Project 2

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

## Loading required package: mlbench

## Warning: package 'mlbench' was built under R version 4.2.2

# if you don't have any required package, use the install.packages() command  
# 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"

str(BreastCancer)

## 'data.frame': 699 obs. of 11 variables:  
## $ Id : chr "1000025" "1002945" "1015425" "1016277" ...  
## $ 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 ...

# some algorithms don't like missing values, so remove rows with missing values  
BreastCancer <- na.omit(BreastCancer)   
# remove the unique identifier, which is useless and would confuse the machine learning algorithms  
BreastCancer$Id <- NULL   
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

library(e1071)

## Warning: package 'e1071' was built under R version 4.2.2

#support vector machine  
mysvm <-svm(Class ~ ., BreastCancer)  
mysvm.pred <-predict(mysvm, BreastCancer)  
table(mysvm.pred,BreastCancer$Class)

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

#install.packages("klar")  
library(klaR)

## Warning: package 'klaR' was built under R version 4.2.2

## Loading required package: MASS

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

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 2

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

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

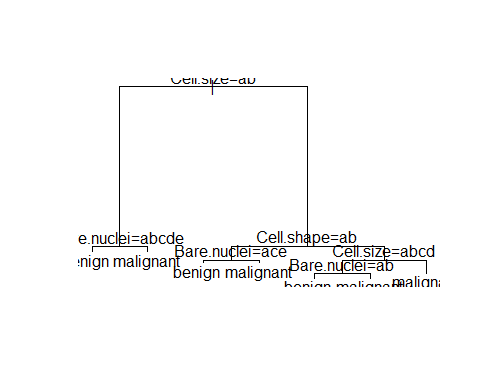
str(mysvm.pred)

## 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"

#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 0.2343096 0.02999988  
## 3 0.02510460 2 0.15481172 0.1548117 0.02475192  
## 4 0.01255230 3 0.12970711 0.1464435 0.02411089  
## 5 0.01000000 6 0.09205021 0.1506276 0.02443403  
##   
## 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

str(mytree)

