Life Expectancy Prediction

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Abstract

We have implemented a Linear Regression model to predict the life expectancy of the human population with an adjusted R-squared value of , MSE of , and MAE of .

Introduction

The goal of this project is to build a Linear Regression model that can predict the life expectancy of the human population based on several factors such as the amount of alcohol consumption, average Body Mass Index (BMI), immunization of various vaccines among 1-year-olds such as Hepatitis B, Polio, and Diphtheria vaccines, and more, and also derive insights into what factors are significant in determining a higher or lower life expectancy of the human population.

Materials and Methods

Dataset

The data related to life expectancy and health factors for 193 countries is taken from the Global Health Observatory (GHO) data repository under the World Health Organization (WHO). Its corresponding economic data was collected from the United Nations website for a period of 16 years (2000-2015).

The dataset is available at https://www.kaggle.com/datasets/kumarajarshi/life-expectancy-who.

```r
life = read.csv('Life Expectancy Data.csv') # Load Dataset
```

`Life Expectancy Data.csv` contains the following fields:

- `Country` - Country Observed.
- `Year` - Year Observed.
- `Status` - Developed or Developing status.
- `Life.expectancy` - Life Expectancy in age.
- `Adult.Mortality` - Adult Mortality Rates on both sexes (probability of dying between 15-60 years/1000 population).
- `infant.deaths` - Number of Infant Deaths per 1000 population.
- `Alcohol` - Alcohol recorded per capita (15+) consumption (in litres of pure alcohol).
- `percentage.expenditure` - Expenditure on health as a percentage of Gross Domestic Product per capita (%).
- `Hepatitis.B` - Hepatitis B (HepB) immunization coverage among 1-year-olds (%).
- `Measles` - Number of reported Measles cases per 1000 population.
- `BMI` - Average Body Mass Index of entire population.
- `under.five.deaths` - Number of under-five deaths per 1000 population.
- `Polio` - Polio (Pol3) immunization coverage among 1-year-olds (%).
- `Total.expenditure` - General government expenditure on health as a percentage of total government expenditure (%).
- `Diphtheria` - Diphtheria tetanus toxoid and pertussis (DTP3) immunization coverage among 1-year-olds (%).
- `HIV.AIDS` - Deaths per 1000 live births due to HIV/AIDS (0-4 years).
- `GDP` - Gross Domestic Product per capita (in USD).
- `Population` - Population of the country.
- `thinness..1.19.years` - Prevalence of thinness among children and adolescents for Age 10 to 19 (%).
- `thinness.5.9.years` - Prevalence of thinness among children for Age 5 to 9 (%).
- `Income.composition.of.resources` - Human Development Index in terms of income composition of resources (index ranging from 0 to 1).
- `Schooling` - Number of years of Schooling (years).

In total, there are 2938 observations of 22 variables with 20 of them being numerical and 2 categorical (`Country` and `Status`).
We will be using `Life.expectancy` to predict the life expectancy of the human population with the given dependent variables in the dataset.

Clean Data

We will drop any observation that does not contain any value in any of its columns.

```r
life = na.omit(life)
```

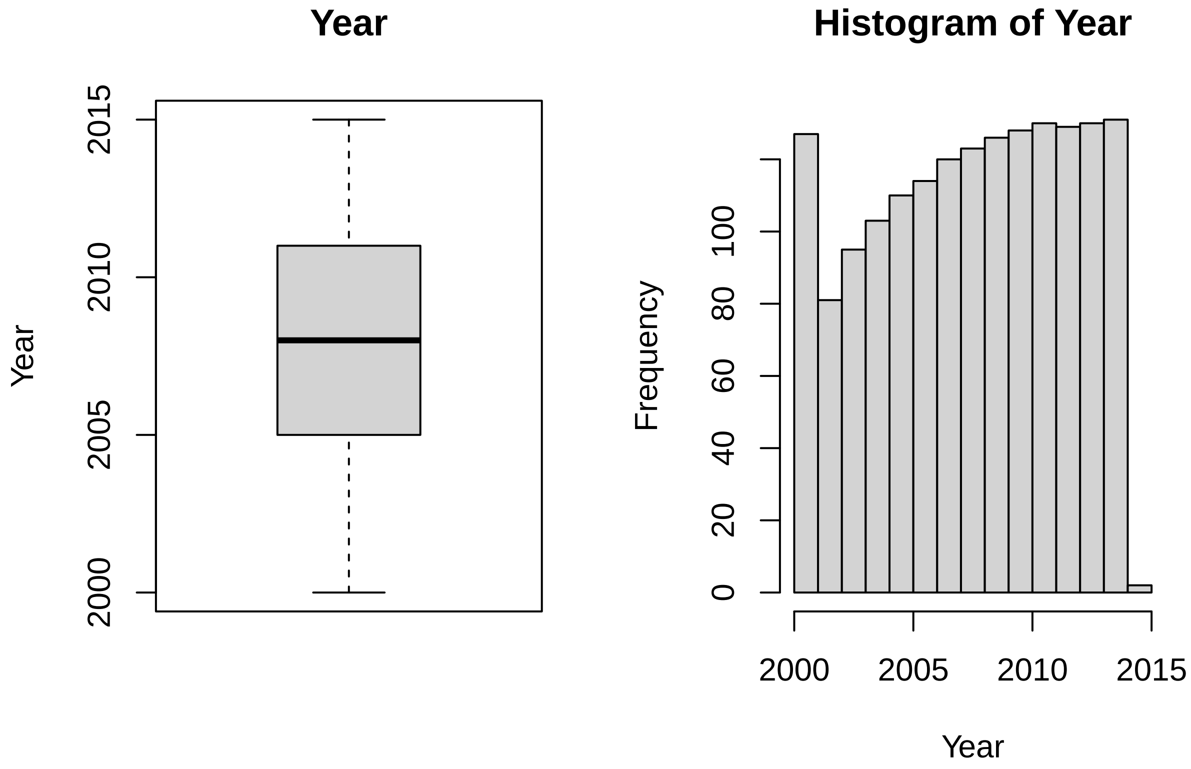
This shrinks our dataset to 1649 observations.

Data Exploration

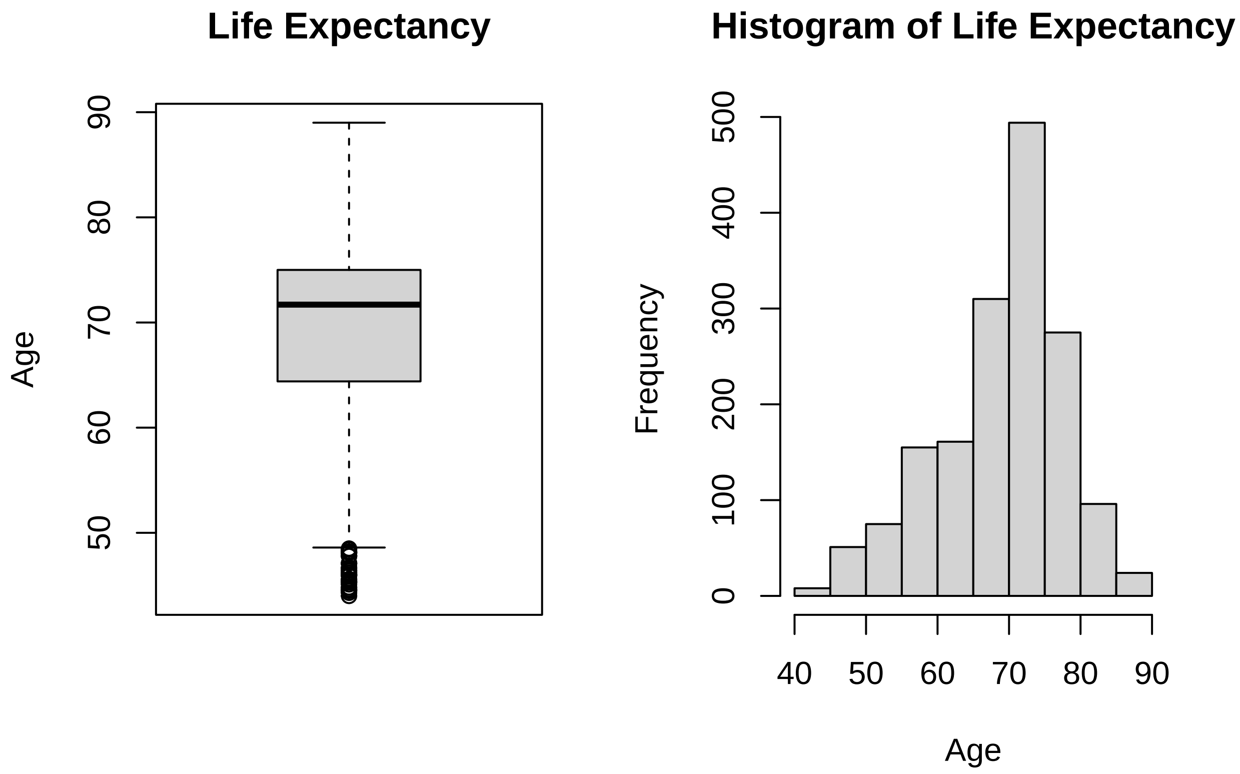
```
summary(life)
```

```
##    Country               Year         Status          Life.expectancy
##  Length:1649        Min.   :2000   Length:1649        Min.   :44.0
##  Class :character   1st Qu.:2005   Class :character   1st Qu.:64.4
##  Mode  :character   Median :2008   Mode  :character   Median :71.7
##                     Mean   :2008                      Mean   :69.3
##                     3rd Qu.:2011                      3rd Qu.:75.0
##                     Max.   :2015                      Max.   :89.0
##  Adult.Mortality infant.deaths        Alcohol       percentage.expenditure
##  Min.   :  1.0   Min.   :   0.00   Min.   : 0.010   Min.   :    0.00
##  1st Qu.: 77.0   1st Qu.:   1.00   1st Qu.: 0.810   1st Qu.:   37.44
##  Median :148.0   Median :   3.00   Median : 3.790   Median :  145.10
##  Mean   :168.2   Mean   :  32.55   Mean   : 4.533   Mean   :  698.97
##  3rd Qu.:227.0   3rd Qu.:  22.00   3rd Qu.: 7.340   3rd Qu.:  509.39
##  Max.   :723.0   Max.   :1600.00   Max.   :17.870   Max.   :18961.35
##   Hepatitis.B       Measles            BMI        under.five.deaths
##  Min.   : 2.00   Min.   :     0   Min.   : 2.00   Min.   :   0.00
##  1st Qu.:74.00   1st Qu.:     0   1st Qu.:19.50   1st Qu.:   1.00
##  Median :89.00   Median :    15   Median :43.70   Median :   4.00
##  Mean   :79.22   Mean   :  2224   Mean   :38.13   Mean   :  44.22
##  3rd Qu.:96.00   3rd Qu.:   373   3rd Qu.:55.80   3rd Qu.:  29.00
##  Max.   :99.00   Max.   :131441   Max.   :77.10   Max.   :2100.00
##      Polio       Total.expenditure   Diphtheria       HIV.AIDS
##  Min.   : 3.00   Min.   : 0.740    Min.   : 2.00   Min.   : 0.100
##  1st Qu.:81.00   1st Qu.: 4.410    1st Qu.:82.00   1st Qu.: 0.100
##  Median :93.00   Median : 5.840    Median :92.00   Median : 0.100
##  Mean   :83.56   Mean   : 5.956    Mean   :84.16   Mean   : 1.984
##  3rd Qu.:97.00   3rd Qu.: 7.470    3rd Qu.:97.00   3rd Qu.: 0.700
##  Max.   :99.00   Max.   :14.390    Max.   :99.00   Max.   :50.600
##       GDP              Population        thinness..1.19.years
##  Min.   :     1.68   Min.   :3.400e+01   Min.   : 0.100
##  1st Qu.:   462.15   1st Qu.:1.919e+05   1st Qu.: 1.600
##  Median :  1592.57   Median :1.420e+06   Median : 3.000
##  Mean   :  5566.03   Mean   :1.465e+07   Mean   : 4.851
##  3rd Qu.:  4718.51   3rd Qu.:7.659e+06   3rd Qu.: 7.100
##  Max.   :119172.74   Max.   :1.294e+09   Max.   :27.200
##  thinness.5.9.years Income.composition.of.resources   Schooling
##  Min.   : 0.100     Min.   :0.0000                  Min.   : 4.20
##  1st Qu.: 1.700     1st Qu.:0.5090                  1st Qu.:10.30
##  Median : 3.200     Median :0.6730                  Median :12.30
##  Mean   : 4.908     Mean   :0.6316                  Mean   :12.12
##  3rd Qu.: 7.100     3rd Qu.:0.7510                  3rd Qu.:14.00
##  Max.   :28.200     Max.   :0.9360                  Max.   :20.70
```

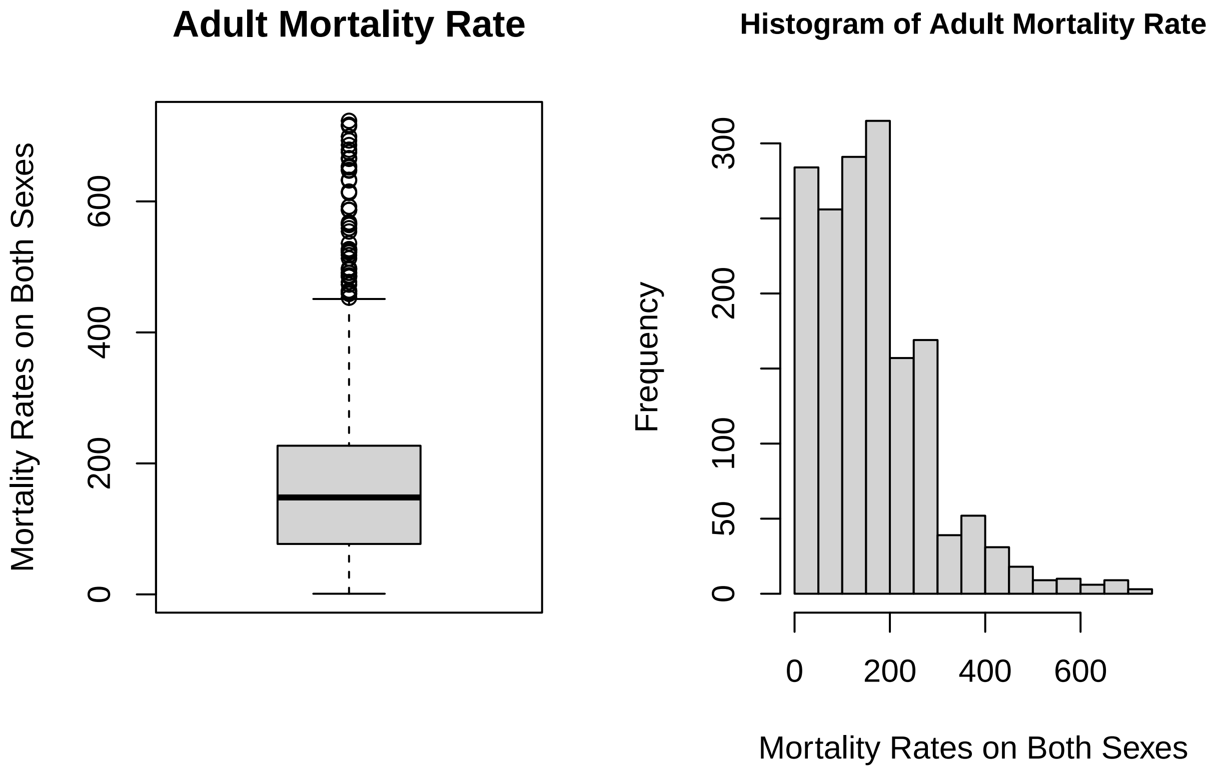
```
par(mfrow = c(1, 2))
boxplot(life$Year, main = 'Year', ylab = 'Year')
hist(life$Year, main = 'Histogram of Year', xlab = 'Year')
```



