Solution Lesson 05: Decision trees

Machine Learning using R

Exercise 1: Diabetes in Pima Indian women

This data set includes the test-results of women who are of Pima Indian heritage and were tested for diabetes according to Wold Health Organization criteria.

a) The Pima.tr data set is available in the MASS package. Load the package to be able to access the data. Get an overview of the data and use the command ?Pima.tr to see the individual variables' meaning.

```
library(MASS)
head(Pima.tr)
##
     npreg glu bp skin bmi
                               ped age type
## 1
           86 68
                     28 30.2 0.364
                                    24
                                          No
## 2
         7 195 70
                     33 25.1 0.163
                                     55
                                         Yes
## 3
         5
           77 82
                     41 35.8 0.156
                                     35
                                          No
         0 165 76
                     43 47.9 0.259
                                     26
                                          No
         0 107 60
## 5
                     25 26.4 0.133
                                     23
                                          No
            97 76
                     27 35.6 0.378
                                     52
                                         Yes
str(Pima.tr)
   'data.frame':
                     200 obs. of 8 variables:
##
    $ npreg: int
                  5 7 5 0 0 5 3 1 3 2 ...
                  86 195 77 165 107 97 83 193 142 128 ...
    $ glu : int
                  68 70 82 76 60 76 58 50 80 78 ...
    $ bp
           : int
##
                  28 33 41 43 25 27 31 16 15 37 ...
    $ skin : int
                  30.2 25.1 35.8 47.9 26.4 35.6 34.3 25.9 32.4 43.3 ...
           : num
    $ ped : num
                  0.364 0.163 0.156 0.259 0.133 ...
                  24 55 35 26 23 52 25 24 63 31 ...
    $ age
           : int
    $ type : Factor w/ 2 levels "No", "Yes": 1 2 1 1 1 2 1 1 1 2 ...
dim(Pima.tr)
## [1] 200
summary(Pima.tr)
##
        npreg
                          glu
                                            bp
                                                             skin
##
    Min.
           : 0.00
                     Min.
                            : 56.0
                                     Min.
                                             : 38.00
                                                        Min.
                                                               : 7.00
##
    1st Qu.: 1.00
                     1st Qu.:100.0
                                      1st Qu.: 64.00
                                                        1st Qu.:20.75
    Median: 2.00
                     Median :120.5
                                     Median : 70.00
                                                        Median :29.00
##
    Mean
           : 3.57
                            :124.0
                                     Mean
                                             : 71.26
                                                        Mean
                                                               :29.21
##
    3rd Qu.: 6.00
                     3rd Qu.:144.0
                                      3rd Qu.: 78.00
                                                        3rd Qu.:36.00
##
    Max.
           :14.00
                     Max.
                            :199.0
                                             :110.00
                                                        Max.
                                                               :99.00
##
         bmi
                          ped
                                            age
                                                         type
##
    Min.
           :18.20
                     Min.
                            :0.0850
                                       Min.
                                              :21.00
                                                        No :132
                     1st Qu.:0.2535
                                                        Yes: 68
    1st Qu.:27.57
                                       1st Qu.:23.00
```

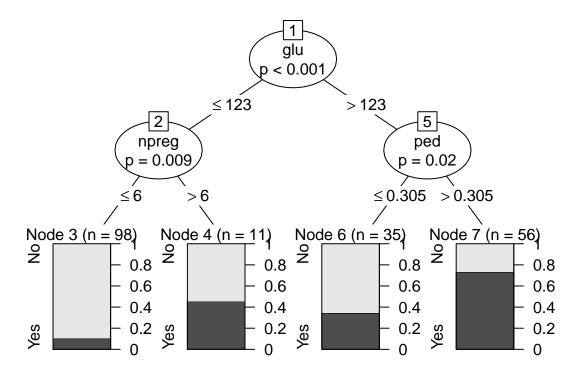
```
## Median :32.80
                    Median :0.3725
                                      Median :28.00
           :32.31
## Mean
                            :0.4608
                                             :32.11
                    Mean
                                      Mean
## 3rd Qu.:36.50
                    3rd Qu.:0.6160
                                      3rd Qu.:39.25
           :47.90
                            :2.2880
## Max.
                    Max.
                                      {\tt Max.}
                                             :63.00
```

b) We want to model the variable type (does the woman have diabetes: Yes/No) using a decision tree. Fit a decision tree to the data using the ctree() function (Hint: library(party))

```
suppressMessages(library(party))
tr <- ctree(type ~ ., data = Pima.tr)</pre>
##
##
     Conditional inference tree with 4 terminal nodes
##
## Response: type
## Inputs: npreg, glu, bp, skin, bmi, ped, age
## Number of observations: 200
##
## 1) glu <= 123; criterion = 1, statistic = 45.693
##
     2) npreg <= 6; criterion = 0.991, statistic = 10.321
##
       3)* weights = 98
##
     2) npreg > 6
##
       4)* weights = 11
## 1) glu > 123
##
     5) ped <= 0.305; criterion = 0.98, statistic = 8.855
##
       6)* weights = 35
     5) ped > 0.305
##
##
       7)* weights = 56
```

c) Plot the tree structure. Which variables were used to split the data? What is the meaning of the p-values printed below the splitting variables?

```
plot(tr)
```



