Machine Learning Lab 2

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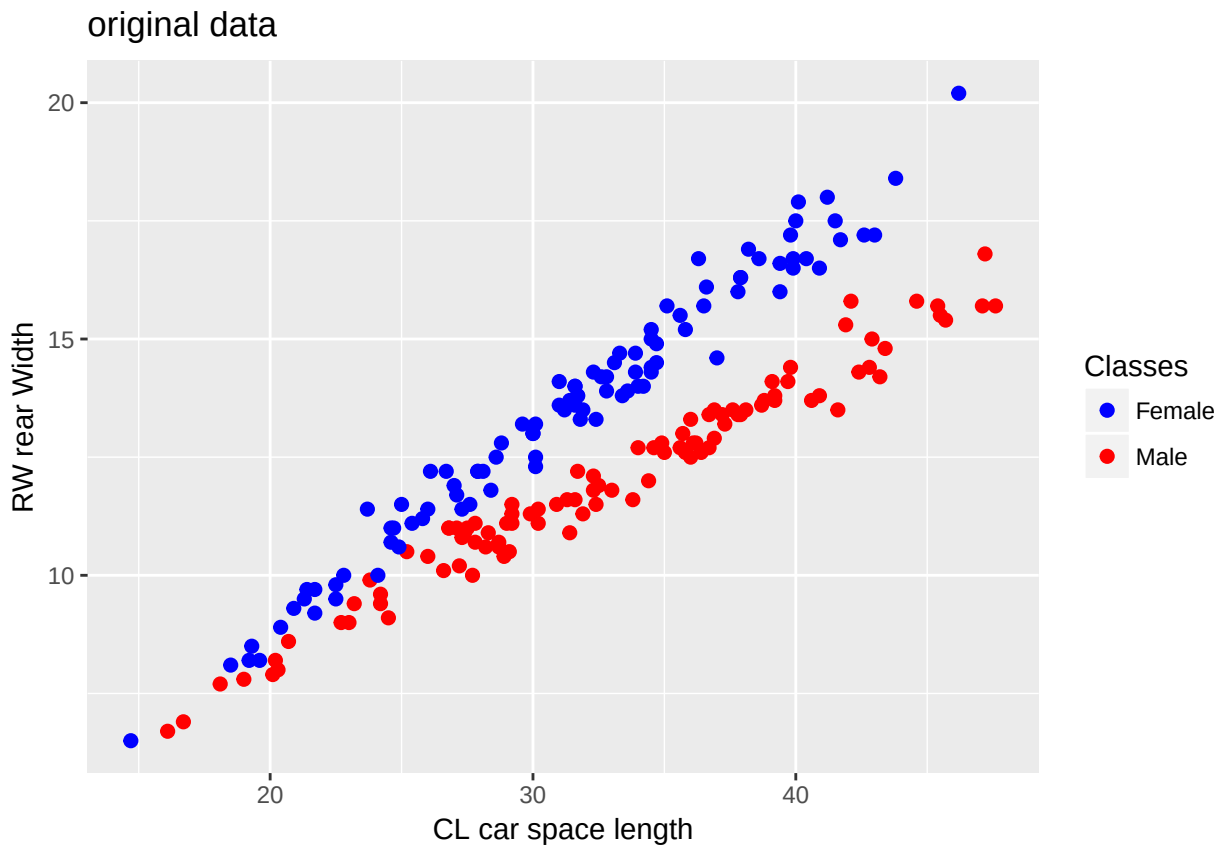
Assignment 1 LDA and Logistic Regression

Part 1



Yes , it is easy to classify the data by linear discriminant function because from the plot it can be observed that the two classes have cooperative distribution having equal covariance.

Part 2

Discriminant function coefficients for male

```
## [1]   2.5658514  -0.2138144 -12.5634175
```

Discriminant function coefficients for Female

```
## [1]   8.248698  -2.161318 -22.428769
```

Decision boundary Equation

$$RW * W_{1R} + CL * W_{1C} + W_{01} = RW * W_{2R} + CL * W_{2C} + W_{02}$$

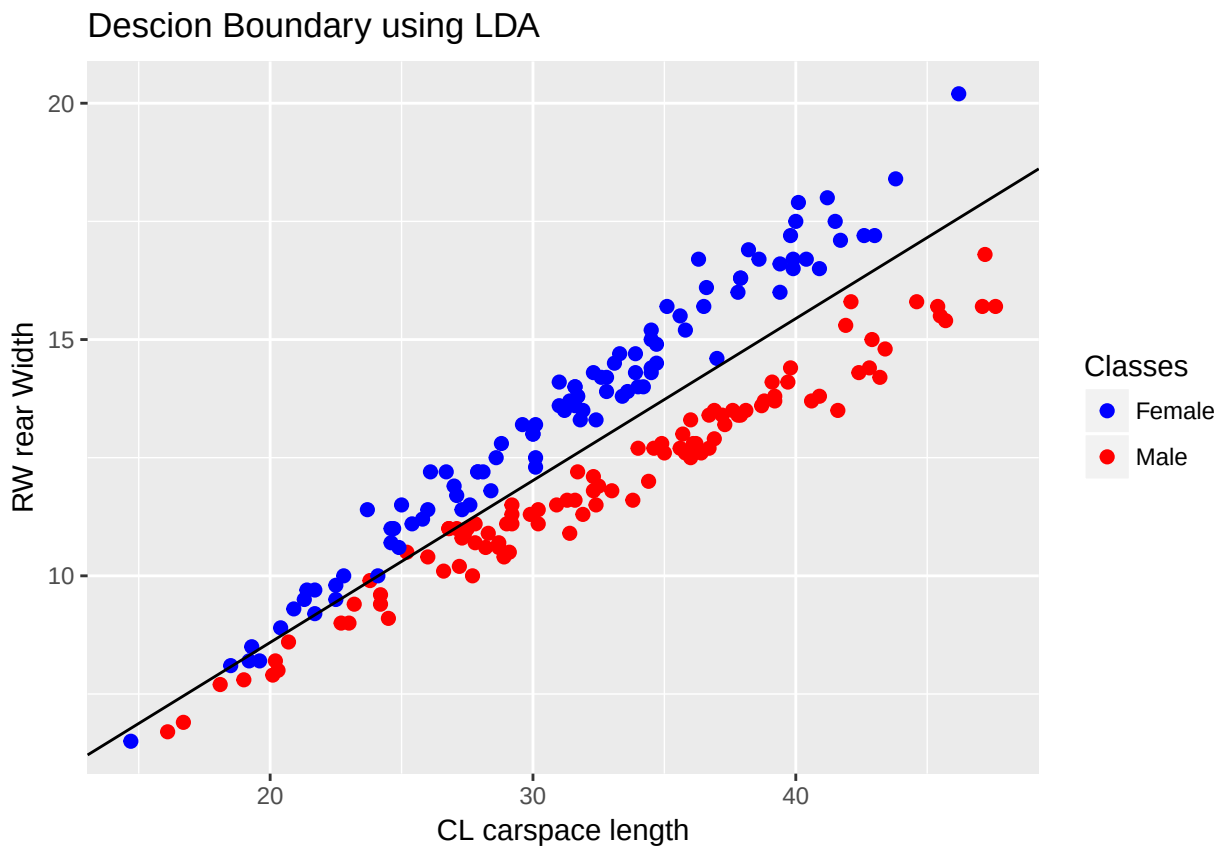
Final equation in term or RW as a Function of CL

