Lab 2

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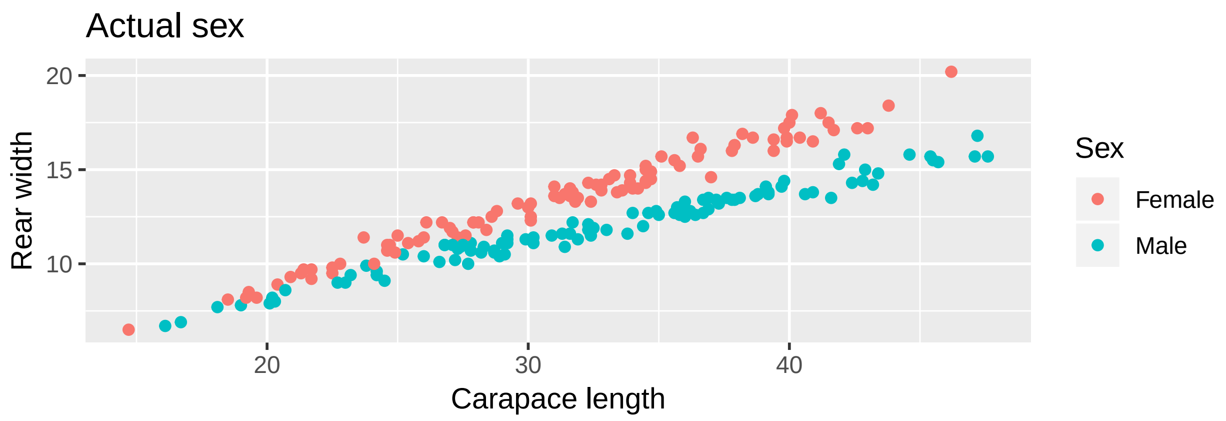
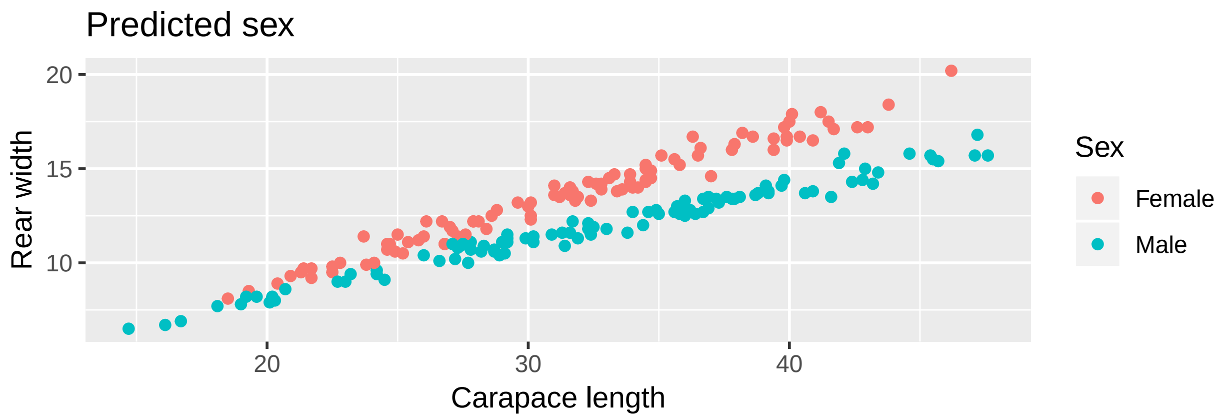
Contents

Assignment 1

Step 1 & 2





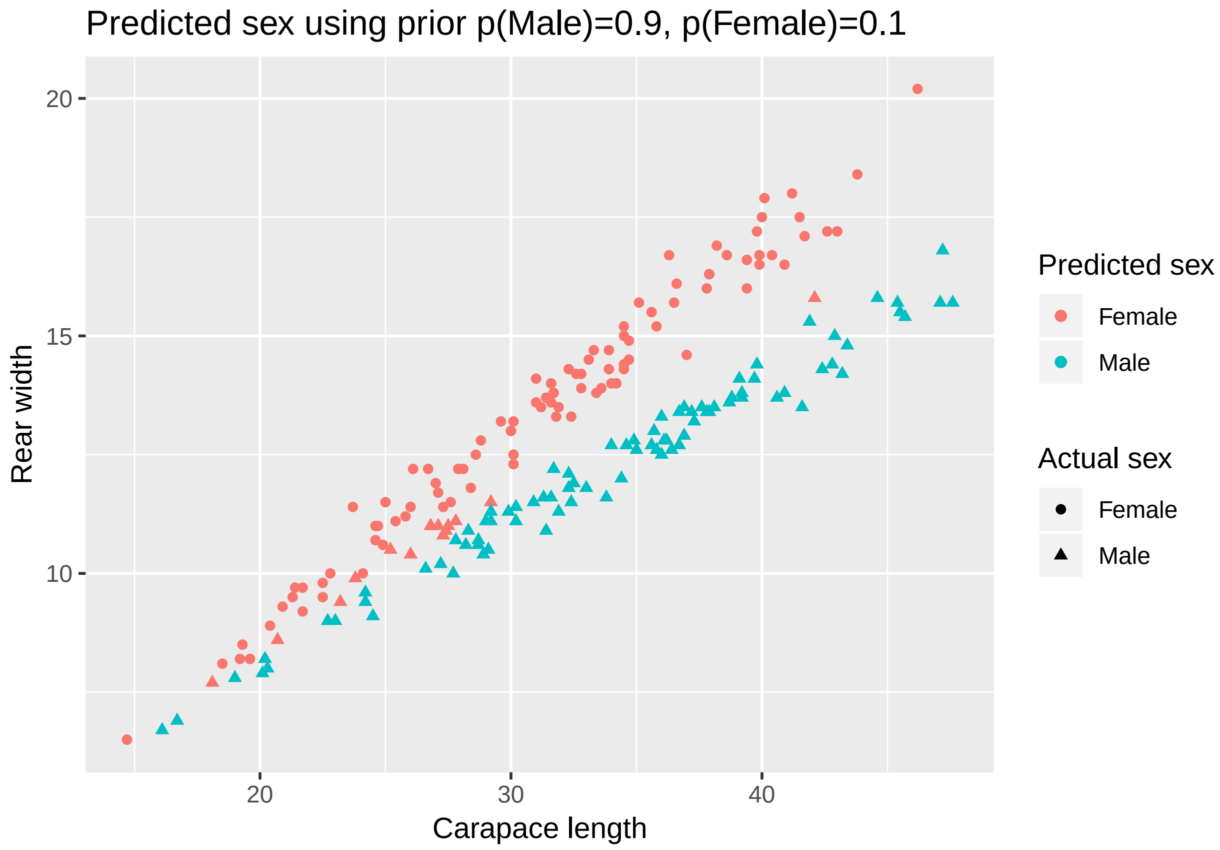
```
## Misclassification rate for lda:  0.035
```

