MVA_Assignment_3

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Assignment 3 - Data Cleaning, EDA, Tests

This document does a preliminary analysis on the Heart Failure Prediction dataset

We will start by loading libraries and data

```
# clear environment
rm(list = ls())

# defining libraries

library(ggplot2)
library(dplyr)
library(PerformanceAnalytics)
library(data.table)
library(sqldf)
library(nortest)
library(tidyverse)
library(MASS)
library(rpart)
library(class)
library(ISLR)
library(scales)
library(ClustOfVar)
library(GGally)
library(reticulate)
library(ggthemes)
library(RColorBrewer)
library(gridExtra)
library(kableExtra)
library(Hmisc)
library(corrplot)
library(energy)
library(nnet)
library(Hotelling)
library(car)
```

```
# reading data
data <- read.csv('/Users/mac/Downloads/heart_failure_clinical_records_dataset.csv')
```

```r
# structure of data
str(data)
```

```
## '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 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 ...
```

```r
glimpse(data)
```

```
## Observations: 299
## Variables: 13
## $ age                      <dbl> 75, 55, 65, 50, 65, 90, 75, 60, 65, 8...
## $ anaemia                  <int> 0, 0, 0, 1, 1, 1, 1, 1, 0, 1, 1, 0, 1...
## $ creatinine_phosphokinase <int> 582, 7861, 146, 111, 160, 47, 246, 31...
## $ diabetes                 <int> 0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 0...
## $ ejection_fraction        <int> 20, 38, 20, 20, 20, 40, 15, 60, 65, 3...
## $ high_blood_pressure      <int> 1, 0, 0, 0, 0, 1, 0, 0, 0, 1, 1, 1, 0...
## $ platelets                <dbl> 265000, 263358, 162000, 210000, 32700...
## $ serum_creatinine         <dbl> 1.90, 1.10, 1.30, 1.90, 2.70, 2.10, 1...
## $ serum_sodium             <int> 130, 136, 129, 137, 116, 132, 137, 13...
## $ sex                      <int> 1, 1, 1, 1, 0, 1, 1, 1, 0, 1, 1, 1, 1...
## $ smoking                  <int> 0, 0, 1, 0, 0, 1, 0, 1, 0, 1, 1, 1, 0...
## $ time                     <int> 4, 6, 7, 7, 8, 8, 10, 10, 10, 10, 10,...
## $ DEATH_EVENT              <int> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1...
```

Let us summarise the data and note observations

summary of data

```r
summary(data)
```

```
##       age           anaemia       creatinine_phosphokinase
##  Min.   :40.00   Min.   :0.0000   Min.   :  23.0          
##  1st Qu.:51.00   1st Qu.:0.0000   1st Qu.: 116.5          
##  Median :60.00   Median :0.0000   Median : 250.0          
##  Mean   :60.83   Mean   :0.4314   Mean   : 581.8          
##  3rd Qu.:70.00   3rd Qu.:1.0000   3rd Qu.: 582.0          
##  Max.   :95.00   Max.   :1.0000   Max.   :7861.0          
##     diabetes      ejection_fraction high_blood_pressure   platelets     
##  Min.   :0.0000   Min.   :14.00     Min.   :0.0000      Min.   : 25100  
##  1st Qu.:0.0000   1st Qu.:30.00     1st Qu.:0.0000      1st Qu.:212500  
##  Median :0.0000   Median :38.00     Median :0.0000      Median :262000  
##  Mean   :0.4181   Mean   :38.08     Mean   :0.3512      Mean   :263358  
##  3rd Qu.:1.0000   3rd Qu.:45.00     3rd Qu.:1.0000      3rd Qu.:303500  
##  Max.   :1.0000   Max.   :80.00     Max.   :1.0000      Max.   :850000  
##  serum_creatinine  serum_sodium        sex              smoking      
##  Min.   :0.500    Min.   :113.0   Min.   :0.0000   Min.   :0.0000  
##  1st Qu.:0.900    1st Qu.:134.0   1st Qu.:0.0000   1st Qu.:0.0000  
##  Median :1.100    Median :137.0   Median :1.0000   Median :0.0000  
##  Mean   :1.394    Mean   :136.6   Mean   :0.6488   Mean   :0.3211  
##  3rd Qu.:1.400    3rd Qu.:140.0   3rd Qu.:1.0000   3rd Qu.:1.0000  
##  Max.   :9.400    Max.   :148.0   Max.   :1.0000   Max.   :1.0000  
##       time         DEATH_EVENT    
##  Min.   :  4.0   Min.   :0.0000  
##  1st Qu.: 73.0   1st Qu.:0.0000  
##  Median :115.0   Median :0.0000  
##  Mean   :130.3   Mean   :0.3211  
##  3rd Qu.:203.0   3rd Qu.:1.0000  
##  Max.   :285.0   Max.   :1.0000
```

Observations -
1. 299 observations for 13 variables
2. Age is between 40 and 95 so not much outliers by intuition
3. Death_event should be converted to factor variable as they take only 2 values
4. Creatinine phosphokinase, platelets clearly has an outlier from max value which we will confirm later by univariate analysis

Missing/ NAs check

```
data2 <- na.omit(data)
```

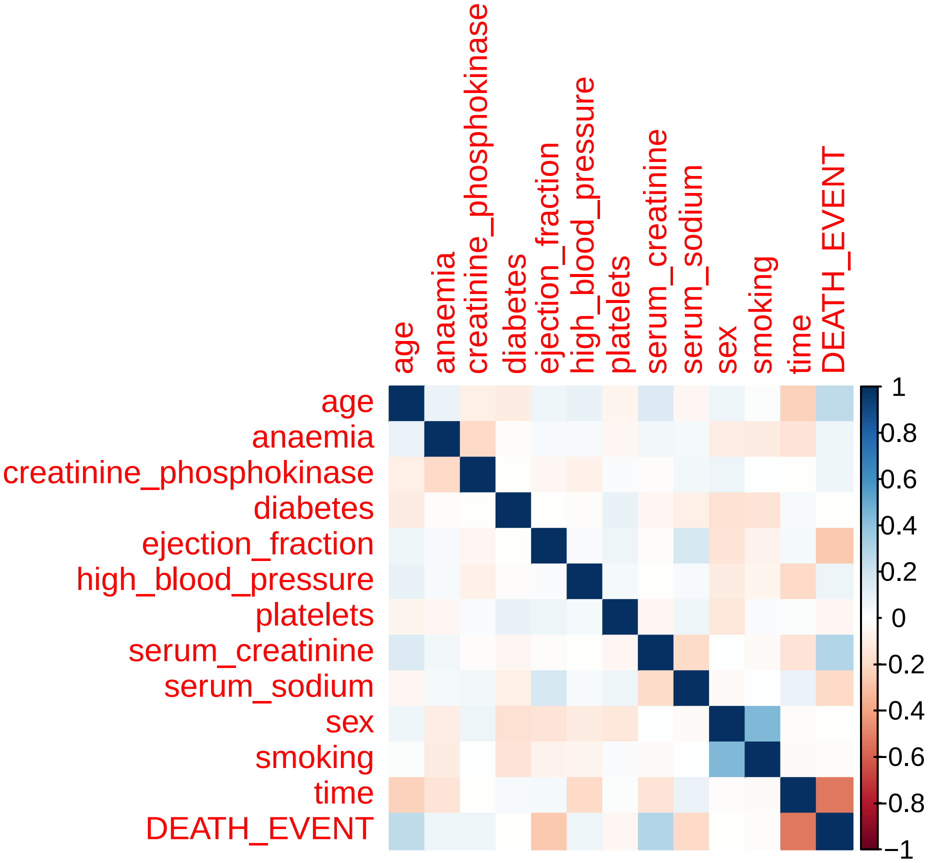
'data2' has same rows as 'data' so there are no missing values in data

Correlation Plot

```
M<-cor(data)
head(round(M,2))
```

```
##                            age anaemia creatinine_phosphokinase diabetes
## age                       1.00    0.09                    -0.08    -0.10
## anaemia                   0.09    1.00                    -0.19    -0.01
## creatinine_phosphokinase -0.08   -0.19                     1.00    -0.01
## diabetes                 -0.10   -0.01                    -0.01     1.00
## ejection_fraction         0.06    0.03                    -0.04     0.00
## high_blood_pressure       0.09    0.04                    -0.07    -0.01
##                          ejection_fraction high_blood_pressure platelets
## age                                   0.06                0.09     -0.05
## anaemia                               0.03                0.04     -0.04
## creatinine_phosphokinase             -0.04               -0.07      0.02
## diabetes                              0.00               -0.01      0.09
## ejection_fraction                     1.00                0.02      0.07
## high_blood_pressure                   0.02                1.00      0.05
##                          serum_creatinine serum_sodium   sex smoking  time
## age                                  0.16        -0.05  0.07    0.02 -0.22
## anaemia                              0.05         0.04 -0.09   -0.11 -0.14
## creatinine_phosphokinase            -0.02         0.06  0.08    0.00 -0.01
## diabetes                            -0.05        -0.09 -0.16   -0.15  0.03
## ejection_fraction                   -0.01         0.18 -0.15   -0.07  0.04
## high_blood_pressure                  0.00         0.04 -0.10   -0.06 -0.20
##                          DEATH_EVENT
## age                             0.25
## anaemia                         0.07
## creatinine_phosphokinase        0.06
## diabetes                        0.00
## ejection_fraction              -0.27
## high_blood_pressure             0.08
```

```
corrplot(M, method="color")
```



We see that age, anameia, creatinine_phosphokinase, high_blood_pressure, serum_creatinine have +ve correlation with death_event

We see that ejection_fraction, platelets, serum_sodium, and time have -ve correlation with death_event

But we will need deeper analysis to confirm these relationships.

Data Information

```r
# Converting to factor (dependent variable)
data$DEATH_EVENT <- factor(data$DEATH_EVENT)

# Let's check how many zeros are in dataset
colSums(data==0)
```

```
##                      age                  anaemia creatinine_phosphokinase
##                        0                      170                        0
##                 diabetes        ejection_fraction      high_blood_pressure
##                      174                        0                      194
##                platelets         serum_creatinine             serum_sodium
##                        0                        0                        0
##                      sex                  smoking                     time
##                      105                      203                        0
##              DEATH_EVENT
##                      203
```

```r
# Let's check their proportion to dataset as well
round(colSums(data==0)/nrow(data)*100,2)
```

```
##                      age                  anaemia creatinine_phosphokinase
##                     0.00                    56.86                     0.00
##                 diabetes        ejection_fraction      high_blood_pressure
##                    58.19                     0.00                    64.88
##                platelets         serum_creatinine             serum_sodium
##                     0.00                     0.00                     0.00
##                      sex                  smoking                     time
##                    35.12                    67.89                     0.00
##              DEATH_EVENT
##                    67.89
```

Smoking, High BP, Diabetes, Anaemia are over 50% while sex is below 35%
The Event rate of survival is ~67.9%

Let's classify independent variables into -
1. Categorical -> Anaemia, Diabetes, High_blood_pressure, Sex, Smoking
2. Numeric -> Age, Creatinine_phosphokinase, Ejection_fraction, Platelets, serum_creatinine, serum_sodium, time

We also see that
Sex - Gender of patient Male = 1, Female =0
Diabetes - 0 = No, 1 = Yes
Anaemia - 0 = No, 1 = Yes
High_blood_pressure - 0 = No, 1 = Yes
Smoking - 0 = No, 1 = Yes
DEATH_EVENT - 0 = No, 1 = Yes

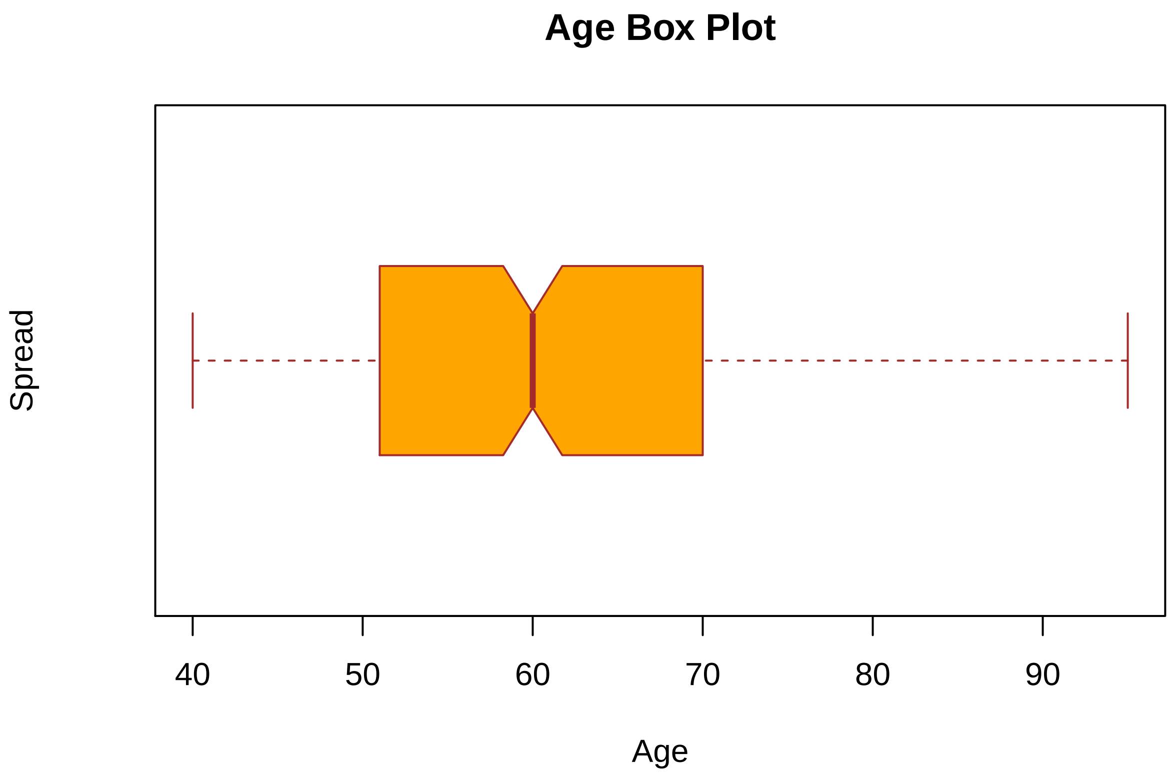
We note the scale of few variables like creatinine_phosphokinase,platelets, ejection_fraction and time. We can normalize the same before modeling but for now we will keep them as-is for the EDA.