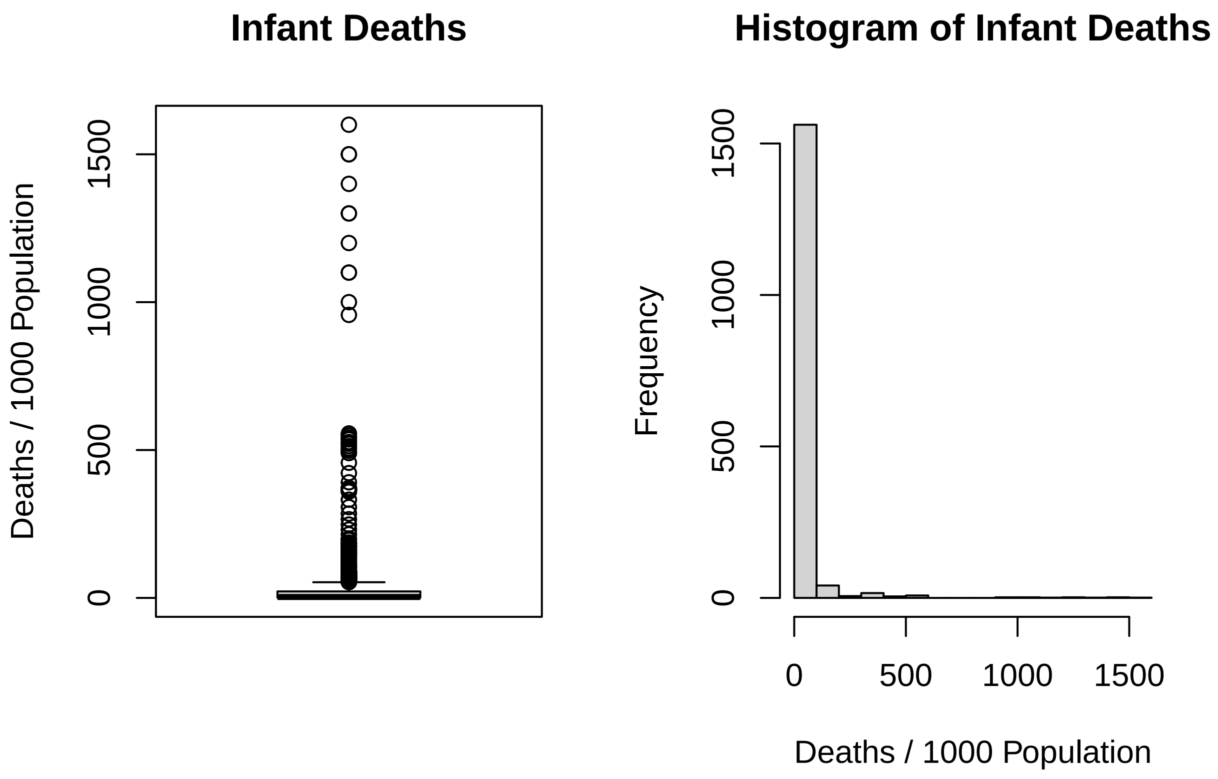
```
par(mfrow = c(1, 2))
boxplot(life$Life.expectancy, main = 'Life Expectancy', ylab = 'Age')
hist(life$Life.expectancy, main = 'Histogram of Life Expectancy', xlab = 'Age')
```



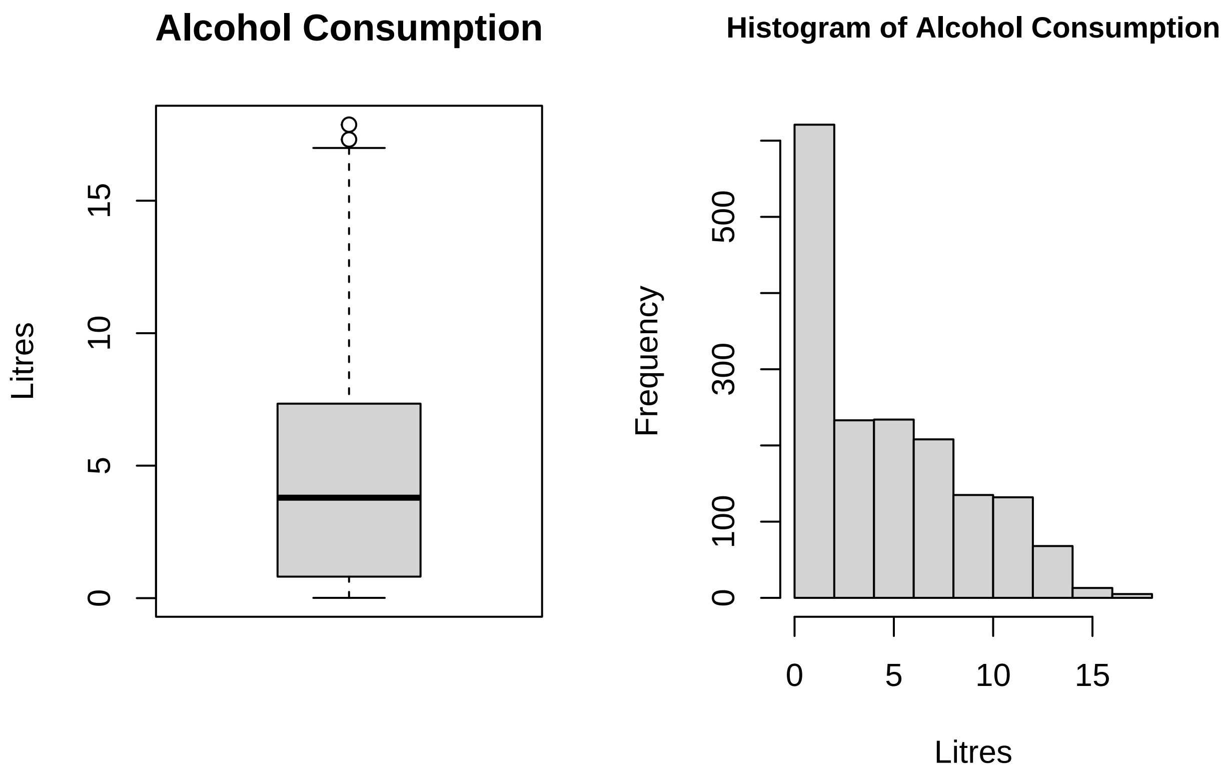
```r
par(mfrow = c(1, 2))
boxplot(life$Adult.Mortality, main = 'Adult Mortality Rate', ylab = 'Mortality Rates on Both Sexes')
hist(
  life$Adult.Mortality,
  main = 'Histogram of Adult Mortality Rate',
  xlab = 'Mortality Rates on Both Sexes',
  cex.main = 0.9
)
```



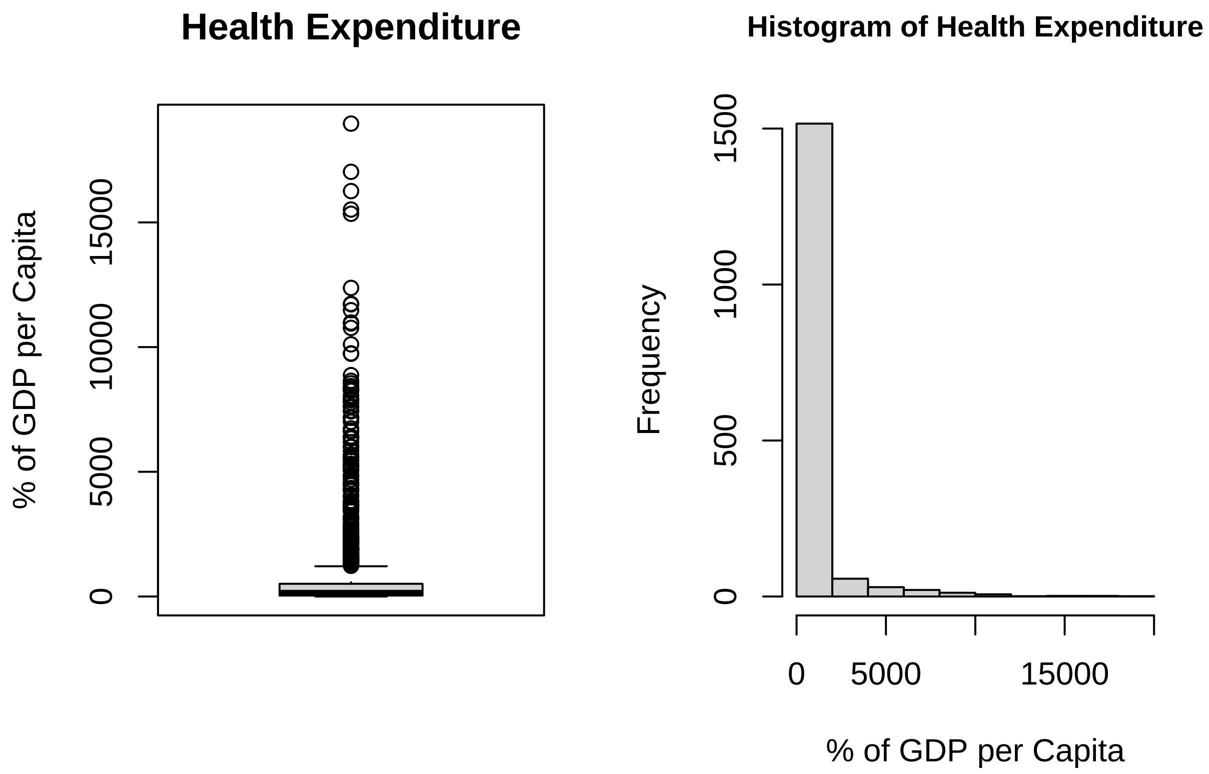
```
par(mfrow = c(1, 2))
boxplot(life$infant.deaths, main = 'Infant Deaths', ylab = 'Deaths / 1000 Population')
hist(life$infant.deaths, main = 'Histogram of Infant Deaths', xlab = 'Deaths / 1000 Population')
```



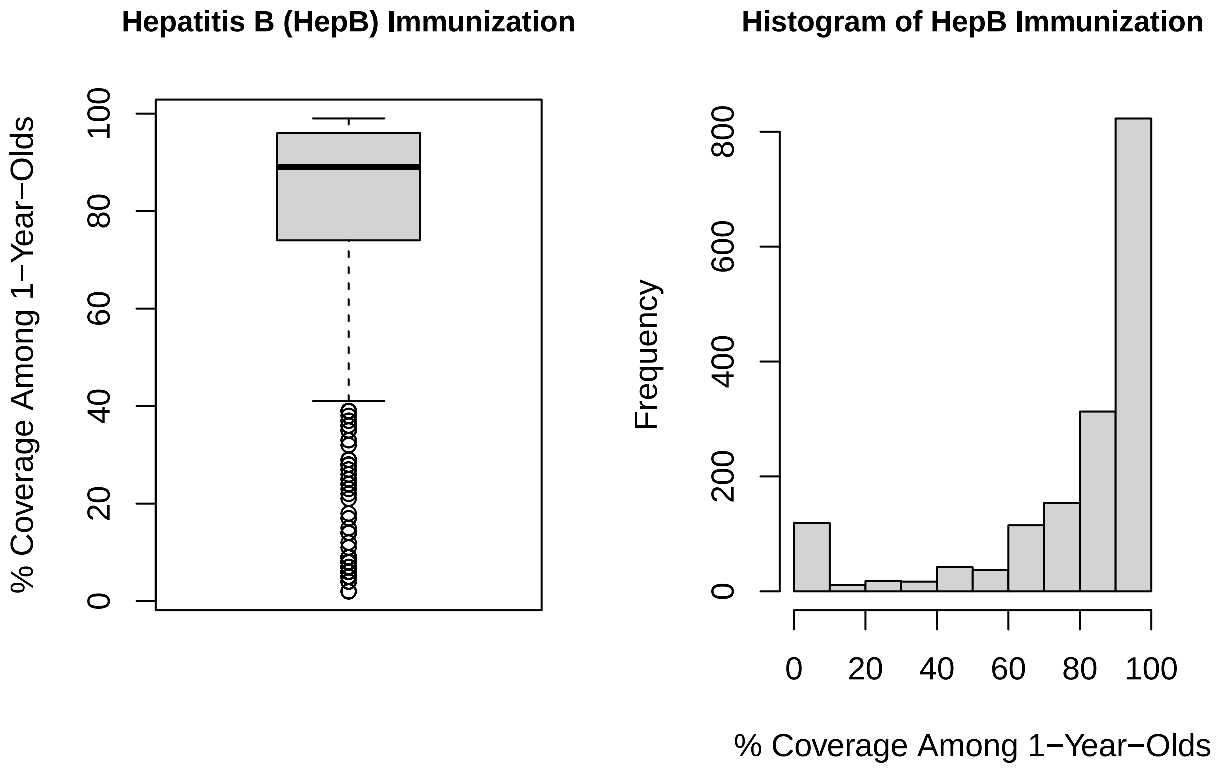
```
par(mfrow = c(1, 2))
boxplot(life$Alcohol, main = 'Alcohol Consumption', ylab = 'Litres')
hist(life$Alcohol,
     main = 'Histogram of Alcohol Consumption',
     xlab = 'Litres',
     cex.main = 0.9)
```



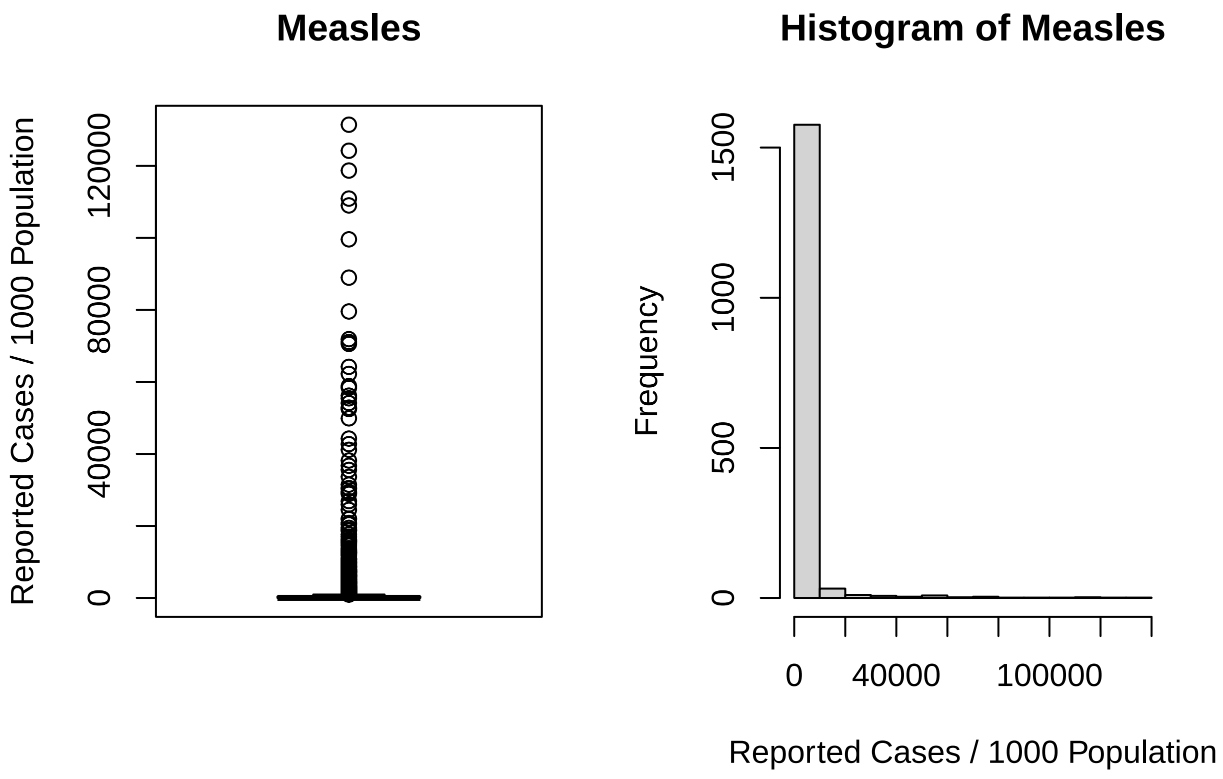
```r
par(mfrow = c(1, 2))
boxplot(life$percentage.expenditure,
        main = 'Health Expenditure',
        ylab = '% of GDP per Capita')
hist(
  life$percentage.expenditure,
  main = 'Histogram of Health Expenditure',
  xlab = '% of GDP per Capita',
  cex.main = 0.9
)
```



