [631] benign benign malignant benign benign benign benign   
## [638] benign benign benign benign malignant malignant benign   
## [645] benign benign benign benign benign benign benign   
## [652] benign malignant malignant malignant benign benign benign   
## [659] benign benign benign benign benign benign malignant  
## [666] malignant benign benign benign benign benign benign   
## [673] benign benign benign malignant benign benign benign   
## [680] benign malignant malignant malignant  
## Levels: benign malignant  
##   
## $posterior  
## benign malignant  
## [1,] 9.999977e-01 2.284877e-06  
## [2,] 3.891195e-06 9.999961e-01  
## [3,] 9.999991e-01 8.907821e-07  
## [4,] 6.827762e-06 9.999932e-01  
## [5,] 9.999979e-01 2.115345e-06  
## [6,] 2.279010e-18 1.000000e+00  
## [7,] 2.162861e-01 7.837139e-01  
## [8,] 9.999997e-01 2.800181e-07  
## [9,] 9.999977e-01 2.321727e-06  
## [10,] 9.999992e-01 8.346701e-07  
## [11,] 9.999999e-01 7.852843e-08  
## [12,] 9.999999e-01 9.041643e-08  
## [13,] 9.959872e-01 4.012776e-03  
## [14,] 9.999992e-01 8.482975e-07  
## [15,] 2.787203e-12 1.000000e+00  
## [16,] 2.872717e-01 7.127283e-01  
## [17,] 9.999995e-01 4.549697e-07  
## [18,] 9.999992e-01 8.044176e-07  
## [19,] 7.021316e-11 1.000000e+00  
## [20,] 9.999924e-01 7.605739e-06  
## [21,] 3.049607e-10 1.000000e+00  
## [22,] 6.476560e-11 1.000000e+00  
## [23,] 9.999998e-01 1.873550e-07  
## [24,] 9.999999e-01 9.093510e-08  
## [25,] 3.990605e-02 9.600939e-01  
## [26,] 9.999997e-01 3.172192e-07  
## [27,] 9.999987e-01 1.294788e-06  
## [28,] 9.999999e-01 9.041643e-08  
## [29,] 9.999998e-01 1.834449e-07  
## [30,] 9.999998e-01 1.629843e-07  
## [31,] 9.999998e-01 1.604781e-07  
## [32,] 4.987136e-09 1.000000e+00  
## [33,] 9.999998e-01 2.322828e-07  
## [34,] 9.999997e-01 3.234519e-07  
## [35,] 9.999999e-01 9.041643e-08  
## [36,] 5.896298e-15 1.000000e+00  
## [37,] 9.980316e-01 1.968409e-03  
## [38,] 5.469323e-09 1.000000e+00  
## [39,] 9.916078e-04 9.990084e-01  
## [40,] 6.172227e-03 9.938278e-01  
## [41,] 2.135101e-15 1.000000e+00  
## [42,] 2.312292e-04 9.997688e-01  
## [43,] 6.210022e-15 1.000000e+00  
## [44,] 9.999999e-01 6.395946e-08  
## [45,] 1.895986e-08 1.000000e+00  
## [46,] 9.999999e-01 5.113621e-08  
## [47,] 9.999979e-01 2.115345e-06  
## [48,] 2.949812e-09 1.000000e+00  
## [49,] 1.514055e-04 9.998486e-01  
## [50,] 9.846732e-01 1.532684e-02  
## [51,] 5.971709e-08 9.999999e-01  
## [52,] 9.326192e-13 1.000000e+00  
## [53,] 5.397670e-10 1.000000e+00  
## [54,] 1.675574e-05 9.999832e-01  
## [55,] 5.646164e-13 1.000000e+00  
## [56,] 4.145859e-01 5.854141e-01  
## [57,] 5.022665e-05 9.999498e-01  
## [58,] 1.970388e-01 8.029612e-01  
## [59,] 3.350530e-04 9.996649e-01  
## [60,] 9.999999e-01 1.410374e-07  
## [61,] 3.110861e-15 