$$RW = \frac{(CL(W_{2C} - W_{1C}) + W_{02} - W_{02})}{W_{1R} - W_{2R}}$$

$$intercept = \frac{CL(W_{2C} - W_{1C})}{W_{1R} - W_{2R}}$$

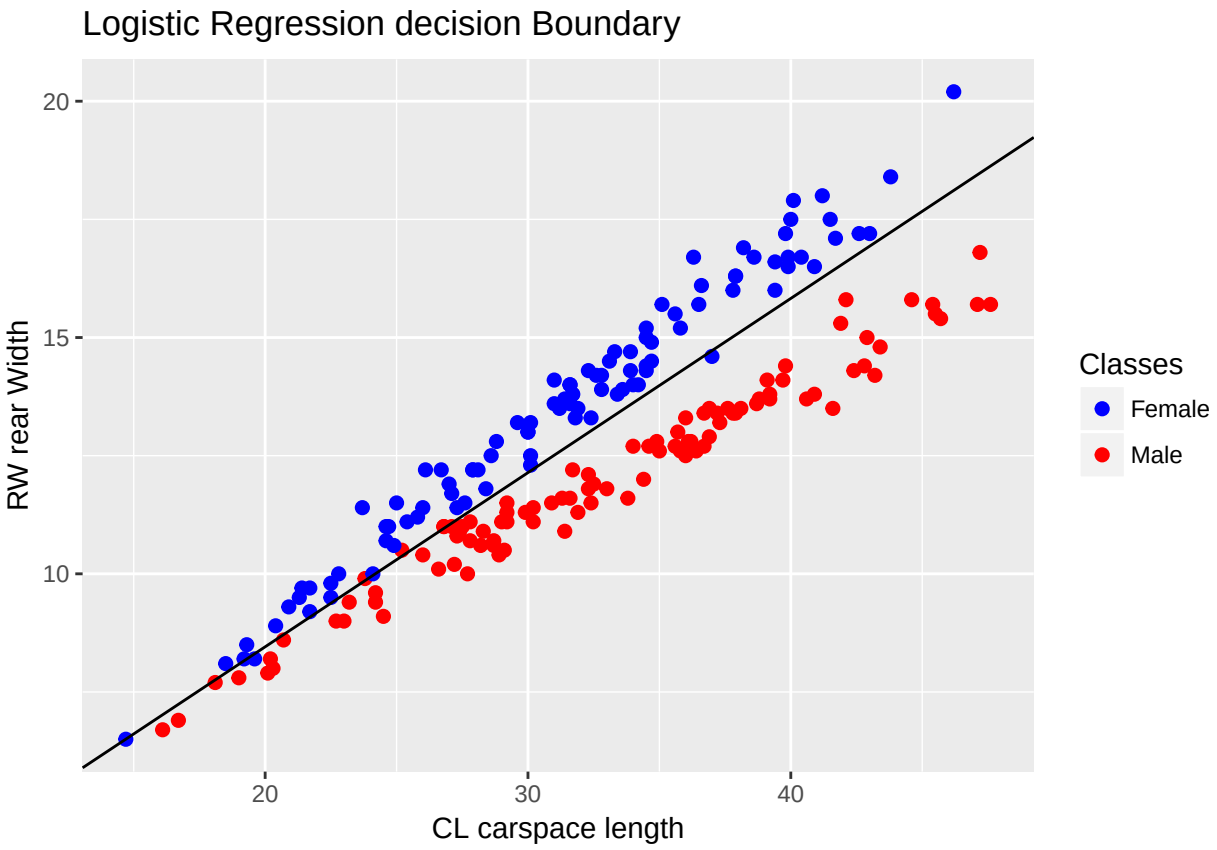
$$slope = \frac{W_{02} - W_{02}}{W_{1R} - W_{2R}}$$

Part 3



It is evident from the plot that decision boundary is separating the data between the two classes classifying points belonging to each class on the respective side of the boundary. There are some points which are misclassified but since there is not a lot of misclassified data that is misclassification rate is low therefore it can be assumed that the quality of fit is good.

Part 4



Decision boundary equation for Logistic Regression

$RW(W_{RW}) + CL(W_{CL}) + W_{01} = 0.5$

In terms of RW

$RW = \frac{-CL*W_{CL}}{W_{RW}} - \frac{W_{01}}{W_{RW}} + \frac{0.5}{W_{RW}}$

$intercept = \frac{-CL(W_{CL})}{W_{RW}}$ $slope = -\frac{W_{01}}{W_{RW}}$

Comaprision

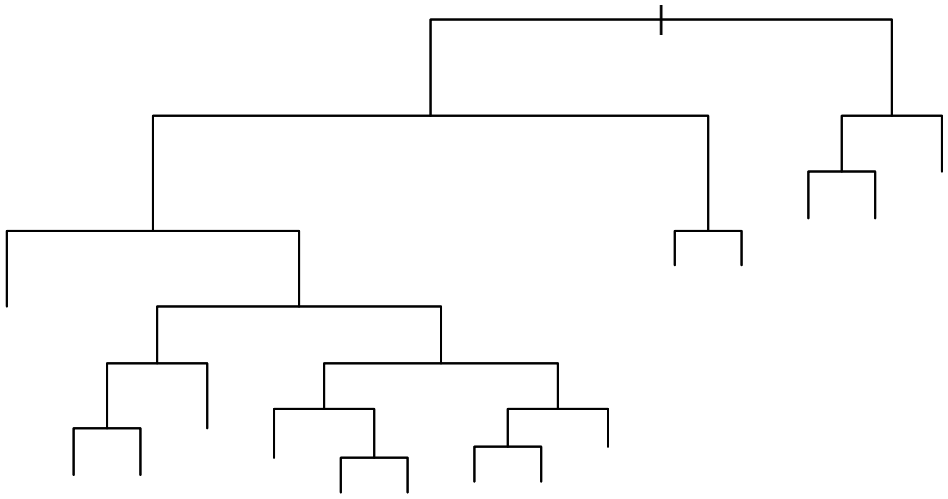
Apparently there are more misclassified points for female in LDA while on applying logistic regression, the female points are classified better than that of male. One more thing which can be observed from the plot is that for LDA, there are very few points which lie on the decision boundary while for Logistic Regression, there are comparatively more points which lie on the decision boundary that iis which are neither classified as male nor as female.

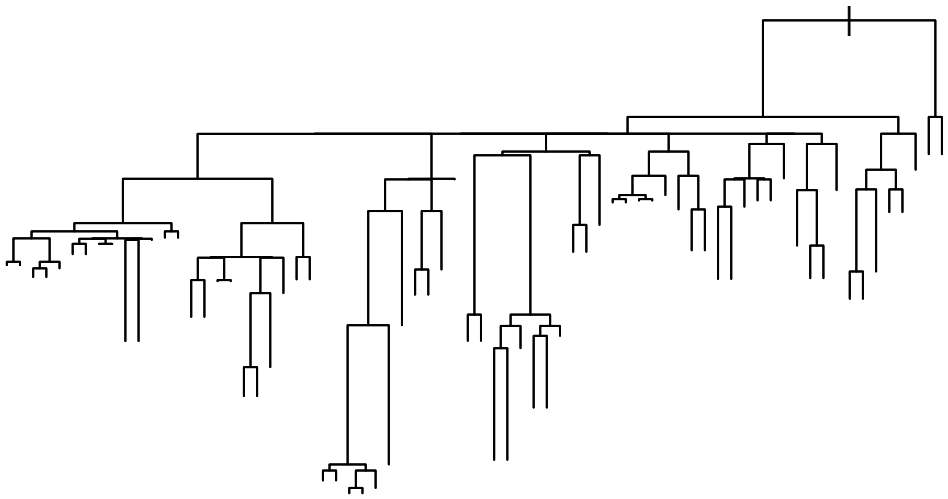
Assignment 2 Analysis of credit scoring

Classification model to find potentially good customers who can manage their loans. The Solution to the tasks are provided below with each step.

