TMA4268 - Project 1

```
# Libraries used throughout the exercise
library(ggplot2)
library(palmerpenguins) # Contains the data set 'penguins'.
library(ggfortify)
library(tidyverse)
library(GGally)
library(MASS)
library(class)
library(base)
library(ROSE)
```

Problem 1

a)

If we have that $y_0 = f(x_0) + \epsilon$, where ϵ is a random error independent of x with 0 mean. And x_0 is a unseen test observation we find,

$$\begin{aligned}
E\left[\left(y_0 - \hat{f}(x_0)\right)^2\right] &= E\left[\left(f(x_0) - \hat{f}(x_0)\right)^2\right] + E\left[\epsilon^2\right] + 2E\left[\left(f(x_0) - \hat{f}(x_0)\right) \cdot \epsilon\right] \\
&= E\left[f(x_0)^2 - 2f(x_0)\hat{f}(x_0) + \hat{f}(x_0)^2\right] + E\left[\epsilon^2\right] + 2E\left[\left(f(x_0) - \hat{f}(x_0)\right)\right] \cdot E[\epsilon] \\
&= f(x_0)^2 - 2f(x_0)E[\hat{f}(x_0)] + E[\hat{f}(x_0)^2] + Var\left[\epsilon\right] \\
&= \left(f(x_0) - E[\hat{f}(x_0)]\right)^2 + Var[\hat{f}(x_0)] + Var\left[\epsilon\right] \\
&= \text{Bias}^2 + \text{Variance} + \text{Irreducible error}
\end{aligned}$$

b)

The irreducible error is a term that can't be reduced by fitting the data well. The variance is a term describing how much uncertainty our statistical model $\hat{f}$, how much $\hat{f}$ changes if we change the training data. The bias is the expected difference between the true model f and our statistical model $\hat{f}$.

c)

i) True
ii) False
iii) True
iv) False

d)

i) False
ii) False
iii) True
iv) False

e)

(iii) 0.76

$$\rho_{x_1,x_2} = \frac{\text{cov}(x_1, x_2)}{\sigma_{x_1}\sigma_{x_2}} = \frac{33}{\sqrt{50}\sqrt{38}} = 0.76$$

Problem 2

a)

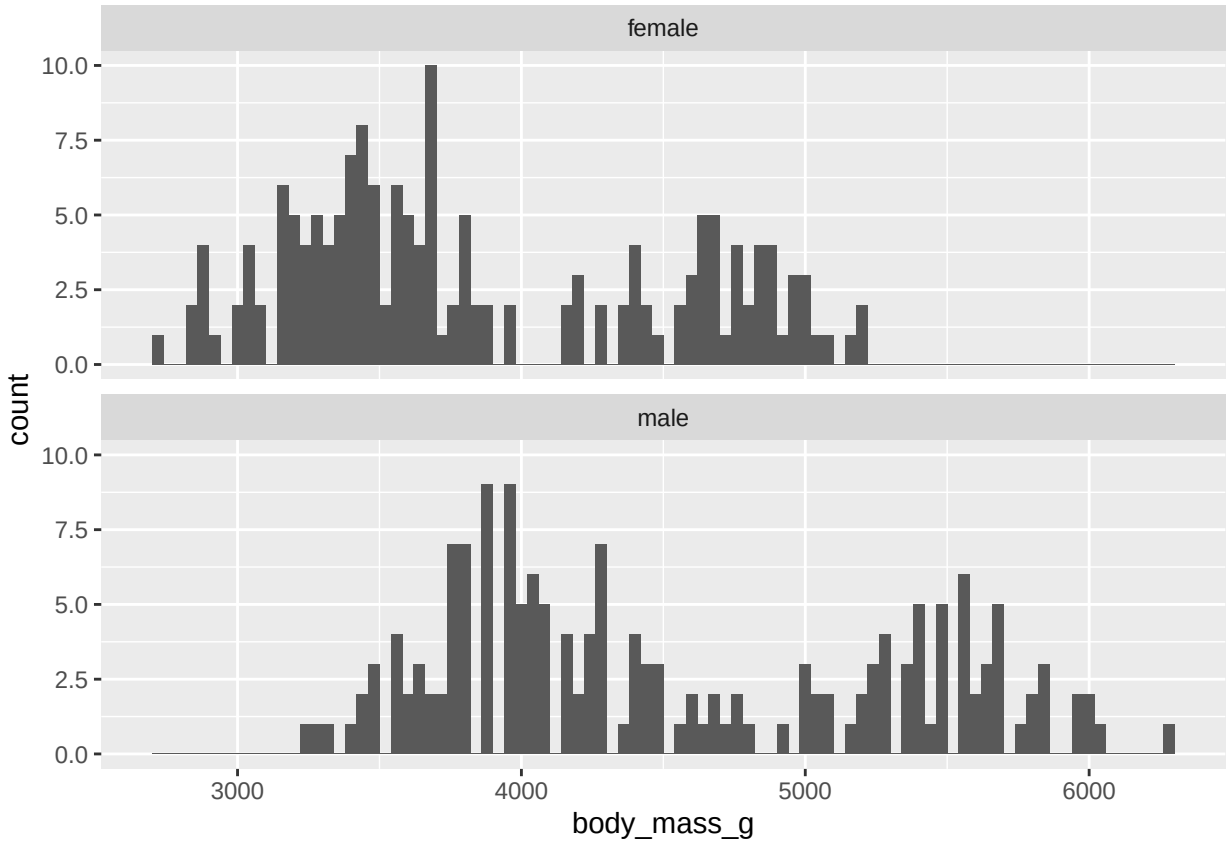
One error made is excluding sex because of a low p-value, the p-value is the probability to observe a result equal or more extreme than the one we did, given that the null hypothesis $H_0 : \beta = 0$, so a lower p-value means the result is more statistically significant.

Another error made is deciding whether to reject the null hypothesis that the species coefficient overall is actually zero based on the p-values of the coefficients. Since the null hypothesis in this case is $H_0 : \beta_{Chinstrap} = \beta_{Gentoo} = 0$ at the same time. We need to do a F-test.