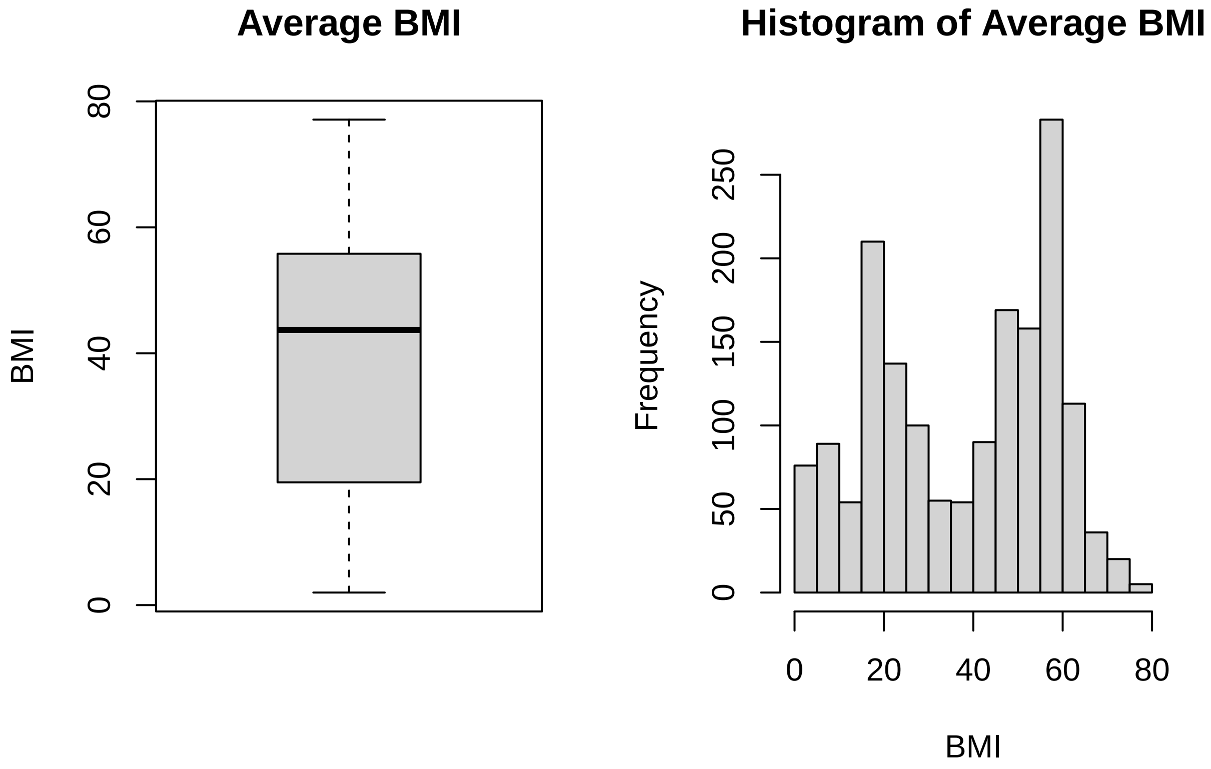
```r
par(mfrow = c(1, 2))
boxplot(life$Hepatitis.B,
        main = 'Hepatitis B (HepB) Immunization',
        ylab = '% Coverage Among 1-Year-Olds',
        cex.main = 0.9)
hist(life$Hepatitis.B,
     main = 'Histogram of HepB Immunization',
     xlab = '% Coverage Among 1-Year-Olds',
     cex.main = 0.9)
```



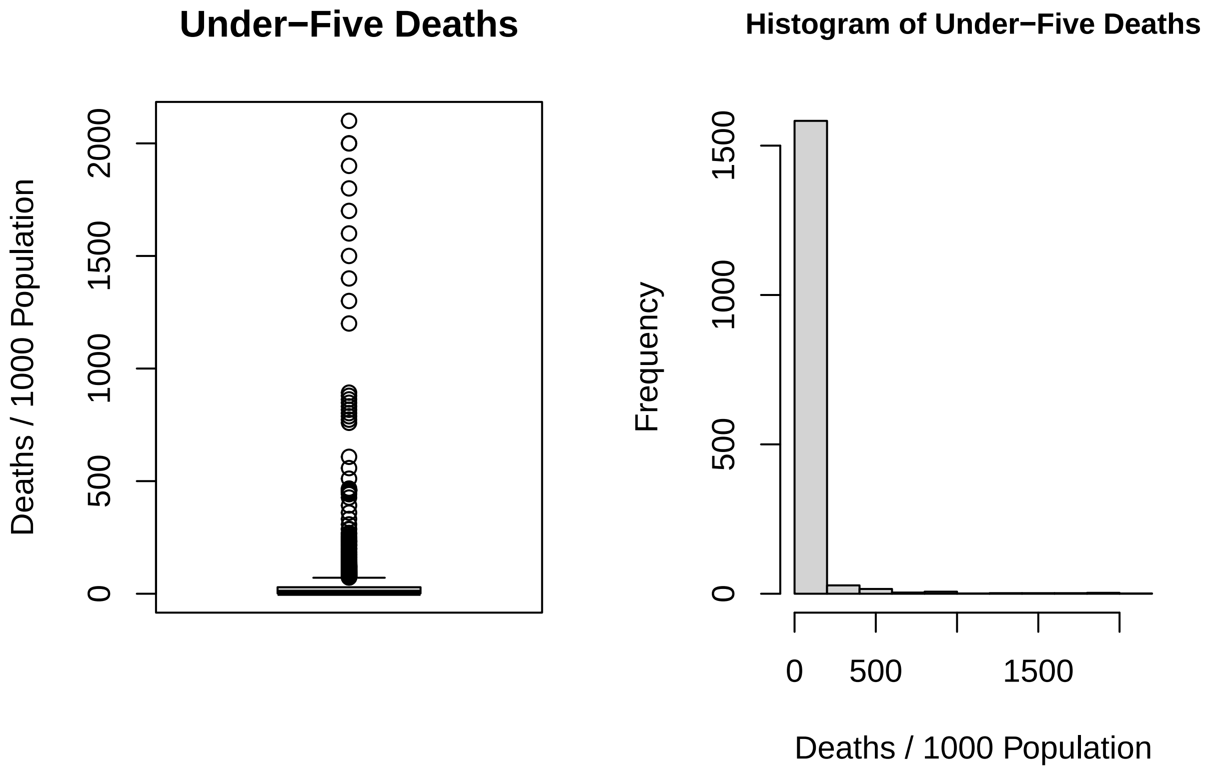
```
par(mfrow = c(1, 2))
boxplot(life$Measles, main = 'Measles', ylab = 'Reported Cases / 1000 Population')
hist(life$Measles, main = 'Histogram of Measles', xlab = 'Reported Cases / 1000 Population')
```



```r
par(mfrow = c(1, 2))
boxplot(life$BMI, main = 'Average BMI', ylab = 'BMI')
hist(life$BMI, main = 'Histogram of Average BMI', xlab = 'BMI')
```



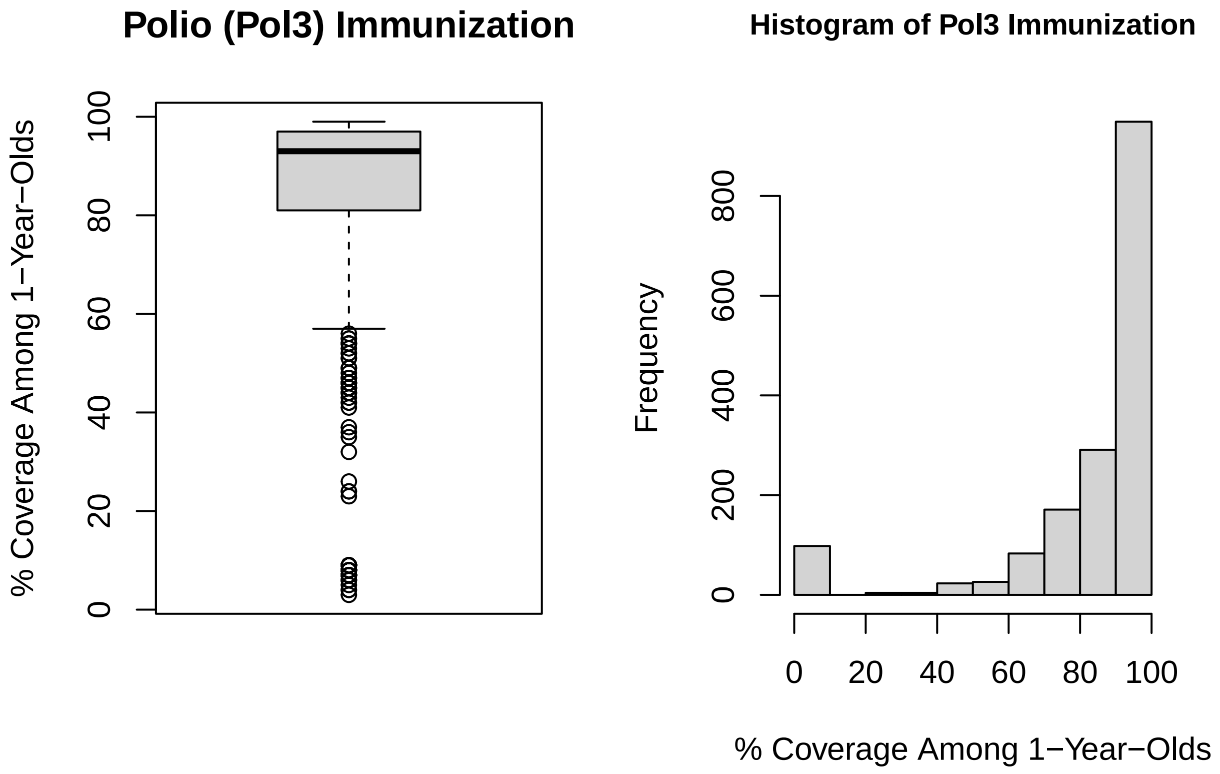
```
par(mfrow = c(1, 2))
boxplot(life$under.five.deaths, main = 'Under-Five Deaths', ylab = 'Deaths / 1000 Population')
hist(
  life$under.five.deaths,
  main = 'Histogram of Under-Five Deaths',
  xlab = 'Deaths / 1000 Population',
  cex.main = 0.9
)
```