1.000000e+00  
## [62,] 2.954845e-02 9.704516e-01  
## [63,] 9.999999e-01 5.113621e-08  
## [64,] 1.144677e-06 9.999989e-01  
## [65,] 9.999992e-01 8.044176e-07  
## [66,] 4.699266e-10 1.000000e+00  
## [67,] 1.733036e-16 1.000000e+00  
## [68,] 9.999998e-01 1.541984e-07  
## [69,] 9.999951e-01 4.920009e-06  
## [70,] 4.969252e-17 1.000000e+00  
## [71,] 9.997135e-01 2.864540e-04  
## [72,] 2.469450e-13 1.000000e+00  
## [73,] 4.619742e-03 9.953803e-01  
## [74,] 9.999984e-01 1.582989e-06  
## [75,] 9.999991e-01 8.554660e-07  
## [76,] 9.999918e-01 8.188156e-06  
## [77,] 9.999970e-01 3.028868e-06  
## [78,] 9.999999e-01 1.461425e-07  
## [79,] 9.999322e-01 6.781660e-05  
## [80,] 9.999993e-01 6.524911e-07  
## [81,] 9.999960e-01 4.015390e-06  
## [82,] 9.998518e-01 1.481627e-04  
## [83,] 2.148705e-15 1.000000e+00  
## [84,] 2.542739e-16 1.000000e+00  
## [85,] 1.783668e-03 9.982163e-01  
## [86,] 8.470140e-10 1.000000e+00  
## [87,] 9.999992e-01 8.044176e-07  
## [88,] 9.999998e-01 2.107355e-07  
## [89,] 9.999999e-01 9.093510e-08  
## [90,] 9.999998e-01 2.086298e-07  
## [91,] 9.999992e-01 8.044176e-07  
## [92,] 9.999999e-01 5.113621e-08  
## [93,] 9.999998e-01 1.604781e-07  
## [94,] 9.999999e-01 9.093510e-08  
## [95,] 9.999999e-01 1.017995e-07  
## [96,] 9.999977e-01 2.284877e-06  
## [97,] 1.898048e-17 1.000000e+00  
## [98,] 1.294129e-14 1.000000e+00  
## [99,] 6.650154e-11 1.000000e+00  
## [100,] 9.562239e-01 4.377611e-02  
## [101,] 9.999987e-01 1.335114e-06  
## [102,] 7.822653e-02 9.217735e-01  
## [103,] 6.905519e-21 1.000000e+00  
## [104,] 2.202028e-02 9.779797e-01  
## [105,] 1.014078e-16 1.000000e+00  
## [106,] 2.323617e-13 1.000000e+00  
## [107,] 9.999998e-01 2.066374e-07  
## [108,] 1.759802e-08 1.000000e+00  
## [109,] 9.999668e-01 3.322949e-05  
## [110,] 5.538446e-06 9.999945e-01  
## [111,] 2.975275e-12 1.000000e+00  
## [112,] 1.362745e-17 1.000000e+00  
## [113,] 9.999821e-01 1.788352e-05  
## [114,] 9.999902e-01 9.804550e-06  
## [115,] 9.960817e-01 3.918286e-03  
## [116,] 2.659781e-14 1.000000e+00  
## [117,] 9.999986e-01 1.356284e-06  
## [118,] 9.999984e-01 1.587554e-06  
## [119,] 9.999998e-01 2.349186e-07  
## [120,] 9.999962e-01 3.769076e-06  
## [121,] 5.783026e-18 1.000000e+00  
## [122,] 2.130614e-07 9.999998e-01  
## [123,] 5.937344e-12 1.000000e+00  
## [124,] 9.999999e-01 5.113621e-08  
## [125,] 2.908502e-10 1.000000e+00  
## [126,] 9.999997e-01 3.318938e-07  
## [127,] 6.814173e-08 9.999999e-01  
## [128,] 9.776827e-01 2.231729e-02  
## [129,] 9.999951e-01 4.920009e-06  
## [130,] 9.999998e-01 1.604781e-07  
## [131,] 1.358017e-15 1.000000e+00  
## [132,] 9.999997e-01 3.221907e-07  
## [133,] 9.999997e-01 3.005865e-07  
## [134,] 9.999789e-01 2.109062e-05  
## [135,] 9.999995e-01 4.549697e-07  
## [136,] 