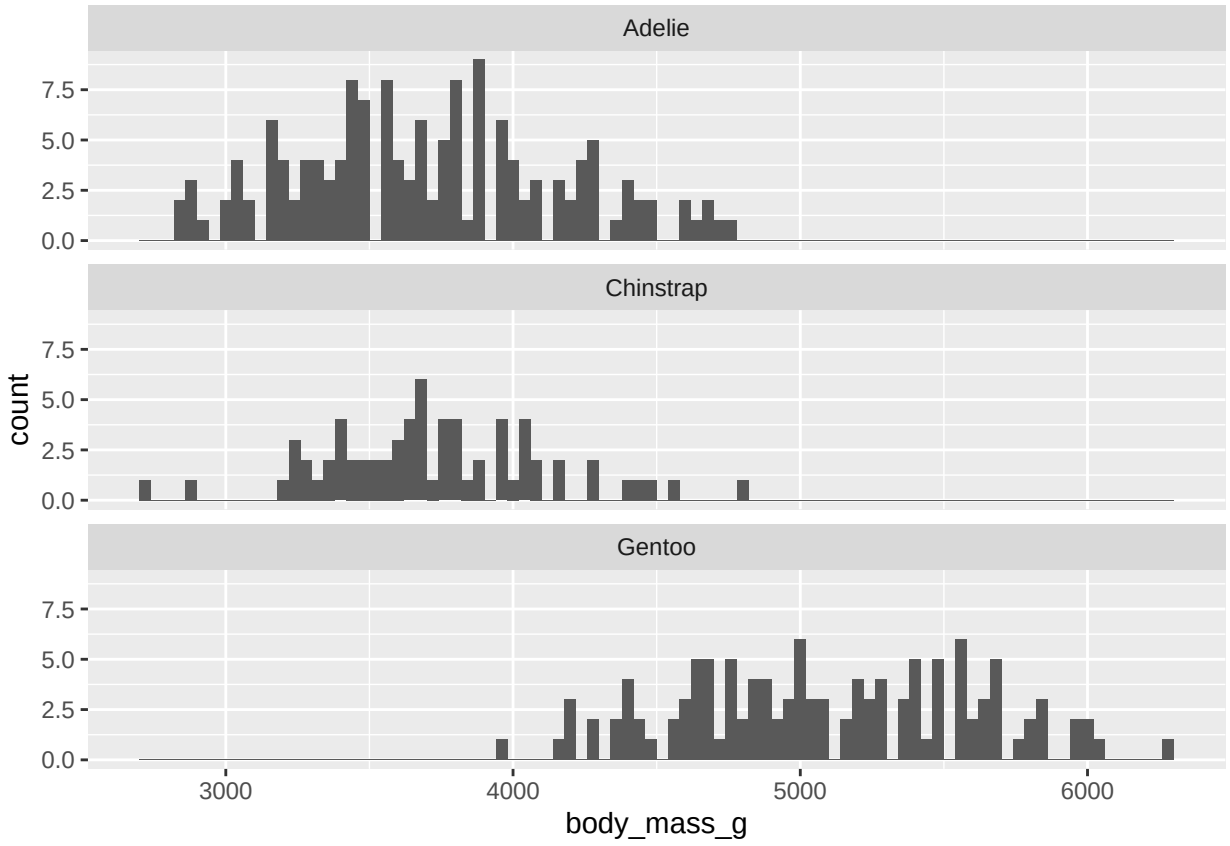
A third error made is claiming that chinstrap penguins are the largest since they have the largest coefficient. Having a large coefficient only means that for a given set of parameters a chinstrap penguin is going to be heavier than another type of penguin. And when we include interaction terms which changes the the slopes, a large coefficient only guarantees it is larger for a range of parameters near zero. And by looking at body mass of the penguins in the data set we find that in fact gentoo penguins have the highest mean body mass.

b)

```
data(penguins)

Penguins <- subset(penguins, select = -c(island, year))
Penguins <- na.omit(Penguins)

ggplot(data = Penguins) +
  geom_histogram(binwidth = 40, mapping = aes(x = body_mass_g)) +
  facet_wrap(~ sex, nrow = 2)
```




```
ggplot(data = Penguins) +
  geom_histogram(binwidth = 40, mapping = aes(x = body_mass_g)) +
  facet_wrap(~ species, nrow = 3)
```



c)

```
Penguins <- subset(penguins, select = -c(island, year))

penguin.model <- lm(body_mass_g ~ flipper_length_mm + sex + bill_depth_mm * species,
                    data = Penguins)
summary(penguin.model)
```

```
##
## Call:
## lm(formula = body_mass_g ~ flipper_length_mm + sex + bill_depth_mm *
##     species, data = Penguins)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -751.2 -183.8   -9.8  191.1  906.9
##
## Coefficients:
##                              Estimate Std. Error t value Pr(>|t|)
## (Intercept)                 -1336.58     646.92  -2.066 0.039615 *
## flipper_length_mm              17.38       2.91   5.971 6.17e-09 ***
## sexmale                       432.90      44.63   9.699  < 2e-16 ***
## bill_depth_mm                  82.98      22.32   3.717 0.000237 ***
## speciesChinstrap             1460.15     680.39   2.146 0.032610 *
```

```
## speciesGentoo                    644.88     542.57   1.189 0.235481
## bill_depth_mm:speciesChinstrap   -83.53      37.01  -2.257 0.024666 *
## bill_depth_mm:speciesGentoo       36.17      34.48   1.049 0.294955
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 286.8 on 325 degrees of freedom
##   (11 observations deleted due to missingness)
## Multiple R-squared:  0.8758, Adjusted R-squared:  0.8732
## F-statistic: 327.5 on 7 and 325 DF,  p-value: < 2.2e-16
```

To test the null hypothesis $H_0 : \beta_{Chinstrap} = \beta_{Gentoo} = 0$, we do a F-test.

