

# Myocard Porject

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## Motivation

This project is a final assessment of the Data Science Professional Certificate. We were encouraged to find any dataset from UCI or Kaggle that we feel comfortable about it. For doing this, we are using the Myocardial infarction complications dataset from UCI repository machine learning. All the variables will explain along with the project.

## 1.0 Introduction

Until the last decade, world healthy has to change, including human behaviour and diseases. The actual world is fighting to prevent infections is the one possible strategy to deal with the increased hallmark of the current time. Prediction disease and chronic disease help the health system help to develop healthy ageing adults. Besides that, the “new world” already has to face many data generations, which can be suitable for data science. Data science has begun to provide a new set of tools that will leverage enhanced laboratory medicine and reinforce its value in a continuously transforming healthcare ecosystem (Gruson D, et al 2019). Using data science tools, it can work with a multidisciplinary field that uses scientific methods, process, algorithm and system to extracts insights from data (Peck, RW 2020). This current project is part of the Data Science Professional Certificate. To do this, we are applying techniques of data visualisation, exploration and linear regression and machine learning. According to this, we are using data from the ULC repository and predicted outcomes of myocardial infarction. We are going to see if the time of hospitalisation predicts new myocardial infarction. The time variable in this project counts how many time the patients were hospitalised.

Myocardial infarction (MI), commonly known as “heart attack”, is irreversible damage caused by prolonged ischemia and hypoxia. That means the heart can receive so much blood (ischemia), or the heart doesn't have blood and oxygen (hypoxia). This a serious medical emergency, meaning the supply of blood to the heart is suddenly blocked, usually by a blood clot. Our heart constantly needs blood and oxygen for a healthy life. When the body stopped or increase the blood flux, can happen a heart attack or MI.

In recent years MI has become one of the most severe diseases in several countries. Despite the treatment, some risk factors can predict MI, increasing the chances of first or second MI, such as age, hypertension, diabetes, and smoking (Fatemeh Kiani, 2016). With advanced medicine, it's easy to find blood tests for helping the diagnostic or prevention of MI. Different of levels enzymes can indicate how good the body and heart are. These enzymes, creatinine phosphokinase, serum creatinine, serum sodium and platelets, are usually inside the cells of your heart. When those cells or heart are injured, these enzymes spread out into your bloodstream. Measuring the levels of these enzymes is a good sign to know how the heart is. Following the World Health Organisation, 85% of deaths cardiovascular diseases caused by MI. It's essential to know to predict this disease to avoiding the patient's deaths.

## 2.0 Objective

This current project is part final assessment Data Science Professional certificate. The main objective is to predict new outcomes of MI in a patient by time. The variable time is how many times the patient admitted to the University of Leicester hospitals. We are trying to predict if the time of hospitalisation and other health issues can predict new MI.

### 3.0 Methods and Exploratory Data Analysis (EDA)

For this project, we are using several packages from CRAN to assist our analysis. All the packages will be load along with the development of the project. First of all, we downloaded the dataset from the website and built a linear regression model. After that, split the data into train and test and built a model for machine learning.

#### 3.1 Explore dataset.

First of all, explore and analyse the data set. It's essential to understand how the data are structured, characteristics for better knowledge.

```
if(!require(tidyverse)) install.packages("tidyverse", repos = "http://cran.us.r-project.org")

## Loading required package: tidyverse

## -- Attaching packages ----- tidyverse 1.3.1 --

## v ggplot2 3.3.4      v purrr  0.3.4
## v tibble  3.1.2      v dplyr  1.0.7
## v tidyr   1.1.3      v stringr 1.4.0
## v readr   1.4.0      v forcats 0.5.1

## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()

if(!require(caret)) install.packages("caret", repos = "http://cran.us.r-project.org")

## Loading required package: caret

## Loading required package: lattice

##
## Attaching package: 'caret'

## The following object is masked from 'package:purrr':
##
## lift

if(!require(data.table)) install.packages("data.table", repos = "http://cran.us.r-project.org")

## Loading required package: data.table

##
## Attaching package: 'data.table'

## The following objects are masked from 'package:dplyr':
##
## between, first, last

## The following object is masked from 'package:purrr':
##
## transpose
```

```

if(!require(dplyr)) install.packages("dplyr", repos = "http://cran.us.r-project.org")
if(!require(RColorBrewer)) install.packages("RColorBrewer", repos = "http://cran.us.r-project.org")

## Loading required package: RColorBrewer

if(!require(broom)) install.packages("broom", repos = "http://cran.us.r-project.org")

## Loading required package: broom

library(tidyverse)
library(dplyr)
library(caret)
library(broom)
library(RColorBrewer)

read_uci <- read.csv("https://archive.ics.uci.edu/ml/machine-learning-databases/00519/heart_failure_clinical_records.dat")

heart_disease <- read_uci

```

### 3.1.2 Analysing the Missing value

Downloaded the dataset, we can analysing if there is missing values.

```

missing_value <- table(is.na(heart_disease))
missing_value

```

```

##
## FALSE
## 3887

```

We observe there is no missig\_value on data set.

### 3.1.3 Exploratory Data Analysis (EDA)

This data collected in patients from Jan 2000 to Jan 2020 at the hospital University of Edx, USA. All the patients have a previous diagnostic of MI and health issue.

```

class(heart_disease)

```

```

## [1] "data.frame"

```

The class funtion tells us kind of R object we have. In our case class heart\_disease is a data\_frame.

```

str(heart_disease)

```

```

## 'data.frame': 299 obs. of 13 variables:
## $ age : num 75 55 65 50 65 90 75 60 65 80 ...
## $ anaemia : int 0 0 0 1 1 1 1 0 1 ...
## $ creatinine_phosphokinase: int 582 7861 146 111 160 47 246 315 157 123 ...
## $ diabetes : int 0 0 0 0 1 0 0 1 0 0 ...

```

```
## $ ejection_fraction      : int  20 38 20 20 20 40 15 60 65 35 ...
## $ high_blood_pressure    : int   1 0 0 0 0 1 0 0 0 1 ...
## $ platelets              : num 265000 263358 162000 210000 327000 ...
## $ serum_creatinine       : num  1.9 1.1 1.3 1.9 2.7 2.1 1.2 1.1 1.5 9.4 ...
## $ serum_sodium           : int  130 136 129 137 116 132 137 131 138 133 ...
## $ sex                    : int   1 1 1 1 0 1 1 1 0 1 ...
## $ smoking                : int   0 0 1 0 0 1 0 1 0 1 ...
## $ time                   : int   4 6 7 7 8 8 10 10 10 10 ...
## $ DEATH_EVENT            : int   1 1 1 1 1 1 1 1 1 1 ...
```

The str function gives us the structure for the heart\_disease dataset. Following this, we can notice the dataset has 299 obs and 13 variables. Also, we can observe the name of the variables on the dataset.

```
dim(heart_disease)
```

```
## [1] 299 13
```

This function dim shows us how many rows and columns we have on dataset heart\_disease. We can observe 299 rows and 13 variables.

```
head(heart_disease)
```

```
##   age anaemia creatinine_phosphokinase diabetes ejection_fraction
## 1  75      0                582      0             20
## 2  55      0                7861     0             38
## 3  65      0                146      0             20
## 4  50      1                111      0             20
## 5  65      1                160      1             20
## 6  90      1                 47      0             40
##   high_blood_pressure platelets serum_creatinine serum_sodium sex smoking time
## 1                   1    265000             1.9         130   1      0      4
## 2                   0    263358             1.1         136   1      0      6
## 3                   0    162000             1.3         129   1      1      7
## 4                   0    210000             1.9         137   1      0      7
## 5                   0    327000             2.7         116   0      0      8
## 6                   1    204000             2.1         132   1      1      8
##   DEATH_EVENT
## 1           1
## 2           1
## 3           1
## 4           1
## 5           1
## 6           1
```

The function head shows us the top few rows or “head” of the dataset heart\_disease.

Our project has the variable “sex”, but we are assuming the 0 is woman and 1 for man. Following this, we can find the proportion for the “sex” in our case.

What’s the proportion of women on dataset heart\_disease?

```
mean(heart_disease$sex == 0)
```

```
## [1] 0.3511706
```

We can observe around 0.3511706 or 35% of heart\_disease is women.

What's the proportion of men on dataset heart\_disease?

```
mean(heart_disease$sex == 1)
```

```
## [1] 0.6488294
```

We can observe around 0.6488294 or 65% of heart\_disease is men.

### 3.2 EDA and Visualisation

In this part of the project, we use the mutate function for better visualisation and add a new variable with gender, male or female.

```
myocard <- heart_disease %>% mutate(gender = ifelse(sex > 0, "male", "female"))
myocard
```

```
##      age anaemia creatinine_phosphokinase diabetes ejection_fraction
## 1  75.000      0                582           0              20
## 2  55.000      0                7861          0              38
## 3  65.000      0                146           0              20
## 4  50.000      1                111           0              20
## 5  65.000      1                160           1              20
## 6  90.000      1                 47           0              40
## 7  75.000      1                246           0              15
## 8  60.000      1                315           1              60
## 9  65.000      0                157           0              65
## 10 80.000      1                123           0              35
## 11 75.000      1                 81           0              38
## 12 62.000      0                231           0              25
## 13 45.000      1                981           0              30
## 14 50.000      1                168           0              38
## 15 49.000      1                 80           0              30
## 16 82.000      1                379           0              50
## 17 87.000      1                149           0              38
## 18 45.000      0                582           0              14
## 19 70.000      1                125           0              25
## 20 48.000      1                582           1              55
## 21 65.000      1                 52           0              25
## 22 65.000      1                128           1              30
## 23 68.000      1                220           0              35
## 24 53.000      0                 63           1              60
## 25 75.000      0                582           1              30
## 26 80.000      0                148           1              38
## 27 95.000      1                112           0              40
## 28 70.000      0                122           1              45
## 29 58.000      1                 60           0              38
## 30 82.000      0                 70           1              30
```

## 31	94.000	0	582	1	38
## 32	85.000	0	23	0	45
## 33	50.000	1	249	1	35
## 34	50.000	1	159	1	30
## 35	65.000	0	94	1	50
## 36	69.000	0	582	1	35
## 37	90.000	1	60	1	50
## 38	82.000	1	855	1	50
## 39	60.000	0	2656	1	30
## 40	60.000	0	235	1	38
## 41	70.000	0	582	0	20
## 42	50.000	0	124	1	30
## 43	70.000	0	571	1	45
## 44	72.000	0	127	1	50
## 45	60.000	1	588	1	60
## 46	50.000	0	582	1	38
## 47	51.000	0	1380	0	25
## 48	60.000	0	582	1	38
## 49	80.000	1	553	0	20
## 50	57.000	1	129	0	30
## 51	68.000	1	577	0	25
## 52	53.000	1	91	0	20
## 53	60.000	0	3964	1	62
## 54	70.000	1	69	1	50
## 55	60.000	1	260	1	38
## 56	95.000	1	371	0	30
## 57	70.000	1	75	0	35
## 58	60.000	1	607	0	40
## 59	49.000	0	789	0	20
## 60	72.000	0	364	1	20
## 61	45.000	0	7702	1	25
## 62	50.000	0	318	0	40
## 63	55.000	0	109	0	35
## 64	45.000	0	582	0	35
## 65	45.000	0	582	0	80
## 66	60.000	0	68	0	20
## 67	42.000	1	250	1	15
## 68	72.000	1	110	0	25
## 69	70.000	0	161	0	25
## 70	65.000	0	113	1	25
## 71	41.000	0	148	0	40
## 72	58.000	0	582	1	35
## 73	85.000	0	5882	0	35
## 74	65.000	0	224	1	50
## 75	69.000	0	582	0	20
## 76	60.000	1	47	0	20
## 77	70.000	0	92	0	60
## 78	42.000	0	102	1	40
## 79	75.000	1	203	1	38
## 80	55.000	0	336	0	45
## 81	70.000	0	69	0	40
## 82	67.000	0	582	0	50
## 83	60.000	1	76	1	25
## 84	79.000	1	55	0	50

## 85	59.000	1	280	1	25
## 86	51.000	0	78	0	50
## 87	55.000	0	47	0	35
## 88	65.000	1	68	1	60
## 89	44.000	0	84	1	40
## 90	57.000	1	115	0	25
## 91	70.000	0	66	1	45
## 92	60.000	0	897	1	45
## 93	42.000	0	582	0	60
## 94	60.000	1	154	0	25
## 95	58.000	0	144	1	38
## 96	58.000	1	133	0	60
## 97	63.000	1	514	1	25
## 98	70.000	1	59	0	60
## 99	60.000	1	156	1	25
## 100	63.000	1	61	1	40
## 101	65.000	1	305	0	25
## 102	75.000	0	582	0	45
## 103	80.000	0	898	0	25
## 104	42.000	0	5209	0	30
## 105	60.000	0	53	0	50
## 106	72.000	1	328	0	30
## 107	55.000	0	748	0	45
## 108	45.000	1	1876	1	35
## 109	63.000	0	936	0	38
## 110	45.000	0	292	1	35
## 111	85.000	0	129	0	60
## 112	55.000	0	60	0	35
## 113	50.000	0	369	1	25
## 114	70.000	1	143	0	60
## 115	60.000	1	754	1	40
## 116	58.000	1	400	0	40
## 117	60.000	1	96	1	60
## 118	85.000	1	102	0	60
## 119	65.000	1	113	1	60
## 120	86.000	0	582	0	38
## 121	60.000	1	737	0	60
## 122	66.000	1	68	1	38
## 123	60.000	0	96	1	38
## 124	60.000	1	582	0	30
## 125	60.000	0	582	0	40
## 126	43.000	1	358	0	50
## 127	46.000	0	168	1	17
## 128	58.000	1	200	1	60
## 129	61.000	0	248	0	30
## 130	53.000	1	270	1	35
## 131	53.000	1	1808	0	60
## 132	60.000	1	1082	1	45
## 133	46.000	0	719	0	40
## 134	63.000	0	193	0	60
## 135	81.000	0	4540	0	35
## 136	75.000	0	582	0	40
## 137	65.000	1	59	1	60
## 138	68.000	1	646	0	25

