wkLdsqR1W2-checkpoint

November 17, 2024

Analyse the **Heart Disease** dataset to predict the presence of heart disease using logistic regression.

The dataset contains medical information about individuals, and the goal is
to explore how various factors contribute to the likelihood of heart disease.
Link to the data set: heart disease link

[208]:

```r
# we want now to check the corelation between variables by the corelation matrix
# needed dependence
install.packages("reshape2")
library(reshape2)
library(ggplot2)

# for our distribution plots
library(gridExtra)
library(gridExtra)
# for bar plot won multiple columns
library(tidyr)
library(pROC)
```

```
Installing package into ‘/home/student/R/x86_64-pc-linux-gnu-library/4.2’
(as ‘lib’ is unspecified)

Type 'citation("pROC")' for a citation.


Attaching package: ‘pROC’


The following objects are masked from ‘package:stats’:

    cov, smooth, var
```

[ ]:

```
```

0.1 Load dataset

[149]:

```
# we sated by importing the dataset
df <- read.csv(file = "../../data/heart.csv",sep=",")
```

We used the **read.csv()** function to read our data after dowloading and placed them into a specific folder.

[ ]:

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```

[150]:

```
# check for some few observations
head(df)
```

A data.frame: 6 × 14

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldp
	<int>	<int>	<int>	<int>	<int>	<int>	<int>	<int>	<int>	<db
1	52	1	0	125	212	0	1	168	0	1.0
2	53	1	0	140	203	1	0	155	1	3.1
3	70	1	0	145	174	0	1	125	1	2.6
4	61	1	0	148	203	0	1	161	0	0.0
5	62	0	0	138	294	1	1	106	0	1.9
6	58	0	0	100	248	0	0	122	0	1.0

By this we get a brief overview about the content and the type of values in our data_set an.

[ ]:

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```

[151]:

```
# check a the description of each column
str(df)
```

```
'data.frame':   1025 obs. of  14 variables:
 $ age     : int  52 53 70 61 62 58 58 55 46 54 …
 $ sex     : int  1 1 1 1 0 0 1 1 1 1 …
 $ cp      : int  0 0 0 0 0 0 0 0 0 0 …
 $ trestbps: int  125 140 145 148 138 100 114 160 120 122 …
 $ chol    : int  212 203 174 203 294 248 318 289 249 286 …
 $ fbs     : int  0 1 0 0 1 0 0 0 0 0 …
 $ restecg : int  1 0 1 1 1 0 2 0 0 0 …
 $ thalach : int  168 155 125 161 106 122 140 145 144 116 …
 $ exang   : int  0 1 1 0 0 0 0 1 0 1 …
 $ oldpeak : num  1 3.1 2.6 0 1.9 1 4.4 0.8 0.8 3.2 …
 $ slope   : int  2 0 0 2 1 1 0 1 2 1 …
 $ ca      : int  2 0 0 1 3 0 3 1 0 2 …
 $ thal    : int  3 3 3 3 2 2 1 3 3 2 …
 $ target  : int  0 0 0 0 0 1 0 0 0 0 …
```

We notice that we get :
14 variables which are all integers except the variable **oldpeak** which is numererical
1025 observations in the dataset

[ ]:

```
```

description of the variables according to [1]

column name	meanin/labeled	values used for this variables
Age	age	measure in years
Sexe	sex	0: for woman , 1: man
Chest Pain	cp	0: for typical angina , 1: for atypical angina, 2: for non-anginal pain, 3: for asymptomatic
Resting Blood Preasure	trestbps	Measure in mm Hg
Cholesterol	chol	Measure in mg/dl
Fasting Blood sugar	fbs	(if greater than 120 mg/dl) :1 for true, :0 for false
Resting Electrocardiogram	restecg	1: for Nomal , 0: for abnormality , 2: Probable or definite left ventricular hypertrophy
Maximum Heart	thalach	Heart rate achieved during the patient's stress testing
Exercise induced Ingima	exang	0: for no , 1: for yes
Stress Test Depression	oldpeak	Numeric value signifying the marker for adverse cardiac events
Slope for peak exercise	slope	2: for upsloping , 0: for flat, 1: for down-sloping
Number of Major Vessels	ca	Number of major vessels [0-3] colored by fluoroscopy
Thalium heart rate	thal	3:Normal, 2:Fixed defect, 1:Reversable defect, 0:bellow the target HR
Heart prediction	target	1: Heart disease , 0: No Heart disease

[ ]:

```

```

0.2 Data cleanin

[ ]:

```
# we check for missing values
missing_vals <- sum(is.na(df))
cat("Number of missing values: ",missing_vals)
```

```
Number of missing values:  0
```

By this we can see that there is not missing values in our data set

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1. 1 2. 0

[ ]:

```
# check for duplicate rows
number_duplicates <- sum(duplicated.data.frame(df))
cat("Number of duplicated rows: ",number_duplicates)
```

```
Number of duplicated rows:  723
```

Ths means that in our data set there are only 1025 - 723 rows that are unique.