9.999999e-01 1.412302e-07  
## [137,] 9.999992e-01 7.660551e-07  
## [138,] 9.999999e-01 1.412302e-07  
## [139,] 9.999999e-01 6.802600e-08  
## [140,] 1.943533e-03 9.980565e-01  
## [141,] 9.999902e-01 9.804550e-06  
## [142,] 9.999999e-01 9.041643e-08  
## [143,] 7.834248e-03 9.921658e-01  
## [144,] 9.999998e-01 2.263966e-07  
## [145,] 6.696455e-02 9.330354e-01  
## [146,] 6.751012e-18 1.000000e+00  
## [147,] 9.999999e-01 7.852843e-08  
## [148,] 3.773832e-07 9.999996e-01  
## [149,] 1.835255e-14 1.000000e+00  
## [150,] 9.999967e-01 3.310221e-06  
## [151,] 1.000000e+00 3.839914e-08  
## [152,] 7.031969e-06 9.999930e-01  
## [153,] 9.999998e-01 1.610140e-07  
## [154,] 9.999998e-01 1.604781e-07  
## [155,] 2.815707e-19 1.000000e+00  
## [156,] 4.683577e-12 1.000000e+00  
## [157,] 9.999987e-01 1.324989e-06  
## [158,] 9.999997e-01 3.318938e-07  
## [159,] 9.986321e-01 1.367942e-03  
## [160,] 9.999965e-01 3.526216e-06  
## [161,] 8.042382e-14 1.000000e+00  
## [162,] 1.374688e-16 1.000000e+00  
## [163,] 9.999997e-01 3.318938e-07  
## [164,] 9.999999e-01 5.054214e-08  
## [165,] 9.999999e-01 1.412302e-07  
## [166,] 9.999999e-01 9.093510e-08  
## [167,] 9.999999e-01 5.113621e-08  
## [168,] 1.056531e-23 1.000000e+00  
## [169,] 3.919658e-08 1.000000e+00  
## [170,] 9.896537e-14 1.000000e+00  
## [171,] 9.999998e-01 1.604781e-07  
## [172,] 1.838619e-11 1.000000e+00  
## [173,] 9.999992e-01 8.044176e-07  
## [174,] 1.552106e-04 9.998448e-01  
## [175,] 9.999999e-01 7.852843e-08  
## [176,] 1.000000e+00 3.839914e-08  
## [177,] 9.999924e-01 7.605739e-06  
## [178,] 1.512469e-13 1.000000e+00  
## [179,] 7.792515e-09 1.000000e+00  
## [180,] 9.999999e-01 1.396164e-07  
## [181,] 1.657670e-10 1.000000e+00  
## [182,] 9.178003e-20 1.000000e+00  
## [183,] 1.160172e-14 1.000000e+00  
## [184,] 9.999994e-01 6.252936e-07  
## [185,] 4.857709e-18 1.000000e+00  
## [186,] 3.645828e-19 1.000000e+00  
## [187,] 9.999987e-01 1.294788e-06  
## [188,] 9.999999e-01 9.093510e-08  
## [189,] 9.999997e-01 3.318938e-07  
## [190,] 9.999992e-01 8.044176e-07  
## [191,] 2.355858e-07 9.999998e-01  
## [192,] 9.999858e-01 1.424361e-05  
## [193,] 1.000000e+00 3.839914e-08  
## [194,] 9.999998e-01 1.873550e-07  
## [195,] 3.948193e-13 1.000000e+00  
## [196,] 1.461687e-16 1.000000e+00  
## [197,] 9.999999e-01 9.093510e-08  
## [198,] 9.999977e-01 2.284877e-06  
## [199,] 9.999999e-01 9.093510e-08  
## [200,] 4.000292e-19 1.000000e+00  
## [201,] 8.438406e-11 1.000000e+00  
## [202,] 9.999999e-01 7.852843e-08  
## [203,] 9.999999e-01 7.852843e-08  
## [204,] 9.999980e-01 2.032632e-06  
## [205,] 7.611835e-22 1.000000e+00  
## [206,] 8.464697e-14 1.000000e+00  
## [207,] 9.999999e-01 9.093510e-08  
## [208,] 1.992509e-21 1.000000e+00  
## [209,] 6.337622e-21 1.000000e+00  
## [210,] 1.972210e-10 1.000000e+00  
## [211,] 9.999999e-01 5.113621e-08  
## [212,] 9.999999e-01 9.093510e-08  
## [213,] 3.747801e-12 1.000000e+00  
## [214,] 9.999733e-01 2.671081e-05  
## [215,] 9.999999e-01 1.333382e-07  
## [216,] 8.754943e-18 1.000000e+00  
## [217,] 9.997957e-01 2.042986e-04  
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## [582,] 9.999992e-01 7.660551e-07  