Step 2

The Misclassification rate and Confusion Matrix for training and test data are presented below along with the tree for deviance and gini index.





```
##
## devi_yfit bad good
##      bad   24   17
##      good  54  155
```

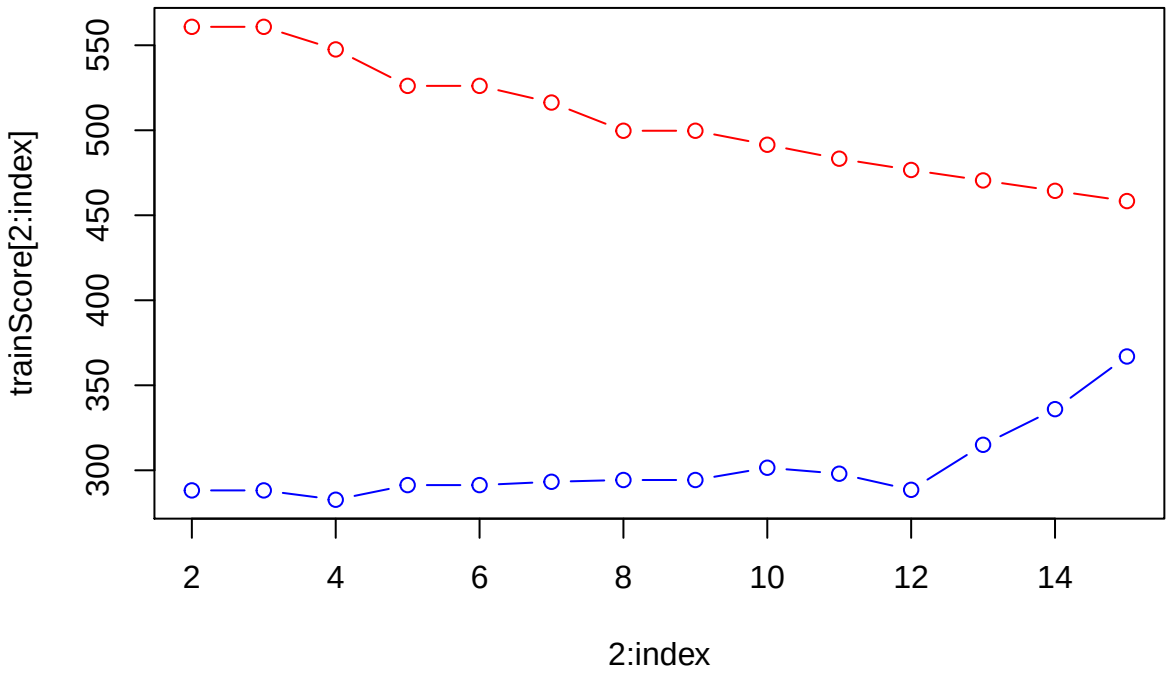
```
## [1] 0.284
```

```
##
## devi_yfit bad good
##      bad   24   17
##      good  54  155
```

```
## [1] 0.284
```

The tree produced by deviance matric is much less complex in comparison to the tree created by gini index.

Step 3

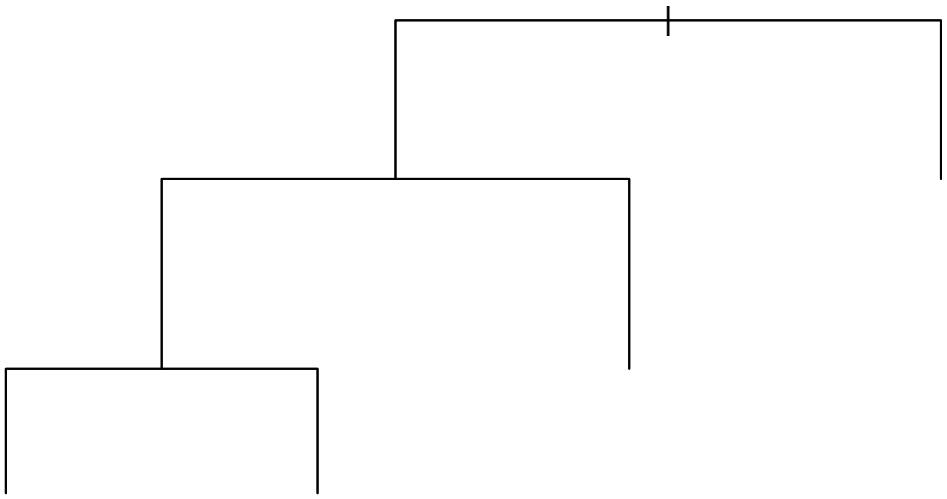



```
## [1] "Confusion Matrix"
```

```
##       yfit
##        bad good
##   bad   22   53
##   good  12  163
```

```
## [1] "Misclassification rate"
```

```
## [1] 0.26
```



In the graph Red line indicates deviance of training data and validation by the blue line. The tree depth of 4 results in the least deviance for the valdation data. The misclassification rate of 0.26 and confusion matrix are also presented above along with the Optimal tree model produced.

Step 4

```
##
## nav_test bad good
##     bad   47   49
##     good  31  123
```

```
##
## nav_train bad good
##      bad   95   98
##      good  52  255
```

```
## Misclassification train data value Using Naive Bayes 0.3
```

```
## Misclassification test data value Using Naive Bayes 0.32
```

The misclassification rate for training and test data are given above the misclassification rate is almost around that given by the decision tree matrix. The misclassification rate of test data is little higher then the rate of train data with more True postive.

Step 5

```
##
```

```
## nav_train bad good
##     FALSE 137  263
##     TRUE   10   90
```

```
## [1] 0.546
```