Analysis

Let's start with Outlier Analysis

Age

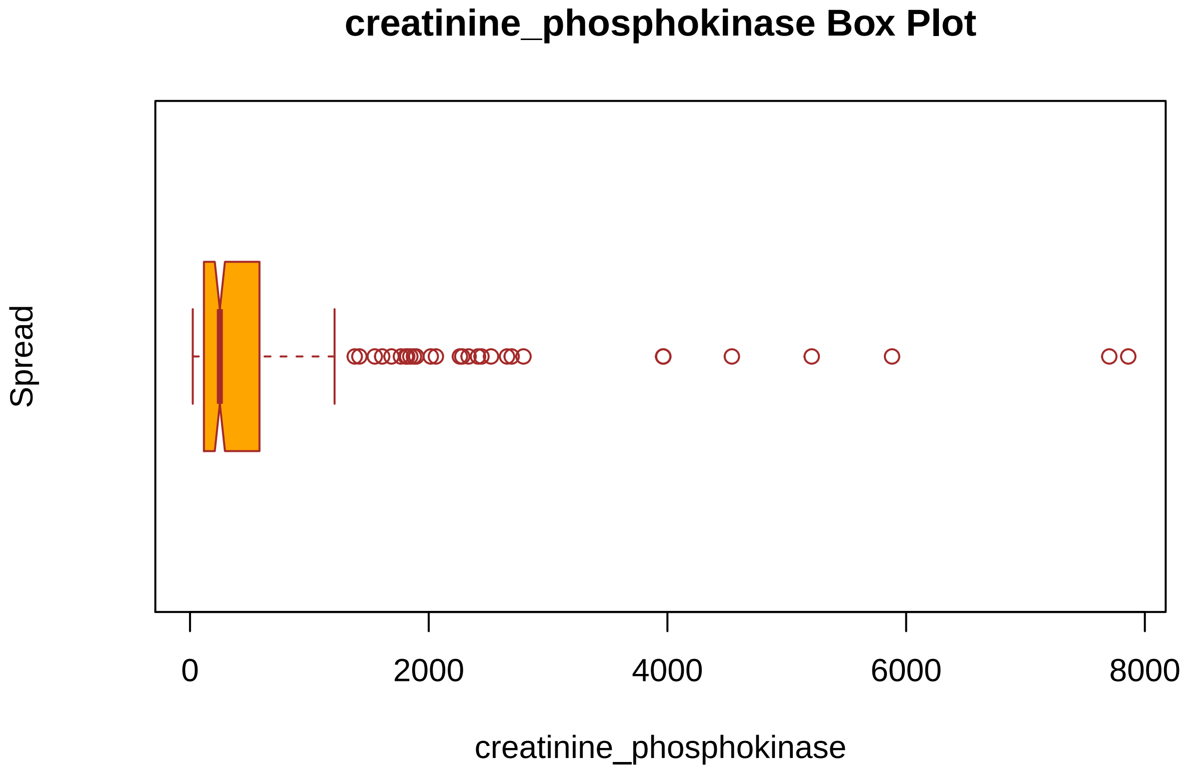
```r
# Outlier Analysis
boxplot(data$age,
        main = "Age Box Plot",
        xlab = "Age",
        ylab = "Spread",
        col = "orange",
        border = "brown",
        horizontal = TRUE,
        notch = TRUE
)
```



We note no observed outlier in age

creatinine_phosphokinase

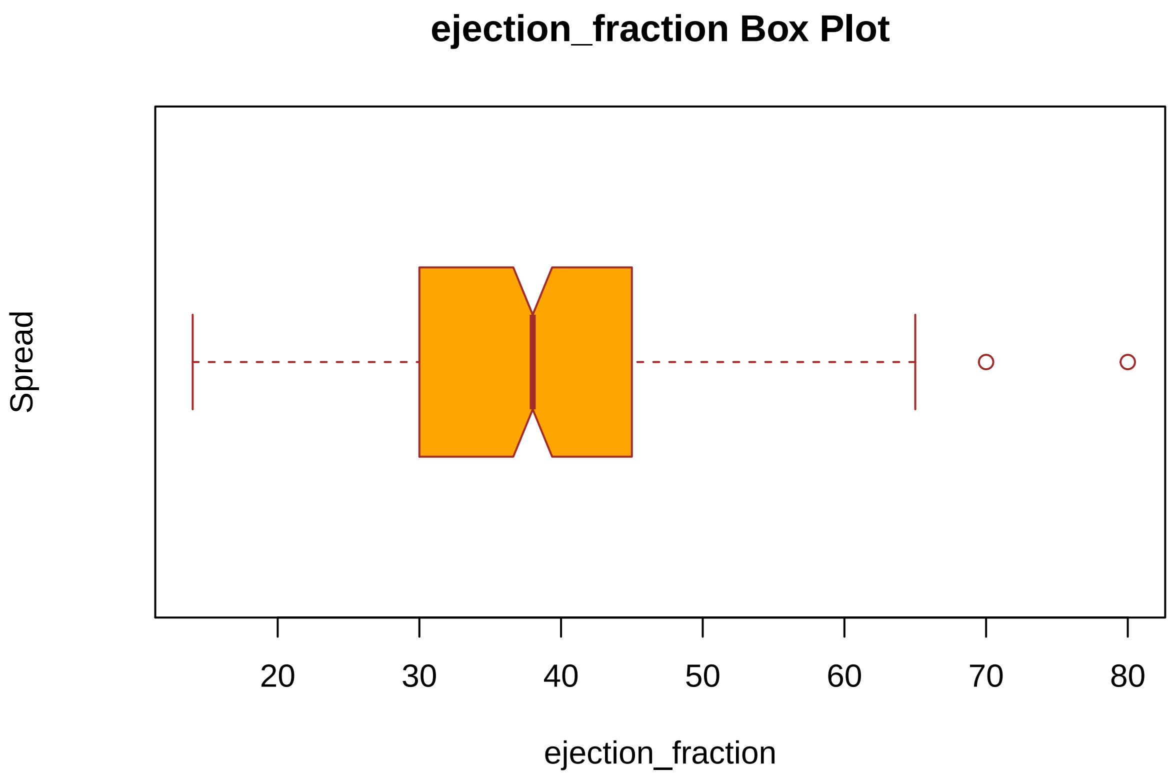
```r
boxplot(data$creatinine_phosphokinase,
        main = "creatinine_phosphokinase Box Plot",
        xlab = "creatinine_phosphokinase",
        ylab = "Spread",
        col = "orange",
        border = "brown",
        horizontal = TRUE,
        notch = TRUE
)
```



We notice some outliers at the positive side in creatinine_phosphokinase with data above median more dispersed

ejection_fraction

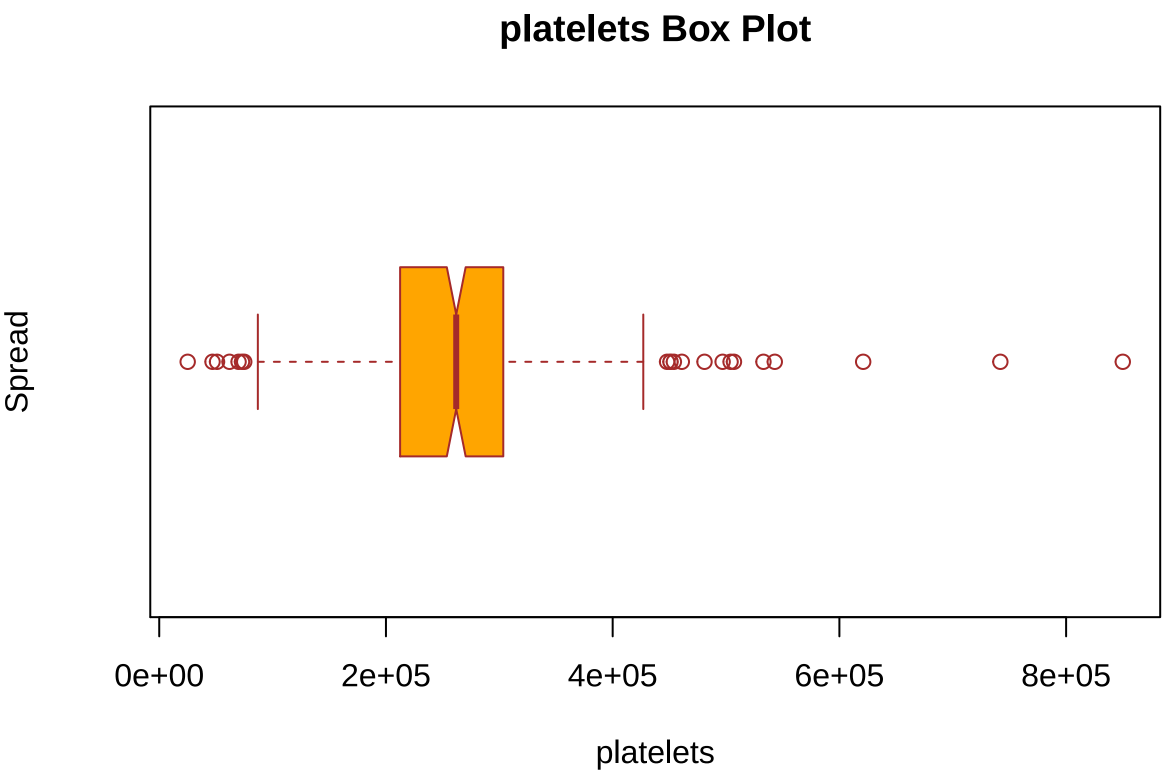
```
boxplot(data$ejection_fraction,
        main = "ejection_fraction Box Plot",
        xlab = "ejection_fraction",
        ylab = "Spread",
        col = "orange",
        border = "brown",
        horizontal = TRUE,
        notch = TRUE
)
```



We notice 2 data points as outliers in ejection_fraction

platelets

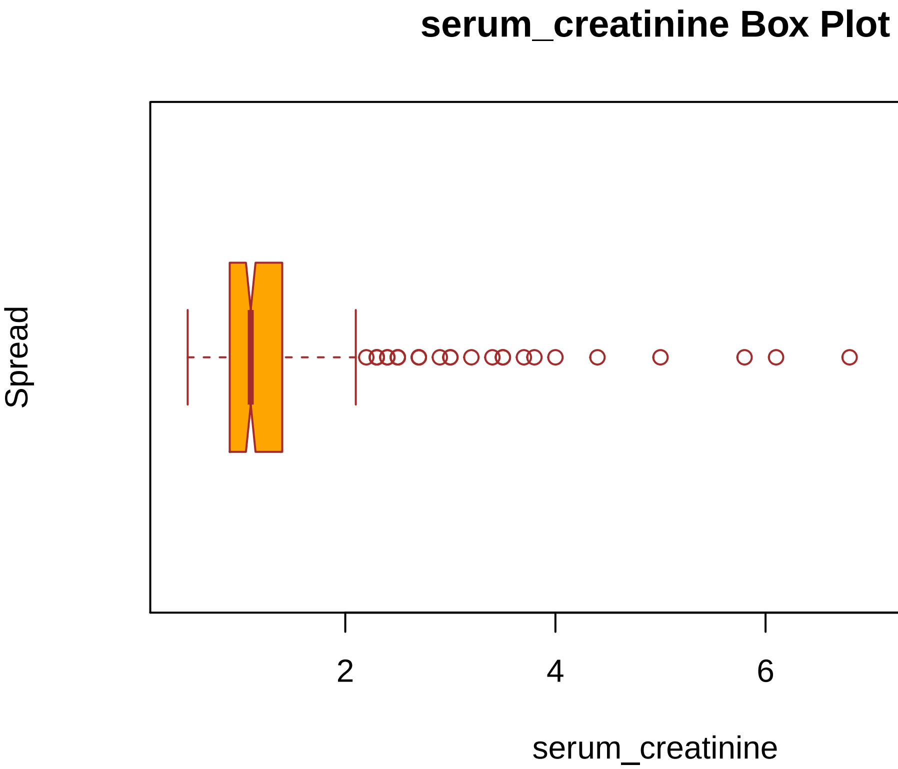
```
boxplot(data$platelets,
        main = "platelets Box Plot",
        xlab = "platelets",
        ylab = "Spread",
        col = "orange",
        border = "brown",
        horizontal = TRUE,
        notch = TRUE
)
```



