Breast Cancer\_Classification model

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##Loading the BreastCancer dataset from mlbench  
  
require(mlbench)

## Loading required package: mlbench

data(BreastCancer)

##Removing null values in the dataset  
library(mice)

##   
## Attaching package: 'mice'

## The following object is masked from 'package:stats':  
##   
## filter

## The following objects are masked from 'package:base':  
##   
## cbind, rbind

dataset\_impute <- mice(BreastCancer[,2:10], print = FALSE)  
  
BreastCancer <- cbind(BreastCancer[,11, drop = FALSE], mice::complete(dataset\_impute, 1))

##SVM Model  
  
head(BreastCancer)

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

library(e1071)  
mysvm <- svm(Class ~ ., BreastCancer)  
mysvm.pred <- predict(mysvm, BreastCancer)  
table(mysvm.pred,BreastCancer$Class)

##   
## mysvm.pred benign malignant  
## benign 443 8  
## malignant 15 233

#Naive Bayes classification model  
library(klaR)

## Loading required package: MASS

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

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## observation 699

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

##   
## benign malignant  
## benign 443 3  
## malignant 15 238

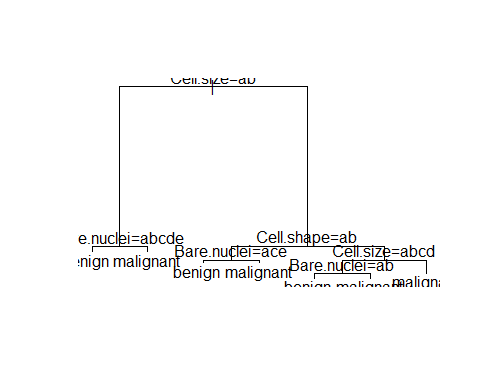
##Neural Network model  
library(nnet)  
mynnet <- nnet(Class ~ ., BreastCancer, size=1)

## # weights: 83  
## initial value 450.259724   
## iter 10 value 110.877224  
## iter 20 value 70.252038  
## iter 30 value 46.153866  
## iter 40 value 31.780288  
## iter 50 value 31.588084  
## iter 60 value 31.545589  
## iter 70 value 31.534510  
## iter 80 value 31.529715  
## iter 90 value 31.527594  
## iter 100 value 31.524918  
## final value 31.524918   
## stopped after 100 iterations

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

##   
## mynnet.pred benign malignant  
## benign 453 1  
## malignant 5 240

library(MASS)  
  
#Decision trees  
library(rpart)  
mytree <- rpart(Class ~ ., BreastCancer)  
plot(mytree); text(mytree) # in "iris\_tree.ps"



summary(mytree)