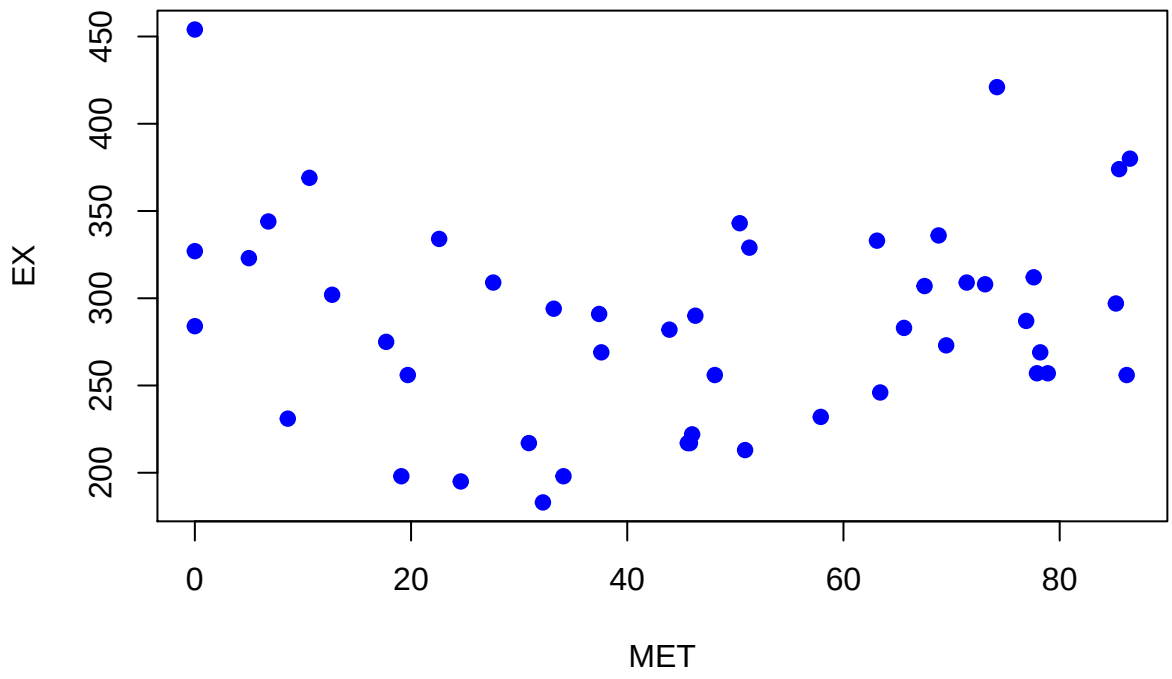
```
##
## nav_test bad good
##    FALSE  70  131
##    TRUE    8   41
```

```
## [1] 0.556
```

The misclassification rate increased by applying the loss matrix from 0.3 to 0.5. Also the False negative decreased and the false positve increased as can be seen above.

