Simple Linear Regression using R

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1. Loading data:

```
setwd("C:/Users/lykha/OneDrive/Documents/1_Qualify-exam-review/5_Applied-regression (Applied)/Prelim-2021-submission")
data <- read.csv("PH1821_data.csv")
data
```

```
##      ID AGE GENDER EDU Hypertension Diabetes Cholesterol HeartAttack Stroke
## 1     1  51      2   2            1        1          20           1      1
## 2     2  61      2   3            2        2          24           2      2
## 3     3  57      2   2            2        2          14           2      2
## 4     4  56      1   2            2        2          11           2      2
## 5     5  56      2   2            2        2          32           2      2
```

```
# Not including the ID column
data <- data[0:nrow(data), 2:ncol(data)]
```

2. Summary stats:

```
## 5 number summary stats:
summary(data)
```

```
##       AGE            GENDER           EDU         Hypertension
##  Min.   :18.00   Min.   :1.000   Min.   :1.000   Min.   :1.000
##  1st Qu.:38.50   1st Qu.:1.000   1st Qu.:3.000   1st Qu.:2.000
##  Median :47.00   Median :2.000   Median :3.000   Median :2.000
##  Mean   :46.89   Mean   :1.632   Mean   :3.071   Mean   :1.847
##  3rd Qu.:55.00   3rd Qu.:2.000   3rd Qu.:3.000   3rd Qu.:2.000
##  Max.   :92.00   Max.   :2.000   Max.   :4.000   Max.   :2.000
##  NA's   :3       NA's   :2       NA's   :6       NA's   :1
##     Diabetes      Cholesterol     HeartAttack        Stroke
##  Min.   :1.000   Min.   :11.00   Min.   :1.000   Min.   :1.000
##  1st Qu.:2.000   1st Qu.:19.50   1st Qu.:2.000   1st Qu.:2.000
##  Median :2.000   Median :25.00   Median :2.000   Median :2.000
##  Mean   :1.941   Mean   :24.53   Mean   :1.992   Mean   :1.995
##  3rd Qu.:2.000   3rd Qu.:30.00   3rd Qu.:2.000   3rd Qu.:2.000
##  Max.   :2.000   Max.   :52.00   Max.   :2.000   Max.   :2.000
```

```
##  NA's   :1       NA's   :7
##  Cardiovascular    Biomarker
##  Min.   :1.000   Min.   :   0.0
##  1st Qu.:2.000   1st Qu.:   0.0
##  Median :2.000   Median :  40.0
##  Mean   :1.989   Mean   : 101.3
##  3rd Qu.:2.000   3rd Qu.: 160.0
##  Max.   :2.000   Max.   :1080.0
##                  NA's   :27
```

NA omit to drop the row with missing data:

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

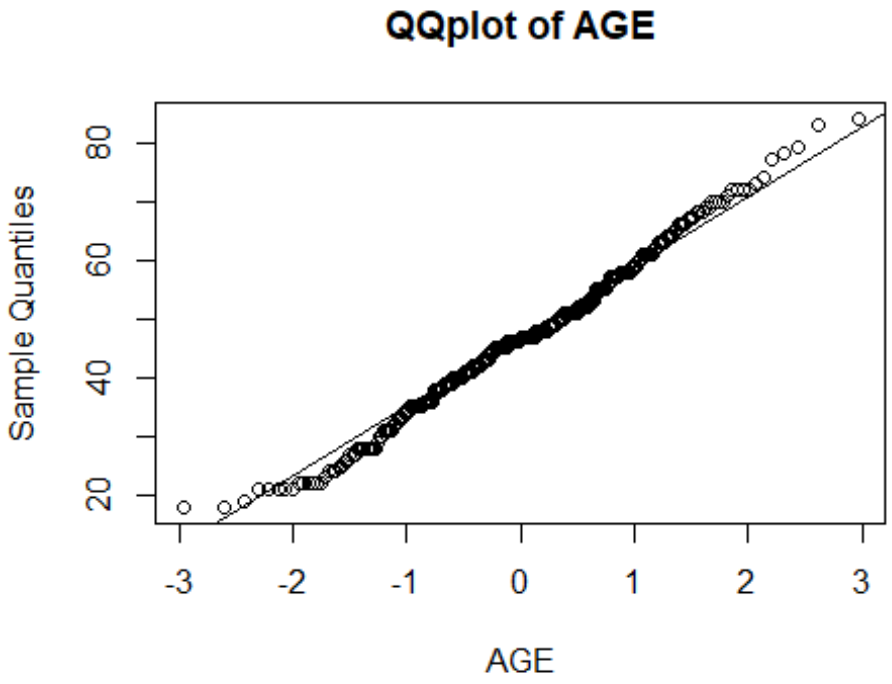
```
## [1] 335
```

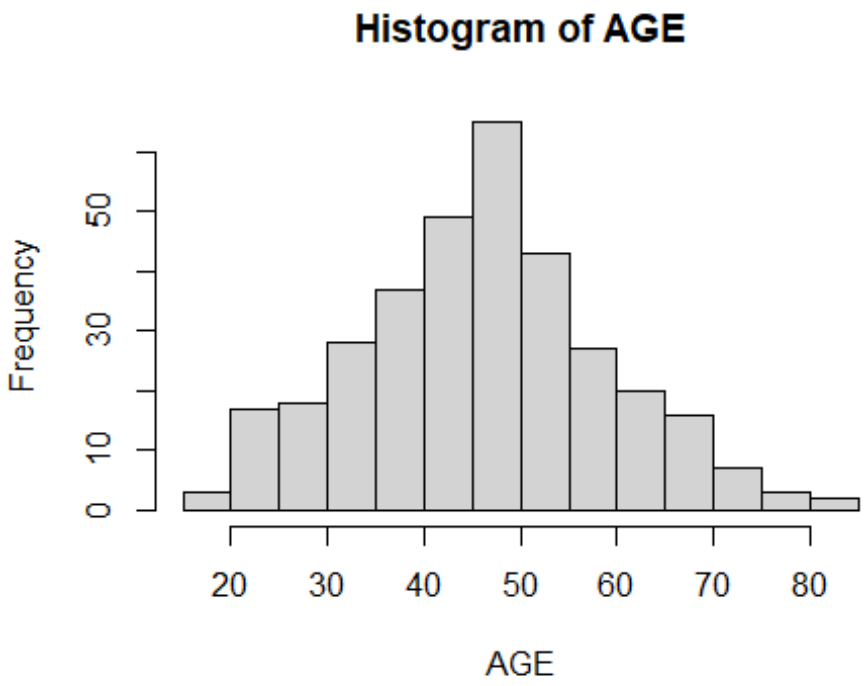
3.1 Normalily checking for continous covariates:

```
s <- data[, c("AGE", "Cholesterol", "Biomarker")]
colnames(s)
```

```
## [1] "AGE"         "Cholesterol" "Biomarker"
```