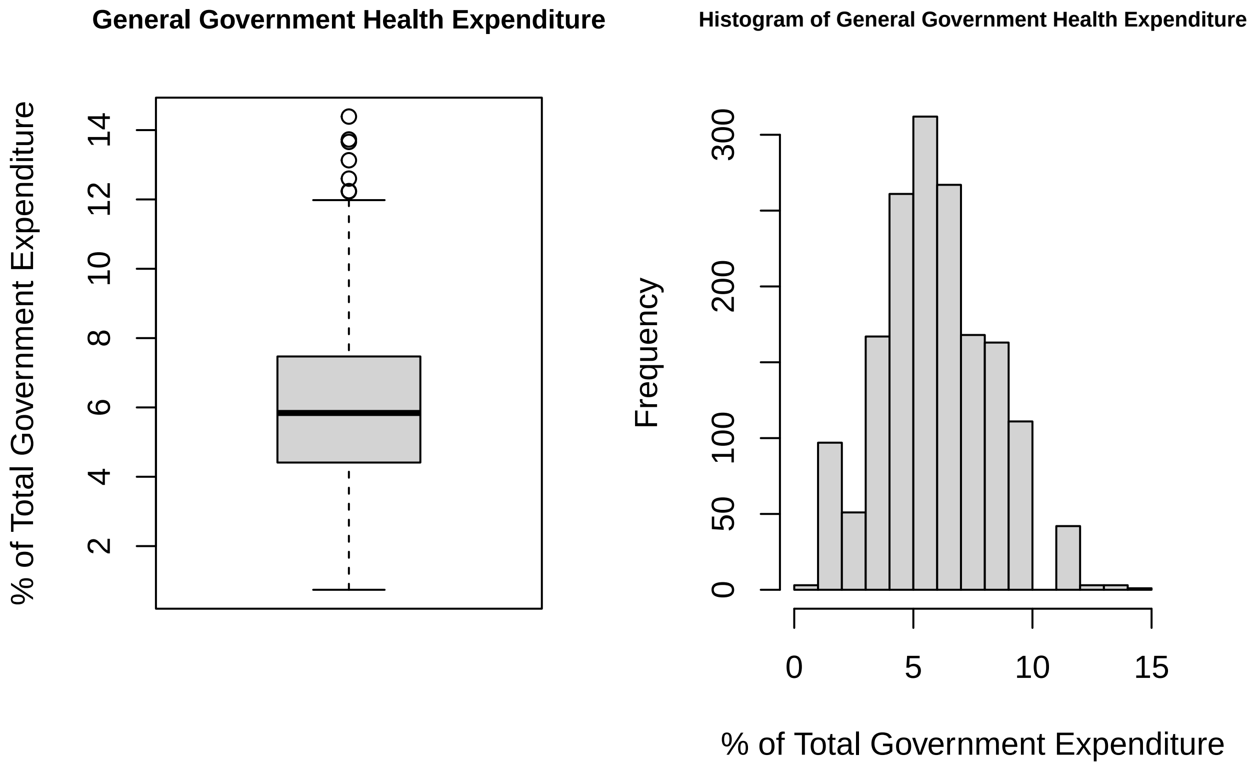
Under−Five Deaths

Histogram of Under−Five Deaths

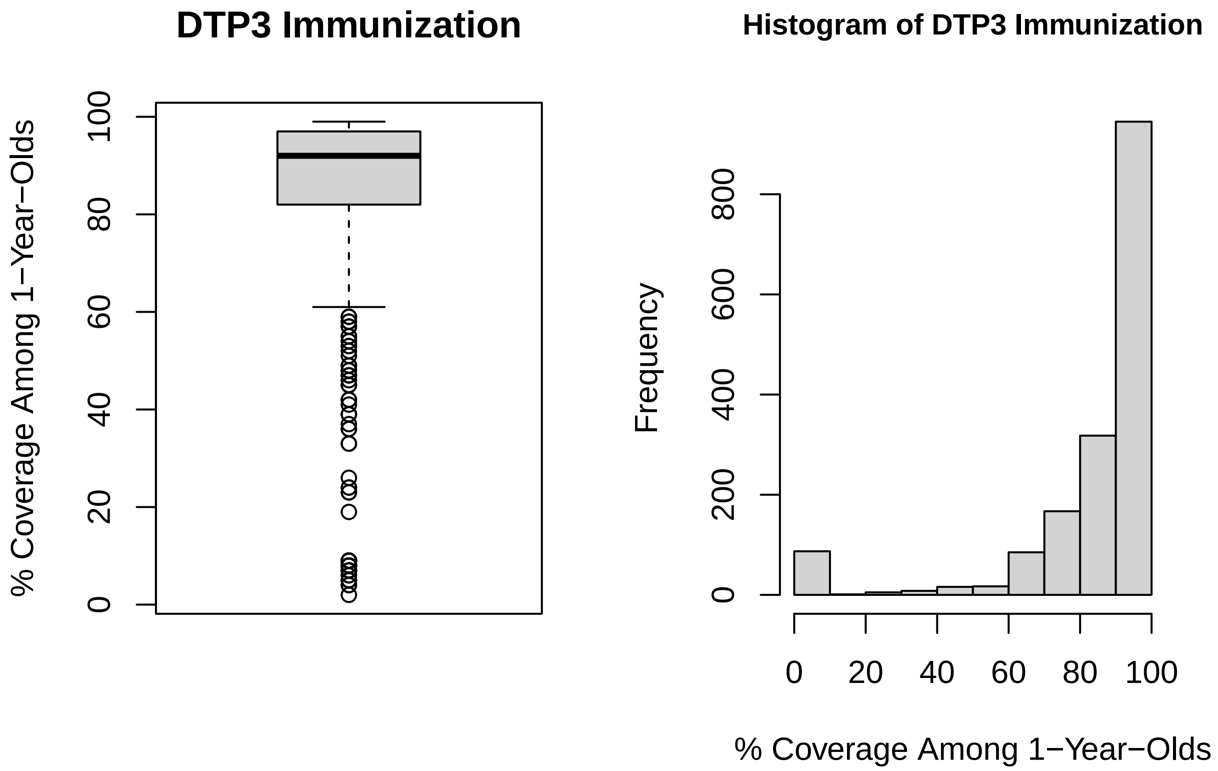
```r
par(mfrow = c(1, 2))
boxplot(life$Polio, main = 'Polio (Pol3) Immunization', ylab = '% Coverage Among 1-Year-Olds')
hist(life$Polio,
     main = 'Histogram of Pol3 Immunization',
     xlab = '% Coverage Among 1-Year-Olds',
     cex.main = 0.9)
```



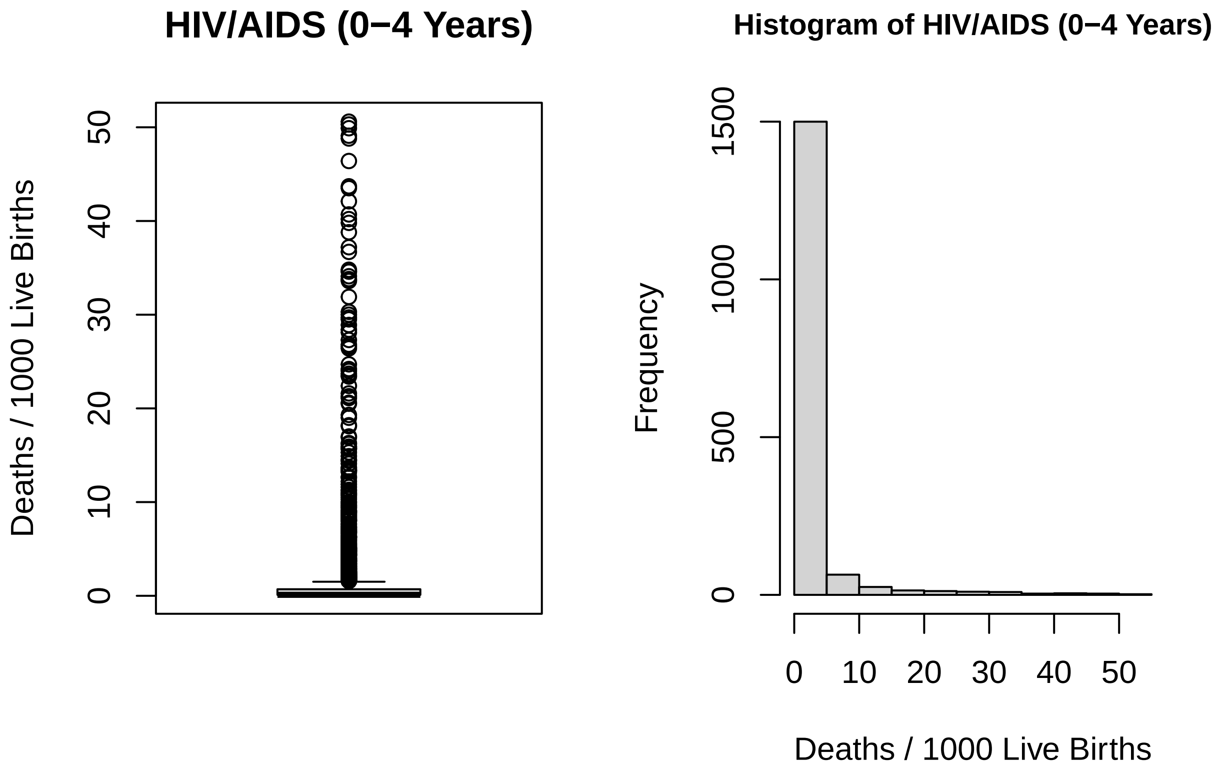
```r
par(mfrow = c(1, 2))
boxplot(
  life$Total.expenditure,
  main = 'General Government Health Expenditure',
  ylab =
    '% of Total Government Expenditure',
  cex.main = 0.8
)
hist(
  life$Total.expenditure,
  main = 'Histogram of General Government Health Expenditure',
  xlab =
    '% of Total Government Expenditure',
  cex.main = 0.7
)
```



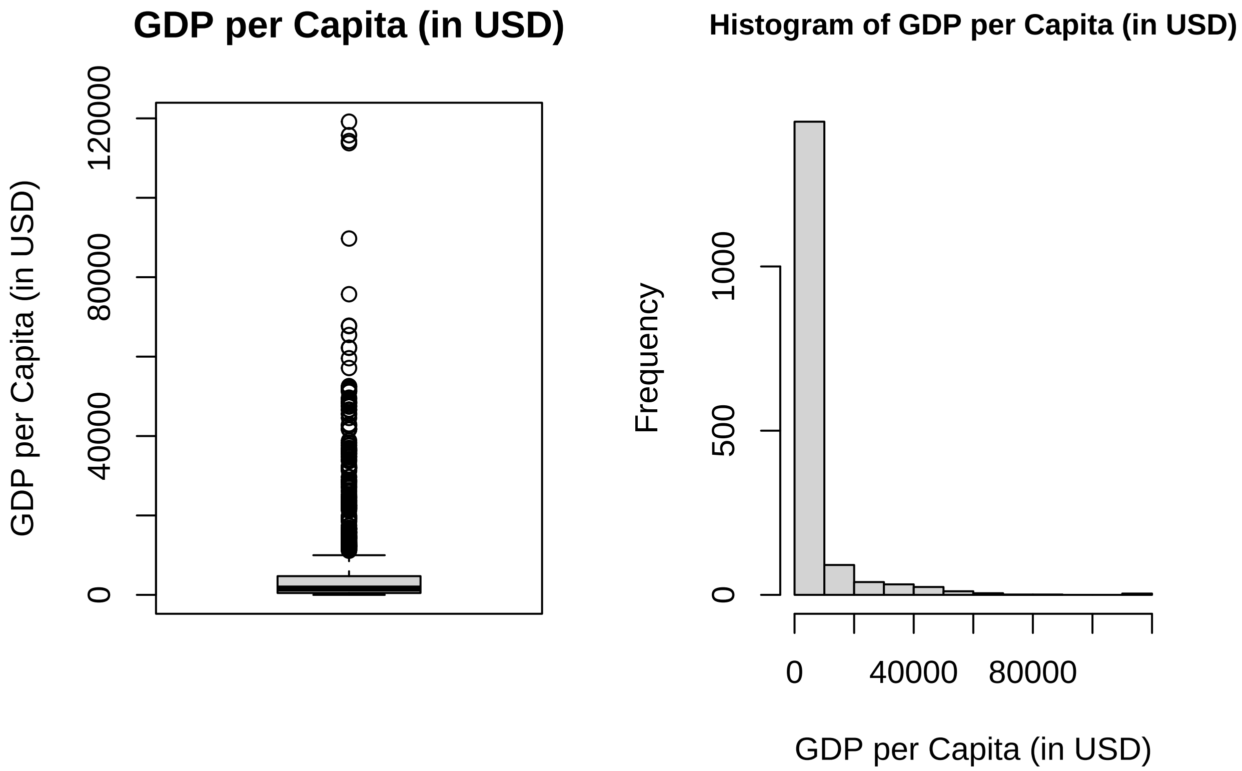
```
par(mfrow = c(1, 2))
boxplot(life$Diphtheria, main = 'DTP3 Immunization', ylab = '% Coverage Among 1-Year-Olds')
hist(life$Diphtheria,
     main = 'Histogram of DTP3 Immunization',
     xlab = '% Coverage Among 1-Year-Olds',
     cex.main = 0.9)
```



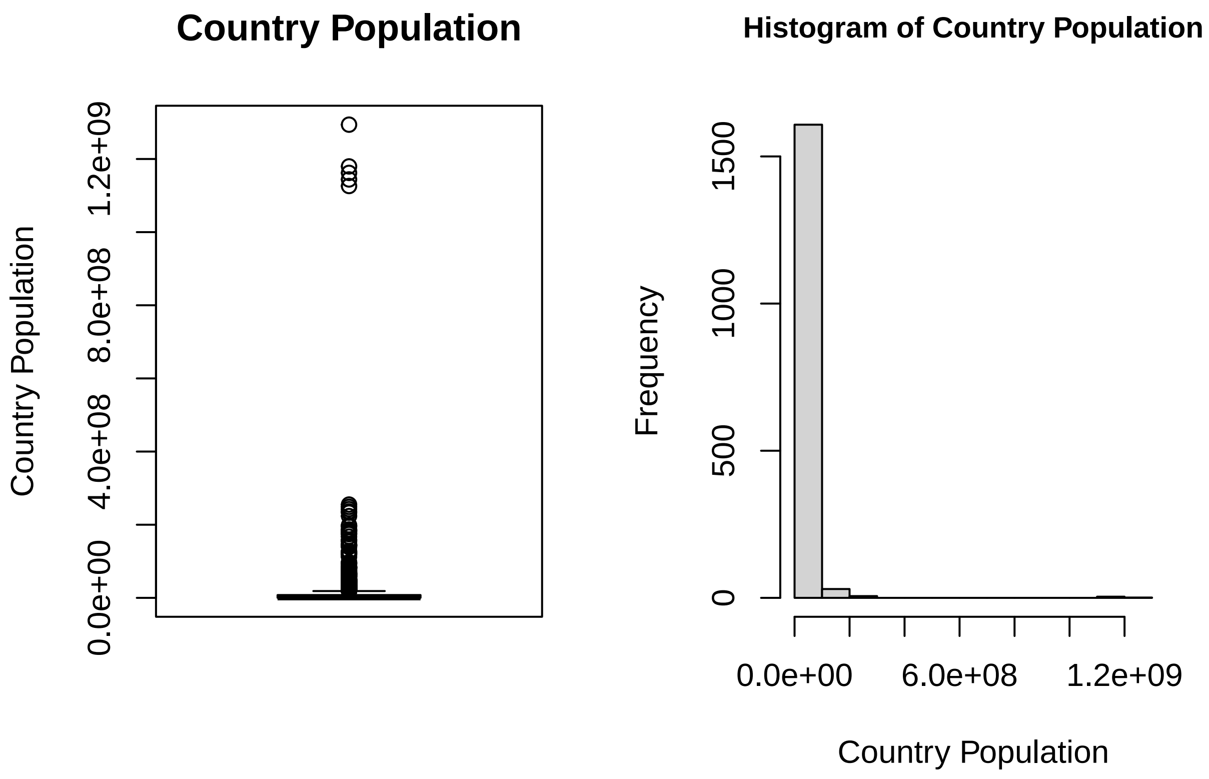
```
par(mfrow = c(1, 2))
boxplot(life$HIV.AIDS, main = 'HIV/AIDS (0-4 Years)', ylab = 'Deaths / 1000 Live Births')
hist(life$HIV.AIDS,
     main = 'Histogram of HIV/AIDS (0-4 Years)',
     xlab = 'Deaths / 1000 Live Births',
     cex.main = 0.9)
```



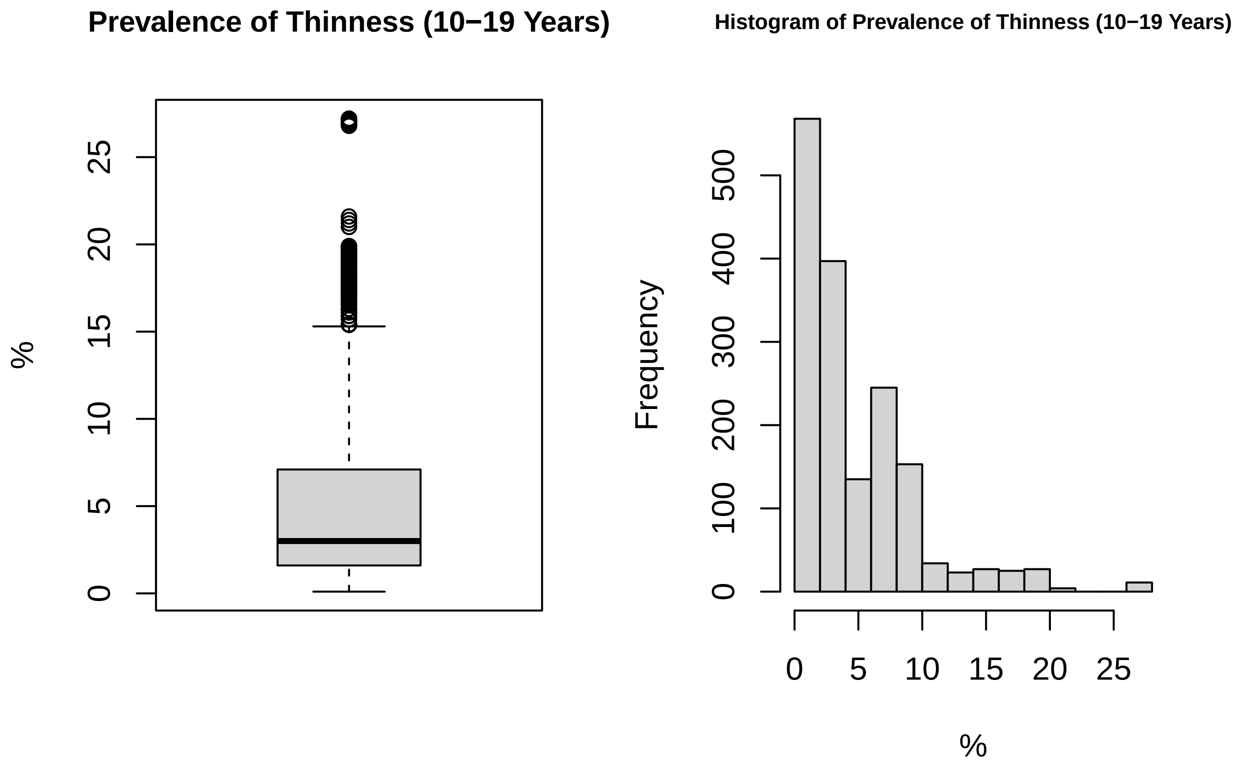
```
par(mfrow = c(1, 2))
boxplot(life$GDP, main = 'GDP per Capita (in USD)', ylab = 'GDP per Capita (in USD)')
hist(life$GDP,
     main = 'Histogram of GDP per Capita (in USD)',
     xlab = 'GDP per Capita (in USD)',
     cex.main = 0.9)
```