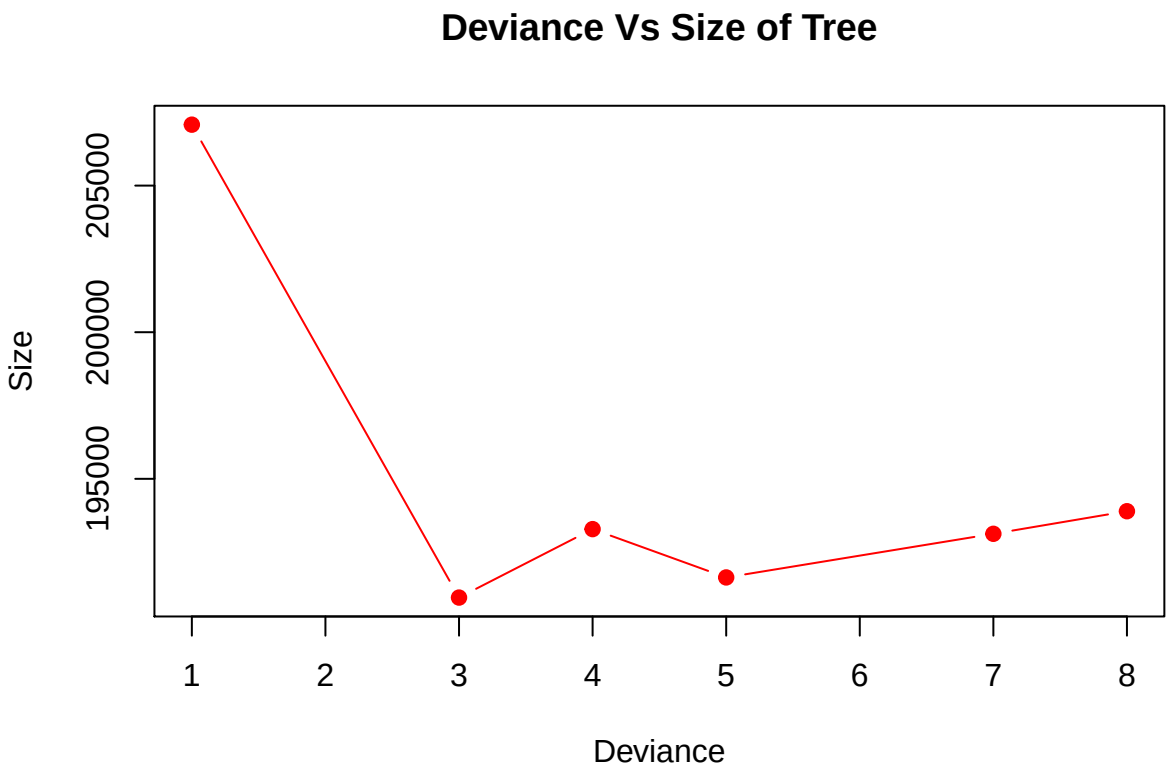
Assignment 3 Uncertainty estimation

Part 1

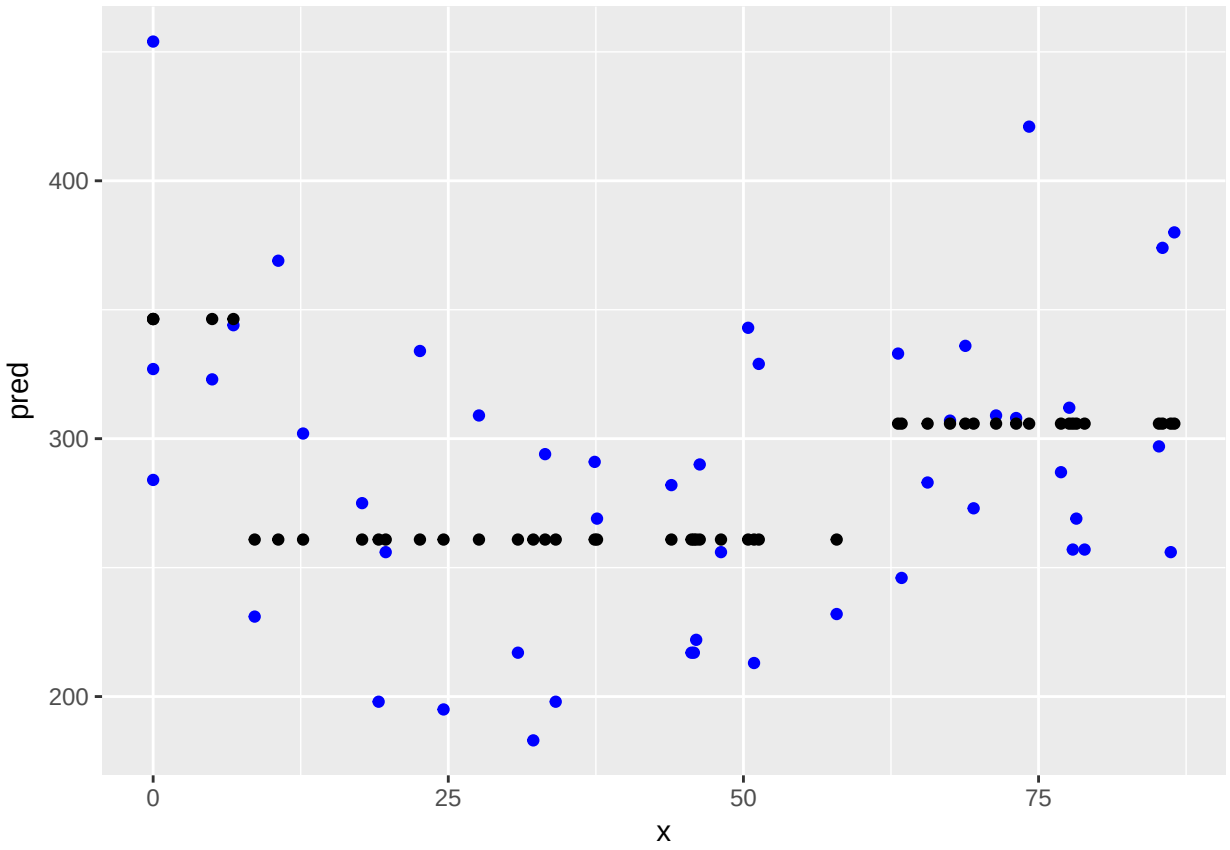


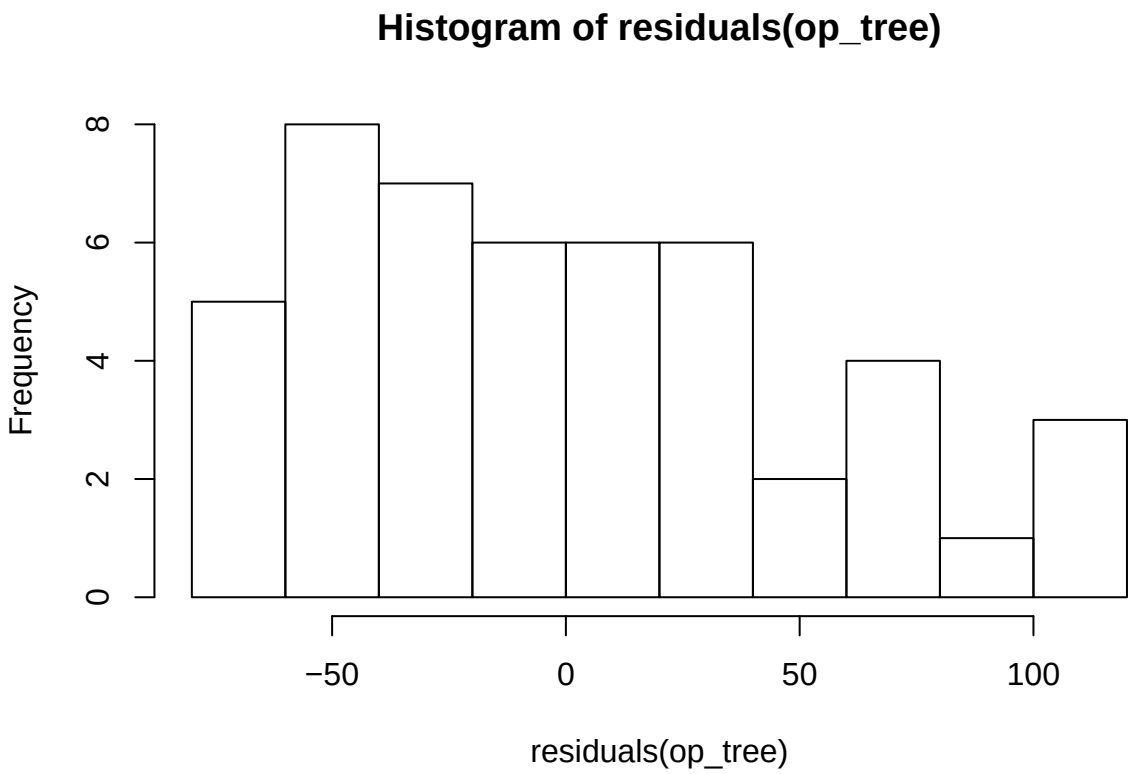
From the plot it can be observed that the data is scattered that is variance is high thus for the this type of data, decision trees would be the appropriate method

Part 2



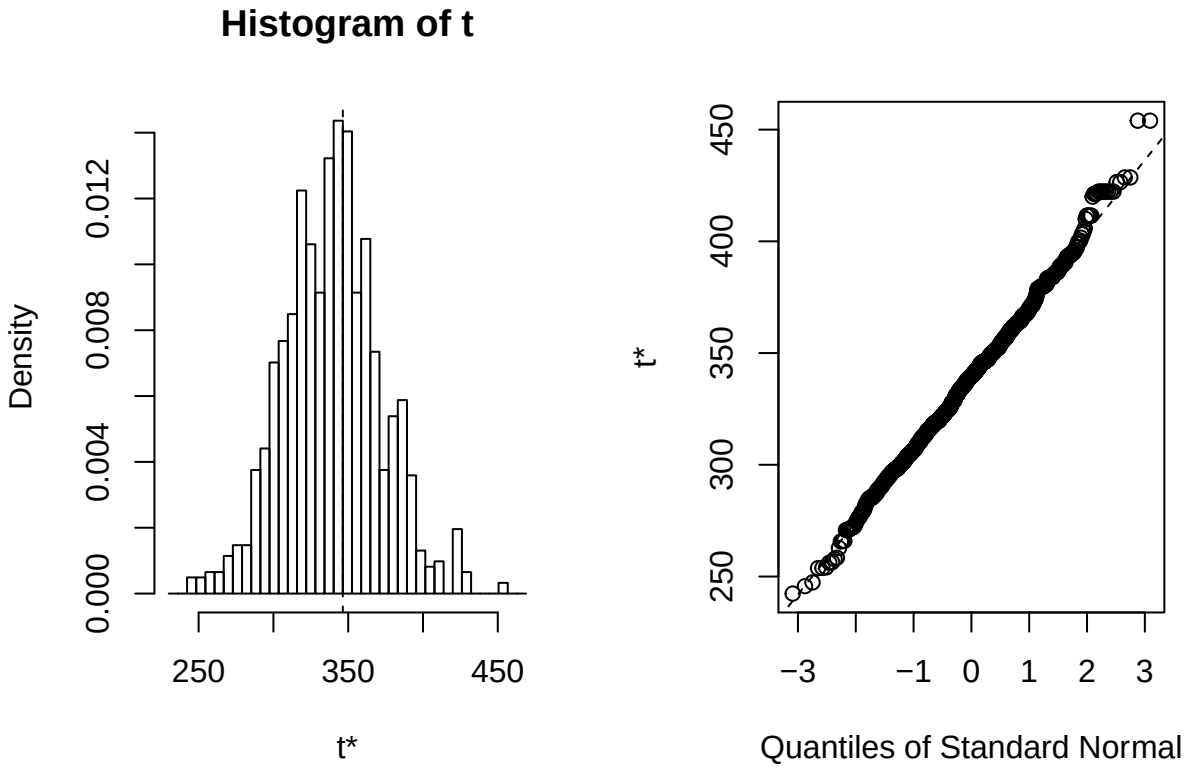
Selected tree is 3 which is selected on the basis of lowest value of deviance