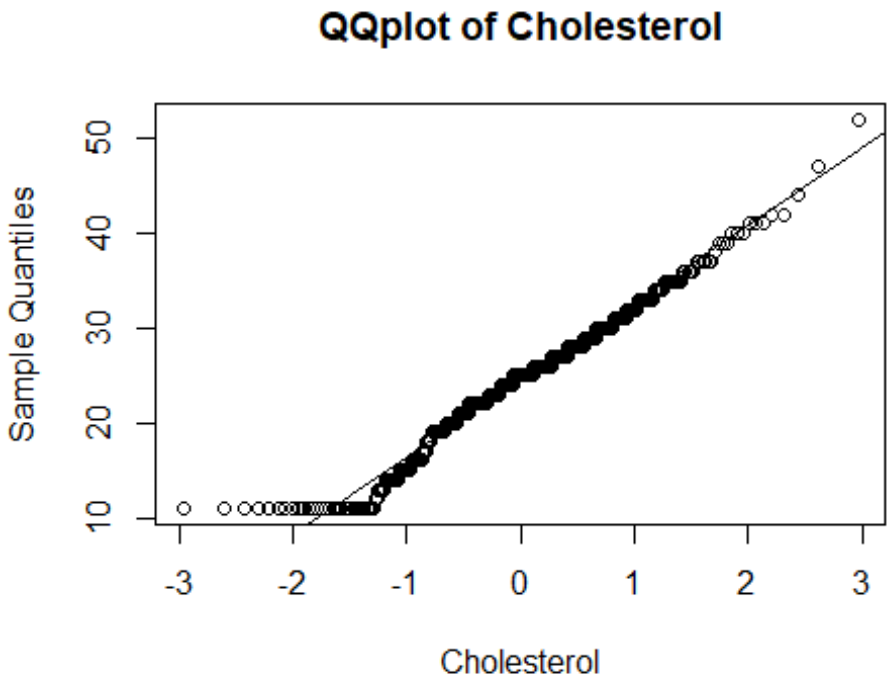
```
for (i in colnames(s)){
  qqnorm(s[,i], main = paste("QQplot of", i), xlab=i)
  qqline(s[,i])
  hist(s[, i], main=paste("Histogram of", i), xlab=i)
  print(paste("Shapiro test for", i))
  print(shapiro.test(s[,i]))
}
```