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```

```

[ ]:

```
# we get only the uniques rows to performe our analysis
df_uniques <- unique.data.frame(df)
head(df_uniques)
```

A data.frame: 6 × 14

	age <int>	sex <int>	cp <int>	trestbps <int>	chol <int>	fbs <int>	restecg <int>	thalach <int>	exang <int>	oldp <dbl
1	52	1	0	125	212	0	1	168	0	1.0
2	53	1	0	140	203	1	0	155	1	3.1
3	70	1	0	145	174	0	1	125	1	2.6
4	61	1	0	148	203	0	1	161	0	0.0
5	62	0	0	138	294	1	1	106	0	1.9
6	58	0	0	100	248	0	0	122	0	1.0

[ ]:

```

```

[ ]:

```
# check the new dim of our sample to verify if it have realy 1025 - 723 rows.
cat("The new data set has",dim(df_uniques)[1],"rows␣
 ↪and",dim(df_uniques)[2],"variables")
```

```
The new data set has 302 rows and 14 variables
```

By this we observed that only “slope” and “oldpeak” are corelated

[ ]:

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[ ]:

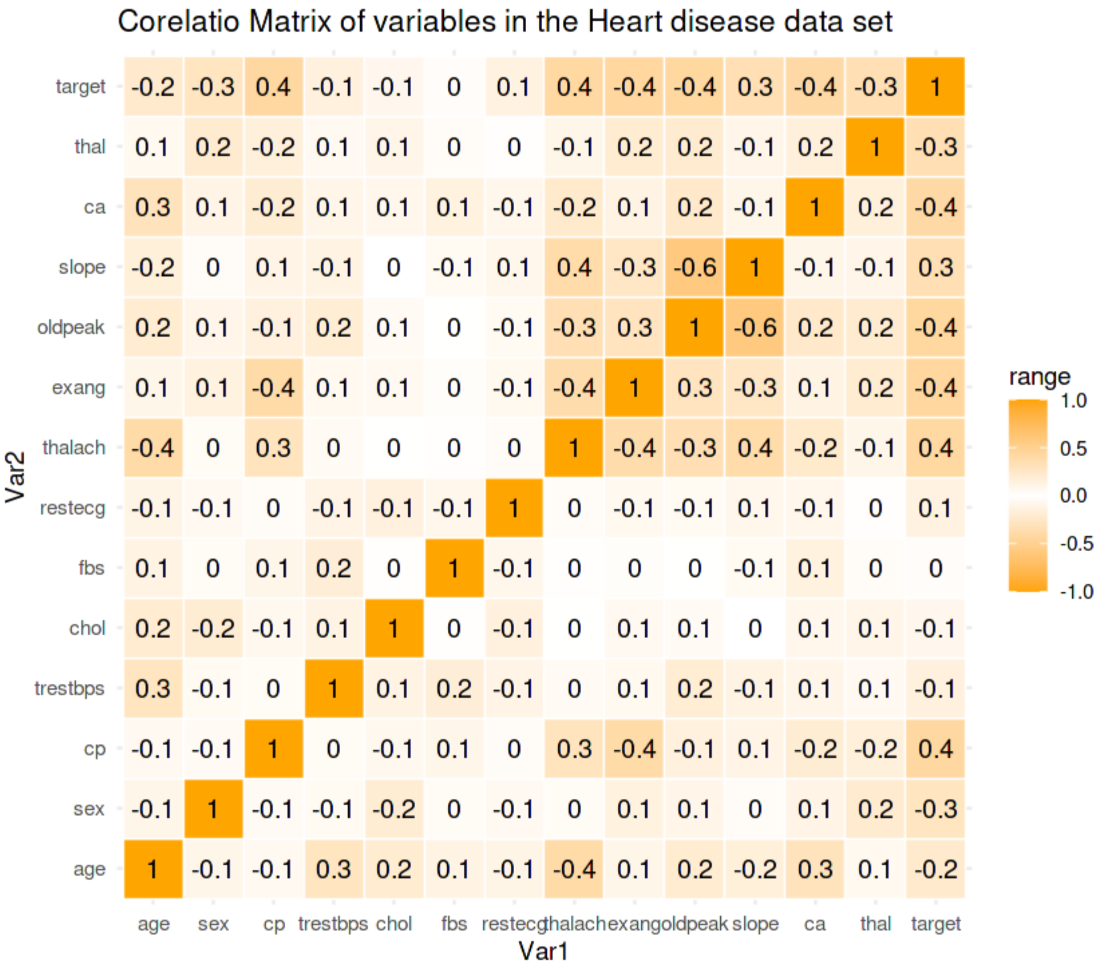
```
# we construct a corelation
cor_matrix_df <- cor(df_uniques)

# we set our data to a good format for the corelation plot with ggplot
cor_matrix_df <- melt(cor_matrix_df)

# we contruct ou plot
plot_cor_matrix_df <- ggplot(cor_matrix_df,aes(x=Var1,y=Var2, fill=value))+
    geom_tile(color="white",size=0.3)+
    geom_text(aes(label=round(value,1)),color="black",size=4)+
   ␣
 ↪scale_fill_gradient2(low="orange",high="orange",mid="white",midpoint=0,limit=c(-1,1),space=
    theme_minimal()+
    labs(title = "Corelatio Matrix of variables in the Heart disease data set")+
    coord_fixed()

# we save our plot to add it in our report
ggsave("cor_plot.png",plot_cor_matrix_df,width=11,height=9, dpi=500,bg="white")

#we show now our plot
plot_cor_matrix_df
```



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```
# Now we selected some variables on which we are going to perform our analysis
# we choose arbitrary the following variables target,age,sex,cp and chol
final_df <- df_uniques[c("age","sex","cp","chol","target")]
head(final_df)
```

A data.frame: 6 × 5

	age	sex	cp	chol	target
	<int>	<int>	<int>	<int>	<int>
1	52	1	0	212	0
2	53	1	0	203	0
3	70	1	0	174	0
4	61	1	0	203	0
5	62	0	0	294	0
6	58	0	0	248	1

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```
# Now we convert the cathegorial variable and the target variable into factor
final_df$sex <- as.factor(final_df$sex)
final_df$cp <- as.factor(final_df$cp)
final_df$target <- as.factor(final_df$target)
str(final_df)
```

```
'data.frame':	302 obs. of  5 variables:
 $ age   : int  52 53 70 61 62 58 58 55 46 54 …
 $ sex   : Factor w/ 2 levels "0","1": 2 2 2 2 1 1 2 2 2 2 …
 $ cp    : Factor w/ 4 levels "0","1","2","3": 1 1 1 1 1 1 1 1 1 1 …
 $ chol  : int  212 203 174 203 294 248 318 289 249 286 …
 $ target: Factor w/ 2 levels "0","1": 1 1 1 1 1 2 1 1 1 1 …
```

[ ]:

