Computer lab 2

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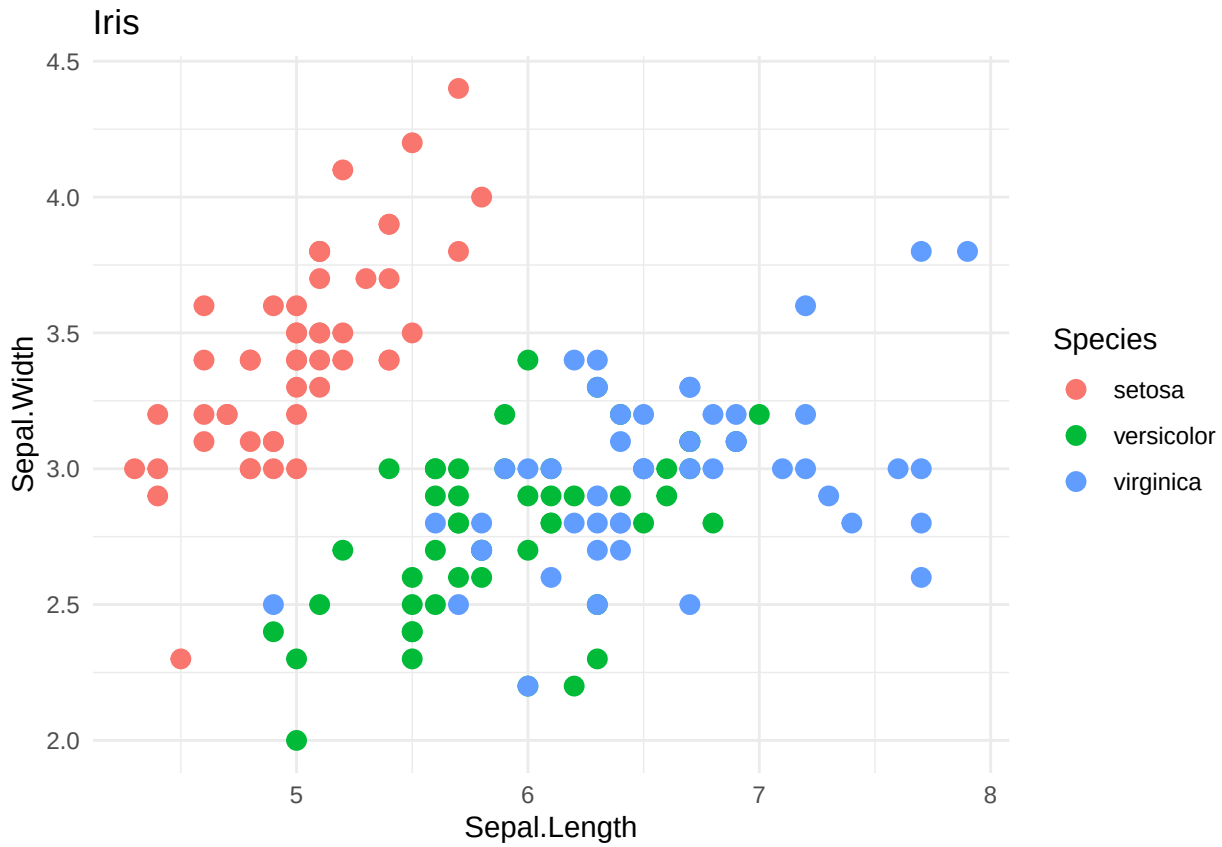
Statement of Contribution

- Assignment 1 - Martynas Lukosevicius
- Assignment 2 - Shwetha Vandagadde Chandramouly
- Assignment 3 - Alejo Perez Gomez

Assignment 1. LDA and logistic regression

1.



It is not easy to classify by LDA because as we can see from scatter plot versicolor overlay virginica. I expect that misclasification rate will be high because part of the virginica data will be predicted as versicolor and vice versa

2.

a)

Setosa: mean - $\begin{bmatrix}5.006\\3.428\end{bmatrix}$, covariance - $\begin{bmatrix}0.124 & 0.099\\0.099 & 0.144\end{bmatrix}$, $\pi_{setosa} - 0.3333333$

Virginica: mean - $\begin{bmatrix}6.588\\2.974\end{bmatrix}$, covariance - $\begin{bmatrix}0.404 & 0.094\\0.094 & 0.104\end{bmatrix}$, $\pi_{virginica} - 0.3333333$

Versicolor: mean - $\begin{bmatrix}5.936\\2.77\end{bmatrix}$, covariance - $\begin{bmatrix}0.266 & 0.085\\0.085 & 0.098\end{bmatrix}$, $\pi_{versicolor} - 0.3333333$

b)

Pooled covariance - $\begin{bmatrix}0.219 & 0.09\\0.09 & 0.114\end{bmatrix}$

c)

