In [1]:

```
#Importing libraries
library(tidyverse)
library(ggplot2)
library(dplyr)
```

```
── Attaching core tidyverse packages ──────────────────────── tidyvers
e 2.0.0 ──
✔ dplyr     1.1.4     ✔ readr     2.1.5
✔ forcats   1.0.0     ✔ stringr   1.5.1
✔ ggplot2   3.4.4     ✔ tibble    3.2.1
✔ lubridate 1.9.3     ✔ tidyr     1.3.1
✔ purrr     1.0.2
── Conflicts ────────────────────────────────────────── tidyverse_conf
licts() ──
✖ purrr::%||%()   masks base::%||%()
✖ dplyr::filter() masks stats::filter()
✖ dplyr::lag()    masks stats::lag()
ℹ Use the conflicted package (<http://conflicted.r-lib.org/>) to force
all conflicts to become errors
```

Dataset Description: Life Expectancy Data

This dataset provides data for 193 countries ranginf from 2000 to 2015 years. This data contains 2938 rowa which are characterized into 22 columns.These features can be categorized into two groups:

Health factors which are originally provided by the Global Health Observatory (GHO) data repository under the World Health Organization (WHO)

Economic factors which have been collected by the United Nation (UN) website. This dataset contains health and economic factors from various countries, influencing life expectancy.

Below is the detailed description of each variable:

Variable	Type	Description
`Country`	Factor	Country name
`Year`	Numeric	Year of the data
`Status`	Factor	Country status of developed or developing
`Life_Expectancy`	Numeric	Life expectancy in age
`Adult_Mortality`	Numeric	Adult Mortality Rates of both sexes (probability of dying between 15 and 60 years per 1000 population)
`infant.deaths`	Numeric	Number of Infant Deaths per 1000 population
`Alcohol`	Numeric	Alcohol, recorded per capita (15+) consumption (in litres of pure alcohol)
`percentage.expenditure`	Numeric	Expenditure on health as a percentage of Gross Domestic Product per capita(%)
`Hepatitis.B`	Numeric	Hepatitis B (HepB) immunization coverage among 1-year-olds (%)
`Measles`	Numeric	Number of reported measles cases per 1000 population
`BMI`	Numeric	Average Body Mass Index of entire population
`under.five.deaths`	Numeric	Number of under-five deaths per 1000 population
`Polio`	Numeric	Polio (Pol3) immunization coverage among 1-year-olds (%)
`Total.expenditure`	Numeric	General government expenditure on health as a percentage of total government expenditure (%)
`Diphtheria`	Numeric	Diphtheria tetanus toxoid and pertussis (DTP3) immunization coverage among 1-year-olds (%)
`HIV.AIDS`	Numeric	Deaths per 1,000 live births HIV/AIDS (0-4 years)
`GDP`	Numeric	Gross Domestic Product per capita (in USD)
`Population`	Numeric	Population of the country
`thinness..1.19.years`	Numeric	Prevalence of thinness among children and adolescents for Age 10 to 19 (%)
`thinness.5.9.years`	Numeric	Prevalence of thinness among children for Age 5 to 9(%)
`Income.composition.of.resources`	Numeric	Human Development Index in terms of income composition of resources (index ranging from 0 to 1)
`Schooling`	Numeric	Number of years of Schooling (years)

```
In [2]: df <- read.csv("/content/Life Expectancy Data.csv")
        head(df)
```

A data.frame: 6 × 22

	Country	Year	Status	Life.expectancy	Adult.Mortality	infant.deaths	Alcohol	percenta
	<chr>	<int>	<chr>	<dbl>	<int>	<int>	<dbl>	
1	Afghanistan	2015	Developing	65.0	263	62	0.01	
2	Afghanistan	2014	Developing	59.9	271	64	0.01	
3	Afghanistan	2013	Developing	59.9	268	66	0.01	
4	Afghanistan	2012	Developing	59.5	272	69	0.01	
5	Afghanistan	2011	Developing	59.2	275	71	0.01	
6	Afghanistan	2010	Developing	58.8	279	74	0.01	

```
In [3]: dim(df)
```

```
2938 · 22
```

Country and Year were removed as they are not useful for our analysis.

```
In [4]: df <- subset(df, select = -c(Country, Year))
```

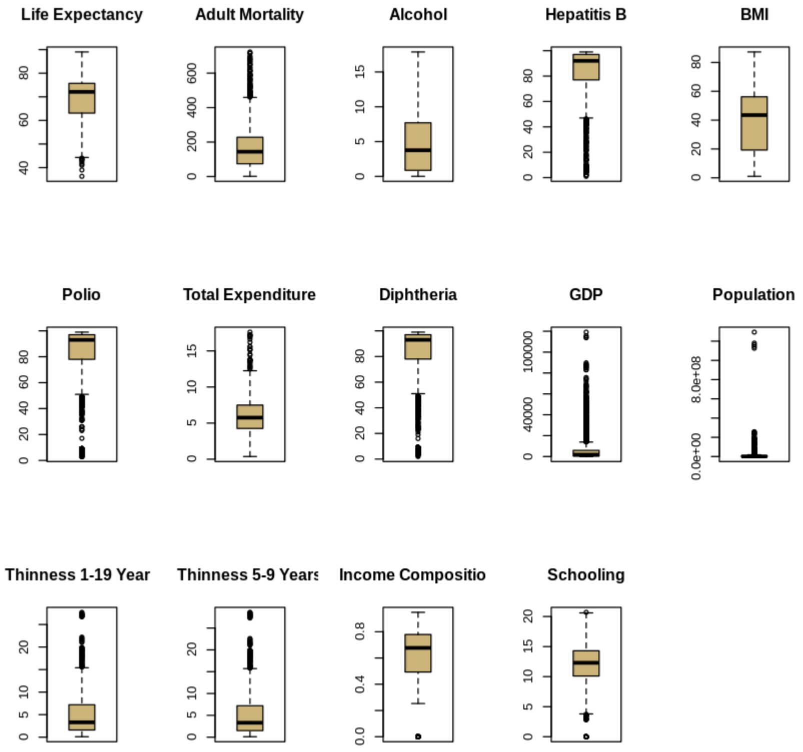
Data Cleaning

In [5]:
```
null_values <- colSums(is.na(df))
print(null_values)
```

```
                         Status                 Life.expectancy 
                              0                              10 
                Adult.Mortality                   infant.deaths 
                             10                               0 
                        Alcohol          percentage.expenditure 
                            194                               0 
                    Hepatitis.B                         Measles 
                            553                               0 
                            BMI                under.five.deaths 
                             34                               0 
                          Polio               Total.expenditure 
                             19                             226 
                     Diphtheria                        HIV.AIDS 
                             19                               0 
                            GDP                      Population 
                            448                             652 
           thinness..1.19.years              thinness.5.9.years 
                             34                              34 
Income.composition.of.resources                       Schooling 
                            167                             163 
```

There are 40% of missing values in the dataset. Hence we will proceed with data cleaning process further.