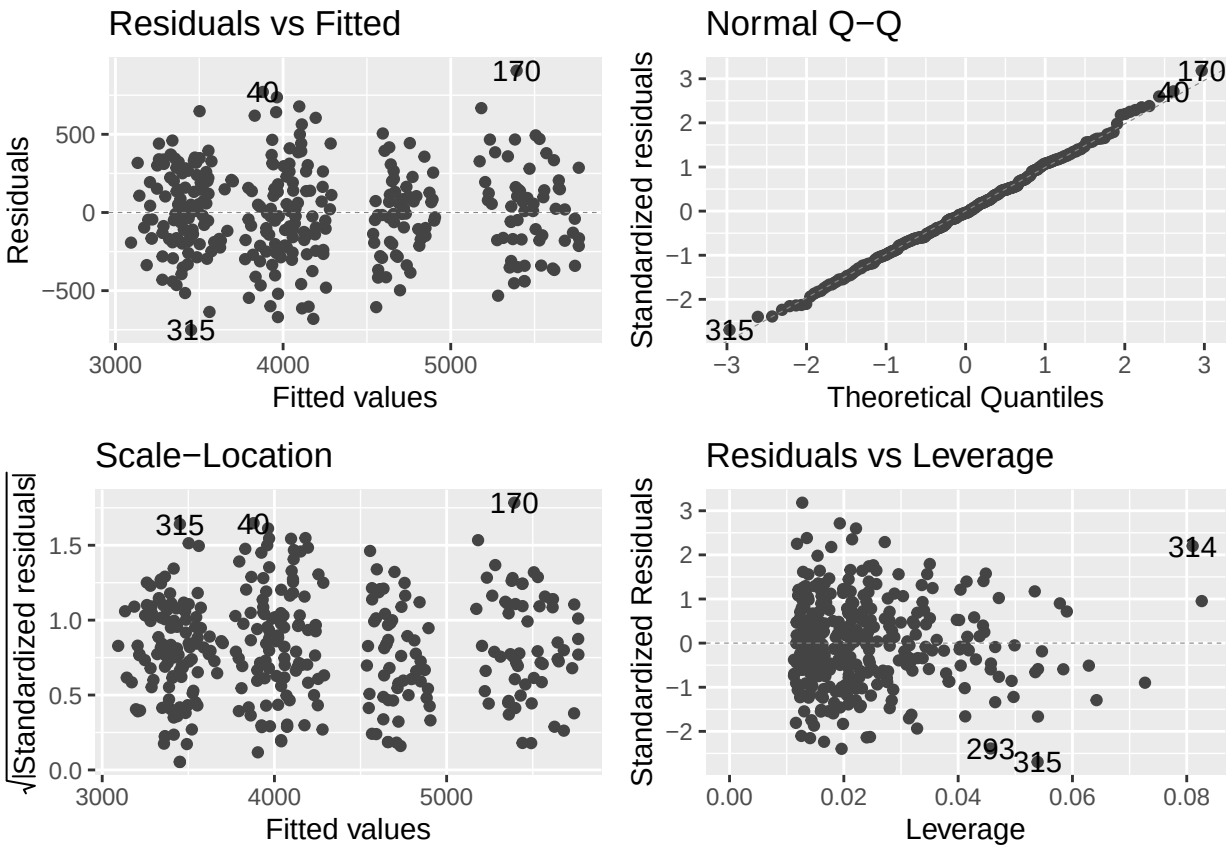
```
anova(penguin.model)
```

```
## Analysis of Variance Table
##
## Response: body_mass_g
##                         Df    Sum Sq   Mean Sq   F value    Pr(>F)
## flipper_length_mm        1 164047703 164047703 1994.7424 < 2.2e-16 ***
## sex                      1   9416589   9416589  114.5013 < 2.2e-16 ***
## bill_depth_mm            1   3667377   3667377   44.5936 1.051e-10 ***
## species                  2  10670525   5335262   64.8743 < 2.2e-16 ***
## bill_depth_mm:species    2    729458    364729    4.4349   0.01258 *
## Residuals              325  26728014     82240
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

We see that the p-value for species is very low, so we do not reject H_0

```
autoplot(penguin.model, smooth.colour = NA)
```

```
## Warning: Removed 333 row(s) containing missing values (geom_path).
## Removed 333 row(s) containing missing values (geom_path).
## Removed 333 row(s) containing missing values (geom_path).
```



Problem 3

Now, the main idea is to classify the species of the penguins for a given body mass and flipper length. The dataset contains 3 type of penguin species, yet, classifying 3 penguin species is not straightforward. So, for simplicity, we define our goal to classify a penguin belonging to the species - Adelie, or not Adelie. This will give us two-class classification problem instead of three.

Since, we will use only three parameters from the dataset, it is wise to create a small dataset, and work with it. First, the variables should be converted to numeric (because knn function cannot handle the int class, and generates errors) and removes any missing observations.

```
penguins$adelie <- ifelse(penguins$species == "Adelie", 1, 0)

# Select only relevant variables and remove all rows with missing values in body
# mass, flipper length, sex or species.
Penguins_reduced <- penguins %>% dplyr::select(body_mass_g, flipper_length_mm,
                    adelie) %>%  mutate(body_mass_g = as.numeric(body_mass_g),
                    flipper_length_mm = as.numeric(flipper_length_mm)) %>% drop_na()
```

Now, we need two datasets: the one to train the model, then to test the model. It is common to divide 70% of dataset as a training dataset, and the rest will be a test dataset.

```
set.seed(4268)

# 70% of the sample size for training set
```

```
training_set_size <- floor(0.7 * nrow(Penguins_reduced))
train_ind <- sample(seq_len(nrow(Penguins_reduced)), size = training_set_size)
train <- Penguins_reduced[train_ind, ]
test <- Penguins_reduced[-train_ind, ]
```

a)

```
log_reg = glm(adelie ~ body_mass_g + flipper_length_mm, data = train, family =
                "binomial")

summary(log_reg)$coef
```

i) Logistic regression

```
##                     Estimate   Std. Error   z value     Pr(>|z|)
## (Intercept)       37.7618776 5.1761640773  7.295340 2.979055e-13
## body_mass_g        0.0007120 0.0004619996  1.541127 1.232859e-01
## flipper_length_mm -0.2055804 0.0324291723 -6.339367 2.307116e-10
```

Here, we train the model using train dataset, and the result is available above.

```
prob_test_lr <- predict(log_reg, newdata = test, type = "response")

pred_test_lr <- ifelse(prob_test_lr > 0.5, 1, 0)
```

predict() gives the probabilities of the species = Adelie (class = 1). Then, we apply a cutoff value of 0.5 to those probabilities, to get predicted classes.

```
adelie_lr_df = bind_rows(mutate(test, pred_test_lr))
adelie_lr_df$pred_test_lr = as.factor(adelie_lr_df$pred_test_lr)