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. Some data may also be crossing this line and get a false classification.

The misclassification rate is really good, which strengthens the argument that the classification method is appropriate.

Step 3

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



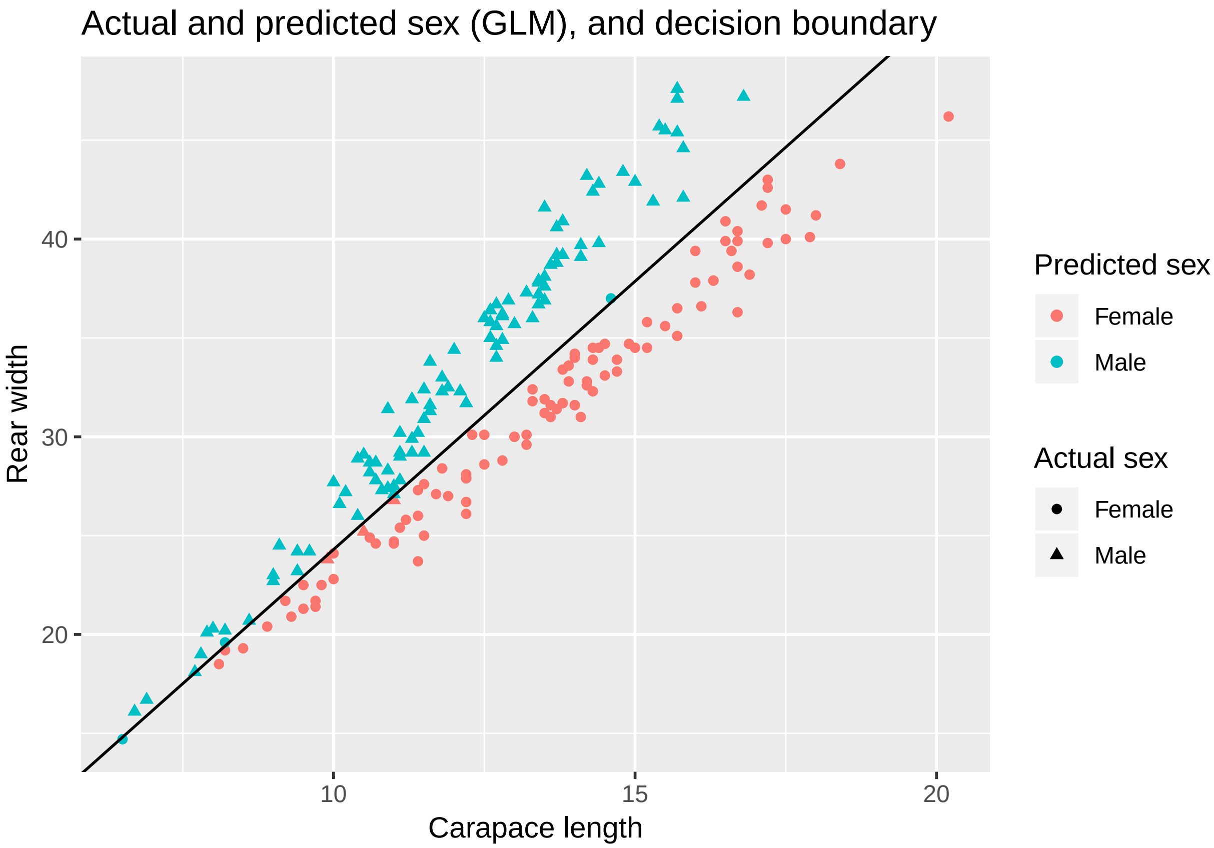
```
## Misclassification rate for lda with p(Male=0.9), p(Female)=0.1:  0.075
```

This time, the misclassification is greater. That is because the priors are not according to the actual distribution of sexes.

Step 4

Here the equation of the decision boundary is plotted together with classification using GLM.

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



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

The misclassification rate is the same as in step 2.

Assignment 2

Step 1

Firstly, the data was separated into training, validation and test data.