In [6]:
```
par(mfrow = c(3, 5))
boxplot(df$Life.expectancy, main = "Life Expectancy", col = "#CFB87C")
boxplot(df$Adult.Mortality, main = "Adult Mortality", col = "#CFB87C")
boxplot(df$Alcohol, main = "Alcohol", col = "#CFB87C")
boxplot(df$Hepatitis.B, main = "Hepatitis B", col = "#CFB87C")
boxplot(df$BMI, main = "BMI", col = "#CFB87C")
boxplot(df$Polio, main = "Polio", col = "#CFB87C")
boxplot(df$Total.expenditure, main = "Total Expenditure", col = "#CFB87C")
boxplot(df$Diphtheria, main = "Diphtheria", col = "#CFB87C")
boxplot(df$GDP, main = "GDP", col = "#CFB87C")
boxplot(df$Population, main = "Population", col = "#CFB87C")
boxplot(df$thinness..1.19.years, main = "Thinness 1-19 Years", col = "#CFB87C")
boxplot(df$thinness.5.9.years, main = "Thinness 5-9 Years", col = "#CFB87C")
boxplot(df$Income.composition.of.resources, main = "Income Composition", col = "#CFB87C")
boxplot(df$Schooling, main = "Schooling", col = "#CFB87C")
```



From the above box plots, we are replacing the boxplots with more outilers with mean and the box plots containing less outliers are replaced with median.

In [7]:
```
# Data Cleaning
Life.expectancy_median <- median(df$Life.expectancy, na.rm = TRUE)
Adult.Mortality_median <- median(df$Adult.Mortality, na.rm = TRUE)
Hepatitis.B_median <- median(df$Hepatitis.B, na.rm = TRUE)
Polio_median <- median(df$Polio, na.rm = TRUE)
Diphtheria_median <- median(df$Diphtheria, na.rm = TRUE)
Total.expenditure_median <- median(df$Total.expenditure, na.rm = TRUE)
GDP_median <- median(df$GDP, na.rm = TRUE)
Population_median <- median(df$Population, na.rm = TRUE)
thinness..1.19.years_median <- median(df$thinness..1.19.years, na.rm = TRUE)
thinness.5.9.years_median <- median(df$thinness.5.9.years, na.rm = TRUE)
Schooling_median <- median(df$Schooling, na.rm = TRUE)
```

In [8]:
```
# Data cleaning
Alcohol_mean <- mean(df$Alcohol,  na.rm = TRUE)
BMI_mean <- mean(df$BMI,  na.rm = TRUE)
Income.composition.of.resources_mean <- mean(df$Income.composition.of.resources,  na.rm = TRUE)
```

In [9]:
```
# Medians
df$Life.expectancy[is.na(df$Life.expectancy)] <- Life.expectancy_median
df$Adult.Mortality[is.na(df$Adult.Mortality)] <- Adult.Mortality_median
df$Hepatitis.B[is.na(df$Hepatitis.B)] <- Hepatitis.B_median
df$Polio[is.na(df$Polio)] <- Polio_median
df$Diphtheria[is.na(df$Diphtheria)] <- Diphtheria_median
df$Total.expenditure[is.na(df$Total.expenditure)] <- Total.expenditure_median
df$GDP[is.na(df$GDP)] <- GDP_median
df$Population[is.na(df$Population)] <- Population_median
df$thinness..1.19.years[is.na(df$thinness..1.19.years)] <- thinness..1.19.years_median
df$thinness.5.9.years[is.na(df$thinness.5.9.years)] <- thinness.5.9.years_median
df$Schooling[is.na(df$Schooling)] <- Schooling_median
# Means
df$Alcohol[is.na(df$Alcohol)] <- Alcohol_mean
df$BMI[is.na(df$BMI)] <- BMI_mean
df$Income.composition.of.resources[is.na(df$Income.composition.of.resources)] <- Income.composition.of.resources_mean
```

In [10]:
```
colSums(is.na(df))
```

```
Status: 0 Life.expectancy: 0 Adult.Mortality: 0 infant.deaths: 0 Alcohol: 0
percentage.expenditure: 0 Hepatitis.B: 0 Measles: 0 BMI: 0 under.five.deaths: 0 Polio: 0
Total.expenditure: 0 Diphtheria: 0 HIV.AIDS: 0 GDP: 0 Population: 0 thinness..1.19.years: 0
thinness.5.9.years: 0 Income.composition.of.resources: 0 Schooling: 0
```

In [11]:
```
df$Status <- as.factor(df$Status)
```

Now, let's procced with the correlation matrix and check that if there is any correlation between variables and see the possibility of collinearity, which we need to avoid in our model.

In [12]:

```
# Install the ggcorrplot package
install.packages("ggcorrplot")

# Load the ggcorrplot package
library(ggcorrplot)
```

