

HEART FAILURE CLINICAL _PROJECT

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Required packages

HEART FAILURE CLINICAL PROJECT LINEAR REGRESSION

```
###* Loading Packages ###* -----
```

```
suppressPackageStartupMessages(library(tidyverse))
suppressPackageStartupMessages(library(caret))
suppressPackageStartupMessages(library(ggcorrplot))
suppressPackageStartupMessages(library(Metrics))
suppressPackageStartupMessages(library(corrplot))
suppressPackageStartupMessages(library(bannerCommenter))
suppressPackageStartupMessages(library(psych))
suppressPackageStartupMessages(library(WVPlots))
suppressPackageStartupMessages(library(PerformanceAnalytics))
suppressPackageStartupMessages(library(car))
suppressPackageStartupMessages(library(dplyr))
suppressPackageStartupMessages(library(ggplot2))
suppressPackageStartupMessages(library(outliers))
suppressPackageStartupMessages(library(broom))
suppressPackageStartupMessages(library(equationmatic))
```

```
##=====
## Reading in the data == ##=====
```

```
download.file("https://raw.githubusercontent.com/ABUALHUSSEIN/test/main/data/heart.csv",
  destfile = "heart.csv")
```

```
##source(destfile) ##ls() ##=====
```

```
setwd("C:/Users/WAFA/Desktop")
heart <- read.csv("heart.csv", header=TRUE)
View(heart)
```

```
txt <- "Explore the data set" #banner(txt, centre = TRUE, bandChar = "-") ##-----
## Explore the data set - ##-----
```

```
##----- - txt <- "Data contents" #banner(txt, centre = TRUE, bandChar = "=")
```

```
##=====
```

```
## Data contents == ##=====
```

```
Hmisc::contents(heart)
```

```
##
```

```
## Data frame:heart 299 observations and 13 variables    Maximum # NAs:0
```

```
##
##
##                               Storage
## anaemia                      integer
## diabetes                     integer
## sex                          integer
## smoking                      integer
## high_blood_pressure          integer
## DEATH_EVENT                  integer
## ejection_fraction            integer
## platelets                    double
## serum_creatinine             double
## serum_sodium                 integer
## time                         integer
## age                          double
## creatinine_phosphokinase     integer
```

```
glimpse(heart)
```

```
## Rows: 299
## Columns: 13
## $ anaemia          <int> 0, 0, 0, 1, 1, 1, 1, 1, 0, 1, 1, 0, 1, 1, 1, ~
## $ diabetes         <int> 0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, ~
## $ sex              <int> 1, 1, 1, 1, 0, 1, 1, 1, 0, 1, 1, 1, 1, 1, 0, ~
## $ smoking          <int> 0, 0, 1, 0, 0, 1, 0, 1, 0, 1, 1, 1, 0, 0, 0, ~
## $ high_blood_pressure <int> 1, 0, 0, 0, 0, 1, 0, 0, 0, 1, 1, 1, 0, 1, 1, ~
## $ DEATH_EVENT      <int> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, ~
## $ ejection_fraction <int> 20, 38, 20, 20, 20, 40, 15, 60, 65, 35, 38, 2~
## $ platelets        <dbl> 265000, 263358, 162000, 210000, 327000, 20400~
## $ serum_creatinine <dbl> 1.90, 1.10, 1.30, 1.90, 2.70, 2.10, 1.20, 1.1~
## $ serum_sodium     <int> 130, 136, 129, 137, 116, 132, 137, 131, 138, ~
## $ time             <int> 4, 6, 7, 7, 8, 8, 10, 10, 10, 10, 10, 10, 11, ~
## $ age              <dbl> 75, 55, 65, 50, 65, 90, 75, 60, 65, 80, 75, 6~
## $ creatinine_phosphokinase <int> 582, 7861, 146, 111, 160, 47, 246, 315, 157, ~
```

```
head(heart, 10)
```

```
##   anaemia diabetes sex smoking high_blood_pressure DEATH_EVENT
## 1      0      0    1      0                      1            1
## 2      0      0    1      0                      0            1
## 3      0      0    1      1                      0            1
## 4      1      0    1      0                      0            1
## 5      1      1    0      0                      0            1
## 6      1      0    1      1                      1            1
## 7      1      0    1      0                      0            1
## 8      1      1    1      1                      0            1
## 9      0      0    0      0                      0            1
## 10     1      0    1      1                      1            1
##   ejection_fraction platelets serum_creatinine serum_sodium time age
## 1                20    265000             1.9          130    4   75
## 2                38    263358             1.1          136    6   55
## 3                20    162000             1.3          129    7   65
## 4                20    210000             1.9          137    7   50
## 5                20    327000             2.7          116    8   65
```

```
## 6          40    204000          2.1          132    8  90
## 7          15    127000          1.2          137   10  75
## 8          60    454000          1.1          131   10  60
## 9          65    263358          1.5          138   10  65
## 10         35    388000          9.4          133   10  80
## creatinine_phosphokinase
## 1          582
## 2         7861
## 3          146
## 4          111
## 5          160
## 6           47
## 7          246
## 8          315
## 9          157
## 10         123
```

```
tail(heart)
```

```
## anaemia diabetes sex smoking high_blood_pressure DEATH_EVENT
## 294      1      1  1      1              0          0
## 295      0      1  1      1              1          0
## 296      0      0  0      0              0          0
## 297      0      1  0      0              0          0
## 298      0      0  1      1              0          0
## 299      0      0  1      1              0          0
## ejection_fraction platelets serum_creatinine serum_sodium time age
## 294          35    179000          0.9          136  270  63
## 295          38    155000          1.1          143  270  62
## 296          38    270000          1.2          139  271  55
## 297          60    742000          0.8          138  278  45
## 298          38    140000          1.4          140  280  45
## 299          45    395000          1.6          136  285  50
## creatinine_phosphokinase
## 294          103
## 295           61
## 296         1820
## 297         2060
## 298         2413
## 299          196
```

```
car::brief(heart)
```

```
## 299 x 13 data.frame (294 rows and 7 columns omitted)
## anaemia diabetes sex smoking . . . age creatinine_phosphokinase
##      [i]      [i] [i]      [i]      [n]      [i]
## 1      0      0  1      0      75      582
## 2      0      0  1      0      55     7861
## 3      0      0  1      1      65      146
## . . .
## 298      0      0  1      1      45     2413
## 299      0      0  1      1      50      196
```

```
str(heart)
```

```
## 'data.frame': 299 obs. of 13 variables:
```

```
## $ anaemia          : int  0 0 0 1 1 1 1 1 0 1 ...
## $ diabetes         : int  0 0 0 0 1 0 0 1 0 0 ...
## $ sex              : int  1 1 1 1 0 1 1 1 0 1 ...
## $ smoking          : int  0 0 1 0 0 1 0 1 0 1 ...
## $ high_blood_pressure : int  1 0 0 0 0 1 0 0 0 1 ...
## $ DEATH_EVENT      : int  1 1 1 1 1 1 1 1 1 1 ...
## $ ejection_fraction : int  20 38 20 20 20 40 15 60 65 35 ...
## $ 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 ...
## $ time              : int  4 6 7 7 8 8 10 10 10 10 ...
## $ age               : num  75 55 65 50 65 90 75 60 65 80 ...
## $ creatinine_phosphokinase : int  582 7861 146 111 160 47 246 315 157 123 ...
```

We have 299 obs. of 13 variables.

```
##=====
## Data Description == ##=====
```

age: age of the patient (years)

anaemia: decrease of red blood cells or hemoglobin (boolean)

high blood pressure: if the patient has hypertension (boolean) creatinine phosphokinase (CPK): level of the CPK enzyme in the blood (mcg/L)

diabetes: if the patient has diabetes (boolean)

ejection fraction: percentage of blood leaving the heart at each contraction (percentage)

platelets: platelets in the blood (kiloplatelets/mL)

** sex: woman or man (binary) ## serum creatinine: level of serum creatinine in the blood (mg/dL) ## serum sodium: level of serum sodium in the blood (mEq/L) ## smoking: if the patient smokes or not (boolean) ## time: follow-up period (days) ## death event**: if the patient deceased during the follow-up period (boolean)

```
##=====
## EDA: Exploratory Data Analysis == ##=====
```

```
heart_data <- heart[, 7:ncol(heart)]
```

Check the column names again,

```
colnames(heart_data)
```

```
## [1] "ejection_fraction"      "platelets"
## [3] "serum_creatinine"      "serum_sodium"
## [5] "time"                  "age"
## [7] "creatinine_phosphokinase"
```

```
#txt <- "Get the summary statistics of the variables" #banner(txt, centre = TRUE, bandChar = ")
##*****
of the variables ##*****
```

```
summary(heart_data)
```

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

```
Hmisc::describe(heart_data)
```

```
## heart_data
##
## 7 Variables      299 Observations
## -----
## ejection_fraction
##      n missing distinct      Info      Mean      Gmd      .05      .10
##    299      0        17    0.986    38.08    13.09      20      25
##    .25    .50    .75    .90    .95
##    30     38     45     60     60
##
## lowest : 14 15 17 20 25, highest: 60 62 65 70 80
##
## Value      14    15    17    20    25    30    35    38    40    45    50
## Frequency      1     2     2    18    36    34    49    40    37    20    21
## Proportion 0.003 0.007 0.007 0.060 0.120 0.114 0.164 0.134 0.124 0.067 0.070
##
## Value      55    60    62    65    70    80
## Frequency      3    31     2     1     1     1
## Proportion 0.010 0.104 0.007 0.003 0.003 0.003
## -----
## platelets
##      n missing distinct      Info      Mean      Gmd      .05      .10
##    299      0        176    0.999    263358    100936    131800    153000
##    .25    .50    .75    .90    .95
##   212500    262000    303500    374600    422500
##
## lowest : 25100 47000 51000 62000 70000, highest: 533000 543000 621000 742000 850000
## -----
## serum_creatinine
##      n missing distinct      Info      Mean      Gmd      .05      .10
##    299      0         40    0.991     1.394     0.783      0.7      0.8
##    .25    .50    .75    .90    .95
```

```
##      0.9      1.1      1.4      2.1      3.0
##
## lowest : 0.50 0.60 0.70 0.75 0.80, highest: 5.80 6.10 6.80 9.00 9.40
## -----
## serum_sodium
##      n missing distinct      Info      Mean      Gmd      .05      .10
##    299      0      27    0.991    136.6    4.683    130.0    132.0
##      .25      .50      .75      .90      .95
##    134.0    137.0    140.0    141.2    144.0
##
## lowest : 113 116 121 124 125, highest: 143 144 145 146 148
## -----
## time
##      n missing distinct      Info      Mean      Gmd      .05      .10
##    299      0      148      1    130.3    89.31    12.9    26.8
##      .25      .50      .75      .90      .95
##    73.0    115.0    203.0    244.0    250.0
##
## lowest : 4 6 7 8 10, highest: 270 271 278 280 285
## -----
## age
##      n missing distinct      Info      Mean      Gmd      .05      .10
##    299      0      47    0.996    60.83    13.44    42.9    45.0
##      .25      .50      .75      .90      .95
##    51.0    60.0    70.0    75.4    82.0
##
## lowest : 40 41 42 43 44, highest: 86 87 90 94 95
## -----
## creatinine_phosphokinase
##      n missing distinct      Info      Mean      Gmd      .05      .10
##    299      0      208    0.996    581.8    710.2    59.0    67.6
##      .25      .50      .75      .90      .95
##    116.5    250.0    582.0    1203.8    2263.0
##
## lowest : 23 30 47 52 53, highest: 4540 5209 5882 7702 7861
## -----
```

```
psych::describe(heart_data, skew = TRUE,
                 IQR = TRUE)
```

```
##      vars      n      mean      sd      median      trimmed
## ejection_fraction      1 299      38.08    11.83      38.0      37.43
## platelets              2 299 263358.03 97804.24 262000.0 256730.09
## serum_creatinine       3 299      1.39      1.03      1.1      1.19
## serum_sodium           4 299     136.63      4.41    137.0     136.82
## time                   5 299     130.26     77.61    115.0     129.28
## age                    6 299      60.83     11.89     60.0     60.22
## creatinine_phosphokinase 7 299     581.84    970.29    250.0     365.49
##      mad      min      max      range      skew      kurtosis
## ejection_fraction      11.86     14.0     80.0     66.0     0.55      0.00
## platelets              65234.40 25100.0 850000.0 824900.0     1.45      6.03
## serum_creatinine        0.30      0.5      9.4      8.9     4.41     25.19
## serum_sodium            4.45    113.0    148.0     35.0    -1.04      3.98
## time                   105.26      4.0    285.0    281.0     0.13     -1.22
## age                     14.83     40.0     95.0     55.0     0.42     -0.22
```

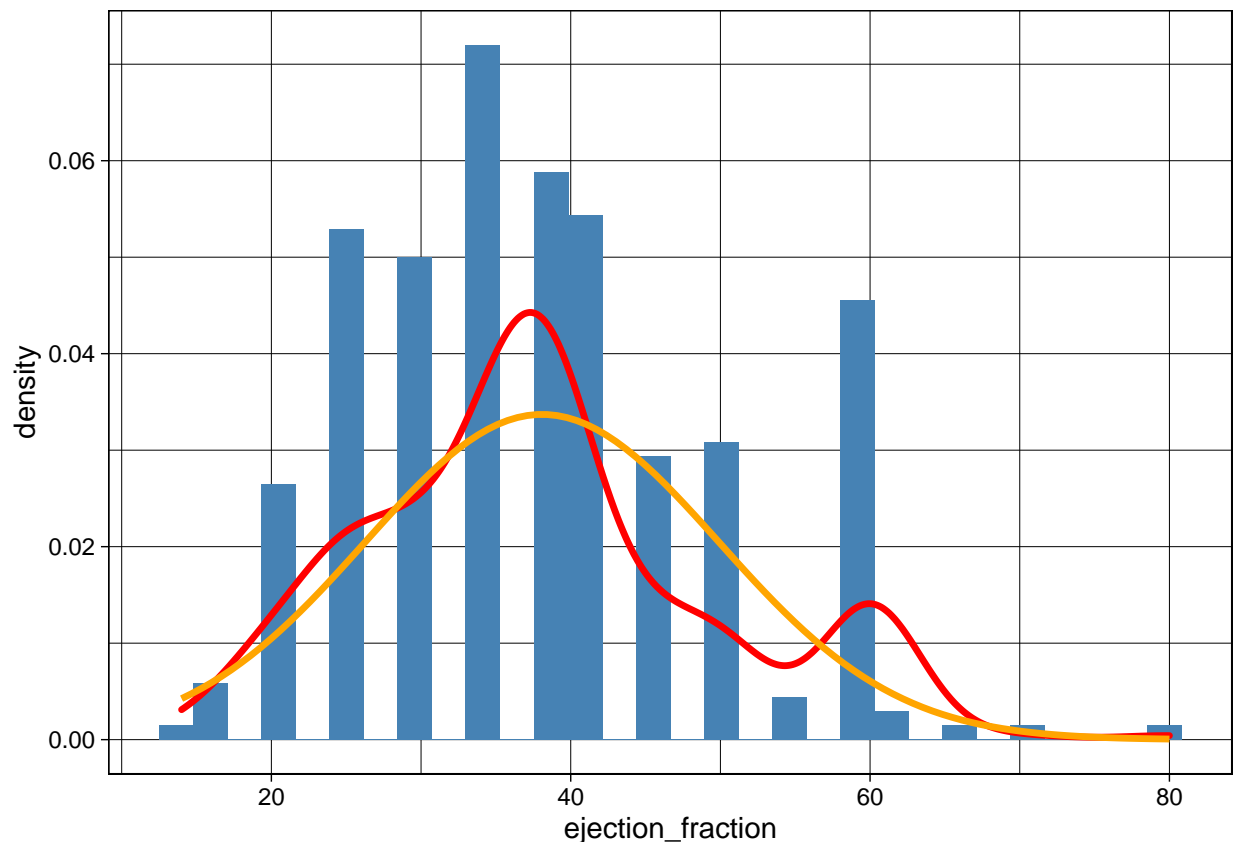
```
## creatinine_phosphokinase 269.83 23.0 7861.0 7838.0 4.42 24.53
##                          se      IQR
## ejection_fraction      0.68 15.0
## platelets              5656.17 91000.0
## serum_creatinine       0.06 0.5
## serum_sodium           0.26 6.0
## time                   4.49 130.0
## age                    0.69 19.0
## creatinine_phosphokinase 56.11 465.5

#txt <- "The Dependent Variables in this study is ejection_fraction" #banner(txt, centre = TRUE, bandChar
= ":")

##:##### ## The Dependent Variables in this study is ejection_fraction
:: ##:#####
```

We are going to explore the distribution of this variable

```
ggplot(heart_data, aes(x = ejection_fraction)) +
  geom_histogram(aes(y = ..density..),
    fill = "steelblue") +
  geom_density(color = "red", lwd = 1.2) +
  stat_function(fun = dnorm, args = list(mean = mean(heart_data$ejection_fraction),
    sd = sd(heart_data$ejection_fraction)),
    color = "orange", lwd = 1.2) +
  theme_linedraw()
```