Step 2

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

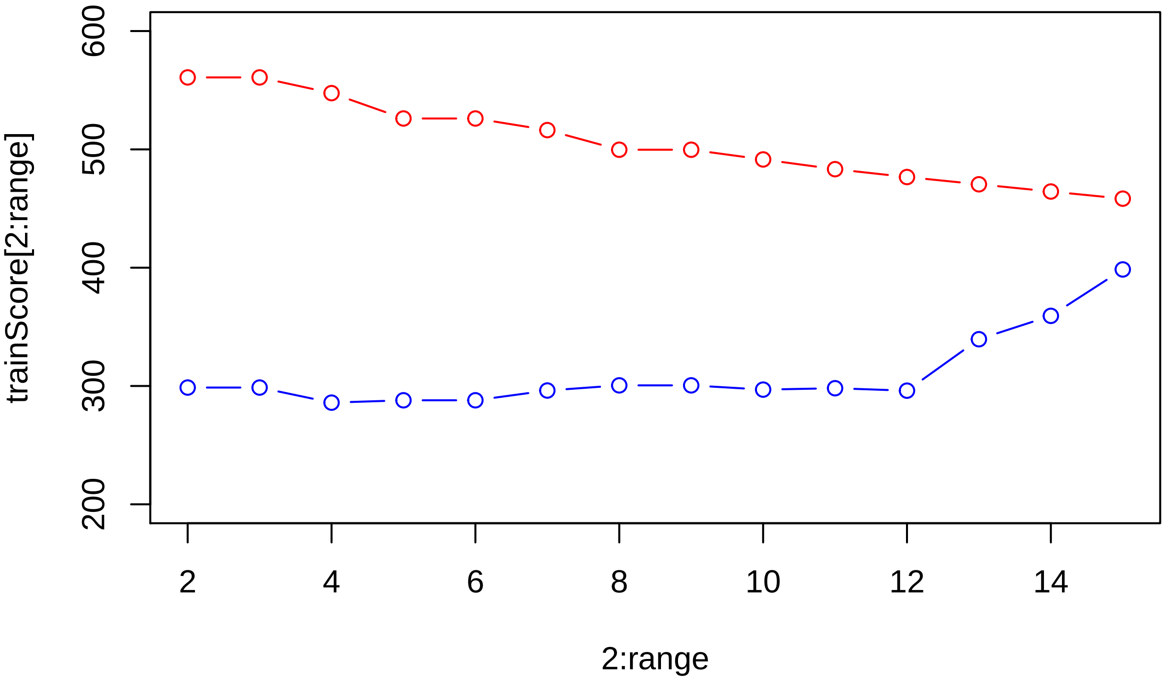
```
## Misclassification on deviance with train:  0.212
```

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

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

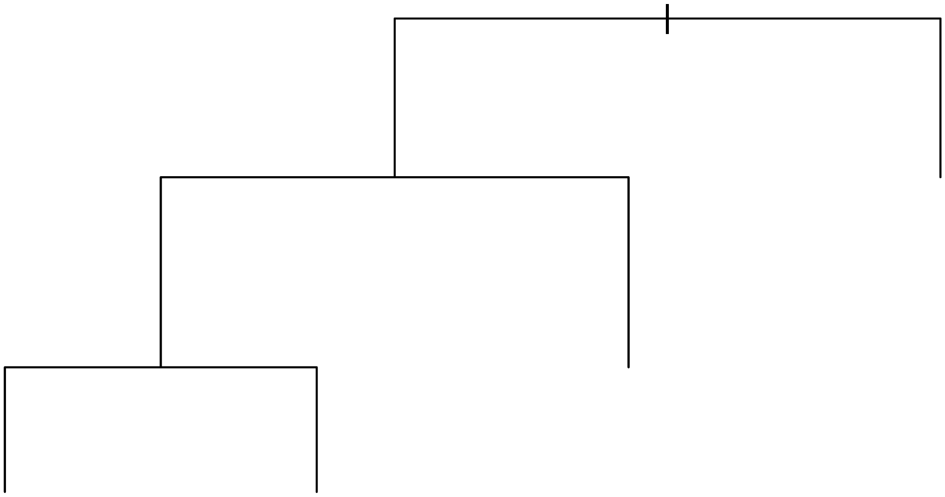
Here, misclassification rate is lower when using deviance as measure of impurity.

Step 3



```
## Misclassification on optimal tree:  0.256
```

```
## Tree depth is 3 as can be seen in the plot.
```



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

Step 4

```
## Confusion table of naïve bayes (test):
```

```
##          Actual
## Predicted bad good
##      bad   46   49
##      good  30  125
## Misclassification with naïve bayes (test):  0.316
```