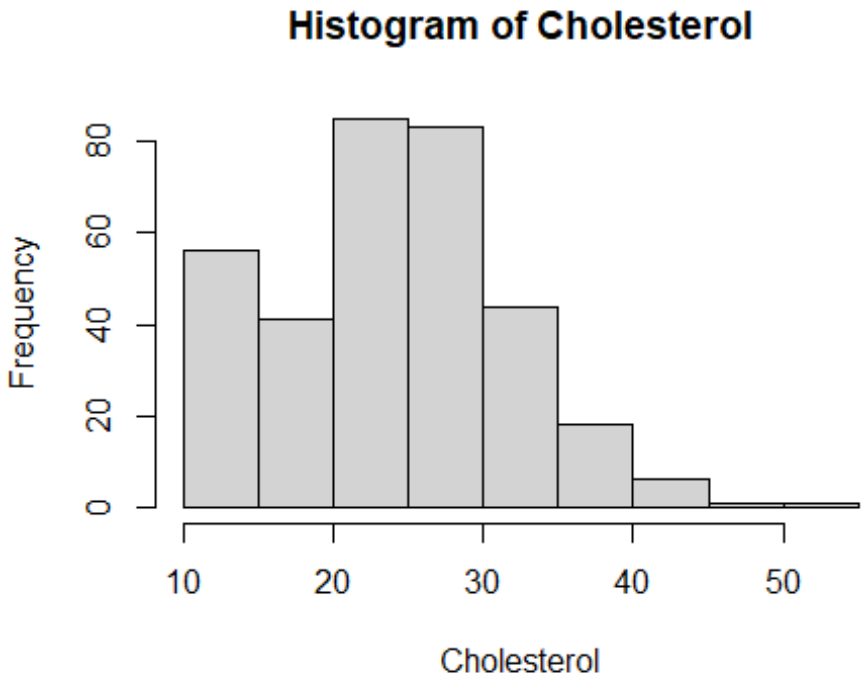




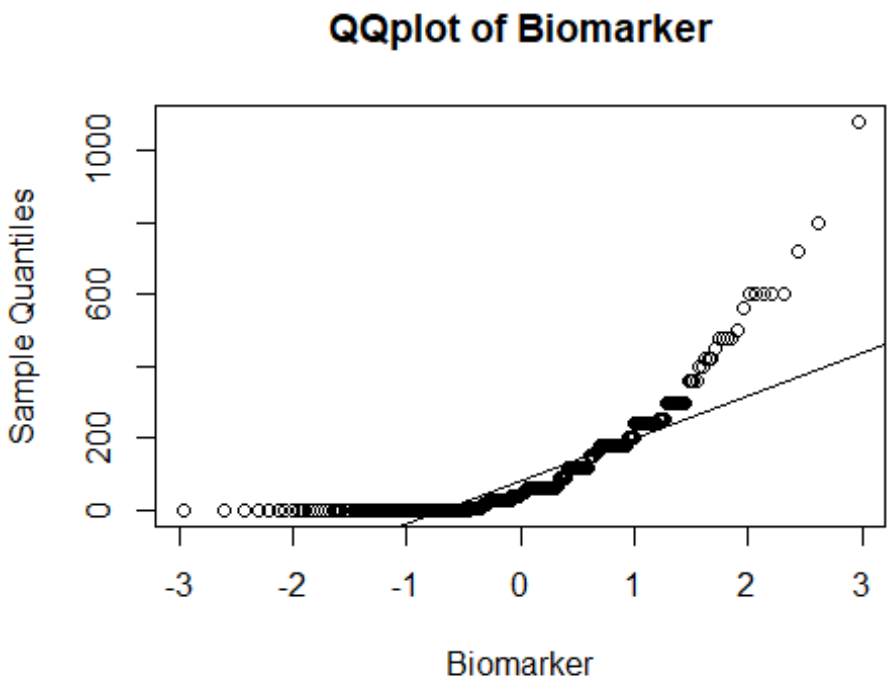

```
## [1] "Shapiro test for AGE"
##
##  Shapiro-Wilk normality test
##
```

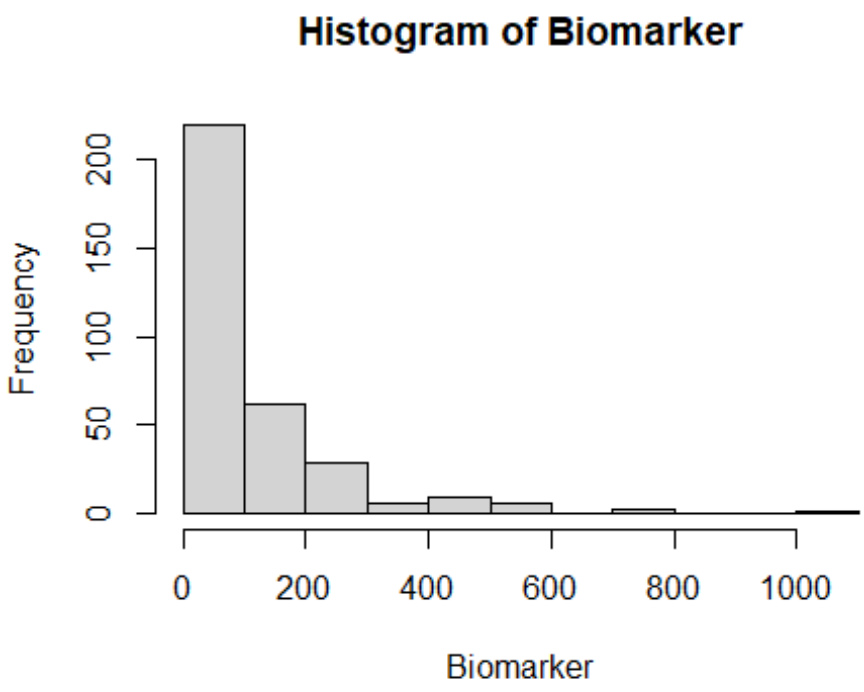
```
## data:  s[, i]
## W = 0.9914, p-value = 0.04838
```





```
## [1] "Shapiro test for Cholesterol"
##
##  Shapiro-Wilk normality test
##
## data:  s[, i]
## W = 0.97614, p-value = 2.366e-05
```






```
## [1] "Shapiro test for Biomarker"
##
##  Shapiro-Wilk normality test
##
```

```
## data:  s[, i]
## W = 0.70935, p-value < 2.2e-16
```