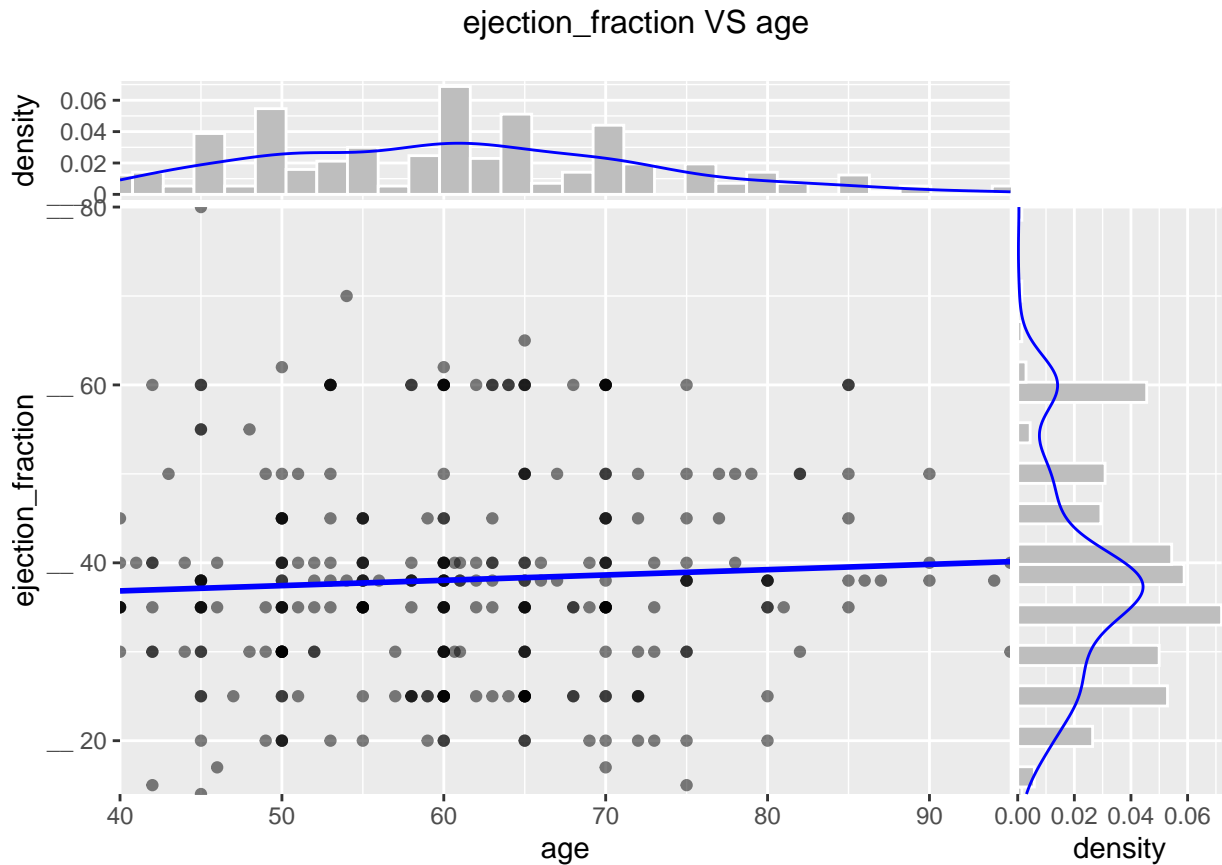


Joint Graphs

```
library(WVPlots)
```

```
#ejection_fraction VS age
```

```
ScatterHist(heart_data, title = "ejection_fraction VS age",  
            xvar = "age", yvar = "ejection_fraction",  
            smoothmethod = "lm")
```



There is a very weak linear relationship between the variables (ejection_fraction VS age)

```
#age VS serum_creatinine
```

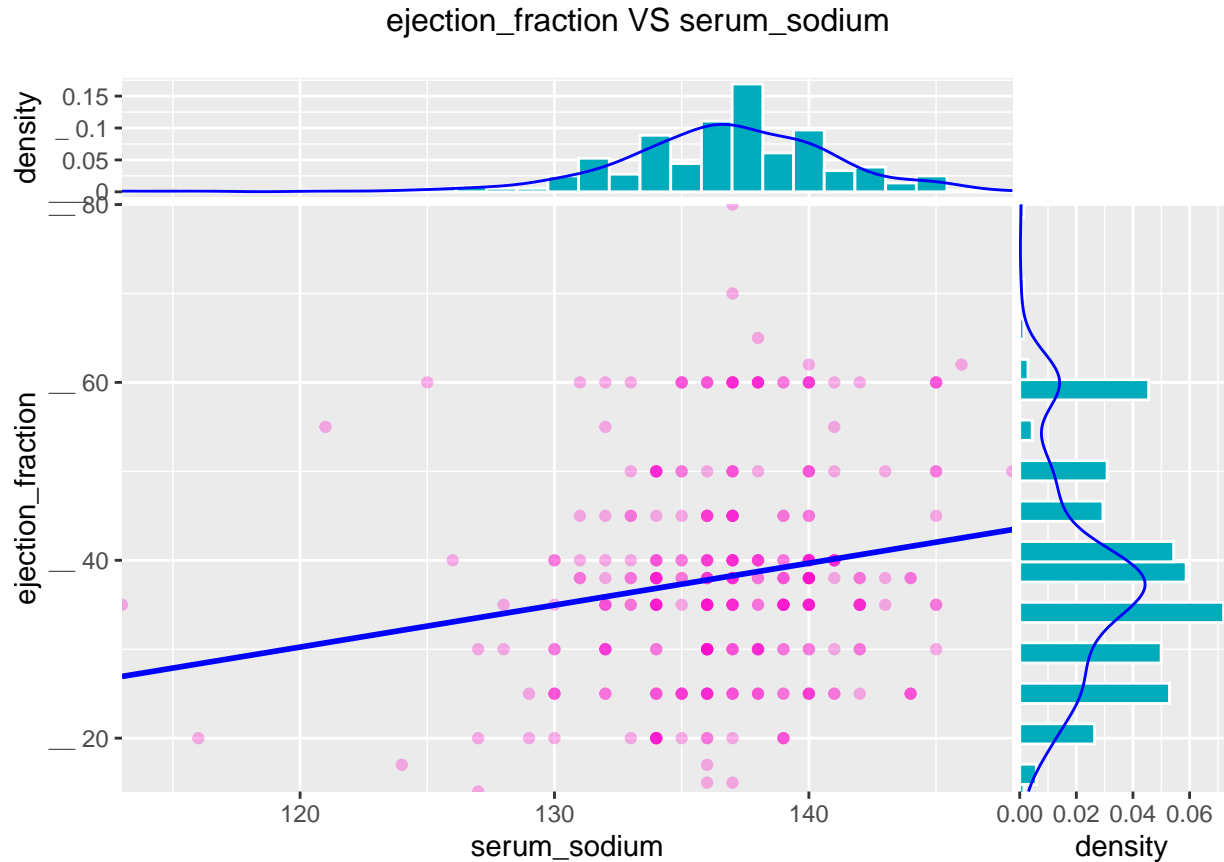
```
ScatterHist(heart_data, title = "age VS serum_creatinine",  
            xvar = "serum_creatinine", yvar = "age",  
            smoothmethod = "lm")
```




There is a positive linear relationship between the variables(age & serum_creatinine)

ejection_fraction VS serum_sodium

```
ScatterHist(heart_data, title = "ejection_fraction VS serum_sodium",
            xvar = "serum_sodium", yvar = "ejection_fraction",
            smoothmethod = "lm", hist_color = "#00ACBB",
            point_alpha = 0.3,
            point_color = "#FF00CC")
```



There is a positive linear relationship between the variables (ejection_fraction & serum_sodium)

```
## ***** ## Study the correlation
## *****
```

```
psych::lowerCor(x = heart_data)
```

```
##          ejct_pltlt srm_c srm_s time  age  crtn_
## ejection_fraction      1.00
## platelets              0.07 1.00
## serum_creatinine      -0.01 -0.04 1.00
## serum_sodium          0.18 0.06 -0.19 1.00
## time                  0.04 0.01 -0.15 0.09 1.00
## age                   0.06 -0.05 0.16 -0.05 -0.22 1.00
## creatinine_phosphokinase -0.04 0.02 -0.02 0.06 -0.01 -0.08 1.00
```

```
psych::corr.test(heart_data)$p
```

```
##          ejection_fraction platelets serum_creatinine
## ejection_fraction      0.00000000 1.0000000      1.00000000
## platelets              0.213329933 0.0000000      1.00000000
## serum_creatinine       0.845686017 0.4778909      0.00000000
## serum_sodium           0.002267684 0.2842728      0.001017081
## time                   0.472229204 0.8563315      0.009720948
## age                    0.300304089 0.3669939      0.005803433
```

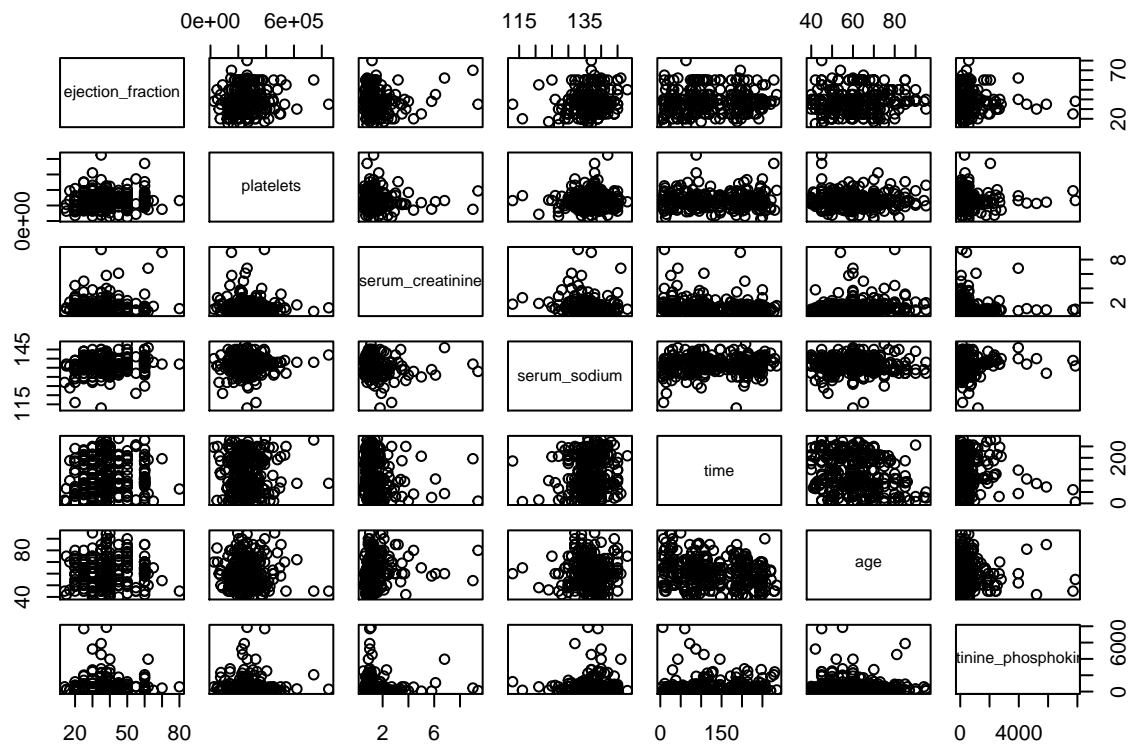
```
## creatinine_phosphokinase      0.447623299 0.6735340      0.777514366
##                               serum_sodium      time      age
## ejection_fraction            0.04308600 1.000000e+00 1.0000000000
## platelets                    1.00000000 1.000000e+00 1.0000000000
## serum_creatinine             0.02034161 1.652561e-01 0.104461793
## serum_sodium                 0.00000000 1.000000e+00 1.0000000000
## time                         0.13053379 0.000000e+00 0.001953672
## age                          0.42841134 9.303199e-05 0.0000000000
## creatinine_phosphokinase     0.30474247 8.721501e-01 0.159381379
##                               creatinine_phosphokinase
## ejection_fraction                                1
## platelets                                         1
## serum_creatinine                                1
## serum_sodium                                    1
## time                                              1
## age                                               1
## creatinine_phosphokinase                        0
```

Plotting the ScatterPlotMatrix

First look at the help, and the arguments

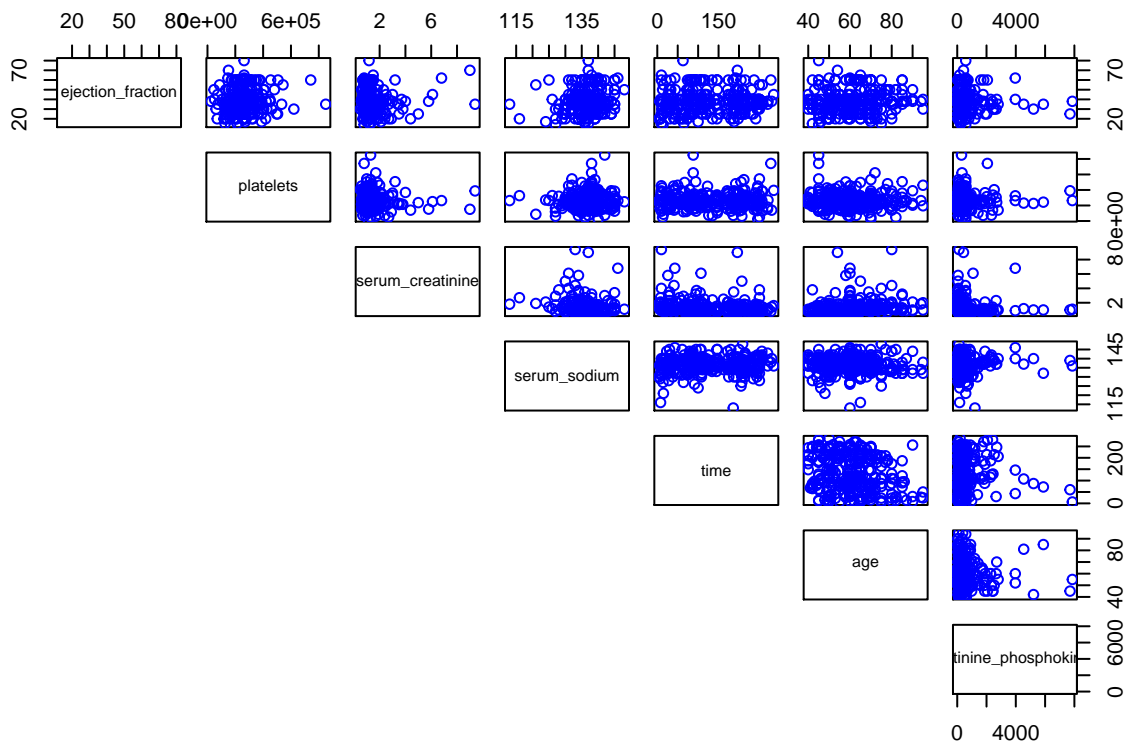
I am going to tweak the knobs a little

```
pairs(heart_data)
```



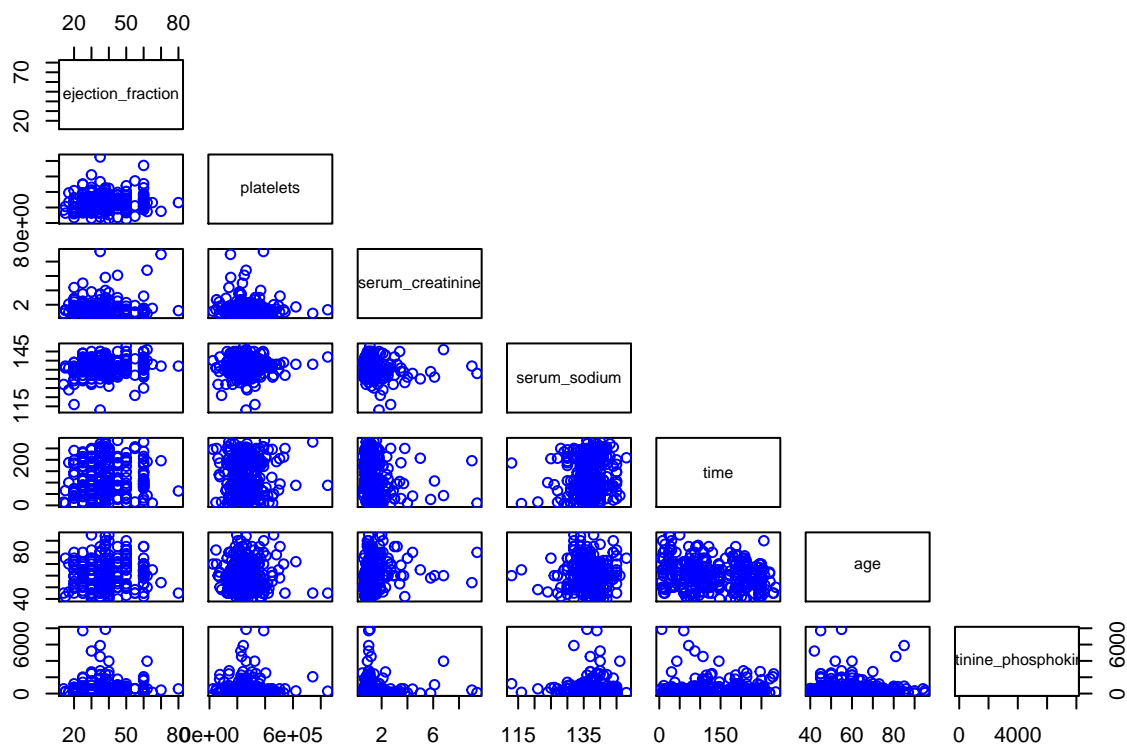
#change the color and get help matrix

```
pairs(heart_data, lower.panel = NULL, col= "blue")
```



Or if you want only the lower part matrix

```
pairs(heart_data, upper.panel = NULL, col= "blue")
```

