Lab 2

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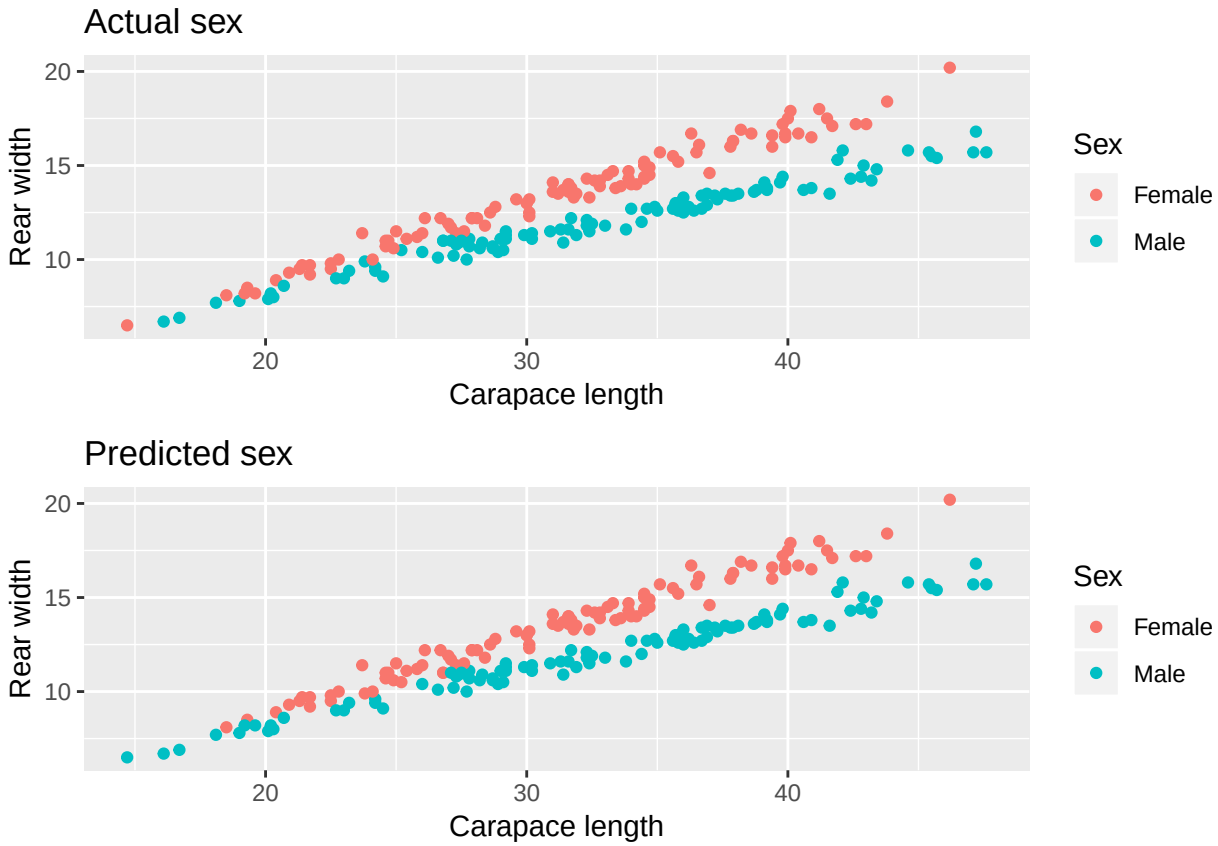
Assignment 1

Step 1 & 2

```
# Add libraries
library("gridExtra")
library("ggplot2")
library("MASS")

# Set working directory
setwd("~/courses/tdde01/lab2")

# Read data
crabs = read.csv("australian-crabs.csv")

crabs.plot = ggplot(data = crabs,
                    mapping = aes(x=CL,
                                  y=RW,
                                  color=sex)) +
geom_point() +
ggtitle("Actual sex") +
scale_x_continuous(name = "Carapace length") +
scale_y_continuous(name = "Rear width") +
scale_color_discrete(name = "Sex")

lda.model = lda(formula = sex~CL+RW, data = crabs)
lda.predict = predict(lda.model, crabs)
crabs.predict = ggplot(data = crabs,
                       mapping = aes(x=CL,
                                     y=RW,
                                     color=lda.predict$class)) +
geom_point() +
ggtitle("Predicted sex") +
scale_x_continuous(name = "Carapace length") +
scale_y_continuous(name = "Rear width") +
scale_color_discrete(name = "Sex")

grid.arrange(crabs.plot, crabs.predict)
```




```
# Calculate misclassification
crabs.misclass = mean(crabs$sex != lda.predict$class)
cat("Misclassification rate for lda: ", crabs.misclass)
```

```
## Misclassification rate for lda:  0.035
```

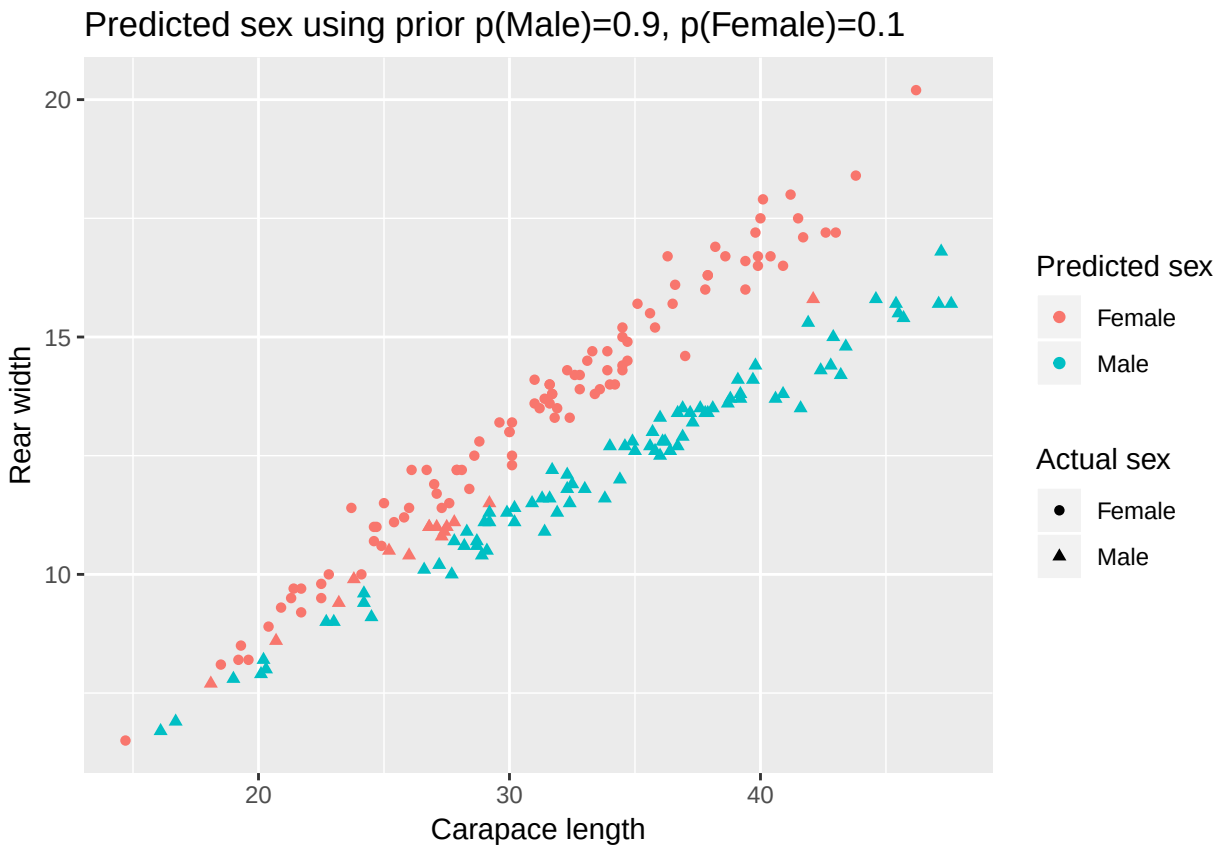
Since the sexes seems to follow two separate lines, they are separatable. Therefore it's appropriate to classify this data with a linear discriminant analysis. The only problem is where these two lines intersect and the sexes are impossible to differ.