3.2 Frequency table of categorical variables:

```
table_x <- table(data$GENDER)
cumsum_table_x <- cumsum(table_x)
n <- nrow(data)
data_freq <- data.frame(Freq = as.numeric(table_x),  # Create data frame with
relevant values
                        Percent = round(as.numeric(table_x / n)*100, 2),
                        Culmulative_freq = as.numeric(cumsum_table_x),
                        Culmulative_percent = round(as.numeric(cumsum_table_x
/ n)*100, 2))
rownames(data_freq) <- c("Male", "Female")
data_freq
```

```
##        Freq Percent Culmulative_freq Culmulative_percent
## Male    129   38.51              129               38.51
## Female  206   61.49              335              100.00
```

```
table_x <- table(data$EDU)
cumsum_table_x <- cumsum(table_x)
n <- nrow(data)
data_freq <- data.frame(Freq = as.numeric(table_x),  # Create data frame with
relevant values
                        Percent = round(as.numeric(table_x / n)*100, 2),
                        Culmulative_freq = as.numeric(cumsum_table_x),
                        Culmulative_percent = round(as.numeric(cumsum_table_x
/ n)*100, 2))
rownames(data_freq) <- c(1, 2, 3, 4)
data_freq
```

```
##   Freq Percent Culmulative_freq Culmulative_percent
## 1    7    2.09                7                2.09
## 2   34   10.15               41               12.24
## 3  207   61.79              248               74.03
## 4   87   25.97              335              100.00
```

```
table_x <- table(data$Hypertension)
cumsum_table_x <- cumsum(table_x)
n <- nrow(data)
data_freq <- data.frame(Freq = as.numeric(table_x),  # Create data frame with
relevant values
                        Percent = round(as.numeric(table_x / n)*100, 2),
                        Culmulative_freq = as.numeric(cumsum_table_x),
                        Culmulative_percent = round(as.numeric(cumsum_table_x
/ n)*100, 2))
rownames(data_freq) <- c("No", "Yes")
data_freq
```

```
##     Freq Percent Culmulative_freq Culmulative_percent
## No    51   15.22               51               15.22
## Yes  284   84.78              335              100.00
```

```
table_x <- table(data$Diabetes)
cumsum_table_x <- cumsum(table_x)
n <- nrow(data)
data_freq <- data.frame(Freq = as.numeric(table_x),  # Create data frame with
relevant values
                        Percent = round(as.numeric(table_x / n)*100, 2),
                        Culmulative_freq = as.numeric(cumsum_table_x),
                        Culmulative_percent = round(as.numeric(cumsum_table_x
/ n)*100, 2))
rownames(data_freq) <- c("No", "Yes")
data_freq
```

```
##     Freq Percent Culmulative_freq Culmulative_percent
## No    19    5.67               19                5.67
## Yes  316   94.33              335              100.00
```

```
table_x <- table(data$HeartAttack)
cumsum_table_x <- cumsum(table_x)
n <- nrow(data)
data_freq <- data.frame(Freq = as.numeric(table_x),  # Create data frame with
relevant values
                        Percent = round(as.numeric(table_x / n)*100, 2),
                        Culmulative_freq = as.numeric(cumsum_table_x),
                        Culmulative_percent = round(as.numeric(cumsum_table_x
/ n)*100, 2))
rownames(data_freq) <- c("No", "Yes")
data_freq
```

```
##     Freq Percent Culmulative_freq Culmulative_percent
## No     3     0.9                3                 0.9
## Yes  332    99.1              335               100.0
```

```
table_x <- table(data$Stroke)
cumsum_table_x <- cumsum(table_x)
n <- nrow(data)
data_freq <- data.frame(Freq = as.numeric(table_x),  # Create data frame with
relevant values
                        Percent = round(as.numeric(table_x / n)*100, 2),
                        Culmulative_freq = as.numeric(cumsum_table_x),
                        Culmulative_percent = round(as.numeric(cumsum_table_x
/ n)*100, 2))
rownames(data_freq) <- c("No", "Yes")
data_freq
```

```
##     Freq Percent Culmulative_freq Culmulative_percent
## No     2     0.6                2                 0.6
## Yes  333    99.4              335               100.0
```

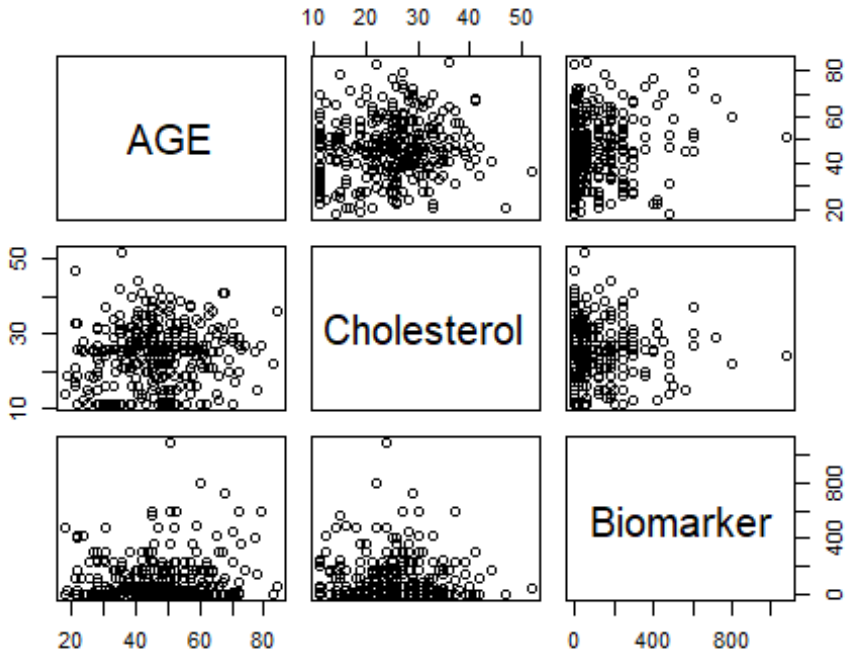
```
table_x <- table(data$Cardiovascular)
cumsum_table_x <- cumsum(table_x)
n <- nrow(data)
data_freq <- data.frame(Freq = as.numeric(table_x),  # Create data frame with
relevant values
                        Percent = round(as.numeric(table_x / n)*100, 2),
                        Culmulative_freq = as.numeric(cumsum_table_x),
                        Culmulative_percent = round(as.numeric(cumsum_table_x
/ n)*100, 2))
rownames(data_freq) <- c("No", "Yes")
data_freq
```

```
##     Freq Percent Culmulative_freq Culmulative_percent
## No     4    1.19                4                1.19
## Yes  331   98.81              335              100.00
```

Row names are always 0 then 1 #find correct matched categories using the given description

3.3 Scatter plot of the continous data:

```
pairs(s)
```




```
for (i in colnames(s)){
  print(paste("Correlation test for:", i))
  print(cor.test(data$Cholesterol, s[, i]))
}
```

```
## [1] "Correlation test for: AGE"
##
##  Pearson's product-moment correlation
##
## data:  data$Cholesterol and s[, i]
## t = 1.9497, df = 333, p-value = 0.05205
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.000926544  0.210990197
## sample estimates:
##      cor
## 0.106238
##
## [1] "Correlation test for: Cholesterol"
##
##  Pearson's product-moment correlation
##
## data:  data$Cholesterol and s[, i]
## t = Inf, df = 333, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  1 1
## sample estimates:
## cor
##   1
##
## [1] "Correlation test for: Biomarker"
##
##  Pearson's product-moment correlation
##
## data:  data$Cholesterol and s[, i]
## t = 0.44256, df = 333, p-value = 0.6584
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.08312477  0.13105877
## sample estimates:
##        cor
## 0.02424523
```