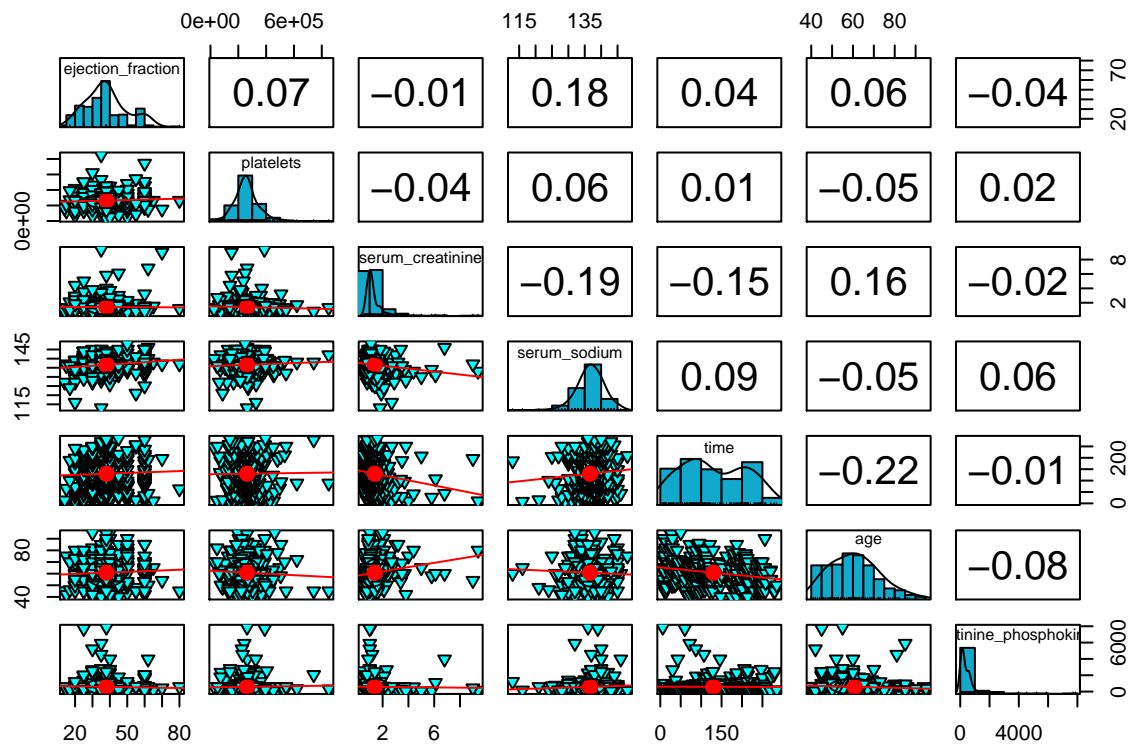


Check the documentation for more information

```
?pairs
```

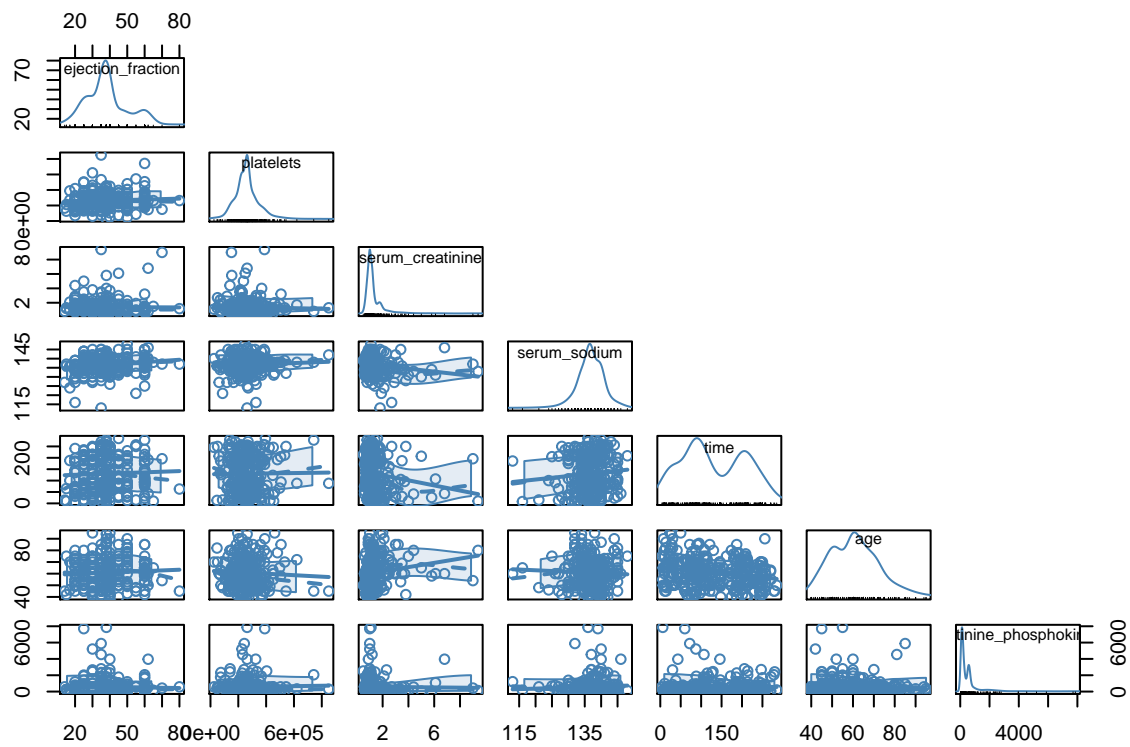
Scatter Matrix with psych package

```
library(psych)
pairs.panels(heart_data,
  method = "pearson", # Correlation method
  hist.col = "#11AACC",
  density = TRUE,
  cex.cor = 1.3,
  col = "red",
  lm = TRUE,
  pch = 25, # point character
  bg = "cyan") # background
```



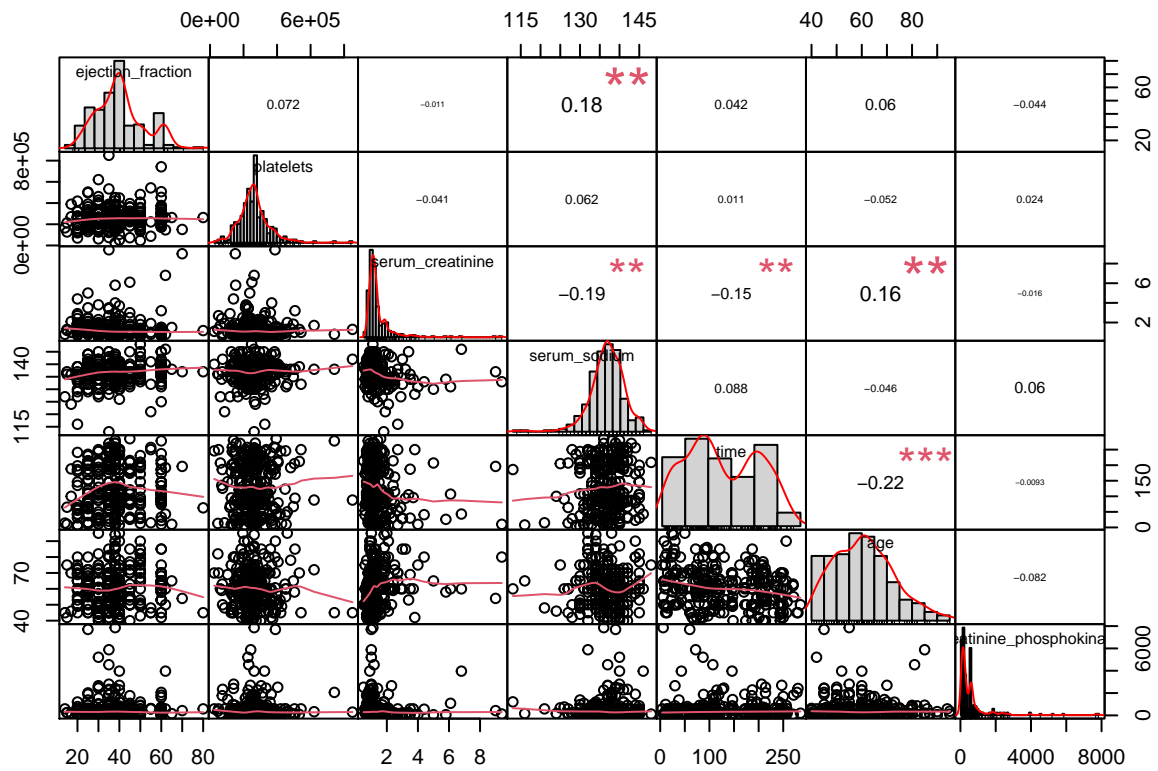
Scatter Matrix with car package

```
car::scatterplotMatrix(heart_data,
  col = "steelblue",
  pch = 21,
  upper.panel = NULL)
```



Lastly

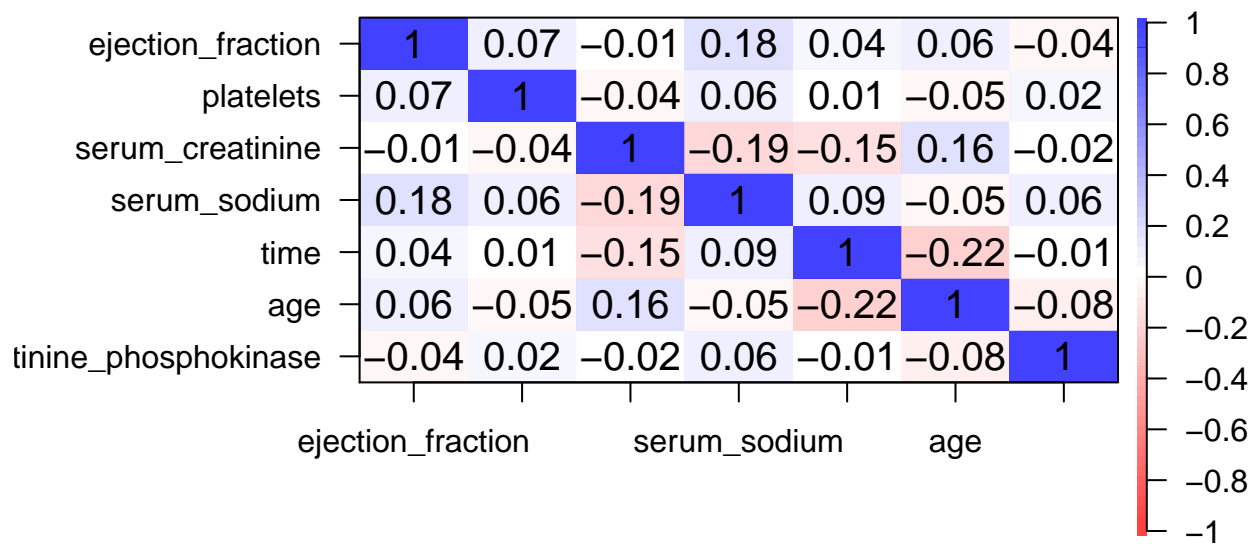
```
library(PerformanceAnalytics)
chart.Correlation(heart_data,
  histogram=TRUE,
  pch=19,
  col = "blue")
```

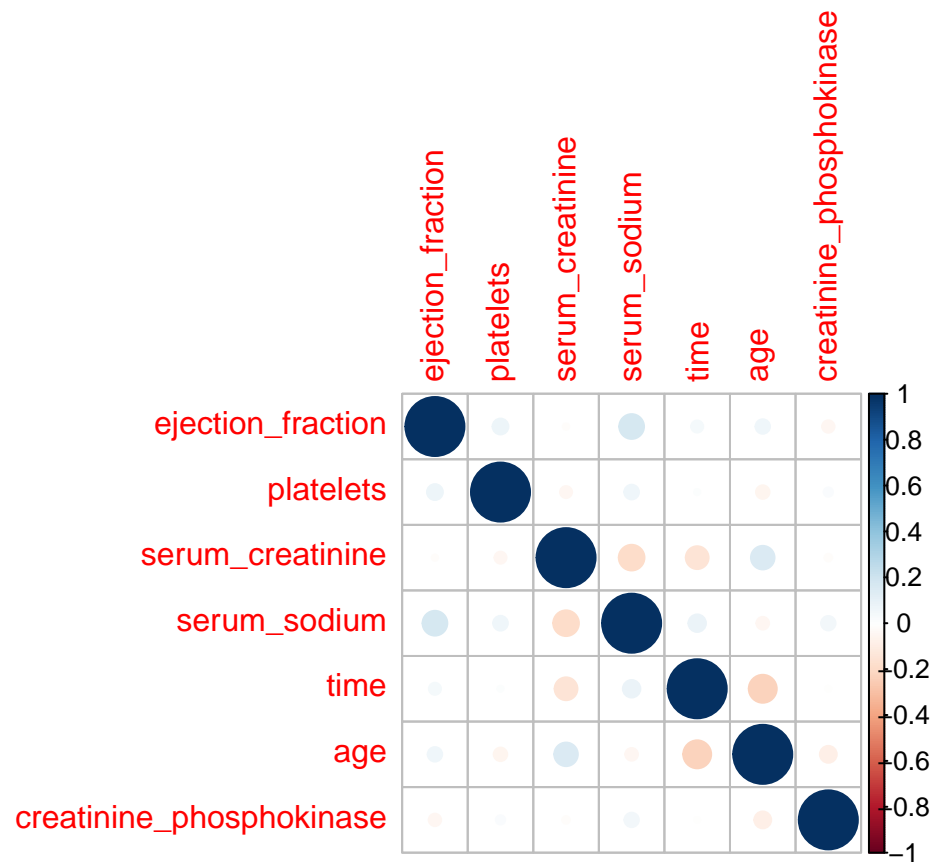
```
## ***** ## correlation plot matrices
## *****
```

```
correl <- cor(heart_data)
```

```
psych::cor.plot(correl)
```

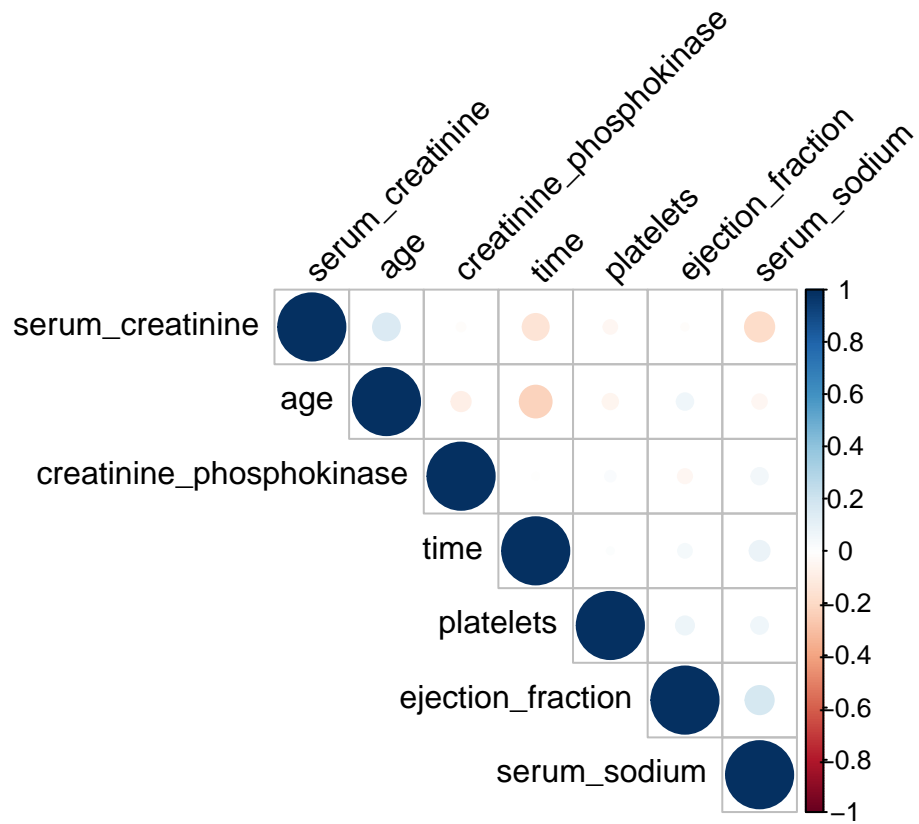


```
corrplot::corrplot(correl)
```



Tweak the knobs

```
corrplot(correl, type = "upper",
         order = "hclust",
         tl.col = "black",
         tl.srt = 45)
```