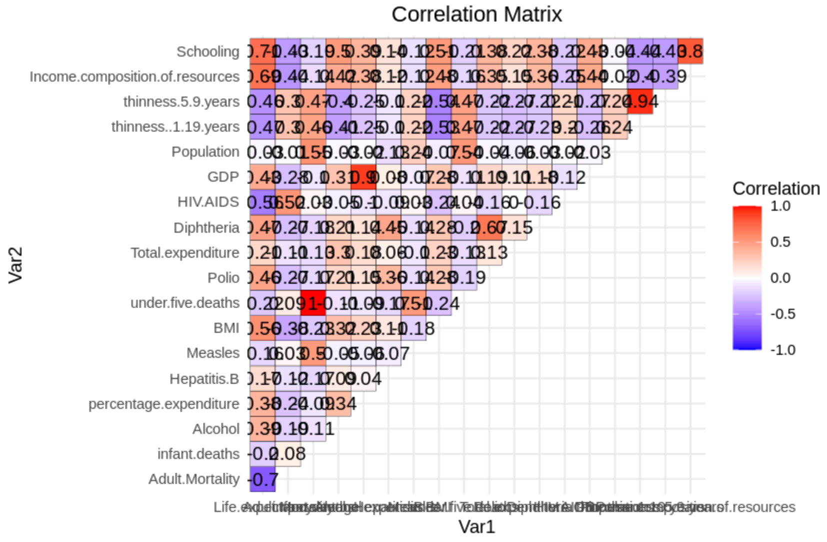
```
Installing package into ‘/usr/local/lib/R/site-library’
(as ‘lib’ is unspecified)

also installing the dependencies ‘plyr’, ‘Rcpp’, ‘reshape2’
```

In [13]:

```
corr <- cor(df[, sapply(df, is.numeric)])

# Create the correlation plot
ggcorrplot(corr, type = "upper", lab = TRUE,
           outline.color = "black", lab_size = 4,
           legend.title = "Correlation") +
  ggtitle("Correlation Matrix") +
  theme_minimal() +
  theme(plot.title = element_text(hjust = 0.5))
```



```
In [14]: corr
```

A matrix: 19 × 19 of type dbl

	Life.expectancy	Adult.Mortality	infant.deaths	Alcohol	perc
Life.expectancy	1.00000000	-0.696390066	-0.19676906	0.39067526	
Adult.Mortality	-0.69639007	1.000000000	0.07889001	-0.18992073	
infant.deaths	-0.19676906	0.078890013	1.00000000	-0.11381227	
Alcohol	0.39067526	-0.189920727	-0.11381227	1.00000000	
percentage.expenditure	0.38141810	-0.242627982	-0.08561222	0.33963429	
Hepatitis.B	0.17021864	-0.123286738	-0.16742088	0.09129769	
Measles	-0.15776659	0.031292960	0.50112834	-0.05105499	
BMI	0.56045296	-0.382143199	-0.22721997	0.31807030	
under.five.deaths	-0.22273822	0.094280105	0.99662888	-0.11077713	
Polio	0.45839934	-0.270001686	-0.17089558	0.21239474	
Total.expenditure	0.20884367	-0.111795861	-0.12626835	0.29548404	
Diphtheria	0.47221082	-0.270300714	-0.17537621	0.21387799	
HIV.AIDS	-0.55670342	0.523886499	0.02523132	-0.04864971	
GDP	0.43046130	-0.281434254	-0.10282895	0.31257906	
Population	-0.02901388	-0.005291655	0.55166746	-0.02734130	
thinness..1.19.years	-0.46800224	0.296135003	0.46481096	-0.41493751	
thinness.5.9.years	-0.46247317	0.301634253	0.47044500	-0.40388078	
Income.composition.of.resources	0.69255953	-0.440143142	-0.14366278	0.41609923	
Schooling	0.71305353	-0.433414640	-0.19095097	0.49933013	

In [15]:
```
corr[corr < 0.75 | corr == 1] <- NA
corr
```

A matrix: 19 × 19 of type dbl

	Life.expectancy	Adult.Mortality	infant.deaths	Alcohol	percenta
Life.expectancy	NA	NA	NA	NA	
Adult.Mortality	NA	NA	NA	NA	
infant.deaths	NA	NA	NA	NA	
Alcohol	NA	NA	NA	NA	
percentage.expenditure	NA	NA	NA	NA	
Hepatitis.B	NA	NA	NA	NA	
Measles	NA	NA	NA	NA	
BMI	NA	NA	NA	NA	
under.five.deaths	NA	NA	0.9966289	NA	
Polio	NA	NA	NA	NA	
Total.expenditure	NA	NA	NA	NA	
Diphtheria	NA	NA	NA	NA	
HIV.AIDS	NA	NA	NA	NA	
GDP	NA	NA	NA	NA	
Population	NA	NA	NA	NA	
thinness..1.19.years	NA	NA	NA	NA	
thinness.5.9.years	NA	NA	NA	NA	
Income.composition.of.resources	NA	NA	NA	NA	
Schooling	NA	NA	NA	NA	

From the correlation matrix we can remove these features: `infant.deaths` , `percentage.expenditure` , `thinness.5.9.years` , `Schooling` as they are highly correlated(greater than 0.75).

In [16]:
```
df <- df %>%
  select(-infant.deaths, -percentage.expenditure, -thinness.5.9.years,
-Schooling)
```

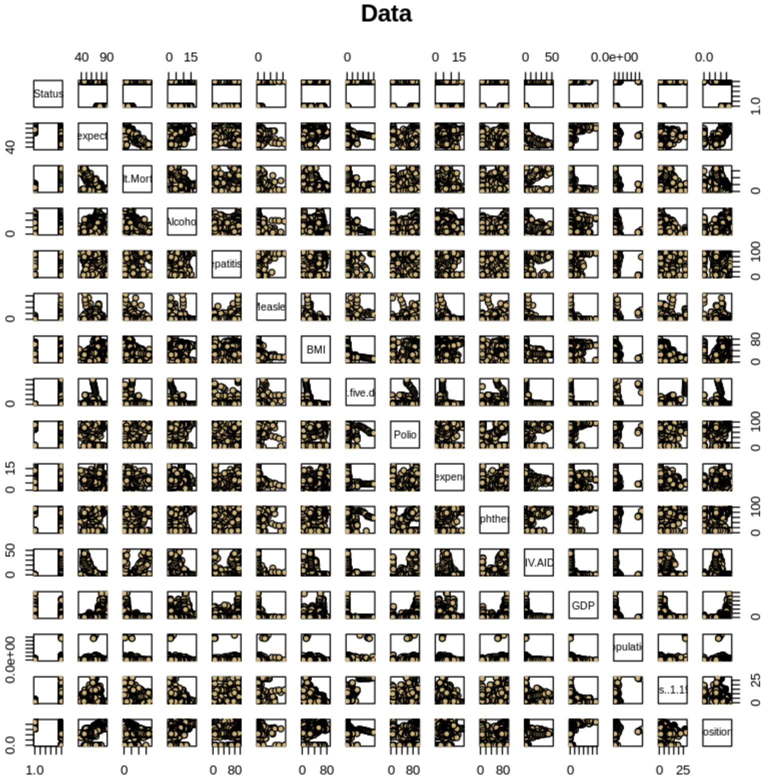
In [17]:
```
colSums(is.na(df))
```

Status: 0 **Life.expectancy:** 0 **Adult.Mortality:** 0 **Alcohol:** 0 **Hepatitis.B:** 0 **Measles:** 0 **BMI:** 0 **under.five.deaths:** 0 **Polio:** 0 **Total.expenditure:** 0 **Diphtheria:** 0 **HIV.AIDS:** 0 **GDP:** 0 **Population:** 0 **thinness..1.19.years:** 0 **Income.composition.of.resources:** 0