Probabilistic model for LDA:

$$P(y = C_i|X, w) \propto P(X|Y = C_i, w)P(Y = C_i|w)$$
$$P(X|Y = C_i, w) \sim N(\mu_i, \Sigma)$$
$$P(Y = C_i|w) = \pi_i$$

$$P(y = C_i|X, w) \propto exp[(\Sigma^{-1}\mu_i)^T X - \frac{1}{2}\mu_i^T\Sigma^{-1}\mu_i + log(\pi_i)] = exp[w_i X + w_{0i}]$$

Where $w_i - (\Sigma^{-1}\mu_i)^T$ and $w_{0i} - -\frac{1}{2}\mu_i^T\Sigma^{-1}\mu_i + log(\pi_i)$

d)

discriminant function $\delta_k(x) = x^T\Sigma^{-1}\mu_k - \frac{1}{2}\mu_k^T + log(\pi_k)$

```
discrim <- function(x,a){
  constant <- (-1/2) * t(a$mean) %*% solve(pcov) %*% a$mean + log(a$prior)
  nonconstant <- t(x) %*% solve(pcov) %*% a$mean
  return(nonconstant+constant)
}
```

e)

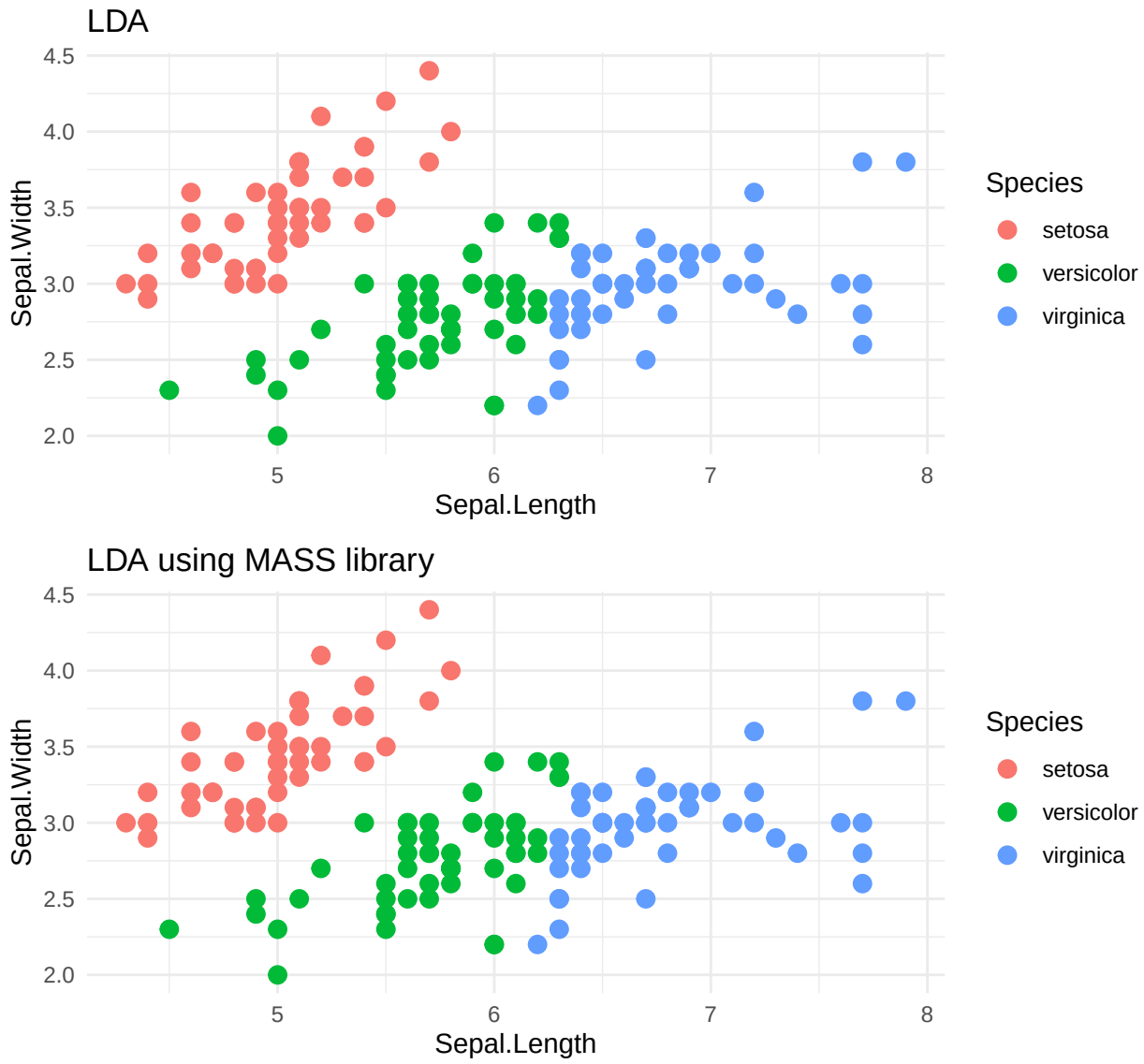
$$(w_i - w_k)x + (w_{0i} - w_{0k}) = 0$$

decision boundaries:

- Setosa - Versicolor: $\begin{pmatrix}-9.8077917\\13.5573492\end{pmatrix} x + (11.6442029) = 0$
- Virginica - Versicolor: $\begin{pmatrix}3.3163254\\-0.827961\end{pmatrix} x + (-18.3889254) = 0$
- Setosa - Versicolor: $\begin{pmatrix}-13.124117\\14.3853102\end{pmatrix} x + (30.0331283) = 0$

LDA assume that $\Sigma_i = \Sigma$, However it is not the case in this situation

3.