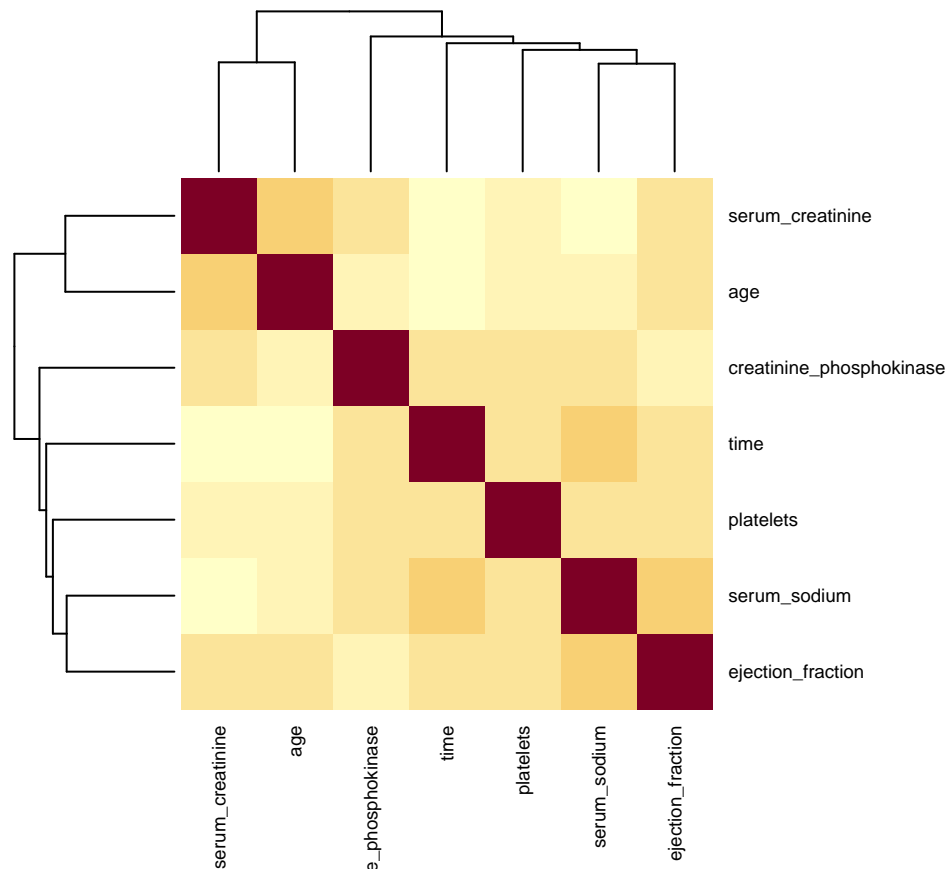


check

```
?corrplot
```

Heatmap

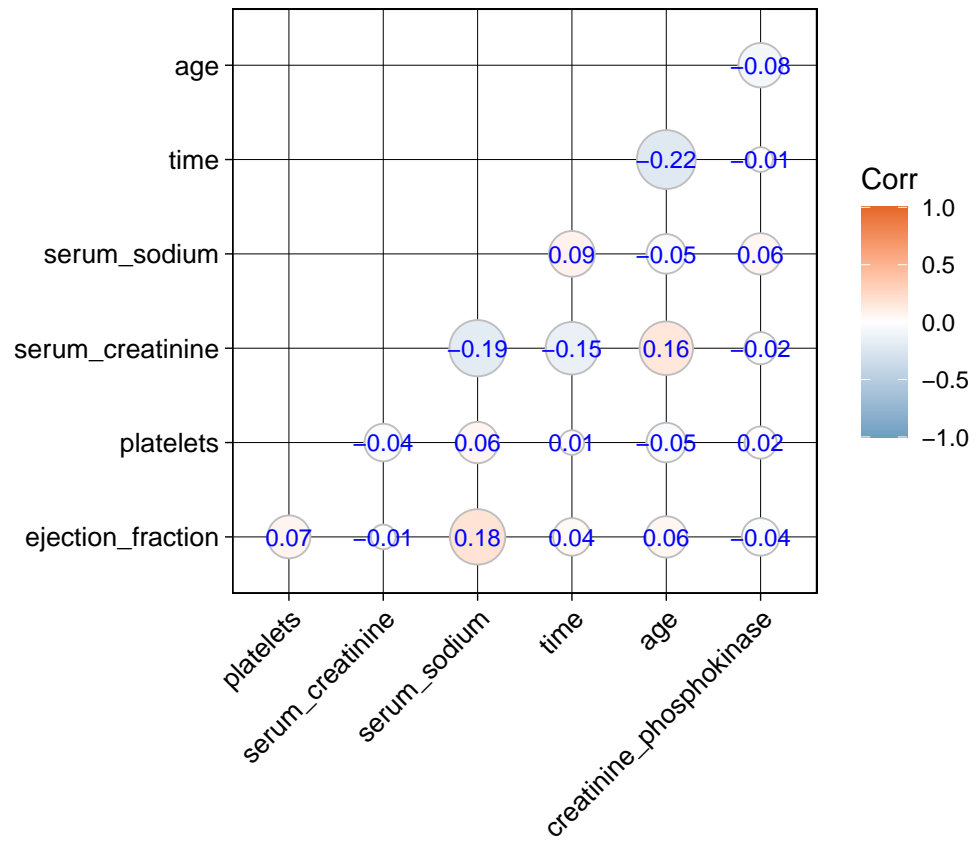
```
heatmap(correl, symm = TRUE,
        cexRow = 0.7,
        cexCol = 0.7)
```



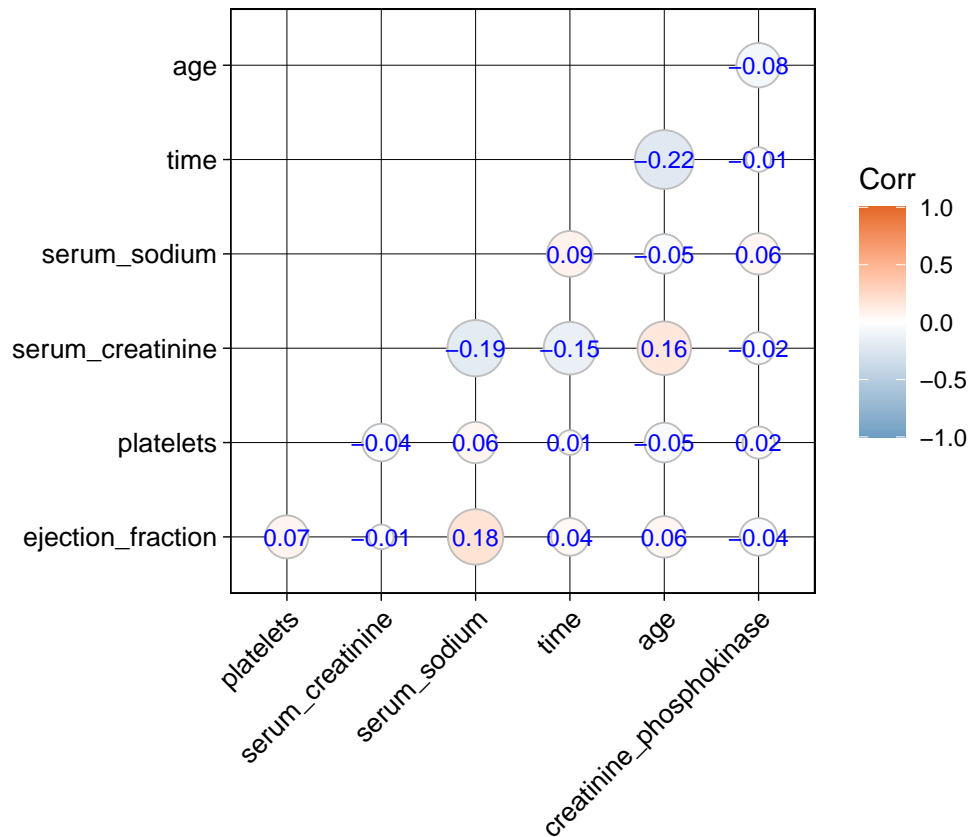
ggcorrplot

```
p <- ggcorrplot::ggcorrplot(correl,
  method = "circle",
  type = "lower",
  ggtheme = ggplot2::theme_linedraw,
  lab_col = "blue",
  lab_size = 3,
  tl.cex = 10,
  lab = TRUE,
  pch.cex = 10,
  colors = c("#6D9EC1", "white", "#E46726"))
```

p



```
p + guides(scale = "none")
```



----- ## Fitting Multiple Regression - ## -----

```
model <- lm(ejection_fraction ~ serum_sodium + age + platelets + serum_creatinine +
            time + creatinine_phosphokinase , data = heart_data)
```

```
model
```

```
##
```

```
## Call:
```

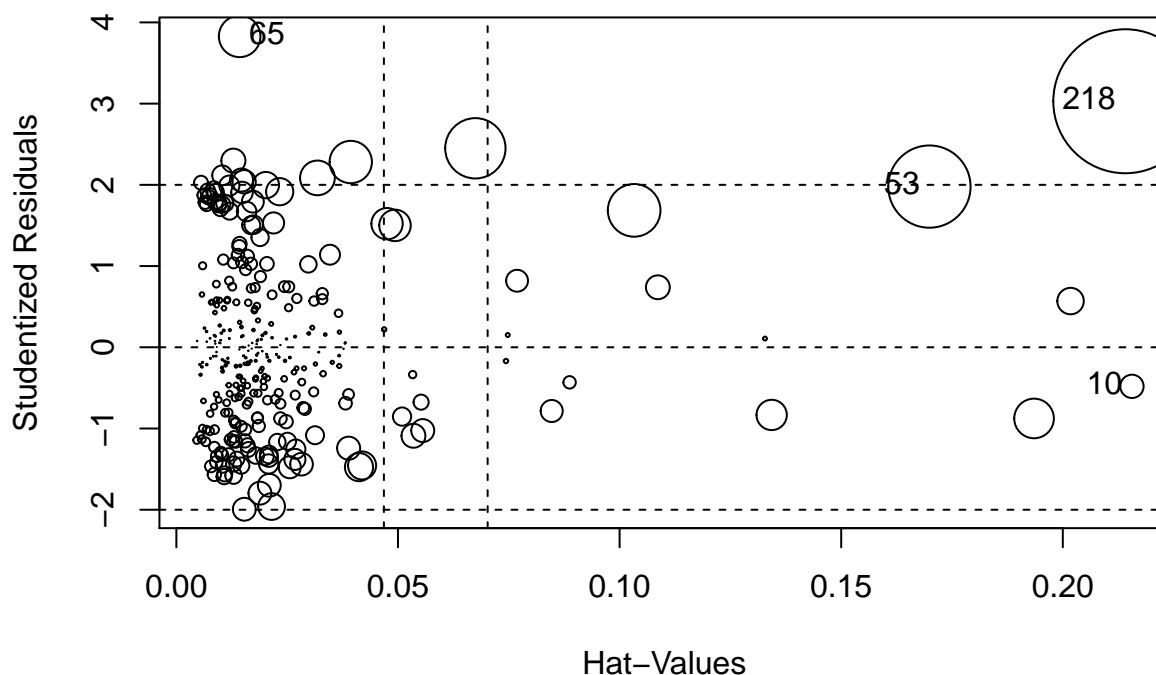
```
## lm(formula = ejection_fraction ~ serum_sodium + age + platelets +
##     serum_creatinine + time + creatinine_phosphokinase, data = heart_data)
```

```
##
```

```
## Coefficients:
```

```
##      (Intercept)      serum_sodium      age
##      -3.456e+01      4.770e-01      7.430e-02
##      platelets      serum_creatinine      time
##      8.055e-06      2.176e-01      6.794e-03
## creatinine_phosphokinase
##      -6.035e-04
```

```
influencePlot(model)
```



```
##      StudRes      Hat      CookD
## 10  -0.4808995 0.21560118 0.009104784
## 53   1.9785962 0.16990708 0.113341065
## 65   3.8282196 0.01427503 0.028964627
## 218  3.0292263 0.21410385 0.347401188
```

```
##-----## Checking lm objects - ##-----
# Show the components of lm object
```

```
str(model)
```

```
## List of 12
## $ coefficients : Named num [1:7] -3.46e+01 4.77e-01 7.43e-02 8.05e-06 2.18e-01 ...
## ..- attr(*, "names")= chr [1:7] "(Intercept)" "serum_sodium" "age" "platelets" ...
## $ residuals : Named num [1:299] -15.24 5.95 -13.34 -16.58 -8.78 ...
## ..- attr(*, "names")= chr [1:299] "1" "2" "3" "4" ...
## $ effects : Named num [1:299] -658.53 35.94 -13.94 13.25 -2.76 ...
## ..- attr(*, "names")= chr [1:299] "(Intercept)" "serum_sodium" "age" "platelets" ...
## $ rank : int 7
## $ fitted.values: Named num [1:299] 35.2 32.1 33.3 36.6 28.8 ...
## ..- attr(*, "names")= chr [1:299] "1" "2" "3" "4" ...
## $ assign : int [1:7] 0 1 2 3 4 5 6
## $ qr :List of 5
## ..$ qr : num [1:299, 1:7] -17.2916 0.0578 0.0578 0.0578 0.0578 ...
## ..- attr(*, "dimnames")=List of 2
## ... ..$ : chr [1:299] "1" "2" "3" "4" ...
## ... ..$ : chr [1:7] "(Intercept)" "serum_sodium" "age" "platelets" ...
```



```
## ..- attr(*, "assign")= int [1:7] 0 1 2 3 4 5 6
## ..$ qraux: num [1:7] 1.06 1 1.02 1.04 1.03 ...
## ..$ pivot: int [1:7] 1 2 3 4 5 6 7
## ..$ tol : num 1e-07
## ..$ rank : int 7
## ..- attr(*, "class")= chr "qr"
## $ df.residual : int 292
## $ xlevels : Named list()
## $ call : language lm(formula = ejection_fraction ~ serum_sodium + age + platelets + serum_creatinine, data = data.frame(...))
## $ terms :Classes 'terms', 'formula' language ejection_fraction ~ serum_sodium + age + platelets + serum_creatinine
## ..- attr(*, "variables")= language list(ejection_fraction, serum_sodium, age, platelets, serum_creatinine)
## ..- attr(*, "factors")= int [1:7, 1:6] 0 1 0 0 0 0 0 0 1 ...
## ..- attr(*, "dimnames")=List of 2
## ..$ : chr [1:7] "ejection_fraction" "serum_sodium" "age" "platelets" "serum_creatinine" ...
## ..$ : chr [1:6] "serum_sodium" "age" "platelets" "serum_creatinine" ...
## ..- attr(*, "term.labels")= chr [1:6] "serum_sodium" "age" "platelets" "serum_creatinine" ...
## ..- attr(*, "order")= int [1:6] 1 1 1 1 1 1
## ..- attr(*, "intercept")= int 1
## ..- attr(*, "response")= int 1
## ..- attr(*, ".Environment")=<environment: R_GlobalEnv>
## ..- attr(*, "predvars")= language list(ejection_fraction, serum_sodium, age, platelets, serum_creatinine)
## ..- attr(*, "dataClasses")= Named chr [1:7] "numeric" "numeric" "numeric" "numeric" "numeric" "numeric" "numeric"
## ..- attr(*, "names")= chr [1:7] "ejection_fraction" "serum_sodium" "age" "platelets" "serum_creatinine" ...
## $ model :'data.frame': 299 obs. of 7 variables:
## ..$ ejection_fraction : int [1:299] 20 38 20 20 20 40 15 60 65 35 ...
## ..$ serum_sodium : int [1:299] 130 136 129 137 116 132 137 131 138 133 ...
## ..$ age : num [1:299] 75 55 65 50 65 90 75 60 65 80 ...
## ..$ platelets : num [1:299] 265000 263358 162000 210000 327000 ...
## ..$ serum_creatinine : num [1:299] 1.9 1.1 1.3 1.9 2.7 2.1 1.2 1.1 1.5 9.4 ...
## ..$ time : int [1:299] 4 6 7 7 8 8 10 10 10 10 ...
## ..$ creatinine_phosphokinase: int [1:299] 582 7861 146 111 160 47 246 315 157 123 ...
## ..- attr(*, "terms")=Classes 'terms', 'formula' language ejection_fraction ~ serum_sodium + age + platelets + serum_creatinine
## ..- attr(*, "variables")= language list(ejection_fraction, serum_sodium, age, platelets, serum_creatinine)
## ..- attr(*, "factors")= int [1:7, 1:6] 0 1 0 0 0 0 0 0 1 ...
## ..- attr(*, "dimnames")=List of 2
## ..$ : chr [1:7] "ejection_fraction" "serum_sodium" "age" "platelets" "serum_creatinine" ...
## ..$ : chr [1:6] "serum_sodium" "age" "platelets" "serum_creatinine" ...
## ..- attr(*, "term.labels")= chr [1:6] "serum_sodium" "age" "platelets" "serum_creatinine" ...
## ..- attr(*, "order")= int [1:6] 1 1 1 1 1 1
## ..- attr(*, "intercept")= int 1
## ..- attr(*, "response")= int 1
## ..- attr(*, ".Environment")=<environment: R_GlobalEnv>
## ..- attr(*, "predvars")= language list(ejection_fraction, serum_sodium, age, platelets, serum_creatinine)
## ..- attr(*, "dataClasses")= Named chr [1:7] "numeric" "numeric" "numeric" "numeric" "numeric" "numeric" "numeric"
## ..- attr(*, "names")= chr [1:7] "ejection_fraction" "serum_sodium" "age" "platelets" "serum_creatinine" ...
## - attr(*, "class")= chr "lm"
```

```
class(model)
```

```
## [1] "lm"
```

```
typeof(model)
```

```
## [1] "list"
```

```
length(model)
```

```
## [1] 12
```

```
names(model)
```

```
## [1] "coefficients" "residuals"      "effects"      "rank"
## [5] "fitted.values" "assign"          "qr"           "df.residual"
## [9] "xlevels"      "call"           "terms"        "model"
```

Summary Function

```
summary(model)
```

```
##
## Call:
## lm(formula = ejection_fraction ~ serum_sodium + age + platelets +
##      serum_creatinine + time + creatinine_phosphokinase, data = heart_data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -23.008  -7.838  -1.393   6.397  43.418
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -3.456e+01  2.191e+01  -1.578   0.1157
## serum_sodium    4.770e-01  1.570e-01   3.037   0.0026 **
## age             7.430e-02  5.918e-02   1.256   0.2103
## platelets       8.055e-06  6.947e-06   1.159   0.2472
## serum_creatinine 2.176e-01  6.784e-01   0.321   0.7486
## time           6.794e-03  9.035e-03   0.752   0.4527
## creatinine_phosphokinase -6.035e-04  7.017e-04  -0.860   0.3905
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 11.69 on 292 degrees of freedom
## Multiple R-squared:  0.0444, Adjusted R-squared:  0.02476
## F-statistic: 2.261 on 6 and 292 DF,  p-value: 0.03778
```

Coefficients Function

```
model$coefficients
```

```
##              (Intercept)          serum_sodium              age
##      -3.456302e+01          4.769850e-01          7.429994e-02
##              platelets      serum_creatinine              time
##      8.054673e-06          2.176059e-01          6.793735e-03
## creatinine_phosphokinase
##      -6.034873e-04
```