In [18]:
```
colnames(df)
```

```
'Status' · 'Life.expectancy' · 'Adult.Mortality' · 'Alcohol' · 'Hepatitis.B' · 'Measles' ·
'BMI' · 'under.five.deaths' · 'Polio' · 'Total.expenditure' · 'Diphtheria' · 'HIV.AIDS' ·
'GDP' · 'Population' · 'thinness..1.19.years' · 'Income.composition.of.resources'
```

In [19]:
```
pairs(df, main = " Data", pch = 21,
      bg = c("#CFB87C"))
```



T Test 1: Life Expectancy by Development Status

Null Hypothesis (H0): The mean life expectancy is the same in developed and developing countries.

Alternative Hypothesis (H1): The mean life expectancy differs between developed and developing countries.

In [20]:

```r
life_expectancy_developed <- filter(df, Status == 'Developed')$Life.expectancy
life_expectancy_developing <- filter(df, Status == 'Developing')$Life.expectancy
t_test1_results <- t.test(life_expectancy_developed, life_expectancy_developing, alternative = 'two.sided', var.equal = FALSE)
t_test1_results
```

```
	Welch Two Sample t-test

data:  life_expectancy_developed and life_expectancy_developing
t = 47.875, df = 1800.5, p-value < 2.2e-16
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 11.57153 12.56012
sample estimates:
mean of x mean of y 
 79.19785  67.13203 
```

We will reject the null hypothesis and conclude that here is a significant difference in life expectancy between developed and developing countries, with developed countries having a higher life expectancy as indicated above.

T Test 2: Impact of Alcohol Consumption on Life Expectancy

Null Hypothesis (H0): There is no difference in mean life expectancy between countries with high alcohol consumption and those with low or moderate alcohol consumption.

Alternative Hypothesis (H1): Countries with high alcohol consumption have a different mean life expectancy compared to those with low or moderate alcohol consumption.

In [21]:

```
high_alcohol <- filter(df, Alcohol > median(df$Alcohol, na.rm = TRUE))$Life.expectancy
low_alcohol <- filter(df, Alcohol <= median(df$Alcohol, na.rm = TRUE))$Life.expectancy
t_test2_results <- t.test(high_alcohol, low_alcohol, alternative = 'two.sided', var.equal = FALSE)
t_test2_results
```

```
	Welch Two Sample t-test

data:  high_alcohol and low_alcohol
t = 18.483, df = 2928.5, p-value < 2.2e-16
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 5.488386 6.791058
sample estimates:
mean of x mean of y 
 72.31503  66.17531 
```

We will reject the null hypothesis and conclude that there is a significant difference in life expectancy between groups with high alcohol consumption and lower alcohol consumption, where higher alcohol consumption is associated with a lower life expectancy.

F-test

Null Hypothesis: H_0 = Reduced model is sufficient
Alternative Hypothesis: H_1 = Reduced model is not sufficient

In [22]:

```
red_model <- lm(Life.expectancy ~ 1, data = df)
ful_model <- lm(Life.expectancy ~ Status + Adult.Mortality + Alcohol + Hepatitis.B + Measles + BMI + under.five.deaths + Polio + Total.expenditure + Diphtheria + HIV.AIDS + GDP + Population + thinness..1.19.years + Income.composition.of.resources, data = df)
```

In [23]:
```
anova(red_model, ful_model)
```

A anova: 2 × 6

	Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
1	2937	265573.14	NA	NA	NA	NA
2	2922	54187.64	15	211385.5	759.9131	0

Based on above output, we reject null hypothesis and conclude that atleast one among all predictors is required for predicting target variable.

Regression Modelling

In [24]:
```
install.packages("car")
library(car)
```

```
Installing package into ‘/usr/local/lib/R/site-library’
(as ‘lib’ is unspecified)

also installing the dependencies ‘numDeriv’, ‘SparseM’, ‘MatrixModel
s’, ‘minqa’, ‘nloptr’, ‘RcppEigen’, ‘carData’, ‘abind’, ‘pbkrtest’, ‘q
uantreg’, ‘lme4’


Loading required package: carData


Attaching package: ‘car’


The following object is masked from ‘package:dplyr’:

    recode


The following object is masked from ‘package:purrr’:

    some
```

In [25]:
```
set.seed(20)
n = floor(0.8 * nrow(df))
index = sample(seq_len(nrow(df)), size = n)
train = df[index, ]
test = df[-index, ]
```

In [26]:

```
model_full<- lm(Life.expectancy~., data = train)
summary(model_full)
```

```
Call:
lm(formula = Life.expectancy ~ ., data = train)

Residuals:
     Min       1Q   Median       3Q      Max
-23.1267  -2.3813  -0.1337   2.3378  19.1048

Coefficients:
                                  Estimate Std. Error t value Pr(>|t|)
(Intercept)                      5.837e+01  7.686e-01  75.942  < 2e-16
***
StatusDeveloping                -2.049e+00  3.245e-01  -6.316 3.20e-10
***
Adult.Mortality                 -2.072e-02  9.550e-04 -21.695  < 2e-16
***
Alcohol                          1.071e-01  3.014e-02   3.555 0.000386
***
Hepatitis.B                     -2.146e-02  4.423e-03  -4.852 1.30e-06
***
Measles                         -2.084e-05  9.100e-06  -2.290 0.022107
*
BMI                              5.324e-02  5.821e-03   9.145  < 2e-16
***
under.five.deaths               -2.597e-03  8.129e-04  -3.195 0.001416
**
Polio                            3.779e-02  5.360e-03   7.051 2.33e-12
***
Total.expenditure                1.055e-01  4.107e-02   2.568 0.010297
*
Diphtheria                       5.120e-02  5.512e-03   9.289  < 2e-16
***
HIV.AIDS                        -4.755e-01  2.169e-02 -21.924  < 2e-16
***
GDP                              5.098e-05  7.936e-06   6.423 1.61e-10
***
Population                       4.163e-09  1.876e-09   2.219 0.026581
*
thinness..1.19.years            -6.074e-02  2.881e-02  -2.109 0.035094
*
Income.composition.of.resources  1.297e+01  6.137e-01  21.130  < 2e-16
***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 4.374 on 2334 degrees of freedom
Multiple R-squared:  0.7935,	Adjusted R-squared:  0.7922 
F-statistic:   598 on 15 and 2334 DF,  p-value: < 2.2e-16
```