gg_p = ggplot(test, aes(x = body_mass_g, y=flipper_length_mm, color=adelie)) +
      geom_point(aes(x = body_mass_g, y=flipper_length_mm, colour=pred_test_lr),
      data=adelie_lr_df, size=2) + xlab("Flipper Length of a penguin (mm)") +
      labs(color = "Adelie") +
      ylab("Body Mass of a penguin (g)") +
      ggtitle("The classification of species using logistic regression") + theme_bw()       +          tl
gg_p
```

Then, we use test dataset for testing the model. The plot illustrates the testing result.

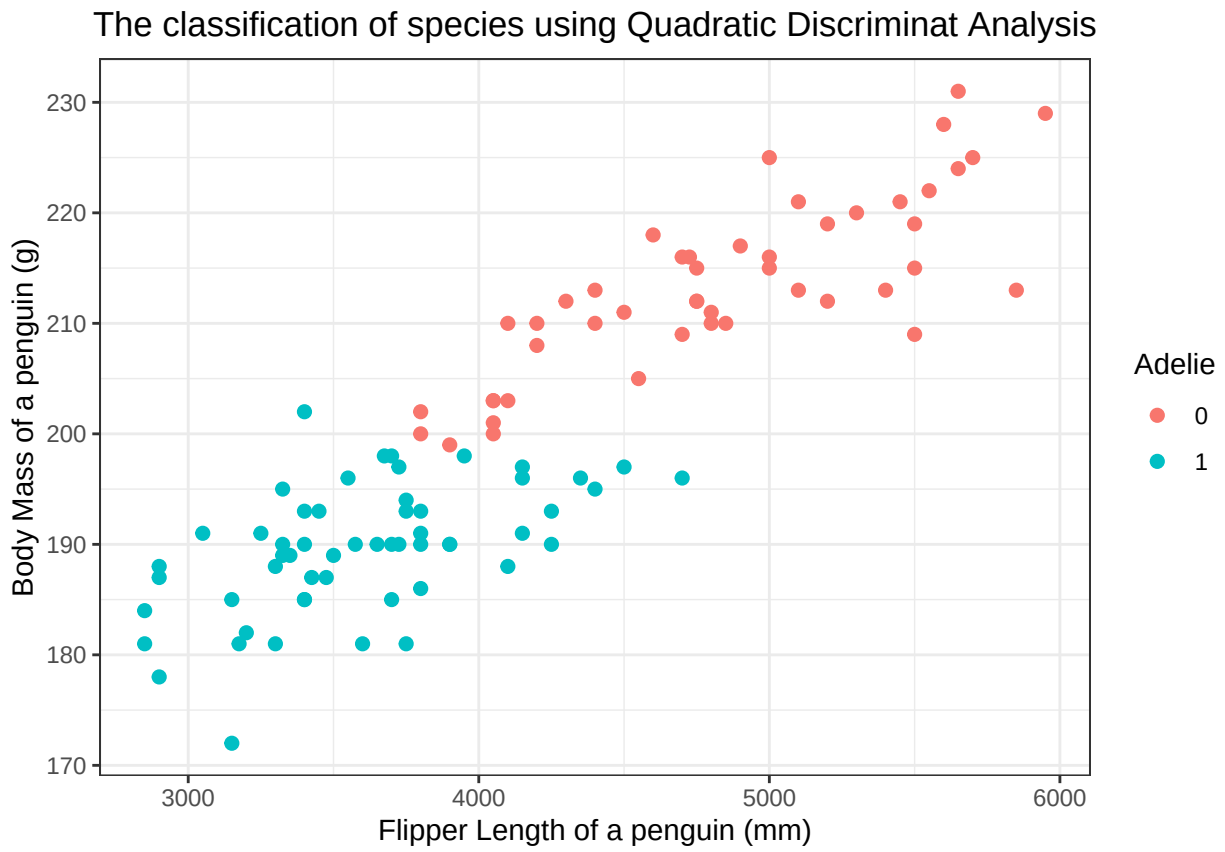
ii) Quadratic Discriminant Analysis We do the same for classification using Quadratic Discriminant Analysis

```
qda_reg = qda(adelie ~ body_mass_g + flipper_length_mm, data = train)

prob_test_qda <- predict(qda_reg, newdata = test, type = "response")$posterior
pred_test_qda <- predict(qda_reg, newdata = test, type = "response")$class
```

Because QDA identifies the probabilities of having species = Adelie (class = 1), and having species = not Adelie (class = 0), predict() function will give both probabilities and already cut-off value (0.5) applied predictions. So, $posteriors will give the probabilities, $class will give 0.5 cut-off value applied corresponding classes.

```
adelie_qda_df = bind_rows(mutate(test, pred_test_qda))
adelie_qda_df$pred_test_qda = as.factor(adelie_qda_df$pred_test_qda)

qda_plot = ggplot(test, aes(x=body_mass_g, y=flipper_length_mm, color=adelie)) +
          geom_point(aes(x = body_mass_g, y=flipper_length_mm, colour=pred_test_qda),
          data=adelie_qda_df, size=2) + xlab("Flipper Length of a penguin (mm)") +
          ylab("Body Mass of a penguin (g)") +
          labs(shape = "Adelie", color = "Adelie") +
          ggtitle("The classification of species using Quadratic Discriminat Analysis") +
  theme_bw() + theme(plot.title = element_text(hjust = 0.5))
```

```
qda_plot
```



Again, this plot illustrates the testing result.

```
knnMod = knn(train = train, test = test, cl = train$adelie, k = 25, prob = T)

knn_r <- data.frame(data.matrix(knnMod), attributes(knnMod)$prob)
```

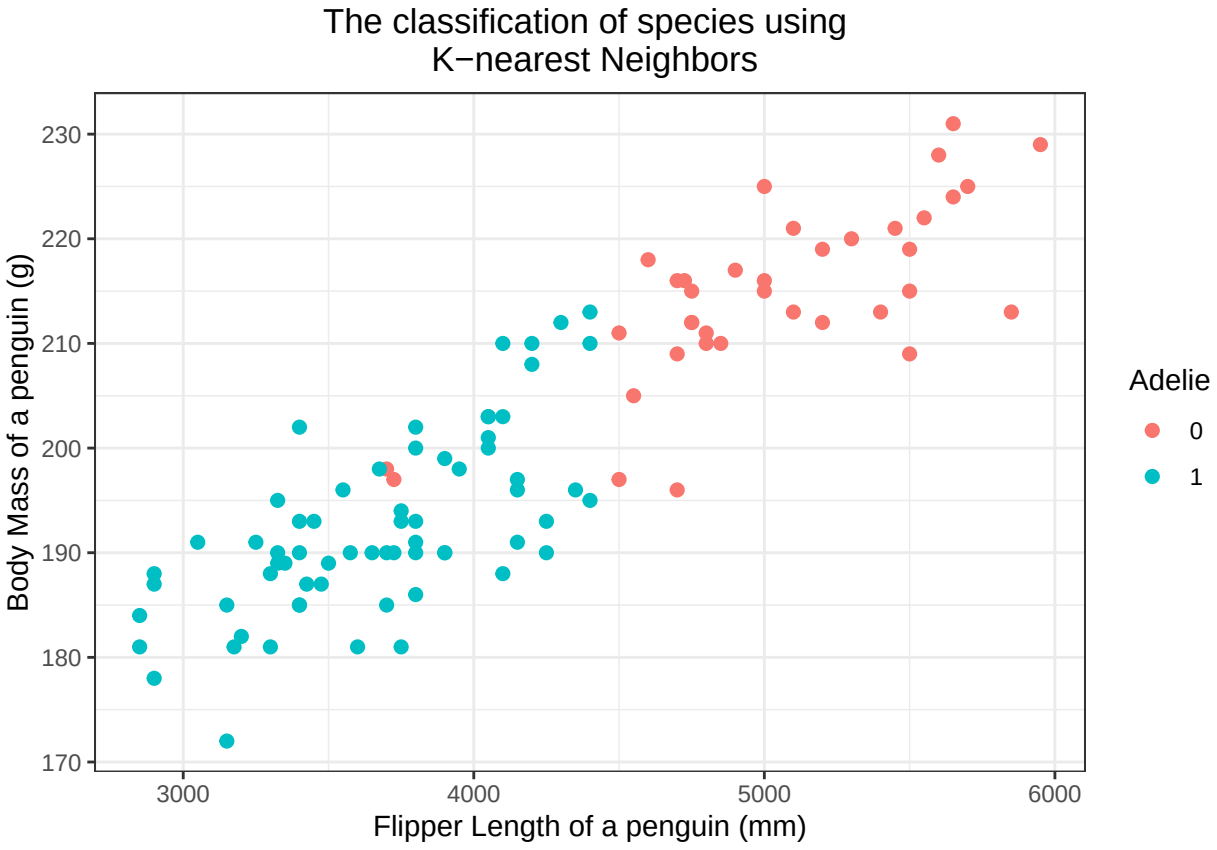
iii) K-nearest Neighbors After having the model, we put the result in matrix form for better usage.