We notice outliers on both spectrum (high and low) in platelets

serum_creatinine

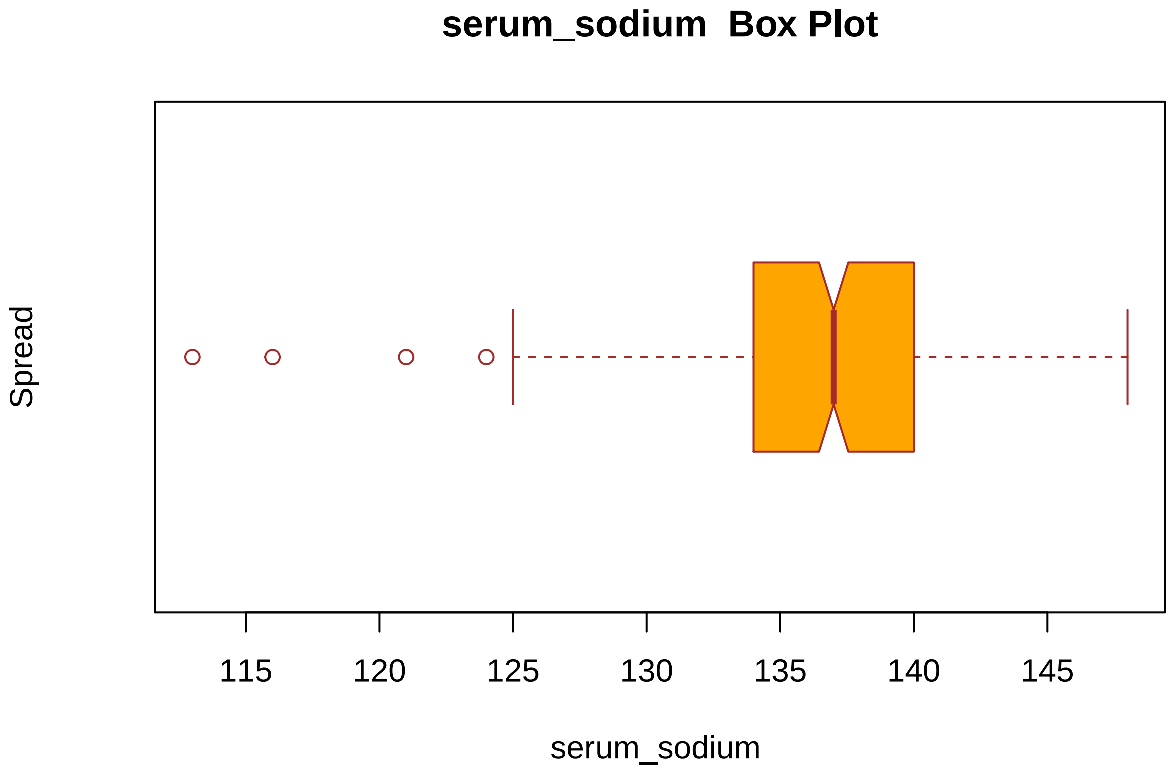
```
boxplot(data$serum_creatinine,
        main = "serum_creatinine Box Plot",
        xlab = "serum_creatinine",
        ylab = "Spread",
        col = "orange",
        border = "brown",
        horizontal = TRUE,
        notch = TRUE
)
```



We notice some outliers in serum_creatinine on higher end (similar to creatinine_phosphokinase). However these are in possible ranges medically.

serum_sodium

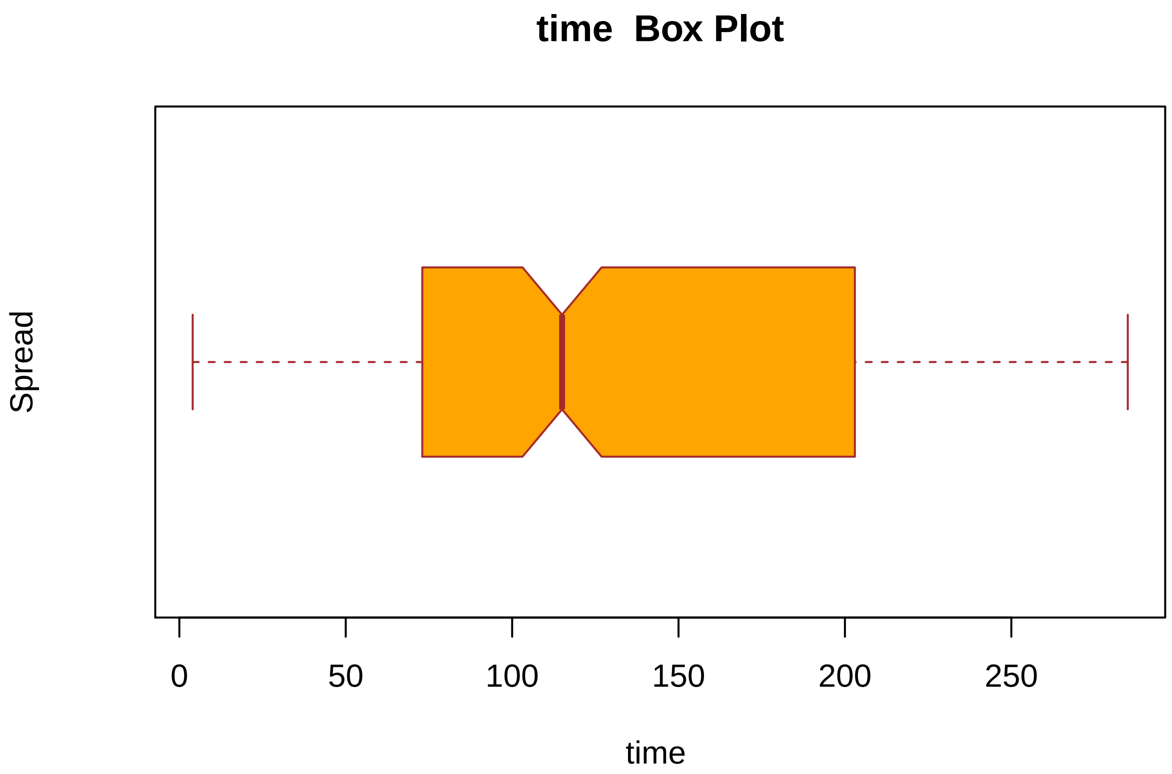
```
boxplot(data$serum_sodium ,
        main = "serum_sodium  Box Plot",
        xlab = "serum_sodium ",
        ylab = "Spread",
        col = "orange",
        border = "brown",
        horizontal = TRUE,
        notch = TRUE
)
```



We notice some outliers in serum_sodium on lower end

time

```r
boxplot(data$time ,
        main = "time  Box Plot",
        xlab = "time ",
        ylab = "Spread",
        col = "orange",
        border = "brown",
        horizontal = TRUE,
        notch = TRUE
)
```



We notice no outliers in time (follow up period) however data above median is more dispersed

Note: While some of these are clear outliers, others must be checked with possible medical range

Data Cleaning - Let's remove these outliers

```
data <- data[data$ejection_fraction <70,]
data <- data[data$creatinine_phosphokinase <7000,]
```

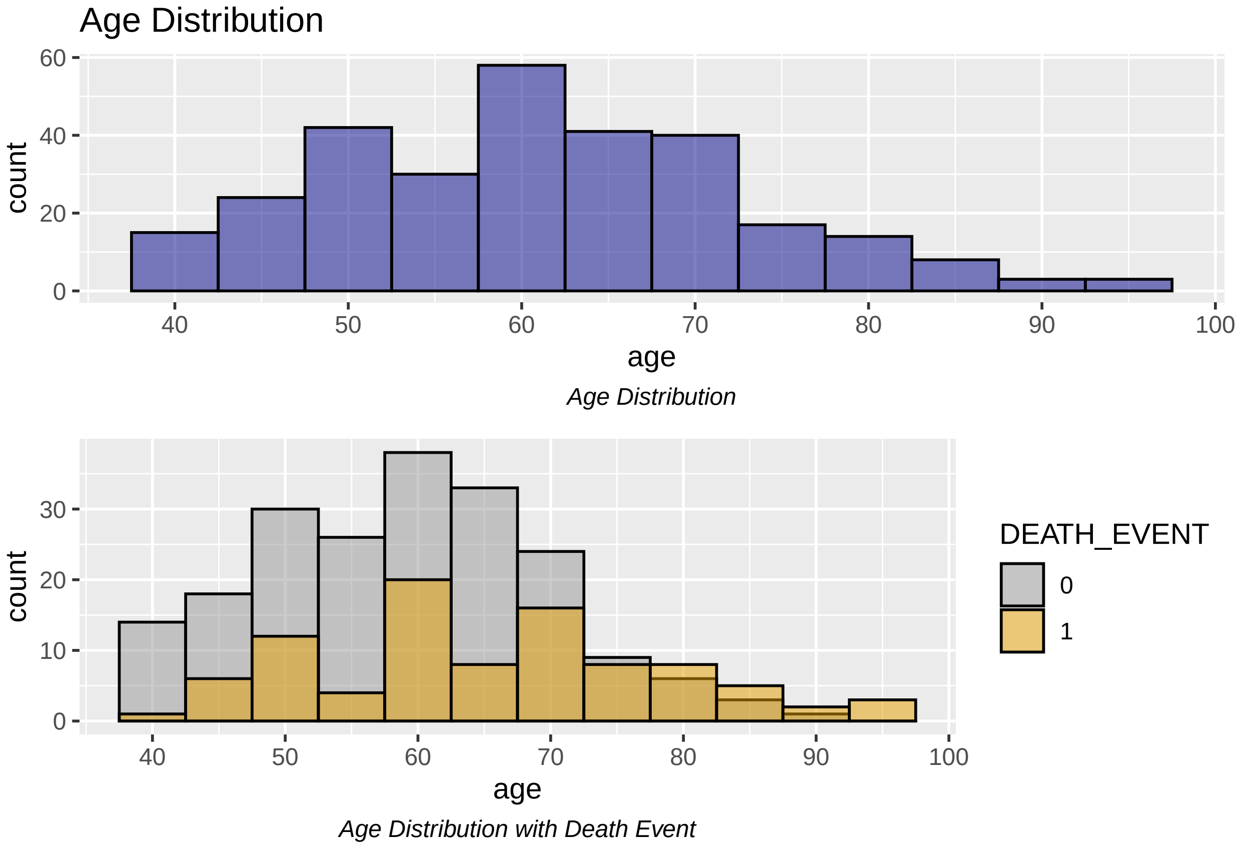
The new data now has only 295 observations - 4 observations were removed

Univariate analysis

We will plot density distributions for numerical variables
And check splits for categorical variables

Age

```
# Let's check Age distribution and see it with death event
a<-ggplot(data,aes(x = age))+geom_histogram(binwidth = 5, color = "black",
                                           fill = "dark blue",alpha = 0.5)+
  labs(title = "Age Distribution",
      caption = "Age Distribution")+
  theme(plot.caption = element_text(hjust = 0.5,face = "italic"))+
  scale_x_continuous(breaks = seq(40,100,10))

b<-ggplot(data,aes(x = age, fill = DEATH_EVENT))+geom_histogram(binwidth = 5,
                        position = "identity",
alpha = 0.5,color = "black")+scale_fill_manual(values = c("#999999", "#E69F00"))+
  labs(caption = "Age Distribution with Death Event")+
  theme(plot.caption = element_text(hjust = 0.5,face = "italic"))+
  scale_x_continuous(breaks = seq(40,100,10))

gridExtra::grid.arrange(a,b)
```



We see that as age increases, chances of death event go up as well

We can also confirm this numerically ;