## List of 15  
## $ frame :'data.frame': 13 obs. of 9 variables:  
## ..$ var : chr [1:13] "Cell.size" "Bare.nuclei" "<leaf>" "<leaf>" ...  
## ..$ n : int [1:13] 683 418 410 8 265 23 16 7 242 68 ...  
## ..$ wt : num [1:13] 683 418 410 8 265 23 16 7 242 68 ...  
## ..$ dev : num [1:13] 239 12 5 1 38 5 0 2 20 17 ...  
## ..$ yval : num [1:13] 1 1 1 2 2 1 1 2 2 2 ...  
## ..$ complexity: num [1:13] 0.7908 0.0251 0 0.01 0.0544 ...  
## ..$ ncompete : int [1:13] 4 4 0 0 4 4 0 0 4 4 ...  
## ..$ nsurrogate: int [1:13] 5 3 0 0 1 5 0 0 5 0 ...  
## ..$ yval2 : num [1:13, 1:6] 1 1 1 2 2 1 1 2 2 2 ...  
## .. ..- attr(\*, "dimnames")=List of 2  
## .. .. ..$ : NULL  
## .. .. ..$ : chr [1:6] "" "" "" "" ...  
## $ where : Named int [1:683] 3 12 3 13 3 13 4 3 3 3 ...  
## ..- attr(\*, "names")= chr [1:683] "1" "2" "3" "4" ...  
## $ call : language rpart(formula = Class ~ ., data = BreastCancer)  
## $ terms :Classes 'terms', 'formula' language Class ~ Cl.thickness + Cell.size + Cell.shape + Marg.adhesion + Epith.c.size + Bare.nuclei + Bl.cromatin + N| \_\_truncated\_\_  
## .. ..- attr(\*, "variables")= language list(Class, Cl.thickness, Cell.size, Cell.shape, Marg.adhesion, Epith.c.size, Bare.nuclei, Bl.cromatin, Norm| \_\_truncated\_\_  
## .. ..- attr(\*, "factors")= int [1:10, 1:9] 0 1 0 0 0 0 0 0 0 0 ...  
## .. .. ..- attr(\*, "dimnames")=List of 2  
## .. .. .. ..$ : chr [1:10] "Class" "Cl.thickness" "Cell.size" "Cell.shape" ...  
## .. .. .. ..$ : chr [1:9] "Cl.thickness" "Cell.size" "Cell.shape" "Marg.adhesion" ...  
## .. ..- attr(\*, "term.labels")= chr [1:9] "Cl.thickness" "Cell.size" "Cell.shape" "Marg.adhesion" ...  
## .. ..- attr(\*, "order")= int [1:9] 1 1 1 1 1 1 1 1 1  
## .. ..- attr(\*, "intercept")= int 1  
## .. ..- attr(\*, "response")= int 1  
## .. ..- attr(\*, ".Environment")=<environment: R\_GlobalEnv>   
## .. ..- attr(\*, "predvars")= language list(Class, Cl.thickness, Cell.size, Cell.shape, Marg.adhesion, Epith.c.size, Bare.nuclei, Bl.cromatin, Norm| \_\_truncated\_\_  
## .. ..- attr(\*, "dataClasses")= Named chr [1:10] "factor" "ordered" "ordered" "ordered" ...  
## .. .. ..- attr(\*, "names")= chr [1:10] "Class" "Cl.thickness" "Cell.size" "Cell.shape" ...  
## $ cptable : num [1:5, 1:5] 0.7908 0.0544 0.0251 0.0126 0.01 ...  
## ..- attr(\*, "dimnames")=List of 2  
## .. ..$ : chr [1:5] "1" "2" "3" "4" ...  
## .. ..$ : chr [1:5] "CP" "nsplit" "rel error" "xerror" ...  
## $ method : chr "class"  
## $ parms :List of 3  
## ..$ prior: num [1:2(1d)] 0.65 0.35  
## .. ..- attr(\*, "dimnames")=List of 1  
## .. .. ..$ : chr [1:2] "1" "2"  
## ..$ loss : num [1:2, 1:2] 0 1 1 0  
## ..$ split: num 1  
## $ control :List of 9  
## ..$ minsplit : int 20  
## ..$ minbucket : num 7  
## ..$ cp : num 0.01  
## ..$ maxcompete : int 4  
## ..$ maxsurrogate : int 5  
## ..$ usesurrogate : int 2  
## ..$ surrogatestyle: int 0  
## ..$ maxdepth : int 30  
## ..$ xval : int 10  
## $ functions :List of 3  
## ..$ summary:function (yval, dev, wt, ylevel, digits)   
## ..$ print :function (yval, ylevel, digits, nsmall)   
## ..$ text :function (yval, dev, wt, ylevel, digits, n, use.n)   
## $ numresp : int 4  
## $ splits : num [1:49, 1:5] 683 683 683 683 683 0 0 0 0 0 ...  
## ..- attr(\*, "dimnames")=List of 2  
## .. ..$ : chr [1:49] "Cell.size" "Cell.shape" "Bare.nuclei" "Bl.cromatin" ...  
## .. ..$ : chr [1:5] "count" "ncat" "improve" "index" ...  
## $ csplit : int [1:49, 1:10] 1 1 1 1 1 1 1 1 1 1 ...  
## $ variable.importance: Named num [1:9] 228 196 178 166 159 ...  
## ..- attr(\*, "names")= chr [1:9] "Cell.size" "Cell.shape" "Bare.nuclei" "Epith.c.size" ...  
## $ y : int [1:683] 1 1 1 1 1 2 1 1 1 1 ...  
## $ ordered : Named logi [1:9] TRUE TRUE TRUE TRUE TRUE FALSE ...  
## ..- attr(\*, "names")= chr [1:9] "Cl.thickness" "Cell.size" "Cell.shape" "Marg.adhesion" ...  
## - attr(\*, "xlevels")=List of 9  
## ..$ Cl.thickness : chr [1:10] "1" "2" "3" "4" ...  
## ..$ Cell.size : chr [1:10] "1" "2" "3" "4" ...  
## ..$ Cell.shape : chr [1:10] "1" "2" "3" "4" ...  
## ..$ Marg.adhesion : chr [1:10] "1" "2" "3" "4" ...  
## ..$ Epith.c.size : chr [1:10] "1" "2" "3" "4" ...  
## ..$ Bare.nuclei : chr [1:10] "1" "2" "3" "4" ...  
## ..$ Bl.cromatin : chr [1:10] "1" "2" "3" "4" ...  
## ..$ Normal.nucleoli: chr [1:10] "1" "2" "3" "4" ...  
## ..$ Mitoses : chr [1:9] "1" "2" "3" "4" ...  
## - attr(\*, "ylevels")= chr [1:2] "benign" "malignant"  
## - attr(\*, "class")= chr "rpart"

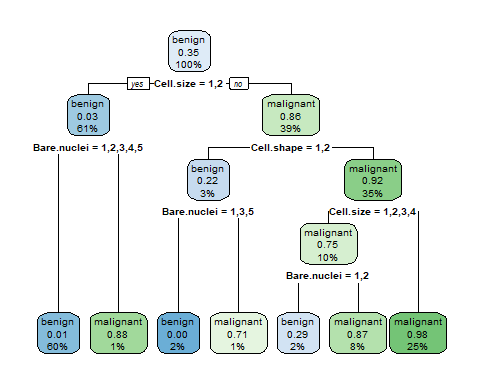
#rpart.plot package  
library(rpart.plot)

## Warning: package 'rpart.plot' was built under R version 4.2.2

rpart.rules(mytree)