```

```

[ ]:

```
# size of our final data set
cat("The new data set has",dim(final_df)[1],"rows␣
 ↪and",dim(final_df)[2],"variables")
```

```
The new data set has 302 rows and 5 variables
```

[ ]:

```

```

0.3 Exploratory data analysis of the final data set

[ ]:

```
# Now we check some few statistic about our selected variables
summary(final_df)
```

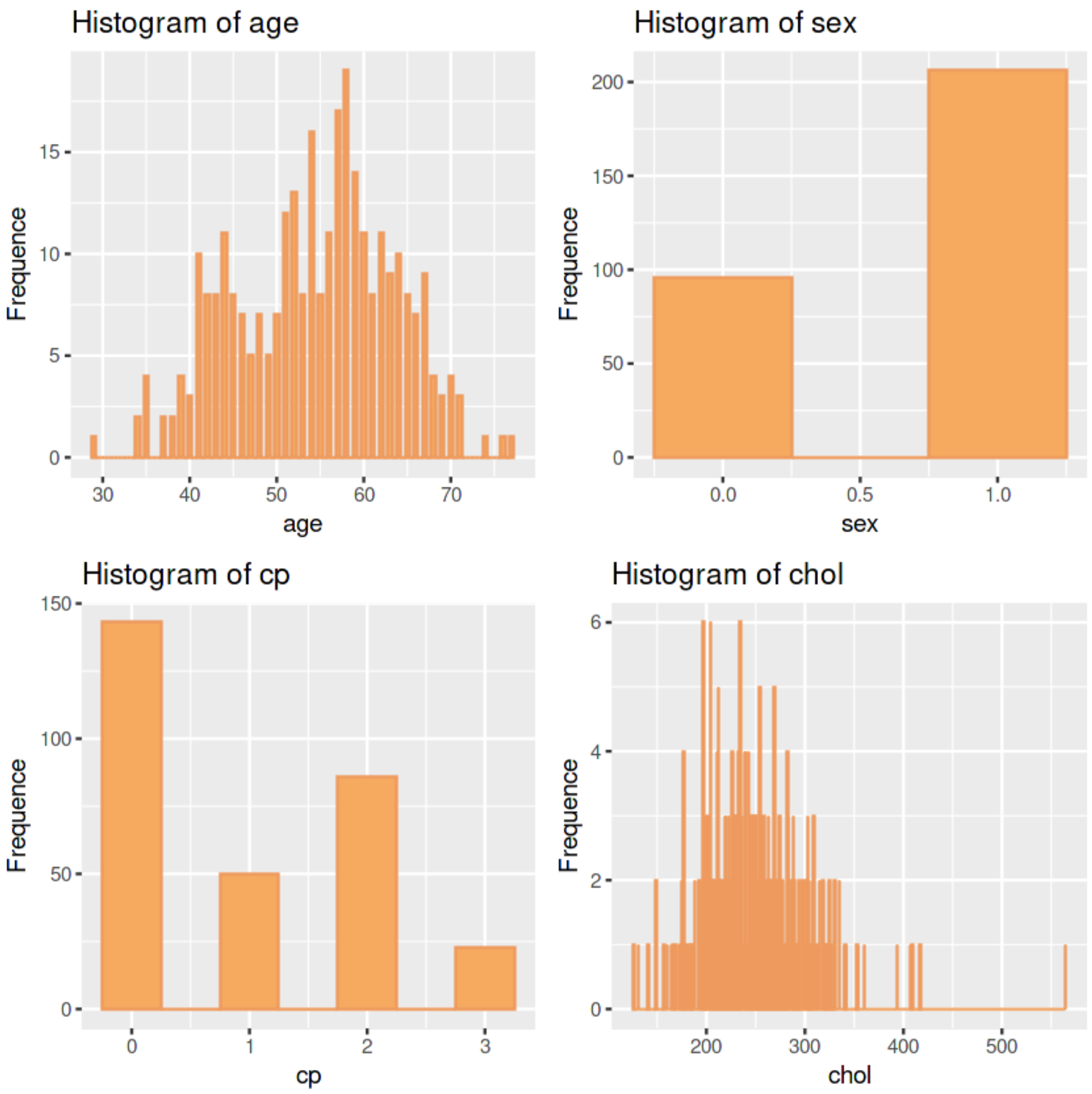
```
      age             sex               cp                chol      
 Min.   :29.00   Min.   :0.0000   Min.   :0.0000   Min.   :126.0  
 1st Qu.:48.00   1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:211.0  
 Median :55.50   Median :1.0000   Median :1.0000   Median :240.5  
 Mean   :54.42   Mean   :0.6821   Mean   :0.9636   Mean   :246.5  
 3rd Qu.:61.00   3rd Qu.:1.0000   3rd Qu.:2.0000   3rd Qu.:274.8  
 Max.   :77.00   Max.   :1.0000   Max.   :3.0000   Max.   :564.0  
     target     
 Min.   :0.000  
 1st Qu.:0.000  
 Median :1.000
 Mean   :0.543
 3rd Qu.:1.000
 Max.   :1.000
```

[ ]:

```

```

[ ]:

```
# check distribution of our selected descriptors ( which are all random␣
 ↪variable )
train_plots <- list()
variables<-colnames(final_df)
for (name in variables[1:4]){
  hist_plot <- ggplot(final_df, aes_string(x = name)) +
    geom_histogram(binwidth = 0.5, fill = "#f5aa5f", color = "#ee9a5e") +
    labs(title = paste("Histogram of", name), x = name, y = "Frequence")

  train_plots[[length(train_plots) + 1]] <- hist_plot
}

grid.arrange(grobs = train_plots, ncol = 2)
```

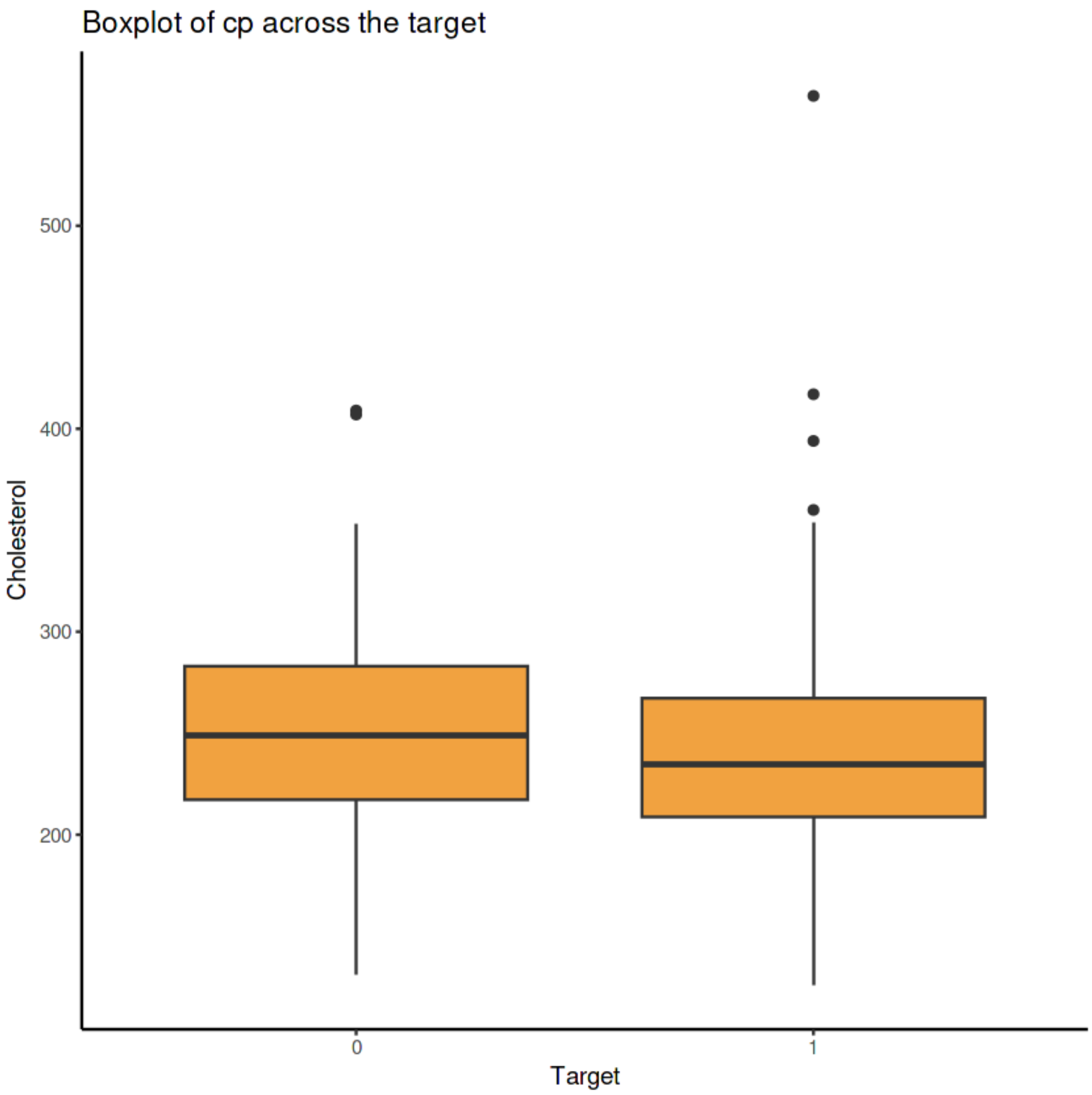


[ ]:

0.3.1 barplot of chest pain with respect to target

[ ]:

```
# Boxplot of mpg by the number of cylinders
ggplot(final_df, aes(x = target, y = chol)) +
  geom_boxplot(fill = "#f1a240") +
  labs(title = "Boxplot of cp across the target",
       x = "Target",
       y = "Cholesterol") +
  theme_classic()
```



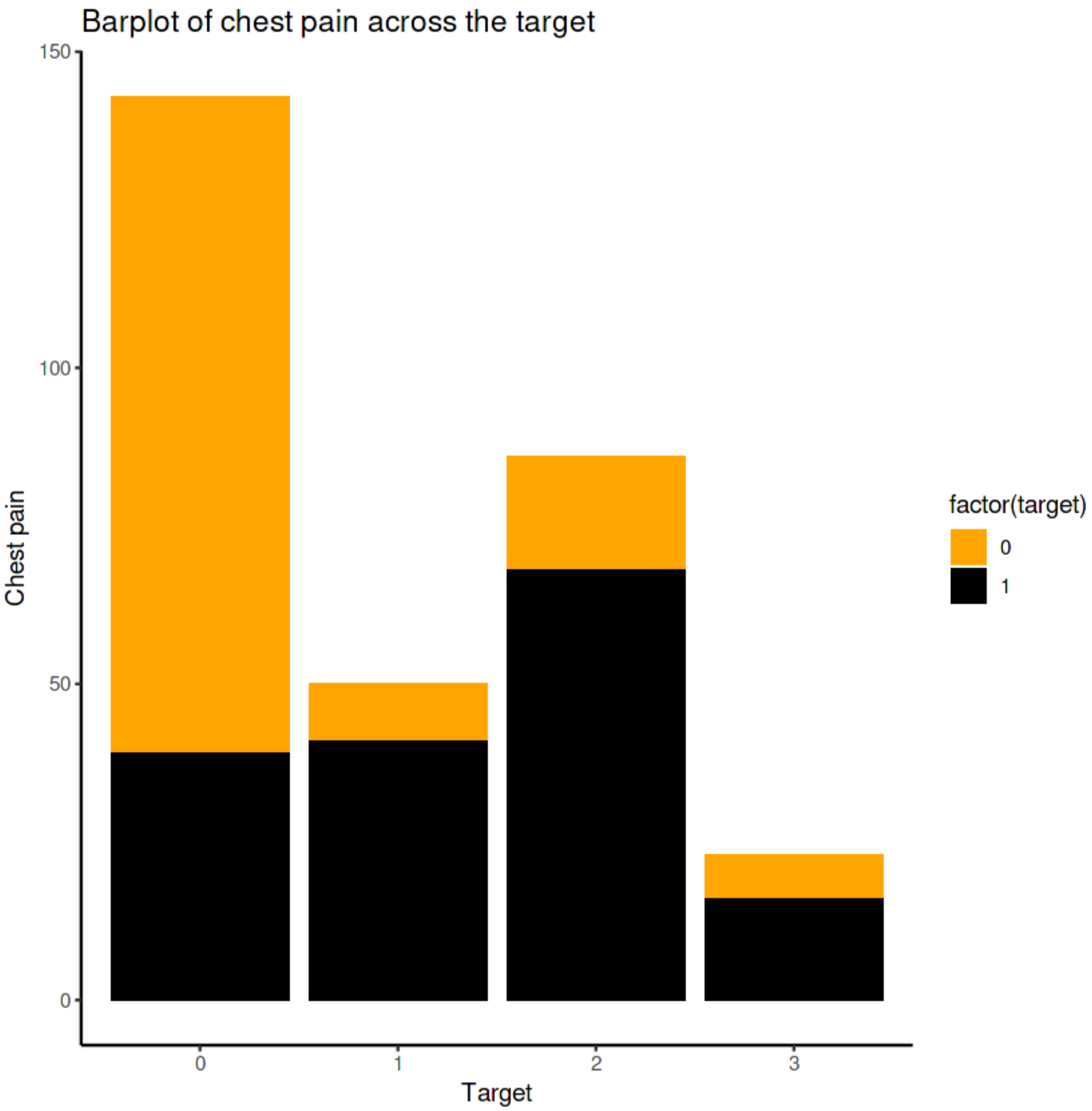
In this plot we can see that the proprtion of people who don’t get the disease but with a significant level of cholesterol is big than the proportion of people who have heart disease with a less quantity of cholesterol.
We also observe that there are some people who have heart disease but with a very big level of cholesterol.

[ ]:

0.3.2 barplot of sexe respect to target

[ ]:

```
ggplot(final_df, aes(x =cp,fill=factor(target))) +
  geom_bar(position = "stack") +
  labs(title = "Barplot of chest pain across the target",
       x = "Target",
       y = "Chest pain") +
       scale_fill_manual(values = c("orange","black"))+
  theme_classic()
```

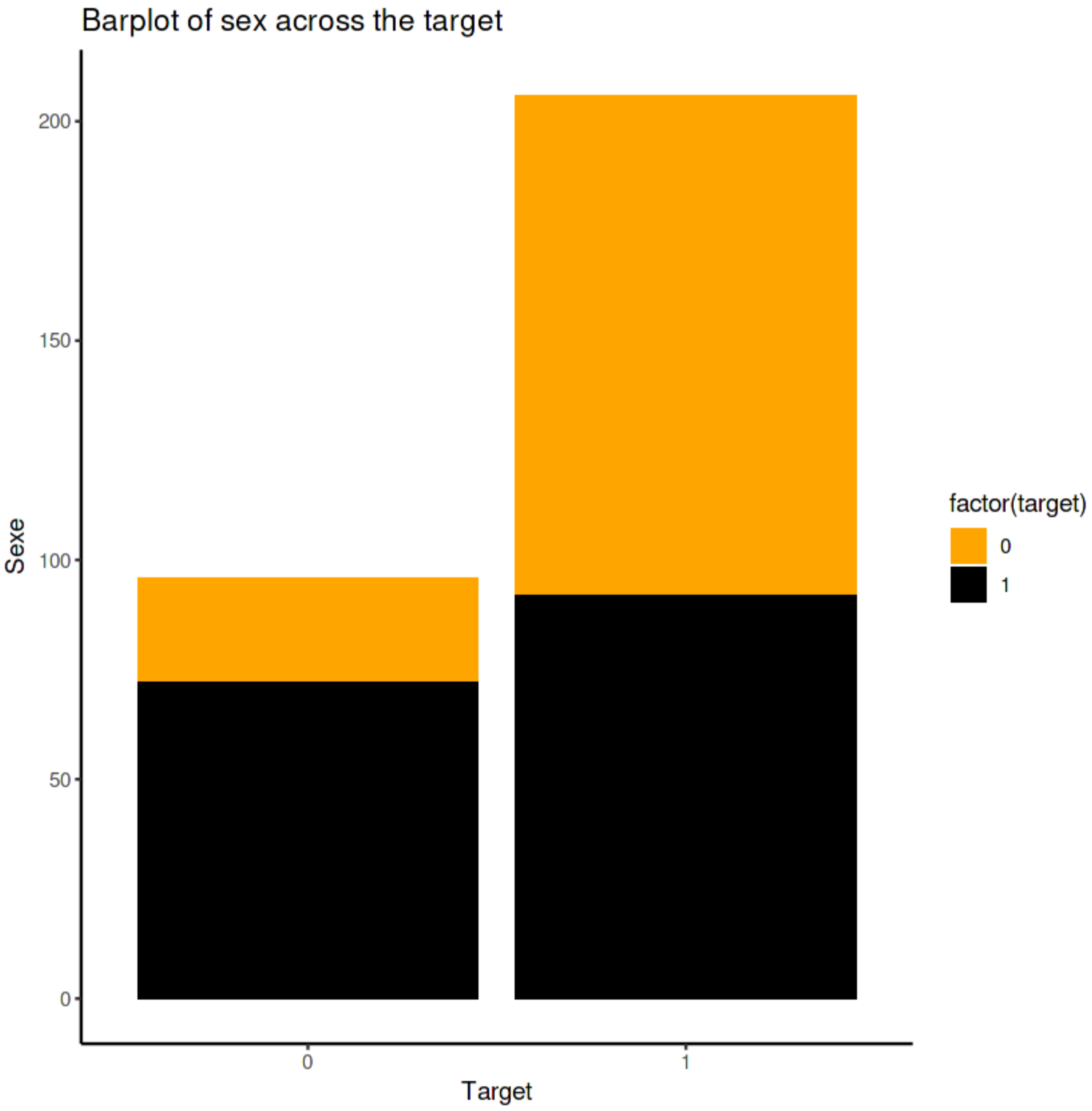


On this plot we can see that between the different type of chest pain there are:
- relatively a small proportion of people who have chest pain of type 0 and get heart heart disease
- for the chest pain 1,2 and 3 we have a significant proportion of people who have heart disease compare to those who don't get heart disease.

this implies that there is diffrence in the heart prevalance of chest pain 0 and chest pain (1,2,3)

[ ]:

```
[ ]: ggplot(final_df, aes(x = sex, fill = factor(target))) +
       geom_bar(position = "stack") +
       labs(title = "Barplot of sex across the target",
            x = "Target",
            y = "Sexe") +
            scale_fill_manual(values = c("orange","black"))+
       theme_classic()
```



By this plot we can see that: - for the female the proportion of those who have heart disease is more important than the proportion of those who don't have the disease. - for the male the proportion is also more for those who have the disease but not significantly

This can be interprate as wemen get more chance to get the disease than men
so there is a difference in heart disease prevalance of wemen and men

[ ]:

```
```

0.4 Fiting a logistic regression model

We start by spliting our data into train and test

[164]:

```
sample_index <- sample(1:nrow(final_df),0.7*nrow(final_df))
train_set <- final_df[sample_index, ]
test_set <- final_df[-sample_index, ]
# we check the dimension of each set
cat("Dimension of the train set:",dim(train_set)[1],"Observations and␣
 ↪",dim(train_set)[2],"features \n")
cat("Dimension of the test set :",dim(test_set)[1],"Observations and␣
 ↪",dim(test_set)[2],"features \n")
```

```
Dimension of the train set: 211 Observations and  5 features
Dimension of the test set : 91 Observations and  5 features
```

[ ]:

```
```

We build now our model and train him in the train_set

[165]:

```
# Fit a logistic model to predict target with age, sex, cp and chol
logistic_model <- glm(target ~ age + sex + cp + chol, data= train_set, family␣
 ↪="binomial")
# we check the summary of our model
cat(" Summary of the logistic model on train_set \n")
summary(logistic_model)
```

```
 Summary of the logistic model on train_set


Call:
glm(formula = target ~ age + sex + cp + chol, family = "binomial",
    data = train_set)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.5423  -0.5596   0.1567   0.6667   2.2980

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  6.814485   1.677713   4.062 4.87e-05 ***
age         -0.090683   0.024600  -3.686 0.000228 ***
```

```
sex1        -2.349896   0.485715  -4.838 1.31e-06 ***
cp1          3.061000   0.576775   5.307 1.11e-07 ***
cp2          2.691461   0.469921   5.727 1.02e-08 ***
cp3          3.014264   0.722424   4.172 3.01e-05 ***
chol        -0.006421   0.003547  -1.810 0.070238 .
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 291.14  on 210  degrees of freedom
Residual deviance: 174.77  on 204  degrees of freedom
AIC: 188.77

Number of Fisher Scoring iterations: 5
```

0.4.1 Interpration of the summary

0.4.2 Here we can see that:

0.4.3 for the p-value and the Estimate:

- **age, sex, cp1, cp2** and **cp3** are hyghly significant since their p-values are less than 0.0001.
- the **age** and **sex1**(being a man) decrease highly-significantly the log-odds respectivly at(0.0906 and 2.349) when they increase.
- the **cp1,cp2** and **cp3**(have the chest pain of type 1,2 or 3) increase highly-significantly the log-odds.
- the **chol** is marginaly significant which means that we can leave this variable out that will not have
  a strong effect on our model. Because high value of **chol** reduce the log-odds but the effect (0.070238) is not significant.

0.4.4 for the residual:

- We can see that our model reduce very well the deviance compare to the null model which implies a that our model fit well the data:
  null-deviance=291.14, residual-deviance=174.7.

about the AIC we can't say anything if we dont have another model to compare their AIC values which aims to see which is the best.

[ ]:

```

```

0.5 Model interpratation

[174]:

```
# we convert the coeffitients into ratio
coefs <- exp(coef(logistic_model))
coefs <- data.frame(coefs)
coefs
```

A data.frame: 7 × 1

	coefs <dbl>
(Intercept)	910.94704085
age	0.91330681
sex1	0.09537908
cp1	21.34889966
cp2	14.75322155
cp3	20.37409213
chol	0.99360004

0.5.1 Insighth:

As we said up here by this we can see clearly that: - the variable sex and cp have significant effect on the odds but here it seems like the chol is also significant

[ ]:

```

```

[176]:

```
# build a reduce model without the chol
reduce_model <- glm(target ~ age + sex + cp , data= train_set, family = "binomial")
# let's check its own summary
cat(" Summary of the reduce logistic model on train_set \n")
summary(reduce_model)
```

```
 Summary of the reduce logistic model on train_set


Call:
glm(formula = target ~ age + sex + cp, family = "binomial", data = train_set)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.4317  -0.5304   0.1952   0.6222   2.4640