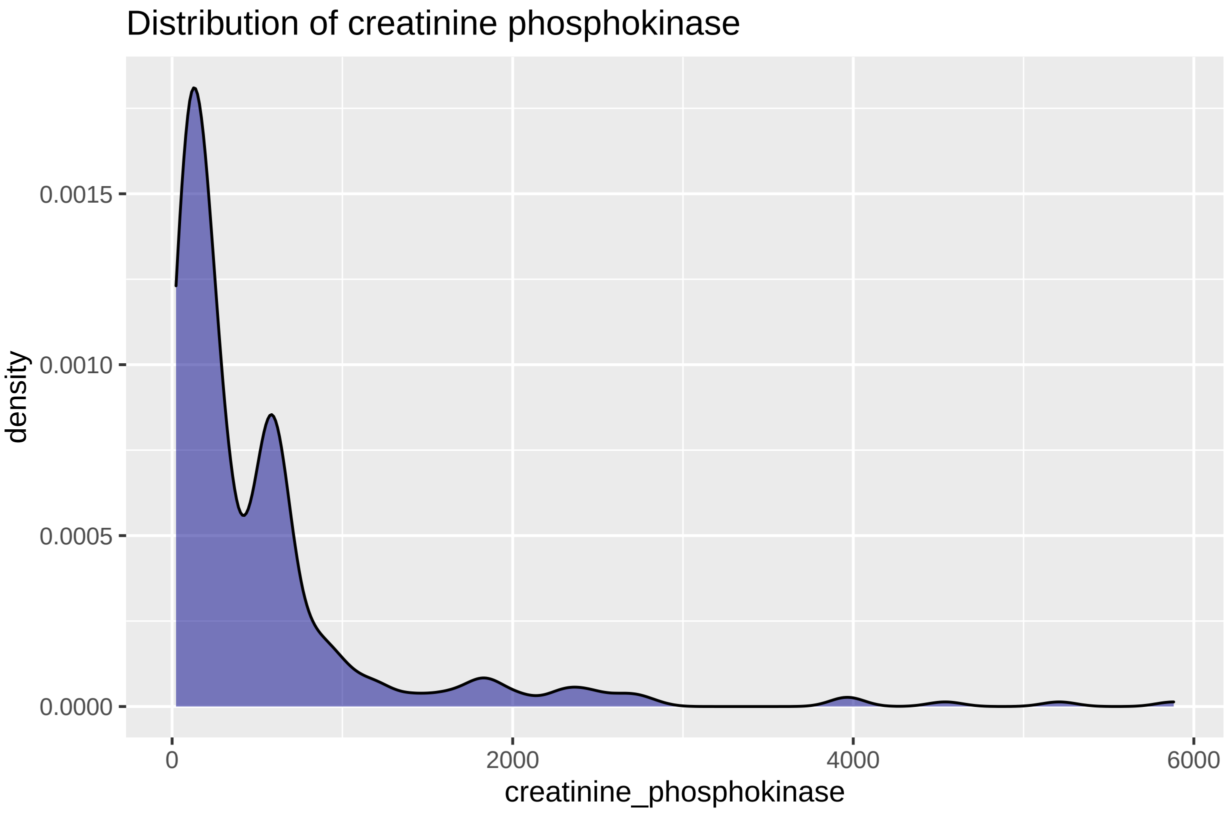
```
# Let's create age ranges
data$age_tr[data$age < 50 & data$age >= 40]="40-50"
data$age_tr[data$age < 60 & data$age >= 50]="50-60"
data$age_tr[data$age < 70 & data$age >= 60]="60-70"
data$age_tr[data$age < 80 & data$age >= 70]="70-80"
data$age_tr[data$age < 90 & data$age >= 80]="80-90"
data$age_tr[data$age < 100 & data$age >= 90]="90-100"

table(data$DEATH_EVENT, data$age_tr)
```

```
##
##     40-50 50-60 60-70 70-80 80-90 90-100
##   0    35    62    66    32     6      1
##   1    10    18    27    20    13      5
```

Numerically, we can confirm the same observation (Higher death rate in higher ages)

Creatinine_phosphokinase

```
# density plot of Creatinine_phosphokinase
ggplot(data,aes(x = creatinine_phosphokinase))+geom_density(fill = "dark blue",
                                                alpha = 0.5)+
  labs(title = "Distribution of creatinine phosphokinase", caption =
    "Density distribution")+
  theme(plot.caption = element_text(hjust = 0.5, face = "italic"))
```



Density distribution

The distribution looks skewed

```
#let's create 10 splits of this variable
data$creatinine_phosphokinase_tr <- cut(data$creatinine_phosphokinase, 10)
table(data$DEATH_EVENT, data$creatinine_phosphokinase_tr)
```

```
##
##     (17.1,609] (609,1.19e+03] (1.19e+03,1.78e+03] (1.78e+03,2.37e+03]
##   0        156             24                   7                   7
##   1         79              6                   2                   3
##
##     (2.37e+03,2.95e+03] (2.95e+03,3.54e+03] (3.54e+03,4.12e+03]
##   0                   5                   0                   1
##   1                   1                   0                   1
##
##     (4.12e+03,4.71e+03] (4.71e+03,5.3e+03] (5.3e+03,5.89e+03]
##   0                   1                  1                  0
##   1                   0                  0                  1
```

Numerically, we can see that for creatinine levels above 4000, death event seems to be higher but what about averages ?

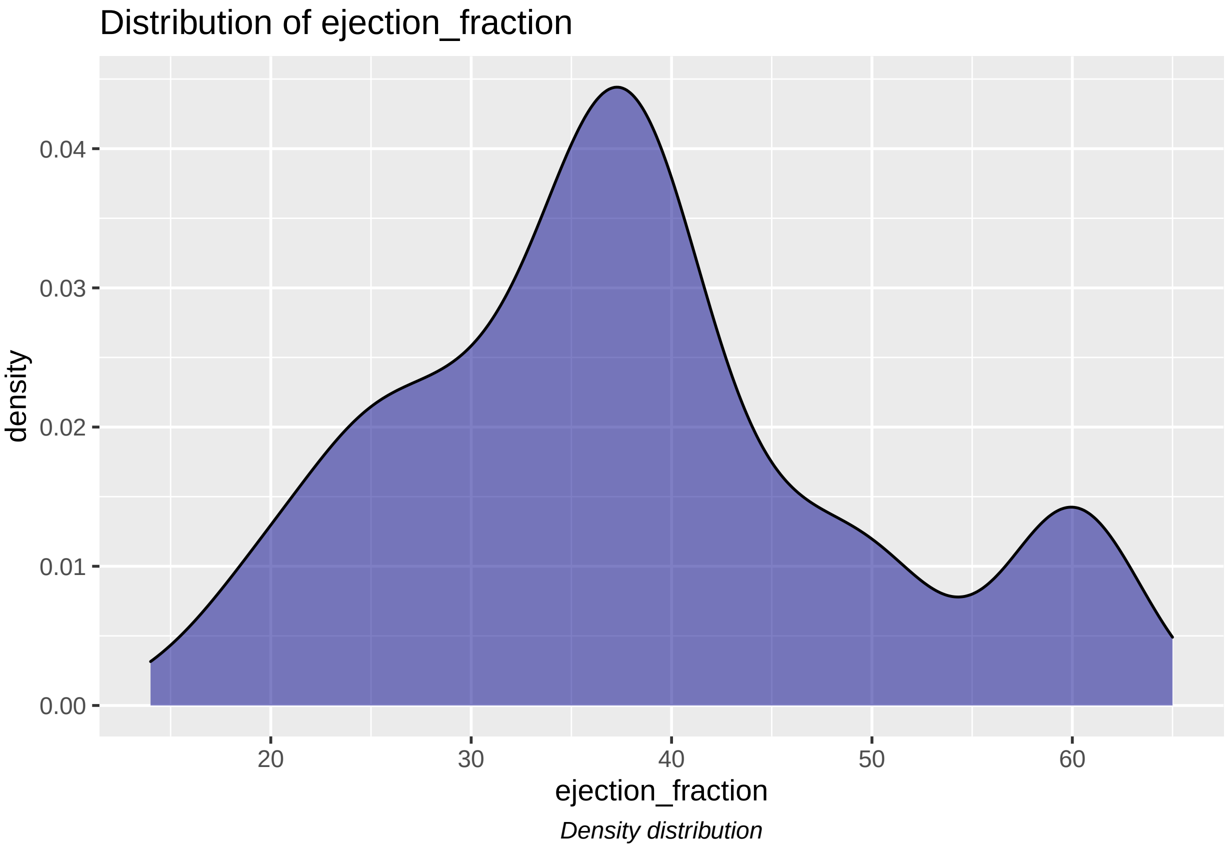
```
aggregate(data[, c('creatinine_phosphokinase')], list(data$DEATH_EVENT), mean)
```

```
##   Group.1        x
## 1       0 539.8465
## 2       1 519.8817
```

Numerically, we can see that average creatinine levels are higher in case of death event

Ejection_fraction

```
ggplot(data,aes(x = ejection_fraction))+geom_density(fill = "dark blue",
                                                     alpha = 0.5)+
  labs(title = "Distribution of ejection_fraction",
       caption = "Density distribution")+
  theme(plot.caption = element_text(hjust = 0.5, face = "italic"))
```



The distribution has a major and a minor peak

```
#let's create 10 splits of this variable
data$ejection_fraction_tr <- cut(data$ejection_fraction, 10)
table(data$DEATH_EVENT, data$ejection_fraction_tr)
```

```
##
##     (13.9,19.1] (19.1,24.2] (24.2,29.3] (29.3,34.4] (34.4,39.5]
##   0           1           2          18          21          67
##   1           4          16          17          13          21
##
##     (39.5,44.6] (44.6,49.7] (49.7,54.8] (54.8,59.9] (59.9,65.1]
##   0          33          15          15           2          28
##   1           4           5           6           1           6
```

Numerically, we can see that ejection fraction is low in case of death event

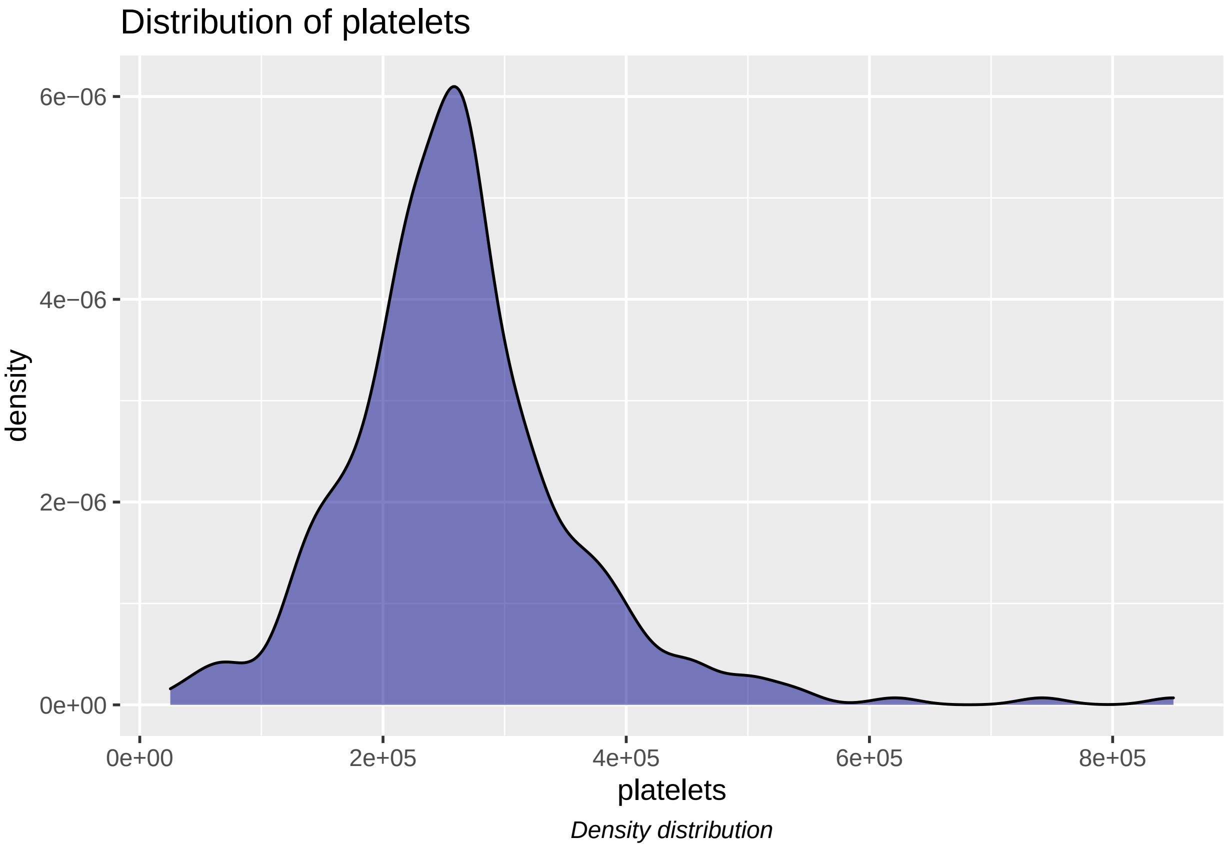
```
aggregate(data[, c('ejection_fraction')], list(data$DEATH_EVENT), mean)
```

```
##   Group.1        x
## 1       0 40.06931
## 2       1 33.11828
```

Numerically, we can see that average ejection fraction is also low in case of death event

platelets

```
ggplot(data,aes(x = platelets ))+geom_density(fill = "dark blue", alpha = 0.5)+
  labs(title = "Distribution of platelets ", caption = "Density distribution")+
  theme(plot.caption = element_text(hjust = 0.5, face = "italic"))
```



The distribution looks pretty normal with some tail noticeable at the right extreme

```
#let's create 10 splits of this variable
data$platelets_tr  <- cut(data$platelets , 10)
table(data$DEATH_EVENT, data$platelets_tr)
```

```
##    
##     (2.43e+04,1.08e+05] (1.08e+05,1.9e+05] (1.9e+05,2.73e+05]
##   0                   4                 31                 91
##   1                   5                 14                 43
##    
```

```
##      (2.73e+05,3.55e+05] (3.55e+05,4.38e+05] (4.38e+05,5.2e+05]
##   0                  49                  18                  5
##   1                  18                   8                  4
##    
##      (5.2e+05,6.03e+05] (6.03e+05,6.85e+05] (6.85e+05,7.68e+05]
##   0                  2                   0                   1
##   1                  0                   1                   0
##    
##      (7.68e+05,8.51e+05]
##   0                   1
##   1                   0
```