```
probKNN = ifelse(knnMod == 0, 1 - attributes(knnMod)$prob, attributes(knnMod)$prob)
predKNN = ifelse(probKNN > 0.5, 1, 0)
```

This is the way to get the probabilities of species = Adelie (class = 1). Then, again we apply 0.5 cut-off value to get the predictions.

```
adelie_knn_df = bind_rows(mutate(test, probKNN, predKNN))
adelie_knn_df$predKNN = as.factor(adelie_knn_df$predKNN)

gg_knn = ggplot(test, aes(x=body_mass_g, y=flipper_length_mm,
      colour=adelie))+geom_point(aes(x=body_mass_g, y=flipper_length_mm,
```

```
      colour=predKNN), data=adelie_knn_df, size=2) +
      xlab("Flipper Length of a penguin (mm)") + ylab("Body Mass of a penguin (g)") +
      labs(shape = "Adelie", color = "Adelie") +
      ggtitle("The classification of species using \n K-nearest Neighbors") +
      theme_bw() + theme(plot.title = element_text(hjust = 0.5))

gg_knn
```



iv) Sensitivity & specificity For Logistic regression

```
predictions_log_reg = data.frame(prob_test_lr, pred_test_lr, test[, "adelie"])
colnames(predictions_log_reg) = c("Estim. prob. of Y=1", "Predicted class",
                                  "True class")
head(predictions_log_reg)
```

```
##   Estim. prob. of Y=1 Predicted class True class
## 1           0.9616473               1          1
## 2           0.9028693               1          1
## 3           0.6321050               1          1
## 4           0.7859021               1          1
## 5           0.9324308               1          1
## 6           0.7688126               1          1
```

```
conf_mat_log_r = table(predicted = predictions_log_reg["Predicted class"][,1], true =
        predictions_log_reg["True class"][,1] )

print("The confusion matrix is:")
```

```
## [1] "The confusion matrix is:"
```

```
conf_mat_log_r
```

```
##          true
## predicted  0  1
##         0 52  1
##         1  8 42
```

```
test_error_rate_lr = (conf_mat_log_r[1, 2] + conf_mat_log_r[2, 1])/sum(conf_mat_log_r)
print(paste( "The test error for Logistic regression -", signif(test_error_rate_lr, digits = 4)))
```

```
## [1] "The test error for Logistic regression - 0.08738"
```

```
sensitivity_lr = conf_mat_log_r[2, 2]/(conf_mat_log_r[1, 2]+conf_mat_log_r[2, 2])
specificity_lr = conf_mat_log_r[1, 1]/(conf_mat_log_r[2, 1]+conf_mat_log_r[1, 1])

print(paste( "The sensitivity - ", signif(sensitivity_lr, digits=4)))
```

```
## [1] "The sensitivity -  0.9767"
```

```
print(paste( "The specificity - ", signif(specificity_lr, digits=4)))
```

```
## [1] "The specificity -  0.8667"
```

For Quadratic Discriminant Analysis

```
predictions_qda = data.frame(pred_test_qda, test[, "adelie"])
colnames(predictions_qda) = c("Predicted class","True class")
head(predictions_qda)
```

```
##   Predicted class True class
## 1               1          1
## 2               1          1
## 3               1          1
## 4               1          1
## 5               1          1
## 6               1          1
```

```
conf_mat_qda = table(predicted = predictions_qda["Predicted class"][,1], true =
        predictions_qda["True class"][,1] )
print("The confusion matrix is:")
```

```
## [1] "The confusion matrix is:"
```

```
conf_mat_qda
```

```
##           true
## predicted  0  1
##         0 46  1
##         1 14 42
```

```
test_error_rate_qda = (conf_mat_qda[1, 2] + conf_mat_qda[2, 1])/sum(conf_mat_qda)
print(paste( "The test error for Quadratic Discriminant Analysis -",
             signif(test_error_rate_qda, digits = 4)))
```

```
## [1] "The test error for Quadratic Discriminant Analysis - 0.1456"
```

```
sensitivity_qda = conf_mat_qda[2, 2]/(conf_mat_qda[1, 2]+conf_mat_qda[2, 2])
specificity_qda = conf_mat_qda[1, 1]/(conf_mat_qda[2, 1]+conf_mat_qda[1, 1])

print(paste( "The sensitivity - ", signif(sensitivity_qda, digits=4)))
```

```
## [1] "The sensitivity -  0.9767"
```

```
print(paste( "The specificity - ", signif(specificity_qda, digits=4)))
```

```
## [1] "The specificity -  0.7667"
```

For K-nearest Neighbors

```
predictions_knn = data.frame(knn_r[, 2], knn_r[, 1], test[, "adelie"])
colnames(predictions_knn) = c("Estim. prob. of Y=1","Predicted class","True class")
head(predictions_knn)
```

```
##   Estim. prob. of Y=1 Predicted class True class
## 1           0.6000000               1          1
## 2           0.6666667               1          1
## 3           0.6800000               1          1
## 4           0.6400000               1          1
## 5           0.6800000               1          1
## 6           0.6400000               1          1
```

```
conf_mat_knn = table(predicted = predictions_knn["Predicted class"][,1], true =
        predictions_knn["True class"][,1] )
print("The confusion matrix is:")
```

```
## [1] "The confusion matrix is:"
```

```
conf_mat_knn
```

```
##           true
## predicted  0  1
##         0 35  2
##         1 25 41
```

```
test_error_rate_knn = (conf_mat_knn[1, 2] + conf_mat_knn[2, 1])/sum(conf_mat_knn)
print(paste( "The test error for K-nearest Neighbors -", signif(test_error_rate_knn, digits = 4)))
```

