Project 2

Dakotah Rector

3/14/2021

library(e1071)  
library(klaR)

## Loading required package: MASS

library(nnet)  
library(MASS)  
library(rpart)  
library(rpart.plot)  
library(randomForest)

## randomForest 4.6-14

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

library(mlbench)  
library(VIM)

## Loading required package: colorspace

## Loading required package: grid

## VIM is ready to use.

## Suggestions and bug-reports can be submitted at: https://github.com/statistikat/VIM/issues

##   
## Attaching package: 'VIM'

## The following object is masked from 'package:datasets':  
##   
## sleep

library(tidyverse)

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

## v ggplot2 3.3.3 v purrr 0.3.4  
## v tibble 3.0.6 v dplyr 1.0.4  
## v tidyr 1.1.2 v stringr 1.4.0  
## v readr 1.4.0 v forcats 0.5.1

## -- Conflicts ------------------------------------------ tidyverse\_conflicts() --  
## x dplyr::combine() masks randomForest::combine()  
## x dplyr::filter() masks stats::filter()  
## x dplyr::lag() masks stats::lag()  
## x ggplot2::margin() masks randomForest::margin()  
## x dplyr::select() masks MASS::select()

library(caret)

## Loading required package: lattice

##   
## Attaching package: 'caret'

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

Load the Data & remove the ID column

data("BreastCancer")  
# remove the Id column  
BreastCancer$Id <- NULL   
BreastCancer <- na.omit(BreastCancer)  
BC.df <- BreastCancer  
summary(BC.df)

## 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

# many of these columns need to be converted into numeric  
str(BC.df)

## '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" ...

BC.df$Cl.thickness<-as.numeric(BC.df$Cl.thickness)  
BC.df$Mitoses<-as.numeric(BC.df$Mitoses)  
BC.df$Cell.size<-as.numeric(BC.df$Cell.size)  
BC.df$Cell.shape<-as.numeric(BC.df$Cell.shape)  
BC.df$Marg.adhesion<-as.numeric(BC.df$Marg.adhesion)  
BC.df$Epith.c.size<-as.numeric(BC.df$Epith.c.size)  
BC.df$Bare.nuclei<-as.numeric(BC.df$Bare.nuclei)  
BC.df$Bl.cromatin<-as.numeric(BC.df$Bl.cromatin)  
BC.df$Normal.nucleoli<-as.numeric(BC.df$Normal.nucleoli)  
  
# convert Class to malignant = 1 and benign = 0  
BC.df$Class <-ifelse(BC.df$Class =="malignant",1,0)  
BC.df$Class <- as.factor(BC.df$Class)  
  
str(BC.df)

## 'data.frame': 683 obs. of 10 variables:  
## $ Cl.thickness : num 5 5 3 6 4 8 1 2 2 4 ...  
## $ Cell.size : num 1 4 1 8 1 10 1 1 1 2 ...  
## $ Cell.shape : num 1 4 1 8 1 10 1 2 1 1 ...  
## $ Marg.adhesion : num 1 5 1 1 3 8 1 1 1 1 ...  
## $ Epith.c.size : num 2 7 2 3 2 7 2 2 2 2 ...  
## $ Bare.nuclei : num 1 10 2 4 1 10 10 1 1 1 ...  
## $ Bl.cromatin : num 3 3 3 3 3 9 3 3 1 2 ...  
## $ Normal.nucleoli: num 1 2 1 7 1 7 1 1 1 1 ...  
## $ Mitoses : num 1 1 1 1 1 1 1 1 5 1 ...  
## $ Class : Factor w/ 2 levels "0","1": 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" ...

View(BC.df)

Support vector machine

BC.svm <- svm(Class ~ ., BC.df)  
BC.svm.pred <- predict(BC.svm, BC.df)  
table(BC.svm.pred, BC.df$Class)

##   
## BC.svm.pred 0 1  
## 0 433 5  
## 1 11 234

Naive Bayes classifier

BC.nb <- NaiveBayes(Class ~ ., BC.df)  
BC.nb.pred <- predict(BC.nb,BC.df)

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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 501