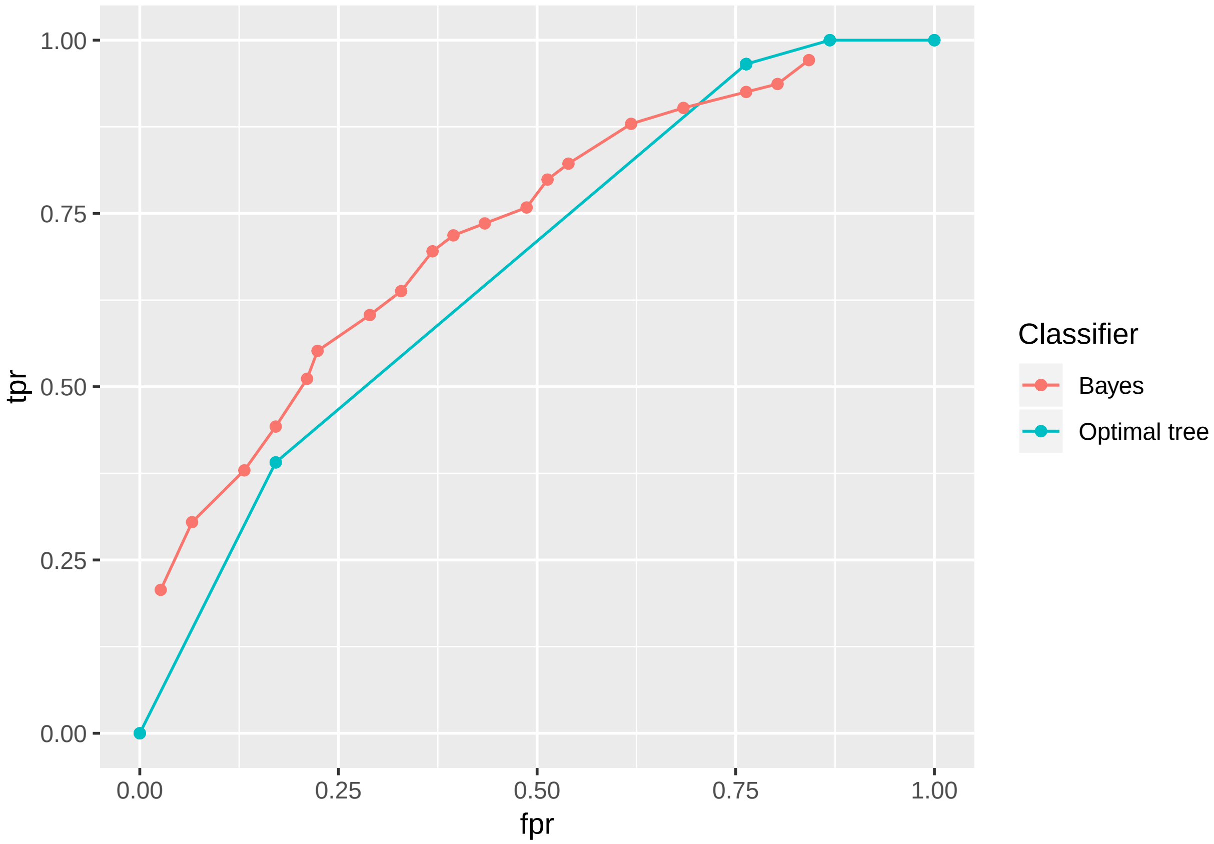
```
## Confusion table of naïve bayes (train):
```

```
##          Actual
## Predicted bad good
##      bad   95   98
##      good  52  255
```

```
## Misclassification with naïve bayes (train):  0.3
```

Naïve Bayes has much better result than in step 3.

Step 5



Naïve Bayes has better ratio between TPR and FPR. The only exception is around $\pi = 0.75$, as can be seen in the graph.

Step 6

Using loss matrix with naïve bayes.

```
## Confusion table of naïve bayes (using test data):
```

```
##          Actual
## Predicted bad good
##      bad   71  122
##      good   5   52
## Misclassification with naïve bayes (using test data):  0.508
```

```
## Confusion table of naïve bayes (using train data):
```

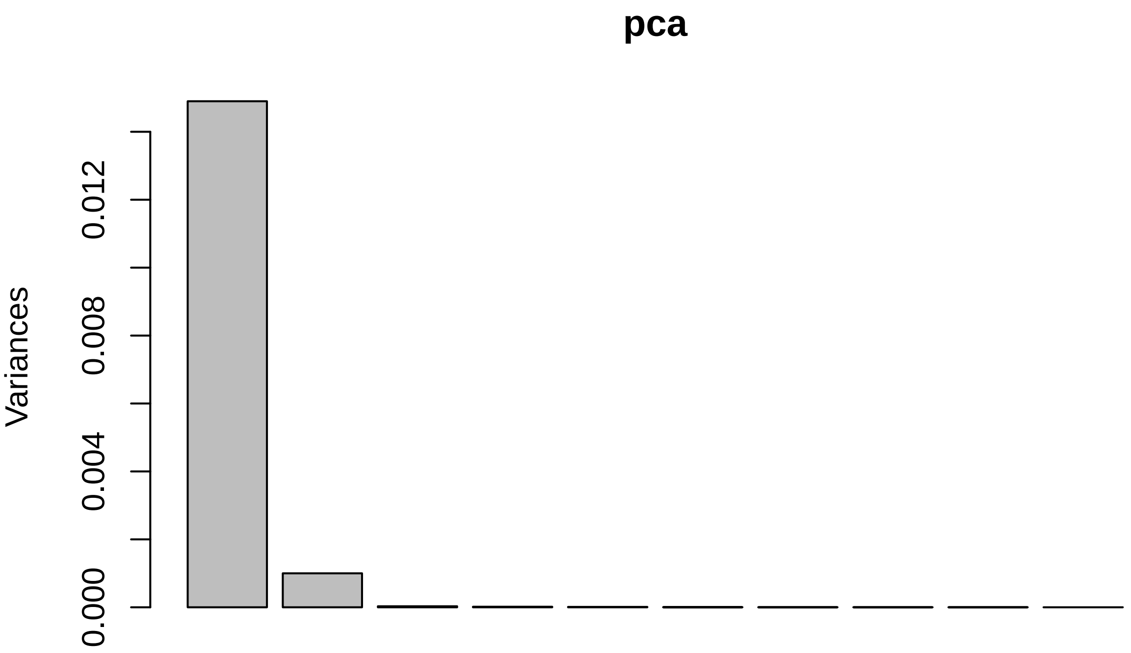
```
##          Actual
## Predicted bad good
##      bad  137  263
##      good  10   90
```

```
## Misclassification with naïve bayes (using train data):  0.546
```

The misclassification is much greater. But the confusion matrix is more favorable from an economic point of view for a company since less are predicted good that are actually bad.