Numerically, we can see that platelets are low in case of death event

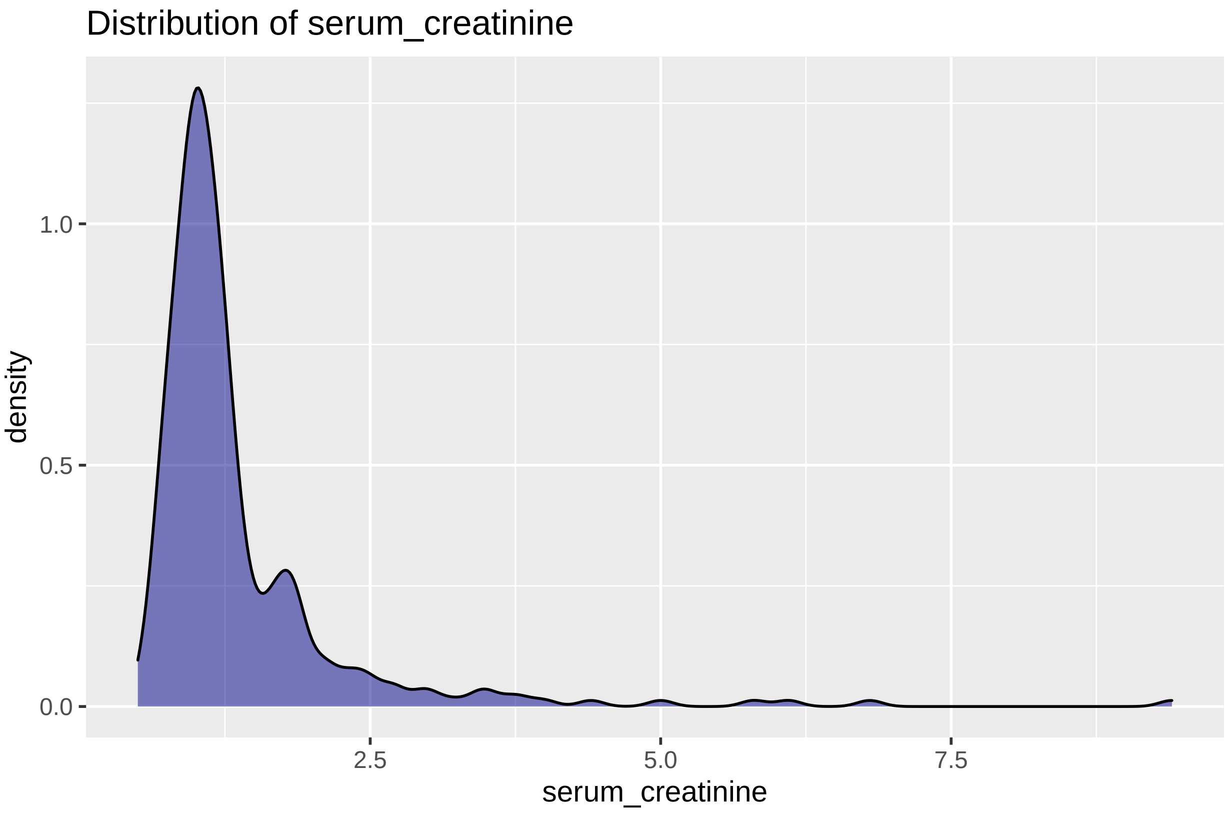
```r
aggregate(data[, c('platelets')], list(data$DEATH_EVENT), mean)
```

```
##   Group.1        x
## 1       0 266673.8
## 2       1 256002.4
```

Numerically, we can see that average platelets are marginally lower in case of death event

serum_creatinine

```r
ggplot(data,aes(x = serum_creatinine ))+geom_density(fill =
                                          "dark blue", alpha = 0.5)+
  labs(title = "Distribution of serum_creatinine ",
       caption = "Density distribution")+
  theme(plot.caption = element_text(hjust = 0.5, face = "italic"))
```



Density distribution

The distribution looks similar to creatinine_phosphokinase

```
#let's create 10 splits of this variable
data$serum_creatinine_tr  <- cut(data$serum_creatinine , 10)
table(data$DEATH_EVENT, data$serum_creatinine_tr)
```

```
##
##     (0.491,1.39] (1.39,2.28] (2.28,3.17] (3.17,4.06] (4.06,4.95]
##   0          168          23           5           4           0
##   1           47          30           9           3           1
##
##     (4.95,5.84] (5.84,6.73] (6.73,7.62] (7.62,8.51] (8.51,9.41]
##   0           1           1           0           0           0
##   1           1           0           1           0           1
```

Numerically, we can see that death event is high when serum_creatinine levels are above 1.39 and very high above 2.28

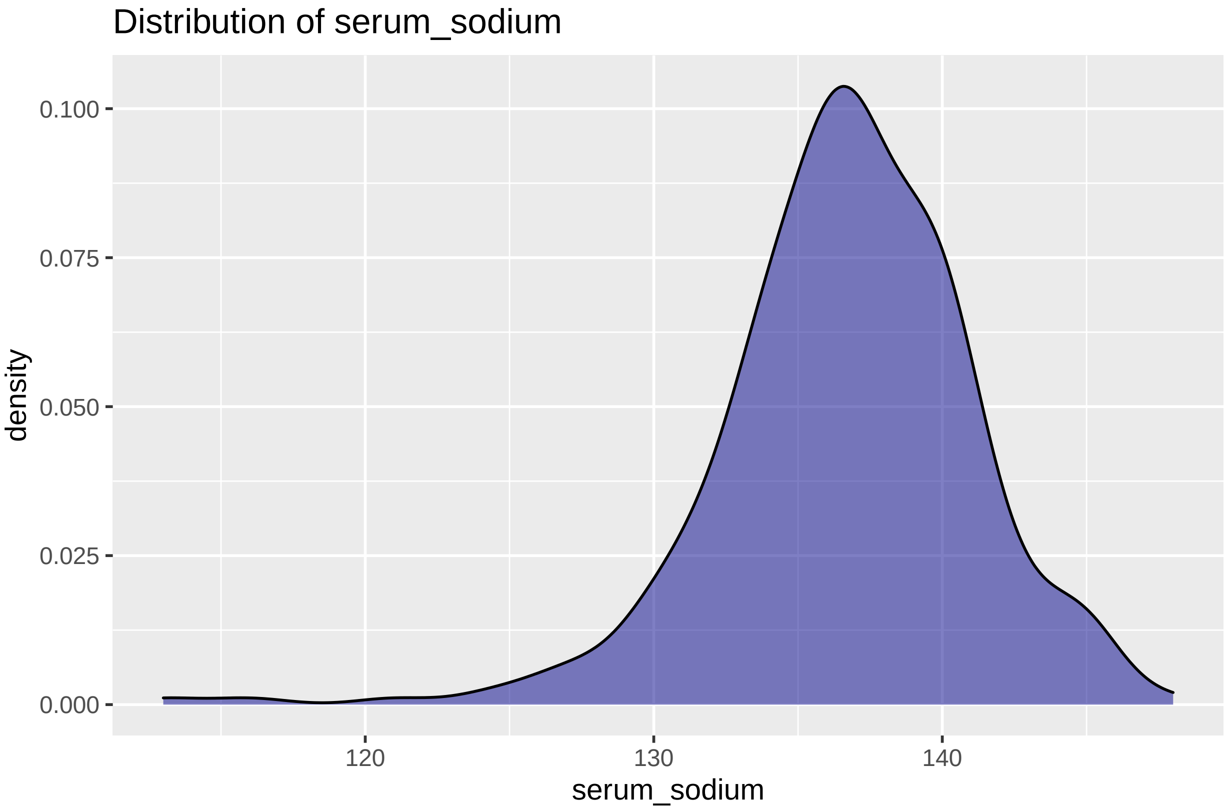
```
aggregate(data[, c('serum_creatinine')], list(data$DEATH_EVENT), mean)
```

```
##   Group.1        x
## 1       0 1.184901
## 2       1 1.775699
```

Numerically, we can see that average serum_creatinine is high in case of death event

serum_sodium

```r
ggplot(data,aes(x = serum_sodium ))+geom_density(fill = "dark blue",
                                                  alpha = 0.5)+
  labs(title = "Distribution of serum_sodium ",
      caption = "Density distribution")+
  theme(plot.caption = element_text(hjust = 0.5, face = "italic"))
```



Density distribution

The distribution looks pretty normal with some tail noticeable at the left extreme

```r
#let's create 10 splits of this variable
data$serum_sodium_tr  <- cut(data$serum_sodium , 10)
table(data$DEATH_EVENT, data$serum_sodium_tr)
```

```
##
##     (113,116] (116,120] (120,124] (124,127] (127,130] (130,134] (134,138]
##   0         1         0         0         2         7        31        69
##   1         1         0         1         4         6        30        22
##
##     (138,141] (141,144] (144,148]
##   0        72        13         7
##   1        19         6         4
```

Numerically, we can see that serum_sodium are low in case of death event

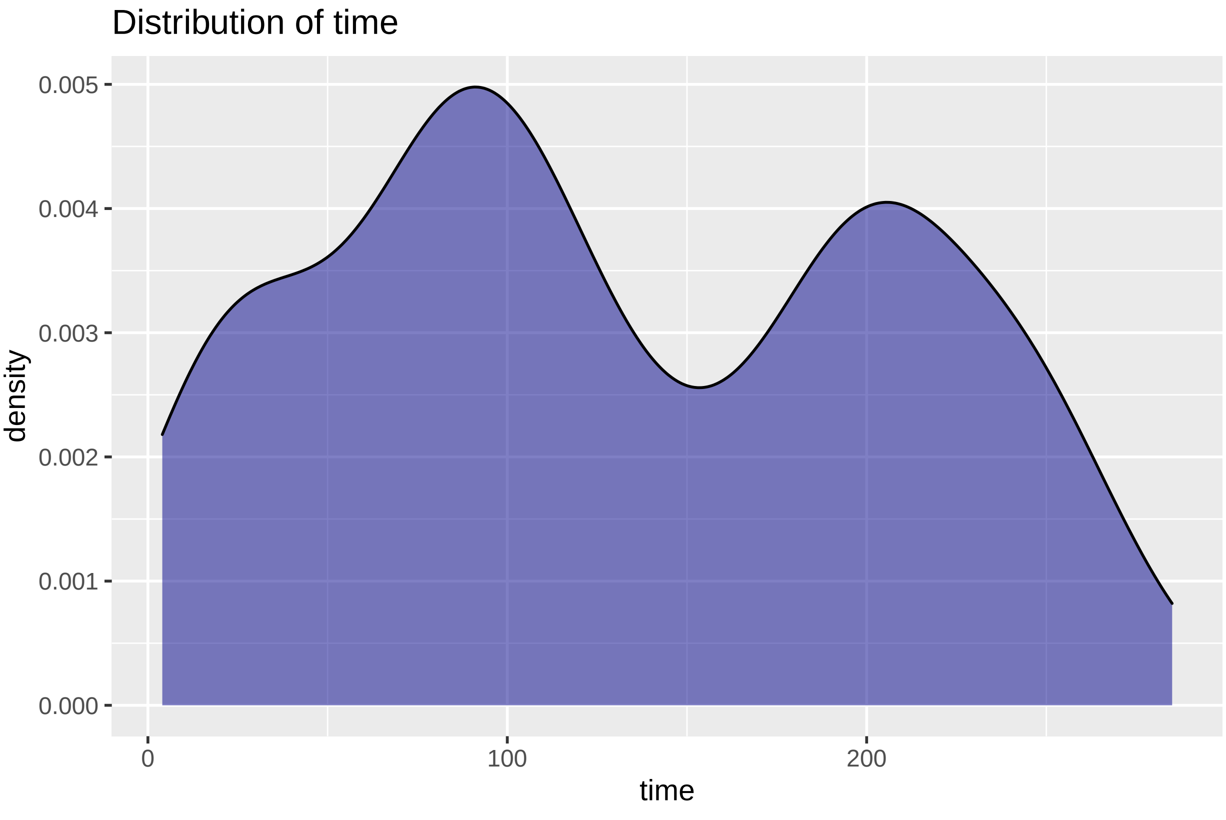
```r
aggregate(data[, c('serum_sodium')], list(data$DEATH_EVENT), mean)
```

```
##   Group.1        x
## 1       0 137.2178
## 2       1 135.3118
```

Numerically, we can see that average serum sodium are marginally lower in case of death event

time

```
ggplot(data,aes(x = time ))+geom_density(fill = "dark blue", alpha = 0.5)+
  labs(title = "Distribution of time ", caption = "Density distribution")+
  theme(plot.caption = element_text(hjust = 0.5, face = "italic"))
```



Density distribution

We note a bi-modal peak

```
#let's create 10 splits of this variable
data$time_tr  <- cut(data$time , 10)
table(data$DEATH_EVENT, data$time_tr)
```

```
##
##     (3.72,32.1] (32.1,60.2] (60.2,88.3] (88.3,116] (116,144] (144,173]
##   0           5           4          33         32        14        13
##   1          36          16          13          9         4         7
##
##     (173,201] (201,229] (229,257] (257,285]
##   0        28        33        31         9
##   1         4         2         2         0
```