Step 3

This time, the same prediction is made, but with the priors $p(Male) = 0.9$ and $p(Female) = 0.1$. See the plot below.

```
prior.male = 0.9
prior.female = 0.1
crabs.predict.prior = predict(lda.model,
                              crabs,
                              prior=c(Male=prior.male,
                                      Female=prior.female))
crabs.plot.prior = ggplot(data=crabs,
                          mapping=aes(x=CL,
                                      y=RW,
                                      shape=sex,
                                      color=crabs.predict.prior$class)) +
geom_point() +
```

```
ggtitle("Predicted sex using prior p(Male)=0.9, p(Female)=0.1") +
scale_x_continuous(name = "Carapace length") +
scale_y_continuous(name = "Rear width") +
scale_color_discrete(name = "Predicted sex") +
scale_shape_discrete(name = "Actual sex")
# Plot
grid.arrange(crabs.plot.prior)
```




```
# Calculate missclassification
crabs.prior.misclass = mean(crabs$sex != crabs.predict.prior$class)
cat("Misclassification rate for lda with p(Male=0.9), p(Female)=0.1: ",
    crabs.prior.misclass)
```

```
## Misclassification rate for lda with p(Male=0.9), p(Female)=0.1:  0.075
```

Step 4

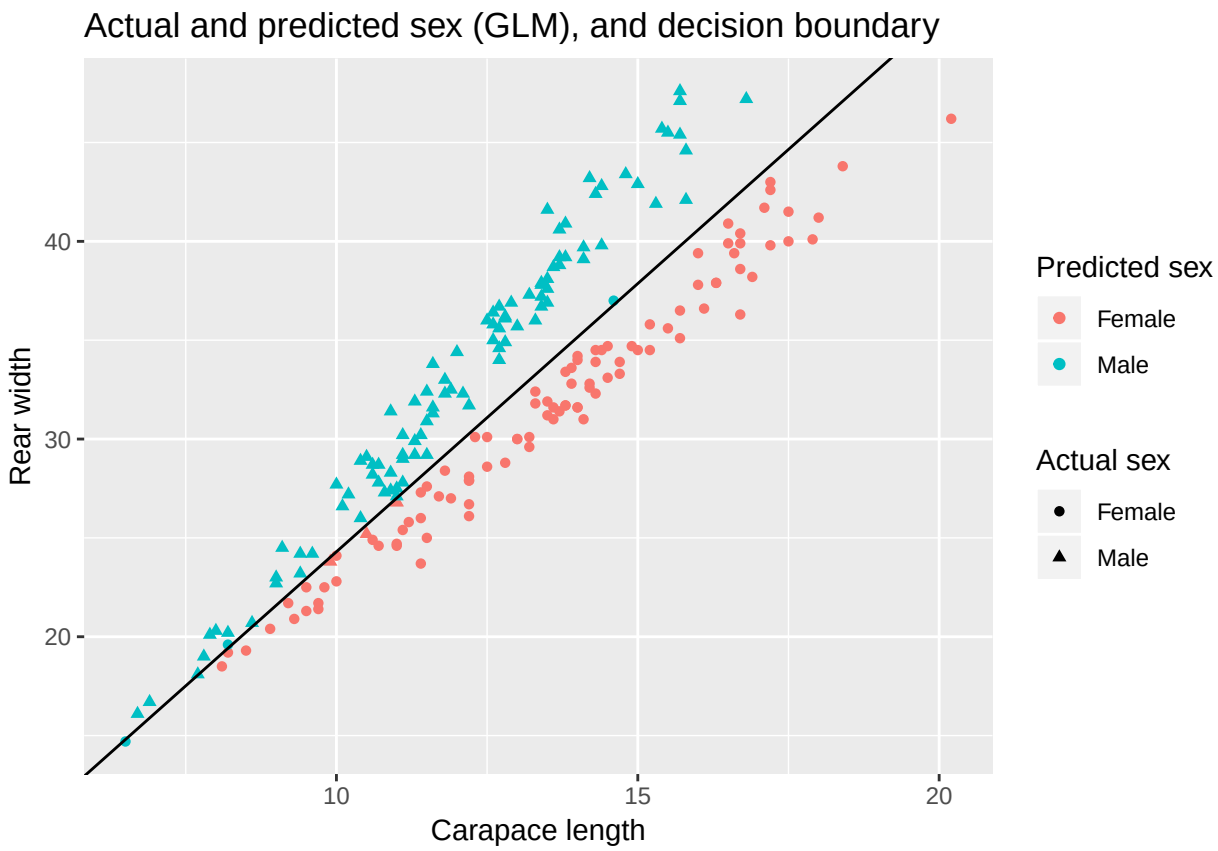
Here the equation of the decision boundary is plotted using GLM.

```
glm.model = glm(formula = sex~RW+CL,
                data = crabs,
                family = 'binomial')
```

```
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

```
glm.predict = predict(object = glm.model,
                      newdata = crabs,
```

```
                      type = 'response')
glm.predicted.sex = ifelse(glm.predict > 0.5, "Male", "Female")

# Calculate line from model
intercept = coef(glm.model)[1]
rw = coef(glm.model)[2]
cl = coef(glm.model)[3]
border = 0.5
k = -rw/cl
m = -(intercept - border)/cl
# Print plot and line
glm.plot = ggplot(data = crabs,
                  mapping = aes(x=RW,
                                y=CL,
                                color=glm.predicted.sex,
                                shape=crabs$sex)) +
geom_point() +
ggtitle("Actual and predicted sex (GLM), and decision boundary") +
scale_x_continuous(name = "Carapace length") +
scale_y_continuous(name = "Rear width") +
scale_color_discrete(name = "Predicted sex") +
scale_shape_discrete(name = "Actual sex") +
geom_abline(intercept = m, slope = k)
grid.arrange(glm.plot)
```




```
# Print misclassification
glm.misclass = mean(crabs$sex != glm.predicted.sex)
```