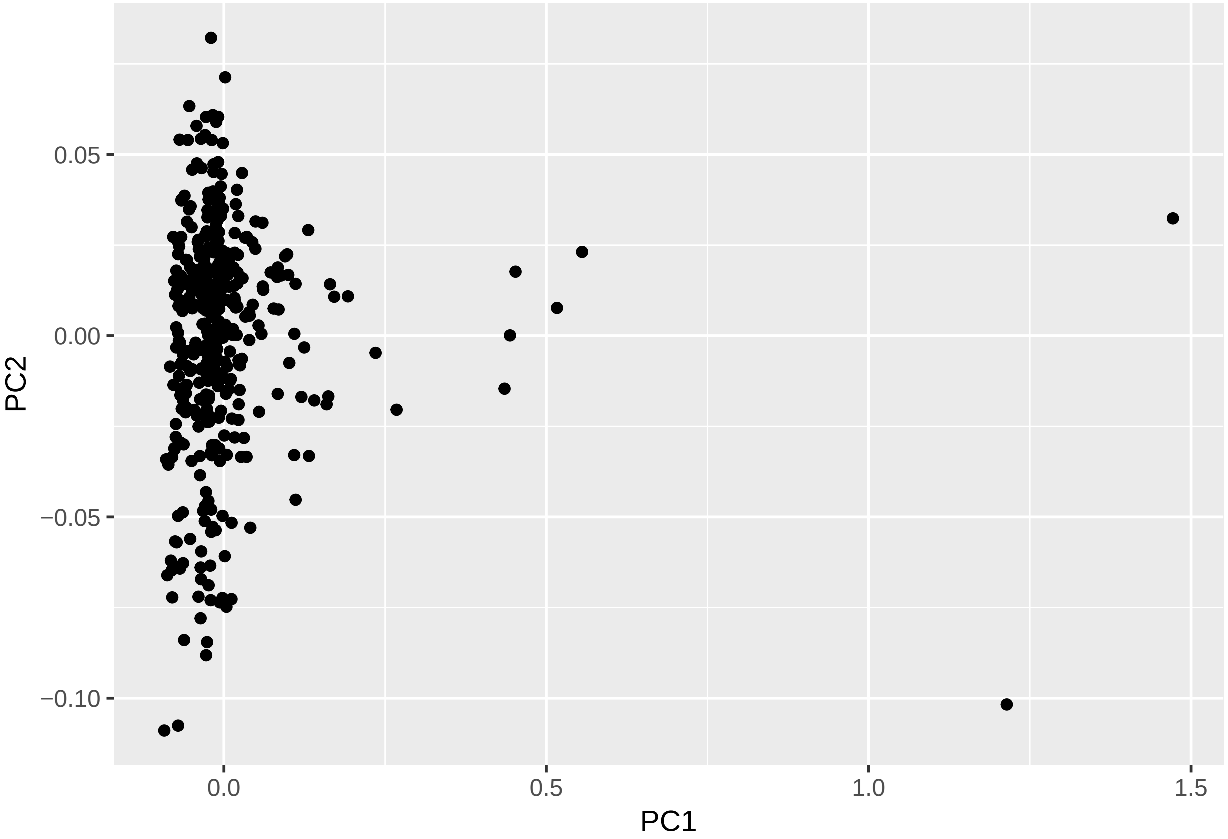
Assignment 4

Step 1



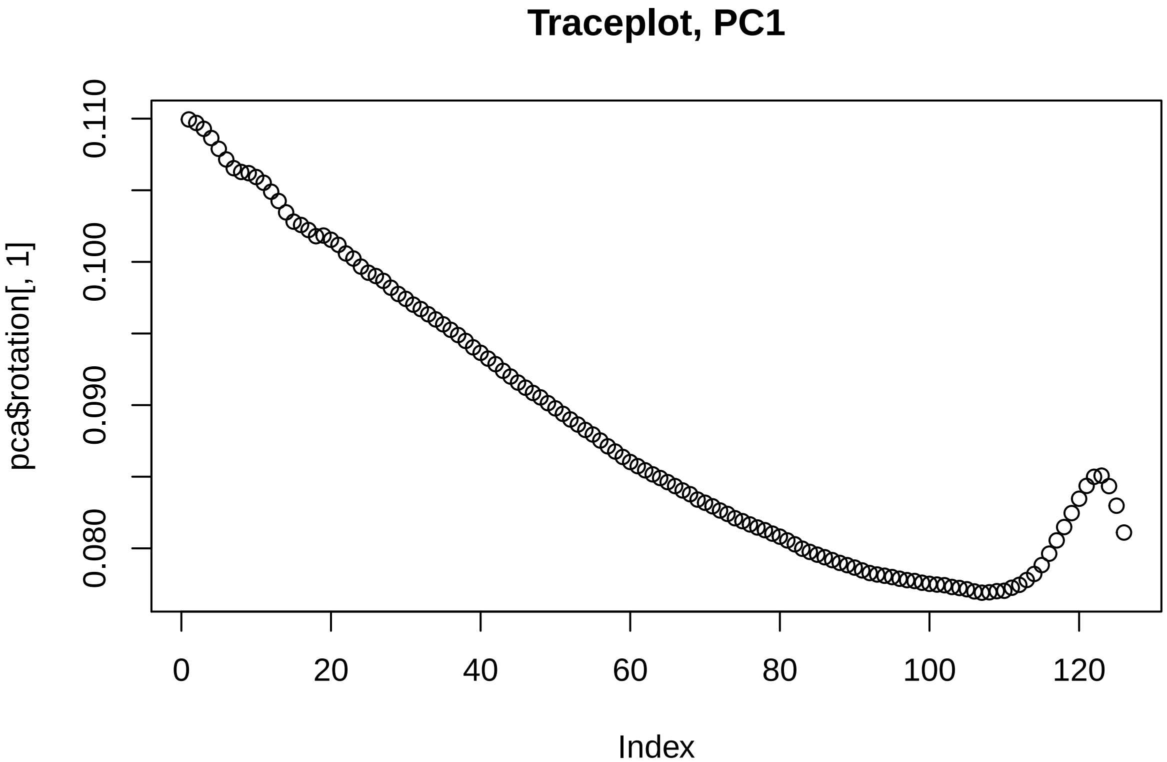
```
##   [1] "93.332" "6.263"  "0.185"  "0.101"  "0.068"  "0.025"  "0.009" 
##   [8] "0.003"  "0.003"  "0.002"  "0.001"  "0.001"  "0.001"  "0.001" 
##  [15] "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000" 
##  [22] "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000"  "0.000" 
##  [29] "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"
```