Numerically, we can see that follow up period was small in case of death event

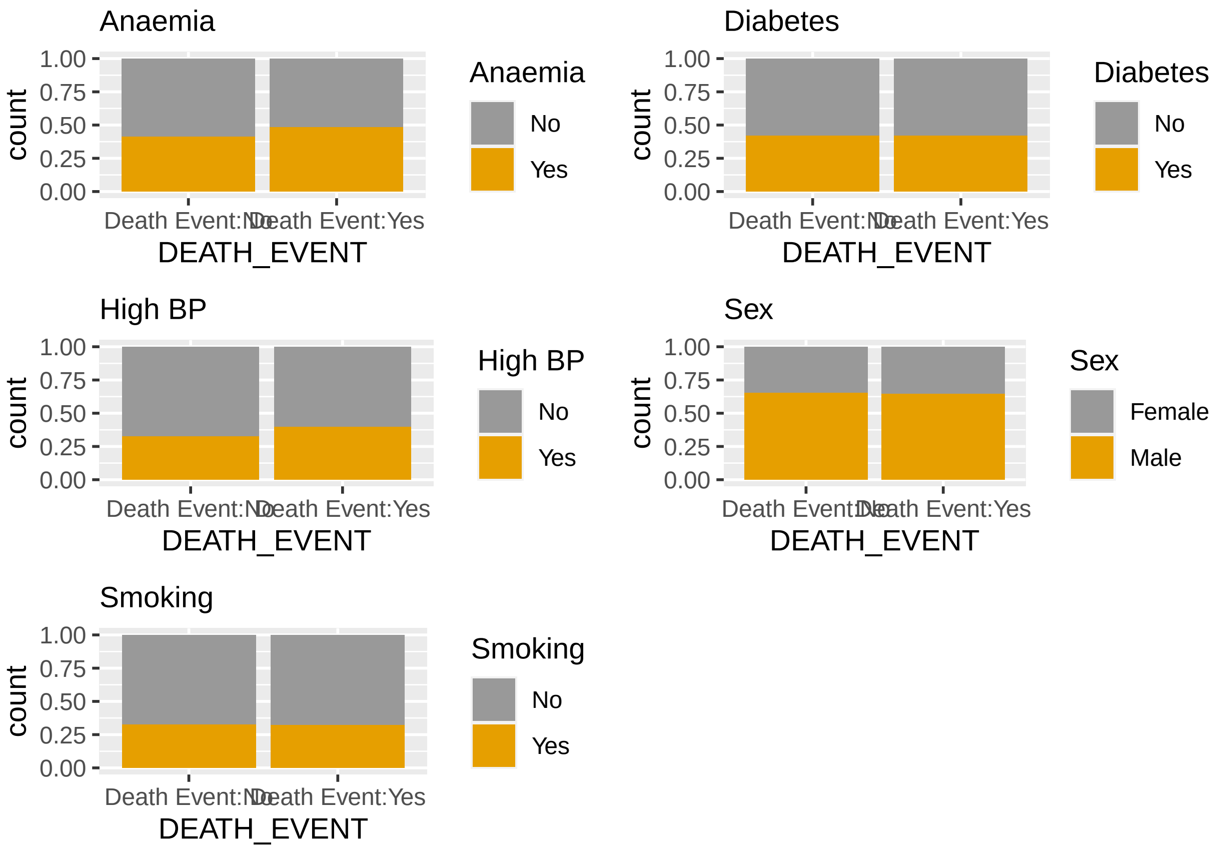
```r
aggregate(data[, c('time')], list(data$DEATH_EVENT), mean)
```

```
##   Group.1         x
## 1       0 158.81188
## 2       1  70.35484
```

Numerically, we can see that average follow up period is low in case of death event. This simply may illustrate that once deemed healthy,the patients may have stopped following up whereas diseased patients would undergo more checkups

Let's do EDA for categorical variables now

```r
# Anaemia, Diabetes, High_blood_pressure, Sex, Smoking

a <- ggplot(data, aes(x = DEATH_EVENT, fill = factor(anaemia)))+
  geom_bar(position = "fill")+
  scale_x_discrete(labels  = c("Death Event:No","Death Event:Yes"))+
  scale_fill_manual(values = c("#999999", "#E69F00"), name = "Anaemia",
  labels = c("No","Yes"))+labs(subtitle = "Anaemia")

b<-ggplot(data, aes(x = DEATH_EVENT, fill = factor(diabetes)))+
  geom_bar(position = "fill")+
  scale_x_discrete(labels  = c("Death Event:No","Death Event:Yes"))+
  scale_fill_manual(values = c("#999999", "#E69F00"), name = "Diabetes",
                    labels = c("No","Yes"))+labs(subtitle = "Diabetes")

c<-ggplot(data, aes(x = DEATH_EVENT, fill = factor(high_blood_pressure)))+
  geom_bar(position = "fill")+
  scale_x_discrete(labels  = c("Death Event:No","Death Event:Yes"))+
  scale_fill_manual(values = c("#999999", "#E69F00"), name = "High BP",
                    labels = c("No","Yes"))+labs(subtitle = "High BP")

d<-ggplot(data, aes(x = DEATH_EVENT, fill = factor(sex)))+
  geom_bar(position = "fill")+
  scale_x_discrete(labels  = c("Death Event:No","Death Event:Yes"))+
  scale_fill_manual(values = c("#999999", "#E69F00"), name = "Sex",
                    labels = c("Female","Male"))+labs(subtitle = "Sex")

e<-ggplot(data, aes(x = DEATH_EVENT, fill = factor(smoking)))+
  geom_bar(position = "fill")+
  scale_x_discrete(labels  = c("Death Event:No","Death Event:Yes"))+
  scale_fill_manual(values = c("#999999", "#E69F00"), name = "Smoking",
                    labels = c("No","Yes"))+labs(subtitle = "Smoking")

grid.arrange(a,b,c,d,e)
```



We can see that Anaemia and High BP has significant difference for death event whereas others not so much

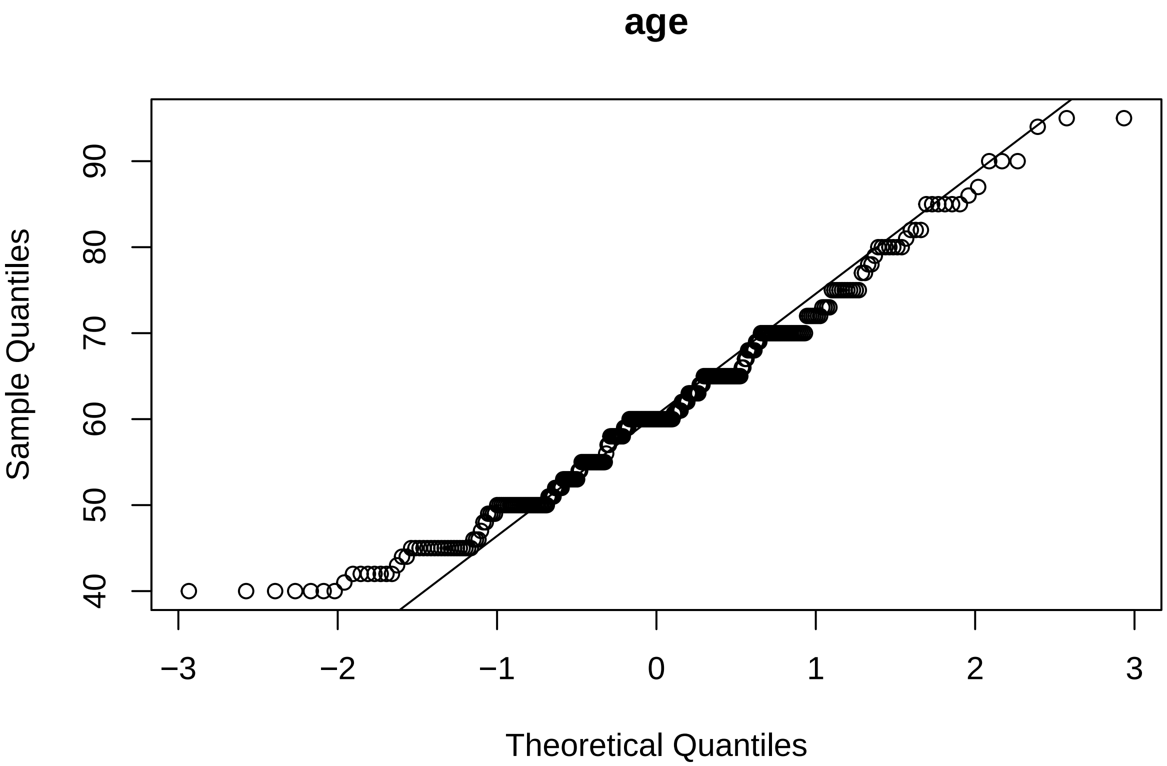
Tests

Normality Test

```
# univariate normality
data <- read.csv('/Users/mac/Downloads/heart_failure_clinical_records_dataset.csv')
cm <- colMeans(data)
S <- cov(data)
d <- apply(data, MARGIN = 1, function(data)t(data - cm) %*% solve(S) %*% (data - cm))
```

Age

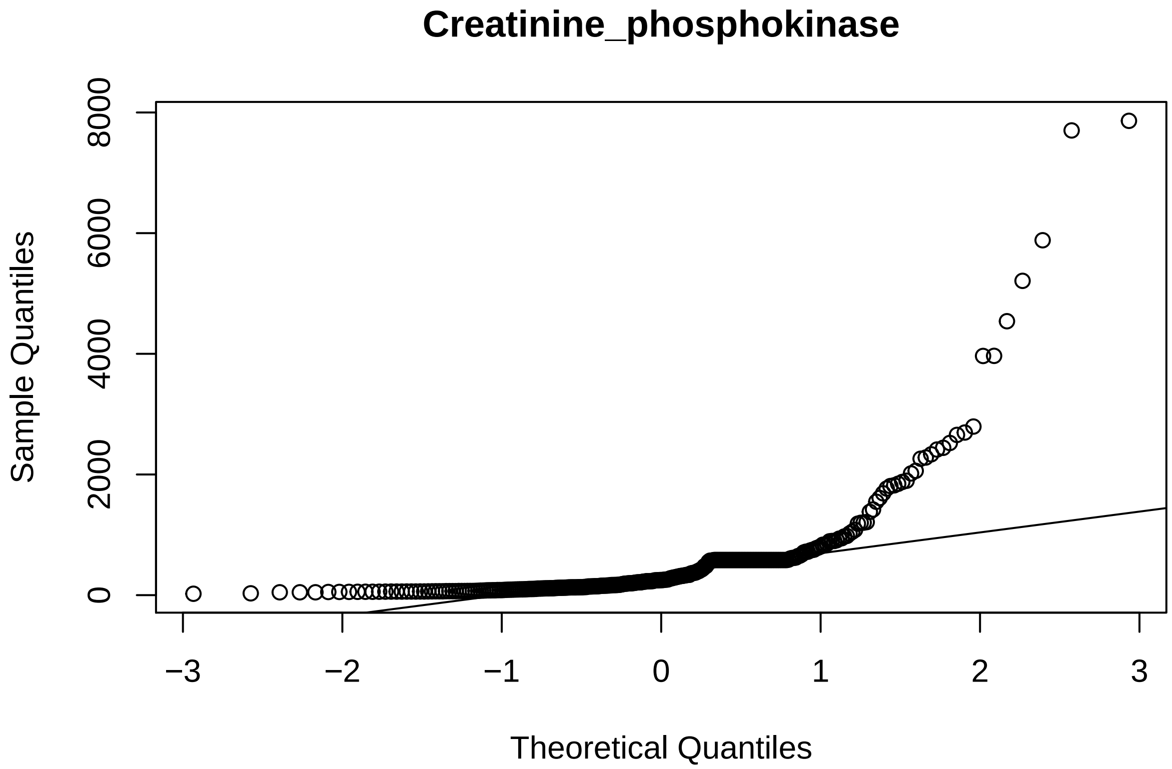
```
qqnorm(data[,"age"], main = "age")
qqline(data[,"age"])
```



Age looks normally distributed

Creatinine_phosphokinase

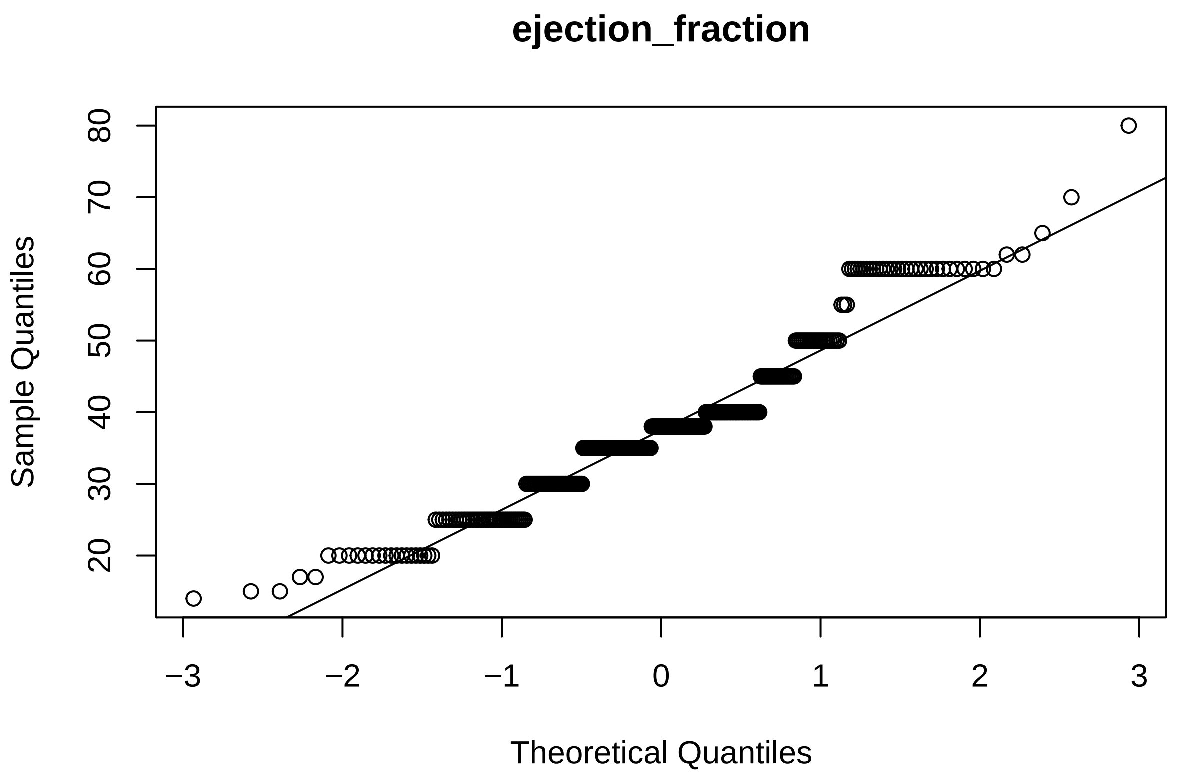
```
qqnorm(data[,"creatinine_phosphokinase"], main = "Creatinine_phosphokinase")
qqline(data[,"creatinine_phosphokinase"])
```