MLR model as follows:

$\hat{\beta}_0 = 54.18, \hat{\beta}_1 = -1.111, \hat{\beta}_2 = -0.01584, , \hat{\beta}_3 = -0.1064, \hat{\beta}_4 = 0.0003945, \hat{\beta}_5 = -0.006863, \hat{\beta}_6 = -0.0000$
$-0.07487, \hat{\beta}_9 = 0.007007, \hat{\beta}_{10} = 0.08049, \hat{\beta}_{11} = 0.0163, \hat{\beta}_{12} = -0.4293, \hat{\beta}_{13} = 0.00000627, \hat{\beta}_{14} = -0.000$
$= 10.61$

$Life.expectancy = 54.18 - 1.111 \times \text{StatusDeveloping} - 0.01584 \times \text{Adult.Mortality} - 0.1064 \times \text{Alcohol} +$
$- 0.006863 \times \text{Hepatitis.B} - 0.00001158 \times \text{Measles} + 0.03477 \times \text{BMI} - 0.07487 \times \text{under.five.deaths} + 0.00$
$\times \text{Total.expenditure} + 0.0163 \times \text{Diphtheria} - 0.4293 \times \text{HIV.AIDS} + 0.00000627 \times \text{GDP} - 0.00000000036$
$\times \text{thinness..1.19.years} + 10.61 \times \text{Income.composition.of.resources}$

In [27]:
```
predicted_values <- predict(model_full, newdata = test)

mspe <- mean((test$Life.expectancy - predicted_values)^2)
print(mspe)
```

```
[1] 16.31475
```

Now, we will try to reduce the predictors and calculate the MSPE for each model. We will be considering the model with least MSPE as the best model. Here we will try to remove `Population` variable.

In [28]:
```
model_full<- update(model_full,.~.-Population)
summary(model_full)
```

```
Call:
lm(formula = Life.expectancy ~ Status + Adult.Mortality + Alcohol + 
    Hepatitis.B + Measles + BMI + under.five.deaths + Polio + 
    Total.expenditure + Diphtheria + HIV.AIDS + GDP + thinness..1.19.y
ears + 
    Income.composition.of.resources, data = train)

Residuals:
     Min       1Q   Median       3Q      Max 
-23.1241  -2.3922  -0.1203   2.3573  19.1356 

Coefficients:
                                  Estimate Std. Error t value Pr(>|t|)
(Intercept)                      5.832e+01  7.689e-01  75.846  < 2e-16
***
StatusDeveloping                -2.042e+00  3.247e-01  -6.288 3.82e-10
***
Adult.Mortality                 -2.075e-02  9.557e-04 -21.710  < 2e-16
***
Alcohol                          1.079e-01  3.016e-02   3.578 0.000353
***
Hepatitis.B                     -2.228e-02  4.411e-03  -5.052 4.71e-07
***
Measles                         -2.179e-05  9.098e-06  -2.395 0.016696
*
BMI                              5.363e-02  5.823e-03   9.209  < 2e-16
***
under.five.deaths               -1.730e-03  7.134e-04  -2.425 0.015371
*
Polio                            3.799e-02  5.363e-03   7.083 1.87e-12
***
Total.expenditure                1.049e-01  4.110e-02   2.551 0.010795
*
Diphtheria                       5.193e-02  5.507e-03   9.431  < 2e-16
***
HIV.AIDS                        -4.759e-01  2.171e-02 -21.921  < 2e-16
***
GDP                              5.104e-05  7.943e-06   6.426 1.58e-10
***
thinness..1.19.years            -5.900e-02  2.882e-02  -2.047 0.040755
*
Income.composition.of.resources  1.301e+01  6.138e-01  21.201  < 2e-16
***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 4.377 on 2335 degrees of freedom
Multiple R-squared:  0.7931,	Adjusted R-squared:  0.7918 
F-statistic: 639.3 on 14 and 2335 DF,  p-value: < 2.2e-16
```

In [29]:
```
predicted_values <- predict(model_full, newdata = test)
mspe <- mean((test$Life.expectancy - predicted_values)^2)
print(mspe)
```

```
[1] 16.33199
```

In [30]:
```
model_full<- update(model_full,.~.-thinness..1.19.years)
summary(model_full)
```

```
Call:
lm(formula = Life.expectancy ~ Status + Adult.Mortality + Alcohol + 
    Hepatitis.B + Measles + BMI + under.five.deaths + Polio + 
    Total.expenditure + Diphtheria + HIV.AIDS + GDP + Income.compositi
on.of.resources, 
    data = train)

Residuals:
     Min       1Q   Median       3Q      Max 
-23.3509  -2.4179  -0.0879   2.3137  19.3684 

Coefficients:
                                  Estimate Std. Error t value Pr(>|t|)
(Intercept)                      5.786e+01  7.366e-01  78.553  < 2e-16
***
StatusDeveloping                -2.084e+00  3.243e-01  -6.425 1.59e-10
***
Adult.Mortality                 -2.079e-02  9.562e-04 -21.738  < 2e-16
***
Alcohol                          1.208e-01  2.952e-02   4.094 4.39e-05
***
Hepatitis.B                     -2.263e-02  4.410e-03  -5.132 3.11e-07
***
Measles                         -2.110e-05  9.098e-06  -2.319 0.020475
*
BMI                              5.741e-02  5.527e-03  10.387  < 2e-16
***
under.five.deaths               -2.339e-03  6.490e-04  -3.603 0.000321
***
Polio                            3.768e-02  5.365e-03   7.023 2.84e-12
***
Total.expenditure                1.136e-01  4.091e-02   2.778 0.005511
**
Diphtheria                       5.183e-02  5.510e-03   9.407  < 2e-16
***
HIV.AIDS                        -4.803e-01  2.161e-02 -22.222  < 2e-16
***
GDP                              5.134e-05  7.947e-06   6.461 1.26e-10
***
Income.composition.of.resources  1.309e+01  6.130e-01  21.356  < 2e-16
***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 4.38 on 2336 degrees of freedom
Multiple R-squared:  0.7927,	Adjusted R-squared:  0.7916 
F-statistic: 687.2 on 13 and 2336 DF,  p-value: < 2.2e-16
```