```
cat("Misclassification rate for GLM: ",
    glm.misclass)
```

```
## Misclassification rate for GLM:  0.035
```

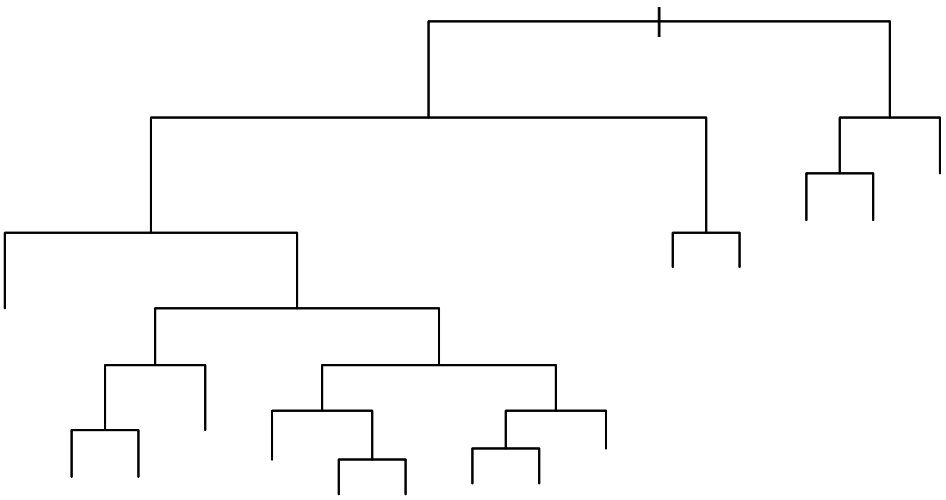
Assignment 2

Step 1

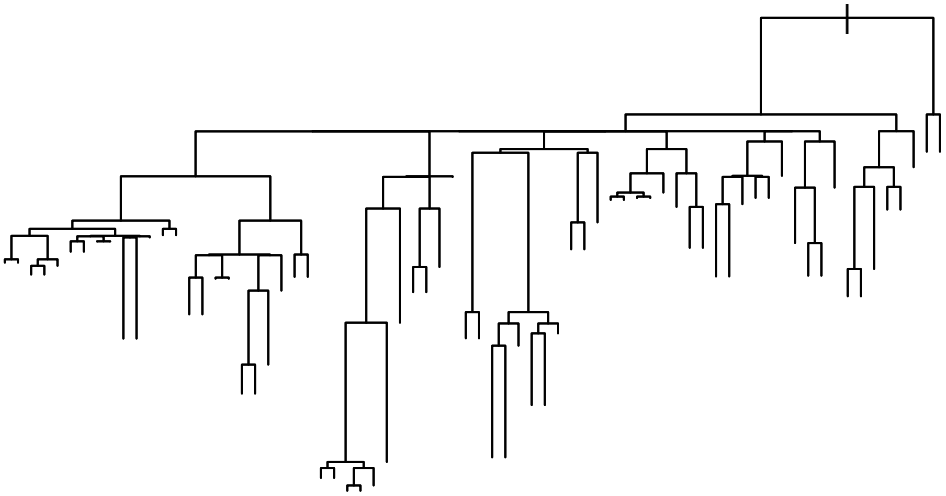
```
# Add libraries
library("gridExtra")
library("ggplot2")
library("tree")
library("MASS")
library("e1071")

# Set working directory
setwd("~/courses/tdde01/lab2")

# Read data
scores = read.csv2("creditscoring.csv")
# Read as strings
scores$good_bad = as.factor(scores$good_bad)

# Split data into train/val/test
n=dim(scores)[1]
set.seed(12345)
id=sample(1:n, floor(n*0.5))
train=scores[id,]
id1=setdiff(1:n, id)
set.seed(12345)
id2=sample(id1, floor(n*0.25))
val=scores[id2,]
id3=setdiff(id1,id2)
test=scores[id3,]
```

Step 2

```
# Create tree
tree.deviance = tree(formula = good_bad~.,
                     data = train,
                     split="deviance")
tree.gini = tree(formula = good_bad~.,
                     data = train,
                     split="gini")
# Plot tree
plot(tree.deviance)
```



```r
plot(tree.gini)
```



```r
# Make predictions
predict.deviance.test = predict(tree.deviance, test, type = "class")
predict.deviance.train = predict(tree.deviance, train, type = "class")
predict.gini.test = predict(tree.gini, test, type = "class")
predict.gini.train = predict(tree.gini, train, type = "class")

# Calculate misclassification rates
misclass = function(predicted, true) {
    return(mean(predicted != true))
}

deviance.test.misclass = misclass(predict.deviance.test, test$good_bad)
deviance.train.misclass = misclass(predict.deviance.train, train$good_bad)
gini.test.misclass = misclass(predict.gini.test, test$good_bad)
gini.train.misclass = misclass(predict.gini.train, train$good_bad)

# Print misclassification rates
cat("Misclassification on deviance with test: ",
    deviance.test.misclass)
```

```
## Misclassification on deviance with test:  0.268
```

```
cat("\nMisclassification on deviance with train: ",
    deviance.train.misclass)
```

```
##
## Misclassification on deviance with train:  0.212
```

```
cat("\nMisclassification on gini with test: ",
    gini.test.misclass)
```

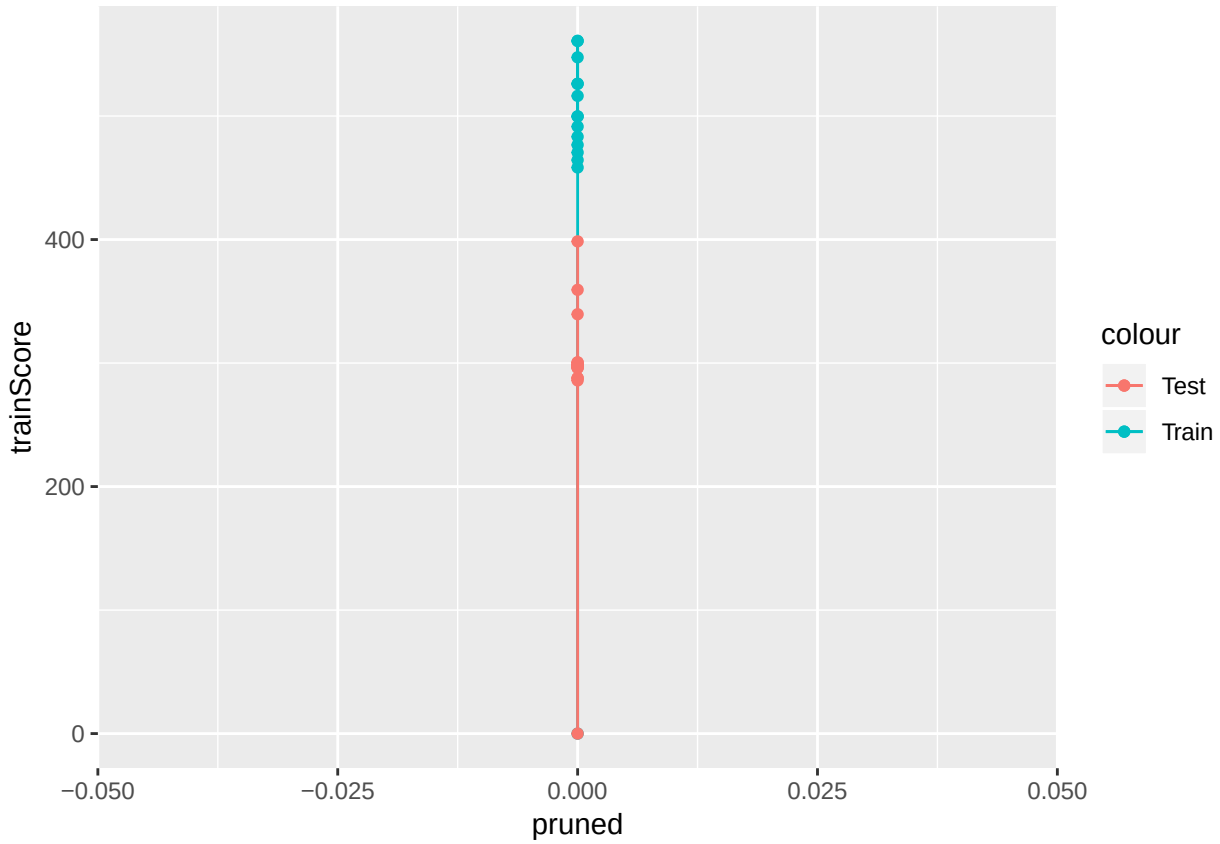
```
##
## Misclassification on gini with test:  0.368
```