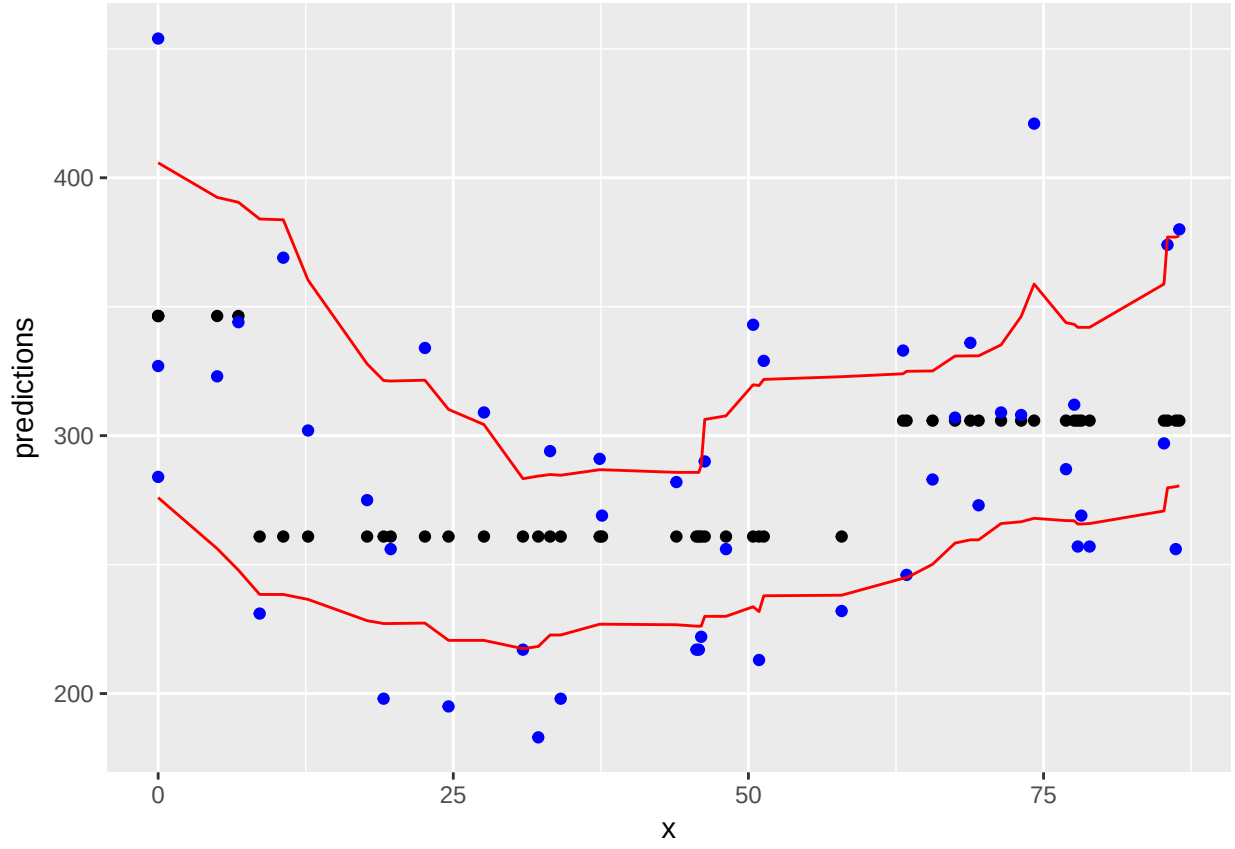

400
300
200
pred
0
25
50
75
x



Residuals seems to be marginally distributed across the data. According to the histogram, residuals represents that fitting of data can be improved that is the residuals can be reduced if better fitting is applied.

Part 3

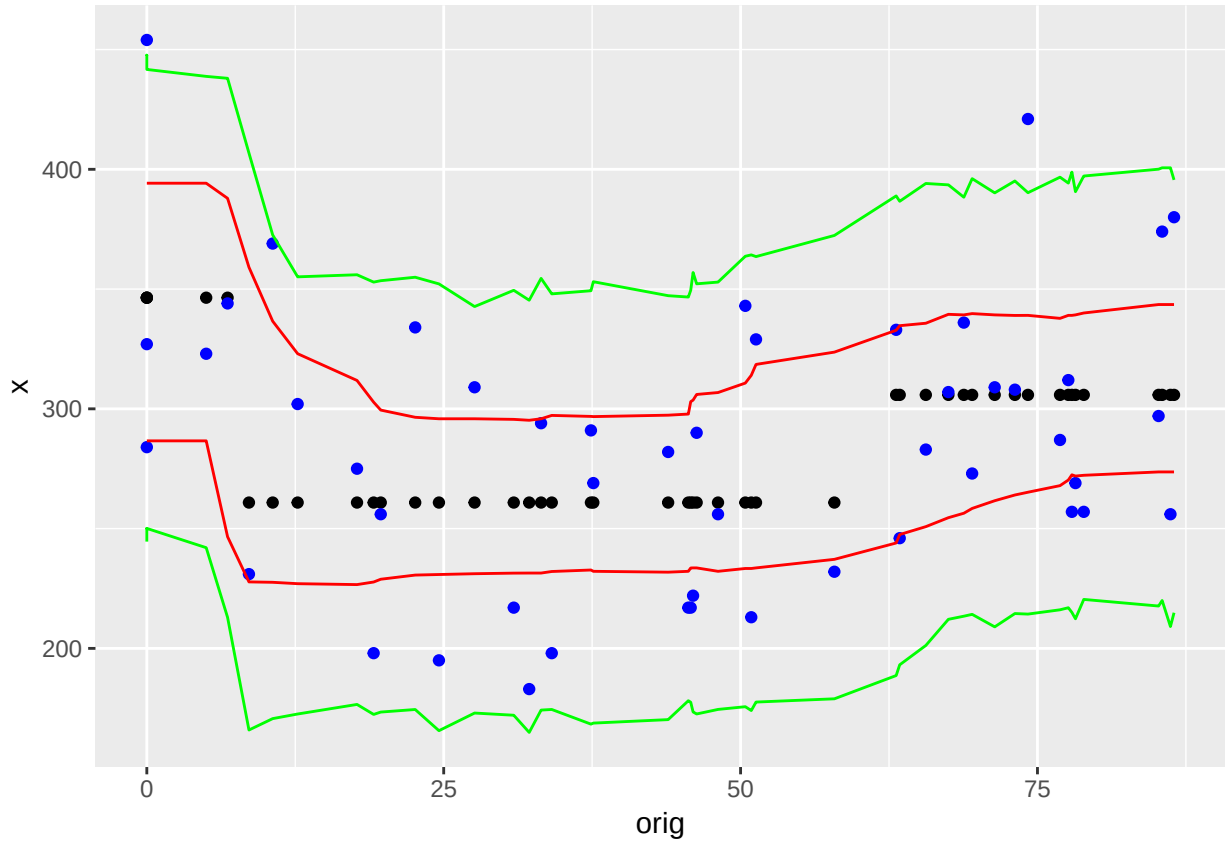

Histogram of t
Density
0.000
0.004
0.008
0.012
250
350
450
t*
t*
250
300
350
400
450
−3
−1
0
1
2
3
Quantiles of Standard Normal


predictions
200
300
400
0
25
50
75
x

Confidence band is the bootstrap percentile interval which is combination of different confidence intervals computed for different replicates of bootstrap.

The confidence band for the parametric bootstrap is bumpy due to the impact of bias on bootstrap.