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  5.30893    1.40777   3.771 0.000162 ***
age         -0.09529    0.02412  -3.951 7.80e-05 ***
sex1        -2.10167    0.45152  -4.655 3.25e-06 ***
cp1          3.02573    0.57024   5.306 1.12e-07 ***
cp2          2.69408    0.46362   5.811 6.21e-09 ***
cp3          3.02896    0.71747   4.222 2.42e-05 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 291.14  on 210  degrees of freedom
Residual deviance: 178.08  on 205  degrees of freedom
```

```
AIC: 190.08

Number of Fisher Scoring iterations: 5
```

[177]:

```
# we perform a anova test to see which of the two model is the best
anova(reduce_model,logistic_model, test="Chisq")
```

A anova: 2 × 5

	Resid. Df	Resid. Dev	Df	Deviance	Pr(>Chi)
	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
1	205	178.0758	NA	NA	NA
2	204	174.7651	1	3.310727	0.06882905

0.5.2 Explanation:

- By this we can confirm that add the chol variable doesn't affect our model since the **p-value** (0.06882905) is greater than 0.05.
- So if we don't compare the **AIC** or the **BIC** of the two models we can say that it is better to chose the reduce_model

[ ]:

```

```

0.5.3 Model prediction and Performance:

[201]:

```
# we test now the performance of the model over the test_set first
# predicted probabilities
test_set$prob <- predict(reduce_model,newdata=test_set ,type = "response")
# probabilities to predicted class
test_set$predicted <- ifelse(test_set$prob > 0.5, 1, 0)

# Confusion matrix
conf_matrx <- table(Predicted = test_set$predicted, Actual= test_set$target)
conf_matrx
```

```
         Actual
Predicted  0  1
        0 30 19
        1 11 31
```

[202]:

```
# accuracy, number of false positive and false negative
cat(" Accuracy :",(conf_matrx[1]+conf_matrx[4])/(conf_matrx[1]+
                                                             ␣
 ↪conf_matrx[4]+conf_matrx[2]+conf_matrx[3]),"\n")
cat("False Positive :", conf_matrx[3],"\n")
cat("False Negative :", conf_matrx[2],"\n")
```

```
 Accuracy : 0.6703297
False Positive : 19
False Negative : 11
```

[ ]:

[206]:

```
# Now we do the same thing over all the observations
# predicted probabilities
final_df$prob <- predict(reduce_model,newdata=final_df ,type = "response")
# probabilities to predicted class
final_df$predicted <- ifelse(final_df$prob > 0.5, 1, 0)

# Confusion matrix
conf_matrx2 <- table(Predicted = final_df$predicted, Actual= final_df$target)
conf_matrx2
```

```
         Actual
Predicted   0   1
        0 107  35
        1  31 129
```

[207]:

```
cat(" Accuracy :",(conf_matrx2[1]+conf_matrx2[4])/(conf_matrx2[1]+
                                                              ␣
 ↪conf_matrx2[4]+conf_matrx2[2]+conf_matrx2[3]),"\n")
cat("False Positive :", conf_matrx2[3],"\n")
cat("False Negative :", conf_matrx2[2],"\n")
```

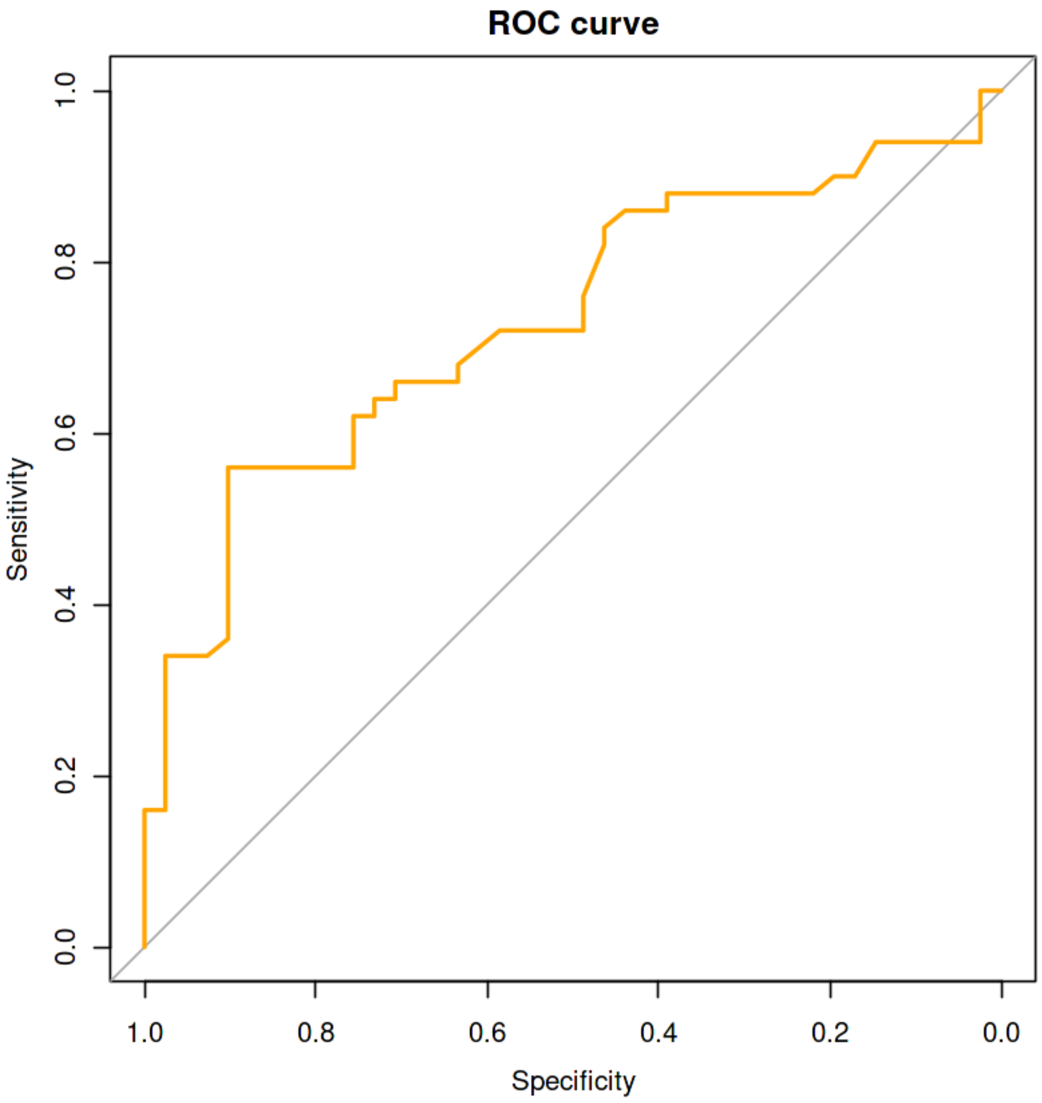
```
 Accuracy : 0.781457
False Positive : 35
False Negative : 31
```

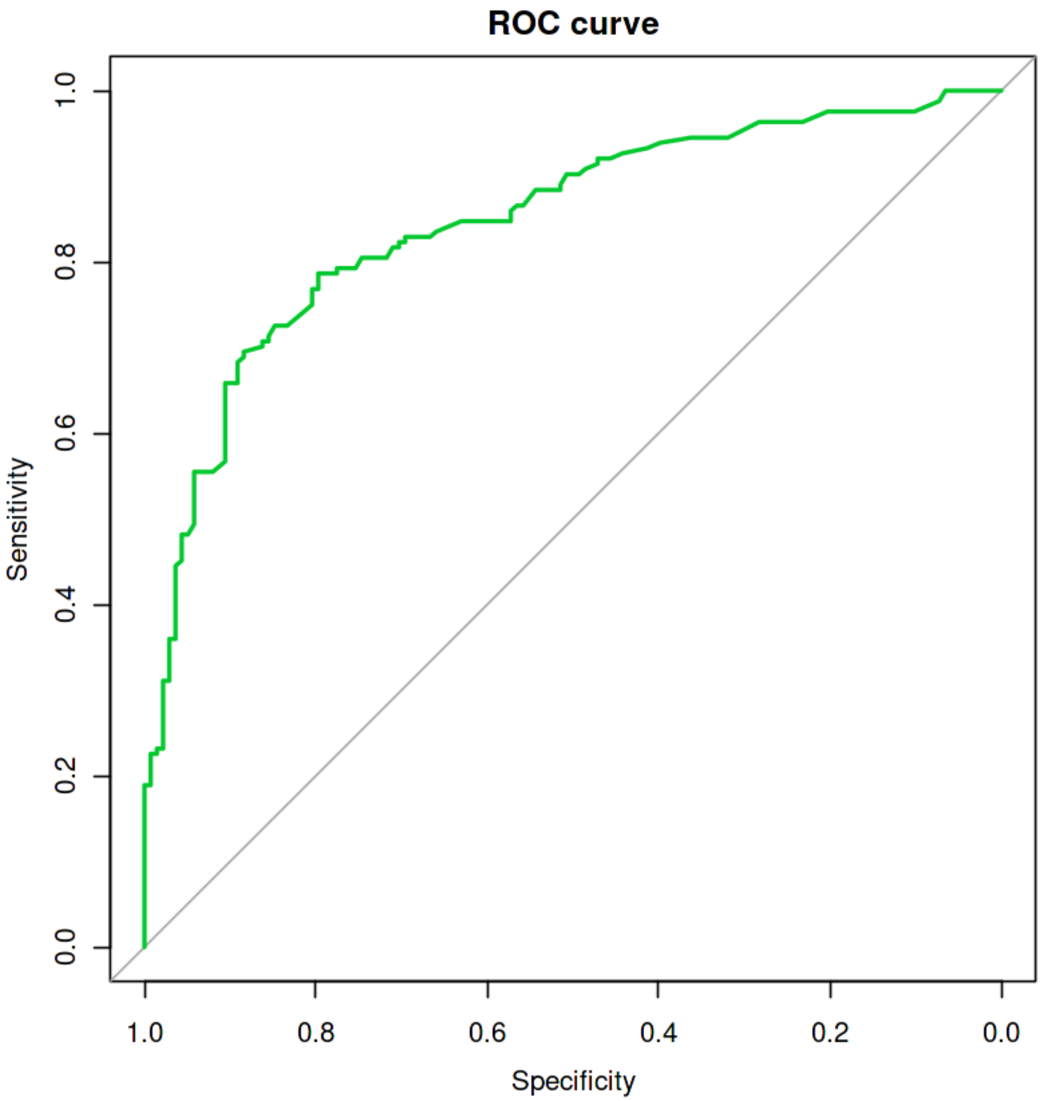
[ ]:

[211]:

```
### ROC curve over the test_set and the full observation
# over the test_set
roc__ <- roc(test_set$target,test_set$prob)
plot(roc__ , main="ROC curve" , col="orange",lwd = 2)
# over all the observations
roc__2 <- roc(final_df$target,final_df$prob)
plot(roc__2, main="ROC curve" , col="#03c82e",lwd = 2)
```

```
Setting levels: control = 0, case = 1

Setting direction: controls < cases

Setting levels: control = 0, case = 1

Setting direction: controls < cases
```


ROC curve
Sensitivity
0.0
0.2
0.4
0.6
0.8
1.0
Specificity
1.0
0.8
0.6
0.4
0.2
0.0



[214]:

```
# AUC only on the test_set
cat("AUC on the test :",auc(roc__))
```

```
AUC on the test : 0.7317073
```

The AUC tel us about our model discriminative ability between the different label of the target. Here we can see that our model has an AUC relatively close to one
but this is not enough for us to say than it has good ability of discrimination between get or not the disease.

[ ]:

```
```

[ ]:

```
```