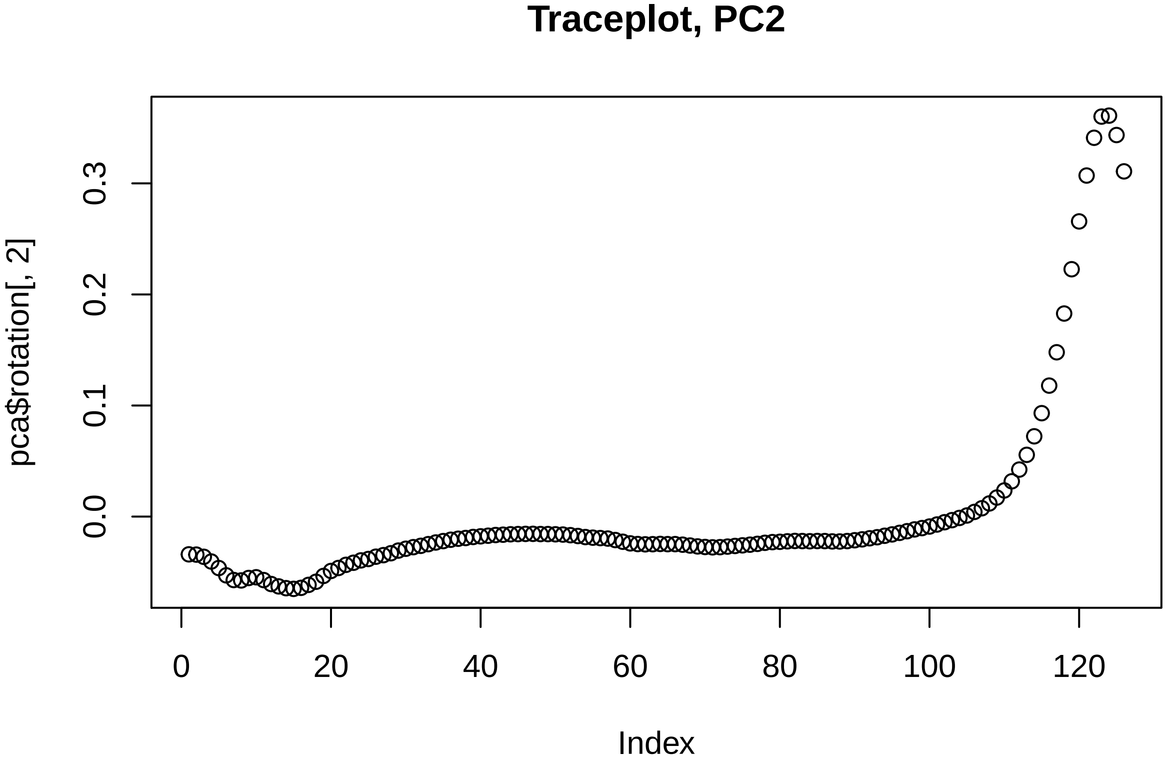
```
## 99% of the variance can be explained by first two PC.
```



Some diesel fuels depend a lot on PC1, compared to other fuels, I would say that these are unusual.