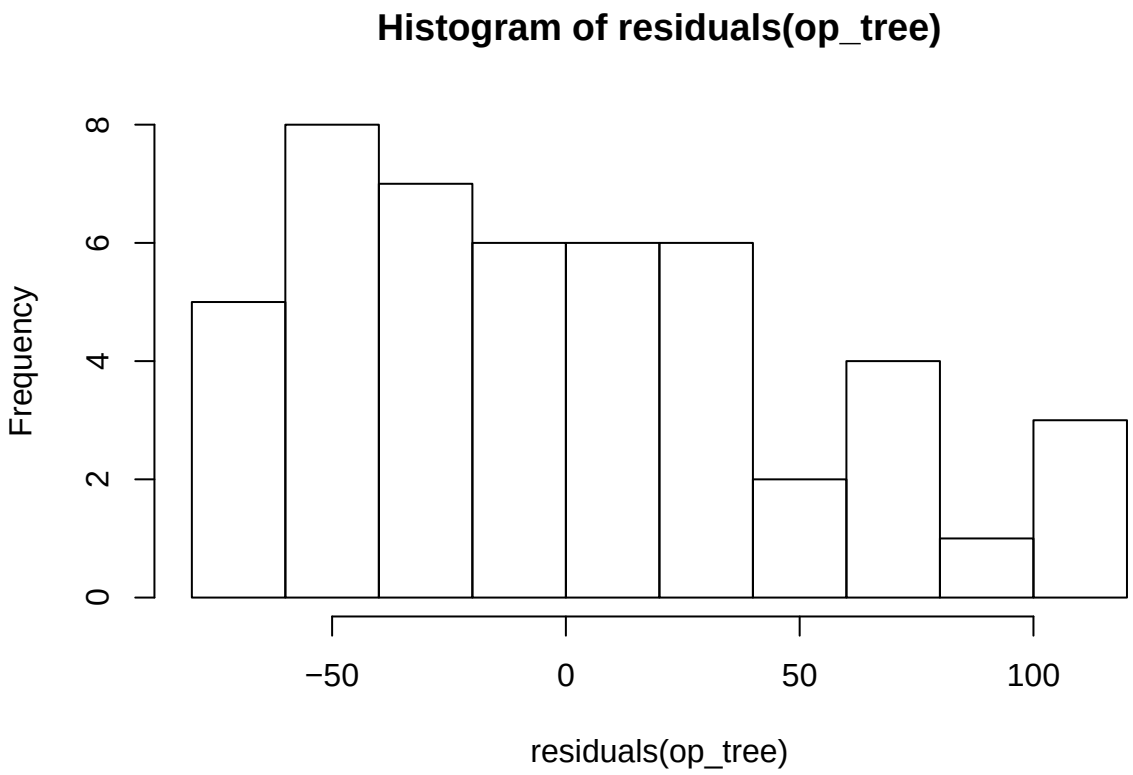
Considering the width of confidence interval, the result of regression model computed in part 2 appears to be reliable as it appears to lie within the confidence band.



The red line in the above plot represents the confidence band.The confidence band seems to enclose the fitted data from step 2 and thus the regression model in step 2 appears to be reliable.

The green lines represent the prediction band. It can be observed that the prediction band encloses almost all the points and only 5% or less data resides outside the prediction band. If the prediction band would enclose all points, it will indicate that there might be overfitting.

Part 5



On the basis of histogram plot from step 2, it can be suggested that the `parametric bootstrap` would be more appropriate model since for the given amount of data, non-parametric bootstrap might gives underfitted values. Moreover, the parametric bootstrap is more reliable if distribution is pre-determined regardless of the size of data.

Apendix

Assignment 1

```
library(ggplot2)
  data<- read.csv2("australian-crabs.csv" ,sep = ",",dec=".")
  p <- ggplot(data, aes(x=CL, y=RW)) + geom_point(aes(color=sex), size=2 ) +
    scale_color_manual (values =  c('blue', 'red')) +
    labs(x="CL carspace length", y="RW rear Width", colour="Classes") +
    ggtitle("original data")
  X<- data.frame(RW=data$RW , CL=data$CL )
  Y <- data$sex

  #1.2
  library(MASS)
  disc_fun=function(label, S)
  {
    X1=X[Y==label,]
```

```
  mean_v <- c(mean(X1$RW) ,mean(X1$CL))
  covaiance_mat_inverse <- solve(S)
  prior_prob <- nrow(X1) / nrow(X)
  w1 <- covaiance_mat_inverse %*% mean_v
  b1 <- ((-1/2) %*% t(mean_v) %*% covaiance_mat_inverse  %*% mean_v) + log(prior_prob)
  w1<- as.vector(w1)

  return(c(w1[1], w1[2], b1[1,1]))
}

X1=X[Y=="Male",]
X2=X[Y=="Female",]

S=cov(X1)*dim(X1)[1]+cov(X2)*dim(X2)[1]
S=S/dim(X)[1]

#discriminant function coefficients
res1=disc_fun("Male",S)
res2=disc_fun("Female",S)
#1.2
#decision boundary coefficients 'res'
res <- c( -(res1[1]-res2[1]) , (res2[2]-res1[2]), (res2[3]-res1[3]))

# classification
d=res[1]*X[,1]+res[2]*X[,2]+res[3]
Yfit=(d>0)
plot(X[,1], X[,2], col=Yfit+1, xlab="CL", ylab="RW")

#slope and intercept
slope <- (res[2] / res[1] ) * -1
intercept <- res[3] /res[1] * -1

#1.3
#plot decision boundary
X<- cbind(X,sex=Y)
p <- ggplot(X, aes(x=CL, y=RW)) + geom_point(aes(color=sex), size=2 ) +
  scale_color_manual (values =  c('blue', 'red')) +
  labs(x="CL carspace length", y="RW rear Width", colour="Classes") +
  geom_abline(slope = slope, intercept = intercept) +
  ggtitle("Descion Boundary LDA")

#1.4
logistic_fit <- glm(sex ~ RW + CL, data= X,
                    family='binomial') #glm fitting
r.unlist <- as.numeric(unlist(logistic_fit$coefficients))
r.unlist <- data.frame(intercept=r[1] ,
                       RW=r[2],
                       CL=r[3]) #convert data into datafreame
glm_intercept <- (-r$intercept/r$RW) #+ (0.5/r$RW)
glm_slope <- (-r$CL / r$RW ) #+ (0.5) / r$RW

p <- ggplot(X, aes(x=CL, y=RW)) + geom_point(aes(color=sex), size=2 ) +
  scale_color_manual (values =  c('blue', 'red')) +
```

```
    labs(x="CL carspace length", y="RW rear Width", colour="Classes") +
    geom_abline(slope = glm_slope,
                intercept = glm_intercept) +
    ggtitle("Logistic Regression
            decision Boundary")
```

