Proj2

Brandon Bainbridge

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

## Loading required package: mlbench

# 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"

# 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)  
  
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)

## 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"

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

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))  
mynnet.pred <- neuralnet::compute(mynnet, BreastCancer)#Get the actual classes out  
predicted.class <- apply(mynnet.pred$net.result,1,which.max)-1  
mynnet.pred <- predicted.class  
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

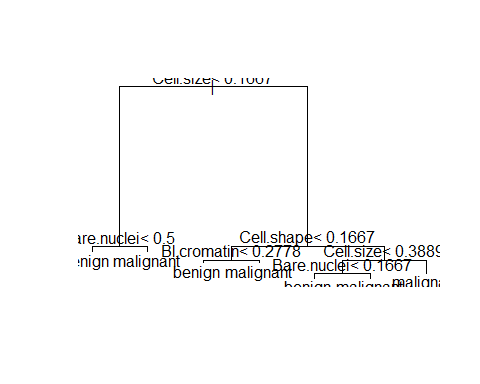
str(mynnet)

## 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] 1.002 1.001 1.001 0.998 1.001 ...  
## .. ..- 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] 2.398 0.967 -3.933 0.625 -0.719 ...  
## .. ..$ : num [1:6, 1:4] 3.91e-01 -1.04e+02 -1.96e+01 -7.26e-03 4.19e+01 ...  
## .. ..$ : num [1:5, 1:2] 0.401 49.239 1.011 0.197 -0.776 ...  
## $ generalized.weights:List of 1  
## ..$ : num [1:683, 1:18] -2.5 20359.86 -8.38 -13085.71 6.05 ...  
## .. ..- 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] 0.761 0.481 -2.852 1.861 0.116 ...  
## .. ..$ : num [1:6, 1:4] 0.33 -1.836 -2.082 0.188 -0.918 ...  
## .. ..$ : num [1:5, 1:2] 0.665 0.556 0.545 0.216 -0.216 ...  
## $ result.matrix : num [1:87, 1] 1.70e-02 9.85e-03 3.90e+04 2.40 9.67e-01 ...  
## ..- attr(\*, "dimnames")=List of 2  
## .. ..$ : chr [1:87] "error" "reached.threshold" "steps" "Intercept.to.1layhid1" ...  
## .. ..$ : NULL  
## - attr(\*, "class")= chr "nn"

table(mynnet.pred,BreastCancer$Class)

##   
## mynnet.pred benign malignant  
## 0 444 0  
## 1 0 239

library(MASS)  
  