## 139 62.000	0	281	1	35
## 140 50.000	0	1548	0	30
## 141 80.000	0	805	0	38
## 142 46.000	1	291	0	35
## 143 50.000	0	482	1	30
## 144 61.000	1	84	0	40
## 145 72.000	1	943	0	25
## 146 50.000	0	185	0	30
## 147 52.000	0	132	0	30
## 148 64.000	0	1610	0	60
## 149 75.000	1	582	0	30
## 150 60.000	0	2261	0	35
## 151 72.000	0	233	0	45
## 152 62.000	0	30	1	60
## 153 50.000	0	115	0	45
## 154 50.000	0	1846	1	35
## 155 65.000	1	335	0	35
## 156 60.000	1	231	1	25
## 157 52.000	1	58	0	35
## 158 50.000	0	250	0	25
## 159 85.000	1	910	0	50
## 160 59.000	1	129	0	45
## 161 66.000	1	72	0	40
## 162 45.000	1	130	0	35
## 163 63.000	1	582	0	40
## 164 50.000	1	2334	1	35
## 165 45.000	0	2442	1	30
## 166 80.000	0	776	1	38
## 167 53.000	0	196	0	60
## 168 59.000	0	66	1	20
## 169 65.000	0	582	1	40
## 170 70.000	0	835	0	35
## 171 51.000	1	582	1	35
## 172 52.000	0	3966	0	40
## 173 70.000	1	171	0	60
## 174 50.000	1	115	0	20
## 175 65.000	0	198	1	35
## 176 60.000	1	95	0	60
## 177 69.000	0	1419	0	40
## 178 49.000	1	69	0	50
## 179 63.000	1	122	1	60
## 180 55.000	0	835	0	40
## 181 40.000	0	478	1	30
## 182 59.000	1	176	1	25
## 183 65.000	0	395	1	25
## 184 75.000	0	99	0	38
## 185 58.000	1	145	0	25
## 186 60.667	1	104	1	30
## 187 50.000	0	582	0	50
## 188 60.000	0	1896	1	25
## 189 60.667	1	151	1	40
## 190 40.000	0	244	0	45
## 191 80.000	0	582	1	35
## 192 64.000	1	62	0	60



## 193 50.000	1	121	1	40
## 194 73.000	1	231	1	30
## 195 45.000	0	582	0	20
## 196 77.000	1	418	0	45
## 197 45.000	0	582	1	38
## 198 65.000	0	167	0	30
## 199 50.000	1	582	1	20
## 200 60.000	0	1211	1	35
## 201 63.000	1	1767	0	45
## 202 45.000	0	308	1	60
## 203 70.000	0	97	0	60
## 204 60.000	0	59	0	25
## 205 78.000	1	64	0	40
## 206 50.000	1	167	1	45
## 207 40.000	1	101	0	40
## 208 85.000	0	212	0	38
## 209 60.000	1	2281	1	40
## 210 49.000	0	972	1	35
## 211 70.000	0	212	1	17
## 212 50.000	0	582	0	62
## 213 78.000	0	224	0	50
## 214 48.000	1	131	1	30
## 215 65.000	1	135	0	35
## 216 73.000	0	582	0	35
## 217 70.000	0	1202	0	50
## 218 54.000	1	427	0	70
## 219 68.000	1	1021	1	35
## 220 55.000	0	582	1	35
## 221 73.000	0	582	0	20
## 222 65.000	0	118	0	50
## 223 42.000	1	86	0	35
## 224 47.000	0	582	0	25
## 225 58.000	0	582	1	25
## 226 75.000	0	675	1	60
## 227 58.000	1	57	0	25
## 228 55.000	1	2794	0	35
## 229 65.000	0	56	0	25
## 230 72.000	0	211	0	25
## 231 60.000	0	166	0	30
## 232 70.000	0	93	0	35
## 233 40.000	1	129	0	35
## 234 53.000	1	707	0	38
## 235 53.000	1	582	0	45
## 236 77.000	1	109	0	50
## 237 75.000	0	119	0	50
## 238 70.000	0	232	0	30
## 239 65.000	1	720	1	40
## 240 55.000	1	180	0	45
## 241 70.000	0	81	1	35
## 242 65.000	0	582	1	30
## 243 40.000	0	90	0	35
## 244 73.000	1	1185	0	40
## 245 54.000	0	582	1	38
## 246 61.000	1	80	1	38

##	247	55.000	0	2017	0	25
##	248	64.000	0	143	0	25
##	249	40.000	0	624	0	35
##	250	53.000	0	207	1	40
##	251	50.000	0	2522	0	30
##	252	55.000	0	572	1	35
##	253	50.000	0	245	0	45
##	254	70.000	0	88	1	35
##	255	53.000	1	446	0	60
##	256	52.000	1	191	1	30
##	257	65.000	0	326	0	38
##	258	58.000	0	132	1	38
##	259	45.000	1	66	1	25
##	260	53.000	0	56	0	50
##	261	55.000	0	66	0	40
##	262	62.000	1	655	0	40
##	263	65.000	1	258	1	25
##	264	68.000	1	157	1	60
##	265	61.000	0	582	1	38
##	266	50.000	1	298	0	35
##	267	55.000	0	1199	0	20
##	268	56.000	1	135	1	38
##	269	45.000	0	582	1	38
##	270	40.000	0	582	1	35
##	271	44.000	0	582	1	30
##	272	51.000	0	582	1	40
##	273	67.000	0	213	0	38
##	274	42.000	0	64	0	40
##	275	60.000	1	257	1	30
##	276	45.000	0	582	0	38
##	277	70.000	0	618	0	35
##	278	70.000	0	582	1	38
##	279	50.000	1	1051	1	30
##	280	55.000	0	84	1	38
##	281	70.000	0	2695	1	40
##	282	70.000	0	582	0	40
##	283	42.000	0	64	0	30
##	284	65.000	0	1688	0	38
##	285	50.000	1	54	0	40
##	286	55.000	1	170	1	40
##	287	60.000	0	253	0	35
##	288	45.000	0	582	1	55
##	289	65.000	0	892	1	35
##	290	90.000	1	337	0	38
##	291	45.000	0	615	1	55
##	292	60.000	0	320	0	35
##	293	52.000	0	190	1	38
##	294	63.000	1	103	1	35
##	295	62.000	0	61	1	38
##	296	55.000	0	1820	0	38
##	297	45.000	0	2060	1	60
##	298	45.000	0	2413	0	38
##	299	50.000	0	196	0	45
##	high_blood_pressure platelets serum_creatinine serum_sodium sex smoking					

## 1	1	265000	1.90	130	1	0
## 2	0	263358	1.10	136	1	0
## 3	0	162000	1.30	129	1	1
## 4	0	210000	1.90	137	1	0
## 5	0	327000	2.70	116	0	0
## 6	1	204000	2.10	132	1	1
## 7	0	127000	1.20	137	1	0
## 8	0	454000	1.10	131	1	1
## 9	0	263358	1.50	138	0	0
## 10	1	388000	9.40	133	1	1
## 11	1	368000	4.00	131	1	1
## 12	1	253000	0.90	140	1	1
## 13	0	136000	1.10	137	1	0
## 14	1	276000	1.10	137	1	0
## 15	1	427000	1.00	138	0	0
## 16	0	47000	1.30	136	1	0
## 17	0	262000	0.90	140	1	0
## 18	0	166000	0.80	127	1	0
## 19	1	237000	1.00	140	0	0
## 20	0	87000	1.90	121	0	0
## 21	1	276000	1.30	137	0	0
## 22	1	297000	1.60	136	0	0
## 23	1	289000	0.90	140	1	1
## 24	0	368000	0.80	135	1	0
## 25	1	263358	1.83	134	0	0
## 26	0	149000	1.90	144	1	1
## 27	1	196000	1.00	138	0	0
## 28	1	284000	1.30	136	1	1
## 29	0	153000	5.80	134	1	0
## 30	0	200000	1.20	132	1	1
## 31	1	263358	1.83	134	1	0
## 32	0	360000	3.00	132	1	0
## 33	1	319000	1.00	128	0	0
## 34	0	302000	1.20	138	0	0
## 35	1	188000	1.00	140	1	0
## 36	0	228000	3.50	134	1	0
## 37	0	226000	1.00	134	1	0
## 38	1	321000	1.00	145	0	0
## 39	0	305000	2.30	137	1	0
## 40	0	329000	3.00	142	0	0
## 41	1	263358	1.83	134	1	1
## 42	1	153000	1.20	136	0	1
## 43	1	185000	1.20	139	1	1
## 44	1	218000	1.00	134	1	0
## 45	0	194000	1.10	142	0	0
## 46	0	310000	1.90	135	1	1
## 47	1	271000	0.90	130	1	0
## 48	1	451000	0.60	138	1	1
## 49	1	140000	4.40	133	1	0
## 50	0	395000	1.00	140	0	0
## 51	1	166000	1.00	138	1	0
## 52	1	418000	1.40	139	0	0
## 53	0	263358	6.80	146	0	0
## 54	1	351000	1.00	134	0	0

## 55	0	255000	2.20	132	0	1
## 56	0	461000	2.00	132	1	0
## 57	0	223000	2.70	138	1	1
## 58	0	216000	0.60	138	1	1
## 59	1	319000	1.10	136	1	1
## 60	1	254000	1.30	136	1	1
## 61	1	390000	1.00	139	1	0
## 62	1	216000	2.30	131	0	0
## 63	0	254000	1.10	139	1	1
## 64	0	385000	1.00	145	1	0
## 65	0	263358	1.18	137	0	0
## 66	0	119000	2.90	127	1	1
## 67	0	213000	1.30	136	0	0
## 68	0	274000	1.00	140	1	1
## 69	0	244000	1.20	142	0	0
## 70	0	497000	1.83	135	1	0
## 71	0	374000	0.80	140	1	1
## 72	0	122000	0.90	139	1	1
## 73	0	243000	1.00	132	1	1
## 74	0	149000	1.30	137	1	1
## 75	0	266000	1.20	134	1	1
## 76	0	204000	0.70	139	1	1
## 77	1	317000	0.80	140	0	1
## 78	0	237000	1.20	140	1	0
## 79	1	283000	0.60	131	1	1
## 80	1	324000	0.90	140	0	0
## 81	0	293000	1.70	136	0	0
## 82	0	263358	1.18	137	1	1
## 83	0	196000	2.50	132	0	0
## 84	1	172000	1.80	133	1	0
## 85	1	302000	1.00	141	0	0
## 86	0	406000	0.70	140	1	0
## 87	1	173000	1.10	137	1	0
## 88	1	304000	0.80	140	1	0
## 89	1	235000	0.70	139	1	0
## 90	1	181000	1.10	144	1	0
## 91	0	249000	0.80	136	1	1
## 92	0	297000	1.00	133	1	0
## 93	0	263358	1.18	137	0	0
## 94	0	210000	1.70	135	1	0
## 95	1	327000	0.70	142	0	0
## 96	1	219000	1.00	141	1	0
## 97	1	254000	1.30	134	1	0
## 98	0	255000	1.10	136	0	0
## 99	1	318000	1.20	137	0	0
## 100	0	221000	1.10	140	0	0
## 101	0	298000	1.10	141	1	0
## 102	1	263358	1.18	137	1	0
## 103	0	149000	1.10	144	1	1
## 104	0	226000	1.00	140	1	1
## 105	1	286000	2.30	143	0	0
## 106	1	621000	1.70	138	0	1
## 107	0	263000	1.30	137	1	0
## 108	0	226000	0.90	138	1	0