## Class   
## 0.00 when Cell.size is 3 or 4 or 5 or 6 or 7 or 8 or 9 or 10 & Bare.nuclei is 1 or 3 or 5 & Cell.shape is 1 or 2  
## 0.01 when Cell.size is 1 or 2 & Bare.nuclei is 1 or 2 or 3 or 4 or 5   
## 0.29 when Cell.size is 1 or 2 or 3 or 4 & Bare.nuclei is 1 or 2 & Cell.shape is 3 or 4 or 5 or 6 or 7 or 8 or 9 or 10  
## 0.71 when Cell.size is 3 or 4 or 5 or 6 or 7 or 8 or 9 or 10 & Bare.nuclei is 2 or 4 or 10 & Cell.shape is 1 or 2  
## 0.87 when Cell.size is 1 or 2 or 3 or 4 & Bare.nuclei is 3 or 4 or 5 or 7 or 8 or 9 or 10 & Cell.shape is 3 or 4 or 5 or 6 or 7 or 8 or 9 or 10  
## 0.88 when Cell.size is 1 or 2 & Bare.nuclei is 6 or 7 or 8 or 10   
## 0.98 when Cell.size is 5 or 6 or 7 or 8 or 9 or 10 & Cell.shape is 3 or 4 or 5 or 6 or 7 or 8 or 9 or 10

rpart.plot(mytree)



#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

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

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

#Random Forests  
library(randomForest)

## Warning: package 'randomForest' was built under R version 4.2.2

## 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(mysvm.pred,myrf.pred,myrda.pred,mytree.pred)  
head(combine.classes)

## mysvm.pred myrf.pred class posterior.benign posterior.malignant  
## 1 benign benign benign 1.000000e+00 6.307604e-33  
## 2 malignant benign malignant 7.011986e-04 9.992988e-01  
## 3 benign benign benign 1.000000e+00 2.567354e-35  
## 4 malignant benign malignant 4.332582e-12 1.000000e+00  
## 5 benign benign benign 1.000000e+00 4.484541e-33  
## 6 malignant malignant malignant 4.399812e-85 1.000000e+00  
## mytree.pred  
## 1 malignant  
## 2 malignant  
## 3 malignant  
## 4 malignant  
## 5 malignant  
## 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 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 6.307604e-33  
## [2,] 7.011986e-04 9.992988e-01  
## [3,] 1.000000e+00 2.567354e-35  
## [4,] 4.332582e-12 1.000000e+00  
## [5,] 1.000000e+00 4.484541e-33  
## [6,] 4.399812e-85 1.000000e+00  
## [7,] 1.000000e+00 1.134189e-26  
## [8,] 1.000000e+00 2.321001e-39  
## [9,] 1.000000e+00 2.123555e-19  
## [10,] 1.000000e+00 4.792881e-37  
## [11,] 1.000000e+00 4.512701e-40  
## [12,] 1.000000e+00 4.526321e-38  
## [13,] 2.519372e-14 1.000000e+00  
## [14,] 1.000000e+00 1.584413e-33  
## [15,] 4.266310e-119 1.000000e+00  
## [16,] 2.099758e-44 1.000000e+00  
## [17,] 1.000000e+00 1.337961e-35  
## [18,] 1.000000e+00 1.223316e-34  
## [19,] 2.662724e-66 1.000000e+00  
## [20,] 1.000000e+00 6.123561e-30  
## [21,] 1.212715e-67 1.000000e+00  
## [22,] 1.548748e-76 1.000000e+00  
## [23,] 1.000000e+00 6.842877e-37  
## [24,] 1.000000e+00 7.134738e-37  
## [25,] 9.753166e-25 1.000000e+00  
## [26,] 1.000000e+00 