4. Regression model:

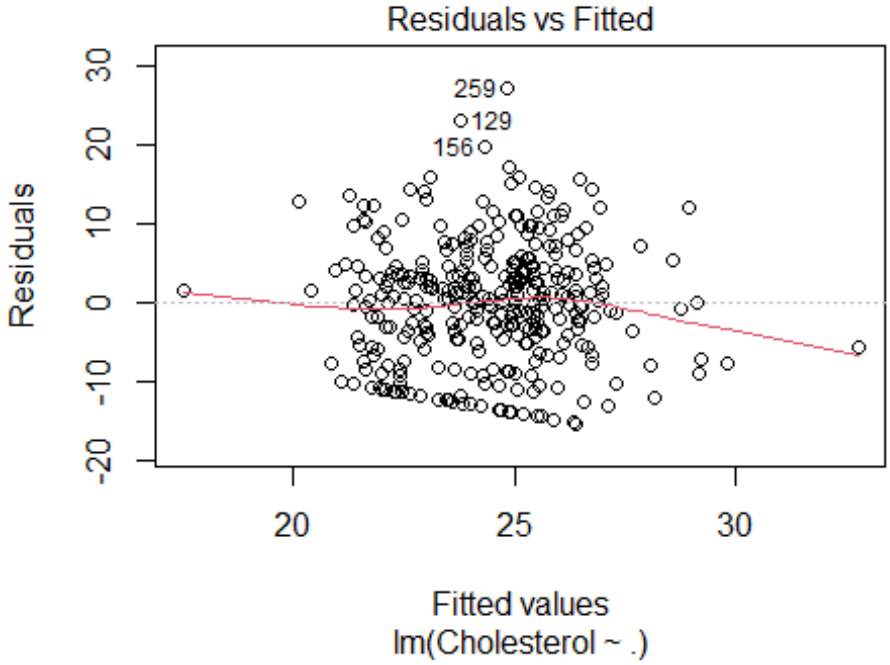
```
attach(data)
mod <- lm(Cholesterol ~ ., data = data)
summary(mod)

##
## Call:
## lm(formula = Cholesterol ~ ., data = data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
```

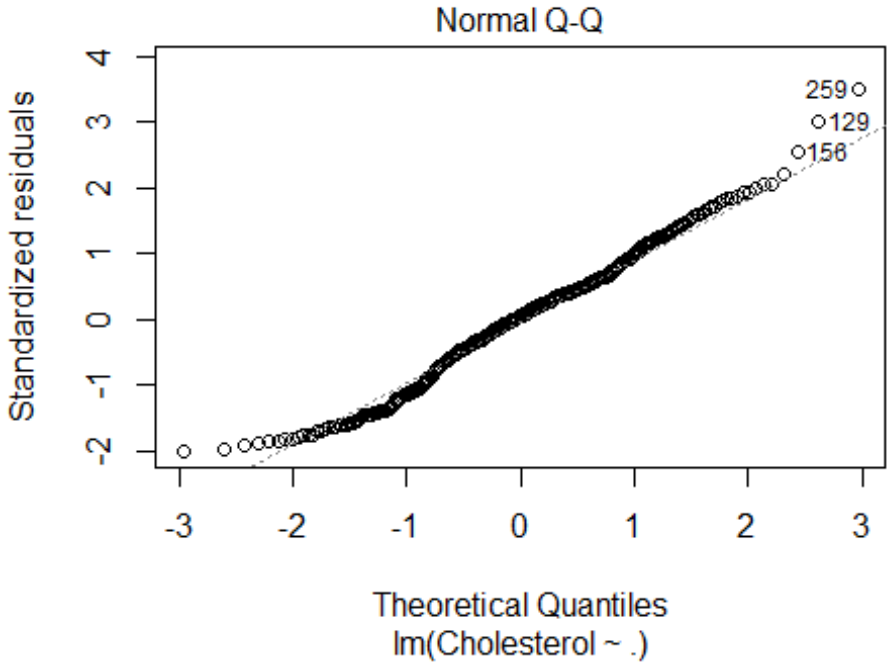
```
## -15.4071  -5.1523   0.4122   4.5665  27.1733
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)    23.951540  14.998770   1.597   0.1113
## AGE             0.063415   0.035540   1.784   0.0753 .
## GENDER          2.328209   0.924255   2.519   0.0122 *
## EDU            -1.047214   0.683895  -1.531   0.1267
## Hypertension    0.390768   1.319737   0.296   0.7673
## Diabetes        1.787375   2.080401   0.859   0.3909
## HeartAttack     4.117977   5.031286   0.818   0.4137
## Stroke         -2.530779   6.293550  -0.402   0.6879
## Cardiovascular -5.271969   4.026906  -1.309   0.1914
## Biomarker       0.001814   0.002946   0.616   0.5385
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.806 on 325 degrees of freedom
## Multiple R-squared:  0.05448,    Adjusted R-squared:  0.0283
## F-statistic: 2.081 on 9 and 325 DF,  p-value: 0.03079
```