#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 0.1715481 0.02597474  
## 4 0.01255230 3 0.12970711 0.1757322 0.02626911  
## 5 0.01000000 6 0.09205021 0.1673640 0.02567599  
##   
## Variable importance  
## Cell.size Cell.shape Bare.nuclei Epith.c.size Bl.cromatin   
## 21 18 16 15 15   
## Normal.nucleoli Cl.thickness   
## 14 1   
##   
## Node number 1: 683 observations, complexity param=0.790795  
## predicted class=benign expected loss=0.3499268 P(node) =1  
## class counts: 444 239  
## probabilities: 0.650 0.350   
## left son=2 (418 obs) right son=3 (265 obs)  
## Primary splits:  
## Cell.size < 0.1666667 to the left, improve=222.3221, (0 missing)  
## Cell.shape < 0.2777778 to the left, improve=216.4111, (0 missing)  
## Bare.nuclei < 0.1666667 to the left, improve=203.7284, (0 missing)  
## Bl.cromatin < 0.2777778 to the left, improve=196.3903, (0 missing)  
## Epith.c.size < 0.1666667 to the left, improve=193.1310, (0 missing)  
## Surrogate splits:  
## Cell.shape < 0.2777778 to the left, agree=0.917, adj=0.785, (0 split)  
## Epith.c.size < 0.1666667 to the left, agree=0.900, adj=0.743, (0 split)  
## Bare.nuclei < 0.1666667 to the left, agree=0.880, adj=0.691, (0 split)  
## Normal.nucleoli < 0.1666667 to the left, agree=0.877, adj=0.683, (0 split)  
## Bl.cromatin < 0.2777778 to the left, agree=0.876, adj=0.679, (0 split)  
##   
## Node number 2: 418 observations, complexity param=0.0251046  
## predicted class=benign expected loss=0.02870813 P(node) =0.6120059  
## class counts: 406 12  
## probabilities: 0.971 0.029   
## left son=4 (410 obs) right son=5 (8 obs)  
## Primary splits:  
## Bare.nuclei < 0.5 to the left, improve=11.68296, (0 missing)  
## Cl.thickness < 0.6111111 to the left, improve=10.32214, (0 missing)  
## Normal.nucleoli < 0.2777778 to the left, improve=10.32214, (0 missing)  
## Bl.cromatin < 0.3888889 to the left, improve= 8.53307, (0 missing)  
## Epith.c.size < 0.2777778 to the left, improve= 4.63208, (0 missing)  
## Surrogate splits:  
## Cl.thickness < 0.8333333 to the left, agree=0.988, adj=0.375, (0 split)  
## Normal.nucleoli < 0.2777778 to the left, agree=0.983, adj=0.125, (0 split)  
##   
## Node number 3: 265 observations, complexity param=0.05439331  
## predicted class=malignant expected loss=0.1433962 P(node) =0.3879941  
## class counts: 38 227  
## probabilities: 0.143 0.857   
## left son=6 (23 obs) right son=7 (242 obs)  
## Primary splits:  
## Cell.shape < 0.1666667 to the left, improve=20.58158, (0 missing)  
## Cell.size < 0.2777778 to the left, improve=18.27650, (0 missing)  
## Bare.nuclei < 0.05555556 to the left, improve=16.81493, (0 missing)  
## Bl.cromatin < 0.1666667 to the left, improve=13.91034, (0 missing)  
## Marg.adhesion < 0.1666667 to the left, improve=11.17148, (0 missing)  
## Surrogate splits:  
## Bl.cromatin < 0.05555556 to the left, agree=0.932, adj=0.217, (0 split)  
##   
## Node number 4: 410 observations  
## predicted class=benign expected loss=0.01219512 P(node) =0.6002928  
## class counts: 405 5  
## probabilities: 0.988 0.012   
##   
## Node number 5: 8 observations  
## predicted class=malignant expected loss=0.125 P(node) =0.01171303  
## class counts: 1 7  
## probabilities: 0.125 0.875   
##   
## Node number 6: 23 observations, complexity param=0.0125523  
## predicted class=benign expected