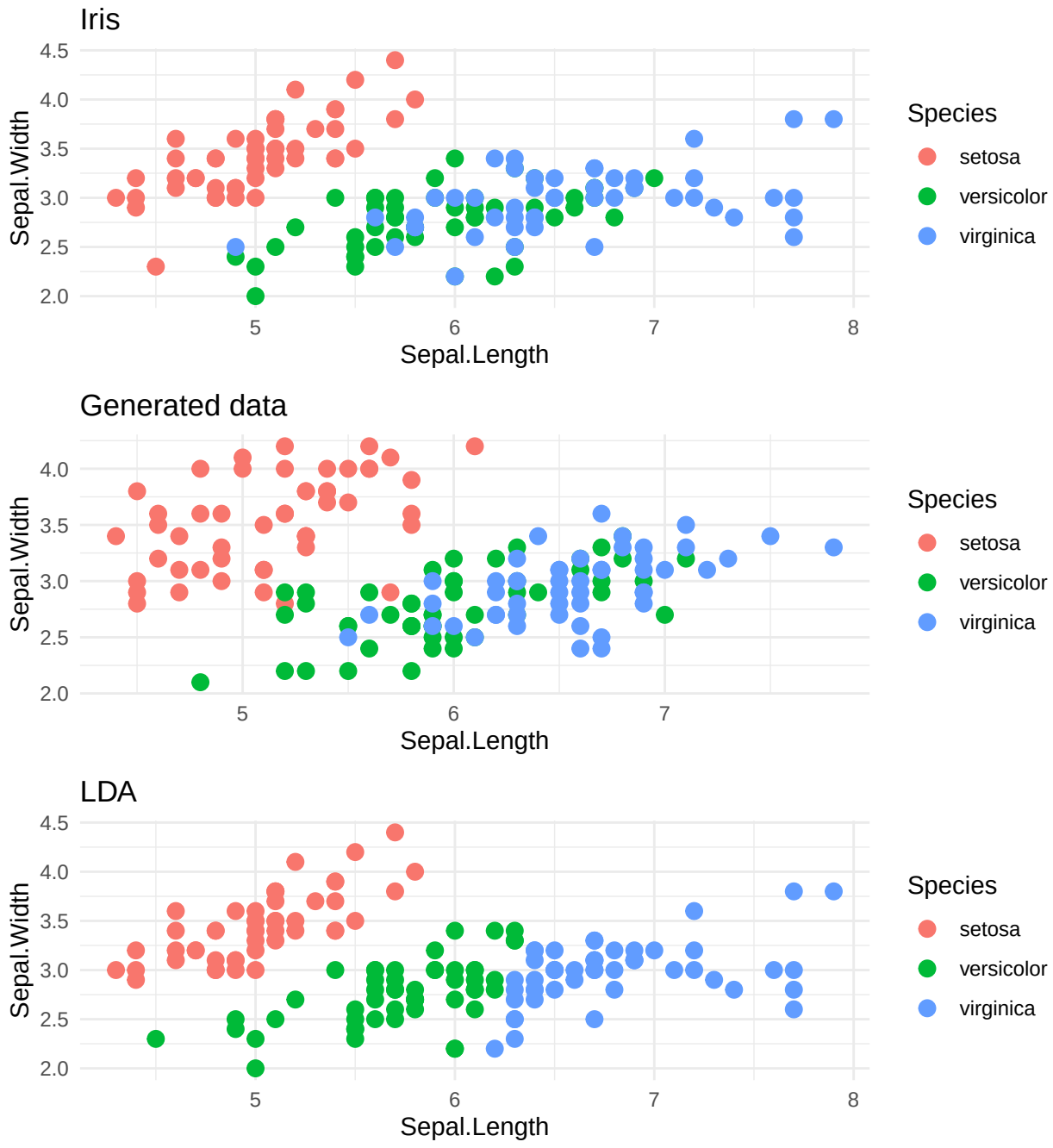


Missclasification rate of LDA: 0.2

Missclasification rate of LDA using MASS library: 0.2

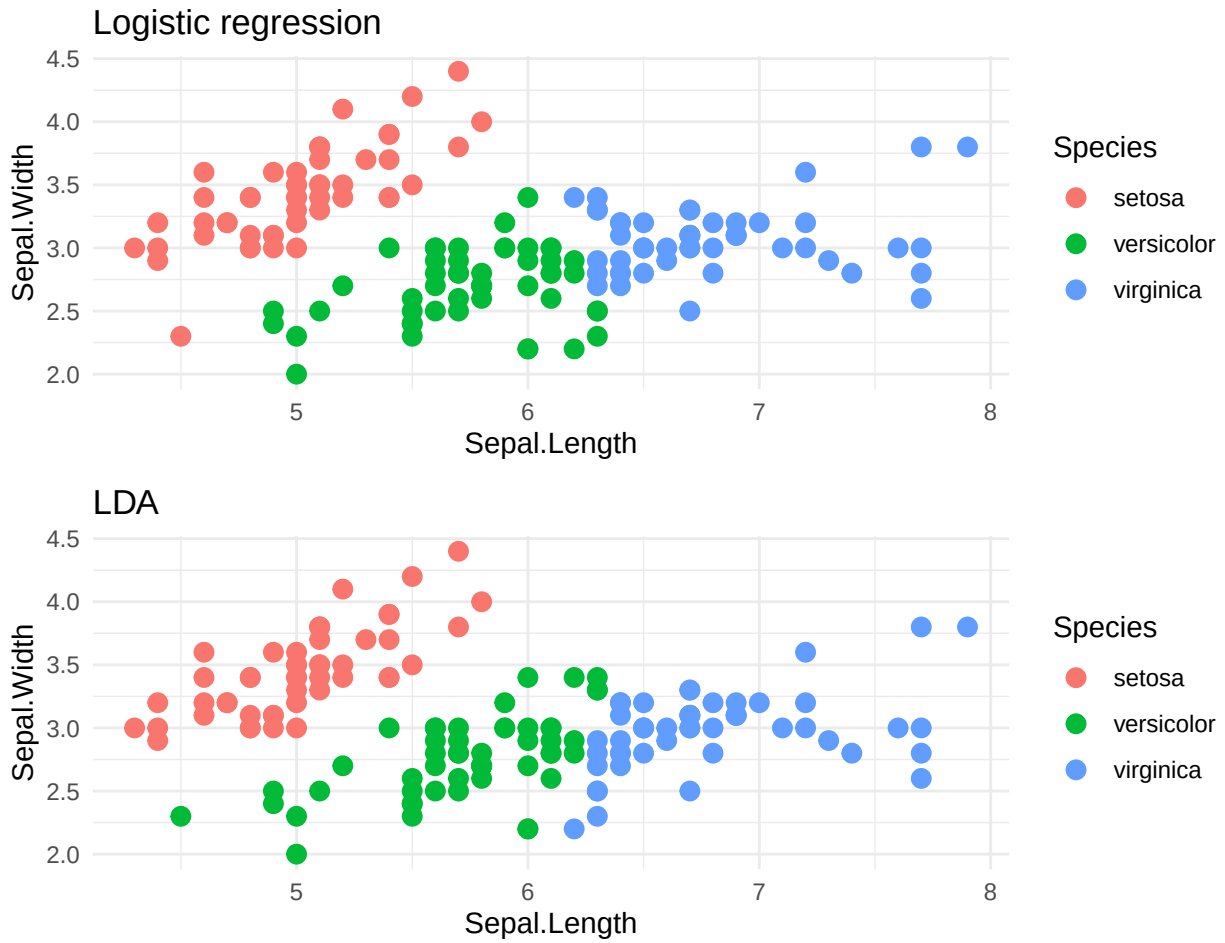
Test errors are the same, Classification methods are identical so and the results are identical

4.



From Plots we can see generated data is spread equally, it is because of LDA assumption that covariances are equal. We can also notice that LDA can not distinguish classes when data overlay.

5.



	Misclasification rate
LDA	0.2000000
LR	0.1666667

From misclasification rate we can see that logistic regresion performed slightly better than LRA.

Assignment 2. Decision trees and Naïve Bayes for bank marketing

1.

Partitioning the data into train , test and validation.

```
bank = read.csv("bank-full.csv", header = TRUE, sep = ";",stringsAsFactors = TRUE)

bank = bank[,-12]
n = nrow(bank)
set.seed(12345)
id1=sample(1:n, floor(n*0.4))
train=bank[id1,]
d2 = bank[-id1,]
```

```
n2 = nrow(d2)
id2=sample(1:n2, floor(n2*0.5))
test=d2[id2,]
validate=d2[-id2,]
```

2.

Fitting decision tree to training data

```
library(tree)
dt_default = tree(y~.,data = train)
dt_size = tree(y~.,data = train, control = tree.control(nrow(train),minsize = 7000))
dt_dev = tree(y~.,data = train, control = tree.control(nrow(train),mindev = 0.0005))
```

Training data missclassification rate:

Default fit : 0.1048441

Min node size is 7000 fit : 0.1048441

Min deviance is .0005 fit : 0.0936187

Validation data missclassification rate:

Default fit : 0.1116927

Min node size is 7000 fit : 0.1116927

Min deviance is .0005 fit : 0.112946

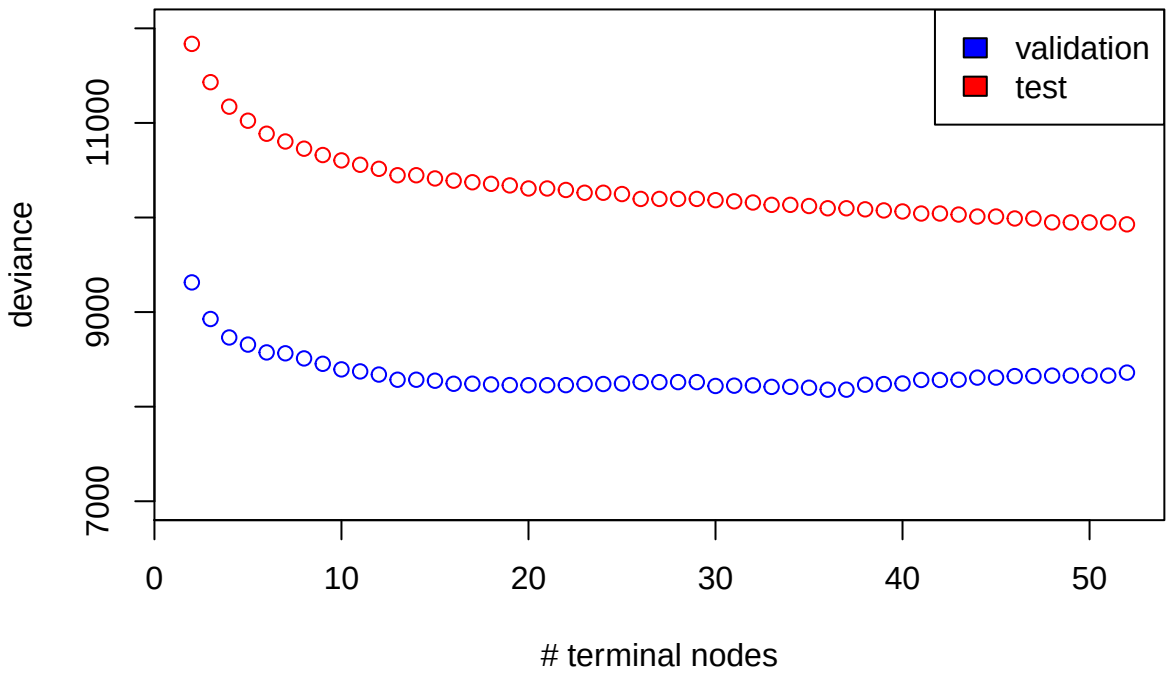
Choosing the best of three fits : Though the misclassification error was least for mindev=0.0005 fit on train data ,it has large tree of 150 terminal nodes, this leads to a overfit tree. As a result of this , on fitting the validation data , the misclassification error rate increases more in this when compared to other two trees. Model a and b , both have same misclassification error , however since the "b" has only 5 terminal nodes whereas "a" has 6 terminal nodes , its better to choose the simpler model ie b. But if we are allowed to find the optimal number of leaves to avoid overfitting, then c would be the best model.

In our case , setting the deviance very small ie 0.0005, made the tree grow more deeper as a large tree with 150 terminal nodes , this did reduce the misclassification on the training data, but ended up overfitting for validation data.

Effect of deviance and nodesize on the tree size : Decreasing the deviance leades to increase in tree size. Increase in the nodesize leads to decrease in the tree size.

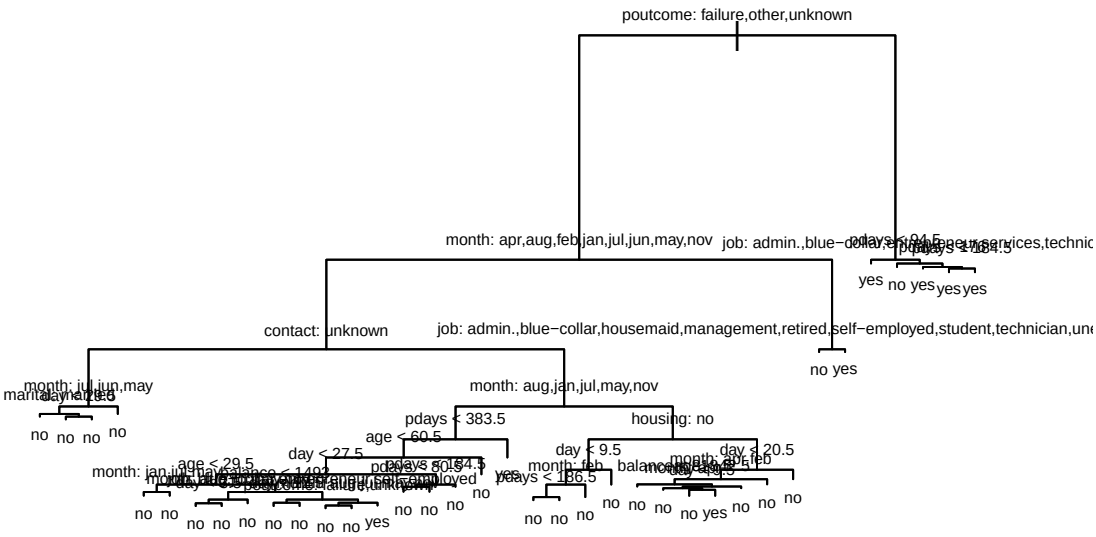
3.