Fitted function

```
model$fitted
```

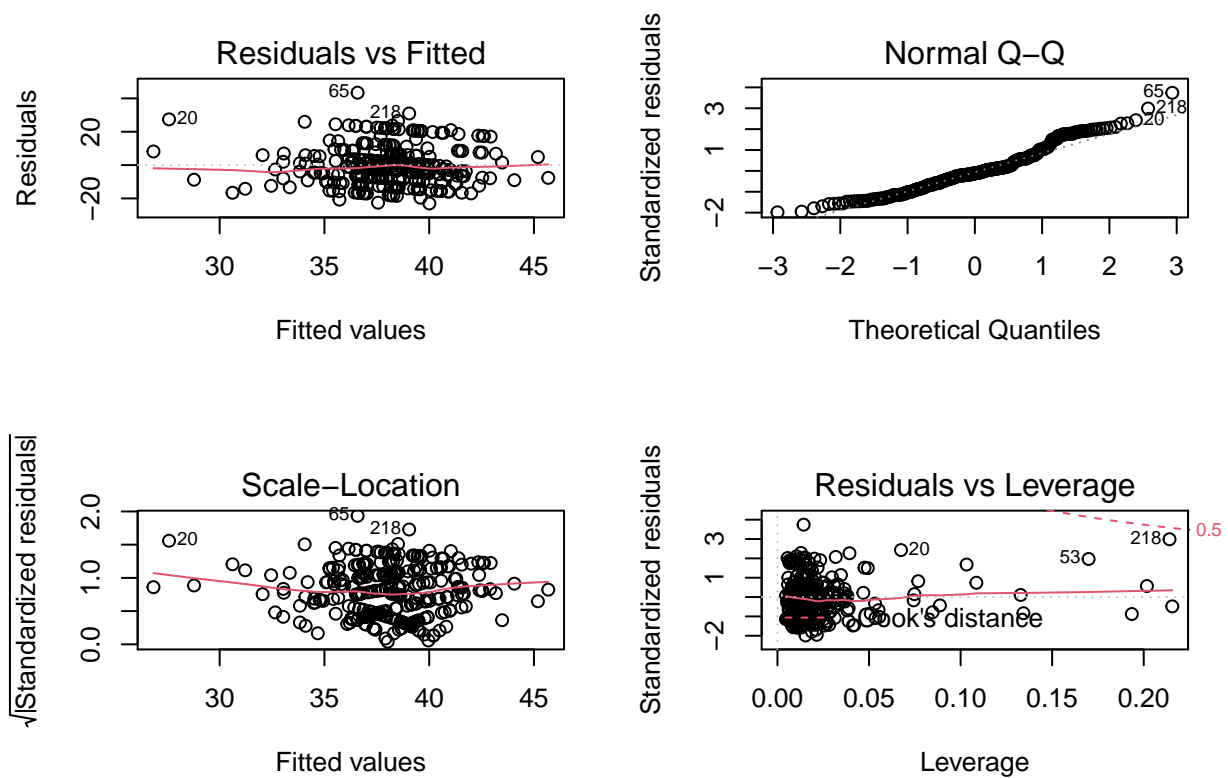
##	1	2	3	4	5	6	7	8
##	35.24141	32.05081	33.34473	36.58442	28.77594	37.21210	37.55997	36.15404
##	9	10	11	12	13	14	15	16
##	38.51127	39.98440	37.34811	38.98368	34.94493	36.93472	38.59180	36.92059
##	17	18	19	20	21	22	23	24
##	40.99034	30.61261	39.56891	27.58345	38.19671	37.93547	39.79403	37.01750
##	25	26	27	28	29	30	31	32
##	37.24997	41.74735	40.21118	38.18136	36.29727	36.49805	38.68885	38.44334
##	33	34	35	36	37	38	39	40
##	33.03306	37.77061	38.91655	36.93033	38.24553	43.18338	36.80004	40.99164
##	41	42	43	44	45	46	47	48
##	36.93282	35.65799	38.56973	36.82364	39.29816	36.34190	33.03834	39.40265
##	49	50	51	52	53	54	55	56
##	36.84991	40.05666	37.81190	39.58450	41.03567	37.85604	35.53848	39.72170
##	57	58	59	60	61	62	63	64
##	39.16723	37.58982	36.65395	38.16647	34.19988	34.09303	38.45149	41.32514
##	65	66	67	68	69	70	71	72
##	36.58223	32.45540	35.71679	40.36427	40.94754	39.44783	38.82037	37.35693
##	73	74	75	76	77	78	79	80
##	33.82882	37.45042	37.02805	38.45895	40.59051	37.94674	36.28477	39.40690
##	81	82	83	84	85	86	87	88
##	38.70577	38.30515	35.45698	37.01949	40.08661	39.91633	37.01159	40.16275
##	89	90	91	92	93	94	95	96
##	37.53827	40.52248	38.19130	35.94599	36.48841	36.81351	40.74142	39.46645
##	97	98	99	100	101	102	103	104
##	36.61633	38.34310	38.54776	39.46267	40.56801	38.97428	41.55545	34.82093
##	105	106	107	108	109	110	111	112
##	41.46703	42.38229	37.41813	36.08631	36.27785	44.06333	37.97394	36.58927
##	113	114	115	116	117	118	119	120
##	36.78863	39.62013	33.06135	37.96270	37.68075	42.93352	39.44573	38.55642
##	121	122	123	124	125	126	127	128
##	36.50647	37.33756	39.26001	40.57076	36.66494	35.65964	31.21869	38.26966
##	129	130	131	132	133	134	135	136
##	37.69904	41.65637	36.98577	35.79503	36.87278	42.55017	36.90672	39.11016
##	137	138	139	140	141	142	143	144
##	37.88599	35.75494	37.47537	36.64905	37.91230	39.19645	35.40946	39.96114
##	145	146	147	148	149	150	151	152
##	40.36491	39.35098	36.76002	37.50203	37.55245	36.21404	38.25708	39.28244
##	153	154	155	156	157	158	159	160
##	35.47813	36.57137	37.81645	39.28125	37.48657	37.01424	38.11707	40.02094
##	161	162	163	164	165	166	167	168
##	37.24571	37.40058	39.75356	37.13126	37.41369	38.01821	35.53031	35.70007
##	169	170	171	172	173	174	175	176
##	39.08267	37.18892	37.17777	37.49054	42.34648	38.07179	38.94502	39.58549
##	177	178	179	180	181	182	183	184
##	36.16233	38.09344	42.61748	39.19572	36.63235	37.60117	38.33991	38.31457
##	185	186	187	188	189	190	191	192
##	38.18585	39.37314	35.24819	42.00205	37.72848	38.63261	39.40395	38.54515
##	193	194	195	196	197	198	199	200
##	34.52245	41.22173	35.40815	43.47940	37.41107	39.51350	36.44523	26.84005

```
##      201      202      203      204      205      206      207      208
## 36.40241 37.98241 39.63487 38.46897 40.19459 38.32498 38.86778 39.45894
##      209      210      211      212      213      214      215      216
## 39.54081 34.10230 40.00809 38.24116 42.40447 34.55707 37.92892 37.66840
##      217      218      219      220      221      222      223      224
## 41.57846 39.04471 37.54975 40.42912 38.29028 42.51881 39.35145 35.08057
##      225      226      227      228      229      230      231      232
## 40.88895 34.05710 35.87193 37.36806 36.64402 38.44964 32.64751 37.64042
##      233      234      235      236      237      238      239      240
## 37.34775 38.67774 38.48652 41.36869 45.18825 36.54125 38.41626 38.57331
##      241      242      243      244      245      246      247      248
## 42.90631 38.51398 36.95820 40.81556 36.97913 39.29107 38.35256 38.45641
##      249      250      251      252      253      254      255      256
## 39.86019 34.76918 38.74765 40.88250 36.32837 37.16957 39.20616 41.29249
##      257      258      259      260      261      262      263      264
## 40.60328 39.78563 36.74700 37.93657 38.74322 37.10203 35.13784 40.67562
##      265      266      267      268      269      270      271      272
## 39.92821 40.49217 36.87266 39.39308 39.49317 34.68318 34.49010 36.42463
##      273      274      275      276      277      278      279      280
## 37.38288 38.63597 38.17710 39.01381 42.53460 39.17744 37.07994 39.92955
##      281      282      283      284      285      286      287      288
## 38.19536 37.85346 33.83012 39.13078 40.49404 38.47979 40.83581 37.68099
##      289      290      291      292      293      294      295      296
## 41.55986 45.68280 39.37243 39.13148 41.01109 38.39762 41.53777 39.00303
##      297      298      299
## 41.40053 37.43671 39.36963
```

```
extract_eq(model, use_cof=TRUE)
```

ejection_fraction = $\alpha + \beta_1(\text{serum_sodium}) + \beta_2(\text{age}) + \beta_3(\text{platelets}) + \beta_4(\text{serum_creatinine}) + \beta_5(\text{time}) + \beta_6(\text{creatinine_phospho})$

```
par(mfrow = c(2, 2))
plot(model)
```



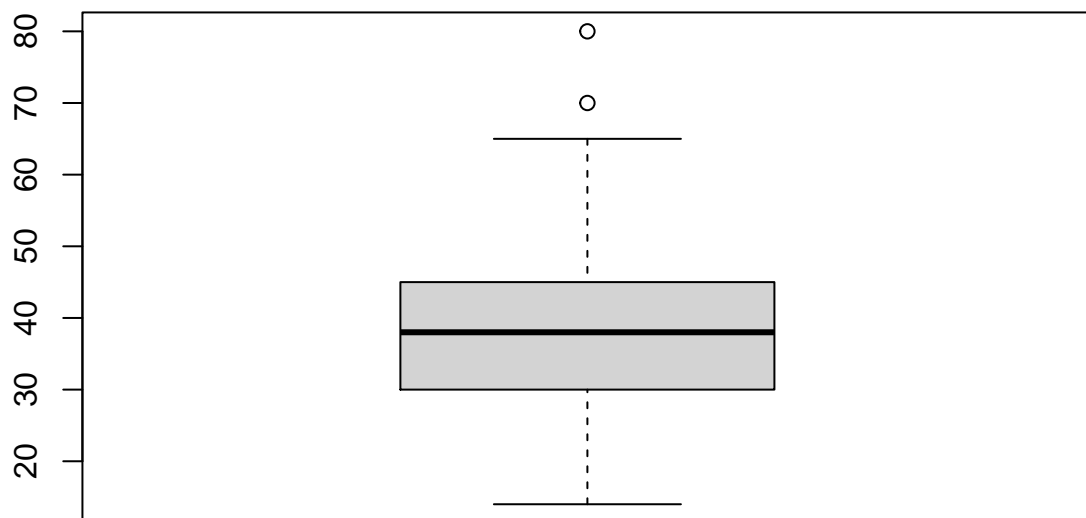
```
vif(model)
```

```
##          serum_sodium          age          platelets
##          1.047593          1.080921          1.007235
##          serum_creatinine          time creatinine_phosphokinase
##          1.074673          1.072699          1.011278
```

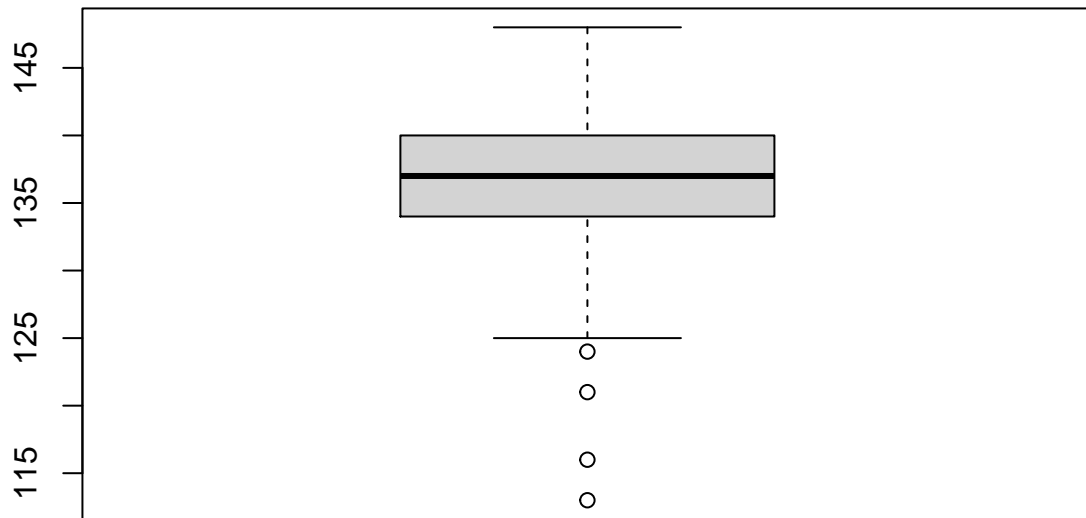
We will improve our result by removing the outlier

```
##create a boxplot to identify outliers
```

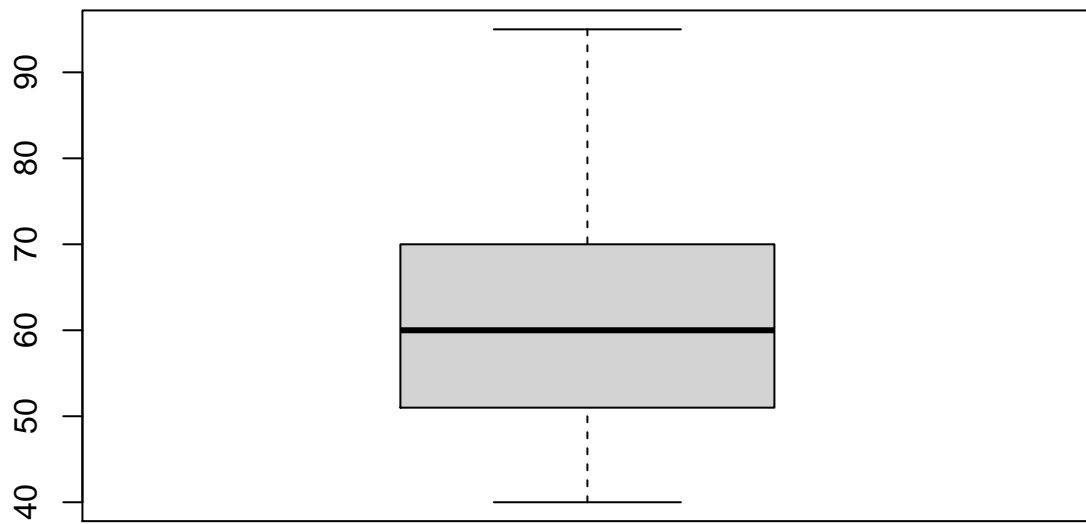
```
boxplot(heart_data$ejection_fraction)
```



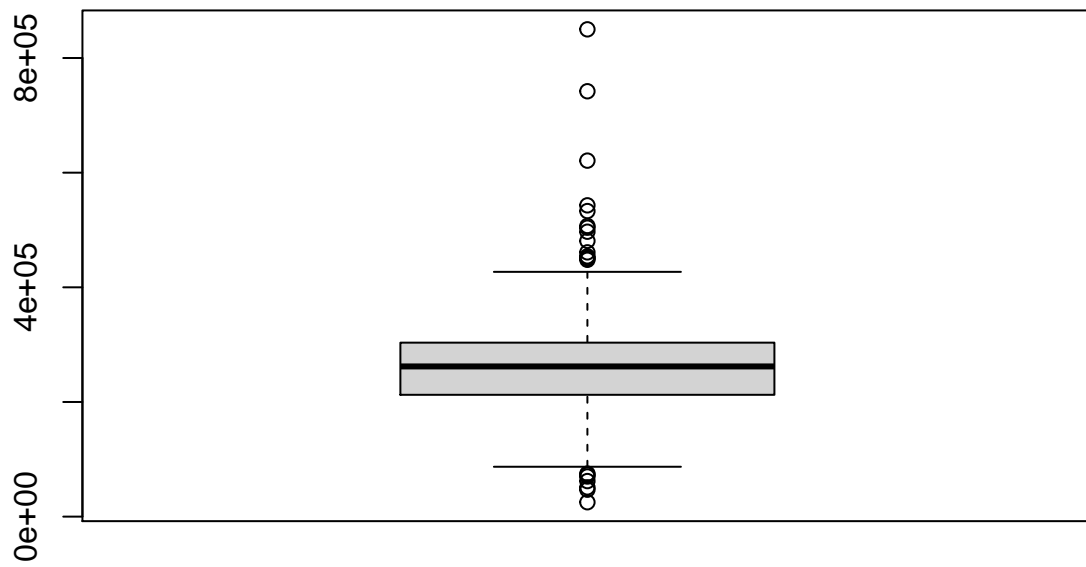
```
boxplot(heart_data$serum_sodium)
```