In [31]:

```
predicted_values <- predict(model_full, newdata = test)
mspe <- mean((test$Life.expectancy - predicted_values)^2)
mspe
```

16.3713190022482

In [32]:

```
model_full<- update(model_full,.~.-Measles)
summary(model_full)
```

```
Call:
lm(formula = Life.expectancy ~ Status + Adult.Mortality + Alcohol + 
    Hepatitis.B + BMI + under.five.deaths + Polio + Total.expenditure 
+ 
    Diphtheria + HIV.AIDS + GDP + Income.composition.of.resources, 
    data = train)

Residuals:
    Min      1Q  Median      3Q     Max 
-23.271  -2.429  -0.077   2.339  19.441 

Coefficients:
                                  Estimate Std. Error t value Pr(>|t|)
(Intercept)                      5.774e+01  7.355e-01  78.505  < 2e-16
***
StatusDeveloping                -2.101e+00  3.245e-01  -6.474 1.16e-10
***
Adult.Mortality                 -2.061e-02  9.539e-04 -21.601  < 2e-16
***
Alcohol                          1.162e-01  2.948e-02   3.942 8.31e-05
***
Hepatitis.B                     -2.307e-02  4.411e-03  -5.231 1.84e-07
***
BMI                              5.799e-02  5.526e-03  10.493  < 2e-16
***
under.five.deaths               -3.087e-03  5.636e-04  -5.477 4.79e-08
***
Polio                            3.789e-02  5.369e-03   7.057 2.24e-12
***
Total.expenditure                1.177e-01  4.091e-02   2.877  0.00405
**
Diphtheria                       5.238e-02  5.510e-03   9.506  < 2e-16
***
HIV.AIDS                        -4.821e-01  2.162e-02 -22.300  < 2e-16
***
GDP                              5.136e-05  7.954e-06   6.456 1.30e-10
***
Income.composition.of.resources  1.315e+01  6.132e-01  21.441  < 2e-16
***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 4.384 on 2337 degrees of freedom
Multiple R-squared:  0.7922,	Adjusted R-squared:  0.7912 
F-statistic: 742.6 on 12 and 2337 DF,  p-value: < 2.2e-16
```

In [33]:
```
predicted_values <- predict(model_full, newdata = test)
mspe <- mean((test$Life.expectancy - predicted_values)^2)
mspe
```

16.3728082899134

In [34]:
```
model_full<- update(model_full,.~.-Total.expenditure)
summary(model_full)
```

```
Call:
lm(formula = Life.expectancy ~ Status + Adult.Mortality + Alcohol + 
    Hepatitis.B + BMI + under.five.deaths + Polio + Diphtheria + 
    HIV.AIDS + GDP + Income.composition.of.resources, data = train)

Residuals:
     Min       1Q   Median       3Q      Max 
-22.5524  -2.4430  -0.0919   2.2913  19.1812 

Coefficients:
                                  Estimate Std. Error t value Pr(>|t|)
(Intercept)                      5.849e+01  6.889e-01  84.912  < 2e-16
***
StatusDeveloping                -2.256e+00  3.206e-01  -7.037 2.56e-12
***
Adult.Mortality                 -2.064e-02  9.553e-04 -21.609  < 2e-16
***
Alcohol                          1.277e-01  2.925e-02   4.364 1.33e-05
***
Hepatitis.B                     -2.365e-02  4.413e-03  -5.359 9.17e-08
***
BMI                              6.016e-02  5.483e-03  10.973  < 2e-16
***
under.five.deaths               -3.197e-03  5.632e-04  -5.676 1.55e-08
***
Polio                            3.820e-02  5.376e-03   7.106 1.58e-12
***
Diphtheria                       5.307e-02  5.514e-03   9.625  < 2e-16
***
HIV.AIDS                        -4.781e-01  2.161e-02 -22.126  < 2e-16
***
GDP                              5.025e-05  7.957e-06   6.315 3.22e-10
***
Income.composition.of.resources  1.301e+01  6.123e-01  21.252  < 2e-16
***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 4.391 on 2338 degrees of freedom
Multiple R-squared:  0.7915,	Adjusted R-squared:  0.7905 
F-statistic: 806.8 on 11 and 2338 DF,  p-value: < 2.2e-16
```

In [35]:
```
predicted_values <- predict(model_full, newdata = test)
mspe <- mean((test$Life.expectancy - predicted_values)^2)
mspe
```

16.426233618976

In [36]:
```
model_full<- update(model_full,.~.-Alcohol)
summary(model_full)
```

```
Call:
lm(formula = Life.expectancy ~ Status + Adult.Mortality + Hepatitis.B
+
    BMI + under.five.deaths + Polio + Diphtheria + HIV.AIDS +
    GDP + Income.composition.of.resources, data = train)

Residuals:
     Min       1Q   Median       3Q      Max
-22.2864  -2.4829  -0.1242   2.3325  19.6660

Coefficients:
                                  Estimate Std. Error t value Pr(>|t|)
(Intercept)                      5.911e+01  6.770e-01  87.314  < 2e-16
***
StatusDeveloping                -2.864e+00  2.898e-01  -9.884  < 2e-16
***
Adult.Mortality                 -2.039e-02  9.573e-04 -21.304  < 2e-16
***
Hepatitis.B                     -2.401e-02  4.429e-03  -5.422 6.50e-08
***
BMI                              6.293e-02  5.467e-03  11.511  < 2e-16
***
under.five.deaths               -3.202e-03  5.654e-04  -5.663 1.67e-08
***
Polio                            3.861e-02  5.396e-03   7.154 1.12e-12
***
Diphtheria                       5.360e-02  5.533e-03   9.687  < 2e-16
***
HIV.AIDS                        -4.716e-01  2.164e-02 -21.793  < 2e-16
***
GDP                              5.087e-05  7.987e-06   6.369 2.28e-10
***
Income.composition.of.resources  1.344e+01  6.067e-01  22.157  < 2e-16
***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 4.408 on 2339 degrees of freedom
Multiple R-squared:  0.7898,    Adjusted R-squared:  0.7889
F-statistic: 878.8 on 10 and 2339 DF,  p-value: < 2.2e-16
```