## Call:  
## rpart(formula = Class ~ ., data = BreastCancer)  
## n= 699   
##   
## CP nsplit rel error xerror xstd  
## 1 0.78008299 0 1.0000000 1.0000000 0.05214175  
## 2 0.05394191 1 0.2199170 0.2738589 0.03207881  
## 3 0.02489627 2 0.1659751 0.1867220 0.02692399  
## 4 0.01244813 3 0.1410788 0.1825726 0.02664351  
## 5 0.01000000 6 0.1037344 0.1618257 0.02517959  
##   
## Variable importance  
## Cell.size Cell.shape Bare.nuclei Epith.c.size Normal.nucleoli   
## 21 18 16 15 15   
## Bl.cromatin Cl.thickness   
## 15 1   
##   
## Node number 1: 699 observations, complexity param=0.780083  
## predicted class=benign expected loss=0.3447783 P(node) =1  
## class counts: 458 241  
## probabilities: 0.655 0.345   
## left son=2 (429 obs) right son=3 (270 obs)  
## Primary splits:  
## Cell.size splits as LLRRRRRRRR, improve=222.9401, (0 missing)  
## Cell.shape splits as LLLRRRRRRR, improve=216.3834, (0 missing)  
## Bare.nuclei splits as LLRRRRRRRR, improve=202.5616, (0 missing)  
## Bl.cromatin splits as LLLRRRRRRR, improve=197.9057, (0 missing)  
## Epith.c.size splits as LLRRRRRRRR, improve=190.5300, (0 missing)  
## Surrogate splits:  
## Cell.shape splits as LLLRRRRRRR, agree=0.916, adj=0.781, (0 split)  
## Epith.c.size splits as LLRRRRRRRR, agree=0.897, adj=0.733, (0 split)  
## Bare.nuclei splits as LLRRRRRRRR, agree=0.881, adj=0.693, (0 split)  
## Normal.nucleoli splits as LLRRRRRRRR, agree=0.880, adj=0.689, (0 split)  
## Bl.cromatin splits as LLLRRRRRRR, agree=0.877, adj=0.681, (0 split)  
##   
## Node number 2: 429 observations, complexity param=0.02489627  
## predicted class=benign expected loss=0.02797203 P(node) =0.6137339  
## class counts: 417 12  
## probabilities: 0.972 0.028   
## left son=4 (421 obs) right son=5 (8 obs)  
## Primary splits:  
## Bare.nuclei splits as LLLLLRRR-R, improve=11.697440, (0 missing)  
## Normal.nucleoli splits as LLLR-RRL-R, improve=11.697440, (0 missing)  
## Cl.thickness splits as LLLLLLRRRR, improve=10.336610, (0 missing)  
## Bl.cromatin splits as LLLLR-R---, improve= 8.548637, (0 missing)  
## Epith.c.size splits as LLLRRRRRRR, improve= 4.645022, (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=0.984, adj=0.125, (0 split)  
##   
## Node number 3: 270 observations, complexity param=0.05394191  
## predicted class=malignant expected loss=0.1518519 P(node) =0.3862661  
## class counts: 41 229  
## probabilities: 0.152 0.848   
## left son=6 (23 obs) right son=7 (247 obs)  
## Primary splits:  
## Cell.shape splits as LLRRRRRRRR, improve=20.00546, (0 missing)  
## Cell.size splits as LLLRRRRRRR, improve=17.38477, (0 missing)  
## Bare.nuclei splits as LRRRRRRRRR, improve=16.15240, (0 missing)  
## Bl.cromatin splits as LLRRRRRRRR, improve=14.86975, (0 missing)  
## Marg.adhesion splits as LLRRRRRRRR, improve=10.74334, (0 missing)  
## Surrogate splits:  
## Bl.cromatin splits as LRRRRRRRRR, agree=0.933, adj=0.217, (0 split)  
##   
## Node number 4: 421 observations  
## predicted class=benign expected loss=0.01187648 P(node) =0.602289  
## class counts: 416 5  
## probabilities: 0.988 0.012   
##   
## Node number 5: 8 observations  
## predicted class=malignant expected loss=0.125 P(node) =0.01144492  
## class counts: 1 7  
## probabilities: 0.125 0.875   
##   
## Node number 6: 23 observations, complexity param=0.01244813  
## predicted class=benign expected loss=0.2173913 P(node) =0.03290415  
## 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: 247 observations, complexity param=0.01244813  
## predicted class=malignant expected loss=0.09311741 P(node) =0.3533619  
## class counts: 23 224  
## probabilities: 0.093 0.907   
## left son=14 (70 obs) right son=15 (177 obs)  
## Primary splits:  
## Cell.size splits as LLLLRRRRRR, improve=5.256228, (0 missing)  
## Bare.nuclei splits as LLLRRLRRRR, improve=4.085830, (0 missing)  
## Cl.thickness splits as LLLLLLRRRR, improve=3.391429, (0 missing)  
## Bl.cromatin splits as LLLLRRRRRR, improve=3.313954, (0 missing)  
## Cell.shape splits as LLLLRRRRRR, improve=3.116243, (0 missing)  
## Surrogate splits:  
## Cell.shape splits as LLLLRRRRRR, agree=0.789, adj=0.257, (0 split)  
## Epith.c.size splits as LLRRRRRRRR, agree=0.777, adj=0.214, (0 split)  
## Marg.adhesion splits as LRRRRRRRRR, agree=0.745, adj=0.100, (0 split)  
## Bl.cromatin splits as LLRRRRRRRR, agree=0.737, adj=0.071, (0 split)  
## Normal.nucleoli splits as RRLRRRRRRR, agree=0.725, adj=0.029, (0 split)  
##   
## Node number 12: 16 observations  
## predicted class=benign expected loss=0 P(node) =0.02288984  
## class counts: 16 0  
## probabilities: 1.000 0.000   
##   
## Node number 13: 7 observations  
## predicted class=malignant expected loss=0.2857143 P(node) =0.01001431  
## class counts: 2 5  
## probabilities: 0.286 0.714   
##   
## Node number 14: 70 observations, complexity param=0.01244813  
## predicted class=malignant expected loss=0.2571429 P(node) =0.1001431  
## class counts: 18 52  
## probabilities: 0.257 0.743   
## left son=28 (14 obs) right son=29 (56 obs)  
## Primary splits:  
## Bare.nuclei splits as LLRRR-RRRR, improve=7.314286, (0 missing)  
## Cl.thickness splits as LLLLLLRRRR, improve=4.114286, (0 missing)  
## Marg.adhesion splits as LLLLLRRRRR, improve=2.742857, (0 missing)  
## Normal.nucleoli splits as LLRRRLLLRR, improve=2.621147, (0 missing)  
## Bl.cromatin splits as LLLRRRRR-R, improve=1.984890, (0 missing)  
##   
## Node number 15: 177 observations  
## predicted class=malignant expected loss=0.02824859 P(node) =0.2532189  
## class counts: 5 172  
## probabilities: 0.028 0.972   
##   
## Node number 28: 14 observations  
## predicted class=benign expected loss=0.2857143 P(node) =0.02002861  
## class counts: 10 4  
## probabilities: 0.714 0.286   
##   
## Node number 29: 56 observations  
## predicted class=malignant expected loss=0.1428571 P(node) =0.08011445  
## class counts: 8 48  
## probabilities: 0.143 0.857