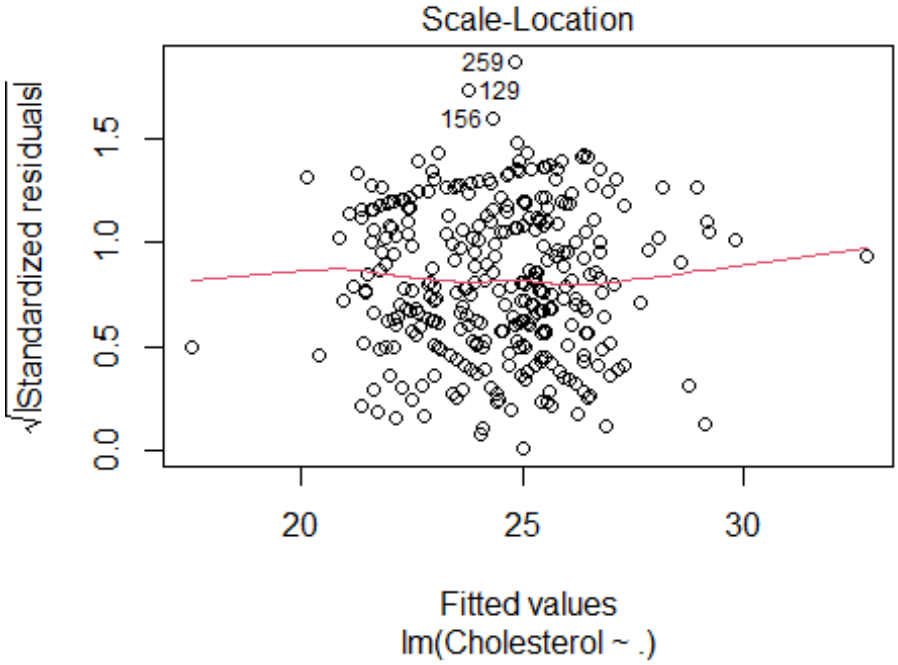
5. Checking the regression model assumptions on residuals:

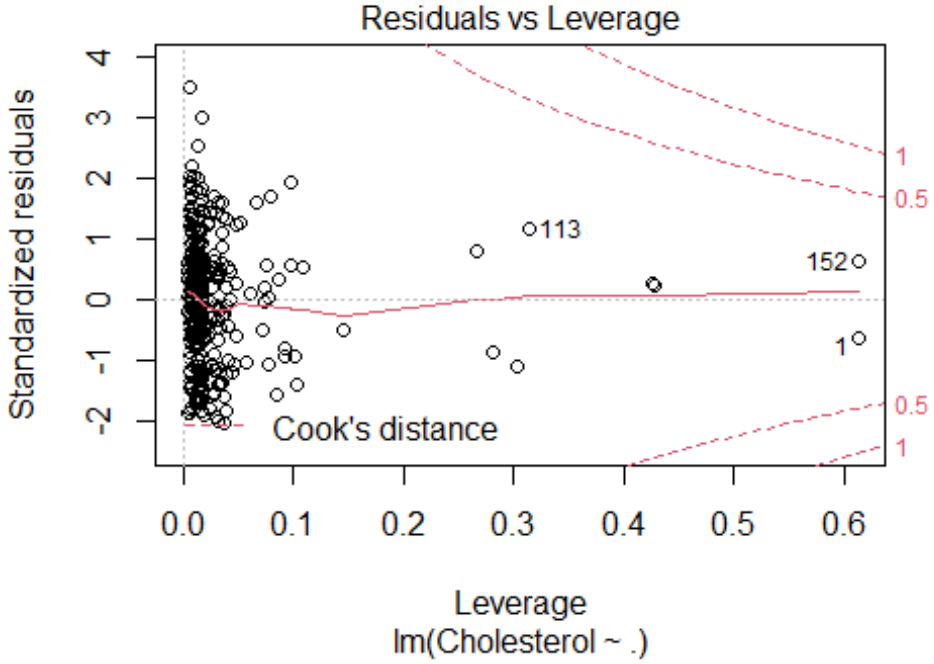
1.linearity 2.normality 3.homoscadescity 4.independency

```
plot(mod)
```


Residuals vs Fitted
259
129
156
Residuals
30
20
10
0
-10
-20
20
25
30
Fitted values
lm(Cholesterol ~ .)


Normal Q-Q
259
129
156
Standardized residuals
4
3
2
1
0
-1
-2
-3
-2
-1
0
1
2
3
Theoretical Quantiles
lm(Cholesterol ~ .)


Scale-Location
259
129
156
√|Standardized residuals|
0.0
0.5
1.0
1.5
20
25
30
Fitted values
lm(Cholesterol ~ .)


Residuals vs Leverage
Standardized residuals
4
3
2
1
0
-1
-2
113
152
1
Cook's distance
1
0.5
0.5
1
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Leverage
lm(Cholesterol ~ .)

In normal q-q plot drawn, the residuals are almost linearly distributed.(but lets check normaly futher using other tests)

In scale-location plot,all the residuals are scattered(i.e none of the points are clustered at one spot). Therefore, HOMOSCADESCITY IS MET on residuals.

Checking for normality on residuals:

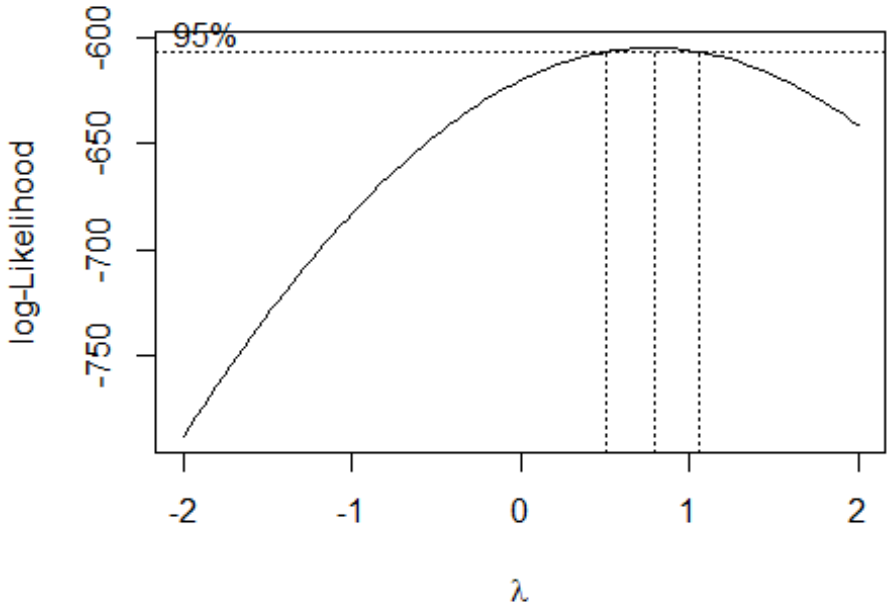
```
shapiro.test(mod$residuals)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  mod$residuals
## W = 0.98705, p-value = 0.00432
```