The decision tree created by ctree() used the variables glu, npreg and ped for splitting. Since ctree() uses a significance test based method for variable selection, it compares the p-values (resulting from testing the relation between each predictor and the target variable statistically) between all predictors. The variable with the lowest p-value is selected for splitting. The p-value of each splitting variable is printed below the variable name.

d) Calculate the training error and show the corresponding confusion matrix (Hint: predict(model, newdata=..., method='response'))

```
pred.tr <- predict(tr, newdata=Pima.tr, method='response')</pre>
# Confusion matrix:
confT <- table(pred.tr, Pima.tr$type)</pre>
confT
##
## pred.tr
             No Yes
##
                  27
        No
            117
        Yes
             15
# Training error:
missMat <- confT
diag(missMat) <- 0</pre>
missCount <- sum(missMat)</pre>
(test.err <- missCount/sum(confT))</pre>
```

e) Yesterday we looked at a cross-validation function for the KNN classifier. Make the appropriate changes in the function so that it can be used for decision trees (generated with ctree()). Evaluate the performance of a ctree-generated decision tree (using default options) on the Pima.tr data set using

[1] 0.21

```
ctree_crossVal <- function(data, label, k_fold=10){</pre>
  stopifnot(nrow(data)==length(label), is.factor(label),
             (1<k_fold & k_fold<=nrow(data)))
  # Create k sub-selections
  n <- nrow(data)
  ind_s <- sample(1:n)</pre>
  ind.L <- list()</pre>
  j1 <- 1
  for (i in 1:k_fold){
    j2 <- (i*n) %/% k_fold
    ind.L[[i]] <- ind_s[j1:j2]</pre>
    j1 <- j2+1
  }
  # Now run ctree on each selection (and collect results):
  confMat <- matrix(0,nrow=nlevels(label), ncol=nlevels(label))</pre>
  for(fold in 1:k_fold){
    ind_fold <- ind.L[[fold]]</pre>
    testDat <- data[ind_fold,]</pre>
    trainDat <- data[-ind_fold,]</pre>
    test.solu <- label[ind_fold]</pre>
    train.solu <- label[-ind_fold]</pre>
    trainDat.tr <- cbind(trainDat, y=train.solu) # needed for ctree function
    tr <- ctree(y~., data = trainDat.tr)</pre>
    tr.pred <- predict(tr, newdata=testDat, type='response')</pre>
    confMat.fold <- table(tr.pred, test.solu)</pre>
    confMat <- confMat + confMat.fold</pre>
  }
  # Calculate estimated test-error
  missMat <- confMat</pre>
  diag(missMat) <- 0</pre>
  missCount <- sum(missMat)</pre>
  test.err <- missCount/n</pre>
  L.res <- list(k_fold=k_fold, Indices=ind.L,</pre>
                 confMatrix=confMat, errorRate=test.err)
  return(L.res)
set.seed(4646)
ctree_crossVal(data = Pima.tr[,-8], label = Pima.tr$type, k_fold = 10)
## $k_fold
## [1] 10
##
## $Indices
## $Indices[[1]]
## [1] 179 146 73 120 193 103 118 152 139 59 42 51 34 167 53 175 107 72 19
## [20] 127
##
## $Indices[[2]]
## [1] 17 65 198 168 86 141 173 32 8 125 64 54 113 89 55 49 26 177 106
```

```
## [20]
##
## $Indices[[3]]
   [1] 166 96 109 67 129 182 165 143 160 184 115 39 164 183 136 108 36 91 178
## [20]
        70
##
## $Indices[[4]]
       48 40 189 82 128 60 104 117 191 188 77 170 74 196 133 123 159 147 21
  [1]
## [20] 79
##
## $Indices[[5]]
             7 102 56 23 61 172 87 171 58 78 148 124 140 131 145 95 181 200
##
   [1] 156
## [20]
       38
##
## $Indices[[6]]
   [1] 187 12
                3 174 135 194 75 199 121 10 22 126 52 111 197 157 90 68 27
## [20] 176
##
## $Indices[[7]]
   [1] 180 14 88 161 155 41 105 85 13 116 47 97 132 158 101
## [20]
       63
##
## $Indices[[8]]
   [1] 195 24 119 28 81 76
                              9 149 2 162 154 151 110 100 99 130
##
## [20] 186
## $Indices[[9]]
   [1] 185 66 150 18 11 144 134 37 31 44 122 163 29 15
                                                             25
                                                                  1 35 20
                                                                            69
## [20]
       46
##
## $Indices[[10]]
   [1] 84 80 192 190 98 153 33 94 142 30 83 93 138 114 45 137 43 169 50
## [20]
        16
##
##
## $confMatrix
         test.solu
## tr.pred No Yes
##
      No 109
              35
##
      Yes 23 33
##
## $errorRate
## [1] 0.29
```

It seems that while the level "No" is predicted relatively well, the prediction of the level "Yes" is not better than random guessing.