2.803918e-42  
## [27,] 1.000000e+00 1.148186e-34  
## [28,] 1.000000e+00 4.526321e-38  
## [29,] 1.000000e+00 4.064728e-35  
## [30,] 1.000000e+00 6.569181e-40  
## [31,] 1.000000e+00 3.012912e-37  
## [32,] 1.369857e-75 1.000000e+00  
## [33,] 1.000000e+00 3.453459e-38  
## [34,] 1.000000e+00 1.086501e-38  
## [35,] 1.000000e+00 4.526321e-38  
## [36,] 6.700450e-81 1.000000e+00  
## [37,] 1.000000e+00 6.610068e-30  
## [38,] 1.203557e-52 1.000000e+00  
## [39,] 8.205863e-56 1.000000e+00  
## [40,] 9.012855e-48 1.000000e+00  
## [41,] 2.431490e-46 1.000000e+00  
## [42,] 1.201602e-45 1.000000e+00  
## [43,] 1.526907e-59 1.000000e+00  
## [44,] 1.000000e+00 8.777483e-32  
## [45,] 3.225707e-67 1.000000e+00  
## [46,] 1.000000e+00 1.787844e-38  
## [47,] 1.000000e+00 4.484541e-33  
## [48,] 1.954026e-60 1.000000e+00  
## [49,] 3.156930e-63 1.000000e+00  
## [50,] 2.006878e-18 1.000000e+00  
## [51,] 3.464524e-44 1.000000e+00  
## [52,] 1.639138e-84 1.000000e+00  
## [53,] 1.854342e-70 1.000000e+00  
## [54,] 7.653517e-52 1.000000e+00  
## [55,] 1.194257e-67 1.000000e+00  
## [56,] 1.336584e-51 1.000000e+00  
## [57,] 1.417449e-17 1.000000e+00  
## [58,] 1.408082e-51 1.000000e+00  
## [59,] 4.233303e-36 1.000000e+00  
## [60,] 1.000000e+00 2.730503e-38  
## [61,] 2.455995e-54 1.000000e+00  
## [62,] 6.541891e-24 1.000000e+00  
## [63,] 1.000000e+00 1.787844e-38  
## [64,] 3.118601e-33 1.000000e+00  
## [65,] 1.000000e+00 1.223316e-34  
## [66,] 2.965816e-44 1.000000e+00  
## [67,] 7.305373e-98 1.000000e+00  
## [68,] 1.000000e+00 1.099210e-40  
## [69,] 1.000000e+00 3.231819e-32  
## [70,] 5.554408e-68 1.000000e+00  
## [71,] 1.000000e+00 5.874335e-24  
## [72,] 3.904478e-73 1.000000e+00  
## [73,] 1.355573e-40 1.000000e+00  
## [74,] 1.000000e+00 5.994280e-34  
## [75,] 1.000000e+00 7.488102e-31  
## [76,] 1.000000e+00 4.730499e-32  
## [77,] 1.000000e+00 3.618961e-32  
## [78,] 1.000000e+00 2.185667e-36  
## [79,] 1.000000e+00 6.982953e-35  
## [80,] 1.000000e+00 3.955780e-36  
## [81,] 1.000000e+00 1.730135e-33  
## [82,] 1.000000e+00 4.383067e-27  
## [83,] 1.423840e-104 1.000000e+00  
## [84,] 5.816222e-67 1.000000e+00  
## [85,] 2.921318e-47 1.000000e+00  
## [86,] 9.303755e-89 1.000000e+00  
## [87,] 1.000000e+00 1.223316e-34  
## [88,] 1.000000e+00 2.104849e-37  
## [89,] 1.000000e+00 7.134738e-37  
## [90,] 1.000000e+00 9.926299e-36  
## [91,] 1.000000e+00 1.223316e-34  
## [92,] 1.000000e+00 1.787844e-38  
## [93,] 1.000000e+00 3.012912e-37  
## [94,] 1.000000e+00 7.134738e-37  
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## [682,] 6.036349e-58 1.000000e+00  
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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)  
str(combine.classes)