Step 2



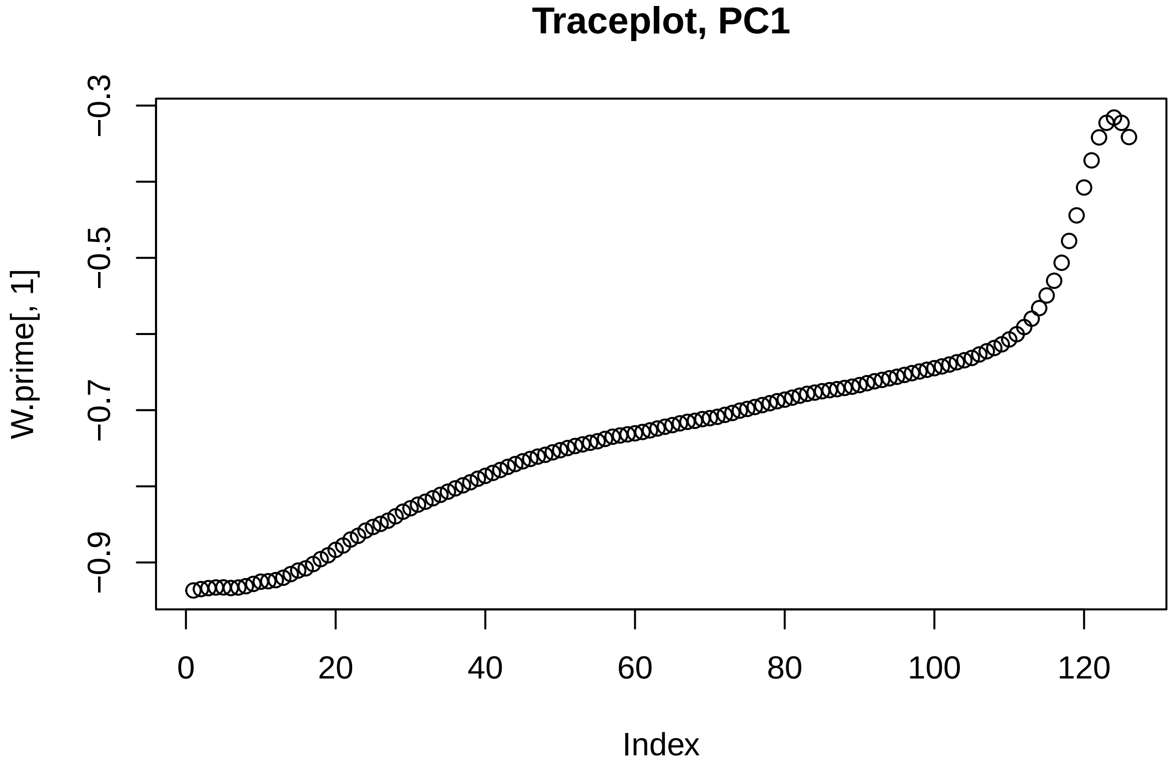


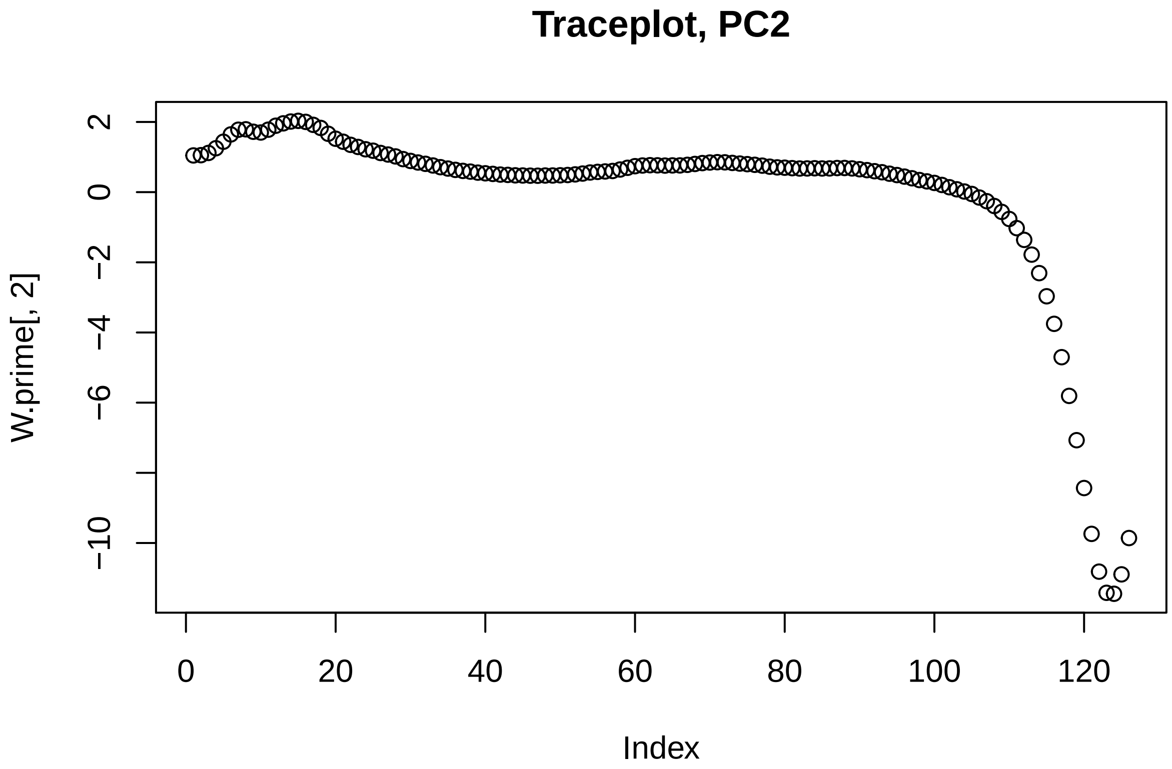
PC2 is explained by mainly a few original features. This can be seen in the graph since it's almost zero until Index is around 100-130.