Creatinine_phosphokinase doesn't looks normal but skewed

ejection_fraction

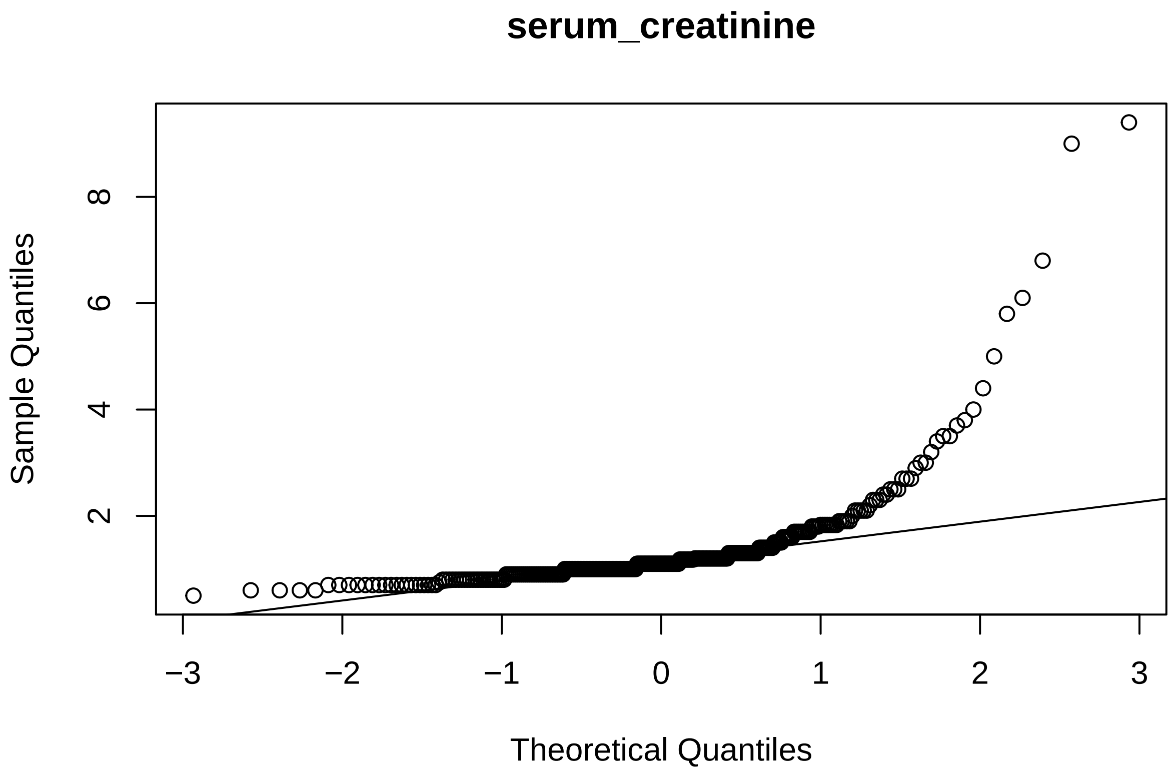
```
qqnorm(data[,"ejection_fraction"], main = "ejection_fraction")
qqline(data[,"ejection_fraction"])
```



ejection_fraction doeesn't look normal as well

serum_creatinine

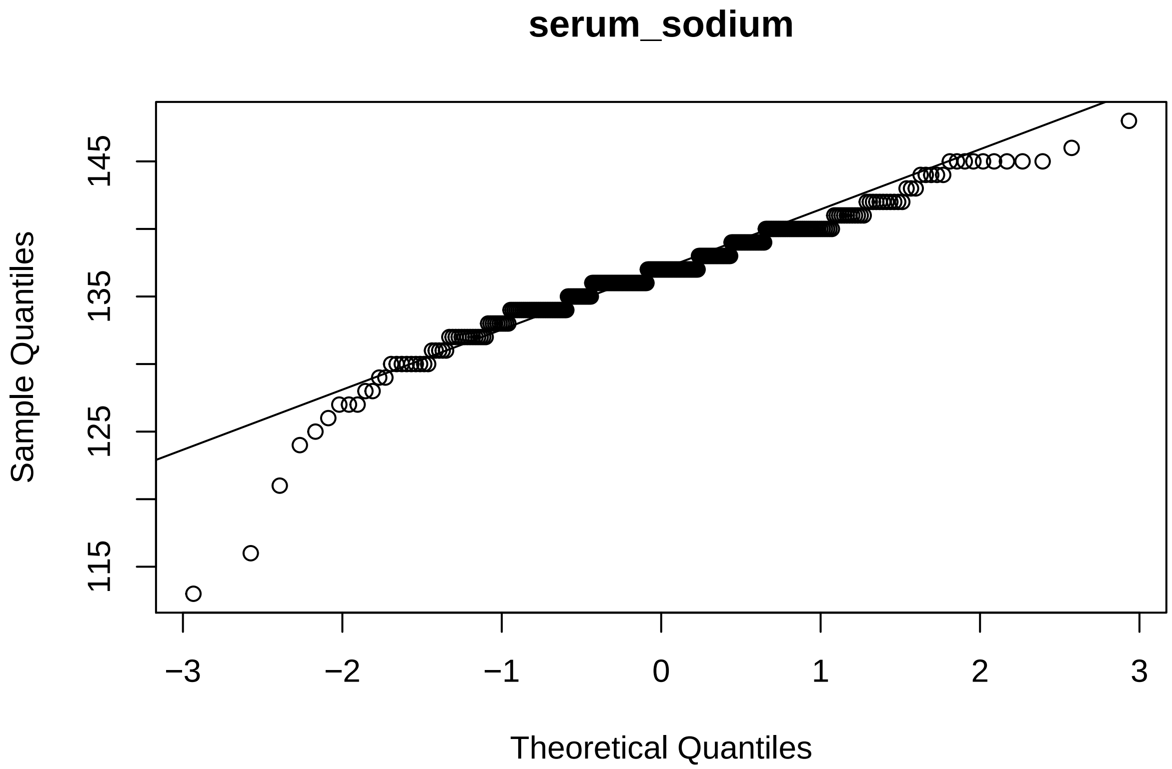
```
qqnorm(data[,"serum_creatinine"], main = "serum_creatinine")
qqline(data[,"serum_creatinine"])
```



serum_creatinine doesn't look normal but skewed

serum_sodium

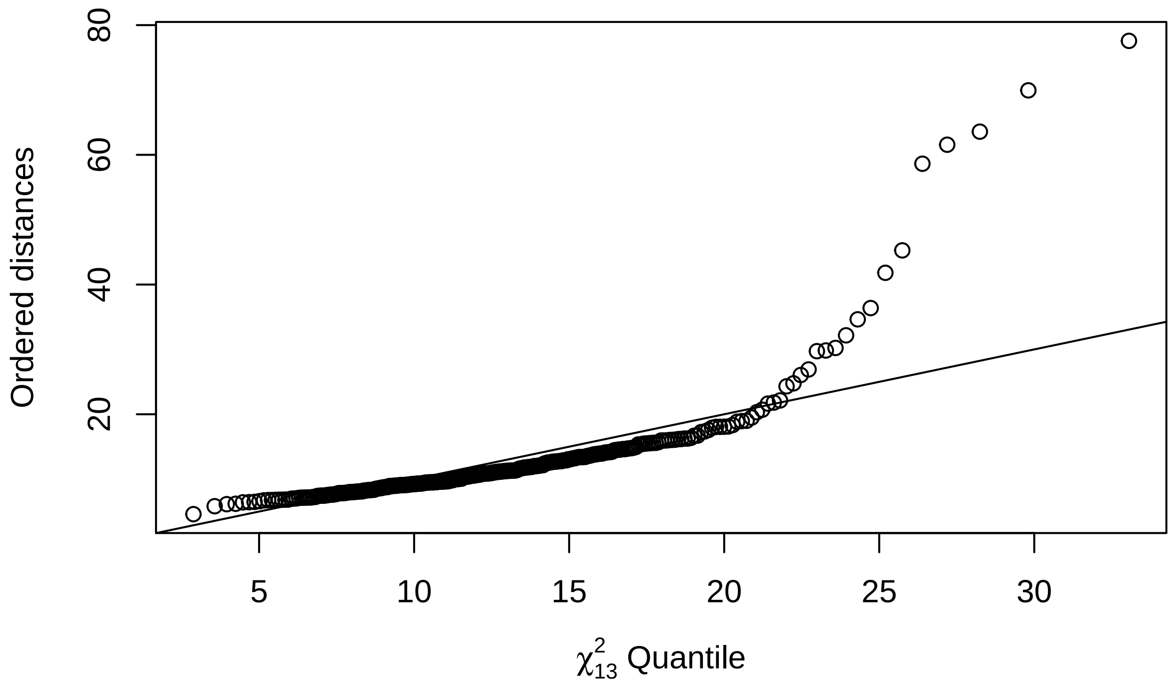
```
qqnorm(data[,"serum_sodium"], main = "serum_sodium")
qqline(data[,"serum_sodium"])
```



serum_sodium looks normal but is slightly skewed on lower end

Multi-variate normality

```
plot(qchisq((1:nrow(data) - 1/2) / nrow(data), df = 13), sort(d),
     xlab = expression(paste(chi[13]^2, " Quantile")),
     ylab = "Ordered distances")
abline(a = 0, b = 1)
```



While plotting for multivariate normality, we see that data is non normal and has some skewness towards positive side