Here the probability value of both Shapiro Wilk is more than 0.05 hence, we accept null hypothesis saying that the residual data is normally distributed. And we also have skewness nearly equal to zero and kurtosis nearly equal to 3 where we can say that residual data is normally distributed. Therefore, NORMALITY IS MET on residuals

No violation so no need for Box-cox transforamtion. # Box-cox transformation (if necessary): #find optimal lambda for Box-Cox transformation

```
library(MASS)
bc <- boxcox(Cholesterol ~., data = data)
```

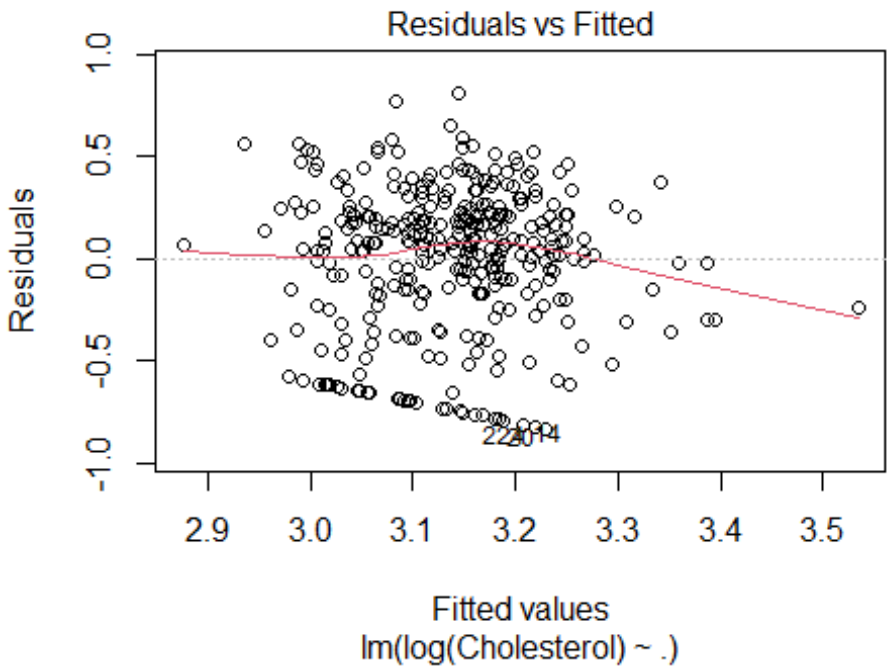


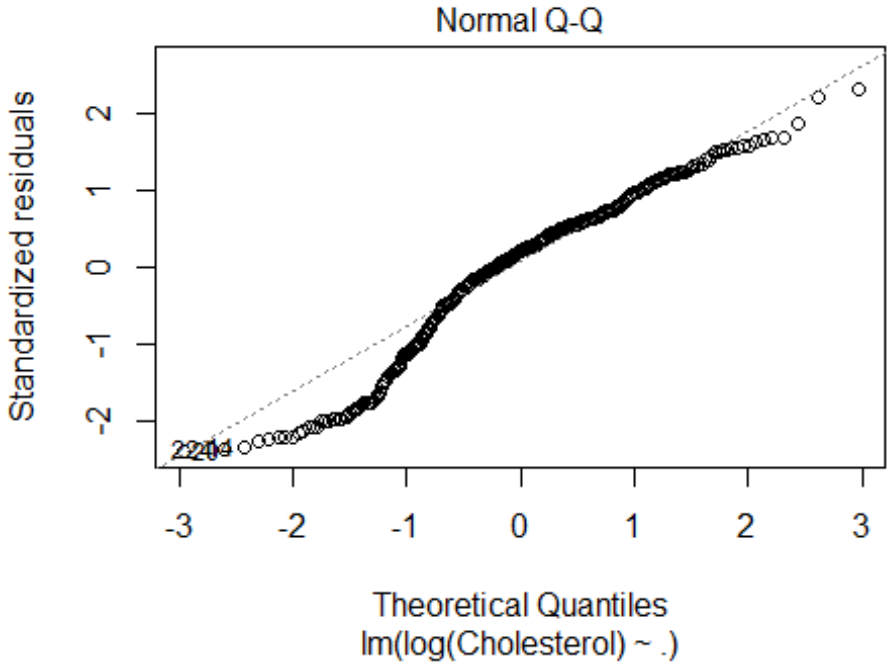

```
(lambda <- bc$x[which.max(bc$y)])
```

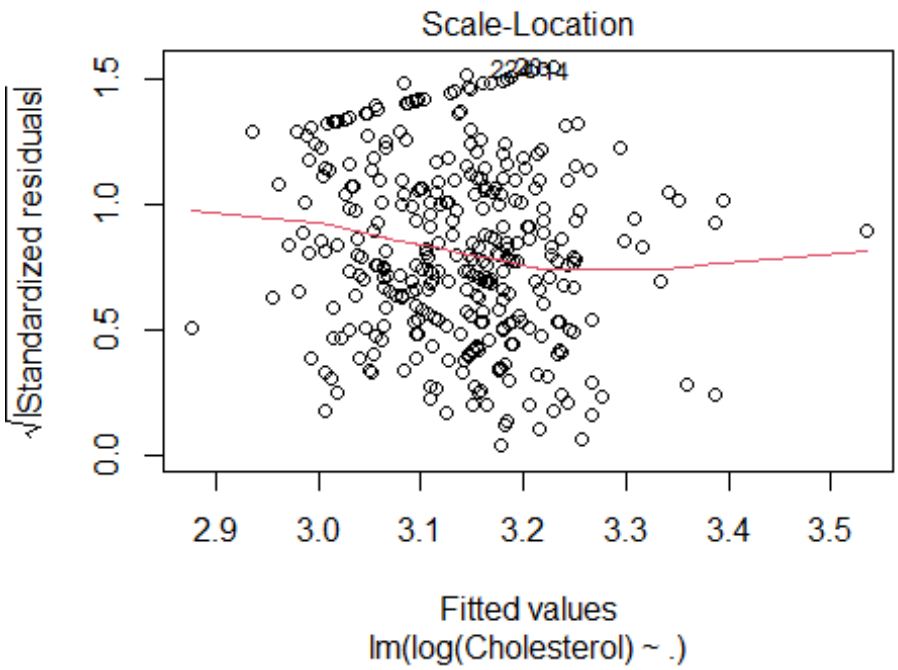
```
## [1] 0.7878788

#fit new linear regression model using the Box-Cox transformation
new_model <- lm(((Cholesterol^lambda-1)/lambda) ~ ., data=data)
```