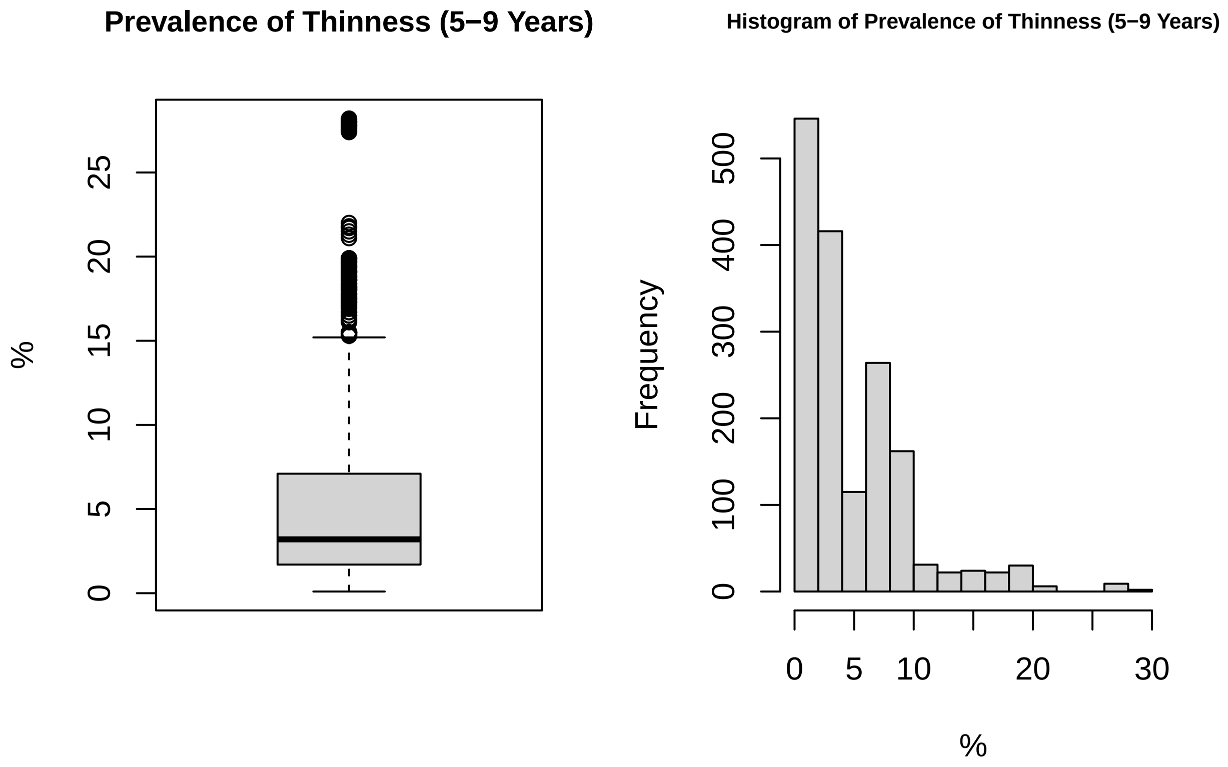
```r
par(mfrow = c(1, 2))
boxplot(life$Population, main = 'Country Population', ylab = 'Country Population')
hist(life$Population,
     main = 'Histogram of Country Population',
     xlab = 'Country Population',
     cex.main = 0.9)
```



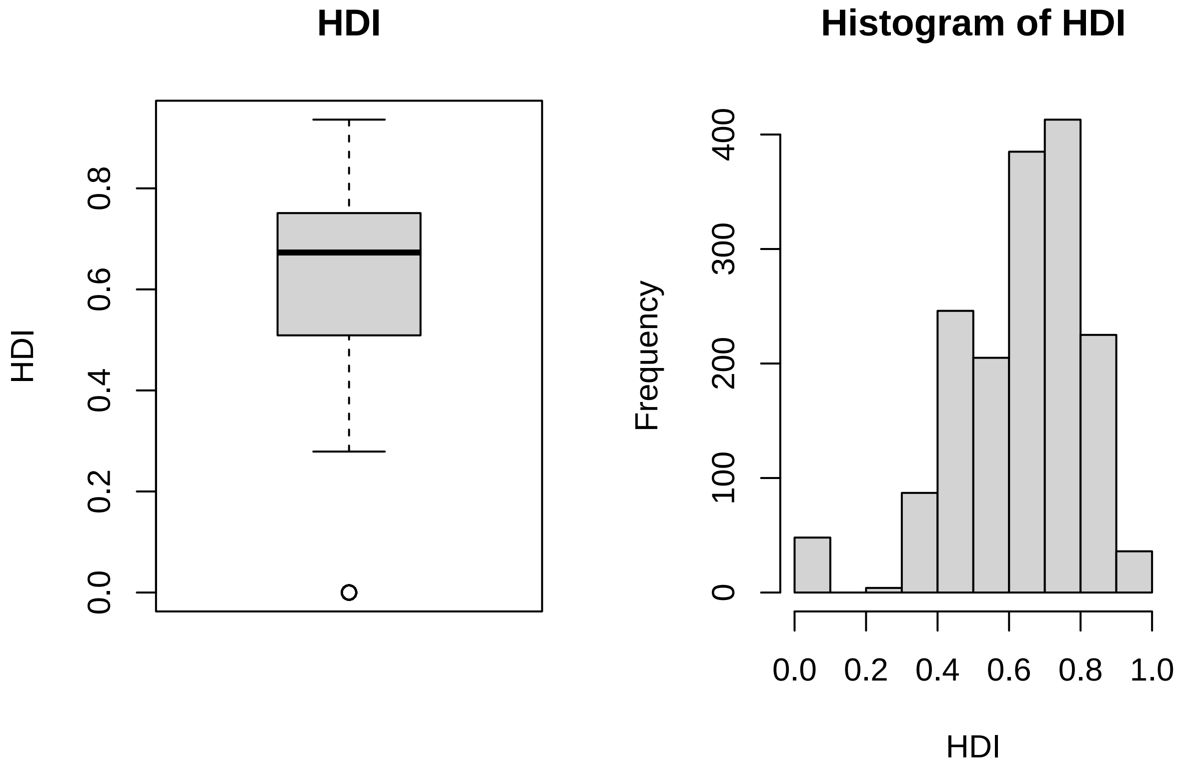
```
par(mfrow = c(1, 2))
boxplot(
  life$thinness..1.19.years,
  main = 'Prevalence of Thinness (10-19 Years)',
  ylab = '%',
  cex.main = 0.9
)
hist(
  life$thinness..1.19.years,
  main = 'Histogram of Prevalence of Thinness (10-19 Years)',
  xlab = '%',
  cex.main = 0.7
)
```



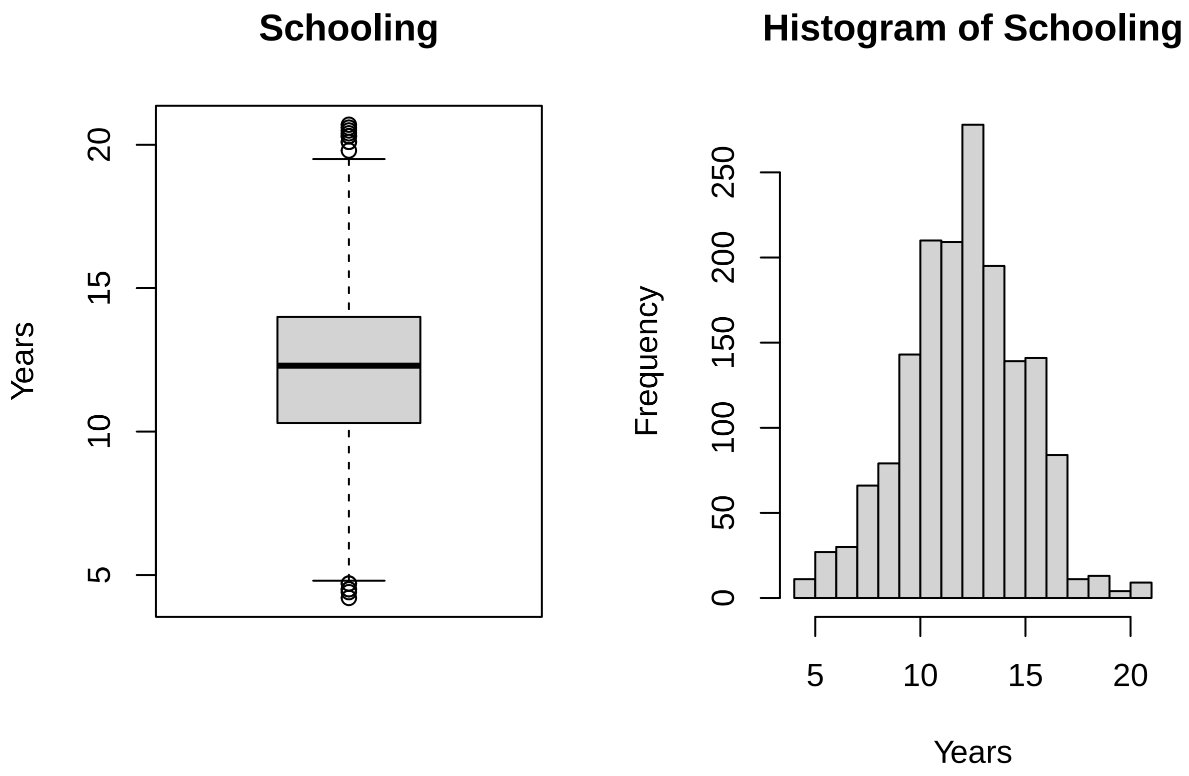
```
par(mfrow = c(1, 2))
boxplot(
  life$thinness.5.9.years,
  main = 'Prevalence of Thinness (5-9 Years)',
  ylab = '%',
  cex.main = 0.9
)
hist(
  life$thinness.5.9.years,
  main = 'Histogram of Prevalence of Thinness (5-9 Years)',
  xlab =
    '%',
  cex.main = 0.7
)
```



```
par(mfrow = c(1, 2))
boxplot(life$Income.composition.of.resources, main = 'HDI', ylab='HDI')
hist(life$Income.composition.of.resources, main = 'Histogram of HDI', xlab='HDI')
```



```r
par(mfrow = c(1, 2))
boxplot(life$Schooling, main = 'Schooling', ylab = 'Years')
hist(life$Schooling, main = 'Histogram of Schooling', xlab = 'Years')
```



Feature Selection

We will be removing some of the variables for building the model due to the reasons mentioned below:
`Country` - Contains too many levels with no additional information to predict `Life.expectancy`.
`Year` - Contains time series data with no additional information to predict `Life.expectancy`.

```r
life = life[, !(names(life) %in% c('Country', 'Year'))]
```

We will be mutating `Hepatitis.B`, `Polio` and `Diphtheria` for building the model since their range between the minimum value and the 1st Quartile is too wide. We will be mutating their values into 2 categorical values: '<90% Covered' and '>=90% Covered'.

```r
life$Hepatitis.B = ifelse(life$Hepatitis.B < 90, '<90% Covered', '>=90% Covered')
life$Polio = ifelse(life$Polio < 90, '<90% Covered', '>=90% Covered')
life$Diphtheria = ifelse(life$Diphtheria < 90, '<90% Covered', '>=90% Covered')
```

This leaves us with 1649 observations of 20 variables with 16 of them being numerical and 4 categorical (`Status`, `Hepatitis.B`, `Polio` and `Diphtheria`).

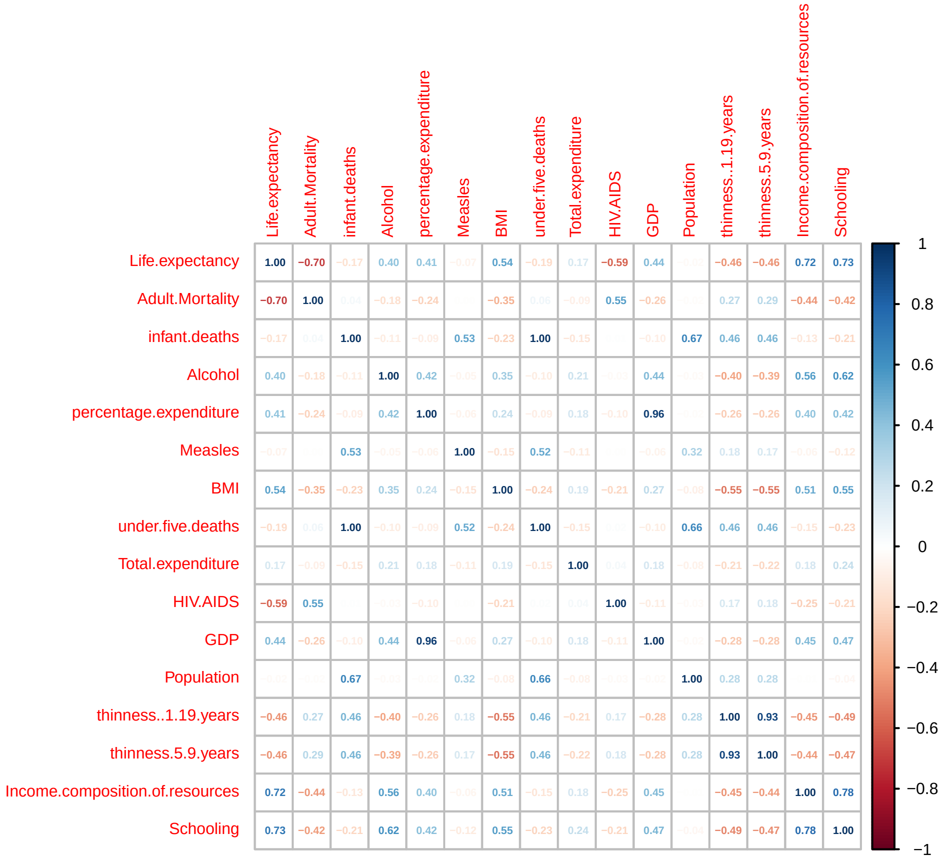
```
summary(life)
```

```
##     Status          Life.expectancy Adult.Mortality infant.deaths
##  Length:1649        Min.   :44.0    Min.   :  1.0   Min.   :   0.00
##  Class :character   1st Qu.:64.4    1st Qu.: 77.0   1st Qu.:   1.00
##  Mode  :character   Median :71.7    Median :148.0   Median :   3.00
##                     Mean   :69.3    Mean   :168.2   Mean   :  32.55
##                     3rd Qu.:75.0    3rd Qu.:227.0   3rd Qu.:  22.00
##                     Max.   :89.0    Max.   :723.0   Max.   :1600.00
##     Alcohol       percentage.expenditure Hepatitis.B          Measles
##  Min.   : 0.010   Min.   :    0.00       Length:1649        Min.   :     0
##  1st Qu.: 0.810   1st Qu.:   37.44       Class :character   1st Qu.:     0
##  Median : 3.790   Median :  145.10       Mode  :character   Median :    15
##  Mean   : 4.533   Mean   :  698.97                          Mean   :  2224
##  3rd Qu.: 7.340   3rd Qu.:  509.39                          3rd Qu.:   373
##  Max.   :17.870   Max.   :18961.35                          Max.   :131441
##       BMI        under.five.deaths    Polio           Total.expenditure
##  Min.   : 2.00   Min.   :   0.00   Length:1649        Min.   : 0.740
##  1st Qu.:19.50   1st Qu.:   1.00   Class :character   1st Qu.: 4.410
##  Median :43.70   Median :   4.00   Mode  :character   Median : 5.840
##  Mean   :38.13   Mean   :  44.22                      Mean   : 5.956
##  3rd Qu.:55.80   3rd Qu.:  29.00                      3rd Qu.: 7.470
##  Max.   :77.10   Max.   :2100.00                      Max.   :14.390
##   Diphtheria           HIV.AIDS          GDP              Population
##  Length:1649        Min.   : 0.100   Min.   :     1.68   Min.   :3.400e+01
##  Class :character   1st Qu.: 0.100   1st Qu.:   462.15   1st Qu.:1.919e+05
##  Mode  :character   Median : 0.100   Median :  1592.57   Median :1.420e+06
##                     Mean   : 1.984   Mean   :  5566.03   Mean   :1.465e+07
##                     3rd Qu.: 0.700   3rd Qu.:  4718.51   3rd Qu.:7.659e+06
##                     Max.   :50.600   Max.   :119172.74   Max.   :1.294e+09
##  thinness..1.19.years thinness.5.9.years Income.composition.of.resources
##  Min.   : 0.100       Min.   : 0.100     Min.   :0.0000
##  1st Qu.: 1.600       1st Qu.: 1.700     1st Qu.:0.5090
##  Median : 3.000       Median : 3.200     Median :0.6730
##  Mean   : 4.851       Mean   : 4.908     Mean   :0.6316
##  3rd Qu.: 7.100       3rd Qu.: 7.100     3rd Qu.:0.7510
##  Max.   :27.200       Max.   :28.200     Max.   :0.9360
##    Schooling
##  Min.   : 4.20
##  1st Qu.:10.30
##  Median :12.30
##  Mean   :12.12
##  3rd Qu.:14.00
##  Max.   :20.70
```