In [37]:
```
predicted_values <- predict(model_full, newdata = test)
mspe <- mean((test$Life.expectancy - predicted_values)^2)
mspe
```

16.592518107029

In [38]:
```
model_full<- update(model_full,.~.-Hepatitis.B)
summary(model_full)
```

```
Call:
lm(formula = Life.expectancy ~ Status + Adult.Mortality + BMI + 
    under.five.deaths + Polio + Diphtheria + HIV.AIDS + GDP + 
    Income.composition.of.resources, data = train)

Residuals:
     Min       1Q   Median       3Q      Max 
-22.5421  -2.4657  -0.0909   2.3511  19.8320 

Coefficients:
                                  Estimate Std. Error t value Pr(>|t|)
(Intercept)                      5.776e+01  6.333e-01  91.207  < 2e-16
***
StatusDeveloping                -2.763e+00  2.909e-01  -9.497  < 2e-16
***
Adult.Mortality                 -2.036e-02  9.631e-04 -21.136  < 2e-16
***
BMI                              6.384e-02  5.498e-03  11.612  < 2e-16
***
under.five.deaths               -2.861e-03  5.653e-04  -5.062 4.47e-07
***
Polio                            3.608e-02  5.409e-03   6.671 3.16e-11
***
Diphtheria                       4.456e-02  5.308e-03   8.395  < 2e-16
***
HIV.AIDS                        -4.726e-01  2.177e-02 -21.709  < 2e-16
***
GDP                              5.086e-05  8.035e-06   6.330 2.92e-10
***
Income.composition.of.resources  1.372e+01  6.082e-01  22.560  < 2e-16
***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 4.435 on 2340 degrees of freedom
Multiple R-squared:  0.7872,	Adjusted R-squared:  0.7863 
F-statistic: 961.5 on 9 and 2340 DF,  p-value: < 2.2e-16
```

In [39]:
```
predicted_values <- predict(model_full, newdata = test)
mspe <- mean((test$Life.expectancy - predicted_values)^2)
mspe
```

```
16.6668862458654
```

In [40]:

```
model_full<- update(model_full,.~.-under.five.deaths)
summary(model_full)
```

```
Call:
lm(formula = Life.expectancy ~ Status + Adult.Mortality + BMI +
    Polio + Diphtheria + HIV.AIDS + GDP + Income.composition.of.resour
ces,
    data = train)

Residuals:
     Min       1Q   Median       3Q      Max
-22.3745  -2.4401  -0.1098   2.3079  20.1081

Coefficients:
                                  Estimate Std. Error t value Pr(>|t|)
(Intercept)                      5.714e+01  6.246e-01  91.478  < 2e-16
***
StatusDeveloping                -2.786e+00  2.924e-01  -9.527  < 2e-16
***
Adult.Mortality                 -2.018e-02  9.675e-04 -20.856  < 2e-16
***
BMI                              6.834e-02  5.453e-03  12.532  < 2e-16
***
Polio                            3.754e-02  5.429e-03   6.915 6.02e-12
***
Diphtheria                       4.626e-02  5.325e-03   8.687  < 2e-16
***
HIV.AIDS                        -4.704e-01  2.188e-02 -21.499  < 2e-16
***
GDP                              5.163e-05  8.076e-06   6.394 1.95e-10
***
Income.composition.of.resources  1.379e+01  6.112e-01  22.557  < 2e-16
***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 4.458 on 2341 degrees of freedom
Multiple R-squared:  0.7848,	Adjusted R-squared:  0.7841
F-statistic:  1067 on 8 and 2341 DF,  p-value: < 2.2e-16
```

In [41]:

```
predicted_values <- predict(model_full, newdata = test)
mspe <- mean((test$Life.expectancy - predicted_values)^2)
mspe
```

16.8999583941662

In [42]:

```
model_full<- update(model_full,.~.-Polio)
summary(model_full)
```

```
Call:
lm(formula = Life.expectancy ~ Status + Adult.Mortality + BMI + 
    Diphtheria + HIV.AIDS + GDP + Income.composition.of.resources, 
    data = train)

Residuals:
     Min       1Q   Median       3Q      Max 
-22.6461  -2.4109  -0.0443   2.2947  20.6678 

Coefficients:
                                  Estimate Std. Error t value Pr(>|t|)
(Intercept)                      5.814e+01  6.136e-01  94.756  < 2e-16
***
StatusDeveloping                -2.834e+00  2.952e-01  -9.598  < 2e-16
***
Adult.Mortality                 -2.037e-02  9.767e-04 -20.852  < 2e-16
***
BMI                              7.056e-02  5.498e-03  12.834  < 2e-16
***
Diphtheria                       6.898e-02  4.232e-03  16.298  < 2e-16
***
HIV.AIDS                        -4.708e-01  2.210e-02 -21.304  < 2e-16
***
GDP                              5.258e-05  8.155e-06   6.448 1.37e-10
***
Income.composition.of.resources  1.412e+01  6.154e-01  22.940  < 2e-16
***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 4.502 on 2342 degrees of freedom
Multiple R-squared:  0.7804,	Adjusted R-squared:  0.7798 
F-statistic:  1189 on 7 and 2342 DF,  p-value: < 2.2e-16
```

In [43]:

```
predicted_values <- predict(model_full, newdata = test)
mspe <- mean((test$Life.expectancy - predicted_values)^2)
mspe
```

