Project 2

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#Install Packages

#install.packages("caret")  
#install.packages("e1071")  
#install.packages("klaR")  
#install.packages("nnet")  
#install.packages("MASS")  
#install.packages("rpart")  
#install.packages("randomForest")  
#install.packages("mlbench")

Library Packages

library(tidyverse)

## -- Attaching packages ------------------------------------------------------------------------------------------------------------------------ tidyverse 1.3.0 --

## v ggplot2 3.3.2 v purrr 0.3.4  
## v tibble 3.0.3 v dplyr 1.0.2  
## v tidyr 1.1.2 v stringr 1.4.0  
## v readr 1.3.1 v forcats 0.5.0

## -- Conflicts --------------------------------------------------------------------------------------------------------------------------- tidyverse\_conflicts() --  
## x dplyr::filter() masks stats::filter()  
## x dplyr::lag() masks stats::lag()

library(readxl)  
library(ggplot2)  
library(gplots)

## Warning: package 'gplots' was built under R version 4.0.3

##   
## Attaching package: 'gplots'

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

library(caret)

## Warning: package 'caret' was built under R version 4.0.4

## Loading required package: lattice

##   
## Attaching package: 'caret'

## The following object is masked from 'package:purrr':  
##   
## lift

library(e1071)

## Warning: package 'e1071' was built under R version 4.0.4

library(rpart)

## Warning: package 'rpart' was built under R version 4.0.4

library(randomForest)

## Warning: package 'randomForest' was built under R version 4.0.4

## randomForest 4.6-14

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

##   
## Attaching package: 'randomForest'

## The following object is masked from 'package:dplyr':  
##   
## combine

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

library(klaR)

## Warning: package 'klaR' was built under R version 4.0.3

## Loading required package: MASS

##   
## Attaching package: 'MASS'

## The following object is masked from 'package:dplyr':  
##   
## select

library(nnet)  
library(MASS)  
library(rpart)  
library(mlbench)

## Warning: package 'mlbench' was built under R version 4.0.4

#Load Data

data(BreastCancer)  
colnames(BreastCancer)

## [1] "Id" "Cl.thickness" "Cell.size" "Cell.shape"   
## [5] "Marg.adhesion" "Epith.c.size" "Bare.nuclei" "Bl.cromatin"   
## [9] "Normal.nucleoli" "Mitoses" "Class"

BreastCancer<-na.omit(BreastCancer)  
BreastCancer$Id <- NULL  
mydata <- BreastCancer  
str(mydata)

## '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" ...

summary(mydata)

## Cl.thickness Cell.size Cell.shape Marg.adhesion Epith.c.size  
## 1 :139 1 :373 1 :346 1 :393 2 :376   
## 5 :128 10 : 67 2 : 58 2 : 58 3 : 71   
## 3 :104 3 : 52 10 : 58 3 : 58 4 : 48   
## 4 : 79 2 : 45 3 : 53 10 : 55 1 : 44   
## 10 : 69 4 : 38 4 : 43 4 : 33 6 : 40   
## 2 : 50 5 : 30 5 : 32 8 : 25 5 : 39   
## (Other):114 (Other): 78 (Other): 93 (Other): 61 (Other): 65   
## Bare.nuclei Bl.cromatin Normal.nucleoli Mitoses Class   
## 1 :402 3 :161 1 :432 1 :563 benign :444   
## 10 :132 2 :160 10 : 60 2 : 35 malignant:239   
## 2 : 30 1 :150 3 : 42 3 : 33   
## 5 : 30 7 : 71 2 : 36 10 : 14   
## 3 : 28 4 : 39 8 : 23 4 : 12   
## 8 : 21 5 : 34 6 : 22 7 : 9   
## (Other): 40 (Other): 68 (Other): 68 (Other): 17

mysvm <- svm(Class ~ ., mydata)  
mysvm.pred <- predict(mysvm, mydata)  
table(mysvm.pred,mydata$Class)

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

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

## 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

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

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

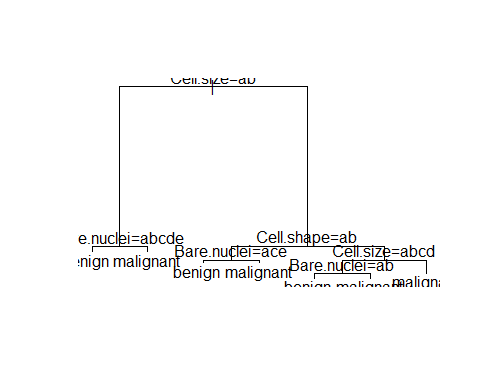
mynnet <- nnet(Class ~ ., mydata, size=1)