Correlations

Since the number of variables is moderately large, we will plot the correlation plot of the dataset rather than looking at the correlation matrix by itself. The color and its shade easily guide us which 2 variables are correlated.

```r
life_nums = unlist(lapply(life, is.numeric), use.names = FALSE)
corrplot(
  cor(life[, life_nums]),
  method = 'number',
  tl.cex = 0.5,
  number.cex = 0.33,
  cl.cex = 0.5
)
```



There are a few takeaways from this correlation plot:

- `Life.expectancy` has a strong positive correlation with `Income.composition.of.resources` and `Schooling`.
- `Life.expectancy` has a negative correlation with `Adult.Mortality`, which makes sense since if the mortality rate of adult is high, then obviously the life expectancy will be low.
- `Life.expectancy` has a very weak correlation with `Measles` and `Population`.
- There is a very strong correlation between `infant.deaths` and `under.five.deaths`, indicating multicollinearity between them. Therefore, we will remove `under.five.deaths` for building the model.

```r
life = life[, !(names(life) %in% c('under.five.deaths'))]
```

Model Building

We will now build a Linear Regression Model using all the remaining variables to predict the life expectancy of the human population.

```r
lmod = lm(Life.expectancy ~ ., data = life)
summary(lmod)
```

```
##
## Call:
## lm(formula = Life.expectancy ~ ., data = life)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -17.0291  -2.1529   0.0557   2.3893  11.5018
##
## Coefficients:
##                                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)                      5.500e+01  8.108e-01  67.833  < 2e-16 ***
## StatusDeveloping                -9.815e-01  3.464e-01  -2.834  0.00466 **
## Adult.Mortality                 -1.780e-02  9.674e-04 -18.399  < 2e-16 ***
## infant.deaths                   -3.007e-03  1.266e-03  -2.376  0.01762 *
## Alcohol                         -1.552e-01  3.380e-02  -4.590 4.77e-06 ***
## percentage.expenditure           3.491e-04  1.862e-04   1.875  0.06094 .
## Hepatitis.B>=90% Covered        -6.372e-01  3.192e-01  -1.996  0.04611 *
## Measles                          1.683e-05  1.079e-05   1.560  0.11906
## BMI                              3.585e-02  6.161e-03   5.819 7.13e-09 ***
## Polio>=90% Covered               5.680e-01  4.439e-01   1.280  0.20087
## Total.expenditure                6.994e-02  4.179e-02   1.674  0.09439 .
## Diphtheria>=90% Covered          9.097e-01  4.899e-01   1.857  0.06352 .
## HIV.AIDS                        -4.279e-01  1.849e-02 -23.142  < 2e-16 ***
## GDP                              9.181e-06  2.925e-05   0.314  0.75368
## Population                       2.496e-09  1.766e-09   1.414  0.15769
## thinness..1.19.years            -5.018e-02  5.469e-02  -0.918  0.35899
## thinness.5.9.years               1.519e-03  5.374e-02   0.028  0.97745
## Income.composition.of.resources  1.048e+01  8.507e-01  12.316  < 2e-16 ***
## Schooling                        8.843e-01  6.172e-02  14.328  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.686 on 1630 degrees of freedom
## Multiple R-squared:  0.8263, Adjusted R-squared:  0.8244
## F-statistic: 430.9 on 18 and 1630 DF,  p-value: < 2.2e-16
```

There are a few takeaways from this model:

- The p-value of the model is 2.2e-16 < 0.05, indicating that it is significant.
- The Adj R-squared value of the model is 0.8244, indicating that about 82.44% of the observed variation can be explained by the variables in the model, which is quite a good result and can possibly be improved even further with model selection.
- `Adult.Mortality`, `Alcohol`, `BMI`, `HIV.AIDS`, `Income.composition.of.resources` and `Schooling` are the most significant variables with p-value < 0.5.
- From the model we can interpret that `StatusDeveloping`, `Adult.Mortality`, `infant.deaths`, `Alcohol`,

HIV.AIDS, and thinness..1.19.years may have a negative effect on life expectancy.

- From the model we can interpret that Income.composition.of.resources has a strong positive effect on life expectancy.
- A peculiar result we can interpret from the model is that Hepatitis.B90% Covered also has a negative effect on life expectancy.

Model Selection

We will now generate models by using different techniques like Forward Selection Method, Backward Elimination Method and Stepwise Selection Method.

Build Model using Forward Selection Method.

```
ols_step_forward_p(lmod)
```

```
##
##                                           Selection Summary
## ----------------------------------------------------------------------------------------------------
##         Variable                                         Adj.
## Step                Entered                R-Square    R-Square      C(p)          AIC         RMSE
## ----------------------------------------------------------------------------------------------------
##    1    Schooling                            0.5294      0.5292    2771.7513    10612.7157    6.0362
##    2    HIV.AIDS                             0.7304      0.7301     887.6286     9696.3271    4.5704
##    3    Adult.Mortality                      0.7871      0.7867     357.3801     9308.9473    4.0627
##    4    Income.composition.of.resources      0.8092      0.8087     152.1307     9130.3986    3.8474
##    5    percentage.expenditure               0.8147      0.8141     102.1617     9083.8457    3.7924
##    6    BMI                                  0.8201      0.8194      54.0203     9037.6049    3.7384
##    7    Diphtheria                           0.8218      0.8211      39.2920     9023.1915    3.7210
##    8    Alcohol                              0.8231      0.8222      29.5343     9013.5567    3.7090
##    9    thinness..1.19.years                 0.8240      0.8230      22.9694     9007.0292    3.7006
##   10    Status                               0.8249      0.8238      16.6366     9000.6904    3.6924
##   11    Hepatitis.B                          0.8252      0.8240      15.5038     8999.5443    3.6900
##   12    Total.expenditure                    0.8255      0.8242      14.8813     8998.9062    3.6881
##   13    infant.deaths                        0.8257      0.8243      14.8516     8998.8614    3.6870
##   14    Measles                              0.8259      0.8244      14.7734     8998.7652    3.6858
##   15    Population                           0.8262      0.8246      14.7661     8998.7380    3.6846
##   16    Polio                                0.8263      0.8246      15.0990     8999.0524    3.6839
## ----------------------------------------------------------------------------------------------------
```

```
lmod_forward = lm(
  Life.expectancy ~  Schooling + HIV.AIDS + Adult.Mortality + Income.composition.of.resources + percenta
    BMI + Diphtheria + Alcohol + thinness..1.19.years + Status + Hepatitis.B +
    Total.expenditure + infant.deaths + Measles + Population + Polio,
  data = life
)
summary(lmod_forward)
```

```
##
## Call:
## lm(formula = Life.expectancy ~ Schooling + HIV.AIDS + Adult.Mortality +
##     Income.composition.of.resources + percentage.expenditure +
##     BMI + Diphtheria + Alcohol + thinness..1.19.years + Status +
##     Hepatitis.B + Total.expenditure + infant.deaths + Measles +
##     Population + Polio, data = life)
##
## Residuals:
```

```
##      Min       1Q   Median       3Q      Max
## -17.0291  -2.1512   0.0485   2.3846  11.4744
##
## Coefficients:
##                                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)                      5.499e+01  8.094e-01  67.942  < 2e-16 ***
## Schooling                        8.858e-01  6.141e-02  14.426  < 2e-16 ***
## HIV.AIDS                        -4.279e-01  1.848e-02 -23.157  < 2e-16 ***
## Adult.Mortality                 -1.779e-02  9.656e-04 -18.428  < 2e-16 ***
## Income.composition.of.resources  1.050e+01  8.481e-01  12.378  < 2e-16 ***
## percentage.expenditure           4.043e-04  6.128e-05   6.597 5.64e-11 ***
## BMI                              3.579e-02  6.096e-03   5.871 5.24e-09 ***
## Diphtheria>=90% Covered          9.024e-01  4.888e-01   1.846  0.06505 .
## Alcohol                         -1.551e-01  3.378e-02  -4.591 4.75e-06 ***
## thinness..1.19.years            -4.903e-02  2.788e-02  -1.758  0.07885 .
## StatusDeveloping                -9.882e-01  3.454e-01  -2.861  0.00428 **
## Hepatitis.B>=90% Covered        -6.299e-01  3.180e-01  -1.981  0.04780 *
## Total.expenditure                6.940e-02  4.169e-02   1.664  0.09621 .
## infant.deaths                   -2.996e-03  1.259e-03  -2.379  0.01746 *
## Measles                          1.682e-05  1.077e-05   1.561  0.11869
## Population                       2.486e-09  1.764e-09   1.409  0.15892
## Polio>=90% Covered               5.728e-01  4.433e-01   1.292  0.19657
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.684 on 1632 degrees of freedom
## Multiple R-squared:  0.8263, Adjusted R-squared:  0.8246
## F-statistic: 485.3 on 16 and 1632 DF,  p-value: < 2.2e-16
```

Build Model using Backward Elimination Method.

```
ols_step_backward_p(lmod)
```

```
##
##
##                                 Elimination Summary
## ------------------------------------------------------------------------------------
##         Variable                           Adj.
## Step         Removed          R-Square    R-Square     C(p)         AIC        RMSE
## ------------------------------------------------------------------------------------
##    1    thinness.5.9.years      0.8263      0.8245    17.0008    9000.9530    3.6849
##    2    GDP                     0.8263      0.8246    15.0990    8999.0524    3.6839
## ------------------------------------------------------------------------------------
```

```
lmod_backward = lm(
  Life.expectancy ~ Status + Adult.Mortality + infant.deaths + Alcohol +
    percentage.expenditure + Hepatitis.B + Measles + BMI + Polio + Total.expenditure +
    Diphtheria + HIV.AIDS + Population + thinness..1.19.years + Income.composition.of.resources +
    Schooling,
  data = life
)
summary(lmod_backward)
```

```
##
## Call:
## lm(formula = Life.expectancy ~ Status + Adult.Mortality + infant.deaths +
##     Alcohol + percentage.expenditure + Hepatitis.B + Measles +
##     BMI + Polio + Total.expenditure + Diphtheria + HIV.AIDS +
##     Population + thinness..1.19.years + Income.composition.of.resources +
##     Schooling, data = life)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -17.0291  -2.1512   0.0485   2.3846  11.4744
##
## Coefficients:
##                                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)                      5.499e+01  8.094e-01  67.942  < 2e-16 ***
## StatusDeveloping                -9.882e-01  3.454e-01  -2.861  0.00428 **
## Adult.Mortality                 -1.779e-02  9.656e-04 -18.428  < 2e-16 ***
## infant.deaths                   -2.996e-03  1.259e-03  -2.379  0.01746 *
## Alcohol                         -1.551e-01  3.378e-02  -4.591 4.75e-06 ***
## percentage.expenditure           4.043e-04  6.128e-05   6.597 5.64e-11 ***
## Hepatitis.B>=90% Covered        -6.299e-01  3.180e-01  -1.981  0.04780 *
## Measles                          1.682e-05  1.077e-05   1.561  0.11869
## BMI                              3.579e-02  6.096e-03   5.871 5.24e-09 ***
## Polio>=90% Covered               5.728e-01  4.433e-01   1.292  0.19657
## Total.expenditure                6.940e-02  4.169e-02   1.664  0.09621 .
## Diphtheria>=90% Covered          9.024e-01  4.888e-01   1.846  0.06505 .
## HIV.AIDS                        -4.279e-01  1.848e-02 -23.157  < 2e-16 ***
## Population                       2.486e-09  1.764e-09   1.409  0.15892
## thinness..1.19.years            -4.903e-02  2.788e-02  -1.758  0.07885 .
## Income.composition.of.resources  1.050e+01  8.481e-01  12.378  < 2e-16 ***
## Schooling                        8.858e-01  6.141e-02  14.426  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.684 on 1632 degrees of freedom
## Multiple R-squared:  0.8263, Adjusted R-squared:  0.8246
## F-statistic: 485.3 on 16 and 1632 DF,  p-value: < 2.2e-16
```