## 'data.frame': 683 obs. of 6 variables:  
## $ mysvm.pred : Factor w/ 2 levels "benign","malignant": 1 2 1 2 1 2 1 1 1 1 ...  
## $ myrf.pred : num 1 1 1 1 1 1 1 1 1 1 ...  
## $ class : num 0 1 0 1 0 1 0 0 0 0 ...  
## $ posterior.benign : num 1.00 7.01e-04 1.00 4.33e-12 1.00 ...  
## $ posterior.malignant: num 6.31e-33 9.99e-01 2.57e-35 1.00 4.48e-33 ...  
## $ mytree.pred : Factor w/ 2 levels "benign","malignant": 2 2 2 2 2 2 2 2 2 2 ...

#combine.cl <- combine.classes[,-c(4,5)] #majority.vote=rowSums(combine.classes[,-c(4,5)]) #head(majority.vote) #data.frame(mysvm.pred,myrf.pred,myrda.pred$Class,#myqda.pred, # mytree.pred,mynb.pred$class)

head(combine.classes)

## mysvm.pred myrf.pred class posterior.benign posterior.malignant mytree.pred  
## 1 benign 1 0 1.000000e+00 6.307604e-33 malignant  
## 2 malignant 1 1 7.011986e-04 9.992988e-01 malignant  
## 3 benign 1 0 1.000000e+00 2.567354e-35 malignant  
## 4 malignant 1 1 4.332582e-12 1.000000e+00 malignant  
## 5 benign 1 0 1.000000e+00 4.484541e-33 malignant  
## 6 malignant 1 1 4.399812e-85 1.000000e+00 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  
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## [673] benign benign benign malignant benign benign benign   
## [680] benign malignant malignant malignant  
## Levels: benign malignant  
##   
## $posterior  
## benign malignant  
## [1,] 1.000000e+00 6.307604e-33  
## [2,] 7.011986e-04 9.992988e-01  
## [3,] 1.000000e+00 2.567354e-35  
## [4,] 4.332582e-12 1.000000e+00  
## [5,] 1.000000e+00 4.484541e-33  
## [6,] 4.399812e-85 1.000000e+00  
## [7,] 1.000000e+00 1.134189e-26  
## [8,] 1.000000e+00 2.321001e-39  
## [9,] 1.000000e+00 2.123555e-19  
## [10,] 1.000000e+00 4.792881e-37  
## [11,] 1.000000e+00 4.512701e-40  
## [12,] 1.000000e+00 4.526321e-38  
## [13,] 2.519372e-14 1.000000e+00  
## [14,] 1.000000e+00 1.584413e-33  
## [15,] 4.266310e-119 1.000000e+00  
## [16,] 2.099758e-44 1.000000e+00  
## [17,] 1.000000e+00 1.337961e-35  
## [18,] 1.000000e+00 1.223316e-34  
## [19,] 2.662724e-66 1.000000e+00  
## [20,] 1.000000e+00 6.123561e-30  
## [21,] 1.212715e-67 1.000000e+00  
## [22,] 1.548748e-76 1.000000e+00  
## [23,] 1.000000e+00 6.842877e-37  
## [24,] 1.000000e+00 7.134738e-37  
## [25,] 9.753166e-25 1.000000e+00  
## [26,] 1.000000e+00 2.803918e-42  
## [27,] 1.000000e+00 1.148186e-34  
## [28,] 1.000000e+00 4.526321e-38  
## [29,] 1.000000e+00 4.064728e-35  
## [30,] 1.000000e+00 6.569181e-40  
## [31,] 1.000000e+00 3.012912e-37  
## [32,] 1.369857e-75 1.000000e+00  
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## [34,] 1.000000e+00 1.086501e-38  
## [35,] 1.000000e+00 4.526321e-38  
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## [37,] 1.000000e+00 6.610068e-30  
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## [39,] 8.205863e-56 1.000000e+00  
## [40,] 9.012855e-48 1.000000e+00  
## [41,] 2.431490e-46 1.000000e+00  
## [42,] 1.201602e-45 1.000000e+00  
## [43,] 1.526907e-59 1.000000e+00  
## [44,] 1.000000e+00 8.777483e-32  
## [45,] 3.225707e-67 1.000000e+00  
## [46,] 1.000000e+00 1.787844e-38  
## [47,] 1.000000e+00 4.484541e-33  
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## [52,] 1.639138e-84 1.000000e+00  
## [53,] 1.854342e-70 1.000000e+00  
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## [55,] 1.194257e-67 1.000000e+00  
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## [444,] 1.000000e+00 5.247281e-35  
## [445,] 1.000000e+00 6.717102e-31  
## [446,] 1.000000e+00 3.594167e-33  
## [447,] 1.000000e+00 7.555823e-30  
## [448,] 1.000000e+00 5.396230e-31  
## [449,] 1.000000e+00 3.828929e-39  
## [450,] 1.000000e+00 5.515325e-35  
## [451,] 5.452781e-106 1.000000e+00  
## [452,] 1.173838e-75 1.000000e+00  
## [453,] 2.445657e-59 1.000000e+00  
## [454,] 1.000000e+00 5.515325e-35  
## [455,] 1.000000e+00 1.076269e-40  
## [456,] 1.000000e+00 6.569181e-40  
## [457,] 1.000000e+00 5.396230e-31  
## [458,] 1.000000e+00 2.277631e-34  
## [459,] 1.000000e+00 5.515325e-35  
## [460,] 1.000000e+00 1.013500e-33  
## [461,] 1.000000e+00 4.992448e-36  
## [462,] 1.000000e+00 1.483177e-36  
## [463,] 1.000000e+00 5.515325e-35  
## [464,] 1.000000e+00 2.651966e-34  
## [465,] 