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

##   
## mytree.pred benign malignant  
## benign 442 9  
## malignant 16 232

# 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 437 22  
## malignant 21 219

#Quadratic Discriminant Analysis  
  
library(MASS)  
df<-BreastCancer  
df2<-df  
#convert to integers   
  
df2$Cl.thickness<-as.integer(df$Cl.thickness)  
df2$Mitoses<-as.integer(df$Mitoses)  
df2$Cell.size<-as.integer(df$Cell.size)  
df2$Cell.shape<-as.integer(df$Cell.shape)  
df2$Marg.adhesion<-as.integer(df$Marg.adhesion)  
df2$Epith.c.size<-as.integer(df$Epith.c.size)  
df2$Bare.nuclei<-as.integer(df$Bare.nuclei)  
df2$Bl.cromatin<-as.integer(df$Bl.cromatin)  
df2$Normal.nucleoli<-as.integer(df$Normal.nucleoli)  
  
head(df2)

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

myqda <- qda(Class ~ ., data=df2)  
myqda.pred <- predict(myqda, df2)  
table(myqda.pred$class,df2$Class)

##   
## benign malignant  
## benign 435 6  
## malignant 23 235

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

##   
## benign malignant  
## benign 445 3  
## malignant 13 238

#Random Forests  
  
library(randomForest)

## randomForest 4.6-14

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

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

##   
## myrf.pred benign malignant  
## benign 458 0  
## malignant 0 241

#The majority vote Ensemble approach   
  
finalPred <-as.factor(ifelse(myrf.pred=='benign' & myrda.pred =='benign','benign',ifelse(myrf.pred=='benign' & myqda.pred=='benign','benign',ifelse(myrda.pred=='benign' & myqda.pred=='benign','benign','malignant'))))

## Warning in myrf.pred == "benign" & myrda.pred == "benign": longer object length  
## is not a multiple of shorter object length

## Warning in myrf.pred == "benign" & myqda.pred == "benign": longer object length  
## is not a multiple of shorter object length

finalPred

## [1] malignant malignant malignant malignant malignant malignant malignant  
## [8] malignant malignant malignant malignant malignant malignant malignant  
## [15] malignant malignant malignant malignant malignant malignant malignant  
## [22] malignant malignant malignant malignant malignant malignant malignant  
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## Levels: malignant