```
## [1] "The test error for K-nearest Neighbors - 0.2621"
```

```
sensitivity_knn = conf_mat_knn[2, 2]/(conf_mat_knn[1, 2]+conf_mat_knn[2, 2])
specificity_knn = conf_mat_knn[1, 1]/(conf_mat_knn[2, 1]+conf_mat_knn[1, 1])

print(paste( "The sensitivity - ", signif(sensitivity_knn, digits=4)))
```

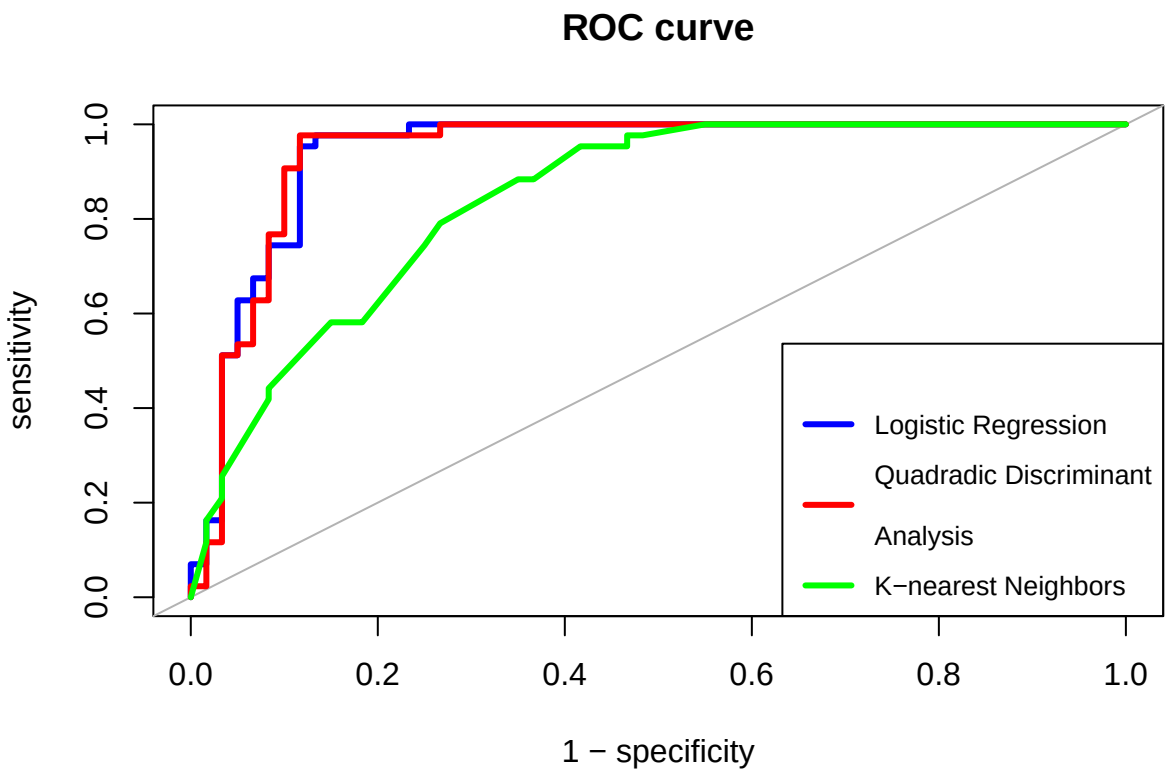
```
## [1] "The sensitivity -  0.9535"
```

```
print(paste( "The specificity - ", signif(specificity_knn, digits=4)))
```

```
## [1] "The specificity -  0.5833"
```

b)

```
lr_roc = roc.curve(test$adelie, prob_test_lr, col = "blue", lwd=3,
                   xlab = "1 - specificity", ylab = "sensitivity")

qda_roc = roc.curve(test$adelie, prob_test_qda[,2], col = "red", lwd=3, add = T)

probKNN = ifelse(knnMod == 0, 1 - attributes(knnMod)$prob, attributes(knnMod)$prob)

knn_roc = roc.curve(test$adelie, probKNN, col = "green", lwd=3, add = T)

legend("bottomright", legend = c("Logistic Regression", "Quadradic Discriminant
        \nAnalysis", "K-nearest Neighbors"), cex=0.8, lwd = 3,
       col = c("blue", "red", "green"))
```



i)

Areas Under Curves:

```
print(paste( "AUC of Logistic Regression ", signif(lr_roc$auc, digits = 4)))
```

```
## [1] "AUC of Logistic Regression  0.9391"
```

```
print(paste( "AUC of Quadradic Discriminant Analysis ", signif(qda_roc$auc, digits = 4)))
```

```
## [1] "AUC of Quadradic Discriminant Analysis  0.938"
```

```
print(paste( "AUC of K-nearest Neighbors ", signif(knn_roc$auc, digits = 4)))
```

```
## [1] "AUC of K-nearest Neighbors  0.8417"
```

ii) ROC curve - Receiver operating characteristics curve displays the relation between False Positive rate and True Positive rate for all possible threshold values (0 to 1). Since True Positive rate is $\frac{True\ Positives}{All\ Positives}$, it is expressed as sensitivity, and False Positive rate as 1 - Specificity. If the model is ideal model, the sensitivity = 1, and specificity = 1, so, the curve will be on the top left. While a straight line will represent a model with random guesses on the outcome.

In order to check the overall performance of the model, AUC (Area Under Curve) values are compared, meaning that if AUC value is high, that means the curve is closer to the ideal situation.

The comparison of the models we have: Logistic regression, Quadratic Discriminant Analysis, K-nearest Neighbors

When we look at the ROC Curves, we clearly see that the model that performs worse than others is K-nearest Neighbors. This is proved by AUC area. (AUC area of KNN = 0.8417).

The performances of Logistic regression and Quadratic Discriminant Analysis are almost the same. Yet, there is a slight difference in AUC areas. Based on AUC areas, Logistic regression performs a bit better than Quadratic Discriminant Analysis (AUC area of LogReg = 0.9391, AUC area of QDA = 0.938). However, the overall conclusion is Logistic Regression and Quadratic Discriminant Analysis are similarly good models for interpreting the data.

iii) If the task is to create an interpretable model, the model that has to be chosen is Logistic Regression. The reason is Logistic Regression outputs a table that contains all the necessary information to analyze the relation between two variable. The features like Intercept, p-value, t-value have key roles in interpretation.

c)

$$odds = \frac{p_i}{1-p_i} = \frac{\mathrm{P}(Y_i = 1 \mid X = x)}{\mathrm{P}(Y_i = 0 \mid X = x)} = exp(\beta_0) \cdot exp(\beta_1 x_1) \cdot exp(\beta_2 x_2)$$

$$odds\ ratio = \frac{odds[Y_i = 1 \mid X = x_1 + 1000]}{odds[Y_i = 1 \mid X = x_1]} = \frac{exp(\beta_0) \cdot exp(\beta_1 (x_1 + 1000)) \cdot exp(\beta_2 x_2)}{exp(\beta_0) \cdot exp(\beta_1 x_1) \cdot exp(\beta_2 x_2)} = exp(\beta_1 * 1000)$$

We find β_1 from coefficient table of Logistic regression

```
summary(log_reg)$coef
```

```
##                     Estimate   Std. Error   z value     Pr(>|z|)
## (Intercept)       37.7618776 5.1761640773  7.295340 2.979055e-13
## body_mass_g        0.0007120 0.0004619996  1.541127 1.232859e-01
## flipper_length_mm -0.2055804 0.0324291723 -6.339367 2.307116e-10
```

So, $\beta_1 = 0.000712$