5.217277e-61 1.000000e+00  
## [466,] 1.000000e+00 1.037498e-37  
## [467,] 1.000000e+00 2.230248e-18  
## [468,] 5.060816e-78 1.000000e+00  
## [469,] 3.808924e-72 1.000000e+00  
## [470,] 1.000000e+00 5.247281e-35  
## [471,] 1.000000e+00 3.245608e-36  
## [472,] 1.000000e+00 6.569181e-40  
## [473,] 1.508147e-75 1.000000e+00  
## [474,] 5.092962e-48 1.000000e+00  
## [475,] 9.919552e-01 8.044791e-03  
## [476,] 1.000000e+00 2.616298e-37  
## [477,] 2.972778e-54 1.000000e+00  
## [478,] 1.000000e+00 4.587300e-38  
## [479,] 3.819873e-73 1.000000e+00  
## [480,] 1.000000e+00 7.920778e-14  
## [481,] 1.000000e+00 6.569181e-40  
## [482,] 1.000000e+00 1.621541e-40  
## [483,] 1.000000e+00 8.779668e-36  
## [484,] 1.000000e+00 1.337961e-35  
## [485,] 1.000000e+00 1.337961e-35  
## [486,] 1.000000e+00 6.123561e-30  
## [487,] 1.000000e+00 1.337961e-35  
## [488,] 1.000000e+00 3.955780e-36  
## [489,] 1.000000e+00 1.223316e-34  
## [490,] 1.000000e+00 2.616298e-37  
## [491,] 1.000000e+00 2.850962e-33  
## [492,] 3.743346e-72 1.000000e+00  
## [493,] 1.000000e+00 4.551401e-28  
## [494,] 1.000000e+00 1.013500e-33  
## [495,] 1.000000e+00 1.754432e-37  
## [496,] 1.000000e+00 2.616298e-37  
## [497,] 1.000000e+00 1.148186e-34  
## [498,] 1.000000e+00 1.013500e-33  
## [499,] 1.000000e+00 6.569181e-40  
## [500,] 1.116360e-77 1.000000e+00  
## [501,] 1.784634e-70 1.000000e+00  
## [502,] 1.000000e+00 1.621541e-40  
## [503,] 1.000000e+00 5.664729e-41  
## [504,] 1.000000e+00 1.381754e-37  
## [505,] 2.079659e-56 1.000000e+00  
## [506,] 1.000000e+00 8.038662e-34  
## [507,] 1.000000e+00 2.632004e-31  
## [508,] 7.036614e-35 1.000000e+00  
## [509,] 1.438101e-67 1.000000e+00  
## [510,] 1.000000e+00 6.842877e-37  
## [511,] 1.000000e+00 9.926299e-36  
## [512,] 1.000000e+00 5.515325e-35  
## [513,] 1.000000e+00 1.223316e-34  
## [514,] 1.000000e+00 6.030581e-29  
## [515,] 1.000000e+00 4.587300e-38  
## [516,] 1.182263e-64 1.000000e+00  
## [517,] 1.000000e+00 5.968007e-35  
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## [519,] 1.000000e+00 6.842877e-37  
## [520,] 1.000000e+00 4.526321e-38  
## [521,] 1.000000e+00 8.602112e-35  
## [522,] 1.000000e+00 6.307604e-33  
## [523,] 1.000000e+00 1.239170e-34  
## [524,] 1.000000e+00 1.337961e-35  
## [525,] 1.000000e+00 5.781283e-31  
## [526,] 1.000000e+00 3.414332e-34  
## [527,] 1.000000e+00 4.992448e-36  
## [528,] 1.000000e+00 4.851401e-31  
## [529,] 1.000000e+00 1.337961e-35  
## [530,] 1.000000e+00 3.433837e-36  
## [531,] 1.000000e+00 1.148186e-34  
## [532,] 9.881147e-43 1.000000e+00  
## [533,] 1.000000e+00 9.020358e-42  
## [534,] 1.000000e+00 9.375130e-40  
## [535,] 7.085286e-71 1.000000e+00  
## [536,] 1.000000e+00 6.842877e-37  
## [537,] 1.000000e+00 7.134738e-37  
## [538,] 1.000000e+00 2.282418e-32  
## [539,] 1.000000e+00 1.891320e-14  
## [540,] 1.000000e+00 4.992448e-36  
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## [543,] 1.000000e+00 3.594167e-33  
## [544,] 1.000000e+00 4.526321e-38  
## [545,] 1.000000e+00 1.148186e-34  
## [546,] 1.000000e+00 6.307604e-33  
## [547,] 1.000000e+00 6.307604e-33  
## [548,] 1.000000e+00 7.134738e-37  
## [549,] 1.000000e+00 6.842877e-37  
## [550,] 1.000000e+00 1.252354e-38  
## [551,] 2.499035e-59 1.000000e+00  
## [552,] 1.000000e+00 1.670197e-37  
## [553,] 1.000000e+00 9.623512e-32  
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## [555,] 9.157972e-75 1.000000e+00  
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## [557,] 1.941774e-94 1.000000e+00  
## [558,] 1.000000e+00 6.842877e-37  
## [559,] 1.000000e+00 1.787844e-38  
## [560,] 1.140148e-55 1.000000e+00  
## [561,] 1.000000e+00 1.239170e-34  
## [562,] 1.000000e+00 1.148186e-34  
## [563,] 1.000000e+00 1.787844e-38  
## [564,] 1.000000e+00 1.787844e-38  
## [565,] 1.000000e+00 7.134738e-37  
## [566,] 1.000000e+00 3.064299e-36  
## [567,] 9.916415e-59 1.000000e+00  
## [568,] 3.136667e-74 1.000000e+00  
## [569,] 1.000000e+00 4.992448e-36  
## [570,] 1.000000e+00 5.055457e-20  
## [571,] 1.000000e+00 2.616298e-37  
## [572,] 1.415681e-57 1.000000e+00  
## [573,] 1.000000e+00 6.129097e-39  
## [574,] 3.367026e-90 1.000000e+00  
## [575,] 1.000000e+00 1.013500e-33  
## [576,] 1.266057e-51 1.000000e+00  
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## [578,] 9.517196e-29 1.000000e+00  