## 109	0	304000	1.10	133	1	1
## 110	0	850000	1.30	142	1	1
## 111	0	306000	1.20	132	1	1
## 112	0	228000	1.20	135	1	1
## 113	0	252000	1.60	136	1	0
## 114	0	351000	1.30	137	0	0
## 115	1	328000	1.20	126	1	0
## 116	0	164000	1.00	139	0	0
## 117	1	271000	0.70	136	0	0
## 118	0	507000	3.20	138	0	0
## 119	1	203000	0.90	140	0	0
## 120	0	263358	1.83	134	0	0
## 121	1	210000	1.50	135	1	1
## 122	1	162000	1.00	136	0	0
## 123	0	228000	0.75	140	0	0
## 124	1	127000	0.90	145	0	0
## 125	0	217000	3.70	134	1	0
## 126	0	237000	1.30	135	0	0
## 127	1	271000	2.10	124	0	0
## 128	0	300000	0.80	137	0	0
## 129	1	267000	0.70	136	1	1
## 130	0	227000	3.40	145	1	0
## 131	1	249000	0.70	138	1	1
## 132	0	250000	6.10	131	1	0
## 133	1	263358	1.18	137	0	0
## 134	1	295000	1.30	145	1	1
## 135	0	231000	1.18	137	1	1
## 136	0	263358	1.18	137	1	0
## 137	0	172000	0.90	137	0	0
## 138	0	305000	2.10	130	1	0
## 139	0	221000	1.00	136	0	0
## 140	1	211000	0.80	138	1	0
## 141	0	263358	1.10	134	1	0
## 142	0	348000	0.90	140	0	0
## 143	0	329000	0.90	132	0	0
## 144	1	229000	0.90	141	0	0
## 145	1	338000	1.70	139	1	1
## 146	0	266000	0.70	141	1	1
## 147	0	218000	0.70	136	1	1
## 148	0	242000	1.00	137	1	0
## 149	0	225000	1.83	134	1	0
## 150	1	228000	0.90	136	1	0
## 151	1	235000	2.50	135	0	0
## 152	1	244000	0.90	139	1	0
## 153	1	184000	0.90	134	1	1
## 154	0	263358	1.18	137	1	1
## 155	1	235000	0.80	136	0	0
## 156	0	194000	1.70	140	1	0
## 157	0	277000	1.40	136	0	0
## 158	0	262000	1.00	136	1	1
## 159	0	235000	1.30	134	1	0
## 160	1	362000	1.10	139	1	1
## 161	1	242000	1.20	134	1	0
## 162	0	174000	0.80	139	1	1

## 163	0	448000	0.90	137	1	1
## 164	0	75000	0.90	142	0	0
## 165	0	334000	1.10	139	1	0
## 166	1	192000	1.30	135	0	0
## 167	0	220000	0.70	133	1	1
## 168	0	70000	2.40	134	1	0
## 169	0	270000	1.00	138	0	0
## 170	1	305000	0.80	133	0	0
## 171	0	263358	1.50	136	1	1
## 172	0	325000	0.90	140	1	1
## 173	1	176000	1.10	145	1	1
## 174	0	189000	0.80	139	1	0
## 175	1	281000	0.90	137	1	1
## 176	0	337000	1.00	138	1	1
## 177	0	105000	1.00	135	1	1
## 178	0	132000	1.00	140	0	0
## 179	0	267000	1.20	145	1	0
## 180	0	279000	0.70	140	1	1
## 181	0	303000	0.90	136	1	0
## 182	0	221000	1.00	136	1	1
## 183	0	265000	1.20	136	1	1
## 184	1	224000	2.50	134	1	0
## 185	0	219000	1.20	137	1	1
## 186	0	389000	1.50	136	1	0
## 187	0	153000	0.60	134	0	0
## 188	0	365000	2.10	144	0	0
## 189	1	201000	1.00	136	0	0
## 190	1	275000	0.90	140	0	0
## 191	0	350000	2.10	134	1	0
## 192	0	309000	1.50	135	0	0
## 193	0	260000	0.70	130	1	0
## 194	0	160000	1.18	142	1	1
## 195	1	126000	1.60	135	1	0
## 196	0	223000	1.80	145	1	0
## 197	1	263358	1.18	137	0	0
## 198	0	259000	0.80	138	0	0
## 199	1	279000	1.00	134	0	0
## 200	0	263358	1.80	113	1	1
## 201	0	73000	0.70	137	1	0
## 202	1	377000	1.00	136	1	0
## 203	1	220000	0.90	138	1	0
## 204	1	212000	3.50	136	1	1
## 205	0	277000	0.70	137	1	1
## 206	0	362000	1.00	136	0	0
## 207	0	226000	0.80	141	0	0
## 208	0	186000	0.90	136	1	0
## 209	0	283000	1.00	141	0	0
## 210	1	268000	0.80	130	0	0
## 211	1	389000	1.00	136	1	1
## 212	1	147000	0.80	140	1	1
## 213	0	481000	1.40	138	1	1
## 214	1	244000	1.60	130	0	0
## 215	1	290000	0.80	134	1	0
## 216	1	203000	1.30	134	1	0

## 217	1	358000	0.90	141	0	0
## 218	1	151000	9.00	137	0	0
## 219	0	271000	1.10	134	1	0
## 220	1	371000	0.70	140	0	0
## 221	0	263358	1.83	134	1	0
## 222	0	194000	1.10	145	1	1
## 223	0	365000	1.10	139	1	1
## 224	0	130000	0.80	134	1	0
## 225	0	504000	1.00	138	1	0
## 226	0	265000	1.40	125	0	0
## 227	0	189000	1.30	132	1	1
## 228	1	141000	1.00	140	1	0
## 229	0	237000	5.00	130	0	0
## 230	0	274000	1.20	134	0	0
## 231	0	62000	1.70	127	0	0
## 232	0	185000	1.10	134	1	1
## 233	0	255000	0.90	137	1	0
## 234	0	330000	1.40	137	1	1
## 235	0	305000	1.10	137	1	1
## 236	1	406000	1.10	137	1	0
## 237	1	248000	1.10	148	1	0
## 238	0	173000	1.20	132	1	0
## 239	0	257000	1.00	136	0	0
## 240	0	263358	1.18	137	1	1
## 241	1	533000	1.30	139	0	0
## 242	0	249000	1.30	136	1	1
## 243	0	255000	1.10	136	1	1
## 244	1	220000	0.90	141	0	0
## 245	0	264000	1.80	134	1	0
## 246	0	282000	1.40	137	1	0
## 247	0	314000	1.10	138	1	0
## 248	0	246000	2.40	135	1	0
## 249	0	301000	1.00	142	1	1
## 250	0	223000	1.20	130	0	0
## 251	1	404000	0.50	139	0	0
## 252	0	231000	0.80	143	0	0
## 253	1	274000	1.00	133	1	0
## 254	1	236000	1.20	132	0	0
## 255	1	263358	1.00	139	1	0
## 256	1	334000	1.00	142	1	1
## 257	0	294000	1.70	139	0	0
## 258	1	253000	1.00	139	1	0
## 259	0	233000	0.80	135	1	0
## 260	0	308000	0.70	135	1	1
## 261	0	203000	1.00	138	1	0
## 262	0	283000	0.70	133	0	0
## 263	0	198000	1.40	129	1	0
## 264	0	208000	1.00	140	0	0
## 265	0	147000	1.20	141	1	0
## 266	0	362000	0.90	140	1	1
## 267	0	263358	1.83	134	1	1
## 268	0	133000	1.70	140	1	0
## 269	0	302000	0.90	140	0	0
## 270	0	222000	1.00	132	1	0

## 271	1	263358	1.60	130	1	1
## 272	0	221000	0.90	134	0	0
## 273	0	215000	1.20	133	0	0
## 274	0	189000	0.70	140	1	0
## 275	0	150000	1.00	137	1	1
## 276	1	422000	0.80	137	0	0
## 277	0	327000	1.10	142	0	0
## 278	0	25100	1.10	140	1	0
## 279	0	232000	0.70	136	0	0
## 280	0	451000	1.30	136	0	0
## 281	0	241000	1.00	137	1	0
## 282	0	51000	2.70	136	1	1
## 283	0	215000	3.80	128	1	1
## 284	0	263358	1.10	138	1	1
## 285	0	279000	0.80	141	1	0
## 286	0	336000	1.20	135	1	0
## 287	0	279000	1.70	140	1	0
## 288	0	543000	1.00	132	0	0
## 289	0	263358	1.10	142	0	0
## 290	0	390000	0.90	144	0	0
## 291	0	222000	0.80	141	0	0
## 292	0	133000	1.40	139	1	0
## 293	0	382000	1.00	140	1	1
## 294	0	179000	0.90	136	1	1
## 295	1	155000	1.10	143	1	1
## 296	0	270000	1.20	139	0	0
## 297	0	742000	0.80	138	0	0
## 298	0	140000	1.40	140	1	1
## 299	0	395000	1.60	136	1	1
##	time	DEATH_EVENT	gender			
## 1	4	1	male			
## 2	6	1	male			
## 3	7	1	male			
## 4	7	1	male			
## 5	8	1	female			
## 6	8	1	male			
## 7	10	1	male			
## 8	10	1	male			
## 9	10	1	female			
## 10	10	1	male			
## 11	10	1	male			
## 12	10	1	male			
## 13	11	1	male			
## 14	11	1	male			
## 15	12	0	female			
## 16	13	1	male			
## 17	14	1	male			
## 18	14	1	male			
## 19	15	1	female			
## 20	15	1	female			
## 21	16	0	female			
## 22	20	1	female			
## 23	20	1	male			
## 24	22	0	male			



## 25	23	1 female
## 26	23	1 male
## 27	24	1 female
## 28	26	1 male
## 29	26	1 male
## 30	26	1 male
## 31	27	1 male
## 32	28	1 male
## 33	28	1 female
## 34	29	0 female
## 35	29	1 male
## 36	30	1 male
## 37	30	1 male
## 38	30	1 female
## 39	30	0 male
## 40	30	1 female
## 41	31	1 male
## 42	32	1 female
## 43	33	1 male
## 44	33	0 male
## 45	33	1 female
## 46	35	1 male
## 47	38	1 male
## 48	40	1 male
## 49	41	1 male
## 50	42	1 female
## 51	43	1 male
## 52	43	1 female
## 53	43	1 female
## 54	44	1 female
## 55	45	1 female
## 56	50	1 male
## 57	54	0 male
## 58	54	0 male
## 59	55	1 male
## 60	59	1 male
## 61	60	1 male
## 62	60	1 female
## 63	60	0 male
## 64	61	1 male
## 65	63	0 female
## 66	64	1 male
## 67	65	1 female
## 68	65	1 male
## 69	66	1 female
## 70	67	1 male
## 71	68	0 male
## 72	71	0 male
## 73	72	1 male
## 74	72	0 male
## 75	73	1 male
## 76	73	1 male
## 77	74	0 female
## 78	74	0 male

## 79	74	0	male
## 80	74	0	female
## 81	75	0	female
## 82	76	0	male
## 83	77	1	female
## 84	78	0	male
## 85	78	1	female
## 86	79	0	male
## 87	79	0	male
## 88	79	0	male
## 89	79	0	male
## 90	79	0	male
## 91	80	0	male
## 92	80	0	male
## 93	82	0	female
## 94	82	1	male
## 95	83	0	female
## 96	83	0	male
## 97	83	0	male
## 98	85	0	female
## 99	85	0	female
## 100	86	0	female
## 101	87	0	male
## 102	87	0	male
## 103	87	0	male
## 104	87	0	male
## 105	87	0	female
## 106	88	1	female
## 107	88	0	male
## 108	88	0	male
## 109	88	0	male
## 110	88	0	male
## 111	90	1	male
## 112	90	0	male
## 113	90	0	male
## 114	90	1	female
## 115	91	0	male
## 116	91	0	female
## 117	94	0	female
## 118	94	0	female
## 119	94	0	female
## 120	95	1	female
## 121	95	0	male
## 122	95	0	female
## 123	95	0	female
## 124	95	0	female
## 125	96	1	male
## 126	97	0	female
## 127	100	1	female
## 128	104	0	female
## 129	104	0	male
## 130	105	0	male
## 131	106	0	male
## 132	107	0	male

## 133	107	0 female
## 134	107	0 male
## 135	107	0 male
## 136	107	0 male
## 137	107	0 female
## 138	108	0 male
## 139	108	0 female
## 140	108	0 male
## 141	109	1 male
## 142	109	0 female
## 143	109	0 female
## 144	110	0 female
## 145	111	1 male
## 146	112	0 male
## 147	112	0 male
## 148	113	0 male
## 149	113	1 male
## 150	115	0 male
## 151	115	1 female
## 152	117	0 male
## 153	118	0 male
## 154	119	0 male
## 155	120	0 female
## 156	120	0 male
## 157	120	0 female
## 158	120	0 male
## 159	121	0 male
## 160	121	0 male
## 161	121	0 male
## 162	121	0 male
## 163	123	0 male
## 164	126	1 female
## 165	129	1 male
## 166	130	1 female
## 167	134	0 male
## 168	135	1 male
## 169	140	0 female
## 170	145	0 female
## 171	145	0 male
## 172	146	0 male
## 173	146	0 male
## 174	146	0 male
## 175	146	0 male
## 176	146	0 male
## 177	147	0 male
## 178	147	0 female
## 179	147	0 male
## 180	147	0 male
## 181	148	0 male
## 182	150	1 male
## 183	154	1 male
## 184	162	1 male
## 185	170	1 male
## 186	171	1 male