```
cat("\nMisclassification on gini with train: ",
    gini.train.misclass, "\n")
```

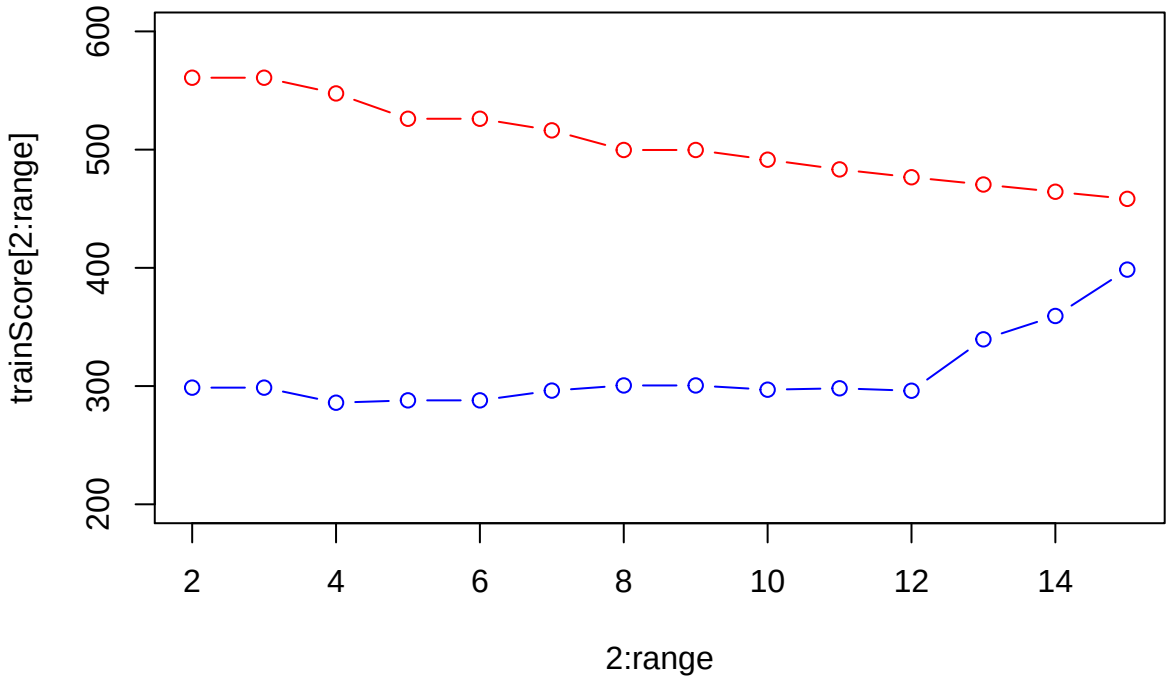
```
##
## Misclassification on gini with train:  0.24
```

Step 3

```
# Lists of scores
range = 15
pruned=rep(0, range)
trainScore=rep(0, range)
testScore=rep(0, range)

test.tree = tree(formula=good_bad~., data=train)
for(i in 2:range) {
    # Prune the tree
    prunedTree=prune.tree(test.tree, best=i)
    # Make trediction on validation data
    pred=predict(prunedTree, newdata=val, type="tree")
    # Append scores
    trainScore[i]=deviance(prunedTree)
    testScore[i]=deviance(pred)
}

df = data.frame(pruned, trainScore, testScore)

ggplot(mapping=aes(col="Test data")) +
    geom_line(data=df, mapping=aes(x=pruned, y=trainScore, col="Train")) +
    geom_point(data=df, mapping=aes(x=pruned, y=trainScore, col="Train")) +
    geom_line(data=df, mapping=aes(x=pruned, y=testScore, col="Test")) +
    geom_point(data=df, mapping=aes(x=pruned, y=testScore, col="Test"))
```




```
# Plot the scores
plot(2:range, trainScore[2:range], type="b", col="red", ylim=c(200, 600))
points(2:range, testScore[2:range], type="b", col="blue")
```




```
optLeaves = 4
```

```
# Info on optimal tree
optTree = prune.tree(tree.deviance, best=optLeaves)
summary(optTree)
```

```
##
## Classification tree:
## snip.tree(tree = tree.deviance, nodes = c(5L, 3L, 9L))
## Variables actually used in tree construction:
## [1] "savings"  "duration" "history"
## Number of terminal nodes:  4
## Residual mean deviance:  1.117 = 547.5 / 490
## Misclassification error rate: 0.251 = 124 / 494
```

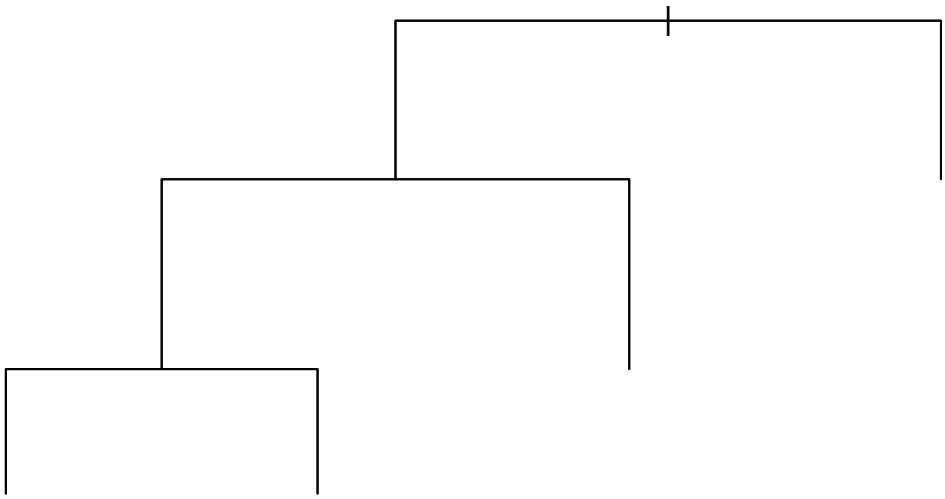
```
optTree.predict = predict(optTree, newdata=test)
optTree.predict.string = ifelse(optTree.predict[2] > 0.5, "good", "bad")
optTree.misclass = misclass(optTree.predict.string, test$good_bad)
cat("\nMisclassification on optimal tree: ",
    optTree.misclass)
```

```
##
## Misclassification on optimal tree:  0.696
```

```
cat("\nTree depth is 5 as can be seen in the plot. \n")
```

```
##
## Tree depth is 5 as can be seen in the plot.
```

```
plot(optTree)
```



```
cat("\n\nUsed variables in optimal tree: \n'savings' 'duration' 'history' 'age' 'purpose'\n\n")
```

```
##
##
## Used variables in optimal tree:
## 'savings' 'duration' 'history' 'age' 'purpose'
```

```
# Step 4
# Create model and classify
model.bayes = naiveBayes(formula = good_bad~., data=train)
predict.bayes.test = predict(model.bayes, newdata=test, type="class")
predict.bayes.train = predict(model.bayes, newdata=train, type="class")
```

```r
# Print info on classification with prediction on test
table.bayes = table(predict.bayes.test, test$good_bad)
cat("Confusion table of naïve bayes:")
```

```
## Confusion table of naïve bayes:
```

```r
print(table.bayes)
```

```
##
## predict.bayes.test bad good
##               bad   46   49
##               good  30  125
```

```r
misclass.bayes = mean(predict.bayes.test != test$good_bad)
cat("Misclassification with naïve bayes: ", misclass.bayes, "\n\n")
```

```
## Misclassification with naïve bayes:  0.316
```

```r
# Print info on classification with prediction on test
table.bayes = table(predict.bayes.train, train$good_bad)
cat("Confusion table of naïve bayes:")
```

```
## Confusion table of naïve bayes:
```

```r
print(table.bayes)
```

```
##
## predict.bayes.train bad good
##                bad   95   98
##                good  52  255
```

```r
misclass.bayes = mean(predict.bayes.train != train$good_bad)
cat("Misclassification with naïve bayes: ", misclass.bayes, "\n\n")
```