t-tests for death events vs not for each variable

```
# age
with(data,t.test(age[DEATH_EVENT=="1"],age[DEATH_EVENT=="0"],var.equal=TRUE))
```

```
##
##  Two Sample t-test
##
## data:  age[DEATH_EVENT == "1"] and age[DEATH_EVENT == "0"]
## t = 4.5206, df = 297, p-value = 8.917e-06
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  3.643992 9.262758
## sample estimates:
## mean of x mean of y
##  65.21528  58.76191
```

```
# anaemia
with(data,t.test(anaemia[DEATH_EVENT=="1"],anaemia[DEATH_EVENT=="0"],var.equal=TRUE))
```

```
##
##  Two Sample t-test
##
## data:  anaemia[DEATH_EVENT == "1"] and anaemia[DEATH_EVENT == "0"]
## t = 1.1446, df = 297, p-value = 0.2533
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.05057162  0.19117096
## sample estimates:
```

```
## mean of x mean of y
## 0.4791667 0.4088670
```

```r
# creatinine_phosphokinase
with(data,t.test(creatinine_phosphokinase[DEATH_EVENT=="1"],
                 creatinine_phosphokinase[DEATH_EVENT=="0"],var.equal=TRUE))
```

```
##
##  Two Sample t-test
##
## data:  creatinine_phosphokinase[DEATH_EVENT == "1"] and creatinine_phosphokinase[DEATH_EVENT == "0"]
## t = 1.0832, df = 297, p-value = 0.2796
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -106.3109  366.5984
## sample estimates:
## mean of x mean of y
##  670.1979  540.0542
```

```r
# diabetes
with(data,t.test(diabetes[DEATH_EVENT=="1"],
                 diabetes[DEATH_EVENT=="0"],var.equal=TRUE))
```

```
##
##  Two Sample t-test
##
## data:  diabetes[DEATH_EVENT == "1"] and diabetes[DEATH_EVENT == "0"]
## t = -0.033483, df = 297, p-value = 0.9733
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.1226917  0.1185866
## sample estimates:
## mean of x mean of y
## 0.4166667 0.4187192
```

```r
# ejection_fraction
with(data,t.test(ejection_fraction[DEATH_EVENT=="1"],
                 ejection_fraction[DEATH_EVENT=="0"],var.equal=TRUE))
```

```
##
##  Two Sample t-test
##
## data:  ejection_fraction[DEATH_EVENT == "1"] and ejection_fraction[DEATH_EVENT == "0"]
## t = -4.8056, df = 297, p-value = 2.453e-06
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -9.580849 -4.013671
## sample estimates:
## mean of x mean of y
##  33.46875  40.26601
```

```r
# high_blood_pressure
with(data,t.test(high_blood_pressure[DEATH_EVENT=="1"],
                 high_blood_pressure[DEATH_EVENT=="0"],var.equal=TRUE))
```

```
##
##  Two Sample t-test
```

```
##
## data:  high_blood_pressure[DEATH_EVENT == "1"] and high_blood_pressure[DEATH_EVENT == "0"]
## t = 1.3718, df = 297, p-value = 0.1711
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.03525453  0.19750823
## sample estimates:
## mean of x mean of y
## 0.4062500 0.3251232
```

```
# platelets
with(data,t.test(platelets[DEATH_EVENT=="1"],
                 platelets[DEATH_EVENT=="0"],var.equal=TRUE))
```

```
##
##  Two Sample t-test
##
## data:  platelets[DEATH_EVENT == "1"] and platelets[DEATH_EVENT == "0"]
## t = -0.84787, df = 297, p-value = 0.3972
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -34129.06  13576.17
## sample estimates:
## mean of x mean of y
##  256381.0  266657.5
```

```
# serum_creatinine
with(data,t.test(serum_creatinine[DEATH_EVENT=="1"],
                 serum_creatinine[DEATH_EVENT=="0"],var.equal=TRUE))
```

```
##
##  Two Sample t-test
##
## data:  serum_creatinine[DEATH_EVENT == "1"] and serum_creatinine[DEATH_EVENT == "0"]
## t = 5.3065, df = 297, p-value = 2.19e-07
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  0.409539 0.892374
## sample estimates:
## mean of x mean of y
##  1.835833  1.184877
```

```
# serum_sodium
with(data,t.test(serum_sodium[DEATH_EVENT=="1"],
                 serum_sodium[DEATH_EVENT=="0"],var.equal=TRUE))
```

```
##
##  Two Sample t-test
##
## data:  serum_sodium[DEATH_EVENT == "1"] and serum_sodium[DEATH_EVENT == "0"]
## t = -3.4301, df = 297, p-value = 0.0006889
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -2.8984440 -0.7850535
## sample estimates:
## mean of x mean of y
##  135.3750  137.2167
```

```
# sex
with(data,t.test(sex[DEATH_EVENT=="1"],
                 sex[DEATH_EVENT=="0"],var.equal=TRUE))
```

```
##
##  Two Sample t-test
##
## data:  sex[DEATH_EVENT == "1"] and sex[DEATH_EVENT == "0"]
## t = -0.074388, df = 297, p-value = 0.9408
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.1211614  0.1123355
## sample estimates:
## mean of x mean of y
## 0.6458333 0.6502463
```

```
# smoking
with(data,t.test(smoking[DEATH_EVENT=="1"],
                 smoking[DEATH_EVENT=="0"],var.equal=TRUE))
```

```
##
##  Two Sample t-test
##
## data:  smoking[DEATH_EVENT == "1"] and smoking[DEATH_EVENT == "0"]
## t = -0.21756, df = 297, p-value = 0.8279
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.1268080  0.1015617
## sample estimates:
## mean of x mean of y
## 0.3125000 0.3251232
```

```
# time
with(data,t.test(time[DEATH_EVENT=="1"],
                 time[DEATH_EVENT=="0"],var.equal=TRUE))
```

```
##
##  Two Sample t-test
##
## data:  time[DEATH_EVENT == "1"] and time[DEATH_EVENT == "0"]
## t = -10.686, df = 297, p-value < 2.2e-16
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -103.5612  -71.3478
## sample estimates:
## mean of x mean of y
##  70.88542 158.33990
```

p-value is below 0.05 for -
1. age
2. serum_sodium
3. serum_creatinine
4. ejection_fraction
5. time
so we may conclude that death event does differ by these variables

t-test multi-variate

```
# Hotelling's T2 test. Comparing multivariate means between death events and non-death event
t2testdata <- hotelling.test(age + anaemia + creatinine_phosphokinase +
              diabetes + ejection_fraction + high_blood_pressure+
                platelets+serum_creatinine + serum_sodium +
                sex+smoking+time
                ~ DEATH_EVENT, data)

cat("T2 statistic =",t2testdata$stat[[1]],"\n")
```

```
## T2 statistic = 212.2908
```

```
print(t2testdata)
```

```
## Test stat:  17.036
## Numerator df:  12
## Denominator df:  286
## P-value:  0
```

The difference in means in the two groups taken together is significant as well

Homoskedasticity check

```
data$DEATH_EVENT <- factor(data$DEATH_EVENT)
leveneTest(age ~ DEATH_EVENT, data=data)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value   Pr(>F)
## group   1  7.1338 0.007981 **
##       297
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
leveneTest(anaemia ~ DEATH_EVENT, data=data)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value Pr(>F)
## group   1  1.3101 0.2533
##       297
```

```
leveneTest(creatinine_phosphokinase ~ DEATH_EVENT, data=data)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value Pr(>F)
## group   1  1.0303 0.3109
##       297
```

```
leveneTest(diabetes ~ DEATH_EVENT, data=data)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value Pr(>F)
## group   1  0.0011 0.9733
##       297
```

```
leveneTest(ejection_fraction ~ DEATH_EVENT, data=data)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value Pr(>F)
## group   1  3.7021 0.0553 .
##       297
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
leveneTest(high_blood_pressure ~ DEATH_EVENT, data=data)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value Pr(>F)
## group   1  1.8819 0.1711
##       297
```

```
leveneTest(platelets ~ DEATH_EVENT, data=data)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value Pr(>F)
## group   1   1.085 0.2984
##       297
```

```
leveneTest(serum_creatinine ~ DEATH_EVENT, data=data)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value    Pr(>F)
## group   1  16.242 7.087e-05 ***
##       297
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
leveneTest(serum_sodium ~ DEATH_EVENT, data=data)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value  Pr(>F)
## group   1   5.274 0.02234 *
##       297
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
leveneTest(sex ~ DEATH_EVENT, data=data)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value Pr(>F)
## group   1  0.0055 0.9408
##       297
```

```
leveneTest(smoking ~ DEATH_EVENT, data=data)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value Pr(>F)
## group   1  0.0473 0.8279
##       297
```

```
leveneTest(time ~ DEATH_EVENT, data=data)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value   Pr(>F)
## group   1  7.9512 0.005129 **
##       297
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

p-value is below 0.05 for -

1. age
2. serum_creatinine
3. ejection_fraction
4. time
5. serum_sodium

so we may conclude that variance between the two groups differ in them

One-way ANOVA tests: comparing univariate means

```r
aov_age <- aov(age ~ DEATH_EVENT, data)
summary(aov_age)
```

```
##              Df Sum Sq Mean Sq F value   Pr(>F)
## DEATH_EVENT   1   2714  2714.4   20.44 8.92e-06 ***
## Residuals   297  39449   132.8
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
aov_anaemia <- aov(anaemia ~ DEATH_EVENT, data)
summary(aov_anaemia)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## DEATH_EVENT   1   0.32  0.3221    1.31  0.253
## Residuals   297  73.02  0.2459
```

```r
aov_creatinine_phosphokinase <- aov(creatinine_phosphokinase ~ DEATH_EVENT, data)
summary(aov_creatinine_phosphokinase)
```

```
##              Df    Sum Sq Mean Sq F value Pr(>F)
## DEATH_EVENT   1   1103933 1103933   1.173   0.28
## Residuals   297 279450722  940912
```

```r
aov_diabetes <- aov(diabetes ~ DEATH_EVENT, data)
summary(aov_diabetes)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## DEATH_EVENT   1   0.00 0.00027   0.001  0.973
## Residuals   297  72.74 0.24492
```

```r
aov_ejection_fraction <- aov(ejection_fraction ~ DEATH_EVENT, data)
summary(aov_ejection_fraction)
```

```
##              Df Sum Sq Mean Sq F value   Pr(>F)
## DEATH_EVENT   1   3011  3011.4   23.09 2.45e-06 ***
## Residuals   297  38728   130.4
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
aov_high_blood_pressure <- aov(high_blood_pressure ~ DEATH_EVENT, data)
summary(aov_high_blood_pressure)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## DEATH_EVENT   1   0.43  0.4290   1.882  0.171
## Residuals   297  67.70  0.2279
```

```
aov_platelets <- aov(platelets ~ DEATH_EVENT, data)
summary(aov_platelets)
```

```
##              Df    Sum Sq   Mean Sq F value Pr(>F)
## DEATH_EVENT   1 6.883e+09 6.883e+09   0.719  0.397
## Residuals   297 2.844e+12 9.575e+09
```

```
aov_serum_creatinine <- aov(serum_creatinine ~ DEATH_EVENT, data)
summary(aov_serum_creatinine)
```

```
##              Df Sum Sq Mean Sq F value   Pr(>F)    
## DEATH_EVENT   1  27.62  27.618   28.16 2.19e-07 ***
## Residuals   297 291.30   0.981                     
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
aov_serum_sodium <- aov(serum_sodium ~ DEATH_EVENT, data)
summary(aov_serum_sodium)
```

```
##              Df Sum Sq Mean Sq F value   Pr(>F)    
## DEATH_EVENT   1    221  221.08   11.77 0.000689 ***
## Residuals   297   5581   18.79                     
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
aov_sex <- aov(sex ~ DEATH_EVENT, data)
summary(aov_sex)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## DEATH_EVENT   1   0.00 0.00127   0.006  0.941
## Residuals   297  68.13 0.22938
```

```
aov_smoking <- aov(smoking ~ DEATH_EVENT, data)
summary(aov_smoking)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## DEATH_EVENT   1   0.01 0.01039   0.047  0.828
## Residuals   297  65.17 0.21942
```

```
aov_time <- aov(time ~ DEATH_EVENT, data)
summary(aov_time)
```

```
##              Df  Sum Sq Mean Sq F value Pr(>F)    
## DEATH_EVENT   1  498494  498494   114.2 <2e-16 ***
## Residuals   297 1296647    4366                   
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

p-value is below 0.05 for -

1. age
2. serum_creatinine
3. ejection_fraction

4. time
5. serum_sodium

so we may conclude that means between the two groups differ in them

Comparing multivariate means (One-way MANOVA)

```
mnv <- manova(as.matrix(data[,-13])~ DEATH_EVENT, data)
summary(mnv)
```

```
##              Df  Pillai approx F num Df den Df    Pr(>F)    
## DEATH_EVENT   1 0.41684   17.036     12    286 < 2.2e-16 ***
## Residuals   297                                            
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

We observe from MANOVA that estimated effects may be unbalanced indicating that mean between groups may be different

Multi-collinearity check

```
# Let us also look at Multicollinearity check
# Earlier we saw the correlation plot
# We will check VIF for this purpose
# In classification, although linear regression isn't to be used
# For VIF, a rudimentary model lets us know the association
# between continuous and categorical variables

data <- read.csv('/Users/mac/Downloads/heart_failure_clinical_records_dataset.csv')
mod <-  lm( DEATH_EVENT ~ age+anaemia+creatinine_phosphokinase+
    diabetes+ejection_fraction+high_blood_pressure+platelets+
    serum_creatinine+serum_sodium+sex+smoking+time, data)
summary(mod)
```

```
## 
## Call:
## lm(formula = DEATH_EVENT ~ age + anaemia + creatinine_phosphokinase + 
##     diabetes + ejection_fraction + high_blood_pressure + platelets + 
##     serum_creatinine + serum_sodium + sex + smoking + time, data = data)
## 
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -0.80866 -0.28041 -0.04205  0.24742  0.96983 
## 
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)    
## (Intercept)               1.664e+00  6.954e-01   2.392  0.01738 *  
## age                       5.767e-03  1.867e-03   3.088  0.00221 ** 
## anaemia                  -2.766e-03  4.438e-02  -0.062  0.95035    
## creatinine_phosphokinase  3.427e-05  2.247e-05   1.525  0.12840    
## diabetes                  1.928e-02  4.410e-02   0.437  0.66236    
## ejection_fraction        -9.834e-03  1.844e-03  -5.333 1.96e-07 ***
## high_blood_pressure      -1.430e-02  4.565e-02  -0.313  0.75438
## platelets                -8.370e-08  2.208e-07  -0.379  0.70492
## serum_creatinine          8.527e-02  2.123e-02   4.017 7.54e-05 ***
## serum_sodium             -7.599e-03  5.024e-03  -1.513  0.13149
## sex                      -6.369e-02  5.108e-02  -1.247  0.21353
## smoking                  -5.733e-03  5.119e-02  -0.112  0.91091
## time                     -2.733e-03  2.903e-04  -9.415  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3646 on 286 degrees of freedom
## Multiple R-squared:  0.4168, Adjusted R-squared:  0.3924
## F-statistic: 17.04 on 12 and 286 DF,  p-value: < 2.2e-16
```

```
vif(mod)
```

```
##                      age                  anaemia creatinine_phosphokinase
##                 1.106067                 1.087163                 1.066014
##                 diabetes        ejection_fraction      high_blood_pressure
##                 1.064324                 1.067758                 1.068377
##                platelets         serum_creatinine             serum_sodium
##                 1.045809                 1.081241                 1.101927
##                      sex                  smoking                     time
##                 1.337716                 1.285049                 1.138009
```

We see that most VIF values are below 1.5
This incdicates absence of multi-collinearity in our data

This concludes our initial EDA for the data