Build Model using Stepwise Selection Method.

```
ols_step_both_p(lmod)
```

```
##
##                                             Stepwise Selection Summary
## ----------------------------------------------------------------------------------------------------
##                                              Added/                   Adj.
## Step               Variable                Removed     R-Square    R-Square      C(p)          AIC
## ----------------------------------------------------------------------------------------------------
##    1               Schooling               addition       0.529       0.529    2771.7510    10612.715
##    2               HIV.AIDS                addition       0.730       0.730     887.6290     9696.327
##    3            Adult.Mortality            addition       0.787       0.787     357.3800     9308.947
##    4    Income.composition.of.resources    addition       0.809       0.809     152.1310     9130.398
##    5        percentage.expenditure         addition       0.815       0.814     102.1620     9083.845
##    6                  BMI                  addition       0.820       0.819      54.0200     9037.604
##    7              Diphtheria               addition       0.822       0.821      39.2920     9023.191
##    8                Alcohol                addition       0.823       0.822      29.5340     9013.550
##    9         thinness..1.19.years          addition       0.824       0.823      22.9690     9007.029
##   10                Status                 addition       0.825       0.824      16.6370     9000.690
##   11              Hepatitis.B              addition       0.825       0.824      15.5040     8999.544
## ----------------------------------------------------------------------------------------------------
```

```
lmod_stepwise = lm(
  Life.expectancy ~ Schooling + HIV.AIDS + Adult.Mortality + Income.composition.of.resources +
    percentage.expenditure + BMI + Diphtheria + Alcohol + thinness..1.19.years +
    Status + Hepatitis.B,
  data = life
)
summary(lmod_stepwise)
```

```
##
## Call:
## lm(formula = Life.expectancy ~ Schooling + HIV.AIDS + Adult.Mortality +
##     Income.composition.of.resources + percentage.expenditure +
##     BMI + Diphtheria + Alcohol + thinness..1.19.years + Status +
##     Hepatitis.B, data = life)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -17.2593  -2.1481   0.0745   2.4046  11.5838
##
## Coefficients:
##                                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)                      5.534e+01  7.750e-01  71.401  < 2e-16 ***
## Schooling                        9.061e-01  6.102e-02  14.848  < 2e-16 ***
## HIV.AIDS                        -4.239e-01  1.833e-02 -23.122  < 2e-16 ***
## Adult.Mortality                 -1.779e-02  9.636e-04 -18.464  < 2e-16 ***
## Income.composition.of.resources  1.037e+01  8.444e-01  12.280  < 2e-16 ***
## percentage.expenditure           4.098e-04  6.119e-05   6.698 2.90e-11 ***
## BMI                              3.610e-02  6.071e-03   5.946 3.36e-09 ***
## Diphtheria>=90% Covered          1.439e+00  3.443e-01   4.181 3.05e-05 ***
## Alcohol                         -1.605e-01  3.353e-02  -4.788 1.84e-06 ***
## thinness..1.19.years            -7.223e-02  2.491e-02  -2.900  0.00378 **
## StatusDeveloping                -1.014e+00  3.454e-01  -2.934  0.00339 **
## Hepatitis.B>=90% Covered        -5.567e-01  3.149e-01  -1.768  0.07723 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.69 on 1637 degrees of freedom
## Multiple R-squared:  0.8252, Adjusted R-squared:  0.824
## F-statistic: 702.7 on 11 and 1637 DF,  p-value: < 2.2e-16
```

Build Model using All Possible Regressions Method.

```
# ols_step_all_possible(lmod, sbc = TRUE)
```

In summary, variables chosen by the methods (x denotes the variable was chosen by the method):

Model Selection Method	Status	Adult.Mortality	infant.deaths	Alcohol
Forward Selection	x	x	x	x
Backward Elimination	x	x	x	x
Stepwise Selection	x	x		x

Model Selection Method	percentage.expenditure	Hepatitis.B	Measles	BMI	Polio
Forward Selection	x	x	x	x	x
Backward Elimination	x	x	x	x	x
Stepwise Selection	x	x		x	

Model Selection Method	Total.expenditure	Diphtheria	HIV.AIDS	GDP	Population
Forward Selection	x	x	x		x
Backward Elimination	x	x	x		x
Stepwise Selection		x	x		

Model Selection Method	thinness..1.19.years	thinness.5.9.years
Forward Selection	x	
Backward Elimination	x	
Stepwise Selection	x	

Model Selection Method	Income.compostition.of.resources	Schooling
Forward Selection	x	x
Backward Elimination	x	x
Stepwise Selection	x	x

Both the Forward Selection method and Backward Elimination method have chosen the same set of variables.

Adj. R-squared values of the above models:

```r
data.frame(
  model = c('lmod', 'lmod_forward', 'lmod_backward', 'lmod_stepwise'),
  AdjRsquare = c(
    summary(lmod)$adj.r.square,
    summary(lmod_forward)$adj.r.square,
    summary(lmod_backward)$adj.r.square,
    summary(lmod_stepwise)$adj.r.square
  )
)
```

```
##           model AdjRsquare
## 1          lmod  0.8244244
## 2  lmod_forward  0.8246289
## 3 lmod_backward  0.8246289
## 4 lmod_stepwise  0.8240486
```

We will be choosing the model chosen by Forward Selection method `lmod_forward` as it has the highest Adj. R-squared value.

```
lmod_final = lmod_forward
summary(lmod_final)
```

```
##
## Call:
## lm(formula = Life.expectancy ~ Schooling + HIV.AIDS + Adult.Mortality +
##     Income.composition.of.resources + percentage.expenditure +
##     BMI + Diphtheria + Alcohol + thinness..1.19.years + Status +
##     Hepatitis.B + Total.expenditure + infant.deaths + Measles +
##     Population + Polio, data = life)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -17.0291  -2.1512   0.0485   2.3846  11.4744
##
## Coefficients:
##                                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)                      5.499e+01  8.094e-01  67.942  < 2e-16 ***
## Schooling                        8.858e-01  6.141e-02  14.426  < 2e-16 ***
## HIV.AIDS                        -4.279e-01  1.848e-02 -23.157  < 2e-16 ***
## Adult.Mortality                 -1.779e-02  9.656e-04 -18.428  < 2e-16 ***
## Income.composition.of.resources  1.050e+01  8.481e-01  12.378  < 2e-16 ***
## percentage.expenditure           4.043e-04  6.128e-05   6.597 5.64e-11 ***
## BMI                              3.579e-02  6.096e-03   5.871 5.24e-09 ***
## Diphtheria>=90% Covered          9.024e-01  4.888e-01   1.846  0.06505 .
## Alcohol                         -1.551e-01  3.378e-02  -4.591 4.75e-06 ***
## thinness..1.19.years            -4.903e-02  2.788e-02  -1.758  0.07885 .
## StatusDeveloping                -9.882e-01  3.454e-01  -2.861  0.00428 **
## Hepatitis.B>=90% Covered        -6.299e-01  3.180e-01  -1.981  0.04780 *
## Total.expenditure                6.940e-02  4.169e-02   1.664  0.09621 .
## infant.deaths                   -2.996e-03  1.259e-03  -2.379  0.01746 *
## Measles                          1.682e-05  1.077e-05   1.561  0.11869
## Population                       2.486e-09  1.764e-09   1.409  0.15892
## Polio>=90% Covered               5.728e-01  4.433e-01   1.292  0.19657
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.684 on 1632 degrees of freedom
## Multiple R-squared:  0.8263, Adjusted R-squared:  0.8246
## F-statistic: 485.3 on 16 and 1632 DF,  p-value: < 2.2e-16
```

Results

Model Error Estimation

We will now use our final model to see how well it performs in predicting the life expectancy of the human population.

```
result = predict(lmod_final, life)
```

Mean Squared Error:

```
mse = mean((life$Life.expectancy - result) ^ 2)
mse
```

```
## [1] 13.43106
```

Root Mean Squared Error:

```
rmse = sqrt(mse)
rmse
```

```
## [1] 3.664841
```

Mean Absolute Error:

```
n = length(result)
sum = 0

for (i in 1:n) {
  sum = sum + abs(life$Life.expectancy[i] - result[i])
}

mae = sum / n
mae
```

```
##        1
## 2.817618
```

In summary,

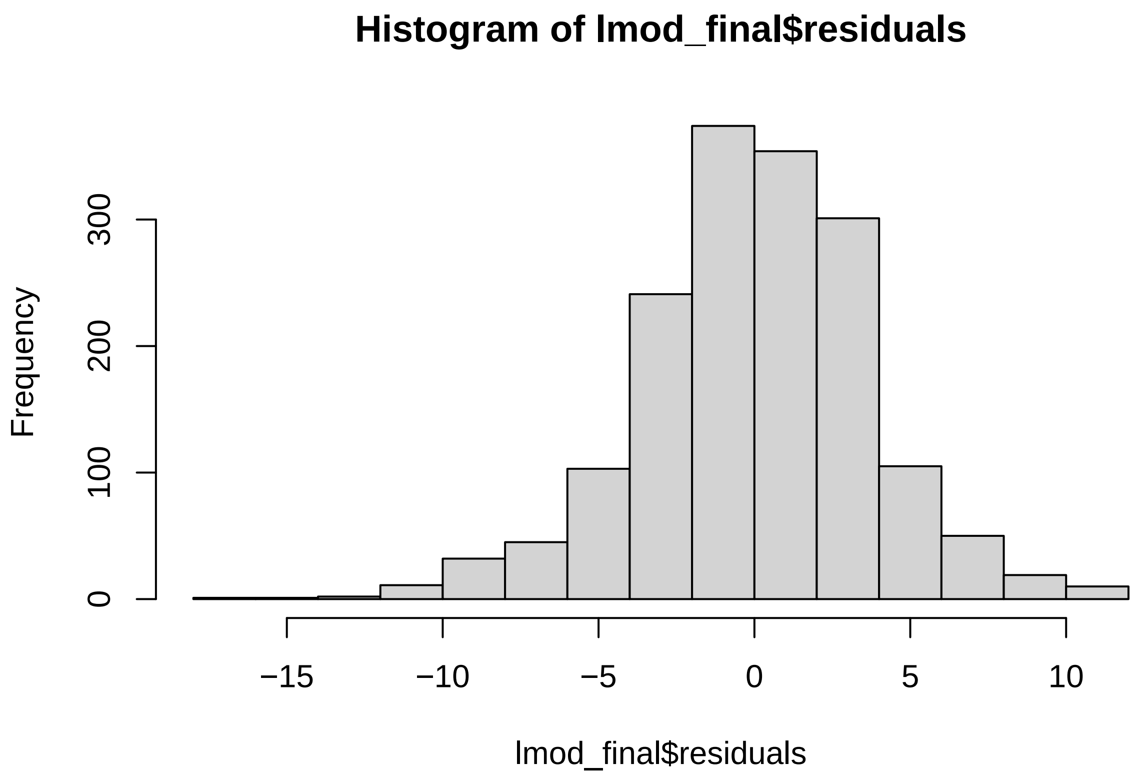
```
data.frame(
  Method = c('MSE', 'RMSE', 'MAE'),
  Result = c(mse, rmse, mae)
)
```

```
##   Method    Result
## 1    MSE 13.431062
## 2   RMSE  3.664841
## 3    MAE  2.817618
```

Model Adequacy Checking

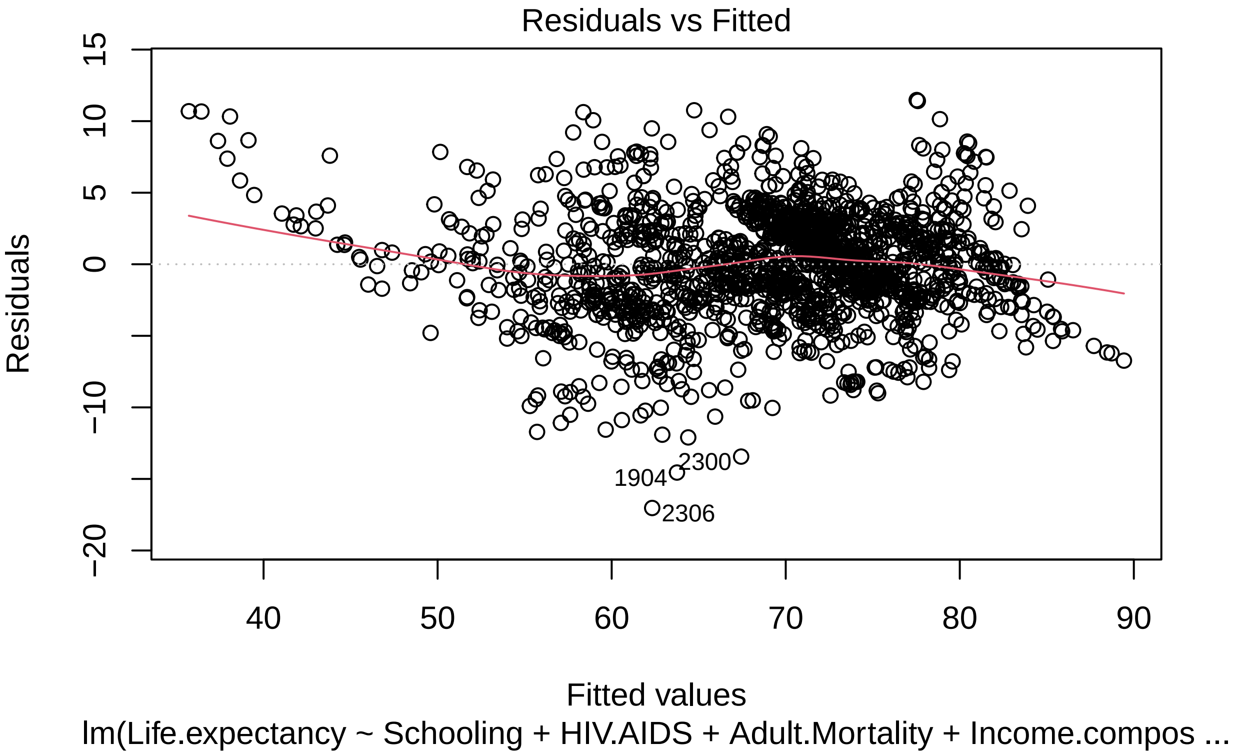
Normality Testing:

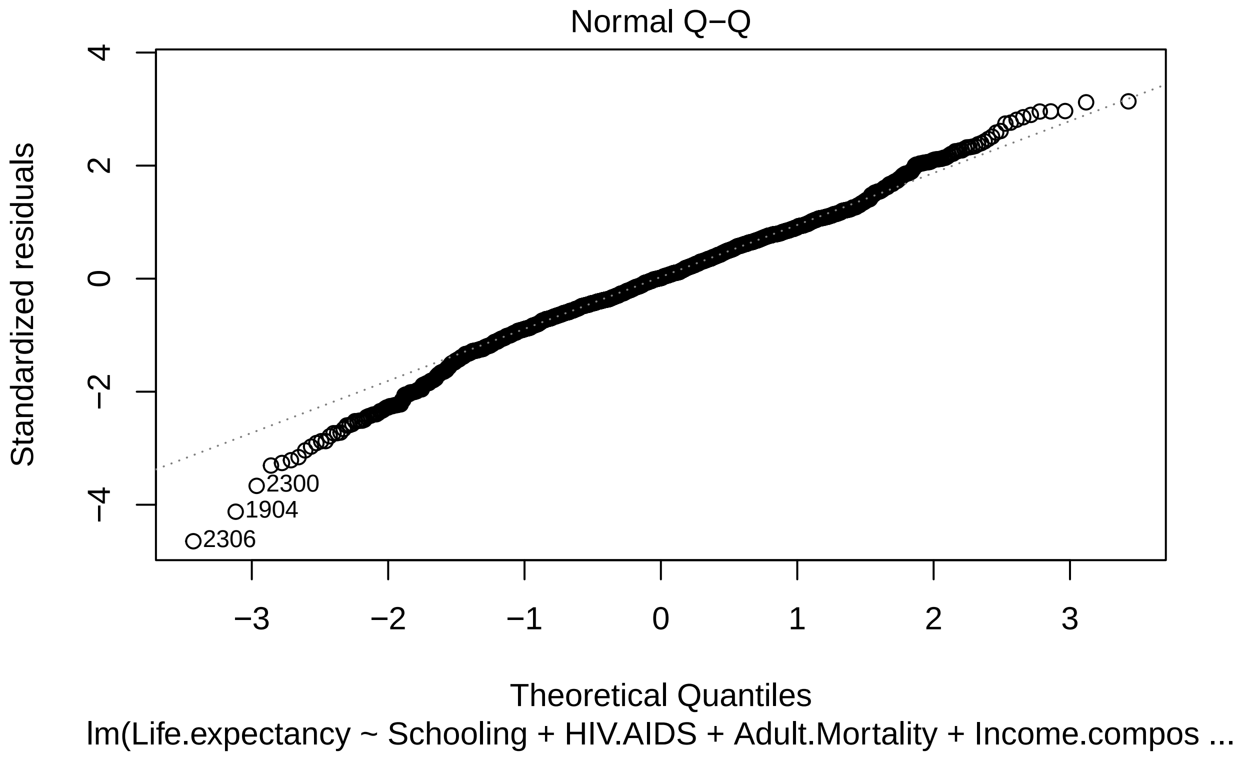
```
hist(lmod_final$residuals, breaks = 20)
```