```
## Misclassification with naïve bayes:  0.3
```

Step 4

```r
# Create model and classify
model.bayes = naiveBayes(formula = good_bad~., data=train)
predict.bayes.test = predict(model.bayes, newdata=test, type="class")
predict.bayes.train = predict(model.bayes, newdata=train, type="class")

# Print info on classification with prediction on test
table.bayes = table(predict.bayes.test, test$good_bad)
cat("Confusion table of naïve bayes:")
```

```
## Confusion table of naïve bayes:
```

```r
print(table.bayes)
```

```
##
## predict.bayes.test bad good
##               bad   46   49
##               good  30  125
```

```r
misclass.bayes = mean(predict.bayes.test != test$good_bad)
cat("Misclassification with naïve bayes: ", misclass.bayes, "\n\n")
```

```
## Misclassification with naïve bayes:  0.316
```

```r
# Print info on classification with prediction on test
table.bayes = table(predict.bayes.train, train$good_bad)
cat("Confusion table of naïve bayes:")
```

```
## Confusion table of naïve bayes:
```

```r
print(table.bayes)
```

```
##
## predict.bayes.train bad good
##                bad   95   98
##                good  52  255
```

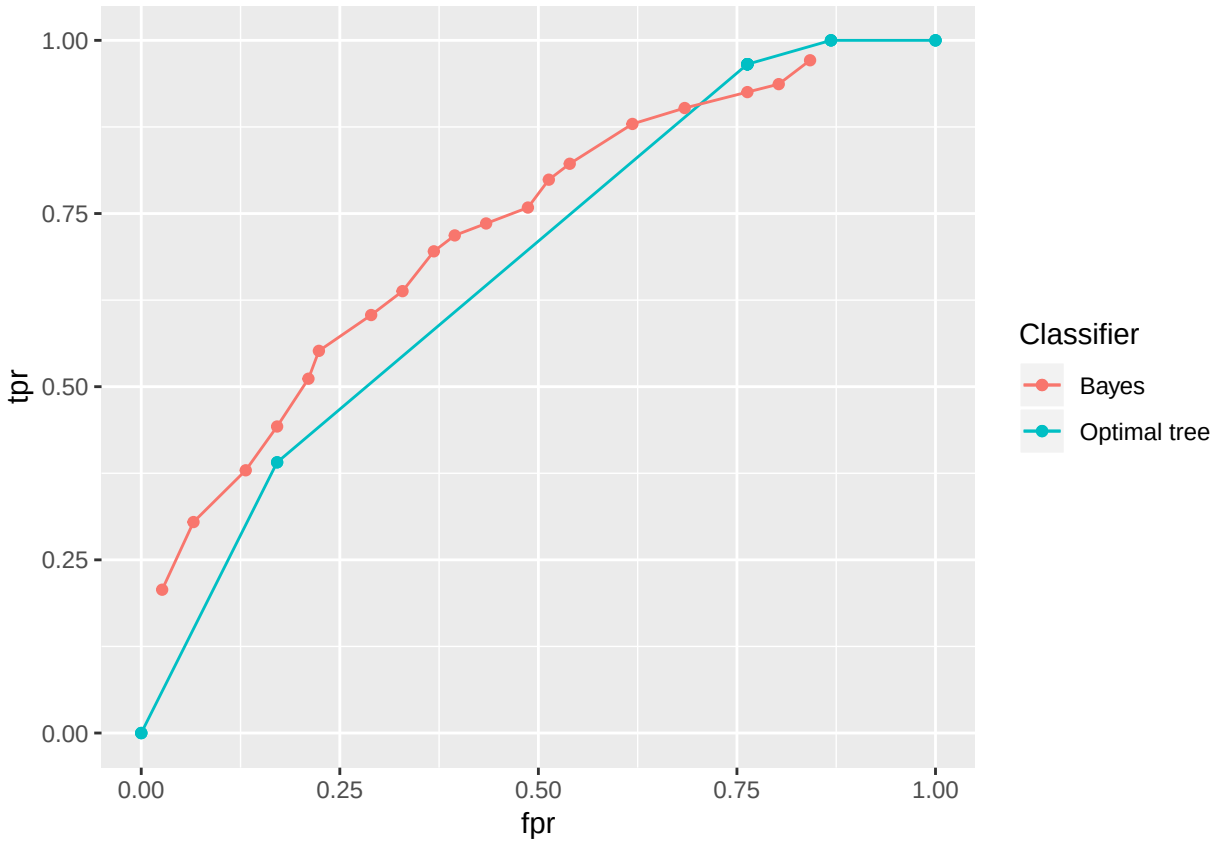
```r
misclass.bayes = mean(predict.bayes.train != train$good_bad)
cat("Misclassification with naïve bayes: ", misclass.bayes, "\n\n")
```

```
## Misclassification with naïve bayes:  0.3
```

Step 5

```r
# Calculate TPR and FPR of optimal tree and bayes
getROC = function(pred, pi) {
    tpr = c()
    fpr = c()
    for (p in pi) {
        # Change probabilities to strings
        tmp = ifelse(pred[,'good'] > p, "good", "bad")
        # Get confusion matrix
        cm = table(predicted=tmp, actual=test$good_bad)
        if('good' %in% rownames(cm)) {
          # Calculate TPR, first dim of cm is predicted
          t = cm['good', 'good'] / sum(cm[,'good'])
          # Calculate FPR
          f = cm['good', 'bad'] / sum(cm[, 'bad'])
          # Append to list of values
          tpr = c(tpr, ifelse(is.finite(t), t, 0))
          fpr = c(fpr, ifelse(is.finite(f), f, 0))
        } else {
          tpr = c(tpr, 0)
          fpr = c(fpr, 0)
        }
    }
    df = data.frame(tpr, fpr)
    return(df)
}

pi = seq(0.05, 0.95, 0.05)
pred.optTree = predict(optTree, newdata=test)
pred.bayes = predict(model.bayes, newdata=test, type='raw')
opt.roc = getROC(pred.optTree, pi)
```

```
bayes.roc = getROC(pred.bayes, pi)

#Plot
roc.plot = ggplot(mapping=aes(col=Classifier)) +
    geom_point(data=opt.roc, aes(x=fpr, y=tpr, col="Optimal tree")) +
    geom_line(data=opt.roc, aes(x=fpr, y=tpr, col="Optimal tree")) +
    geom_point(data=bayes.roc, aes(x=fpr, y=tpr, col="Bayes")) +
    geom_line(data=bayes.roc, aes(x=fpr, y=tpr, col="Bayes"))