## # weights: 83  
## initial value 485.518671   
## iter 10 value 58.344725  
## iter 20 value 28.410335  
## iter 30 value 23.316778  
## iter 40 value 20.832106  
## iter 50 value 19.384374  
## iter 60 value 18.964360  
## iter 70 value 18.749391  
## iter 80 value 18.680738  
## iter 90 value 18.665486  
## iter 100 value 18.660076  
## final value 18.660076   
## stopped after 100 iterations

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

##   
## mynnet.pred benign malignant  
## benign 442 1  
## malignant 2 238

mytree <- rpart(Class ~ ., mydata)  
plot(mytree); text(mytree) # in "mydata\_tree.ps"



summary(mytree)

## Call:  
## rpart(formula = Class ~ ., data = mydata)  
## n= 683   
##   
## CP nsplit rel error xerror xstd  
## 1 0.79079498 0 1.00000000 1.0000000 0.05215335  
## 2 0.05439331 1 0.20920502 0.2468619 0.03071921  
## 3 0.02510460 2 0.15481172 0.1882845 0.02712741  
## 4 0.01255230 3 0.12970711 0.1589958 0.02506475  
## 5 0.01000000 6 0.09205021 0.1548117 0.02475192  
##   
## Variable importance  
## Cell.size Cell.shape Bare.nuclei Epith.c.size Bl.cromatin   
## 21 18 16 15 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,mydata,type="class")  
table(mytree.pred,mydata$Class)

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

# Leave-1-Out Cross Validation (LOOCV)

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

#Quadratic Discriminant Analysis

#myqda <- qda(Class ~ ., mydata)  
#myqda.pred <- predict(myqda, mydata)  
#table(myqda.pred$class,mydata$Class)

#Regularised Discriminant Analysis

myrda <- rda(Class ~ ., mydata)  
myrda.pred <- predict(myrda, mydata)  
table(myrda.pred$class,mydata$Class)

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

#Random Forests

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

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

classifier1<- c(0,1,0,1, 0)  
classifier2<-c(0,0,0,1,0)  
classifier3<-c(0,0,0,1,0)  
classifier4<-c(0,0,0,1,0)  
classifier5<-c(0,0,0,1,0)  
combine.df<-cbind(classifier1, classifier2, classifier3, classifier4, classifier5)

head(myrf.pred)

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

head(mysvm.pred)

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

classifier1<-myrf.pred  
classifier2<-mysvm.pred  
classifier3<-myrda.pred$class  
classifier4<-mytree.pred  
classifier5<-mynb.pred$class  
classifier6<-mynnet.pred  
combine.df<-data.frame(classifier1, classifier2, classifier3, classifier4, classifier5, classifier6)  
head(combine.df)

## classifier1 classifier2 classifier3 classifier4 classifier5 classifier6  
## 1 benign benign benign benign benign benign  
## 2 benign malignant malignant malignant malignant benign  
## 3 benign benign benign benign benign benign  
## 4 benign malignant malignant malignant malignant benign  
## 5 benign benign benign benign benign benign  
## 6 malignant malignant malignant malignant malignant malignant

combine.df[,1]<-ifelse(combine.df[,1]=="benign",0,1)  
combine.df[,2]<-ifelse(combine.df[,2]=="benign",0,1)  
combine.df[,3]<-ifelse(combine.df[,3]=="benign",0,1)  
combine.df[,4]<-ifelse(combine.df[,4]=="benign",0,1)  
combine.df[,5]<-ifelse(combine.df[,5]=="benign",0,1)  
combine.df[,6]<-ifelse(combine.df[,6]=="benign",0,1)  
  
# Checking  
head(combine.df)

## classifier1 classifier2 classifier3 classifier4 classifier5 classifier6  
## 1 0 0 0 0 0 0  
## 2 0 1 1 1 1 0  
## 3 0 0 0 0 0 0  
## 4 0 1 1 1 1 0  
## 5 0 0 0 0 0 0  
## 6 1 1 1 1 1 1

#combine.df[,7]<-NULL

#combine.df[,7]<-rowSums(combine.df)  
  
combine.df[,7]<- ifelse(rowSums(combine.df)>=4,"malignant","benign")  
head(combine.df)

## classifier1 classifier2 classifier3 classifier4 classifier5 classifier6  
## 1 0 0 0 0 0 0  
## 2 0 1 1 1 1 0  
## 3 0 0 0 0 0 0  
## 4 0 1 1 1 1 0  
## 5 0 0 0 0 0 0  
## 6 1 1 1 1 1 1  
## V7  
## 1 benign  
## 2 malignant  
## 3 benign  
## 4 malignant  
## 5 benign  
## 6 malignant

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

##   
## benign malignant  
## benign 435 2  
## malignant 9 237