loss=0.2173913 P(node) =0.03367496  
## class counts: 18 5  
## probabilities: 0.783 0.217   
## left son=12 (16 obs) right son=13 (7 obs)  
## Primary splits:  
## Bl.cromatin < 0.2777778 to the left, improve=4.968944, (0 missing)  
## Cl.thickness < 0.3888889 to the left, improve=3.381643, (0 missing)  
## Bare.nuclei < 0.05555556 to the left, improve=2.826087, (0 missing)  
## Mitoses < 0.0625 to the left, improve=2.522516, (0 missing)  
## Epith.c.size < 0.1666667 to the left, improve=1.992754, (0 missing)  
## Surrogate splits:  
## Cl.thickness < 0.5 to the left, agree=0.870, adj=0.571, (0 split)  
## Marg.adhesion < 0.6666667 to the left, agree=0.826, adj=0.429, (0 split)  
## Normal.nucleoli < 0.1666667 to the left, agree=0.826, adj=0.429, (0 split)  
## Mitoses < 0.0625 to the left, agree=0.826, adj=0.429, (0 split)  
## Epith.c.size < 0.3333333 to the left, agree=0.783, adj=0.286, (0 split)  
##   
## Node number 7: 242 observations, complexity param=0.0125523  
## predicted class=malignant expected loss=0.08264463 P(node) =0.3543192  
## class counts: 20 222  
## probabilities: 0.083 0.917   
## left son=14 (68 obs) right son=15 (174 obs)  
## Primary splits:  
## Cell.size < 0.3888889 to the left, improve=5.297663, (0 missing)  
## Bare.nuclei < 0.1666667 to the left, improve=4.093695, (0 missing)  
## Cell.shape < 0.3888889 to the left, improve=2.958548, (0 missing)  
## Bl.cromatin < 0.2777778 to the left, improve=2.805426, (0 missing)  
## Marg.adhesion < 0.5 to the left, improve=2.754821, (0 missing)  
## Surrogate splits:  
## Cell.shape < 0.3888889 to the left, agree=0.789, adj=0.250, (0 split)  
## Epith.c.size < 0.1666667 to the left, agree=0.777, adj=0.206, (0 split)  
## Marg.adhesion < 0.05555556 to the left, agree=0.744, adj=0.088, (0 split)  
## Bl.cromatin < 0.1666667 to the left, agree=0.736, adj=0.059, (0 split)  
##   
## Node number 12: 16 observations  
## predicted class=benign expected loss=0 P(node) =0.02342606  
## class counts: 16 0  
## probabilities: 1.000 0.000   
##   
## Node number 13: 7 observations  
## predicted class=malignant expected loss=0.2857143 P(node) =0.0102489  
## class counts: 2 5  
## probabilities: 0.286 0.714   
##   
## Node number 14: 68 observations, complexity param=0.0125523  
## predicted class=malignant expected loss=0.25 P(node) =0.09956076  
## class counts: 17 51  
## probabilities: 0.250 0.750   
## left son=28 (14 obs) right son=29 (54 obs)  
## Primary splits:  
## Bare.nuclei < 0.1666667 to the left, improve=7.600529, (0 missing)  
## Cl.thickness < 0.6111111 to the left, improve=3.558824, (0 missing)  
## Marg.adhesion < 0.5 to the left, improve=2.615385, (0 missing)  
## Normal.nucleoli < 0.1666667 to the left, improve=1.937690, (0 missing)  
## Bl.cromatin < 0.2777778 to the left, improve=1.525641, (0 missing)  
##   
## Node number 15: 174 observations  
## predicted class=malignant expected loss=0.01724138 P(node) =0.2547584  
## class counts: 3 171  
## probabilities: 0.017 0.983   
##   
## Node number 28: 14 observations  
## predicted class=benign expected loss=0.2857143 P(node) =0.0204978  
## class counts: 10 4  
## probabilities: 0.714 0.286   
##   
## Node number 29: 54 observations  
## predicted class=malignant expected loss=0.1296296 P(node) =0.07906296  
## class counts: 7 47  
## probabilities: 0.130 0.870