Selecting optimal tree by training and validation



Optimal amount of leaves = 36

```
optimal_tree = prune.tree(dt_dev, best = 36)
plot(optimal_tree)
text(optimal_tree, pretty = 0, cex = 0.5)
```



Variable : poutcome is the most important for decision making in this tree.

Tree sturcture : variable included = poutcome, month, contact, marital, day, pdays, age, balance, job and housing Number of leaves = 37 First variable considered in the tree is "poutcome", the partition is made by taking the condition poutcome = failure, other or unknown, if this is true , the data goes to left side to the next condition on variable month. If the poutcome was not satisfied , ie say poutcome was "success" then the data flows to right part , where next node condition is on pdays < 94.5. The tree continues until the number of leaves are 37.

Confusion matrix and missclassification rate for test data.

confusion matrix :

	no	yes
no	11868	122
yes	1347	226

Missclassification rate : 0.1083094

we can see that the misclassification rate for the test data has reduced for the optimal tree. Hence this is a better fit compared to the previously tried tree fits.

4.

Loss Matrix :

	no	yes
no	0	1
yes	5	0

Confusion matrix :

	no	yes
no	10965	1025
yes	745	828

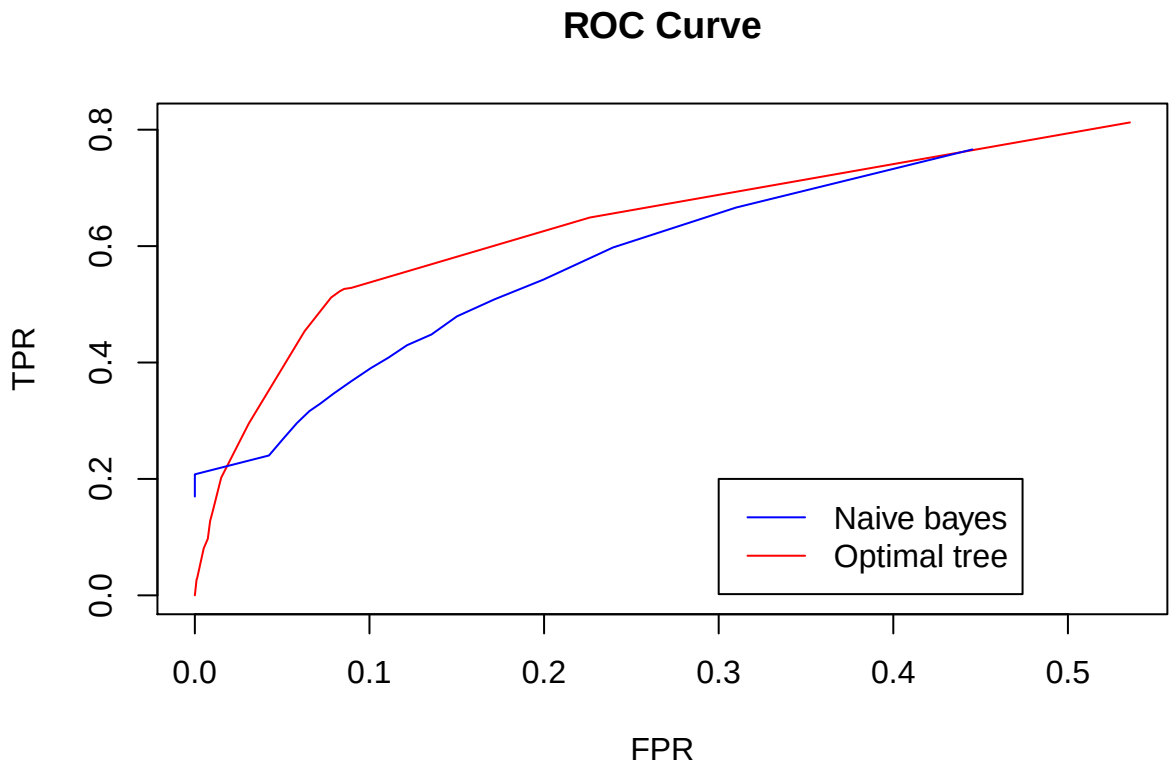
Missclassification rate : 0.1305021

Here in the loss function we can see that , penalty for predicting observed yes as no is 5 and no as yes is 1. So on applying loss function , as expected , the misclassification of an observed yes as no is reduced in the confusion matrix here. Previously observed yes predicted as no was 1347 , and now it is 745. However the missclassification error rate has increased.

We can try different loss matrix (assigning the loss function with suitable costs for the respective senario) and choose the one which gives the lowest misclassification rate.

5.

Fitting naive bayes model, computing TPR and FPR for both models and plotting the ROC curve



Conclusion : Area under the curve is more for Optimal tree fit hence this is the best classifier.