grid.arrange(roc.plot)
```



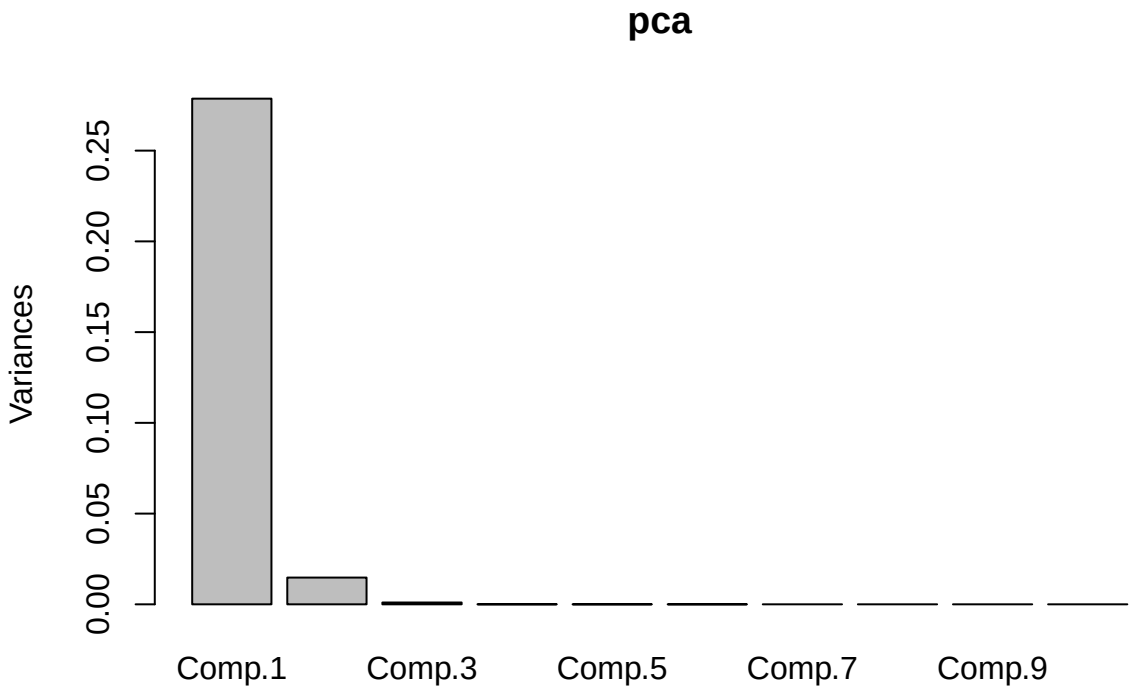
Step 6

Assignment 4

Step 1

```
# Add libraries
library("gridExtra")
library("ggplot2")
library("MASS")
library("stats")
library("fastICA")
```

```r
# Set working directory
setwd("~/courses/tdde01/lab2")

# Read data
spectra = read.csv2("NIRSpectra.csv")

# Calculate principal components
pca = princomp(spectra)

# Get eigen values
lambda = pca$sdev^2
# Plot variance of each component
screeplot(pca)
```




```r
# Print proportion of variation
sprintf("%2.3f",lambda/sum(lambda)*100)
```

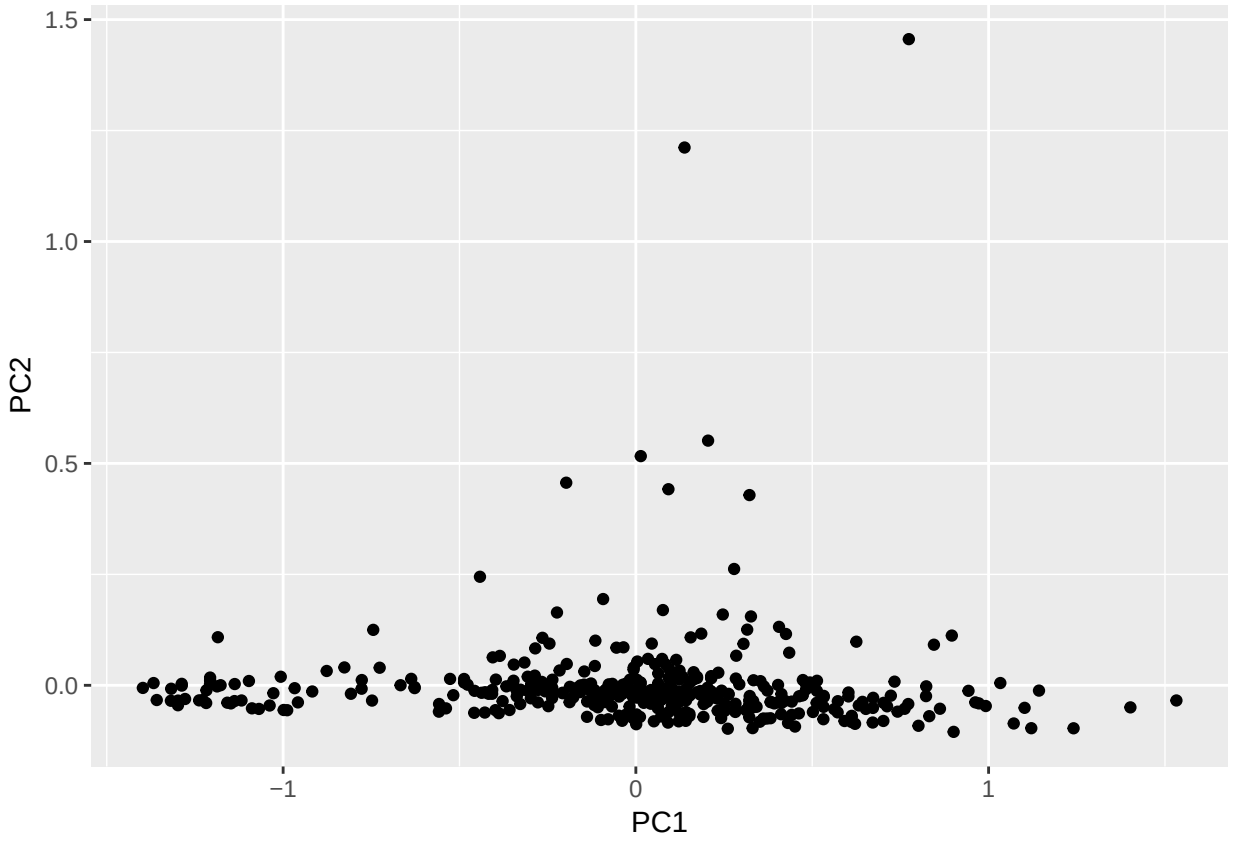
```
##   [1] "94.635" "5.008"  "0.337"  "0.010"  "0.004"  "0.004"  "0.001"
##   [8] "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"
##  [15] "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"
##  [22] "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"
##  [29] "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"
##  [36] "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"
##  [43] "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"
##  [50] "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"
##  [57] "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"
##  [64] "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"
##  [71] "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"
##  [78] "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"
##  [85] "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"
##  [92] "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"
##  [99] "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"
```

```
## [106] "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"
## [113] "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"
## [120] "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"
## [127] "0.000"
```

```
cat("99% of the variance can be explained by first two PC.\n\n")
```

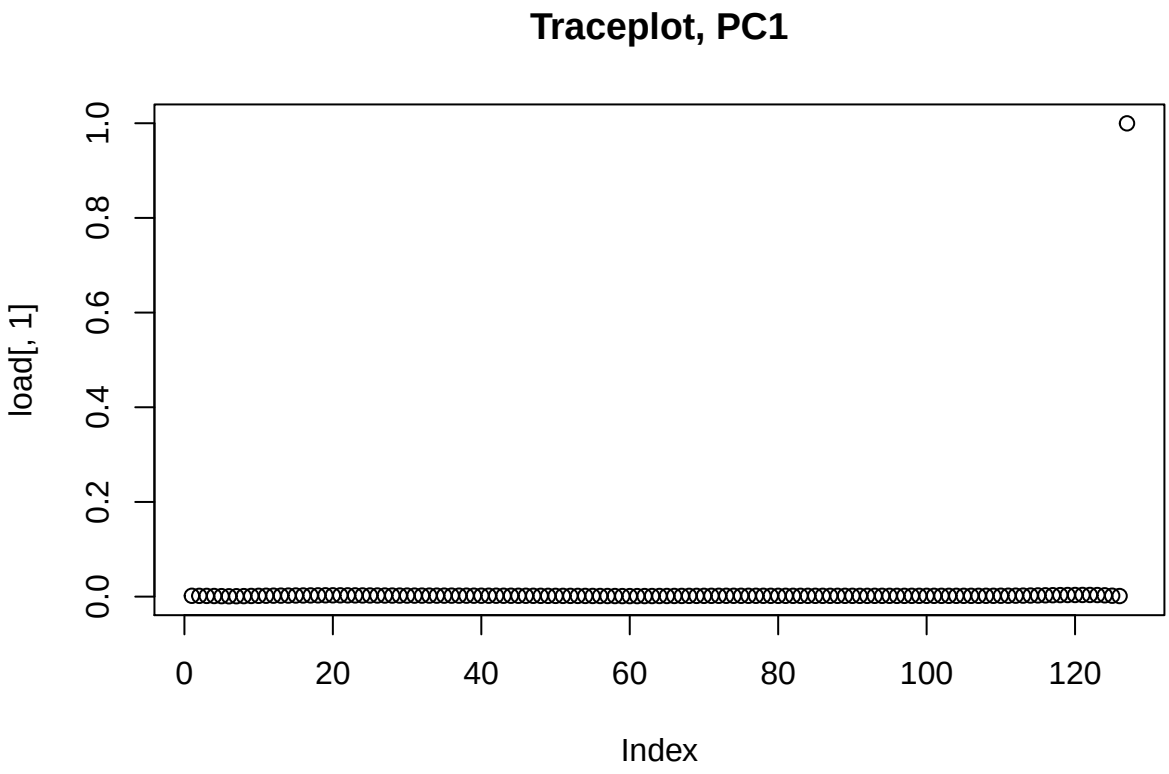
```
## 99% of the variance can be explained by first two PC.
```