## 187	172	1 female
## 188	172	1 female
## 189	172	0 female
## 190	174	0 female
## 191	174	0 male
## 192	174	0 female
## 193	175	0 male
## 194	180	0 male
## 195	180	1 male
## 196	180	1 male
## 197	185	0 female
## 198	186	0 female
## 199	186	0 female
## 200	186	0 male
## 201	186	0 male
## 202	186	0 male
## 203	186	0 male
## 204	187	0 male
## 205	187	0 male
## 206	187	0 female
## 207	187	0 female
## 208	187	0 male
## 209	187	0 female
## 210	187	0 female
## 211	188	0 male
## 212	192	0 male
## 213	192	0 male
## 214	193	1 female
## 215	194	0 male
## 216	195	0 male
## 217	196	0 female
## 218	196	1 female
## 219	197	0 male
## 220	197	0 female
## 221	198	1 male
## 222	200	0 male
## 223	201	0 male
## 224	201	0 male
## 225	205	0 male
## 226	205	0 female
## 227	205	0 male
## 228	206	0 male
## 229	207	0 female
## 230	207	0 female
## 231	207	1 female
## 232	208	0 male
## 233	209	0 male
## 234	209	0 male
## 235	209	0 male
## 236	209	0 male
## 237	209	0 male
## 238	210	0 male
## 239	210	0 female
## 240	211	0 male

##	241	212	0	female
##	242	212	0	male
##	243	212	0	male
##	244	213	0	female
##	245	213	0	male
##	246	213	0	male
##	247	214	1	male
##	248	214	0	male
##	249	214	0	male
##	250	214	0	female
##	251	214	0	female
##	252	215	0	female
##	253	215	0	male
##	254	215	0	female
##	255	215	0	male
##	256	216	0	male
##	257	220	0	female
##	258	230	0	male
##	259	230	0	male
##	260	231	0	male
##	261	233	0	male
##	262	233	0	female
##	263	235	1	male
##	264	237	0	female
##	265	237	0	male
##	266	240	0	male
##	267	241	1	male
##	268	244	0	male
##	269	244	0	female
##	270	244	0	male
##	271	244	0	male
##	272	244	0	female
##	273	245	0	female
##	274	245	0	male
##	275	245	0	male
##	276	245	0	female
##	277	245	0	female
##	278	246	0	male
##	279	246	0	female
##	280	246	0	female
##	281	247	0	male
##	282	250	0	male
##	283	250	0	male
##	284	250	0	male
##	285	250	0	male
##	286	250	0	male
##	287	250	0	male
##	288	250	0	female
##	289	256	0	female
##	290	256	0	female
##	291	257	0	female
##	292	258	0	male
##	293	258	0	male
##	294	270	0	male

```
## 295 270      0 male
## 296 271      0 female
## 297 278      0 female
## 298 280      0 male
## 299 285      0 male
```

Following this, we can visualise that str, dim with new variable and mean for both genders doesn't affect by mutate function.

```
str(myocard)
```

```
## 'data.frame': 299 obs. of 14 variables:
## $ age : num 75 55 65 50 65 90 75 60 65 80 ...
## $ anaemia : int 0 0 0 1 1 1 1 1 0 1 ...
## $ creatinine_phosphokinase: int 582 7861 146 111 160 47 246 315 157 123 ...
## $ diabetes : int 0 0 0 0 1 0 0 1 0 0 ...
## $ ejection_fraction : int 20 38 20 20 20 40 15 60 65 35 ...
## $ high_blood_pressure : int 1 0 0 0 0 1 0 0 0 1 ...
## $ platelets : num 265000 263358 162000 210000 327000 ...
## $ serum_creatinine : num 1.9 1.1 1.3 1.9 2.7 2.1 1.2 1.1 1.5 9.4 ...
## $ serum_sodium : int 130 136 129 137 116 132 137 131 138 133 ...
## $ sex : int 1 1 1 1 0 1 1 1 0 1 ...
## $ smoking : int 0 0 1 0 0 1 0 1 0 1 ...
## $ time : int 4 6 7 7 8 8 10 10 10 10 ...
## $ DEATH_EVENT : int 1 1 1 1 1 1 1 1 1 1 ...
## $ gender : chr "male" "male" "male" "male" ...
```

```
dim(myocard)
```

```
## [1] 299 14
```

```
mean(myocard$gender == "female")
```

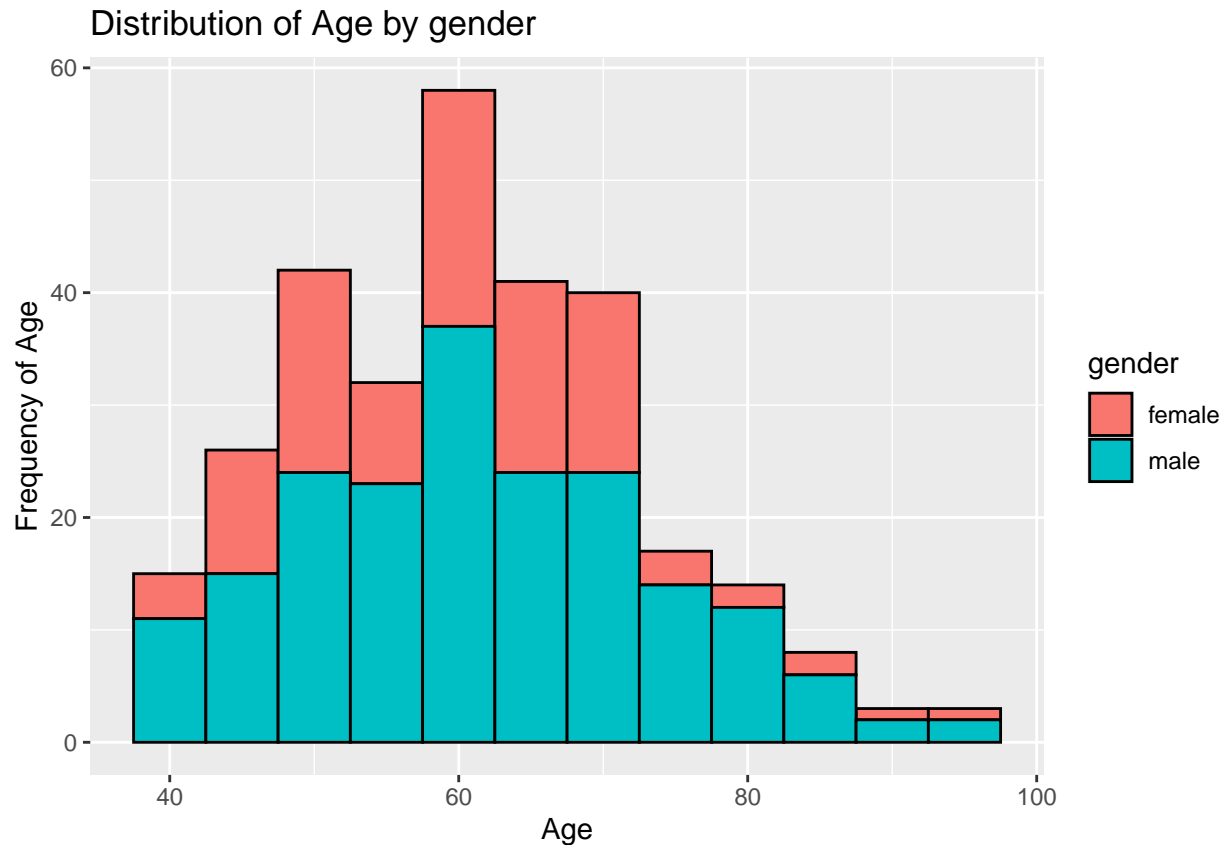
```
## [1] 0.3511706
```

```
mean(myocard$gender == "male")
```

```
## [1] 0.6488294
```

### 3.2.1 Distribution of Age

```
myocard %>% ggplot(aes(age, fill = gender)) + geom_histogram(bins = 30, binwidth = 5, color = "black")
```

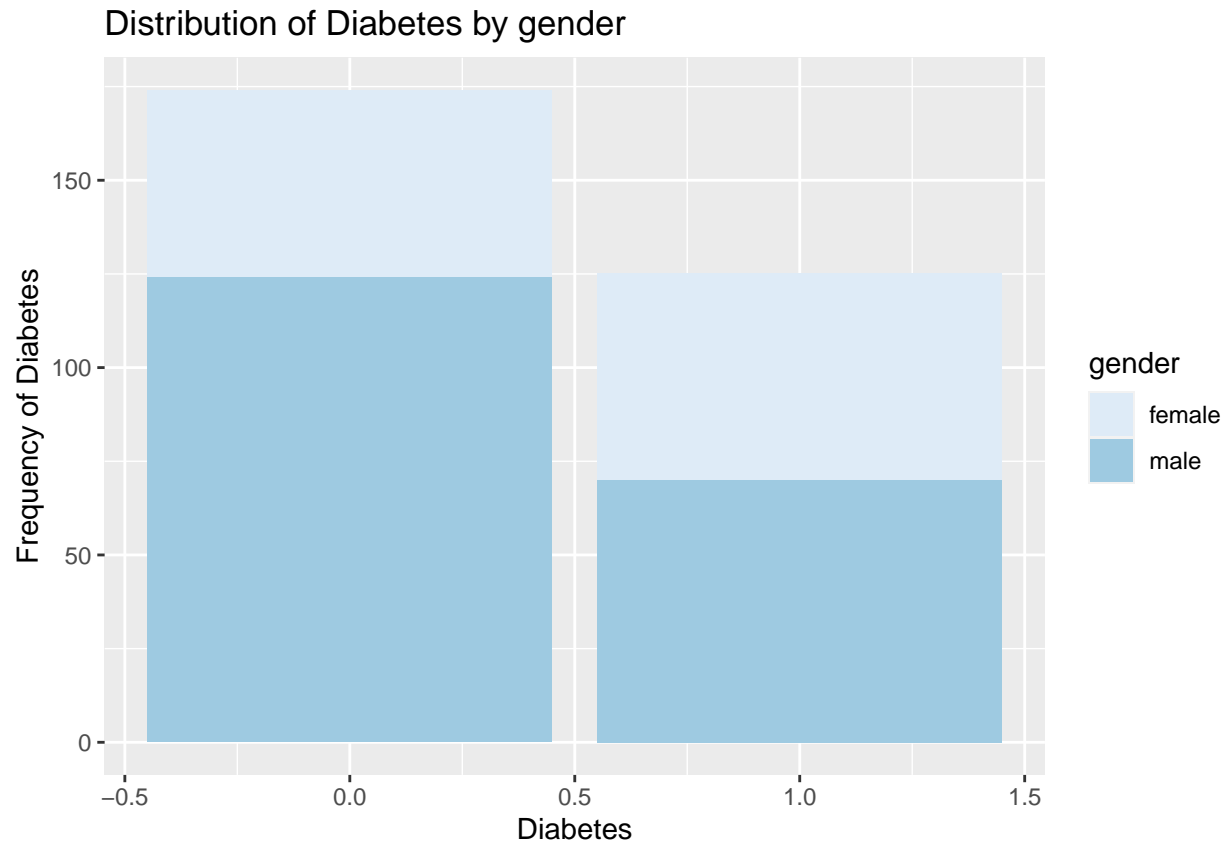


Age is one of most risk for developing predictions of diseases (Nicolli T, 2012). In our case, we can notice the distribution of age by gender. We see that the peak of age is around 60 and previous see before, and there is more man than a woman in our case.

### 3.2.2 Distribution of Diabetes

Diabetes is a common disease where your blood glucose is too high. That means your body doesn't produce enough insulin or can't produce any at all. The diagnostic of Diabetes can lead to several predictions of disease, such as MI. In our case, we are assuming that all patients who have Diabetes are 1 and without Diabetes is 0.

```
myocard %>% ggplot(aes(diabetes)) + geom_bar(aes(fill = gender)) + scale_fill_brewer(palette="Blues") +
  xlab("Diabetes") + ylab("Frequency of Diabetes") + ggtitle("Distribution of Diabetes by gender")
```



```
myocard %>% group_by(diabetes) %>% summarise(n = n()) %>% head()
```

```
## # A tibble: 2 x 2
##   diabetes     n
##   <int> <int>
## 1     0   174
## 2     1   125
```

We can visualise the number of patients who have Diabetes as around 125 and without Diabetes as 174.