```
print(paste( "The odds will be multiplied by ", signif(exp(coef(log_reg)[2]*1000), digits = 4)))
```

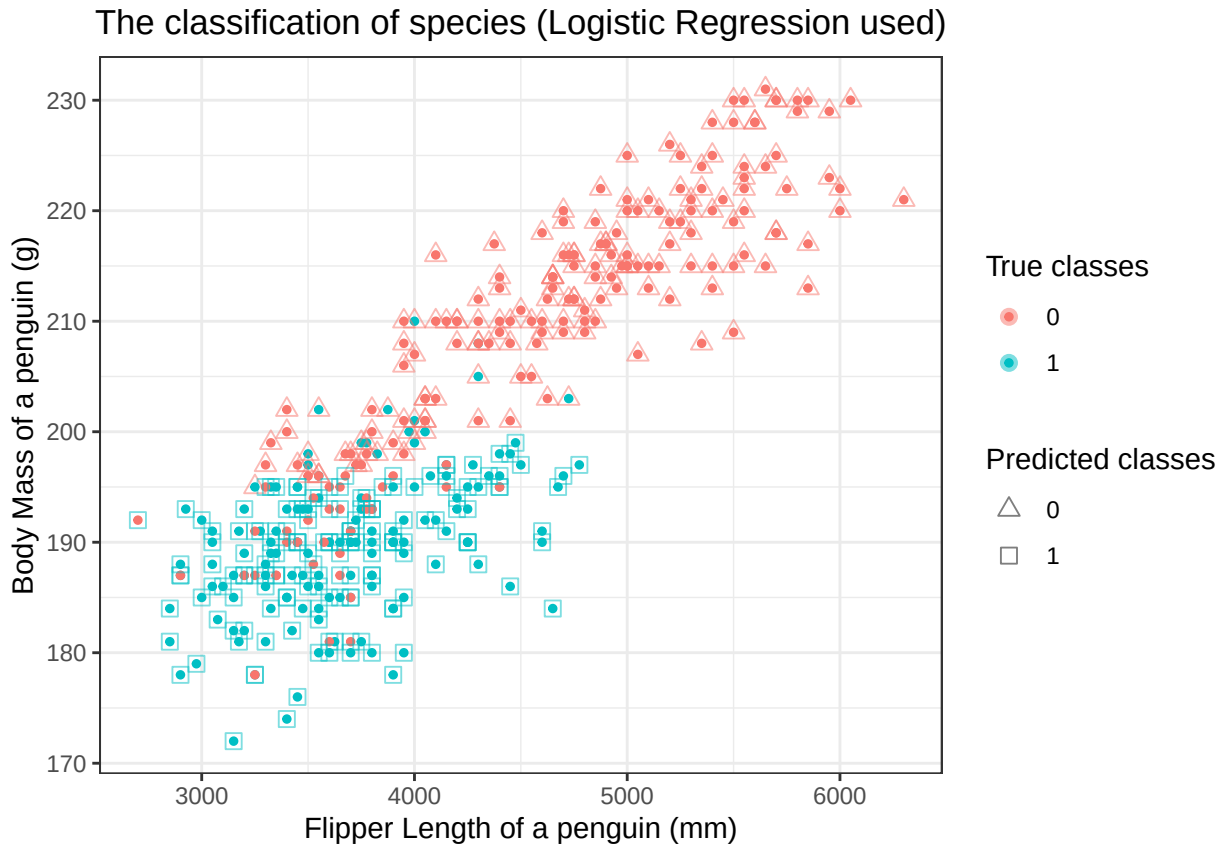
```
## [1] "The odds will be multiplied by  2.038"
```

The answer is III.

d)

```
prob_whole_lr <- predict(log_reg, newdata = Penguins_reduced, type = "response")

pred_whole_lr <- ifelse(prob_whole_lr > 0.5, 1, 0)

pred_whole_lr_sh = pred_whole_lr

whole_lr_df = bind_rows(mutate(Penguins_reduced, pred_whole_lr, pred_whole_lr_sh))
whole_lr_df$pred_whole_lr = as.factor(whole_lr_df$pred_whole_lr)
```

```
whole_lr_df$pred_whole_lr_sh = as.factor(whole_lr_df$pred_whole_lr_sh)
Penguins_reduced$adelie = as.factor(Penguins_reduced$adelie)


data = ggplot(Penguins_reduced, aes(x=body_mass_g, y=flipper_length_mm, color=adelie)) +
      geom_point(size=1) + theme_bw()


data_plot = data +
            geom_point(aes(x = body_mass_g, y=flipper_length_mm, colour = pred_whole_lr,
            shape = pred_whole_lr_sh), data=whole_lr_df,
            size=2.5, alpha = 1/2) + scale_shape_manual(values=c(2, 0))+
            labs(shape = "Predicted classes", color = "True classes") +
            xlab("Flipper Length of a penguin (mm)") +
            ylab("Body Mass of a penguin (g)") +
            ggtitle("The classification of species (Logistic Regression used)") +
            theme_bw() + theme(plot.title = element_text(hjust = 0.5))

data_plot
```



Problem 4

a)

Answers for the questions are as follows: (i) True; (ii) False; (iii) True; (iv) False;

b)

The given data for the problem was loaded into R firstly. The heart disease (chd) predicting function was created using global linear function and three variables sex, systolic blood pressure (sbp) and if a person smokes or not. The data-frame representing a non-smoking male with sbp 150 was insterted into the predicting function.

```
#Accessing the data

id<-"1chRpybM5cJn4Eow3-_xwDKPKyddL9M2N"
d.chd<-read.csv(sprintf("https://docs.google.com/uc?id=%s&export=download",id))

#Creating a predicting model

glm_fit = glm(chd~sex+sbp+smoking, data = d.chd, family = binomial)