## [583,] 9.999916e-01 8.436211e-06  
## [584,] 9.999998e-01 1.873550e-07  
## [585,] 9.999827e-01 1.734518e-05  
## [586,] 9.999998e-01 1.873550e-07  
## [587,] 1.000000e+00 4.382869e-08  
## [588,] 9.999995e-01 4.549697e-07  
## [589,] 9.390618e-08 9.999999e-01  
## [590,] 1.685021e-08 1.000000e+00  
## [591,] 2.914178e-13 1.000000e+00  
## [592,] 9.999995e-01 5.010790e-07  
## [593,] 1.000000e+00 3.839914e-08  
## [594,] 3.302553e-21 1.000000e+00  
## [595,] 9.999990e-01 9.797832e-07  
## [596,] 4.536591e-12 1.000000e+00  
## [597,] 1.178685e-12 1.000000e+00  
## [598,] 2.864870e-26 1.000000e+00  
## [599,] 9.999995e-01 4.648358e-07  
## [600,] 9.999999e-01 7.807329e-08  
## [601,] 9.999982e-01 1.817541e-06  
## [602,] 9.999998e-01 1.873550e-07  
## [603,] 9.999995e-01 4.549697e-07  
## [604,] 9.999987e-01 1.294788e-06  
## [605,] 9.999998e-01 1.873550e-07  
## [606,] 9.904237e-01 9.576299e-03  
## [607,] 9.999357e-01 6.430856e-05  
## [608,] 1.000000e+00 3.839914e-08  
## [609,] 9.999983e-01 1.651864e-06  
## [610,] 9.999656e-01 3.439140e-05  
## [611,] 1.225776e-06 9.999988e-01  
## [612,] 9.999830e-01 1.699196e-05  
## [613,] 9.999999e-01 6.802600e-08  
## [614,] 9.999997e-01 3.436206e-07  
## [615,] 9.999818e-01 1.819336e-05  
## [616,] 9.999987e-01 1.294788e-06  
## [617,] 1.000000e+00 3.839914e-08  
## [618,] 5.261437e-07 9.999995e-01  
## [619,] 9.999999e-01 1.412302e-07  
## [620,] 9.999979e-01 2.122869e-06  
## [621,] 1.015363e-15 1.000000e+00  
## [622,] 9.999544e-01 4.564229e-05  
## [623,] 9.999997e-01 3.436206e-07  
## [624,] 9.999973e-01 2.683643e-06  
## [625,] 9.999990e-01 9.658691e-07  
## [626,] 9.999998e-01 1.873550e-07  
## [627,] 9.999998e-01 1.873550e-07  
## [628,] 1.000000e+00 3.839914e-08  
## [629,] 9.999999e-01 6.802600e-08  
## [630,] 9.999998e-01 1.873550e-07  
## [631,] 9.999999e-01 1.261166e-07  
## [632,] 9.999999e-01 1.166520e-07  
## [633,] 1.564250e-22 1.000000e+00  
## [634,] 9.999998e-01 1.873550e-07  
## [635,] 9.999876e-01 1.239496e-05  
## [636,] 9.999997e-01 2.745715e-07  
## [637,] 9.999978e-01 2.183907e-06  
## [638,] 9.999995e-01 4.549697e-07  
## [639,] 9.999997e-01 3.318938e-07  
## [640,] 9.999998e-01 1.873550e-07  
## [641,] 9.999987e-01 1.294788e-06  
## [642,] 1.394618e-01 8.605382e-01  
## [643,] 3.074248e-12 1.000000e+00  
## [644,] 1.000000e+00 3.839914e-08  
## [645,] 9.999999e-01 5.113621e-08  
## [646,] 9.999992e-01 