### 3.2.3 Distribution of Diabetes by gender

What's the proportion of Diabetes by gender?

```
myocard %>% group_by(gender) %>% summarise(diabetes = mean(diabetes == 0)) %>%
  filter(gender == "female")
```

```
## # A tibble: 1 x 2
##   gender diabetes
##   <chr>     <dbl>
## 1 female    0.476
```

```
myocard %>% group_by(gender) %>% summarise(diabetes = mean(diabetes == 1)) %>%
  filter(gender == "female")
```



```
## # A tibble: 1 x 2
##   gender diabetes
##   <chr>      <dbl>
## 1 female    0.524
```

```
myocard %>% group_by(gender) %>% summarise(diabetes = mean(diabetes == 0)) %>%
  filter(gender == "male")
```

```
## # A tibble: 1 x 2
##   gender diabetes
##   <chr>      <dbl>
## 1 male     0.639
```

```
myocard %>% group_by(gender) %>% summarise(diabetes = mean(diabetes == 1)) %>%
  filter(gender == "male")
```

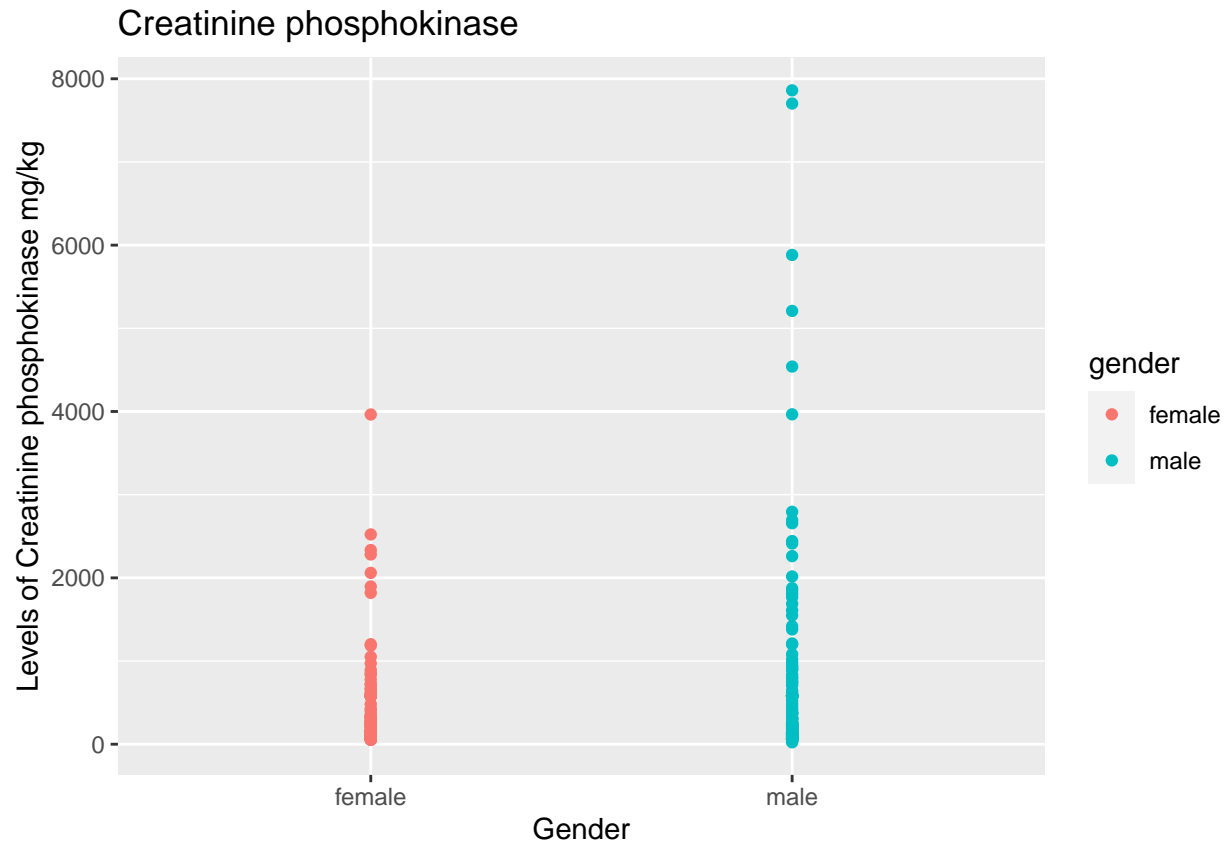
```
## # A tibble: 1 x 2
##   gender diabetes
##   <chr>      <dbl>
## 1 male     0.361
```

Filtering by gender, we can find more women with Diabetes (0.524) than men (0.361).

### 3.2.4 Levels of Creatinine phosphokinase

Creatinine phosphokinase, also known as Creatine Kinase (CK), is an enzyme found in our body. It is located mainly in the heart, brain, and skeletal muscle. When your body has damage, CK increases in your body, meaning something is not right. Also, CK levels are important MI markers. Elevated levels of CK have been used to diagnose a case of MI (Patel R, 2021).

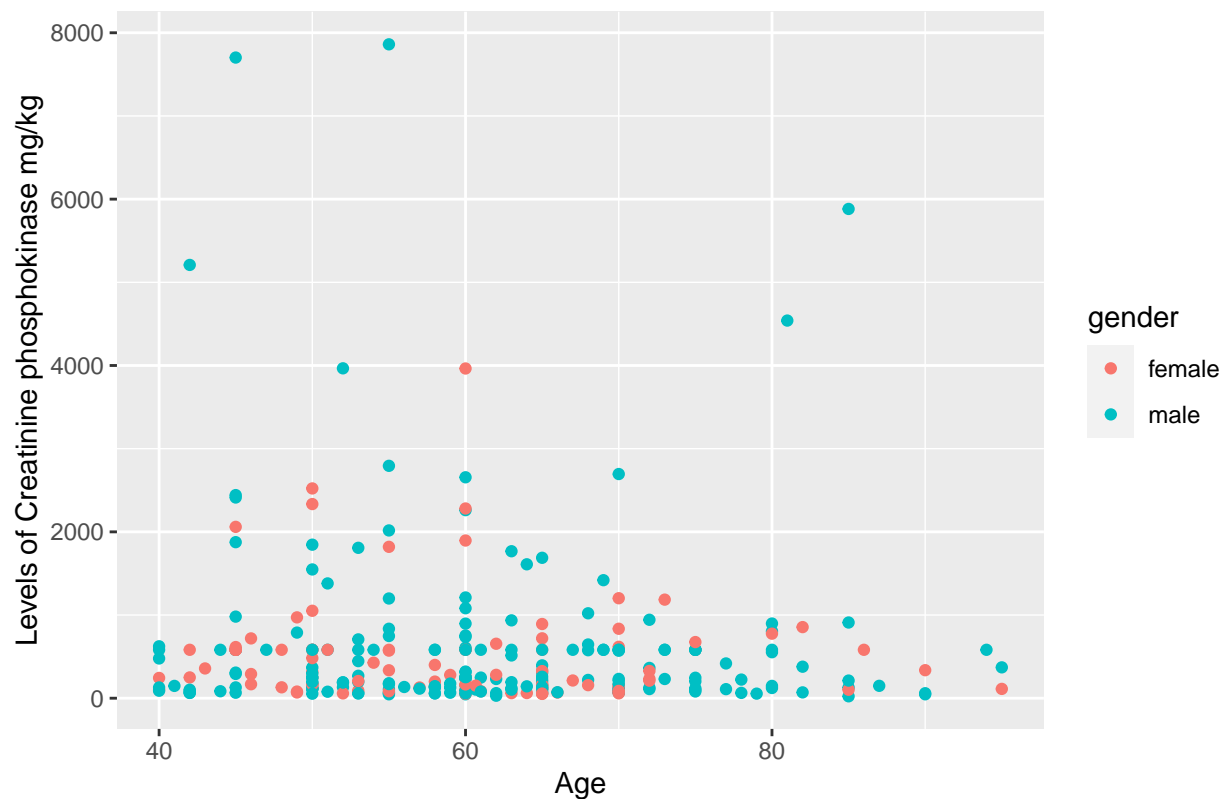
```
myocard %>% ggplot(aes(gender, creatinine_phosphokinase)) + geom_point(aes(color = gender)) +
  ylab("Levels of Creatinine phosphokinase mg/kg") + xlab("Gender") +
  ggtitle("Creatinine phosphokinase")
```



We can notice that's men have a little higher levels of CK rather than women.

```
myocard %>% ggplot(aes(age, creatinine_phosphokinase)) + geom_point(aes(color = gender)) +  
  ylab("Levels of Creatinine phosphokinase mg/kg") + xlab("Age") +  
  ggtitle("Creatinine phosphokinase by Age and Gender")
```

## Creatinine phosphokinase by Age and Gender



As shown before, age can be a risk factor for some disease. We can analyse the CK by age and gender. Following this, what are the mean levels between women and men?

```
myocard %>% group_by(gender) %>% summarise(creatinine_phosphokinase = mean(creatinine_phosphokinase))
```

```
## # A tibble: 2 x 2
##   gender creatinine_phosphokinase
##   <chr>                <dbl>
## 1 female                477.
## 2 male                 639.
```

```
myocard %>% group_by(gender) %>% summarise(creatinine_phosphokinase = sd(creatinine_phosphokinase))
```

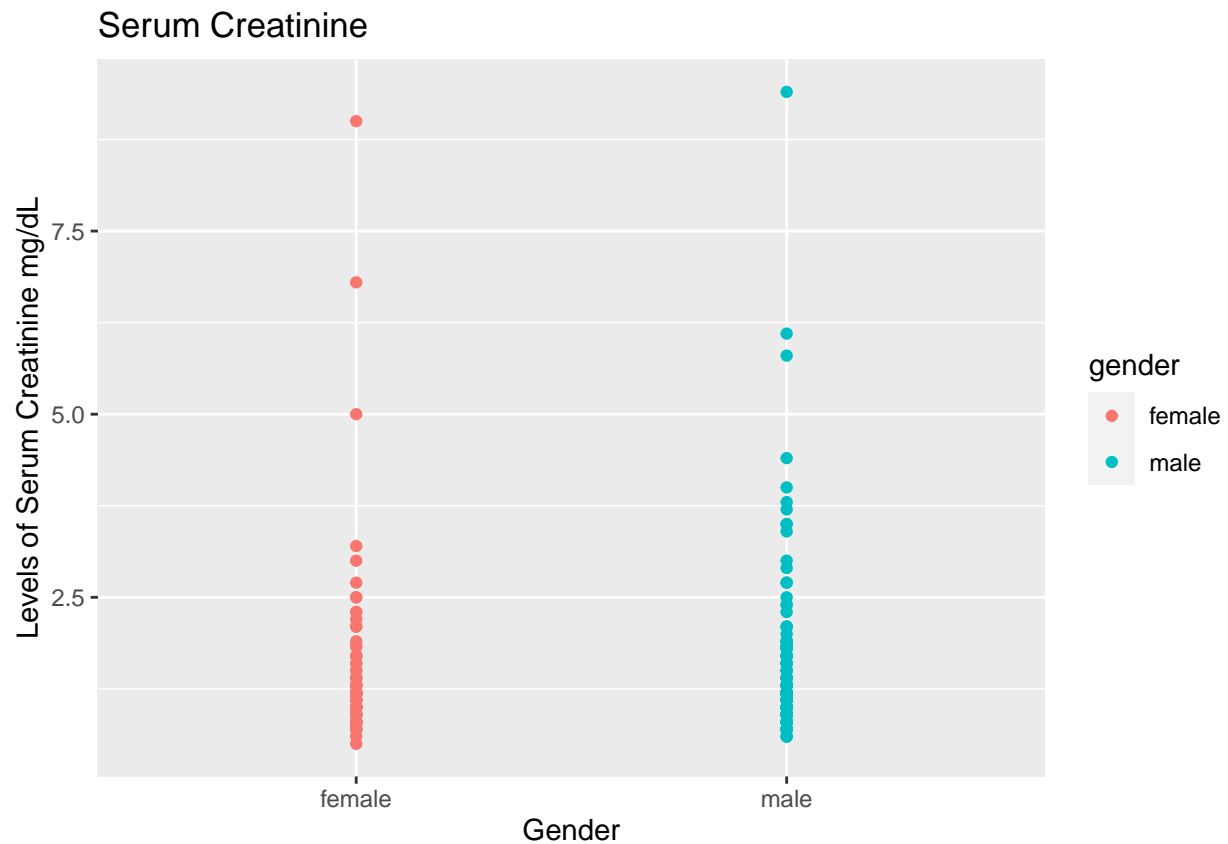
```
## # A tibble: 2 x 2
##   gender creatinine_phosphokinase
##   <chr>                <dbl>
## 1 female                611.
## 2 male                1115.
```

According to the literature, the normal levels of CK are around 200 U/L. We can see that men have a mean and standard deviation higher than women, showing to us that men have a higher risk than women.

### 3.2.5 Serum Creatinine

The creatinine levels measure how well your kidneys perform their work of filtering waste from your blood. That means if your kidney has an injury or damage, the levels of creatinine can rise.