```
# Extract principal components
PC1 = pca$scores[,'Comp.1']
PC2 = pca$scores[,'Comp.2']
plane = matrix(c(PC1, PC2), ncol=2)
colnames(plane)=c("PC1", "PC2")
# Project data onto PC1 and PC2
projection = spectra*plane

# Plot the data projected onto PC 1 and 2
plot.projection = ggplot() +
    geom_point(data=projection, mapping=aes(x=PC1, y=PC2))
grid.arrange(plot.projection)
```

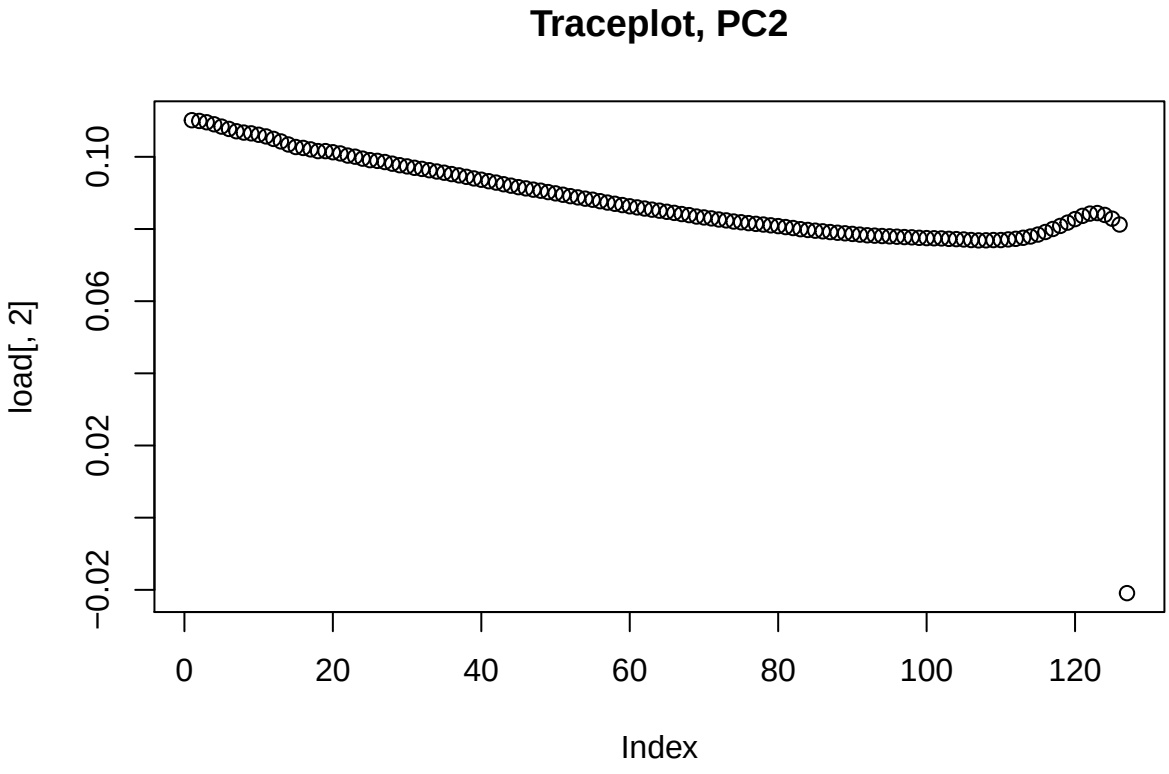


Step 2

```
load = loadings(pca)