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 505

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 508

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 509

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 516

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 532

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 535

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 539

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 541

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 551

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 554

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 555

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 556

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 557

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 560

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 567

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 568

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 570

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 572

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 574

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 576

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 577

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 578

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 580

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 589

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 590

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 591

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 594

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 596

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 597

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 598

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 606

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 611

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 618

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 621

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 633

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 642

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 643

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 653

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 654

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 655

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 665

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 666

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 674

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 676

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## 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(BC.nb.pred$class,BC.df$Class)

##   
## 0 1  
## 0 424 5  
## 1 20 234

Neural Network

#set.seed(1)  
BC.nnet <- nnet(Class ~ ., BC.df, size=1)

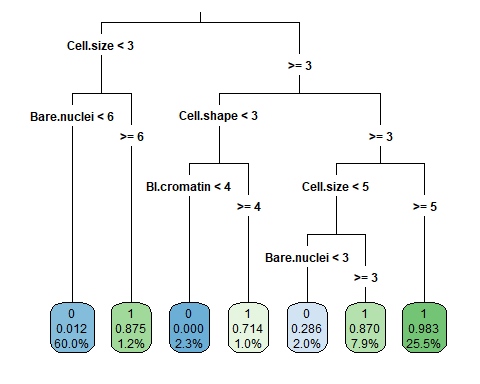
## # weights: 12  
## initial value 459.760992   
## iter 10 value 351.267393  
## iter 20 value 144.614019  
## iter 30 value 118.877352  
## iter 40 value 110.522426  
## iter 50 value 76.964969  
## iter 60 value 55.212186  
## iter 70 value 51.229480  
## iter 80 value 50.255645  
## iter 90 value 49.992151  
## iter 100 value 48.762850  
## final value 48.762850   
## stopped after 100 iterations

BC.nnet.pred <- predict(BC.nnet,BC.df,type="class")  
table(BC.nnet.pred,BC.df$Class)

##   
## BC.nnet.pred 0 1  
## 0 432 1  
## 1 12 238

Decision trees

BC.tree <- rpart(Class ~ ., BC.df)  
rpart.plot(BC.tree, type=3, digits = 3, fallen.leaves = TRUE)



BC.tree.pred <- predict(BC.tree,BC.df,type="class")  
table(BC.tree.pred,BC.df$Class)

##   
## BC.tree.pred 0 1  
## 0 431 9  
## 1 13 230

Leave-1-Out Cross Validation (LOOCV)

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

##   
## ans 0 1  
## 0 431 24  
## 1 13 215

Quadratic Discriminant Analysis

BC.qda <- qda(Class ~ ., BC.df)  
BC.qda.pred <- predict(BC.qda, BC.df)  
table(BC.qda.pred$class,BC.df$Class)

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

Regularised Discriminant Analysis

BC.rda <- rda(Class ~ ., BC.df)  
BC.rda.pred <- predict(BC.rda, BC.df)  
table(BC.rda.pred$class,BC.df$Class)

##   
## 0 1  
## 0 433 8  
## 1 11 231

Random Forests

BC.rf <- randomForest(Class ~ .,BC.df)  
BC.rf.pred <- predict(BC.rf, BC.df)  
table(BC.rf.pred, BC.df$Class)

##   
## BC.rf.pred 0 1  
## 0 444 0  
## 1 0 239

Creating the Ensemble

combine.classes<-data.frame(BC.rf.pred, BC.rda.pred$class,BC.qda.pred,  
BC.tree.pred,BC.nnet.pred,BC.svm.pred, BC.nb.pred$class)  
#head(combine.classes)  
#head(BC.rf.pred)  
#head(BC.rda.pred)  
combine.classes$BC.rf.pred<-ifelse(combine.classes$BC.rf.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)  
combine.classes$BC.nnet.pred <- as.numeric(combine.classes$BC.nnet.pred)  
combine.classes$BC.svm.pred <- as.numeric(combine.classes$BC.svm.pred)  
combine.classes$BC.nb.pred.class <- as.numeric(combine.classes$BC.nb.pred.class)  
  
majority.vote = rowSums(combine.classes)  
#head(majority.vote)  
  
combine.classes[,7]<-rowSums(combine.classes)  
combine.classes[,8]<-ifelse(combine.classes[,7]>=4, "malignant", "benign")  
table(combine.classes[,8], BreastCancer$Class)

##   
## benign malignant  
## malignant 444 239