Appendix

```
knitr::opts_chunk$set(echo = TRUE)
library(datasets)
y <- iris

library(ggplot2)
plotiris <- ggplot(iris, aes(x=Sepal.Length, y=Sepal.Width, color=Species)) +
  geom_point(size=3) + theme_minimal() + ggtitle("Iris")
plotiris

a2 <- function(x){
y1 <- iris[as.numeric(iris$Species) == x, ][1:2]
mean1 <- apply(y1, 2,mean)
covar <- cov(y1)
prior <- dim(y1)[1]/ dim(iris)[1]

return(list(data = y1, mean = unname(mean1), covariance = covar, prior = prior, n = dim(y1)[1]))
}


pooledcov <- function(a,b,c){
  temp <- (a$cov * a$n) + (b$cov * b$n) + (b$cov * b$n)
  return(temp/dim(iris)[1])
}

Setosa <- a2(1)
Versicolor <- a2(2)
virginica <- a2(3)

# print("Setosa")
# print(Setosa[c(-1,-5)])
#
# print("Versicolor")
# print(Versicolor[c(-1,-5)])
#
# print("Virginica")
# print(virginica[c(-1,-5)])

write_matex <- function(x) {
  begin <- "\\begin{bmatrix}"
  end <- "\\end{bmatrix}"
  X <-
    apply(x, 1, function(x) {
      paste(
        paste(x, collapse = "&"),
        "\\\\"
      )
    })
  writeLines(c(begin, X, end))
}
```

```r
pcov <- pooledcov(Setosa,Versicolor,virginica)
discrim <- function(x,a){
  constant <- (-1/2) * t(a$mean) %*% solve(pcov) %*% a$mean + log(a$prior)
  nonconstant <- t(x) %*% solve(pcov) %*% a$mean
  return(nonconstant+constant)
}
w0 <- function(a){
  constant <- (-1/2) * t(a$mean) %*% solve(pcov) %*% a$mean + log(a$prior)
  return(constant)
}

w <- function(a){
  nonconstant <- solve(pcov) %*% a$mean
  return(nonconstant)
}

predictLDA <- function(x){
  values <- c(discrim(x, Setosa), discrim(x,Versicolor), discrim(x,virginica))
  return(which.max(values))
}

res <- cbind(iris[1:2],cut(apply(iris[1:2], 1, predictLDA),3, c("setosa","versicolor","virginica")))
colnames(res) <- c("Sepal.Length", "Sepal.Width", "Species")
plotcustom <- ggplot(res, aes(x=Sepal.Length, y=Sepal.Width, color=Species)) +
  geom_point(size=3) + theme_minimal() + ggtitle("LDA")

# a <- table(iris$Species, res$Species)
# knitr::kable(a, caption = "Confusion matrix ")


library(MASS)
fitLDA <- lda(Species ~ Sepal.Length + Sepal.Width, data = iris)
resLDA <- cbind(iris[1:2], predict(fitLDA, iris[1:2]))
colnames(resLDA) <- c("Sepal.Length", "Sepal.Width", "Species")

library(gridExtra)

plotLDA <- ggplot(resLDA, aes(x=Sepal.Length, y=Sepal.Width, color=Species)) +
  geom_point(size=3) + theme_minimal() + ggtitle("LDA using MASS library")

grid.arrange(plotcustom, plotLDA, nrow=2)
library(mvtnorm)
set.seed(12345)
gen <- rbind(rmvnorm(50, Setosa$mean, pcov),
             rmvnorm(50, Versicolor$mean, pcov),
             rmvnorm(50, virginica$mean, pcov))
gen <- round(gen,1)
gen <- as.data.frame(cbind(gen, c(rep("setosa",50), rep("versicolor",50), rep("virginica",50) )))
colnames(gen) <- c("Sepal.Length", "Sepal.Width", "Species")

plotfromequation <- ggplot(gen, aes(x=as.numeric(Sepal.Length), y=as.numeric(Sepal.Width), color=Species
  geom_point(size=3) + ggtitle("Generated data")  + theme_minimal() + xlab("Sepal.Length") + ylab("Sepal
grid.arrange(plotiris, plotfromequation,  plotcustom,  nrow=3)
```

```
library(nnet)
fitlr <- multinom(Species ~ Sepal.Length + Sepal.Width, data = iris)
reslr <- predict(fitlr,iris[1:2])

reslr <- cbind(iris[1:2], reslr, deparse.level = 1)
names(reslr)[3] <- c("Species")

plotlr <- ggplot(reslr, aes(x=Sepal.Length, y=Sepal.Width, color=Species)) +
  geom_point(size=3) + ggtitle("Logistic regression")  + theme_minimal()

grid.arrange(plotlr,  plotcustom,  nrow=2)
table <- matrix(c(mean(iris$Species != resLDA$Species),mean(iris$Species != reslr$Species)))
colnames(table) <- c("Misclasification rate")
row.names(table) <- c("LDA", "LR")
knitr::kable(table)