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## [581,] 1.000000e+00 1.148186e-34  
## [582,] 1.000000e+00 1.854699e-37  
## [583,] 1.000000e+00 1.152426e-29  
## [584,] 1.000000e+00 6.842877e-37  
## [585,] 1.000000e+00 1.945685e-28  
## [586,] 1.000000e+00 6.842877e-37  
## [587,] 1.000000e+00 5.664729e-41  
## [588,] 1.000000e+00 1.337961e-35  
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## [590,] 1.972266e-41 1.000000e+00  
## [591,] 2.956612e-79 1.000000e+00  
## [592,] 1.000000e+00 1.793315e-35  
## [593,] 1.000000e+00 2.616298e-37  
## [594,] 1.974742e-40 1.000000e+00  
## [595,] 1.000000e+00 1.013500e-33  
## [596,] 5.005195e-36 1.000000e+00  
## [597,] 3.710550e-52 1.000000e+00  
## [598,] 4.109229e-73 1.000000e+00  
## [599,] 1.000000e+00 3.095818e-35  
## [600,] 1.000000e+00 1.189711e-41  
## [601,] 1.000000e+00 8.408338e-34  
## [602,] 1.000000e+00 6.842877e-37  
## [603,] 1.000000e+00 1.337961e-35  
## [604,] 1.000000e+00 1.148186e-34  
## [605,] 1.000000e+00 6.842877e-37  
## [606,] 9.999988e-01 1.239073e-06  
## [607,] 1.000000e+00 4.558629e-18  
## [608,] 1.000000e+00 2.616298e-37  
## [609,] 1.000000e+00 2.126929e-38  
## [610,] 1.000000e+00 4.810832e-23  
## [611,] 1.154782e-99 1.000000e+00  
## [612,] 1.000000e+00 1.533749e-30  
## [613,] 1.000000e+00 1.754432e-37  
## [614,] 1.000000e+00 5.515325e-35  
## [615,] 1.000000e+00 1.843211e-25  
## [616,] 1.000000e+00 1.148186e-34  
## [617,] 1.000000e+00 2.616298e-37  
## [618,] 4.062485e-55 1.000000e+00  
## [619,] 1.000000e+00 4.992448e-36  
## [620,] 1.000000e+00 1.603297e-28  
## [621,] 8.035073e-100 1.000000e+00  
## [622,] 1.000000e+00 2.100701e-24  
## [623,] 1.000000e+00 5.515325e-35  
## [624,] 1.000000e+00 3.594167e-33  
## [625,] 1.000000e+00 1.212318e-33  
## [626,] 1.000000e+00 6.842877e-37  
## [627,] 1.000000e+00 6.842877e-37  
## [628,] 1.000000e+00 2.616298e-37  
## [629,] 1.000000e+00 1.754432e-37  
## [630,] 1.000000e+00 6.842877e-37  
## [631,] 1.000000e+00 1.065292e-36  
## [632,] 1.000000e+00 1.333912e-36  
## [633,] 3.439738e-53 1.000000e+00  
## [634,] 1.000000e+00 6.842877e-37  
## [635,] 1.000000e+00 6.556318e-26  
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## [639,] 1.000000e+00 1.428988e-35  
## [640,] 1.000000e+00 6.842877e-37  
## [641,] 1.000000e+00 1.148186e-34  
## [642,] 2.281959e-07 9.999998e-01  
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## [645,] 1.000000e+00 1.787844e-38  
## [646,] 1.000000e+00 1.223316e-34  
## [647,] 1.000000e+00 1.179643e-36  
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## [655,] 2.747487e-56 1.000000e+00  
## [656,] 1.000000e+00 2.361693e-37  
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## [659,] 1.000000e+00 1.787844e-38  
## [660,] 1.000000e+00 4.219720e-28  
## [661,] 1.000000e+00 1.076269e-40  
## [662,] 1.000000e+00 1.013500e-33  
## [663,] 1.000000e+00 2.616298e-37  
## [664,] 1.000000e+00 1.754432e-37  
## [665,] 3.159616e-77 1.000000e+00  
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## [667,] 1.000000e+00 6.000980e-37  
## [668,] 1.000000e+00 2.616298e-37  
## [669,] 1.000000e+00 2.616298e-37  
## [670,] 1.000000e+00 2.616298e-37  
## [671,] 1.000000e+00 2.616298e-37  
## [672,] 1.000000e+00 1.487144e-31  
## [673,] 1.000000e+00 5.515325e-35  
## [674,] 1.000000e+00 1.876616e-18  
## [675,] 1.000000e+00 1.333912e-36  
## [676,] 9.877012e-56 1.000000e+00  
## [677,] 1.000000e+00 4.992448e-36  
## [678,] 1.000000e+00 3.653375e-30  
## [679,] 1.000000e+00 1.992388e-32  
## [680,] 1.000000e+00 1.754432e-37  
## [681,] 3.381135e-49 1.000000e+00  
## [682,] 6.036349e-58 1.000000e+00  
## [683,] 2.985939e-72 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 6 variables:  
## $ mysvm.pred : Factor w/ 2 levels "benign","malignant": 1 2 1 2 1 2 1 1 1 1 ...  
## $ myrf.pred : num 1 1 1 1 1 1 1 1 1 1 ...  
## $ class : num 1 1 1 1 1 1 1 1 1 1 ...  
## $ posterior.benign : num 1 1 1 1 1 1 1 1 1 1 ...  
## $ posterior.malignant: num 1 1 1 1 1 1 1 1 1 1 ...  
## $ mytree.pred : Factor w/ 2 levels "benign","malignant": 2 2 2 2 2 2 2 2 2 2 ...

