Iris\_multipleClassifier

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#SVM  
  
data(iris)  
mydata <- cbind(iris[5],iris[1:4])   
  
library(e1071)  
mysvm <- svm(Species ~ ., iris)  
mysvm.pred <- predict(mysvm, iris)  
table(mysvm.pred,iris$Species)

##   
## mysvm.pred setosa versicolor virginica  
## setosa 50 0 0  
## versicolor 0 48 2  
## virginica 0 2 48

#Naive Bayes  
  
installed.packages("klaR")

## Package LibPath Version Priority Depends Imports LinkingTo Suggests  
## Enhances License License\_is\_FOSS License\_restricts\_use OS\_type Archs  
## MD5sum NeedsCompilation Built

library(klaR)

## Loading required package: MASS

mynb <- NaiveBayes(Species ~ ., iris)  
mynb.pred <- predict(mynb,iris)  
table(mynb.pred$class,iris$Species)

##   
## setosa versicolor virginica  
## setosa 50 0 0  
## versicolor 0 47 3  
## virginica 0 3 47

# setosa versicolor virginica  
# setosa 50 0 0  
# versicolor 0 47 3  
# virginica 0 3 47

# Neural Network  
  
library(nnet)  
mynnet <- nnet(Species ~ ., iris, size=1)

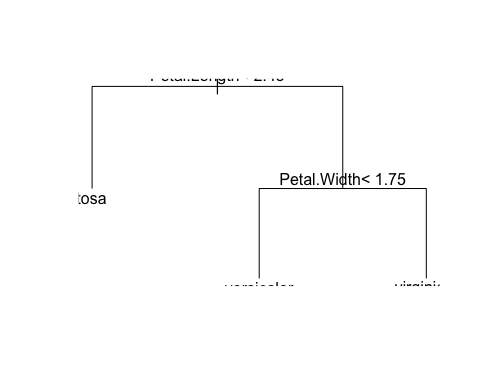
## # weights: 11  
## initial value 180.124842   
## iter 10 value 50.421778  
## iter 20 value 8.535818  
## iter 30 value 6.070173  
## iter 40 value 5.988921  
## iter 50 value 5.972936  
## iter 60 value 5.971885  
## iter 70 value 5.969110  
## iter 80 value 5.967027  
## iter 90 value 5.965416  
## iter 100 value 5.957352  
## final value 5.957352   
## stopped after 100 iterations

mynnet.pred <- predict(mynnet,iris,type="class")  
table(mynnet.pred,iris$Species)

##   
## mynnet.pred setosa versicolor virginica  
## setosa 50 0 0  
## versicolor 0 49 1  
## virginica 0 1 49

# mynnet.pred setosa versicolor virginica  
# setosa 50 0 0  
# versicolor 0 49 1  
# virginica 0 1 49  
  
library(MASS)  
data(iris)

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



summary(mytree)

## Call:  
## rpart(formula = Species ~ ., data = iris)  
## n= 150   
##   
## CP nsplit rel error xerror xstd  
## 1 0.50 0 1.00 1.15 0.05180090  
## 2 0.44 1 0.50 0.68 0.06096994  
## 3 0.01 2 0.06 0.08 0.02751969  
##   
## Variable importance  
## Petal.Width Petal.Length Sepal.Length Sepal.Width   
## 34 31 21 14   
##   
## Node number 1: 150 observations, complexity param=0.5  
## predicted class=setosa expected loss=0.6666667 P(node) =1  
## class counts: 50 50 50  
## probabilities: 0.333 0.333 0.333   
## left son=2 (50 obs) right son=3 (100 obs)  
## Primary splits:  
## Petal.Length < 2.45 to the left, improve=50.00000, (0 missing)  
## Petal.Width < 0.8 to the left, improve=50.00000, (0 missing)  
## Sepal.Length < 5.45 to the left, improve=34.16405, (0 missing)  
## Sepal.Width < 3.35 to the right, improve=19.03851, (0 missing)  
## Surrogate splits:  
## Petal.Width < 0.8 to the left, agree=1.000, adj=1.00, (0 split)  
## Sepal.Length < 5.45 to the left, agree=0.920, adj=0.76, (0 split)  
## Sepal.Width < 3.35 to the right, agree=0.833, adj=0.50, (0 split)  
##   
## Node number 2: 50 observations  
## predicted class=setosa expected loss=0 P(node) =0.3333333  
## class counts: 50 0 0  
## probabilities: 1.000 0.000 0.000   
##   
## Node number 3: 100 observations, complexity param=0.44  
## predicted class=versicolor expected loss=0.5 P(node) =0.6666667  
## class counts: 0 50 50  
## probabilities: 0.000 0.500 0.500   
## left son=6 (54 obs) right son=7 (46 obs)  
## Primary splits:  
## Petal.Width < 1.75 to the left, improve=38.969400, (0 missing)  
## Petal.Length < 4.75 to the left, improve=37.353540, (0 missing)  
## Sepal.Length < 6.15 to the left, improve=10.686870, (0 missing)  
## Sepal.Width < 2.45 to the left, improve= 3.555556, (0 missing)  
## Surrogate splits:  
## Petal.Length < 4.75 to the left, agree=0.91, adj=0.804, (0 split)  
## Sepal.Length < 6.15 to the left, agree=0.73, adj=0.413, (0 split)  
## Sepal.Width < 2.95 to the left, agree=0.67, adj=0.283, (0 split)  
##   
## Node number 6: 54 observations  
## predicted class=versicolor expected loss=0.09259259 P(node) =0.36  
## class counts: 0 49 5  
## probabilities: 0.000 0.907 0.093   
##   
## Node number 7: 46 observations  
## predicted class=virginica expected loss=0.02173913 P(node) =0.3066667  
## class counts: 0 1 45  
## probabilities: 0.000 0.022 0.978

mytree.pred <- predict(mytree,iris,type="class")  
table(mytree.pred,iris$Species)

##   
## mytree.pred setosa versicolor virginica  
## setosa 50 0 0  
## versicolor 0 49 5  
## virginica 0 1 45

# Leave-1-Out Cross Validation (LOOCV)  
ans <- numeric(length(iris[,1]))  
for (i in 1:length(iris[,1])) {  
 mytree <- rpart(Species ~ ., iris[-i,])  
 mytree.pred <- predict(mytree,iris[i,],type="class")  
 ans[i] <- mytree.pred  
}  
ans <- factor(ans,labels=levels(iris$Species))  
table(ans,iris$Species)

##   
## ans setosa versicolor virginica  
## setosa 50 0 0  
## versicolor 0 45 5  
## virginica 0 5 45

# The same as above in this case

#Quadratic Discriminant Analysis  
library(MASS)  
myqda <- qda(Species ~ ., iris)  
myqda.pred <- predict(myqda, iris)  
table(myqda.pred$class,iris$Species)

##   
## setosa versicolor virginica  
## setosa 50 0 0  
## versicolor 0 48 1  
## virginica 0 2 49

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

##   
## setosa versicolor virginica  
## setosa 50 0 0  
## versicolor 0 48 1  
## virginica 0 2 49

#Random Forests  
library(randomForest)

## randomForest 4.7-1.1

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

myrf <- randomForest(Species ~ .,iris)  
myrf.pred <- predict(myrf, iris)  
table(myrf.pred, iris$Species)

##   
## myrf.pred setosa versicolor virginica  
## setosa 50 0 0  
## versicolor 0 50 0  
## virginica 0 0 50

# (Suspiciously correct! - need to read the manual)