Assignment 2

```
library(readxl)
library(tree)
library(e1071)
library(MASS)

# Importing Data - 2.1
data <- read_excel("creditscoring.xls")
data <- as.data.frame(data)
data$good_bad <- as.factor(data$good_bad)
# Dividing Data into three Train(50%) Test(25%) Validation(25%)
n = nrow(data)
set.seed(12345)

n=dim(data)[1]
set.seed(12345)
# 50% Training Data
id=sample(1:n, floor(n*0.5))
train=data[id,]
#train$good_bad <- as.factor(train$good_bad)

# 25% validation & testing Data
Sub_id = data[-id,]
m = dim(Sub_id)[1]
part1 = sample(1:m, floor(m*0.5))
validation = Sub_id[part1,]
testing = Sub_id[-part1,]

# Fitting data using Deviance and gini - 2.2
tree_deviance = tree(as.factor(good_bad) ~ ., data = train, split = "deviance")
tree_gini = tree(as.factor(good_bad) ~ ., data = train, split = "gini")

# Prediction
devi_yfit = predict(tree_deviance, newdata = testing,type="class")
gini_yfit = predict(tree_gini, newdata = testing,type="class")
plot(tree_deviance)
plot(tree_gini)

devi_table = table(devi_yfit,testing$good_bad)
geni_table = table(devi_yfit,testing$good_bad)

devi_table
# Missclassification rate Deviance
missclass_devi <- 1-sum(diag(devi_table))/sum(devi_table)
```

```
geni_table
# Missclassification rate Gigi
missclass_geni <- 1-sum(diag(geni_table))/sum(geni_table)

index = summary(tree_deviance)[4]$size
trainScore = rep(0,index)
testScore = rep(0,index)

# Graph training and validation
for(i in 2:index) {
  prunedTree=prune.tree(tree_deviance,best=i)
  pred=predict(prunedTree, newdata=validation,type="tree")
  trainScore[i]=deviance(prunedTree)
  testScore[i]=deviance(pred)
}

plot(2:index,trainScore[2:index], col="Red",type = "b", ylim=c(min(testScore[2:index]),max(trainScore))
points(2:index,testScore[2:index],col="Blue",type="b")

# misclassification rate for test data
missclass_test_t = prune.tree(tree_deviance, best = 4)
yfit = predict(missclass_test_t, newdata = validation, type="class")
valid_ = table(validation$good_bad,yfit)
valid_
mc <- 1-sum(diag(valid_))/sum(valid_)
plot(missclass_test_t)


# Naïve Bayes 2.4
naye = naiveBayes(good_bad ~., data=train)

nav_test = predict(naye, newdata = testing, type = "class")
nav_train = predict(naye,newdata = train[,-ncol(train)])

# Confusion Matrix Using Naive Bayes
naive_table = table(nav_test,testing$good_bad)
print(naive_table)
naive_table_train <- table(nav_train,train$good_bad)
print(naive_table_train)

# Missclassification train data value Using Naive Bayes
mc_nav_train <- 1-sum(diag(naive_table_train))/sum(naive_table_train)
mc_nav_train

# Missclassification test data value Using Naive Bayes
mc_nav_test <- 1-sum(diag(naive_table))/sum(naive_table)
mc_nav_test

# Naive Bayes With loss matrix 2.5
naye = naiveBayes(good_bad ~ ., data = train)

# Predicting using Naive
nav_test = predict(naye, testing[,-ncol(testing)] , type="raw")
```

```
nav_train = predict(naye, train[,-ncol(train)] , type="raw")

# applying loss matrix if greater then 10 True else False
nav_test =  (nav_test[, 2] / nav_test[, 1]) > 10
nav_train =  (nav_train[, 2] / nav_train[, 1]) > 10

# confusion matrix for train & test
naive_table = table(nav_test , testing$good_bad)
naive_table_train = table(nav_train , train$good_bad)

# missclasification for train & test
naive_table_train
1-sum(diag(naive_table_train))/sum(naive_table_train)

naive_table
1-sum(diag(naive_table))/sum(naive_table)
```

Assignment 3

```
library(tree)

# 3.1 Data import, reorder and Plot
set.seed(12345)

data = read.csv2("State.csv", header = TRUE)
data = data[order(data$MET),]
plot(EX ~ MET, data = data, pch = 19, cex = 1,col="blue")

# 3.2
set.seed(12345)

control_parameter = tree.control(nobs = nrow(data),minsize = 8)

fit_tree = tree(formula = EX ~ MET,data = data,control = control_parameter)
leave_fit = cv.tree(fit_tree)
plot(leave_fit$size, leave_fit$dev, main = "Deviance Vs Size of Tree" ,
     xlab="Deviance", ylab = "Size", type="b",col="red", pch= 19,cex=1)


op_tree = prune.tree(fit_tree,best = leave_fit$size[which.min(leave_fit$dev)])

fitted_val = predict(op_tree, newdata=data)

df = data.frame(x = data$MET, pred = fitted_val, ex_val = data$EX)
fit_original_plot = ggplot(df, aes(x, pred, ex_val)) +
  geom_point(aes(x,ex_val), colour = "blue") +
  geom_point(aes(x, pred))
fit_original_plot

hist(residuals(op_tree))
```

```r
# 3.3 Non-Paramatric Bootstrap
library(boot)


f_np = function(data,index){
  sample = data[index,]
  Ctrl = tree.control(nrow(sample), minsize = 8)
  fit = tree( EX ~ MET, data=sample, control = Ctrl)
  optimal_tree = prune.tree(fit, best= leave_fit$size[which.min(leave_fit$dev)])
  return(predict(optimal_tree, newdata=data))
}

np_bs = boot(data, statistic = f_np, R=1000)
conf_bound = envelope(np_bs,level=0.95)
predictions = predict(op_tree,data)

plot(np_bs)

fig_data = data.frame(orig = data$EX, x=data$MET, pred=predictions,
                      upper=conf_bound$point[1,], lower=conf_bound$point[2,])
fig = ggplot(fig_data, aes(x,predictions,upper,lower))
p = fig + geom_point(aes(x, pred)) +
  geom_point(aes(x, orig),colour="blue") +
  geom_line(aes(x,upper),colour="red") +
  geom_line(aes(x,lower),colour="red")
p


# 3.4 Paramatric Bootstrap
set.seed(12345)

parama_conf = function(data){
  controll = tree.control(nrow(data), minsize = 8)
  fit = tree( EX ~ MET, data=data, control = controll)
  op_tree = prune.tree(fit, best=leave_fit$size[which.min(leave_fit$dev)])
  return(predict(op_tree, newdata=data))
}

param_predict = function(data){
  controll = tree.control(nrow(data), minsize = 8)
  fit = tree( EX ~ MET, data=data, control = controll)
  op_tree = prune.tree(fit, best=leave_fit$size[which.min(leave_fit$dev)])
  predictions = predict(op_tree, newdata=data)
  return(rnorm(nrow(data),predictions,sd(resid(fit))))
}

rnd = function(data, model){
  sample = data.frame(MET=data$MET, EX=data$EX)
  sample$EX = rnorm(nrow(data), predict(model,newdata=data),sd(resid(model)))
  return(sample)
}

set.seed(12345)
```

```
param_boot_conf = boot(data, statistic = parama_conf, R=1000, mle = op_tree,
                       ran.gen = rnd, sim = "parametric")
confidence_bound_param = envelope(param_boot_conf, level=0.95)

param_boot_predict = boot(data, statistic = param_predict, R=1000, mle = op_tree, ran.gen = rnd, sim =
prediction_bound_param = envelope(param_boot_predict, level=0.95)

plot(param_boot_conf)
plot(param_boot_predict)

predictions = predict(op_tree,data)
fig_data = data.frame(orig = data$EX, x=data$MET, pred=predictions,
                      upper_c=confidence_bound_param$point[1,],
                      lower_c=confidence_bound_param$point[2,],
                      upper_p=prediction_bound_param$point[1,],
                      lower_p=prediction_bound_param$point[2,])

para_plot = ggplot(fig_data, aes(orig,x,pred,upper_c,lower_c, upper_p, lower_p))
para_plot = para_plot +
  geom_point(aes(x, pred)) +
  geom_point(aes(x, orig),colour="blue") +
  geom_line(aes(x,upper_c),colour="red") +
  geom_line(aes(x,lower_c),colour="red") +
  geom_line(aes(x,upper_p),colour="green")+
  geom_line(aes(x,lower_p),colour="green")
para_plot
```