Step 3

a

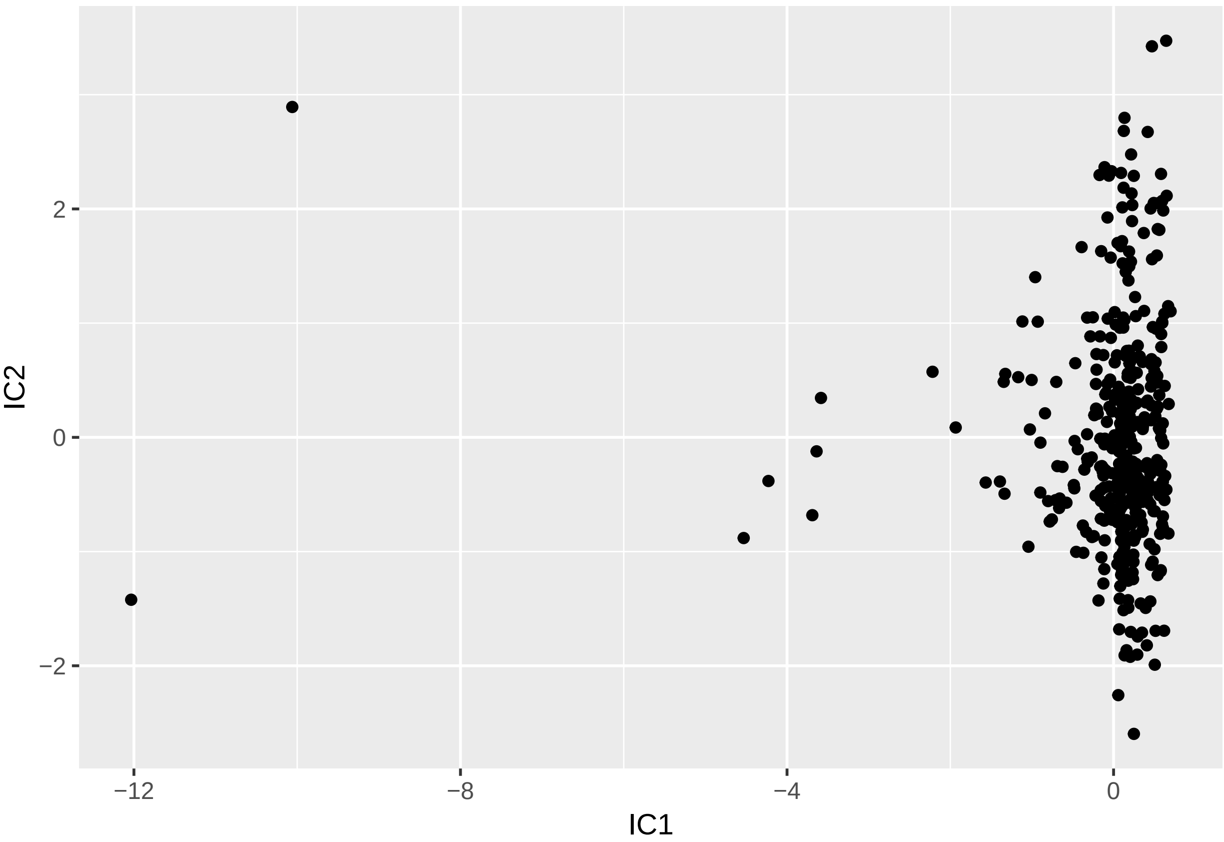
```
## Centering

## Whitening

## Symmetric FastICA using logcosh approx. to neg-entropy function

## Iteration 1 tol = 0.01930239

## Iteration 2 tol = 0.01303959

## Iteration 3 tol = 0.002393582

## Iteration 4 tol = 0.0006708454

## Iteration 5 tol = 0.0001661602

## Iteration 6 tol = 3.521604e-05
```





W’ is an estimation of an un-mixing matrix.

b



This plot is very similar to the one in step 1, but it is flipped and scaled.

Appendix

Assignment 1

```
# 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)

# Step 3
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)

# Step 4
glm.model = glm(formula = sex~RW+CL,
                data = crabs,
                family = 'binomial')
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)
```

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")

# 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)
cat("\nMisclassification on deviance with train: ",
    deviance.train.misclass)
cat("\nMisclassification on gini with test: ",
    gini.test.misclass)
cat("\nMisclassification on gini with train: ",
    gini.train.misclass, "\n")

# 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)
}

# 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)
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)

cat("\nTree depth is 5 as can be seen in the plot. \n")
plot(optTree)
cat("\n\nUsed variables in optimal tree: \n'savings' 'duration' 'history' 'age' 'purpose'\n\n")

# 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")

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

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

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

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

# Step 5
# 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
# Create model and classify
model.bayes = naiveBayes(formula = good_bad~., data=train)
predict.bayes.test = predict(model.bayes, newdata=test, type="raw")
predict.bayes.train = predict(model.bayes, newdata=train, type="raw")

# Print info on classification with prediction on test
loss = 10/1
predict.bayes.test.loss = ifelse(predict.bayes.test[, 'good'] /
                                 predict.bayes.test[, 'bad'] > loss,
                                 'good',
                                 'bad')
table.bayes = table(Predict=predict.bayes.test.loss, Actual=test$good_bad)
cat("Confusion table of naïve bayes (using test data):")
print(table.bayes)

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

```
# Print info on classification with prediction on train
predict.bayes.train.loss = ifelse(predict.bayes.train[, 'good'] /
                                   predict.bayes.train[, 'bad'] > loss,
                                  'good',
                                  'bad')
table.bayes = table(Predict=predict.bayes.train.loss, Actual=train$good_bad)
cat("Confusion table of naïve bayes (using train data): ")
print(table.bayes)

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

Assignment 4

```
# Step 1
# Add libraries
library("gridExtra")
library("ggplot2")
library("MASS")
library("stats")
library("fastICA")

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

# Read data
spectra = data.frame(read.csv2("NIRSpectra.csv"))
spectra = subset(spectra, select=-Viscosity)

# Calculate principal components
pca = prcomp(spectra)

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

# Print proportion of variation
sprintf("%2.3f",lambda/sum(lambda)*100)
cat("99% of the variance can be explained by first two PC.\n\n")

# Extract principal components
PC1 = pca$x[,1]
PC2 = pca$x[,2]

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

# Step 2
plot(pca$rotation[,1], main="Traceplot, PC1")
plot(pca$rotation[,2], main="Traceplot, PC2")
```

```
# Step 3a
set.seed(12345)
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)

W.prime = res$K %*% res$W
# Traceplots of fastICA
plot(W.prime[,1], main="Traceplot, PC1")
plot(W.prime[,2], main="Traceplot, PC2")

# Step 3b
# Extract ICs
IC1 = res$S[,1]
IC2 = res$S[,2]

# Plot the data projected onto PC 1 and 2
plot.projection = ggplot() +
    geom_point(data=spectra, mapping=aes(x=IC1, y=IC2))
grid.arrange(plot.projection)
```