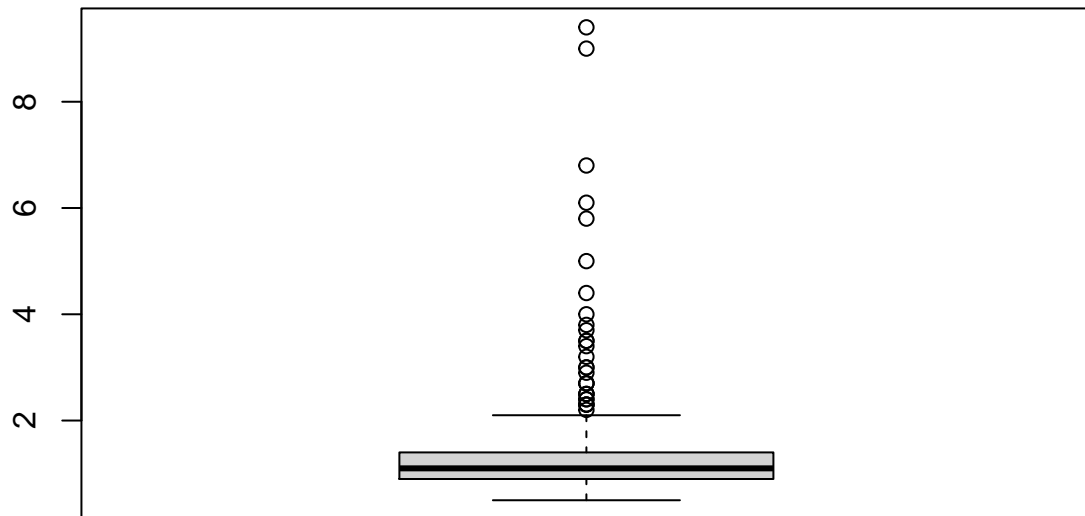
```
boxplot(heart_data$age)
```



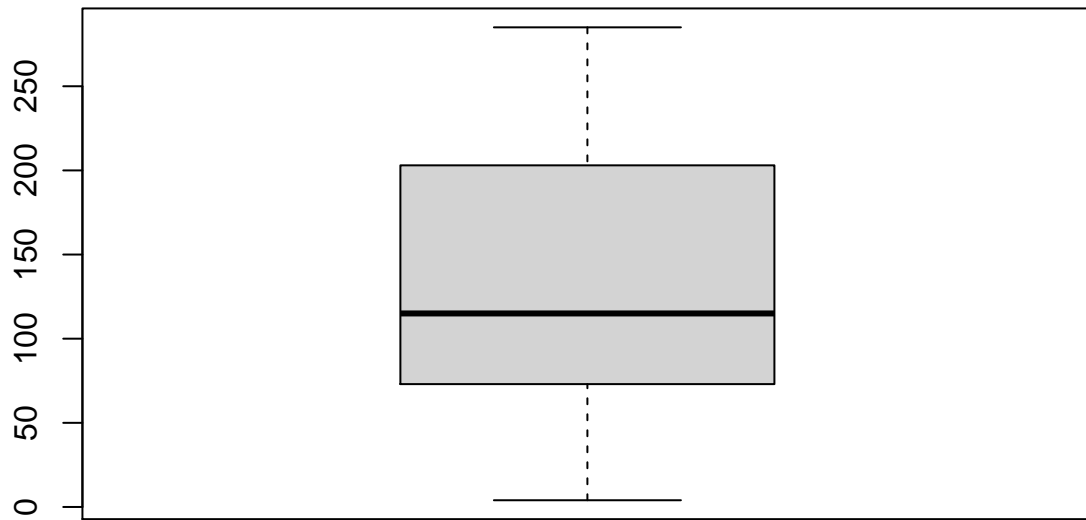
```
boxplot(heart_data$platelets)
```

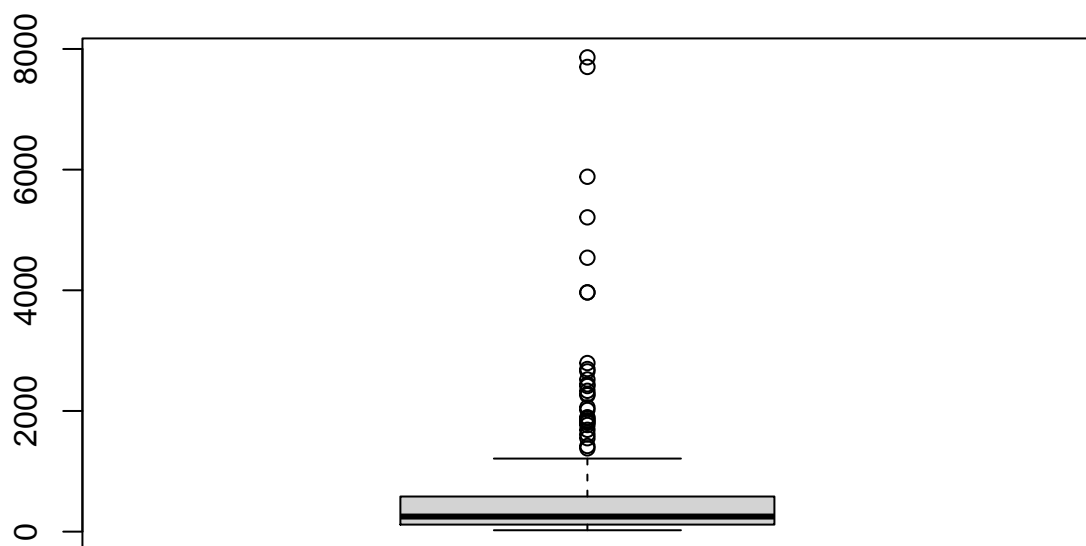
```
boxplot(heart_data$serum_creatinine)
```



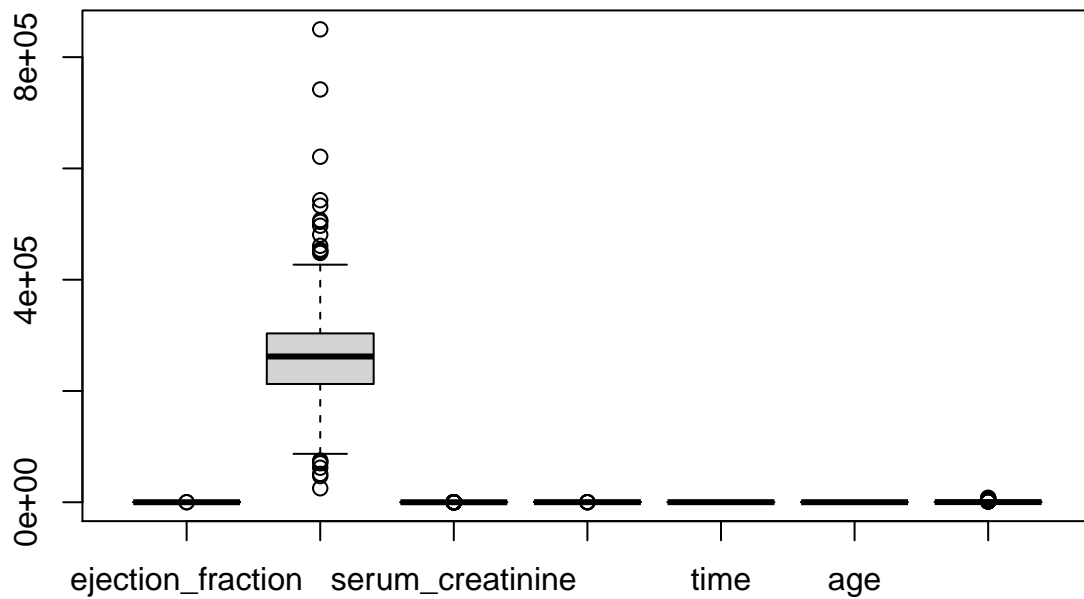
```
boxplot(heart_data$time)
```



```
boxplot(heart_data$creatinine_phosphokinase)
```



```
boxplot(heart_data)
boxplot(heart_data)$out
```



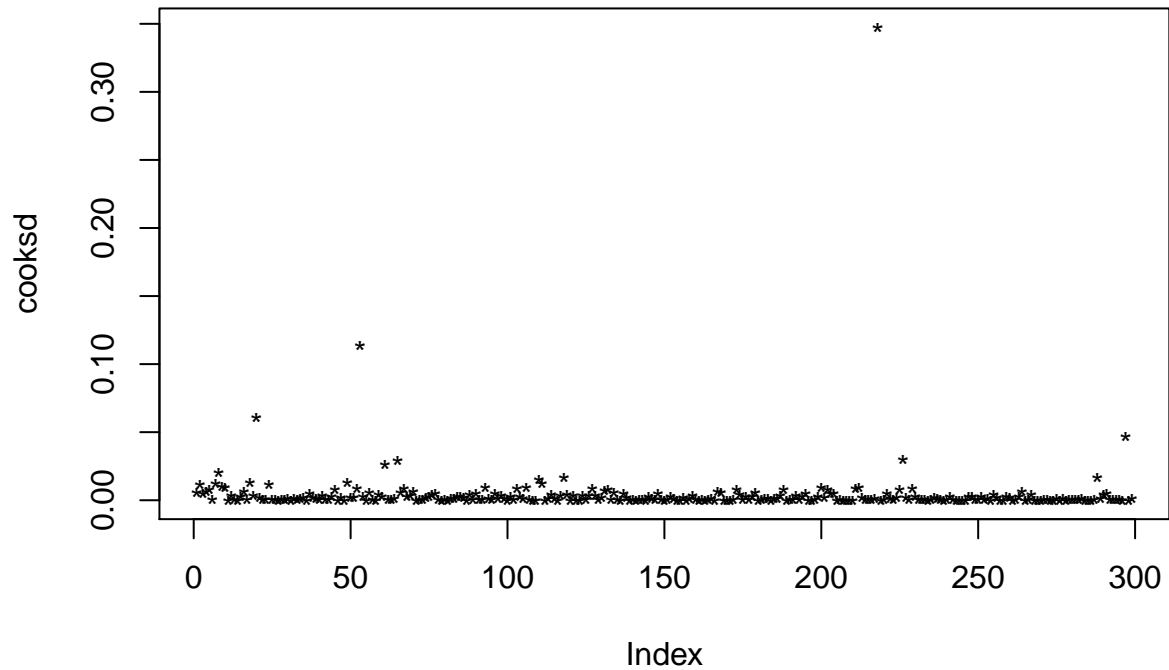
```
## [1]      80.0      70.0 454000.0  47000.0 451000.0 461000.0 497000.0 621000.0
## [9] 850000.0 507000.0 448000.0  75000.0 70000.0  73000.0 481000.0 504000.0
## [17] 62000.0 533000.0  25100.0 451000.0 51000.0 543000.0 742000.0      2.7
## [25]    9.4     4.0     5.8     3.0     3.5     2.3     3.0     4.4
## [33]    6.8     2.2     2.7     2.3     2.9     2.5     2.3     3.2
## [41]    3.7     3.4     6.1     2.5     2.4     2.5     3.5     9.0
## [49]    5.0     2.4     2.7     3.8    116.0    121.0    124.0    113.0
## [57]  7861.0   2656.0   1380.0   3964.0   7702.0   5882.0   5209.0   1876.0
## [65]  1808.0   4540.0   1548.0   1610.0   2261.0   1846.0   2334.0   2442.0
## [73]  3966.0   1419.0   1896.0   1767.0   2281.0   2794.0   2017.0   2522.0
## [81]  2695.0   1688.0   1820.0   2060.0   2413.0
```

###How to Remove Outliers from Multiple Columns in R

```
cooksds<-cooks.distance((model))
```

```
plot(cooksds,pch="*",cex=1,main="Influential obs by cooks distance")
```

Influential obs by cooks distance



cooks_d

##	1	2	3	4	5	6
##	5.284681e-03	1.171972e-02	4.912216e-03	6.245319e-03	8.141469e-03	2.653447e-04
##	7	8	9	10	11	12
##	1.194381e-02	2.019379e-02	9.687037e-03	9.104784e-03	1.831718e-05	3.394552e-03
##	13	14	15	16	17	18
##	7.667166e-04	2.265372e-05	2.342132e-03	6.653790e-03	2.857165e-04	1.317423e-02
##	19	20	21	22	23	24
##	3.724945e-03	6.097901e-02	2.279553e-03	7.651668e-04	3.730553e-04	1.161865e-02
##	25	26	27	28	29	30
##	7.472761e-04	5.201301e-04	1.900456e-06	5.728536e-04	2.648348e-04	1.068289e-03
##	31	32	33	34	35	36
##	1.702930e-05	1.487766e-03	1.284833e-04	1.061639e-03	2.072173e-03	8.540088e-05
##	37	38	39	40	41	42
##	4.572457e-03	1.710926e-03	1.369558e-03	2.682449e-04	3.203227e-03	6.881869e-04
##	43	44	45	46	47	48
##	6.016504e-04	2.594720e-03	8.008238e-03	4.448462e-05	1.664264e-03	4.984561e-05
##	49	50	51	52	53	54
##	1.330929e-02	2.012071e-03	2.290776e-03	8.774700e-03	1.133411e-01	2.354134e-03
##	55	56	57	58	59	60
##	7.839482e-05	5.588178e-03	2.623447e-04	6.646141e-05	3.850300e-03	3.011220e-03
##	61	62	63	64	65	66
##	2.633563e-02	6.881912e-04	1.329521e-04	1.380565e-03	2.896463e-02	5.409143e-03
##	67	68	69	70	71	72
##	8.790110e-03	2.973094e-03	3.731132e-03	6.211757e-03	3.803257e-05	9.246817e-05
##	73	74	75	76	77	78

##	2.533409e-04	1.780941e-03	2.409340e-03	3.926756e-03	4.850425e-03	9.242458e-05
##	79	80	81	82	83	84
##	6.217289e-05	3.590252e-04	1.355204e-05	8.580346e-04	1.520130e-03	2.917386e-03
##	85	86	87	88	89	90
##	2.433875e-03	2.096440e-03	4.741065e-05	4.178946e-03	1.142178e-04	5.240252e-03
##	91	92	93	94	95	96
##	4.479522e-04	7.868025e-04	9.111827e-03	1.012419e-03	1.087684e-04	4.921409e-03
##	97	98	99	100	101	102
##	8.407937e-04	3.753156e-03	1.290173e-03	2.705104e-06	2.358255e-03	3.521267e-04
##	103	104	105	106	107	108
##	8.572764e-03	2.596878e-03	1.402845e-03	9.573433e-03	3.510242e-04	2.314998e-05
##	109	110	111	112	113	114
##	2.702955e-05	1.539698e-02	1.240126e-02	2.071835e-05	1.275086e-03	4.206122e-03
##	115	116	117	118	119	120
##	1.446532e-03	4.503556e-05	3.740700e-03	1.662530e-02	4.294496e-03	6.537544e-06
##	121	122	123	124	125	126
##	3.247024e-03	4.535887e-06	1.518915e-05	3.041305e-03	2.599806e-04	3.142591e-03
##	127	128	129	130	131	132
##	8.895245e-03	3.149970e-03	3.844198e-04	1.949019e-03	6.783257e-03	7.993333e-03
##	133	134	135	136	137	138
##	1.022391e-04	5.751694e-03	3.300314e-04	7.347130e-06	4.610002e-03	1.662575e-03
##	139	140	141	142	143	144
##	3.444767e-05	5.687146e-04	1.242432e-07	2.726775e-04	4.229062e-04	1.472794e-08
##	145	146	147	148	149	150
##	2.593485e-03	1.100202e-03	4.393990e-04	4.551796e-03	5.800149e-04	2.415411e-05
##	151	152	153	154	155	156
##	4.716964e-04	2.953297e-03	1.158468e-03	3.074422e-05	4.862289e-05	1.859283e-03
##	157	158	159	160	161	162
##	4.507423e-05	1.155256e-03	3.145229e-03	2.300947e-04	5.101938e-05	9.903583e-05
##	163	164	165	166	167	168
##	1.071340e-06	1.795456e-04	1.341500e-03	5.423067e-09	6.606950e-03	5.613007e-03
##	169	170	171	172	173	174
##	4.180093e-06	5.974847e-05	2.966692e-05	3.398817e-04	7.471013e-03	3.807119e-03
##	175	176	177	178	179	180
##	9.003808e-05	3.013658e-03	2.943979e-04	2.577543e-03	5.516997e-03	4.721195e-06
##	181	182	183	184	185	186
##	6.950263e-04	9.006640e-04	8.674883e-04	1.516047e-06	1.056627e-03	1.033790e-03
##	187	188	189	190	191	192
##	3.339629e-03	8.146482e-03	3.736027e-05	7.102899e-04	4.347388e-04	3.508900e-03
##	193	194	195	196	197	198
##	5.763194e-04	2.542098e-03	4.607915e-03	6.840248e-05	3.675433e-06	7.318874e-04
##	199	200	201	202	203	204
##	2.592985e-03	9.521235e-03	2.062839e-03	7.733730e-03	4.573590e-03	4.525863e-03
##	205	206	207	208	209	210
##	6.974020e-07	5.452967e-04	2.675198e-05	6.007895e-05	4.148692e-06	1.591460e-05
##	211	212	213	214	215	216
##	8.750738e-03	8.936827e-03	2.123926e-03	4.019204e-04	9.448173e-05	1.029148e-04
##	217	218	219	220	221	222
##	1.295557e-03	3.474012e-01	7.750182e-05	3.729277e-04	4.637201e-03	1.320985e-03
##	223	224	225	226	227	228
##	3.683757e-04	2.014246e-03	7.453644e-03	3.000988e-02	1.684352e-03	1.961317e-04
##	229	230	231	232	233	234
##	8.837211e-03	2.615989e-03	2.904187e-04	1.081326e-04	9.737810e-05	4.447544e-06
##	235	236	237	238	239	240

```
## 3.607094e-04 1.994600e-03 9.546182e-04 8.098831e-04 2.355419e-05 3.435480e-04
##          241          242          243          244          245          246
## 2.697206e-03 6.566114e-04 6.968474e-05 1.331616e-05 1.114431e-05 1.486776e-05
##          247          248          249          250          251          252
## 2.984275e-03 2.502847e-03 5.043576e-04 5.216583e-04 2.461028e-03 5.369566e-04
##          253          254          255          256          257          258
## 1.018217e-03 8.212610e-05 4.023192e-03 2.011645e-03 8.080747e-05 3.535551e-05
##          259          260          261          262          263          264
## 2.316954e-03 2.013333e-03 2.024340e-05 1.329005e-04 2.646723e-03 6.392683e-03
##          265          266          267          268          269          270
## 7.220088e-05 5.219092e-04 4.482996e-03 4.342987e-05 3.775377e-05 2.587794e-06
##          271          272          273          274          275          276
## 5.387748e-04 1.966122e-04 7.054131e-06 4.394479e-05 1.148183e-03 2.543075e-05
##          277          278          279          280          281          282
## 1.271522e-03 5.740894e-05 7.601651e-04 1.003344e-04 1.225563e-04 1.910696e-04
##          283          284          285          286          287          288
## 9.126335e-04 2.516511e-05 4.289123e-06 3.668249e-05 5.405292e-04 1.643697e-02
##          289          290          291          292          293          294
## 8.598465e-04 3.818555e-03 5.012986e-03 3.705568e-04 1.907882e-04 2.387322e-04
##          295          296          297          298          299
## 3.666463e-04 2.235451e-05 4.647102e-02 1.365131e-05 8.839829e-04
```

```
influential<-cooksds[(cooksds>(3*mean(cooksds,na.rm=TRUE)))]
```

```
names_of_influential<-names(influential)
names_of_influential
```

```
## [1] "8" "20" "53" "61" "65" "110" "118" "218" "226" "288" "297"
```

```
outliers <- heart_data[names_of_influential,]
heart_data_without_outliers <-heart_data %>% anti_join(outliers)
heart_data_without_outliers
```

```
##      ejection_fraction platelets serum_creatinine serum_sodium time      age
## 1              20      265000              1.90          130      4 75.000
## 2              38      263358              1.10          136      6 55.000
## 3              20      162000              1.30          129      7 65.000
## 4              20      210000              1.90          137      7 50.000
## 5              20      327000              2.70          116      8 65.000
## 6              40      204000              2.10          132      8 90.000
## 7              15      127000              1.20          137     10 75.000
## 8              65      263358              1.50          138     10 65.000
## 9              35      388000              9.40          133     10 80.000
## 10             38      368000              4.00          131     10 75.000
## 11             25      253000              0.90          140     10 62.000
## 12             30      136000              1.10          137     11 45.000
## 13             38      276000              1.10          137     11 50.000
## 14             30      427000              1.00          138     12 49.000
## 15             50      47000              1.30          136     13 82.000
## 16             38      262000              0.90          140     14 87.000
## 17             14      166000              0.80          127     14 45.000
## 18             25      237000              1.00          140     15 70.000
## 19             25      276000              1.30          137     16 65.000
## 20             30      297000              1.60          136     20 65.000
## 21             35      289000              0.90          140     20 68.000
```


