

CS771A Assignment 1: Decision Trees

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```
library(rpart)
library(rpart.plot)
set.seed(10)
rawData = read.csv(file="data", header=F, sep=",")
originalData = rawData[sample(nrow(rawData)),]
colnames(originalData) = c("PregnantCount", "Glucose", "BP", "Triceps",
                           "Insulin", "BMI", "DPF", "Age", "Class")

N = nrow(originalData)
K = 5
foldWidth = floor(N/K)
Accuracy = 0
for (i in (1:K))
{
  data = originalData
  data$Glucose[data$Glucose==0] = NA          # Missing Data # c
  data$BP[data$BP==0] = NA
  data$Triceps[data$Triceps==0] = NA
  data$Insulin[data$Insulin==0] = NA
  data$BMI[data$BMI==0] = NA
  start = as.integer((i-1)*foldWidth)+1
  end = as.integer(i*foldWidth)
  if(i==K)
  {
    end = N
  }
  testData = data[c(start:end),]
  learnData = data[c(-start:-end),]
  diabStat = factor(learnData$Class, levels=0:1, labels=c('ND','D'))
  #' Any split that does not decrease the overall lack of fit by a factor
  #' of cp is not attempted. By setting appropriate (here, 0.03), we are
  #' controlling the growth of tree by thresholding impurity decrease.
  cfit = rpart(
    diabStat ~ PregnantCount+Glucose+BP+Triceps+Insulin+BMI+DPF+Age,
    data = learnData,
    na.action = na.rpart,
    method = 'class',
    parms = list(split = "gini"),
    control = rpart.control(
      cp = 0.03,
    )
  )
  predictedFactor = predict(cfit, testData, type="class")
  predictedFrame = as.data.frame.factor(predictedFactor)
  predicted = c(predictedFrame[,1]) - 1 # gives 1 for ND, 2 for D
  actual = testData$Class
  TP = sum(predicted & actual)
  TN = nrow(testData) - sum(predicted | actual)
```

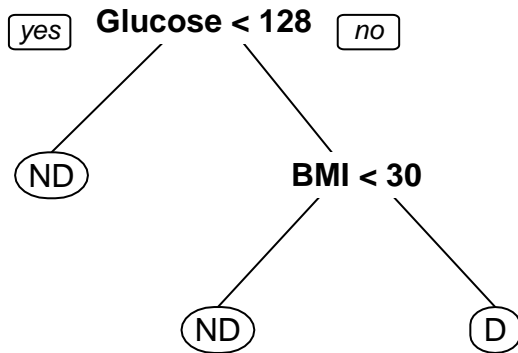
```

# Accuracy
print((TP+TN)/nrow(testData))
Accuracy = Accuracy + (TP+TN)/nrow(testData)
rpart.plot(cfit)
}

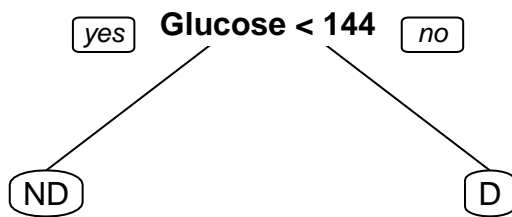
```

```
## [1] 0.751634
```

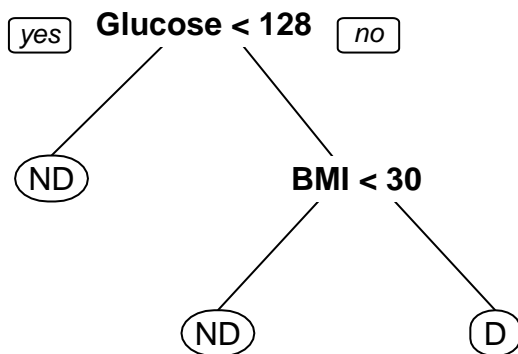
```
## [1] 0.7777778
```



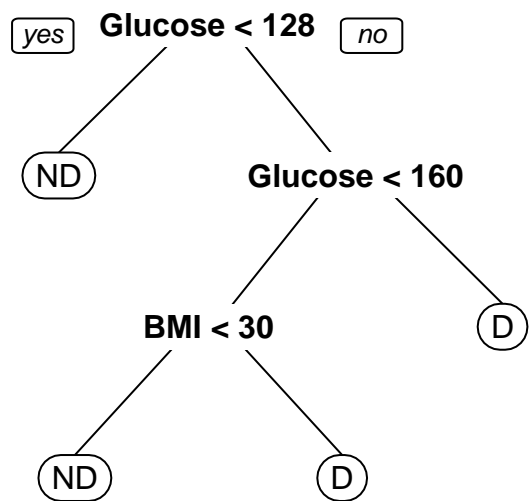
```
## [1] 0.6993464
```



```
## [1] 0.7647059
```



```
## [1] 0.8012821
```



```
# Mean Accuracy  
print(Accuracy/K)
```

```
## [1] 0.7589492
```