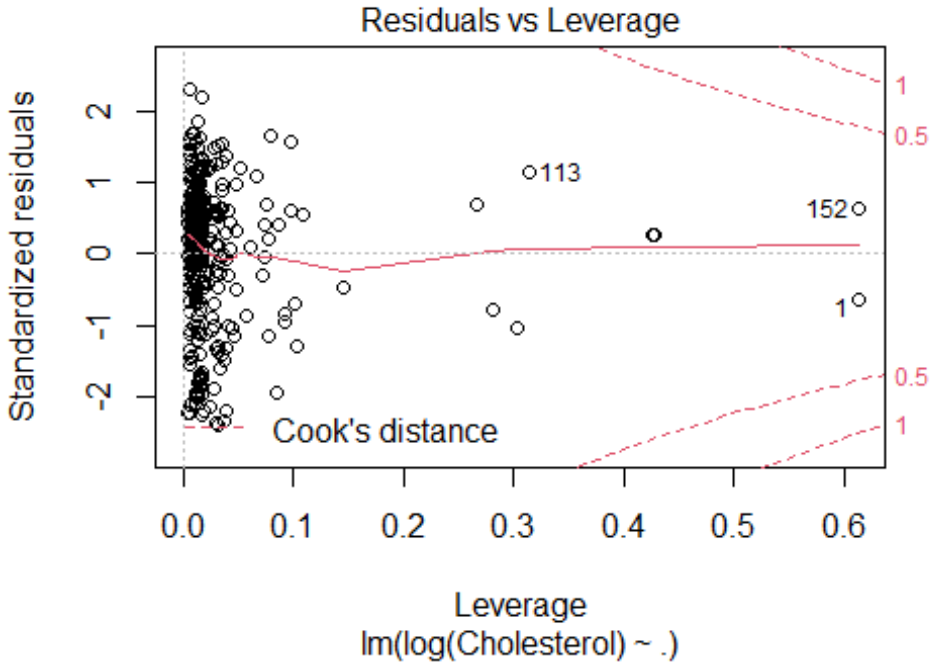
For convinient, the log transformation is performed to save time:

```
trans.mod <- lm(log(Cholesterol) ~., data = data)
summary(trans.mod)

##
## Call:
## lm(formula = log(Cholesterol) ~ ., data = data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.83105 -0.17185  0.06837  0.22225  0.80741
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)     3.2037268  0.6786322   4.721  3.5e-06 ***
## AGE             0.0035566  0.0016080   2.212   0.0277 *
## GENDER          0.1027026  0.0418187   2.456   0.0146 *
## EDU            -0.0413272  0.0309434  -1.336   0.1826
## Hypertension    0.0271980  0.0597126   0.455   0.6491
## Diabetes        0.0824822  0.0941295   0.876   0.3815
## HeartAttack     0.1296525  0.2276448   0.570   0.5694
## Stroke         -0.1392443  0.2847570  -0.489   0.6252
## Cardiovascular -0.2380750  0.1822008  -1.307   0.1923
## Biomarker       0.0001323  0.0001333   0.992   0.3217
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3532 on 325 degrees of freedom
## Multiple R-squared:  0.05724,    Adjusted R-squared:  0.03113
## F-statistic: 2.192 on 9 and 325 DF,  p-value: 0.02229

plot(trans.mod)
```


Residuals vs Fitted
Residuals
1.0
0.5
0.0
-0.5
-1.0
2.9
3.0
3.1
3.2
3.3
3.4
3.5
Fitted values
lm(log(Cholesterol) ~ .)


Normal Q-Q
Standardized residuals
2
1
0
-1
-2
-3
-2
-1
0
1
2
3
Theoretical Quantiles
lm(log(Cholesterol) ~ .)






```
shapiro.test(mod$residuals)

##
##  Shapiro-Wilk normality test
```

```
##
## data:  mod$residuals
## W = 0.98705, p-value = 0.00432
```

6. Stepwise selection for multiple covariates:

```
library(MASS)
# Fit the full model
full.model <- lm(log(Cholesterol) ~., data = data)
# Stepwise regression model
step.model <- stepAIC(full.model, direction = "both", scope = list(lower = ~
Biomarker),
                      trace = FALSE)
summary(step.model)
```

```
##
## Call:
## lm(formula = log(Cholesterol) ~ AGE + GENDER + Biomarker, data = data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.85837 -0.18054  0.06003  0.23485  0.81283
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.7654163  0.0990560  27.918  < 2e-16 ***
## AGE         0.0035852  0.0015156   2.366  0.01858 *
## GENDER      0.1185996  0.0400153   2.964  0.00326 **
## Biomarker   0.0001346  0.0001314   1.024  0.30645
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3525 on 331 degrees of freedom
## Multiple R-squared:  0.04344,    Adjusted R-squared:  0.03477
## F-statistic: 5.011 on 3 and 331 DF,  p-value: 0.00207
```

Final model

```
exp(0.0001346)
```

```
## [1] 1.000135
```