Project Two – Breast Cancer Dataset

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#load the mlbench package which has the BreastCancer data set  
#install.packages("mlbench")  
require(mlbench)

## Loading required package: mlbench

## Warning: package 'mlbench' was built under R version 4.0.5

# if you don't have any required package, use the install.packages() command  
# load the data set  
data(BreastCancer)  
# 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  
mydata <- BreastCancer  
df <-BreastCancer

# SVM Prediction

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

mysvm

##   
## Call:  
## svm(formula = Class ~ ., data = BreastCancer)  
##   
##   
## Parameters:  
## SVM-Type: C-classification   
## SVM-Kernel: radial   
## cost: 1   
##   
## Number of Support Vectors: 174

mysvm.pred

## 1 2 3 4 5 6 7 8   
## benign malignant benign malignant benign malignant benign benign   
## 9 10 11 12 13 14 15 16   
## benign benign benign benign benign benign malignant malignant   
## 17 18 19 20 21 22 23 25   
## benign benign malignant benign malignant malignant benign benign   
## 26 27 28 29 30 31 32 33   
## benign benign benign benign benign benign benign malignant   
## 34 35 36 37 38 39 40 42   
## benign benign benign malignant benign malignant malignant malignant   
## 43 44 45 46 47 48 49 50   
## malignant malignant malignant benign malignant benign benign malignant   
## 51 52 53 54 55 56 57 58   
## malignant benign malignant malignant malignant malignant malignant malignant   
## 59 60 61 62 63 64 65 66   
## malignant malignant malignant benign malignant malignant benign malignant   
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## malignant benign benign benign benign benign benign benign   
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## benign benign malignant malignant malignant malignant benign benign   
## 91 92 93 94 95 96 97 98   
## benign benign benign benign benign benign benign benign   
## 99 100 101 102 103 104 105 106   
## malignant malignant malignant benign benign malignant malignant malignant   
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## malignant malignant malignant benign malignant benign malignant benign   
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## benign benign malignant benign benign benign benign benign   
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## benign benign benign malignant benign benign malignant benign   
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## benign malignant malignant malignant malignant malignant benign malignant   
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## malignant benign malignant malignant benign malignant benign benign   
## 327 328 329 330 331 332 333 334   
## benign benign malignant malignant malignant benign benign malignant   
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## malignant malignant benign benign benign benign benign benign   
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## benign benign benign benign malignant benign benign benign   
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## benign malignant benign benign benign benign benign benign   
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## benign benign benign benign benign malignant benign malignant   
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## benign malignant benign benign benign benign malignant benign   
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## benign benign benign malignant malignant malignant benign benign   
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## benign malignant benign benign benign benign benign benign   
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## benign benign malignant benign benign benign malignant benign   
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## benign malignant malignant benign benign benign benign benign   
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## benign benign malignant malignant malignant benign benign benign   
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## benign benign benign benign benign benign benign benign   
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## malignant benign benign malignant malignant benign benign benign   
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## malignant malignant benign benign malignant benign malignant benign   
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## benign benign benign benign benign benign malignant malignant   
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## benign benign benign malignant benign malignant benign malignant   
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## malignant malignant benign malignant benign benign benign benign   
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## benign benign benign benign malignant malignant malignant benign   
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## benign malignant benign malignant malignant malignant benign benign   
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## benign benign malignant benign benign benign benign benign   
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## benign malignant benign benign malignant benign benign benign   
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## benign benign benign benign benign benign benign benign   
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## malignant benign benign benign benign benign benign benign   
## 657 658 659 660 661 662 663 664   
## benign malignant malignant benign benign benign benign benign   
## 665 666 667 668 669 670 671 672   
## benign benign benign benign malignant malignant malignant benign   
## 673 674 675 676 677 678 679 680   
## benign benign benign benign benign benign benign benign   
## 681 682 683 684 685 686 687 688   
## malignant malignant benign benign benign benign benign benign   
## 689 690 691 692 693 694 695 696   
## benign benign benign malignant benign benign benign benign   
## 697 698 699   
## malignant malignant malignant   
## Levels: benign malignant

# NaiveBayes Prediction

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

## Warning: package 'klaR' was built under R version 4.0.5

## 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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## observation 681

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 682

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

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

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

# Neural Net Prediction

library(nnet)  
mynnet <- nnet(Class ~ ., BreastCancer, size=1)

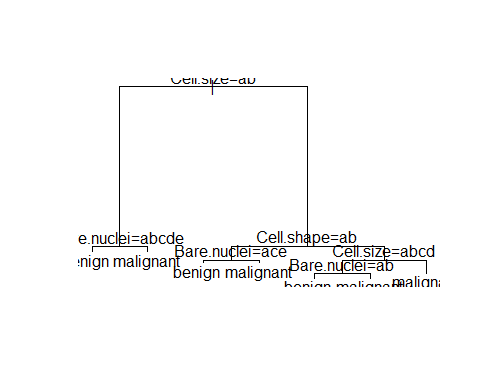
## # weights: 83  
## initial value 475.770629   
## iter 10 value 143.917142  
## iter 20 value 65.311421  
## iter 30 value 42.822426  
## iter 40 value 38.983580  
## iter 50 value 35.287080  
## iter 60 value 35.251944  
## iter 70 value 35.228132  
## iter 80 value 31.861248  
## iter 90 value 31.494387  
## iter 100 value 31.469196  
## final value 31.469196   
## stopped after 100 iterations

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

##   
## mynnet.pred benign malignant  
## benign 439 1  
## malignant 5 238

# Decision tree Prediction

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



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 0.2384937 0.03024241  
## 3 0.02510460 2 0.15481172 0.1673640 0.02567599  
## 4 0.01255230 3 0.12970711 0.1464435 0.02411089  
## 5 0.01000000 6 0.09205021 0.1297071 0.02276126  
##   
## 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

# Leave-1-Out Cross Validation (LOOCV) Prediction

# 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

# The same as above in this case

# Quadratic Discriminant Analysis Prediction

df2<-df  
#convert to integers #There are better ways to do this conversion  
df2$Cl.thickness<-as.integer(df$Cl.thickness)  
df2$Class<-ifelse(as.integer(df$Class)==2,1,0) #I had Class converted to a dummy variable  
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)  
  
myqda <- qda(Class ~ ., data=df2)  
myqda.pred <- predict(myqda, df2)  
table(myqda.pred$class,df2$Class)

##   
## 0 1  
## 0 422 6  
## 1 22 233

# Regularised Discriminant Analysis (RDA) Prediction

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

##   
## benign malignant  
## benign 433 3  
## malignant 11 236

# Random Forests Prediction

#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 444 0  
## malignant 0 239

# Combination of Classifiers Prediction

combine.classes<-data.frame(myrf.pred, myrda.pred$class,mytree.pred,mynnet.pred,mysvm.pred,mynb.pred$class)  
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)  
majority.vote=rowSums(combine.classes)  
combine.classes[,7]<-rowSums(combine.classes)  
combine.classes[,8]<-ifelse(combine.classes[,7]>=4, "malignant", "benign")  
table(combine.classes[,8], BreastCancer$Class)

##   
## benign malignant  
## benign 433 3  
## malignant 11 236