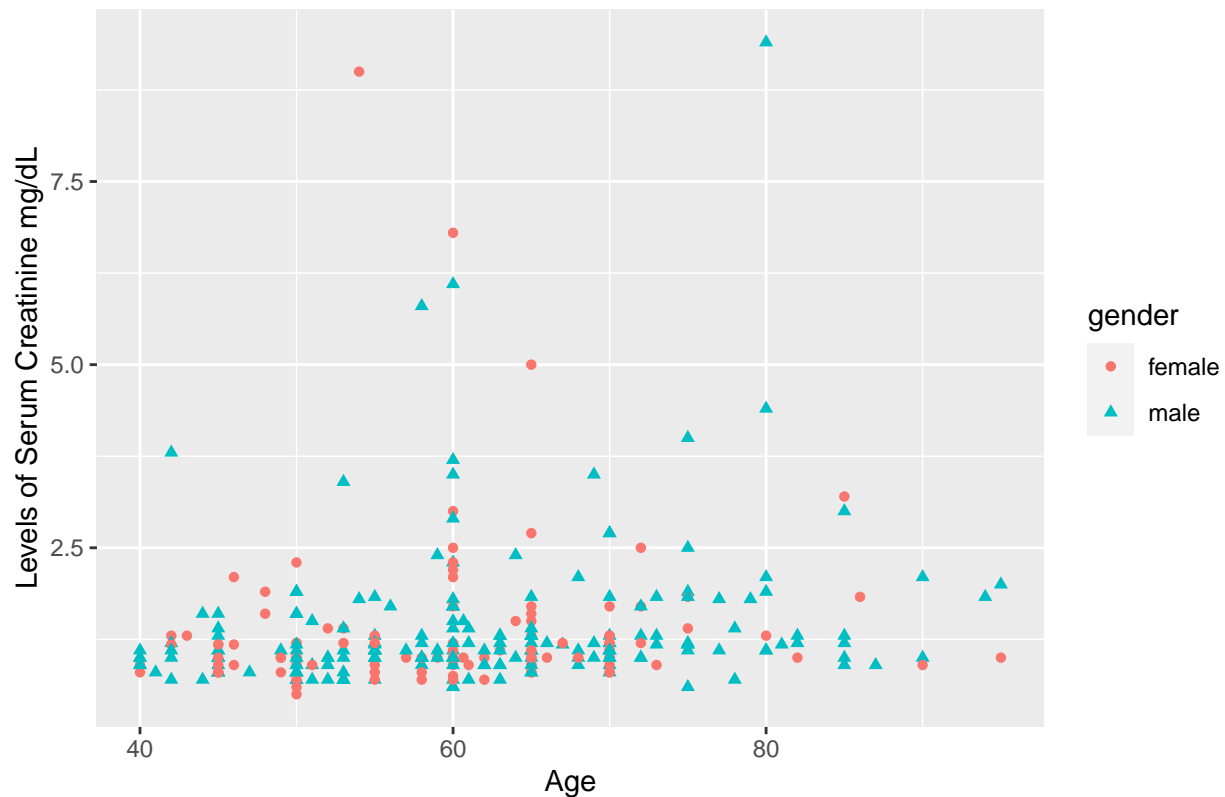
```
myocard %>% ggplot(aes(gender, serum_creatinine)) + geom_point(aes(color = gender)) +
  ylab("Levels of Serum Creatinine mg/dL") + xlab("Gender") +
  ggtitle("Serum Creatinine")
```



The levels of Serum creatinine is slightly the same between gender.

```
myocard %>% ggplot(aes(age, serum_creatinine)) + geom_point(aes(color = gender, shape = gender)) +
  ylab("Levels of Serum Creatinine mg/dL") + xlab("Age") +
  ggtitle("Serum Creatinine by Age and Gender")
```

## Serum Creatinine by Age and Gender



We can visualise the Serum creatine Age and gender. We can see there are no differences between gender. The levels of Serum creatinine between woman and men are quite the same. We can see this by the mean and standard deviation.

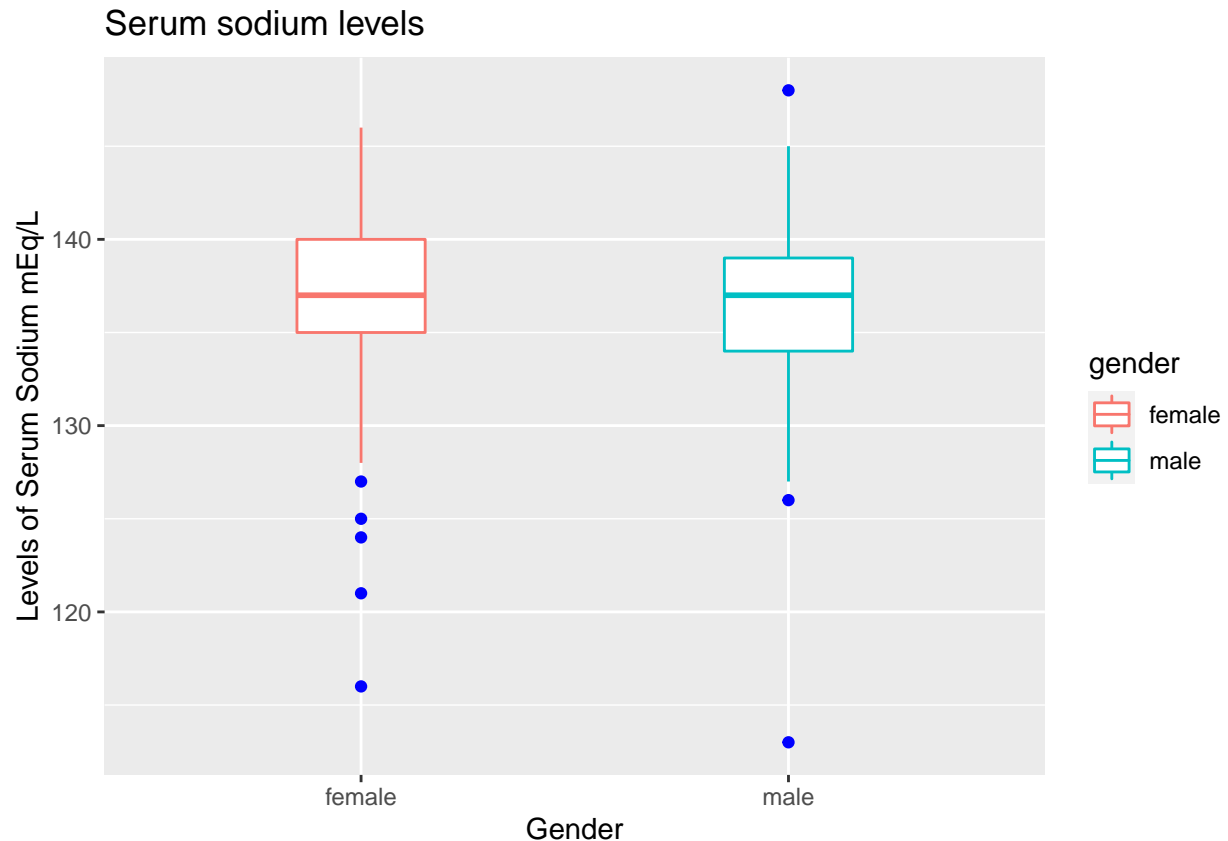
```
myocard %>% group_by(gender) %>% summarise(mean(serum_creatinine), sd(serum_creatinine))
```

```
## # A tibble: 2 x 3
##   gender 'mean(serum_creatinine)' 'sd(serum_creatinine)'
##   <chr>          <dbl>          <dbl>
## 1 female          1.38          1.12
## 2 male           1.40          0.989
```

### 3.2.6 Serum Sodium Levels

Alterations in sodium levels is a risk for any disease. High levels of serum sodium can lead to high pressure, but lower levels can predict MI. This graph shows us the Sodium serum levels, and we can notice for both gender is around 137. Normals levels are about 135 to 145 mEq/L.

```
myocard %>% ggplot(aes(gender, serum_sodium)) +
  geom_boxplot(aes(color = gender), outlier.colour = "blue", width = 0.3) +
  ylab("Levels of Serum Sodium mEq/L") + xlab("Gender") +
  ggtitle("Serum sodium levels")
```



We can see, the levels of serum sodium in both gender in our case doesn't have difference. Also, that can observe by the mean and standard deviation.

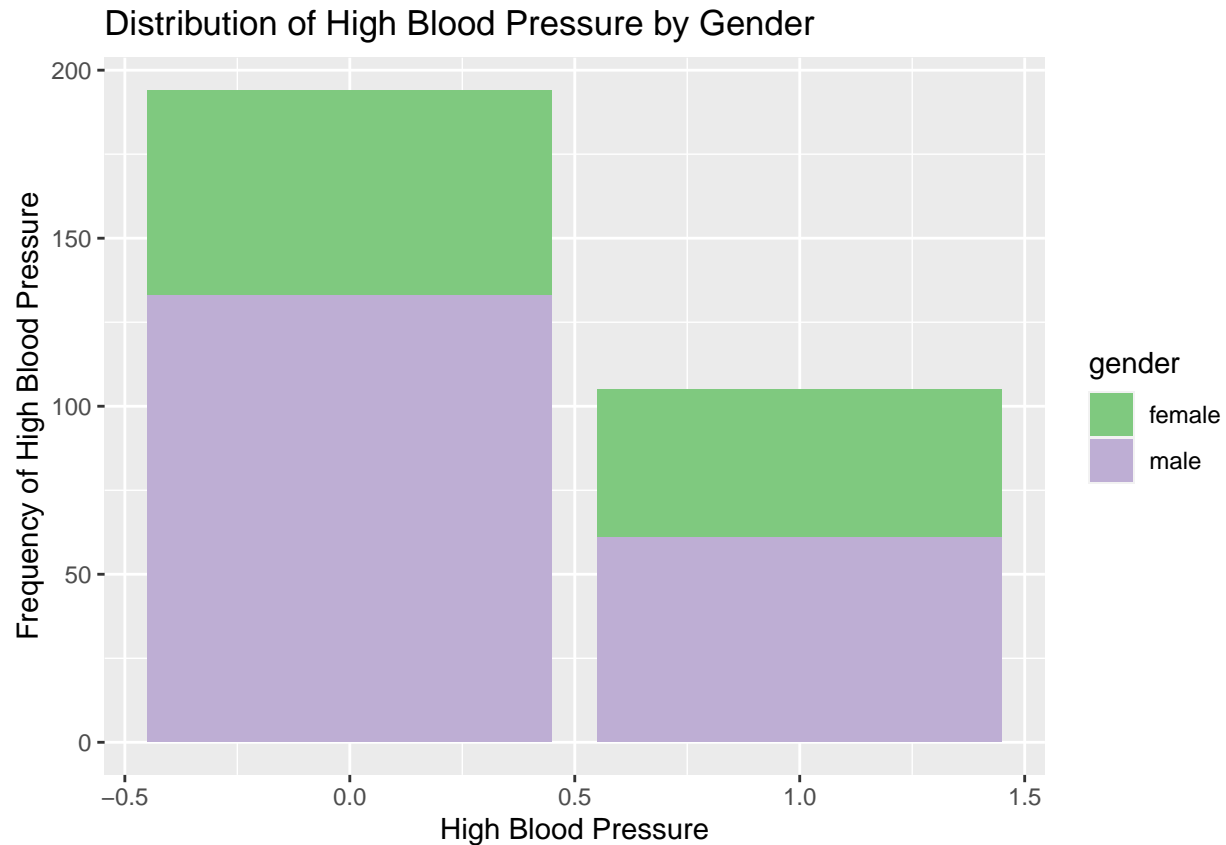
```
myocard %>% group_by(gender) %>% summarise(mean(sodium), sd(sodium))
```

```
## # A tibble: 2 x 3
##   gender 'mean(sodium)' 'sd(sodium)'
##   <chr>      <dbl>      <dbl>
## 1 female      137.      4.90
## 2 male       137.      4.13
```

### 3.2.7 High Blood Pressure

High blood pressure is medically known as hypertension. When somebody has high blood pressure, the heart is working too hard to pump the blood for all the body. In our case, the variable high blood pressure is measurable by meaning the number 1 is the patients who have high pressure and 0 who don't have pressure.

```
myocard %>% ggplot(aes(high_blood_pressure)) + geom_bar(aes(fill = gender)) +
  scale_fill_brewer(palette = "Accent") + ylab("Frequency of High Blood Pressure") +
  xlab("High Blood Pressure") + ggtitle("Distribution of High Blood Pressure by Gender")
```



We can see the more patients doesn't have high blood pressure. We can easily see by the code below the proportions of males and females in high blood pressure.

```
myocard %>% group_by(gender) %>% summarise(high_blood_pressure = mean(high_blood_pressure == 0)) %>% fi
```

```
## # A tibble: 1 x 2
##   gender high_blood_pressure
##   <chr>      <dbl>
## 1 male          0.686
```

```
myocard %>% group_by(gender) %>% summarise(high_blood_pressure = mean(high_blood_pressure == 1)) %>% fi
```

```
## # A tibble: 1 x 2
##   gender high_blood_pressure
##   <chr>      <dbl>
## 1 male          0.314
```

```
myocard %>% group_by(gender) %>% summarise(high_blood_pressure = mean(high_blood_pressure == 0)) %>% fi
```

```
## # A tibble: 1 x 2
##   gender high_blood_pressure
##   <chr>      <dbl>
## 1 female        0.581
```

```
myocard %>% group_by(gender) %>% summarise(high_blood_pressure = mean(high_blood_pressure == 1)) %>% fi
```