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

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

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

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

# The same as above in this case

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

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

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

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

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

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

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

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

#Random Forests  
library(randomForest)

## randomForest 4.7-1.1

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

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

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

table(myrf.pred, BreastCancer$Class)

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

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

## myrf.pred myrda.pred.class mytree.pred mynnet.pred mysvm.pred mynb.pred.class  
## 1 benign benign malignant 0 benign benign  
## 2 benign malignant malignant 0 malignant malignant  
## 3 benign benign malignant 0 benign benign  
## 4 benign malignant malignant 0 malignant malignant  
## 5 benign benign malignant 0 benign benign  
## 6 malignant malignant malignant 1 malignant malignant

head(myrf.pred)

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

head(myrda.pred)

## $class  
## [1] benign malignant benign malignant benign malignant benign   
## [8] benign benign benign benign benign benign benign   
## [15] malignant malignant benign benign malignant benign malignant  
## [22] malignant benign benign malignant benign benign benign   
## [29] benign benign benign malignant benign benign benign   
## [36] malignant benign malignant malignant malignant malignant malignant  
## [43] malignant benign malignant benign benign malignant malignant  
## [50] benign malignant malignant malignant malignant malignant benign   
## [57] malignant malignant malignant benign malignant malignant benign   
## [64] malignant benign malignant malignant benign benign malignant  
## [71] benign malignant malignant benign benign benign benign   
## [78] benign benign benign benign benign malignant malignant  
## [85] malignant malignant benign benign benign benign benign   
## [92] benign benign benign benign benign malignant malignant  
## [99] malignant benign benign malignant malignant malignant malignant  
## [106] malignant benign malignant benign malignant malignant malignant  
## [113] benign benign benign malignant benign benign benign   
## [120] benign malignant malignant malignant benign malignant benign   
## [127] malignant benign benign benign malignant benign benign   
## [134] benign benign benign benign benign benign malignant  
## [141] benign benign malignant benign benign malignant benign   
## [148] malignant malignant benign benign malignant benign benign   
## [155] malignant malignant benign benign benign benign malignant  
## [162] malignant benign benign benign benign benign malignant  
## [169] malignant malignant benign malignant benign malignant benign   
## [176] benign benign malignant malignant benign malignant malignant  
## [183] malignant benign malignant malignant benign benign benign   
## [190] benign malignant benign benign benign malignant malignant  
## [197] benign benign benign malignant malignant benign benign   
## [204] benign malignant malignant benign malignant malignant malignant  
## [211] benign benign malignant benign benign malignant benign   
## [218] malignant malignant benign malignant malignant benign malignant  
## [225] malignant malignant benign malignant benign malignant malignant  
## [232] malignant malignant benign benign benign benign benign   
## [239] benign malignant malignant benign benign malignant malignant  
## [246] malignant malignant malignant benign benign benign malignant  
## [253] malignant malignant malignant malignant malignant benign malignant  
## [260] malignant malignant benign malignant benign malignant benign   
## [267] benign benign benign benign malignant benign benign   
## [274] malignant malignant malignant malignant malignant benign malignant  
## [281] malignant benign benign malignant malignant malignant benign   
## [288] malignant malignant benign malignant benign malignant malignant  
## [295] benign benign malignant benign benign benign malignant  
## [302] benign benign malignant malignant benign malignant malignant  
## [309] benign malignant benign benign malignant benign malignant  
## [316] malignant malignant benign benign malignant malignant benign   
## [323] malignant benign benign malignant malignant benign benign   
## [330] benign malignant benign benign benign malignant malignant  
## [337] benign benign malignant malignant benign benign benign   
## [344] malignant malignant malignant malignant malignant benign benign   
## [351] benign benign malignant malignant benign benign benign   
## [358] benign benign benign benign benign benign benign   
## [365] benign benign benign malignant benign benign benign   
## [372] benign malignant benign benign benign benign malignant  
## [379] benign benign benign benign benign benign