## 22	60	368000	0.80	135	22 53.000
## 23	30	263358	1.83	134	23 75.000
## 24	38	149000	1.90	144	23 80.000
## 25	40	196000	1.00	138	24 95.000
## 26	45	284000	1.30	136	26 70.000
## 27	38	153000	5.80	134	26 58.000
## 28	30	200000	1.20	132	26 82.000
## 29	38	263358	1.83	134	27 94.000
## 30	45	360000	3.00	132	28 85.000
## 31	35	319000	1.00	128	28 50.000
## 32	30	302000	1.20	138	29 50.000
## 33	50	188000	1.00	140	29 65.000
## 34	35	228000	3.50	134	30 69.000
## 35	50	226000	1.00	134	30 90.000
## 36	50	321000	1.00	145	30 82.000
## 37	30	305000	2.30	137	30 60.000
## 38	38	329000	3.00	142	30 60.000
## 39	20	263358	1.83	134	31 70.000
## 40	30	153000	1.20	136	32 50.000
## 41	45	185000	1.20	139	33 70.000
## 42	50	218000	1.00	134	33 72.000
## 43	60	194000	1.10	142	33 60.000
## 44	38	310000	1.90	135	35 50.000
## 45	25	271000	0.90	130	38 51.000
## 46	38	451000	0.60	138	40 60.000
## 47	20	140000	4.40	133	41 80.000
## 48	30	395000	1.00	140	42 57.000
## 49	25	166000	1.00	138	43 68.000
## 50	20	418000	1.40	139	43 53.000
## 51	50	351000	1.00	134	44 70.000
## 52	38	255000	2.20	132	45 60.000
## 53	30	461000	2.00	132	50 95.000
## 54	35	223000	2.70	138	54 70.000
## 55	40	216000	0.60	138	54 60.000
## 56	20	319000	1.10	136	55 49.000
## 57	20	254000	1.30	136	59 72.000
## 58	40	216000	2.30	131	60 50.000
## 59	35	254000	1.10	139	60 55.000
## 60	35	385000	1.00	145	61 45.000
## 61	20	119000	2.90	127	64 60.000
## 62	15	213000	1.30	136	65 42.000
## 63	25	274000	1.00	140	65 72.000
## 64	25	244000	1.20	142	66 70.000
## 65	25	497000	1.83	135	67 65.000
## 66	40	374000	0.80	140	68 41.000
## 67	35	122000	0.90	139	71 58.000
## 68	35	243000	1.00	132	72 85.000
## 69	50	149000	1.30	137	72 65.000
## 70	20	266000	1.20	134	73 69.000
## 71	20	204000	0.70	139	73 60.000
## 72	60	317000	0.80	140	74 70.000
## 73	40	237000	1.20	140	74 42.000
## 74	38	283000	0.60	131	74 75.000
## 75	45	324000	0.90	140	74 55.000

## 76	40	293000	1.70	136	75 70.000
## 77	50	263358	1.18	137	76 67.000
## 78	25	196000	2.50	132	77 60.000
## 79	50	172000	1.80	133	78 79.000
## 80	25	302000	1.00	141	78 59.000
## 81	50	406000	0.70	140	79 51.000
## 82	35	173000	1.10	137	79 55.000
## 83	60	304000	0.80	140	79 65.000
## 84	40	235000	0.70	139	79 44.000
## 85	25	181000	1.10	144	79 57.000
## 86	45	249000	0.80	136	80 70.000
## 87	45	297000	1.00	133	80 60.000
## 88	60	263358	1.18	137	82 42.000
## 89	25	210000	1.70	135	82 60.000
## 90	38	327000	0.70	142	83 58.000
## 91	60	219000	1.00	141	83 58.000
## 92	25	254000	1.30	134	83 63.000
## 93	60	255000	1.10	136	85 70.000
## 94	25	318000	1.20	137	85 60.000
## 95	40	221000	1.10	140	86 63.000
## 96	25	298000	1.10	141	87 65.000
## 97	45	263358	1.18	137	87 75.000
## 98	25	149000	1.10	144	87 80.000
## 99	30	226000	1.00	140	87 42.000
## 100	50	286000	2.30	143	87 60.000
## 101	30	621000	1.70	138	88 72.000
## 102	45	263000	1.30	137	88 55.000
## 103	35	226000	0.90	138	88 45.000
## 104	38	304000	1.10	133	88 63.000
## 105	60	306000	1.20	132	90 85.000
## 106	35	228000	1.20	135	90 55.000
## 107	25	252000	1.60	136	90 50.000
## 108	60	351000	1.30	137	90 70.000
## 109	40	328000	1.20	126	91 60.000
## 110	40	164000	1.00	139	91 58.000
## 111	60	271000	0.70	136	94 60.000
## 112	60	203000	0.90	140	94 65.000
## 113	38	263358	1.83	134	95 86.000
## 114	60	210000	1.50	135	95 60.000
## 115	38	162000	1.00	136	95 66.000
## 116	38	228000	0.75	140	95 60.000
## 117	30	127000	0.90	145	95 60.000
## 118	40	217000	3.70	134	96 60.000
## 119	50	237000	1.30	135	97 43.000
## 120	17	271000	2.10	124	100 46.000
## 121	60	300000	0.80	137	104 58.000
## 122	30	267000	0.70	136	104 61.000
## 123	35	227000	3.40	145	105 53.000
## 124	60	249000	0.70	138	106 53.000
## 125	45	250000	6.10	131	107 60.000
## 126	40	263358	1.18	137	107 46.000
## 127	60	295000	1.30	145	107 63.000
## 128	35	231000	1.18	137	107 81.000
## 129	40	263358	1.18	137	107 75.000

## 130	60	172000	0.90	137	107	65.000
## 131	25	305000	2.10	130	108	68.000
## 132	35	221000	1.00	136	108	62.000
## 133	30	211000	0.80	138	108	50.000
## 134	38	263358	1.10	134	109	80.000
## 135	35	348000	0.90	140	109	46.000
## 136	30	329000	0.90	132	109	50.000
## 137	40	229000	0.90	141	110	61.000
## 138	25	338000	1.70	139	111	72.000
## 139	30	266000	0.70	141	112	50.000
## 140	30	218000	0.70	136	112	52.000
## 141	60	242000	1.00	137	113	64.000
## 142	30	225000	1.83	134	113	75.000
## 143	35	228000	0.90	136	115	60.000
## 144	45	235000	2.50	135	115	72.000
## 145	60	244000	0.90	139	117	62.000
## 146	45	184000	0.90	134	118	50.000
## 147	35	263358	1.18	137	119	50.000
## 148	35	235000	0.80	136	120	65.000
## 149	25	194000	1.70	140	120	60.000
## 150	35	277000	1.40	136	120	52.000
## 151	25	262000	1.00	136	120	50.000
## 152	50	235000	1.30	134	121	85.000
## 153	45	362000	1.10	139	121	59.000
## 154	40	242000	1.20	134	121	66.000
## 155	35	174000	0.80	139	121	45.000
## 156	40	448000	0.90	137	123	63.000
## 157	35	75000	0.90	142	126	50.000
## 158	30	334000	1.10	139	129	45.000
## 159	38	192000	1.30	135	130	80.000
## 160	60	220000	0.70	133	134	53.000
## 161	20	70000	2.40	134	135	59.000
## 162	40	270000	1.00	138	140	65.000
## 163	35	305000	0.80	133	145	70.000
## 164	35	263358	1.50	136	145	51.000
## 165	40	325000	0.90	140	146	52.000
## 166	60	176000	1.10	145	146	70.000
## 167	20	189000	0.80	139	146	50.000
## 168	35	281000	0.90	137	146	65.000
## 169	60	337000	1.00	138	146	60.000
## 170	40	105000	1.00	135	147	69.000
## 171	50	132000	1.00	140	147	49.000
## 172	60	267000	1.20	145	147	63.000
## 173	40	279000	0.70	140	147	55.000
## 174	30	303000	0.90	136	148	40.000
## 175	25	221000	1.00	136	150	59.000
## 176	25	265000	1.20	136	154	65.000
## 177	38	224000	2.50	134	162	75.000
## 178	25	219000	1.20	137	170	58.000
## 179	30	389000	1.50	136	171	60.667
## 180	50	153000	0.60	134	172	50.000
## 181	25	365000	2.10	144	172	60.000
## 182	40	201000	1.00	136	172	60.667
## 183	45	275000	0.90	140	174	40.000

## 184	35	350000	2.10	134	174	80.000
## 185	60	309000	1.50	135	174	64.000
## 186	40	260000	0.70	130	175	50.000
## 187	30	160000	1.18	142	180	73.000
## 188	20	126000	1.60	135	180	45.000
## 189	45	223000	1.80	145	180	77.000
## 190	38	263358	1.18	137	185	45.000
## 191	30	259000	0.80	138	186	65.000
## 192	20	279000	1.00	134	186	50.000
## 193	35	263358	1.80	113	186	60.000
## 194	45	73000	0.70	137	186	63.000
## 195	60	377000	1.00	136	186	45.000
## 196	60	220000	0.90	138	186	70.000
## 197	25	212000	3.50	136	187	60.000
## 198	40	277000	0.70	137	187	78.000
## 199	45	362000	1.00	136	187	50.000
## 200	40	226000	0.80	141	187	40.000
## 201	38	186000	0.90	136	187	85.000
## 202	40	283000	1.00	141	187	60.000
## 203	35	268000	0.80	130	187	49.000
## 204	17	389000	1.00	136	188	70.000
## 205	62	147000	0.80	140	192	50.000
## 206	50	481000	1.40	138	192	78.000
## 207	30	244000	1.60	130	193	48.000
## 208	35	290000	0.80	134	194	65.000
## 209	35	203000	1.30	134	195	73.000
## 210	50	358000	0.90	141	196	70.000
## 211	35	271000	1.10	134	197	68.000
## 212	35	371000	0.70	140	197	55.000
## 213	20	263358	1.83	134	198	73.000
## 214	50	194000	1.10	145	200	65.000
## 215	35	365000	1.10	139	201	42.000
## 216	25	130000	0.80	134	201	47.000
## 217	25	504000	1.00	138	205	58.000
## 218	25	189000	1.30	132	205	58.000
## 219	35	141000	1.00	140	206	55.000
## 220	25	237000	5.00	130	207	65.000
## 221	25	274000	1.20	134	207	72.000
## 222	30	62000	1.70	127	207	60.000
## 223	35	185000	1.10	134	208	70.000
## 224	35	255000	0.90	137	209	40.000
## 225	38	330000	1.40	137	209	53.000
## 226	45	305000	1.10	137	209	53.000
## 227	50	406000	1.10	137	209	77.000
## 228	50	248000	1.10	148	209	75.000
## 229	30	173000	1.20	132	210	70.000
## 230	40	257000	1.00	136	210	65.000
## 231	45	263358	1.18	137	211	55.000
## 232	35	533000	1.30	139	212	70.000
## 233	30	249000	1.30	136	212	65.000
## 234	35	255000	1.10	136	212	40.000
## 235	40	220000	0.90	141	213	73.000
## 236	38	264000	1.80	134	213	54.000
## 237	38	282000	1.40	137	213	61.000

## 238	25	314000	1.10	138	214	55.000
## 239	25	246000	2.40	135	214	64.000
## 240	35	301000	1.00	142	214	40.000
## 241	40	223000	1.20	130	214	53.000
## 242	30	404000	0.50	139	214	50.000
## 243	35	231000	0.80	143	215	55.000
## 244	45	274000	1.00	133	215	50.000
## 245	35	236000	1.20	132	215	70.000
## 246	60	263358	1.00	139	215	53.000
## 247	30	334000	1.00	142	216	52.000
## 248	38	294000	1.70	139	220	65.000
## 249	38	253000	1.00	139	230	58.000
## 250	25	233000	0.80	135	230	45.000
## 251	50	308000	0.70	135	231	53.000
## 252	40	203000	1.00	138	233	55.000
## 253	40	283000	0.70	133	233	62.000
## 254	25	198000	1.40	129	235	65.000
## 255	60	208000	1.00	140	237	68.000
## 256	38	147000	1.20	141	237	61.000
## 257	35	362000	0.90	140	240	50.000
## 258	20	263358	1.83	134	241	55.000
## 259	38	133000	1.70	140	244	56.000
## 260	38	302000	0.90	140	244	45.000
## 261	35	222000	1.00	132	244	40.000
## 262	30	263358	1.60	130	244	44.000
## 263	40	221000	0.90	134	244	51.000
## 264	38	215000	1.20	133	245	67.000
## 265	40	189000	0.70	140	245	42.000
## 266	30	150000	1.00	137	245	60.000
## 267	38	422000	0.80	137	245	45.000
## 268	35	327000	1.10	142	245	70.000
## 269	38	25100	1.10	140	246	70.000
## 270	30	232000	0.70	136	246	50.000
## 271	38	451000	1.30	136	246	55.000
## 272	40	241000	1.00	137	247	70.000
## 273	40	51000	2.70	136	250	70.000
## 274	30	215000	3.80	128	250	42.000
## 275	38	263358	1.10	138	250	65.000
## 276	40	279000	0.80	141	250	50.000
## 277	40	336000	1.20	135	250	55.000
## 278	35	279000	1.70	140	250	60.000
## 279	35	263358	1.10	142	256	65.000
## 280	38	390000	0.90	144	256	90.000
## 281	55	222000	0.80	141	257	45.000
## 282	35	133000	1.40	139	258	60.000
## 283	38	382000	1.00	140	258	52.000
## 284	35	179000	0.90	136	270	63.000
## 285	38	155000	1.10	143	270	62.000
## 286	38	270000	1.20	139	271	55.000
## 287	38	140000	1.40	140	280	45.000
## 288	45	395000	1.60	136	285	50.000
##	creatinine_phosphokinase					
## 1		582				
## 2		7861				

## 3	146
## 4	111
## 5	160
## 6	47
## 7	246
## 8	157
## 9	123
## 10	81
## 11	231
## 12	981
## 13	168
## 14	80
## 15	379
## 16	149
## 17	582
## 18	125
## 19	52
## 20	128
## 21	220
## 22	63
## 23	582
## 24	148
## 25	112
## 26	122
## 27	60
## 28	70
## 29	582
## 30	23
## 31	249
## 32	159
## 33	94
## 34	582
## 35	60
## 36	855
## 37	2656
## 38	235
## 39	582
## 40	124
## 41	571
## 42	127
## 43	588
## 44	582
## 45	1380
## 46	582
## 47	553
## 48	129
## 49	577
## 50	91
## 51	69
## 52	260
## 53	371
## 54	75
## 55	607
## 56	789

## 57	364
## 58	318
## 59	109
## 60	582
## 61	68
## 62	250
## 63	110
## 64	161
## 65	113
## 66	148
## 67	582
## 68	5882
## 69	224
## 70	582
## 71	47
## 72	92
## 73	102
## 74	203
## 75	336
## 76	69
## 77	582
## 78	76
## 79	55
## 80	280
## 81	78
## 82	47
## 83	68
## 84	84
## 85	115
## 86	66
## 87	897
## 88	582
## 89	154
## 90	144
## 91	133
## 92	514
## 93	59
## 94	156
## 95	61
## 96	305
## 97	582
## 98	898
## 99	5209
## 100	53
## 101	328
## 102	748
## 103	1876
## 104	936
## 105	129
## 106	60
## 107	369
## 108	143
## 109	754
## 110	400

## 111	96
## 112	113
## 113	582
## 114	737
## 115	68
## 116	96
## 117	582
## 118	582
## 119	358
## 120	168
## 121	200
## 122	248
## 123	270
## 124	1808
## 125	1082
## 126	719
## 127	193
## 128	4540
## 129	582
## 130	59
## 131	646
## 132	281
## 133	1548
## 134	805
## 135	291
## 136	482
## 137	84
## 138	943
## 139	185
## 140	132
## 141	1610
## 142	582
## 143	2261
## 144	233
## 145	30
## 146	115
## 147	1846
## 148	335
## 149	231
## 150	58
## 151	250
## 152	910
## 153	129
## 154	72
## 155	130
## 156	582
## 157	2334
## 158	2442
## 159	776
## 160	196
## 161	66
## 162	582
## 163	835
## 164	582

## 165	3966
## 166	171
## 167	115
## 168	198
## 169	95
## 170	1419
## 171	69
## 172	122
## 173	835
## 174	478
## 175	176
## 176	395
## 177	99
## 178	145
## 179	104
## 180	582
## 181	1896
## 182	151
## 183	244
## 184	582
## 185	62
## 186	121
## 187	231
## 188	582
## 189	418
## 190	582
## 191	167
## 192	582
## 193	1211
## 194	1767
## 195	308
## 196	97
## 197	59
## 198	64
## 199	167
## 200	101
## 201	212
## 202	2281
## 203	972
## 204	212
## 205	582
## 206	224
## 207	131
## 208	135
## 209	582
## 210	1202
## 211	1021
## 212	582
## 213	582
## 214	118
## 215	86
## 216	582
## 217	582
## 218	57