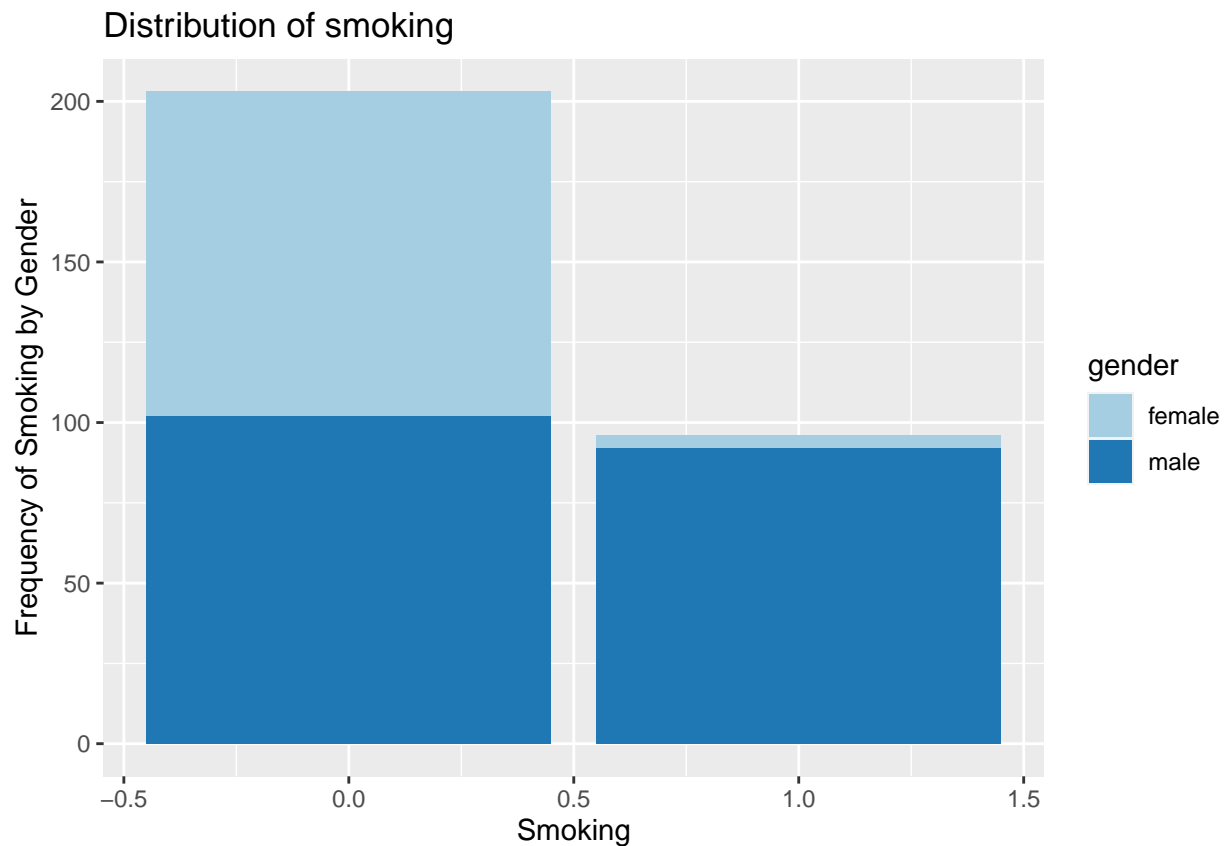
```
## # A tibble: 1 x 2
##   gender high_blood_pressure
##   <chr>         <dbl>
## 1 female         0.419
```

We can quickly notice that there are more patients male with high blood pressure than males don't have.

### 3.2.8 Distribution of Smoking

Smoking is the most significant health issue worldwide. Besides that, smoking causes problems breathing and lung cancer. People who smoke are two to four times more likely to get MI. In our case, the variable smoking is measurable by meaning the number 1 is the patients who smoking and 0 who don't smoking.

```
myocard %>% ggplot(aes(smoking)) + geom_bar(aes(fill = gender)) +
  scale_fill_brewer(palette = "Paired") + ylab("Frequency of Smoking by Gender") +
  xlab("Smoking") + ggtitle("Distribution of smoking")
```



And now, what the proportion of woman and men smoking?

```
myocard %>% group_by(gender) %>% summarise(smoking = mean(smoking == 0)) %>% filter(gender == "male")
```

```
## # A tibble: 1 x 2
##   gender smoking
##   <chr>     <dbl>
## 1 male      0.526
```



```
myocard %>% group_by(gender) %>% summarise(smoking = mean(smoking == 1)) %>% filter(gender == "male")
```

```
## # A tibble: 1 x 2
##   gender smoking
##   <chr>     <dbl>
## 1 male      0.474
```

```
myocard %>% group_by(gender) %>% summarise(smoking = mean(smoking == 0)) %>% filter(gender == "female")
```

```
## # A tibble: 1 x 2
##   gender smoking
##   <chr>     <dbl>
## 1 female    0.962
```

```
myocard %>% group_by(gender) %>% summarise(smoking = mean(smoking == 1)) %>% filter(gender == "female")
```

```
## # A tibble: 1 x 2
##   gender smoking
##   <chr>     <dbl>
## 1 female    0.0381
```

We can notice the number of women doesn't smoke higher than woman smoking, either comparing with man smoking or not.

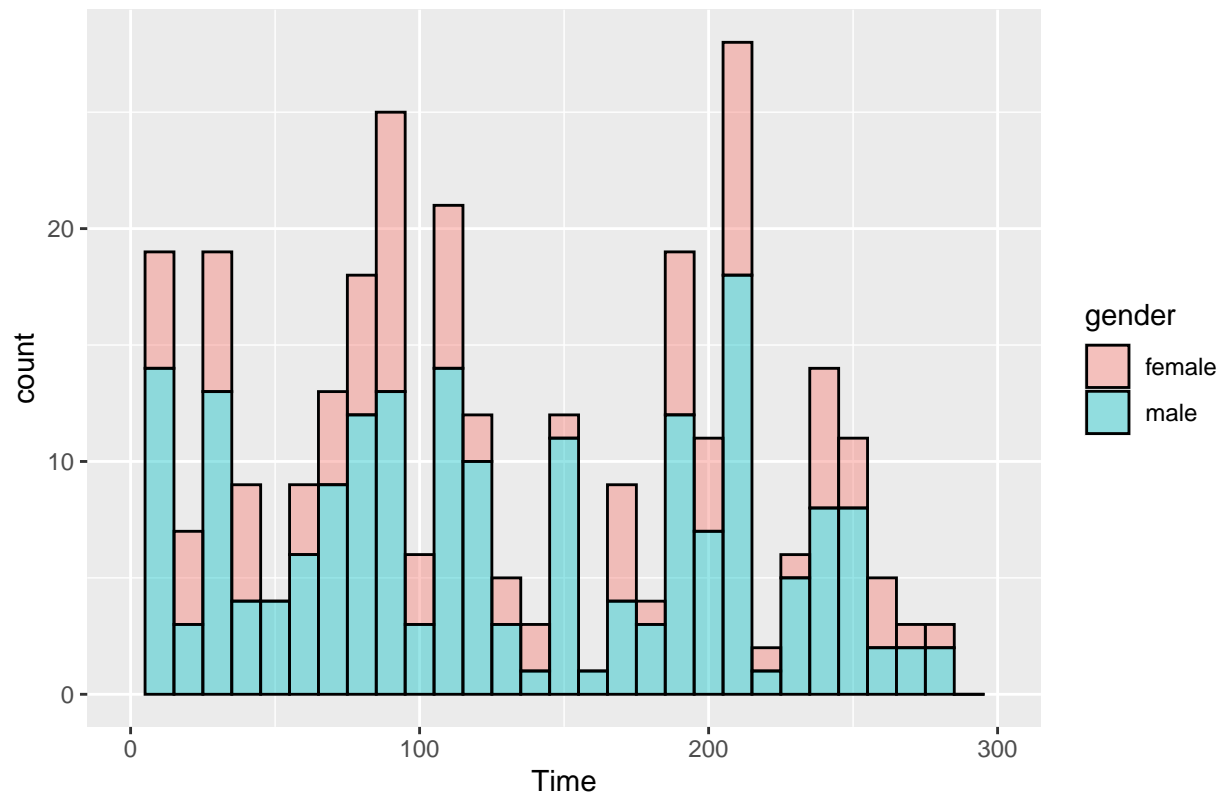
### 3.2.9 Distribution of Time (Hospitalisation)

Time of hospitalisation is another risk for MI. Studies have shown the times of hospitalisation associated with comorbidity increase of risk for MI. As sad before, the Time variable is counting how many time the patients has of hospitalisation.

```
myocard %>% ggplot(aes(time, fill = gender)) +
  geom_histogram(binwidth = 10, bins = 5, color = "black", alpha = 0.4) +
  xlim(c(0,300)) +
  xlab("Time") + ggtitle("Distribution of Hospitalisation")
```

```
## Warning: Removed 4 rows containing missing values (geom_bar).
```

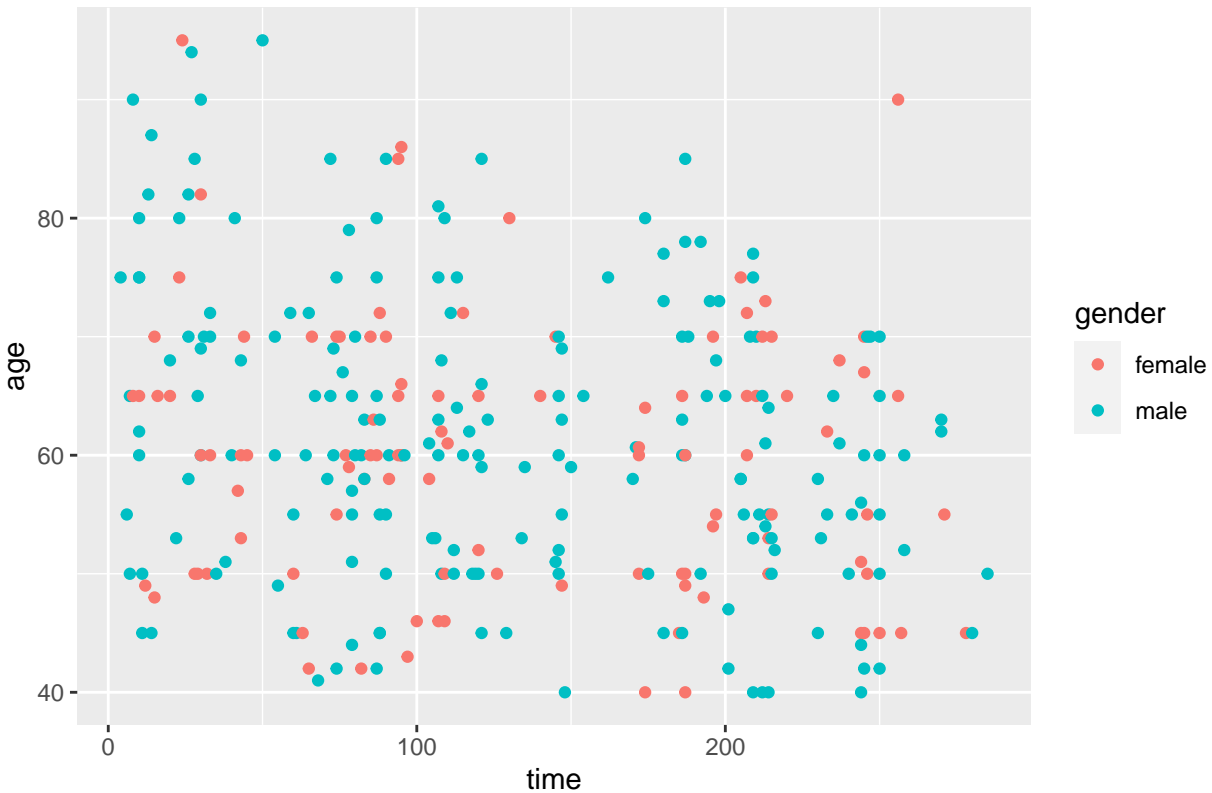
# Distribution of Hospitalisation



Observing this histogram graph, we can see the distribution of data by the time is not a normal distribution. We can see a high peak in around 200 times.

```
myocard %>% ggplot(aes(time, age)) + geom_point(aes(color = gender)) + ggtitle("Time hospitalisation by
```

Time hospitalisation by Age and gender



We can notice in this graph that it's hard to know the distribution, but we can see a man has shown more in the scatterplot, but the number of man in our case is higher than the woman.

#### 4.0 Linear Regression

Until now, we have observed the distribution of comorbidity in our case MI. The second part of this project is to build a machine learning model, and a linear regression model is considered a machine learning model.

Multiple Linear Regression is a technique statistical that use several variables exploratory to predict the outcome of a response variable. We have several variable exploratories (independent variable) and response (in our case, time-variable) outcomes.

```
fit <- lm(time ~ age + sex + high_blood_pressure + smoking + creatinine_phosphokinase + serum_creatinine)
fit
```

```
##
## Call:
## lm(formula = time ~ age + sex + high_blood_pressure + smoking +
##      creatinine_phosphokinase + serum_creatinine + serum_sodium,
##      data = myocard)
##
## Coefficients:
##              (Intercept)                age                sex
##              67.925116             -1.232983             -0.408229
##      high_blood_pressure              smoking creatinine_phosphokinase
##              -30.351623             -5.279724             -0.003481
##      serum_creatinine              serum_sodium
##              -8.168100              1.195768
```

```
summary(fit)
```

```
##
## Call:
## lm(formula = time ~ age + sex + high_blood_pressure + smoking +
##      creatinine_phosphokinase + serum_creatinine + serum_sodium,
##      data = myocard)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -152.453  -59.491   -9.518   68.181  152.762
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    67.925116  139.584667   0.487  0.62689
## age           -1.232983   0.371034  -3.323  0.00100 **
## sex            -0.408229   10.183948  -0.040  0.96805
## high_blood_pressure -30.351623   9.134630  -3.323  0.00101 **
## smoking        -5.279724   10.312968  -0.512  0.60907
## creatinine_phosphokinase -0.003481   0.004492  -0.775  0.43904
## serum_creatinine  -8.168100   4.296581  -1.901  0.05828 .
## serum_sodium      1.195768   0.997905   1.198  0.23178
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 74.41 on 291 degrees of freedom
## Multiple R-squared:  0.1025, Adjusted R-squared:  0.08087
## F-statistic: 4.745 on 7 and 291 DF,  p-value: 4.572e-05
```

```
tidy(fit)
```

```
## # A tibble: 8 x 5
##   term                estimate std.error statistic p.value
##   <chr>              <dbl>    <dbl>    <dbl>    <dbl>
## 1 (Intercept)        67.9      140.        0.487  0.627
## 2 age               -1.23      0.371     -3.32  0.00100
## 3 sex                -0.408     10.2     -0.0401 0.968
## 4 high_blood_pressure -30.4      9.13     -3.32  0.00101
## 5 smoking            -5.28     10.3     -0.512  0.609
## 6 creatinine_phosphokinase -0.00348  0.00449  -0.775  0.439
## 7 serum_creatinine    -8.17      4.30     -1.90  0.0583
## 8 serum_sodium         1.20      0.998      1.20  0.232
```

## 4.1 Linear Regression and Results

The overall quality of the multiple linear regression can be assessing following three quantify display in summary function.