#combine.cl <- combine.classes[,-c(6,7)]  
#majority.vote=rowSums(combine.classes[,-c(6,7)])  
#head(majority.vote)  
#head(combine.cl)  
#combine.classes[,6]<- rowSums(combine.classes[,-c(6,7)])  
#combine.classes[,7]<-ifelse(combine.classes[,6]>=4, "malignant", benign)  
head(combine.classes)

## mysvm.pred myrf.pred class posterior.benign posterior.malignant mytree.pred  
## 1 benign 1 1 1 1 malignant  
## 2 malignant 1 1 1 1 malignant  
## 3 benign 1 1 1 1 malignant  
## 4 malignant 1 1 1 1 malignant  
## 5 benign 1 1 1 1 malignant  
## 6 malignant 1 1 1 1 malignant

#table(combine.classes[,7], BreastCancer$Class)

# partition the data set for 80% training and 20% evaluation (adapted from ?randomForest)  
set.seed(2)  
  
ind <- sample(2, nrow(BreastCancer), replace = TRUE, prob=c(0.8, 0.2))  
  
# create model using recursive partitioning on the training data set  
require(rpart)  
x.rp <- rpart(Class ~ ., data=BreastCancer[ind == 1,])  
# predict classes for the evaluation data set  
x.rp.pred <- predict(x.rp, type="class", newdata=BreastCancer[ind == 2,])  
# score the evaluation data set (extract the probabilities)  
x.rp.prob <- predict(x.rp, type="prob", newdata=BreastCancer[ind == 2,])  
  
# To view the decision tree, uncomment this line.  
# plot(x.rp, main="Decision tree created using rpart")  
  
# create model using conditional inference trees  
require(party)

## Loading required package: party

## Warning: package 'party' was built under R version 4.2.2

## Loading required package: grid

## Loading required package: mvtnorm

## Loading required package: modeltools

## Loading required package: stats4

## Loading required package: strucchange

## Warning: package 'strucchange' was built under R version 4.2.2

## Loading required package: zoo

## Warning: package 'zoo' was built under R version 4.2.2

##   
## Attaching package: 'zoo'

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

## Loading required package: sandwich

## Warning: package 'sandwich' was built under R version 4.2.2

x.ct <- ctree(Class ~ ., data=BreastCancer[ind == 1,])  
x.ct.pred <- predict(x.ct, newdata=BreastCancer[ind == 2,])  
x.ct.prob <- 1- unlist(treeresponse(x.ct, BreastCancer[ind == 2,]), use.names=F)[seq(1,nrow(BreastCancer[ind == 2,])\*2,2)]  
  
# To view the decision tree, uncomment this line.  
# plot(x.ct, main="Decision tree created using condition inference trees")  
  
# create model using random forest and bagging ensemble using conditional inference trees  
x.cf <- cforest(Class ~ ., data=BreastCancer[ind == 1,], control = cforest\_unbiased(mtry = ncol(BreastCancer)-2))  
x.cf.pred <- predict(x.cf, newdata=BreastCancer[ind == 2,])  
x.cf.prob <- 1- unlist(treeresponse(x.cf, BreastCancer[ind == 2,]), use.names=F)[seq(1,nrow(BreastCancer[ind == 2,])\*2,2)]  
  
# create model using bagging (bootstrap aggregating)  
require(ipred)

## Loading required package: ipred

## Warning: package 'ipred' was built under R version 4.2.2

x.ip <- bagging(Class ~ ., data=BreastCancer[ind == 1,])  
x.ip.prob <- predict(x.ip, type="prob", newdata=BreastCancer[ind == 2,])  
  
# create model using svm (support vector machine)  
require(e1071)  
  
# svm requires tuning  
x.svm.tune <- tune(svm, Class~., data = BreastCancer[ind == 1,],  
 ranges = list(gamma = 2^(-8:1), cost = 2^(0:4)),  
 tunecontrol = tune.control(sampling = "fix"))  
# display the tuning results (in text format)  
x.svm.tune

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

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

## Loading required package: ROCR

## Warning: package 'ROCR' was built under R version 4.2.2

# create an ROCR prediction object from rpart() probabilities  
x.rp.prob.rocr <- prediction(x.rp.prob[,2], BreastCancer[ind == 2,'Class'])  
# prepare an ROCR performance object for ROC curve (tpr=true positive rate, fpr=false positive rate)  
x.rp.perf <- performance(x.rp.prob.rocr, "tpr","fpr")  
# plot it  
plot(x.rp.perf, col=2, main="ROC curves comparing classification performance of five machine learning models")  
  
# Draw a legend.  
legend(0.6, 0.6, c('rpart', 'ctree', 'cforest','bagging','svm'), 2:6)  
  
# ctree  
x.ct.prob.rocr <- prediction(x.ct.prob, BreastCancer[ind == 2,'Class'])  
x.ct.perf <- performance(x.ct.prob.rocr, "tpr","fpr")  
# add=TRUE draws on the existing chart   
plot(x.ct.perf, col=3, add=TRUE)  
  
  
# cforest  
x.cf.prob.rocr <- prediction(x.cf.prob, BreastCancer[ind == 2,'Class'])  
x.cf.perf <- performance(x.cf.prob.rocr, "tpr","fpr")  
plot(x.cf.perf, col=4, add=TRUE)  
  
# bagging  
x.ip.prob.rocr <- prediction(x.ip.prob[,2], BreastCancer[ind == 2,'Class'])  
x.ip.perf <- performance(x.ip.prob.rocr, "tpr","fpr")  
plot.new()  
plot(x.ip.perf, col=5, add=TRUE)  
# svm  
x.svm.prob.rocr <- prediction(attr(x.svm.prob, "probabilities")[,2], BreastCancer[ind == 2,'Class'])  
x.svm.perf <- performance(x.svm.prob.rocr, "tpr","fpr")  
  
plot(x.svm.perf, col=6, add=TRUE)  
  
# Close and save the PNG file.  
dev.off()

## png   
## 2