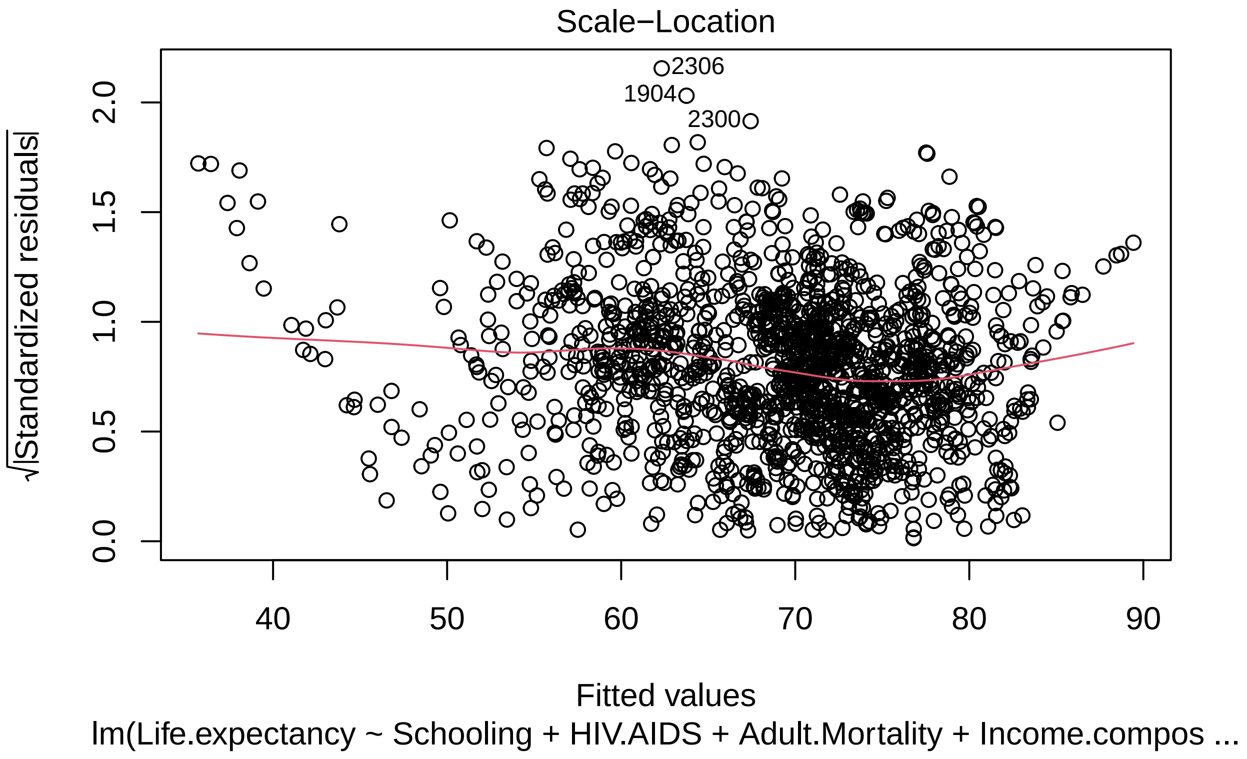


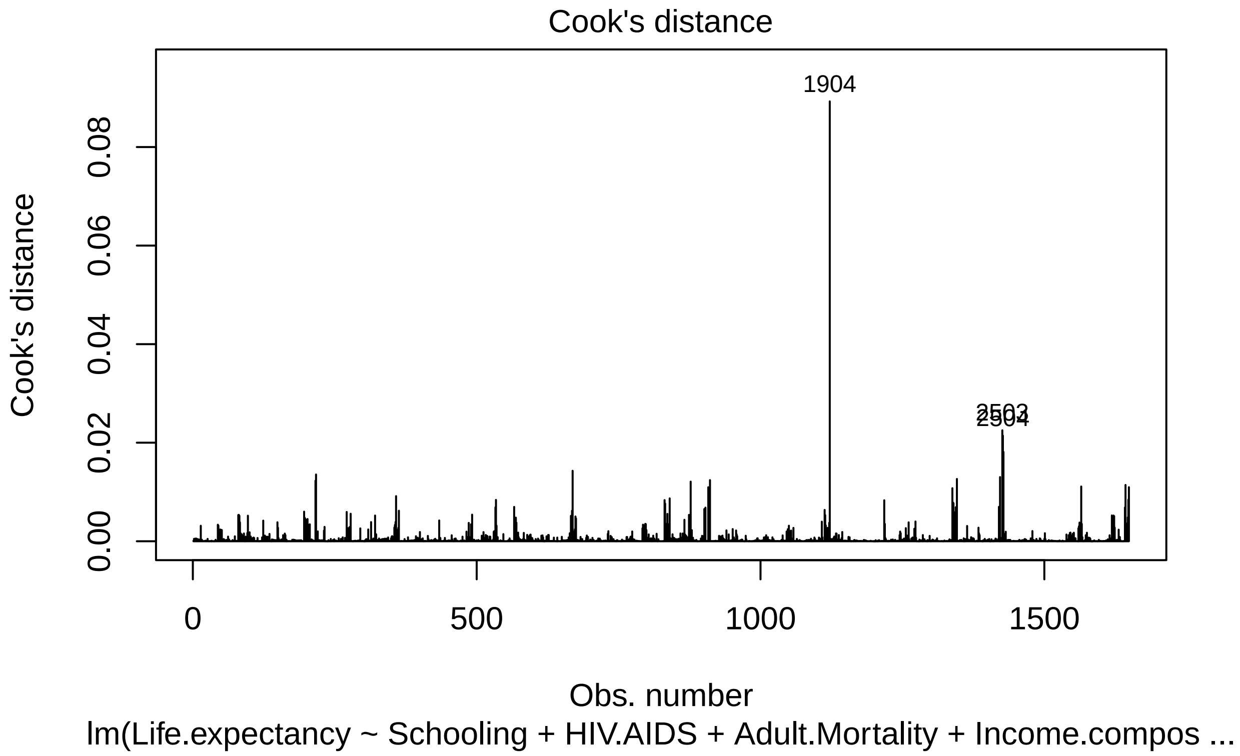
Most of the residuals seem to be distributed in the center, indicating that they are distributed normally.

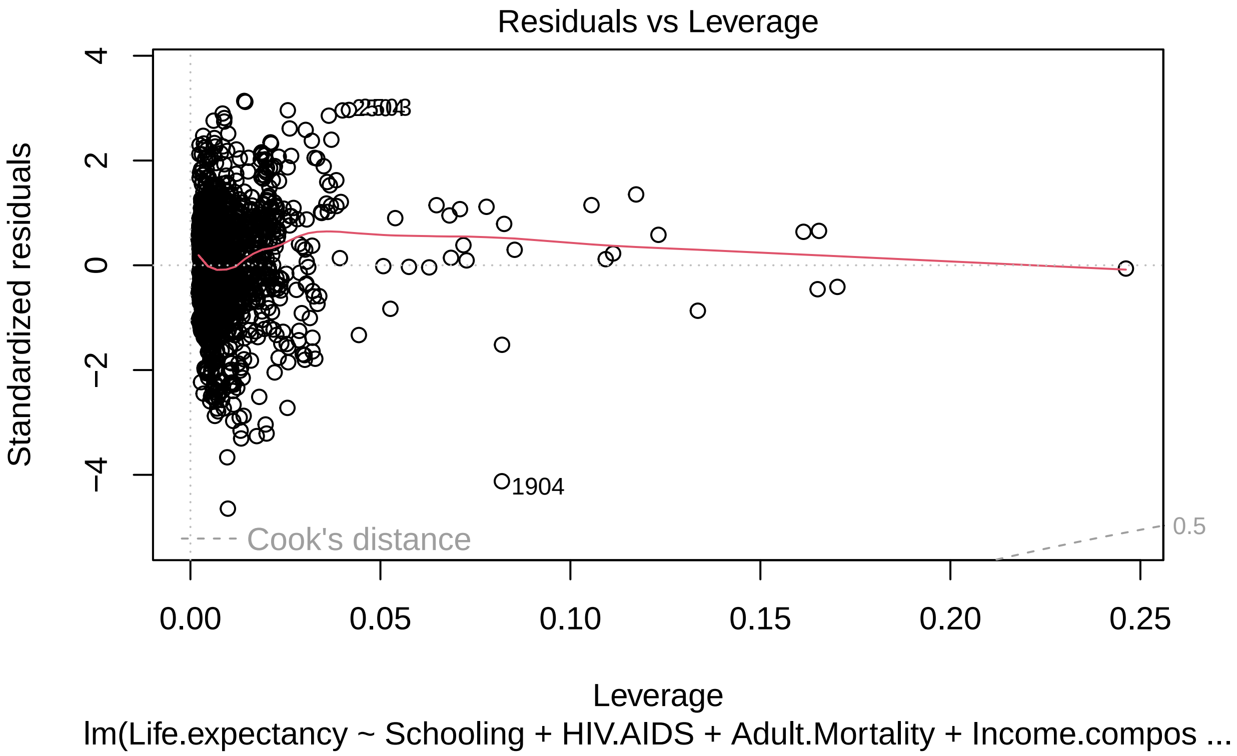
```
plot(lmod_final, which = c(1:6))
```

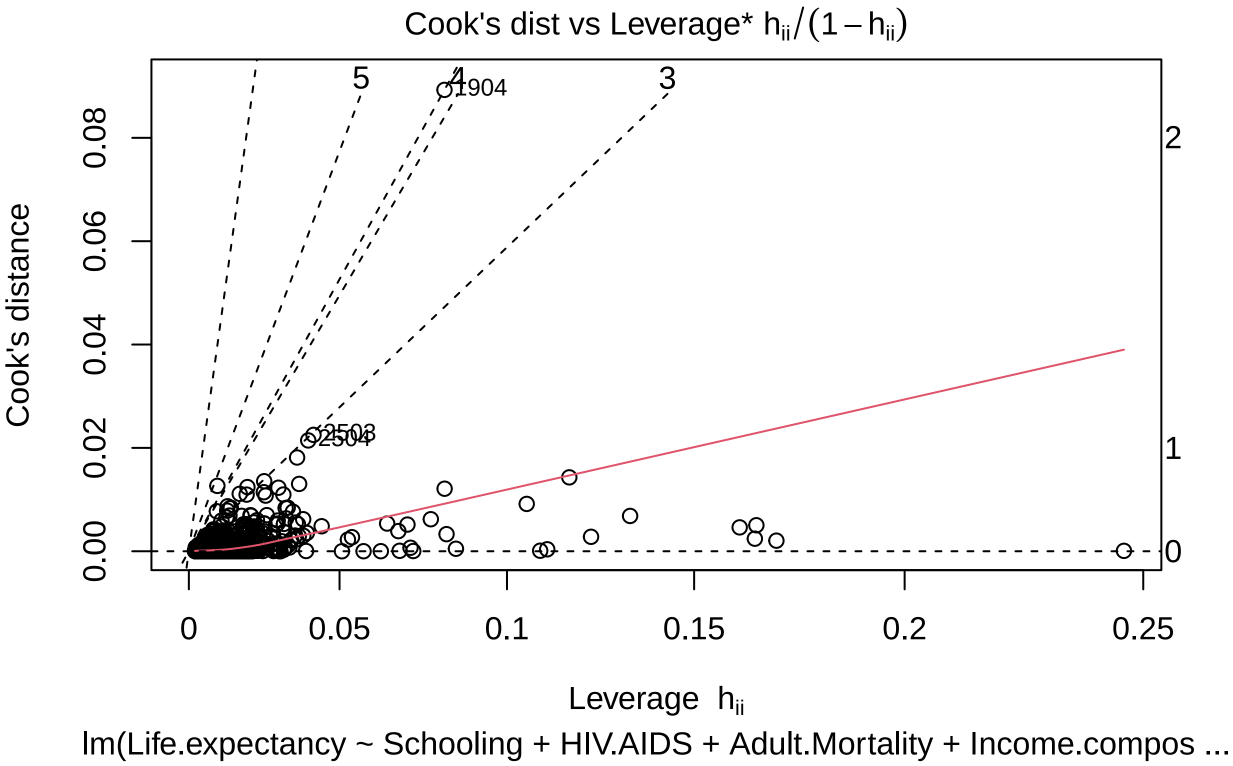



Normal Q−Q
Standardized residuals
4
2
0
−2
−4
2300
1904
2306
−3
−2
−1
0
1
2
3
Theoretical Quantiles
lm(Life.expectancy ~ Schooling + HIV.AIDS + Adult.Mortality + Income.compos ...


Scale−Location
2306
1904
2300
√|Standardized residuals|
0.0
0.5
1.0
1.5
2.0
40
50
60
70
80
90
Fitted values
lm(Life.expectancy ~ Schooling + HIV.AIDS + Adult.Mortality + Income.compos ...


Cook's distance
Cook's distance
0.00
0.02
0.04
0.06
0.08
1904
2503
2504
0
500
1000
1500
Obs. number
lm(Life.expectancy ~ Schooling + HIV.AIDS + Adult.Mortality + Income.compos ...


Residuals vs Leverage
Standardized residuals
4
2
0
−2
−4
2504
2503
1904
Cook's distance
0.5
0.00
0.05
0.10
0.15
0.20
0.25
Leverage
lm(Life.expectancy ~ Schooling + HIV.AIDS + Adult.Mortality + Income.compos ...



There is no obvious observable pattern in the above plots, indicating that the model is appropriate.

Multicollinearity Test:

```
vif(lmod_final)
```

```
##                       Schooling                        HIV.AIDS
##                        3.578091                        1.509013
##                 Adult.Mortality Income.composition.of.resources
##                        1.778090                        2.927679
##          percentage.expenditure                             BMI
##                        1.411270                        1.761017
##                      Diphtheria                         Alcohol
##                        7.102613                        2.249650
##            thinness..1.19.years                          Status
##                        1.996547                        1.815140
##                     Hepatitis.B               Total.expenditure
##                        3.072344                        1.116175
##                   infant.deaths                         Measles
##                        2.811727                        1.433389
##                      Population                           Polio
##                        1.876386                        5.834447
```

A VIF > 10 implies serious problems with multicollinearity.
Since the VIF for all of the predictors is less than 10, there seems to be no issue with multicollinearity.

Discussion