bank = read.csv("bank-full.csv", header = TRUE, sep = ";",stringsAsFactors = TRUE)

bank = bank[,-12]
n = nrow(bank)
set.seed(12345)
id1=sample(1:n, floor(n*0.4))
train=bank[id1,]
d2 = bank[-id1,]
n2 = nrow(d2)
id2=sample(1:n2, floor(n2*0.5))
test=d2[id2,]
validate=d2[-id2,]

library(tree)
dt_default = tree(y~.,data = train)
dt_size = tree(y~.,data = train, control = tree.control(nrow(train),minsize = 7000))
dt_dev = tree(y~.,data = train, control = tree.control(nrow(train),mindev = 0.0005))
#summary(dt_default)
#summary(dt_size)
#summary(dt_dev)

mce_default_train = summary(dt_default)$misclass[1]/summary(dt_default)$misclass[2]
mce_size_train = summary(dt_size)$misclass[1]/summary(dt_size)$misclass[2]
mce_dev_train = summary(dt_dev)$misclass[1]/summary(dt_dev)$misclass[2]

y_default = predict(dt_default, validate, type = "class")
y_size = predict(dt_size, validate, type = "class")
y_dev = predict(dt_dev, validate, type = "class")

missclass = function(y,y1){
  n = length(y)
  return( 1 - sum(diag(table(y,y1)))/n)
}

mce_default_val = missclass(validate$y,y_default)
mce_size_val = missclass(validate$y,y_size)
mce_dev_val =  missclass(validate$y,y_dev)
```

```
train_score = validate_score = rep(0,52)
for(i in 2:52){
  pruned_tree = prune.tree(dt_dev,best = i)
  pred = predict(pruned_tree, newdata=validate, type="tree")
  train_score[i] = deviance(pruned_tree)
  validate_score[i] = deviance(pred)
}
plot(2:52, train_score[2:52], type="p", col="red", ylim =c(7000,12000), xlab = "# terminal nodes", ylab
points(2:52, validate_score[2:52], type="p", col="blue")
legend("topright", c("validation", "test"), fill=c("blue", "red"))
optimal_tree = prune.tree(dt_dev, best = 36)
plot(optimal_tree)
text(optimal_tree, pretty = 0, cex = 0.5)

optimal_pred = predict(optimal_tree, test, type = "class")
confusion_matrix = table(test$y,optimal_pred)
missclassification_rate = missclass(test$y,optimal_pred)
knitr::kable(confusion_matrix)

loss_mat = t(matrix(c(0,1,5,0),2,2))
row.names(loss_mat) = colnames(loss_mat) = c("no","yes")
op = predict(optimal_tree, test)
loss_fit = ifelse(loss_mat[1,2]*op[,1] > loss_mat[2,1]*op[,2] ,"no","yes")#1 is no , 2 is yes
loss_confusion_matrix = table(test$y,loss_fit)
m = missclass(test$y,loss_fit)
knitr::kable(loss_mat)
knitr::kable(loss_confusion_matrix)
library(e1071)
naive_model = naiveBayes(y~., train)
naive_y = predict(naive_model, test, type = "raw")

pi = seq(0.05,0.95,0.05)
prob_naive_yes = naive_y[,2]
prob_dt_yes = op[,2]
real_y = ifelse(test$y == "yes",1,0) # yes is 1 , no is 0
NAIVE = DT = matrix(0,ncol = 3,nrow = length(pi))


for(i in 1:length(pi)){
  dt_assign = ifelse(prob_dt_yes > pi[i],1,0)
  naive_assign = ifelse(prob_naive_yes > pi[i],1,0)

  cm_dt = table(real_y,dt_assign)
  cm_naive = table(real_y,naive_assign)

  if(all(dim(cm_dt) == c(2,2))== TRUE){
  tpr_dt = cm_dt[2,2]/sum(cm_dt[2,])
  } else {
  tpr_dt = 0
  }
  if(all(dim(cm_naive) == c(2,2))){
  tpr_naive = cm_naive[2,2]/sum(cm_naive[2,])
  } else {
```

```
  tpr_naive = 0
  }

  if(all(dim(cm_dt) == c(2,2))== TRUE){
  fpr_dt = cm_dt[1,2]/sum(cm_dt[1,])
  }else {
  fpr_dt = 0
  }
  if(all(dim(cm_dt) == c(2,2))== TRUE){
  fpr_naive = cm_naive[1,2]/sum(cm_naive[1,])
  }else {
  fpr_naive = 0
  }

  NAIVE[i,] = c(pi[i],tpr_naive,fpr_naive)
  DT[i,] = c(pi[i],tpr_dt,fpr_dt)


}
colnames(NAIVE) = c("pi","TPR","FPR")
colnames(DT) = c("pi","TPR","FPR")

#ROC curve
plot(DT[,3],DT[,2],ylab = "TPR",xlab = "FPR", type = "l", col = "red")
lines(NAIVE[,3],NAIVE[,2],col= "blue")
title("ROC Curve")
legend(0.3, 0.2, legend = c("Naive bayes","Optimal tree"), col=c("blue","red"), lty = c(1,1))
```