plot(load[,1], main="Traceplot, PC1")
```




```
plot(load[,2], main="Traceplot, PC2")
```

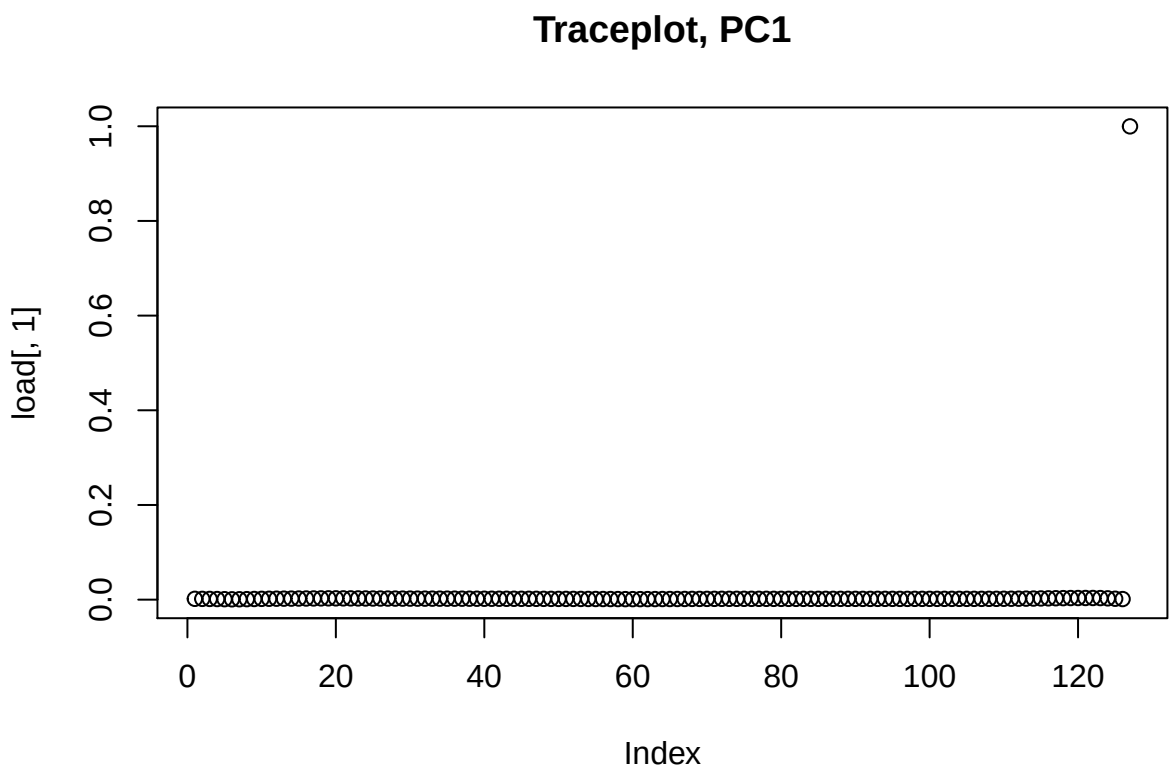


Step 3a

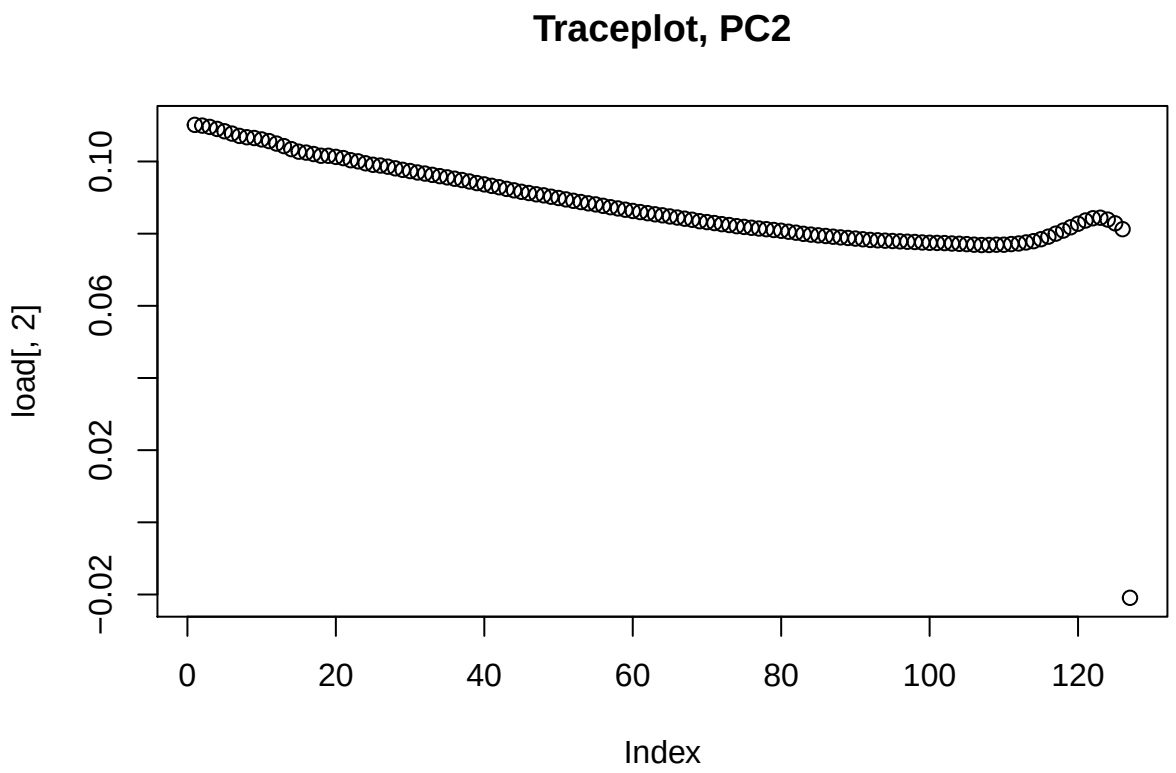
```
res = fastICA(X=spectra,
        n.comp=2,
        alg.typ= "parallel",
        fun = "logcosh",
        alpha = 1,
        method = "R",
        row.norm = FALSE,
        maxit= 200,
        tol = 0.0001,
        verbose = TRUE)
```

```
## Centering
## Whitening
## Symmetric FastICA using logcosh approx. to neg-entropy function
## Iteration 1 tol = 0.01710046
## Iteration 2 tol = 0.02060934
## Iteration 3 tol = 0.005733105
## Iteration 4 tol = 0.0001228216
## Iteration 5 tol = 1.722824e-06
```

```
W.prime = res$K %*% res$W
# Traceplots of fastICA
plot(load[,1], main="Traceplot, PC1")
```



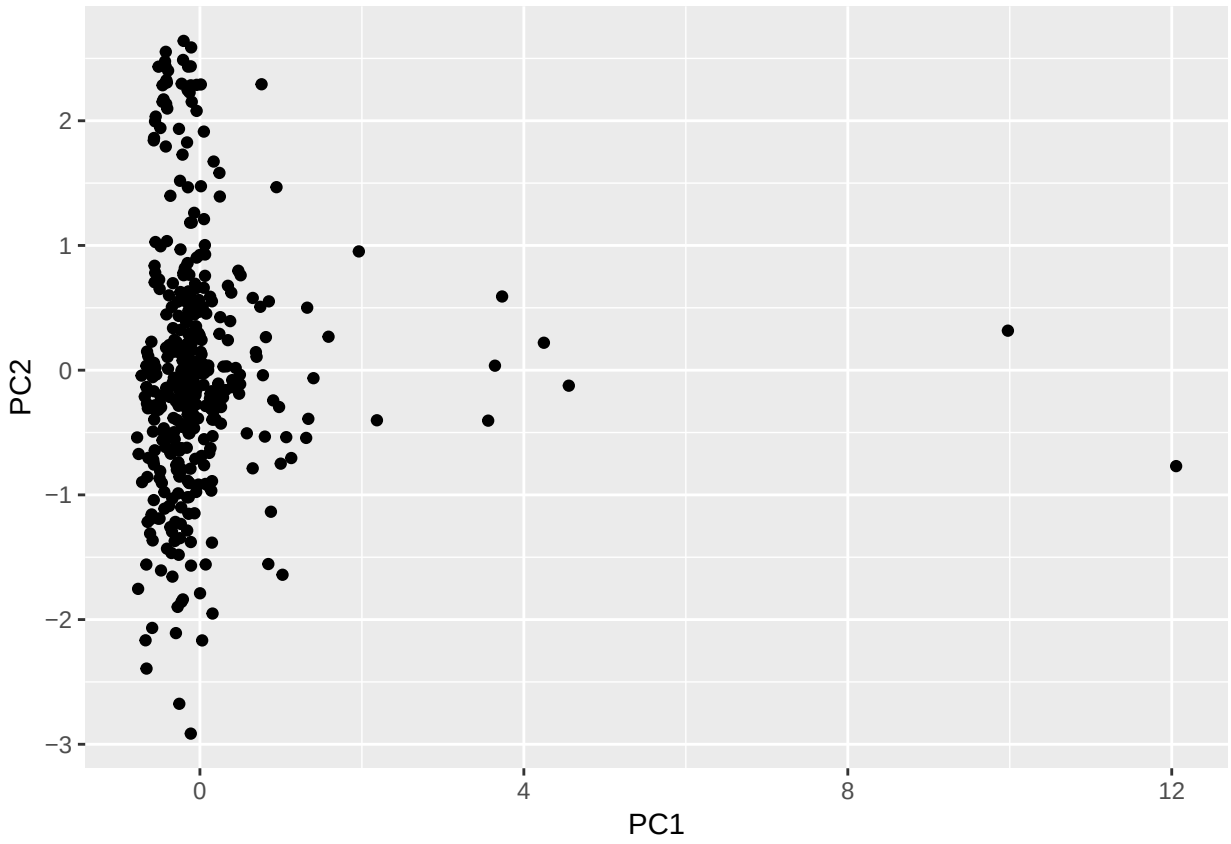
```r
plot(load[,2], main="Traceplot, PC2")
```




```r
# These look identical to step 2
```

Step 3b

```r
# Extract principal components
PC1 = res$S[,1]
PC2 = res$S[,2]
plane = matrix(c(PC1, PC2), ncol=2)
colnames(plane)=c("PC1", "PC2")
projection = spectra*plane

# Plot the data projected onto PC 1 and 2
plot.projection = ggplot() +
    geom_point(data=projection, mapping=aes(x=PC1, y=PC2))
grid.arrange(plot.projection)
```




```
# Plot looks mirrored to step 1
```