Project2

2023-03-21

#load the mlbench package which has the BreastCancer data set install.packages(‘mlbench’) require(mlbench) # if you don’t have any required package, use the install.packages() command # load the data set data(BreastCancer)

mydata <- cbind(BreastCancer[5],BreastCancer[1:4]) head(BreastCancer) #Id Cl.thickness Cell.size Cell.shape Marg.adhesion Epith.c.size #1 1000025 5 1 1 1 2 #2 1002945 5 4 4 5 7 #3 1015425 3 1 1 1 2 #4 1016277 6 8 8 1 3 #5 1017023 4 1 1 3 2 #6 1017122 8 10 10 8 7 #Bare.nuclei Bl.cromatin Normal.nucleoli Mitoses Class #1 1 3 1 1 benign #2 10 3 2 1 benign #3 2 3 1 1 benign #4 4 3 7 1 benign #5 1 3 1 1 benign #6 10 9 7 1 malignant library(e1071)

install.packages(“klaR”)

library(klaR) mynb <- NaiveBayes(Class ~ ., BreastCancer) mynb.pred <- predict(mynb, BreastCancer) table(mynb.predClass)

#benign malignant #benign 443 2 #malignant 15 239

library(nnet) mynnet <- nnet(Class ~ ., BreastCancer, size=1) mynnet.pred <- predict(mynnet,BreastCancer,type=“class”) table(mynnet.pred,BreastCancer$Class)

# weights: 712

#initial value 473.466909 #iter 10 value 88.200941 #iter 20 value 82.608418 #iter 30 value 78.436176 #iter 40 value 78.203689 #iter 50 value 70.797846 #iter 60 value 65.896378 #iter 70 value 61.456267 #iter 80 value 61.311028 #iter 90 value 61.308693 #iter 100 value 61.306768 #final value 61.306768 #stopped after 100 iterations

#mynnet.pred benign malignant #benign 435 4 #malignant 9 235

#Decision trees library(rpart) mytree <- rpart(Class ~ ., BreastCancer) plot(mytree); text(mytree) # in “iris\_tree.ps” summary(mytree) mytree.pred <- predict(mytree,BreastCancer,type=“class”) table(mytree.pred,BreastCancer$Class)

#mytree.pred benign malignant #benign 455 1 #malignant 3 240

# mytree <- rpart(Class ~ ., BreastCancer[-i,])

#mytree.pred <- predict(mytree,BreastCancer[i,],type=“class”) #ans[i] <- mytree.pred

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

#Random Forests library(randomForest) myrf <- randomForest(Class ~ .,BreastCancer) myrf.pred <- predict(myrf, BreastCancer) table(myrf.pred, BreastCancer$Class)

combine.df <- c(mynb.pred, mynnet.pred, mytree.pred, myrda.pred) combine.df