Residual Standard Error (RSE): this represents the average of the outcomes and the predicted values by the model. Which lowest RSE, is better for fit the model in our data. We can notice we have 74.41 RSE in our project results, and meaning is a high value for RSE. Multiple R-square and Adjust R-square: the multiple correlations between three or more variables. It tells us how useful the predictor variables are at predicting the value of the response variable. In our case, we can see the Multiple R-square is 0.1025. It is a good

result however, it doesn't mean it is a good fit. Adjust R-square: This is a correction for the number of x variables included in the predictive model. Adjust R-square near to 1 indicates that the regression model has explained a large proportion of the variability in the outcome. In our case is around 0.080. F-statistical: It's the overall significance of the model. It assesses whether at least one predictor variable has a non-zero coefficient. In statistical p-value significant is  $\leq 0.05$ , our case show  $4.572e-05$  for p-value, showing us very strong p-value.

What the intercept of the model?

```
fit$coef[1]
```

```
## (Intercept)
##      67.92512
```

Looking back at the display of the summary function, we can see the age and high\_blood\_pressure has to asterisk. We can see the strong p-value between time and these two variables. However, we can see the plot doesn't show strong relation when we plot the linear regression model.

#### 4.1.2 Predict age by time

```
time_vs_age_hbp <- lm(time ~ age + high_blood_pressure, data = myocard)
time_vs_age_hbp
```

```
##
## Call:
## lm(formula = time ~ age + high_blood_pressure, data = myocard)
##
## Coefficients:
##      (Intercept)              age  high_blood_pressure
##      222.740             -1.354             -28.744
```

```
tidy(time_vs_age_hbp)
```

```
## # A tibble: 3 x 5
##   term                estimate std.error statistic  p.value
##   <chr>              <dbl>    <dbl>    <dbl>    <dbl>
## 1 (Intercept)        223.      22.6      9.87 4.64e-20
## 2 age                -1.35     0.365    -3.71 2.48e- 4
## 3 high_blood_pressure -28.7     9.08     -3.16 1.71e- 3
```

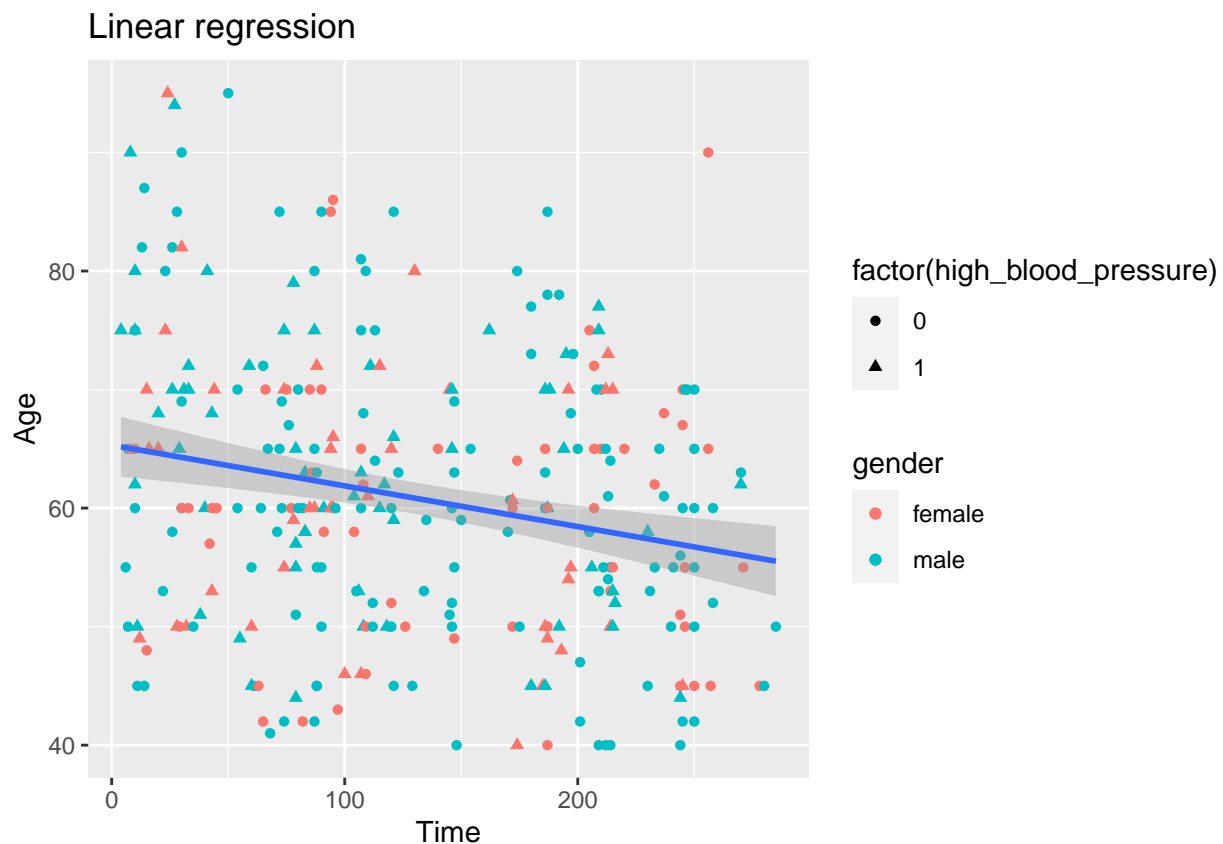
```
summary(time_vs_age_hbp)
```

```
##
## Call:
## lm(formula = time ~ age + high_blood_pressure, data = myocard)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -150.798  -60.870   -9.381   67.473  159.969
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)          222.7404      22.5594   9.874 < 2e-16 ***
## age                  -1.3543       0.3651  -3.709 0.000248 ***
## high_blood_pressure -28.7444      9.0830  -3.165 0.001714 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 74.64 on 296 degrees of freedom
## Multiple R-squared:  0.08129,    Adjusted R-squared:  0.07508
## F-statistic: 13.1 on 2 and 296 DF,  p-value: 3.551e-06
```

```
myocard %>% ggplot(aes(time, age)) + geom_point(aes(color = gender, shape = factor(high_blood_pressure)))
```

```
## 'geom_smooth()' using formula 'y ~ x'
```



We can see for each increase at the variable age, the time decrease -1.35 and high\_blood\_pressure -28.7.

#### 4.1.3 Conclusion

Until now, we made a multiple linear regression, trying to find out if the comorbidity or health issue predicts the time in hospitals in patients MI. In our results, we found a significant relationship between age and high\_blood\_pressure with time. Specially we found for each new data add in age the time decrease -1.354 and each new data in high\_blood\_pressure decrease time in -28.744.

#### 5.0 Machine Learning

The large of information in data healthcare have increasingly risen in the last decade. Understanding and quantify extensive healthcare data can lead to the expected risk and predict disease in patients. Machine

learning is the study of tools and methods for identifying data patterns (Wienns J, 2017). Understanding these methods can be used to predict the risk for disease and predict the future. This project uses two parameters in machine learning, LDA (Linear Discriminant Analysis) and QDA (Quadratic Discriminant Analysis).

### 5.1 Linear Discriminant Analysis - LDA

Linear discriminant analysis is used as a tool for classification, dimension reduction, and data visualisation. Also is a linear machine learning algorithm used for multi-class classification. LDA seeks to best separate (or discriminate) the samples in the training dataset by their class value. For this, we are classifying the data by the median in the time. We are using the mean value on time and considering this “high” or “low” for hospitalisation time. Value is separated into “high” for risk to MI and “low” risk to MI. At this part of the project, we are going to use all the variables in it. For this step, we are split the myocard data set into train and test. The train data set has 10%, and the test has 90% of the original data. Also, it is an important method that evaluates the accuracy of the dataset.

Until now, we create the gender variable for better visualisation of data. However, for doing a machine learning algorithm, we are going to exclude this variable.

```
myocard <- subset(myocard, select = -14)
```

```
mean(myocard$time)
```

```
## [1] 130.2609
```

```
myocard <- myocard %>% mutate(time = ifelse(time > 130, "high", "low"))
```

```
myocard$time <- factor(myocard$time, levels = c("high", "low"))
```

```
set.seed(1)
```

```
test_index <- createDataPartition(myocard$time, times = 1, p = 0.1, list = FALSE)
```

```
train_set <- myocard[-test_index, ]
```

```
test_set <- myocard[test_index, ]
```

```
lda_fit <- train(time ~., method = "lda", data = train_set)
```

```
lda_predict <- predict(lda_fit, test_set)
```

```
confusionMatrix(lda_predict, test_set$time)
```

```
## Confusion Matrix and Statistics
```

```
##
```

```
##           Reference
```

```
## Prediction high low
```

```
##      high      9      7
```

```
##      low       5     10
```

```
##
```

```
##              Accuracy : 0.6129
```

```
##              95% CI : (0.4219, 0.7815)
```

```
##      No Information Rate : 0.5484
```

```
##      P-Value [Acc > NIR] : 0.2960
```

```
##
```

```
##              Kappa : 0.2282
```

```
##
```

```
##      McNemar's Test P-Value : 0.7728
```

```
##
##          Sensitivity : 0.6429
##          Specificity : 0.5882
##          Pos Pred Value : 0.5625
##          Neg Pred Value : 0.6667
##          Prevalence : 0.4516
##          Detection Rate : 0.2903
##          Detection Prevalence : 0.5161
##          Balanced Accuracy : 0.6155
##
##          'Positive' Class : high
##
```

When we look at our results on sensitivity and specificity parameters, we also conclude that on our model LDA: the sensitivity 0.6429 means 64% of patients have the risk for MI and fails in 36%. While specificity 0.5882 means 58% doesn't have relations with time and fails 42% and an Accuracy of 0.6129.

## 5.2 Quadratic Discriminant Analysis - QDA

QDA is a variant of LDA in which an individual covariance matrix is estimated for every class of observations. Discriminant analysis is used to determine which variables discriminate between two or more naturally occurring groups.

```
qda_fit <- train(time ~., method = "qda", data = train_set)
qda_predict <- predict(qda_fit, test_set)
confusionMatrix(qda_predict, test_set$time)
```

```
## Confusion Matrix and Statistics
##
##          Reference
## Prediction high low
##          high      8  11
##          low       6   6
##
##          Accuracy : 0.4516
##          95% CI : (0.2732, 0.6397)
##          No Information Rate : 0.5484
##          P-Value [Acc > NIR] : 0.8965
##
##          Kappa : -0.0733
##
##          Mcnemar's Test P-Value : 0.3320
##
##          Sensitivity : 0.5714
##          Specificity : 0.3529
##          Pos Pred Value : 0.4211
##          Neg Pred Value : 0.5000
##          Prevalence : 0.4516
##          Detection Rate : 0.2581
##          Detection Prevalence : 0.6129
##          Balanced Accuracy : 0.4622
##
##          'Positive' Class : high
##
```



In our case, when we look at our results on sensitivity and specificity parameters, we also conclude that on our model QDA: the sensitivity 0.5714 means 57% of patients have the risk for MI and fails in 43%. While specificity 0.3529 means 35% doesn't have relations with time and fails 65% and an Accuracy of 0.4516.

Accuracy is a parameter that generally describes how the model performs across the data. It's a relation between the number of correct prediction to the total prediction on test data. For example, in our data, we can find the better Accuracy on the LDA model is 0.6129. This algorithm has 61% classifying patients low or high time in hospitalisation.

## 6.0 Conclusion

Our project tried whether the patient's time in the hospital is at risk for myocardial infarction. For this, we performed a linear regression analysis in the first part, verifying the relationship between the variables. In this part, we saw that age and time are related. In the second part, we set up a machine learning LDA and QDA model. We were checking the specificity and sensitivity of the model. We can conclude that our model can predict with an accuracy of around 60% that the time of the hospitalized patient added to the other comorbidities increases the risk of MI.

## 7.0 References

Zumel Nina, Mount Jhon: Practical Data Science with R. ed; Manning, 2019. book <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4804079/> <https://www.sciencedirect.com/science/article/abs/pii/S0009912018311974?via%3Dihub> <https://ascpt.onlinelibrary.wiley.com/doi/10.1002/cpt.1803> <https://www.sciencedirect.com/science/article/pii/S0960982212008159> <https://www.ncbi.nlm.nih.gov/books/NBK546624/>