8.044176e-07  
## [647,] 9.999998e-01 2.373729e-07  
## [648,] 9.999998e-01 2.373729e-07  
## [649,] 9.999995e-01 5.227315e-07  
## [650,] 1.000000e+00 3.839914e-08  
## [651,] 9.999954e-01 4.644634e-06  
## [652,] 9.999997e-01 3.318938e-07  
## [653,] 3.557647e-06 9.999964e-01  
## [654,] 4.476421e-14 1.000000e+00  
## [655,] 6.762476e-11 1.000000e+00  
## [656,] 9.999992e-01 8.380822e-07  
## [657,] 9.999998e-01 1.604781e-07  
## [658,] 9.999906e-01 9.369622e-06  
## [659,] 9.999999e-01 5.113621e-08  
## [660,] 9.999952e-01 4.791524e-06  
## [661,] 9.999999e-01 9.281248e-08  
## [662,] 9.999990e-01 9.797832e-07  
## [663,] 1.000000e+00 3.839914e-08  
## [664,] 9.999999e-01 6.802600e-08  
## [665,] 5.424249e-25 1.000000e+00  
## [666,] 2.864380e-16 1.000000e+00  
## [667,] 9.999963e-01 3.727240e-06  
## [668,] 1.000000e+00 3.839914e-08  
## [669,] 1.000000e+00 3.839914e-08  
## [670,] 1.000000e+00 3.839914e-08  
## [671,] 1.000000e+00 3.839914e-08  
## [672,] 9.999993e-01 7.283203e-07  
## [673,] 9.999997e-01 3.436206e-07  
## [674,] 9.982174e-01 1.782597e-03  
## [675,] 9.999999e-01 1.166520e-07  
## [676,] 7.905355e-09 1.000000e+00  
## [677,] 9.999999e-01 1.412302e-07  
## [678,] 9.999998e-01 2.375625e-07  
## [679,] 9.999994e-01 6.239970e-07  
## [680,] 9.999999e-01 6.802600e-08  
## [681,] 1.210812e-12 1.000000e+00  
## [682,] 3.335739e-07 9.999997e-01  
## [683,] 1.648048e-08 1.000000e+00

combine.classes$myrf.pred<-ifelse(combine.classes$myrf.pred=="benign", 0, 1)  
combine.classes[,2]<-ifelse(combine.classes[,2]=="benign", 0, 1)  
combine.classes[,3]<-ifelse(combine.classes[,3]=="benign", 0, 1)  
combine.classes[,4]<-ifelse(combine.classes[,4]=="benign", 0, 1)  
combine.classes[,5]<-ifelse(combine.classes[,5]=="benign", 0, 1)  
combine.classes[,6]<-ifelse(combine.classes[,6]=="benign", 0, 1)  
str(combine.classes)

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

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

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

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

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

confusionMatrix(table(combine.classes[,8], BreastCancer$Class))

## Confusion Matrix and Statistics  
##   
##   
## benign malignant  
## benign 428 0  
## malignant 16 239  
##   
## Accuracy : 0.9766   
## 95% CI : (0.9622, 0.9866)  
## No Information Rate : 0.6501   
## P-Value [Acc > NIR] : < 2.2e-16   
##   
## Kappa : 0.9493   
##   
## Mcnemar's Test P-Value : 0.0001768   
##   
## Sensitivity : 0.9640   
## Specificity : 1.0000   
## Pos Pred Value : 1.0000   
## Neg Pred Value : 0.9373   
## Prevalence : 0.6501   
## Detection Rate : 0.6266   
## Detection Prevalence : 0.6266   
## Balanced Accuracy : 0.9820   
##   
## 'Positive' Class : benign   
##