#Predicting the disease probability

temp_d <- data.frame(sex=1, sbp=150, smoking=0)
predict(glm_fit,temp_d,type = 'response')
```

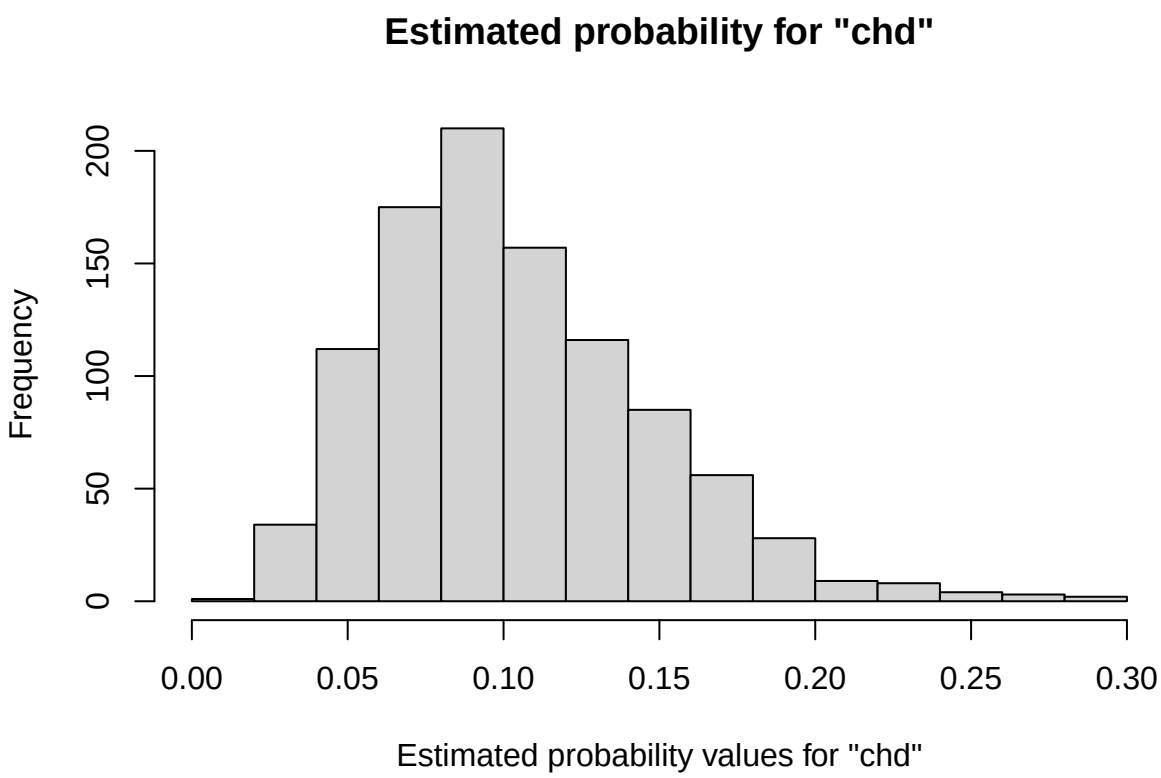
```
##       1
## 0.10096
```

The chd probability for a non-smoking male with sbp 150 equals to 0.10096 according to our predicting function.

c)

The function of the interest (which is chd predicting function for the male above) was created for bootstrapping. The bootstrapping was performed on function of the interest by replacing a row in the supplied data by another row in this data 1000 times. Each iteration result was saved in variable "A" and they were plotted as a histogram.

```
#Create function of interest
func_interest <- function(used_data){
  glm_fit = glm(chd~sex+sbp+smoking, data = used_data, family = binomial)
  predict(glm_fit,data.frame(sex=1, sbp=150, smoking=0),type = 'response')
}

#Implement bootstrap for 1000 iterations and save the results in A
B = 1000
A = replicate(B,0)
for (i in 1:B){
  A[i]=func_interest(d.chd[sample(1:nrow(d.chd), 500, replace = T),])
}

hist(A, main = 'Estimated probability for "chd"', xlab = 'Estimated probability values for "chd"')
```



As one can see most of the prediction values are between 0.05 and 0.15.

We created the function that takes prediction values above for calculating the standard error.

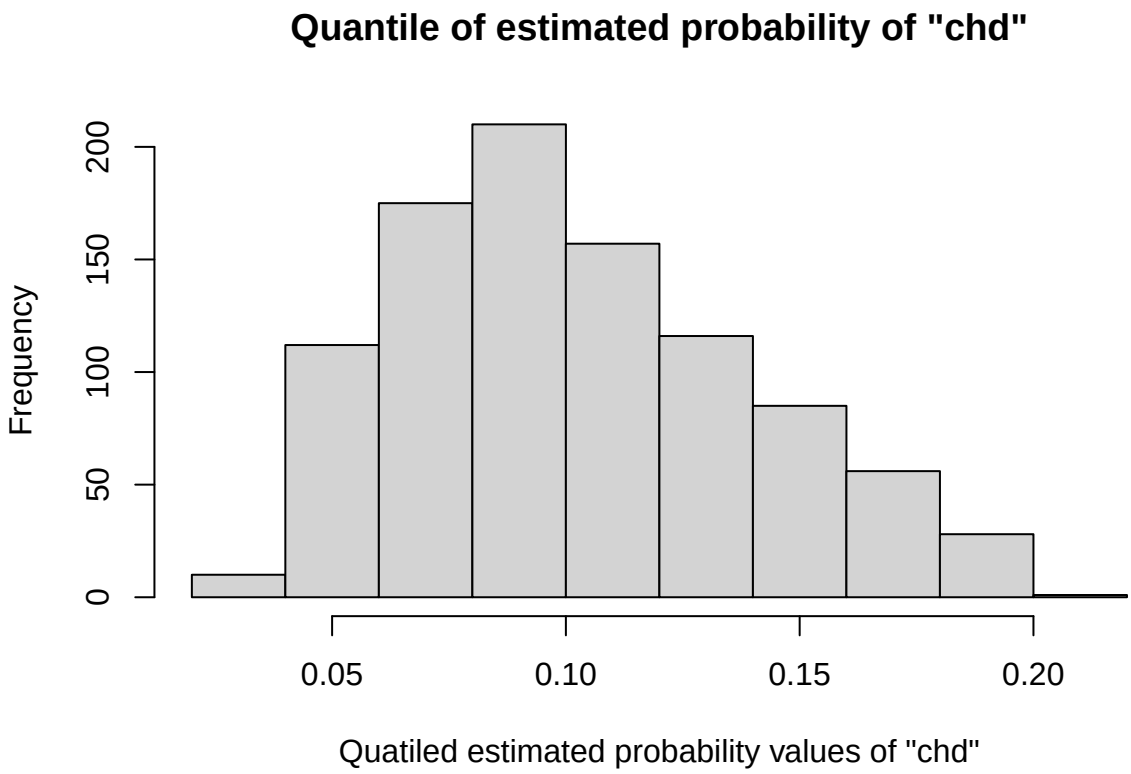
```
#Calculating standard error
std_error_func <- function(x) sd(x) / sqrt(length(x))
Std_error <- std_error_func(A)
print(Std_error)
```

```
## [1] 0.001387751
```

The standard error derived from predictions above equals to 0.00134.

2.5 % and 97.5 % quantile values of the predictions were defined using "quantile" function. The values below and above these quantile values were deleted from the predictions data and plotted as a histogram.

```
#Deriving quantiles and sorting bootstrap results within them
q = quantile(A,probs = c(0.025, 0.975))

After_q <-A[A<q[2]]
After_q <-After_q[After_q>q[1]]

hist(After_q, main = 'Quantile of estimated probability of "chd"', xlab = 'Quatiled estimated probabili
```



The remaining 95 % quantile interval for the bootstrap samples lies between 0.03915905 and 0.20153356. One can see how they distributed in the histogram above.

```
#Calculating values probabilities and expected probability value

EP = 0
for(i in 1:length(After_q)){
  EP = EP+After_q[i]*((1/950))
}
print(EP)
```

```
## [1] 0.1025979
```

The expected probability value is 0.1036039. In my opinion the range of plausible values are from 0.06 to 0.12.

d)

The answers for the questions in problem d) are as follows. (i) True, (ii) Fal- se, (iii) True, (iv) False.