benign   
## [386] benign malignant benign benign benign benign benign   
## [393] benign benign benign benign benign malignant benign   
## [400] malignant benign malignant benign benign benign benign   
## [407] malignant benign benign benign malignant benign malignant  
## [414] benign benign benign benign benign benign malignant  
## [421] malignant malignant benign benign benign malignant benign   
## [428] benign benign benign benign benign benign benign   
## [435] malignant benign benign benign malignant benign 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,] 9.999974e-01 2.593893e-06  
## [2,] 3.319185e-05 9.999668e-01  
## [3,] 9.999989e-01 1.117365e-06  
## [4,] 9.042385e-05 9.999096e-01  
## [5,] 9.999977e-01 2.294104e-06  
## [6,] 9.942388e-16 1.000000e+00  
## [7,] 7.260883e-01 2.739117e-01  
## [8,] 9.999997e-01 3.008570e-07  
## [9,] 9.999993e-01 7.163984e-07  
## [10,] 9.999990e-01 9.915542e-07  
## [11,] 9.999999e-01 6.707261e-08  
## [12,] 9.999999e-01 9.550853e-08  
## [13,] 9.945659e-01 5.434086e-03  
## [14,] 9.999991e-01 8.617679e-07  
## [15,] 1.751470e-10 1.000000e+00  
## [16,] 4.923742e-01 5.076258e-01  
## [17,] 9.999995e-01 5.324052e-07  
## [18,] 9.999991e-01 9.415752e-07  
## [19,] 1.911445e-09 1.000000e+00  
## [20,] 9.999921e-01 7.924560e-06  
## [21,] 2.199372e-08 1.000000e+00  
## [22,] 1.676884e-09 1.000000e+00  
## [23,] 9.999998e-01 2.141305e-07  
## [24,] 9.999999e-01 8.377734e-08  
## [25,] 8.937188e-02 9.106281e-01  
## [26,] 9.999997e-01 3.342710e-07  
## [27,] 9.999985e-01 1.468024e-06  
## [28,] 9.999999e-01 9.550853e-08  
## [29,] 9.999999e-01 1.383612e-07  
## [30,] 9.999998e-01 1.722427e-07  
## [31,] 9.999998e-01 1.692162e-07  
## [32,] 7.483356e-08 9.999999e-01  
## [33,] 9.999998e-01 2.449783e-07  
## [34,] 9.999996e-01 3.781360e-07  
## [35,] 9.999999e-01 9.550853e-08  
## [36,] 4.699416e-12 1.000000e+00  
## [37,] 9.992441e-01 7.559231e-04  
## [38,] 1.755160e-07 9.999998e-01  
## [39,] 4.464943e-03 9.955351e-01  
## [40,] 1.668216e-02 9.833178e-01  
## [41,] 8.448717e-13 1.000000e+00  
## [42,] 9.635469e-03 9.903645e-01  
## [43,] 4.978332e-12 1.000000e+00  
## [44,] 9.999999e-01 5.595322e-08  
## [45,] 3.706247e-07 9.999996e-01  
## [46,] 1.000000e+00 4.724254e-08  
## [47,] 9.999977e-01 2.294104e-06  
## [48,] 5.403818e-08 9.999999e-01  
## [49,] 2.988709e-03 9.970113e-01  
## [50,] 9.812378e-01 1.876218e-02  
## [51,] 1.269586e-06 9.999987e-01  
## [52,] 4.635782e-10 1.000000e+00  
## [53,] 1.338124e-08 1.000000e+00  
## [54,] 5.432149e-05 9.999457e-01  
## [55,] 1.321292e-10 1.000000e+00  
## [56,] 7.114209e-01 2.885791e-01  
## [57,] 5.170591e-04 9.994829e-01  
## [58,] 3.710069e-01 6.289931e-01  
## [59,] 4.005644e-03 9.959944e-01  
## [60,] 9.999999e-01 1.418905e-07  
## [61,] 1.797416e-12 1.000000e+00  
## [62,] 1.619807e-01 8.380193e-01  
## [63,] 1.000000e+00 4.724254e-08  
## [64,] 2.291900e-04 9.997708e-01  
## [65,] 9.999991e-01 9.415752e-07  
## [66,] 3.232278e-08 1.000000e+00  
## [67,] 2.825789e-13 1.000000e+00  
## [68,] 9.999999e-01 1.441979e-07  
## [69,] 9.999946e-01 5.391744e-06  
## [70,] 1.969670e-12 1.000000e+00  
## [71,] 9.998830e-01 1.169652e-04  
## [72,] 2.354258e-11 1.000000e+00  
## [73,] 1.485241e-02 9.851476e-01  
## [74,] 9.999985e-01 1.542492e-06  
## [75,] 9.999994e-01 5.743120e-07  
## [76,] 9.999912e-01 8.809025e-06  
## [77,] 9.999962e-01 3.839878e-06  
## [78,] 9.999999e-01 1.489187e-07  
## [79,] 9.999729e-01 2.709041e-05  
## [80,] 9.999992e-01 7.685999e-07  
## [81,] 9.999953e-01 4.689849e-06  
## [82,] 9.999278e-01 7.218884e-05  
## [83,] 2.660186e-12 1.000000e+00  
## [84,] 4.242437e-12 1.000000e+00  
## [85,] 5.545649e-03 9.944544e-01  
## [86,] 2.330529e-08 1.000000e+00  
## [87,] 9.999991e-01 9.415752e-07  
## [88,] 9.999998e-01 2.153612e-07  
## [89,] 9.999999e-01 8.377734e-08  
## [90,] 9.999998e-01 2.160362e-07  
## [91,] 9.999991e-01 9.415752e-07  
## [92,] 1.000000e+00 4.724254e-08  
## [93,] 9.999998e-01 1.692162e-07  
## [94,] 9.999999e-01 8.377734e-08  
## [95,] 9.999999e-01 9.700391e-08  
## [96,] 9.999974e-01 2.593893e-06  
## [97,] 1.577849e-13 1.000000e+00  
## [98,] 2.459229e-12 1.000000e+00  
## [99,] 9.865171e-09 1.000000e+00  
## [100,] 9.732847e-01 2.671526e-02  
## [101,] 9.999984e-01 1.619002e-06  
## [102,] 2.524970e-01 7.475030e-01  
## [103,] 4.591481e-16 1.000000e+00  
## [104,] 1.834799e-01 8.165201e-01  
## [105,] 8.368023e-14 1.000000e+00  
## [106,] 9.522309e-11 1.000000e+00  
## [107,] 9.999998e-01 1.746342e-07  
## [108,] 2.280536e-07 9.999998e-01  
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## [547,] 9.999974e-01 2.593893e-06  
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## [682,] 8.128896e-06 9.999919e-01  
## [683,] 5.838489e-07 9.999994e-01

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

## 'data.frame': 683 obs. of 6 variables:  
## $ myrf.pred : num 0 0 0 0 0 1 0 0 0 0 ...  
## $ myrda.pred.class: num 0 1 0 1 0 1 0 0 0 0 ...  
## $ mytree.pred : num 1 1 1 1 1 1 1 1 1 1 ...  
## $ mynnet.pred : 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 : num 0 1 0 1 0 1 0 0 0 0 ...

combine.classes$wwcd<- rowSums(combine.classes)  
combine.classes$mv <- ifelse(combine.classes$wwcd >= 3, 'Malignant', 'Benign')  
table(combine.classes$mv, BreastCancer$Class)

##   
## benign malignant  
## Benign 429 0  
## Malignant 15 239