## 219	2794
## 220	56
## 221	211
## 222	166
## 223	93
## 224	129
## 225	707
## 226	582
## 227	109
## 228	119
## 229	232
## 230	720
## 231	180
## 232	81
## 233	582
## 234	90
## 235	1185
## 236	582
## 237	80
## 238	2017
## 239	143
## 240	624
## 241	207
## 242	2522
## 243	572
## 244	245
## 245	88
## 246	446
## 247	191
## 248	326
## 249	132
## 250	66
## 251	56
## 252	66
## 253	655
## 254	258
## 255	157
## 256	582
## 257	298
## 258	1199
## 259	135
## 260	582
## 261	582
## 262	582
## 263	582
## 264	213
## 265	64
## 266	257
## 267	582
## 268	618
## 269	582
## 270	1051
## 271	84
## 272	2695

## 273	582
## 274	64
## 275	1688
## 276	54
## 277	170
## 278	253
## 279	892
## 280	337
## 281	615
## 282	320
## 283	190
## 284	103
## 285	61
## 286	1820
## 287	2413
## 288	196

Other Ways of Removing Outliers

```

outliers <- function(x) {

  Q1 <- quantile(x, probs=.25)
  Q3 <- quantile(x, probs=.75)
  iqr = Q3-Q1

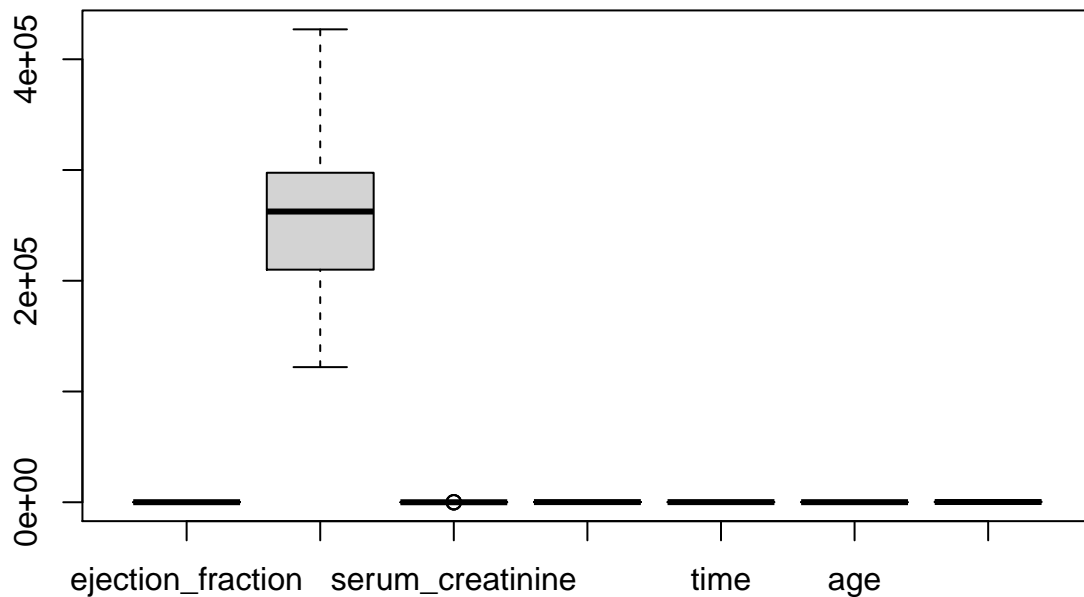
  upper_limit = Q3 + (iqr*1.5)
  lower_limit = Q1 - (iqr*1.5)

  x > upper_limit | x < lower_limit
}

remove_outliers <- function(heart_data, cols = names(heart_data)) {
  for (col in cols) {
    heart_data <- heart_data[!outliers(heart_data[[col]]),]
  }
  heart_data
}

heart_data_without_outliers <- remove_outliers(heart_data)
boxplot(heart_data_without_outliers)

```



```
mode2 <- lm(ejection_fraction ~ serum_sodium + age + platelets + serum_creatinine + time +
  creatinine_phosphokinase , data = heart_data_without_outliers)
mode2

##
## Call:
## lm(formula = ejection_fraction ~ serum_sodium + age + platelets +
##     serum_creatinine + time + creatinine_phosphokinase, data = heart_data_without_outliers)
##
## Coefficients:
##             (Intercept)          serum_sodium              age
##             -2.268e+01           4.174e-01           1.429e-01
##             platelets        serum_creatinine              time
##             1.336e-05           -7.241e+00           8.623e-03
## creatinine_phosphokinase
##             -4.521e-03

summary(mode2)

##
## Call:
## lm(formula = ejection_fraction ~ serum_sodium + age + platelets +
##     serum_creatinine + time + creatinine_phosphokinase, data = heart_data_without_outliers)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -25.7044  -7.3759  -0.9897   6.6674  28.7599
```

```
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -2.268e+01  3.123e+01  -0.726  0.46852
## serum_sodium     4.174e-01  2.193e-01   1.903  0.05834 .
## age             1.429e-01  6.778e-02   2.108  0.03616 *
## platelets       1.336e-05  1.126e-05   1.186  0.23692
## serum_creatinine -7.241e+00  2.462e+00  -2.941  0.00363 **
## time            8.623e-03  1.032e-02   0.835  0.40455
## creatinine_phosphokinase -4.522e-03  2.758e-03  -1.639  0.10262
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 11.15 on 213 degrees of freedom
## Multiple R-squared:  0.09792,    Adjusted R-squared:  0.07251
## F-statistic: 3.853 on 6 and 213 DF,  p-value: 0.001136
```

Other Ways of Removing Outliers

To detect the outlier, we can use the influencePlot

```
##influencePlot(model)

##mode2 <- lm(ejection_fraction ~ serum_sodium + age + platelets + serum_creatinine + time +
creatinine_phosphokinase , data = heart_data[!(row.names(heart_data)=="218"&"65")])

##mode2
```

Coefficients Function & Fitted function

```
mode2$coefficients
```

```
##              (Intercept)              serum_sodium              age
##          -2.268009e+01          4.173797e-01          1.429044e-01
##              platelets          serum_creatinine              time
##          1.335629e-05          -7.240539e+00          8.622597e-03
## creatinine_phosphokinase
##          -4.521499e-03
```

```
mode2$fitted
```

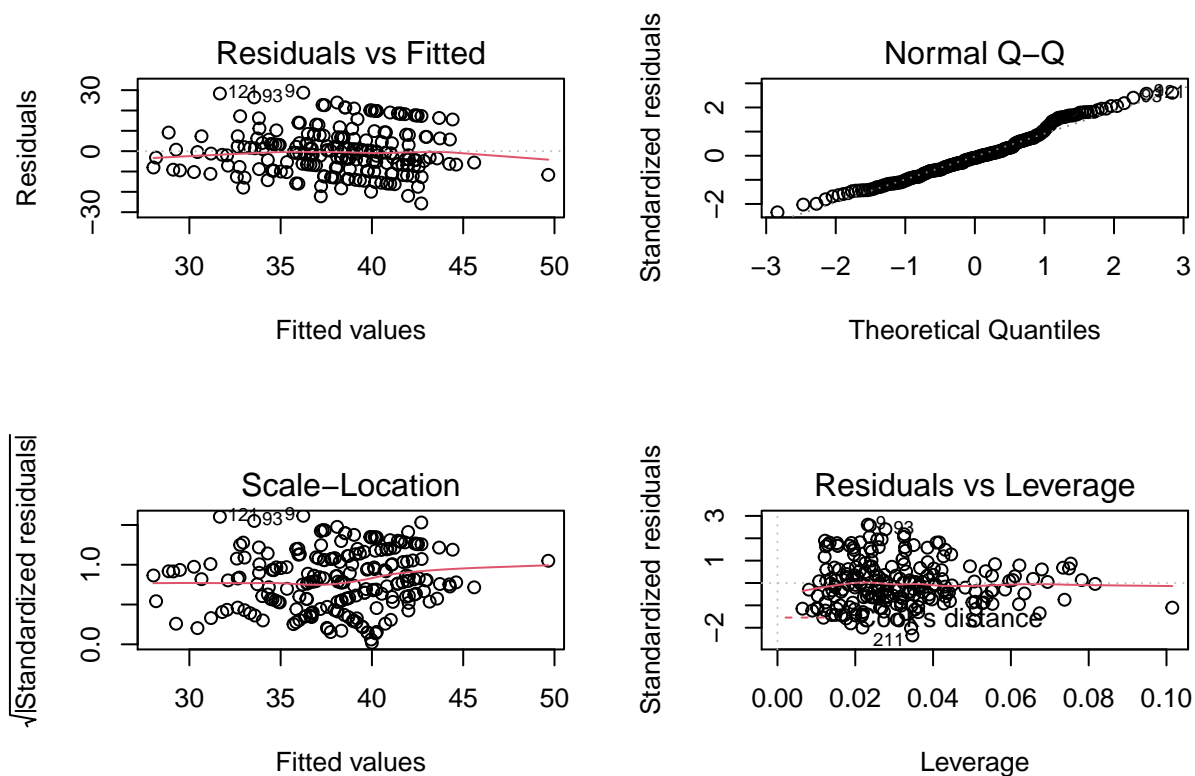
```
##          1          3          4          6          7          9         12         13
## 29.48247 32.60191 30.25242 32.65145 37.20030 36.24012 40.51756 30.44275
##          14          15          17          19          21          22          23          24
## 36.70313 40.12497 44.61563 41.24543 37.96619 35.34799 41.99177 40.26763
##          25          26          27          28          30          31          33          34
## 31.80073 36.61714 43.57205 38.13991 38.02248 34.55040 34.02543 36.93962
##          35          37          38          41          42          43          44          45
## 40.13733 41.87556 42.99775 31.15519 34.29889 36.82403 38.91935 37.41452
##          46          50          51          52          54          58          59          60
## 28.86509 41.71269 37.37428 38.31511 40.76703 39.75428 34.28871 37.21537
##          63          64          67          68          69          71          72          74
## 38.64785 40.06676 32.94782 42.52437 41.00255 40.73213 36.71782 35.97511
##          75          76          77          78          79          80          81          82
## 35.97126 41.98320 44.41998 36.40873 41.87020 40.54261 36.02604 37.07298
##          84          85          86          87          88          89          90          91
```

```
## 33.80905 40.80141 43.72398 37.17539 43.68346 39.99521 40.18225 42.01153
##      92      93      94      95      96      97      98      99
## 34.76598 33.55211 32.74708 44.23999 40.25771 34.62319 39.99427 38.66141
##      100     101     102     103     107     109     111     112
## 40.20892 40.84592 38.31106 39.57029 33.83738 34.45677 40.15204 36.38724
##      113     114     116     117     119     120     121     122
## 32.11729 39.90905 37.55009 41.58545 41.53629 33.99350 31.67125 38.95010
##      123     124     126     128     129     133     134     136
## 42.32724 39.78163 32.78149 40.99629 41.07389 33.71984 41.42032 38.48351
##      137     138     139     141     142     143     144     145
## 40.22636 28.17566 38.31552 37.53409 40.08228 36.19749 41.99840 34.52365
##      146     147     149     152     153     155     156     157
## 41.92932 39.72677 32.06444 41.81141 36.83258 40.23864 34.59978 35.84998
##      158     159     160     161     162     166     167     169
## 37.39192 36.05046 41.09749 37.94184 38.75349 35.86248 38.54456 39.14841
##      170     171     173     174     175     176     178     179
## 38.59078 32.64712 42.71511 39.95174 41.38999 41.58246 38.23341 42.43633
##      180     181     182     183     185     186     187     189
## 39.76291 36.44506 38.72372 37.76499 37.83599 38.09215 36.94477 38.99755
##      190     191     192     193     194     195     196     197
## 39.02283 33.01953 37.29833 38.09060 41.12062 29.11545 38.45117 34.86895
##      198     199     202     203     205     206     207     208
## 42.72266 35.85217 38.52021 42.50873 45.60184 39.68054 40.26847 42.85208
##      210     211     212     214     215     216     217     219
## 33.58617 42.70441 38.09326 31.18460 41.68085 36.02933 40.69401 35.70345
##      220     221     222     223     224     227     230     232
## 42.56676 33.02387 42.94626 39.59242 35.01081 35.32403 39.33972 39.13142
##      233     234     235     236     238     239     240     242
## 38.32532 34.95111 37.35455 44.27191 36.80109 38.11963 38.33982 36.48183
##      243     244     245     246     249     250     252     253
## 36.66204 39.50300 30.66382 38.32271 38.10753 34.35230 41.42538 37.14181
##      254     255     256     257     258     259     260     261
## 38.33674 39.02384 42.23819 36.66527 41.14911 39.10123 42.02408 39.95948
##      262     263     264     265     266     267     268     269
## 39.45042 33.81823 42.34182 37.57439 41.93880 28.03260 34.71670 39.17328
##      270     271     272     273     274     275     276     277
## 33.32717 29.27209 36.44457 37.73842 41.03418 38.78861 40.25657 42.31230
##      279     285     286     287     289     290     291     292
## 36.62812 43.16113 38.71197 36.75653 39.60371 49.66009 39.20910 36.32733
##      293     294     295     299
## 42.41121 40.82320 42.02320 36.49087
```

```
extract_eq(mode2, use_cof=TRUE)
```

ejection_fraction = $\alpha + \beta_1(\text{serum_sodium}) + \beta_2(\text{age}) + \beta_3(\text{platelets}) + \beta_4(\text{serum_creatinine}) + \beta_5(\text{time}) + \beta_6(\text{creatinine_phospho})$

```
par(mfrow = c(2, 2))
plot(mode2)
```



We can see here, that the coefficient is different between our new model and our previous model

Also, after removing the outlier from our dataset the residual standard error is decreasing, while the R^2 is increasing

It means that our new model fits better to our data compared to the previous model

VIF for new model

```
vif(mode2)
```

```
##          serum_sodium          age          platelets
##          1.059446          1.150795          1.011299
##          serum_creatinine          time creatinine_phosphokinase
##          1.158148          1.097319          1.040899
```

```
glance(mode2)
```

```
## # A tibble: 1 x 12
##   r.squared adj.r.squared sigma statistic p.value    df logLik   AIC   BIC
##   <dbl>      <dbl> <dbl>      <dbl>  <dbl> <dbl> <dbl> <dbl> <dbl>
## 1    0.0979      0.0725  11.2        3.85 0.00114     6 -839. 1694. 1722.
## # ... with 3 more variables: deviance <dbl>, df.residual <int>, nobs <int>
```

```
tidy(mode2)
```

```
## # A tibble: 7 x 5
##   term                estimate std.error statistic p.value
##   <chr>              <dbl>      <dbl>      <dbl>   <dbl>
## 1 (Intercept)       -22.7        31.2        -0.726 0.469
## 2 serum_sodium        0.417        0.219         1.90 0.0583
## 3 age                 0.143        0.0678        2.11 0.0362
## 4 platelets          0.0000134 0.0000113      1.19 0.237
## 5 serum_creatinine   -7.24         2.46        -2.94 0.00363
## 6 time                0.00862      0.0103         0.835 0.405
## 7 creatinine_phosphokinase -0.00452 0.00276      -1.64 0.103
```

vif<10 for all variables the model good.

```
#####
### SPLITTING THE DATA ### TRAINING AND TEST SETS ###
#####
###*
```

Let's say we want to split the data in 80:20 for train :test dataset

```
set.seed(299)
ind <- createDataPartition(heart_data$ ejection_fraction,
                           p = 0.8, times = 1, list = FALSE)
length(ind)
```

```
## [1] 241
```

```
train_set <- heart_data[ind, ]
test_set <- heart_data[-ind, ]
nrow(train_set); nrow(test_set)
```

```
## [1] 241
```

```
## [1] 58
```

Training the model

```
lm_fit <- lm(ejection_fraction ~ . , data = train_set)
broom::tidy(lm_fit)
```

```
## # A tibble: 7 x 5
##   term                estimate std.error statistic p.value
##   <chr>              <dbl>      <dbl>      <dbl>   <dbl>
## 1 (Intercept)       -39.2        22.4        -1.75 0.0813
## 2 platelets          0.00000350 0.00000760     0.461 0.645
## 3 serum_creatinine    0.280        0.709         0.395 0.693
## 4 serum_sodium        0.541        0.161         3.36 0.000918
## 5 time                0.00760      0.00979         0.777 0.438
## 6 age                 0.0133       0.0646         0.205 0.838
## 7 creatinine_phosphokinase 0.000392 0.00105         0.372 0.710
```

```
broom::glance(lm_fit)
```

```
## # A tibble: 1 x 12
```



```
##   r.squared adj.r.squared sigma statistic p.value    df logLik   AIC    BIC
##      <dbl>         <dbl> <dbl>      <dbl>   <dbl> <dbl> <dbl> <dbl> <dbl>
## 1    0.0527         0.0284  11.5        2.17  0.0468    6  -927. 1869. 1897.
## # ... with 3 more variables: deviance <dbl>, df.residual <int>, nobs <int>
```

We've built a machine learning model and trained it on `train_set`

```
###* *** Prediction *** # -----
```

```
pred <- predict(object = lm_fit, newdata = test_set, type = "response")
head(pred)
```

```
##          2          3          7          8          11          28
## 39.43998 32.47492 36.84354 34.54559 35.16405 36.88770
```

```
**** Model Evaluation *** # -----
```

```
actual <- test_set$sejection_fraction
mae <- Metrics::mae(actual = actual, predicted = pred)
mse <- Metrics::mse(actual = actual, predicted = pred)
rmse <- Metrics::rmse(actual = actual, predicted = pred)
```

These common metrics are used to evaluate the model.

Table of results

```
knitr::kable(cbind(mae, mse, rmse))
```

mae	mse	rmse
10.22927	165.1528	12.85118