17.1751004677239

In [44]:
```
model_full<- update(model_full,.~.-GDP)
summary(model_full)
```

```
Call:
lm(formula = Life.expectancy ~ Status + Adult.Mortality + BMI + 
    Diphtheria + HIV.AIDS + Income.composition.of.resources, 
    data = train)

Residuals:
     Min       1Q   Median       3Q      Max 
-22.6238  -2.4055  -0.1096   2.3140  21.1466 

Coefficients:
                                  Estimate Std. Error t value Pr(>|t|)    
(Intercept)                     58.4420236  0.6170919   94.71   <2e-16 
***
StatusDeveloping                -3.4211264  0.2832455  -12.08   <2e-16 
***
Adult.Mortality                 -0.0207673  0.0009831  -21.12   <2e-16 
***
BMI                              0.0714517  0.0055437   12.89   <2e-16 
***
Diphtheria                       0.0686565  0.0042685   16.09   <2e-16 
***
HIV.AIDS                        -0.4658259  0.0222743  -20.91   <2e-16 
***
Income.composition.of.resources 15.0467324  0.6035087   24.93   <2e-16 
***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 4.541 on 2343 degrees of freedom
Multiple R-squared:  0.7765,    Adjusted R-squared:  0.776 
F-statistic:  1357 on 6 and 2343 DF,  p-value: < 2.2e-16
```

In [45]:
```
predicted_values <- predict(model_full, newdata = test)
mspe <- mean((test$Life.expectancy - predicted_values)^2)
mspe
```

17.4380394865856

I have removed features one by one as part of backward selection process, however I observed very little or no change in MSPE and Adj R^2. Upon observing these values over iterations, hardly MSPE increased from xx to 17.43 and R_a^2 decreased from xx to 77.6\%. I see this as a trade-off between complexity of model and prediction accuracy. Also, I would tend to select a more interpretable and less complicated model if we could achieve reasonably good accuracies by sacrificing few predictors. I believe it's worth doing that as industry needs simple and straightforward models without compromising on performance. We will one more iteration to see any significant change in these values. If there is, we need to stop at that iteration and can chooxse model.

In [46]:
```
model_full<- update(model_full,.~.-Income.composition.of.resources)
summary(model_full)
```

```
Call:
lm(formula = Life.expectancy ~ Status + Adult.Mortality + BMI + 
    Diphtheria + HIV.AIDS, data = train)

Residuals:
     Min       1Q   Median       3Q      Max 
-26.3407  -2.8041   0.1956   2.8426  15.5823 

Coefficients:
                  Estimate Std. Error t value Pr(>|t|)    
(Intercept)      67.155424   0.571968  117.41   <2e-16 ***
StatusDeveloping -5.662961   0.302066  -18.75   <2e-16 ***
Adult.Mortality  -0.025609   0.001084  -23.63   <2e-16 ***
BMI               0.113388   0.005941   19.09   <2e-16 ***
Diphtheria        0.090665   0.004697   19.30   <2e-16 ***
HIV.AIDS         -0.472104   0.025048  -18.85   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 5.107 on 2344 degrees of freedom
Multiple R-squared:  0.7172,    Adjusted R-squared:  0.7166 
F-statistic:  1189 on 5 and 2344 DF,  p-value: < 2.2e-16
```

In [47]:
```
predicted_values <- predict(model_full, newdata = test)
mspe <- mean((test$Life.expectancy - predicted_values)^2)
mspe
```

21.6409493929237

As described above, there is a significant drop of around 6\% in R_a^2 and remarkable increase in MSPE to 21.64 after dropping `Income.composition.of.resources` . This means that we need to stop our iterations here and best model would be Life.expectancy ~ Status + Adult.Mortality + BMI + Diphtheria + HIV.AIDS + Income.composition.of.resources, data = train

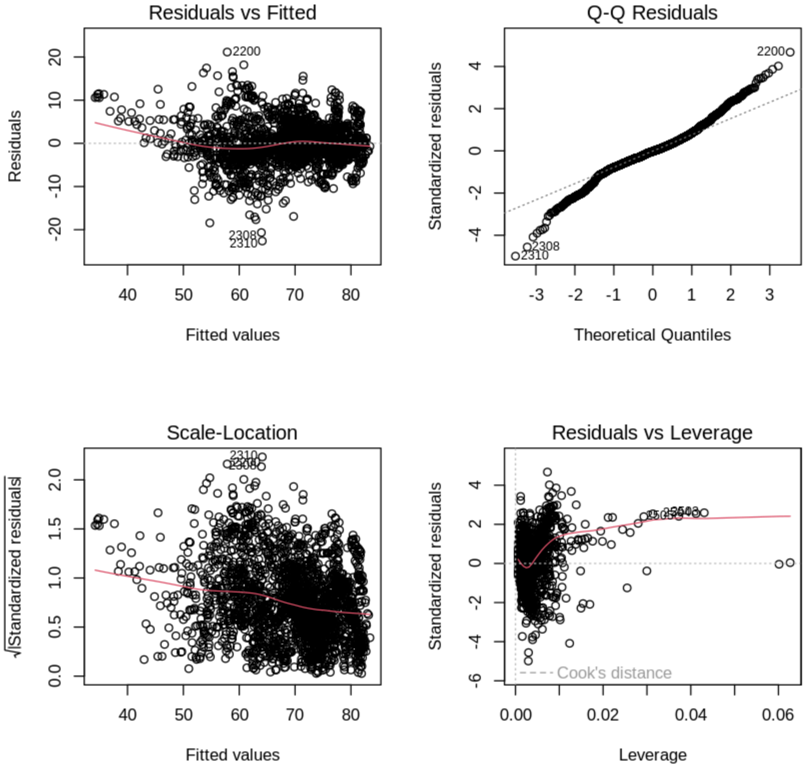
In [48]:
```
model_full <- lm(Life.expectancy ~ Status + Adult.Mortality + BMI + 
    Diphtheria + HIV.AIDS + Income.composition.of.resources, 
    data = train)
```

In [49]:
```
model_full
```

```
Call:
lm(formula = Life.expectancy ~ Status + Adult.Mortality + BMI + 
    Diphtheria + HIV.AIDS + Income.composition.of.resources, 
    data = train)

Coefficients:
                    (Intercept)                StatusDeveloping  
                       58.44202                        -3.42113  
                Adult.Mortality                             BMI  
                       -0.02077                         0.07145  
                     Diphtheria                        HIV.AIDS  
                        0.06866                        -0.46583  
Income.composition.of.resources  
                       15.04673  
```

In [50]:
```
# Model Diagnostics
par(mfrow=c(2,2))
plot(model_full)
```



From the above Residual vs Fitted graph, we can see that the points are scattered randomly, without having any pattern, this shows that the homoscedasticity is met.

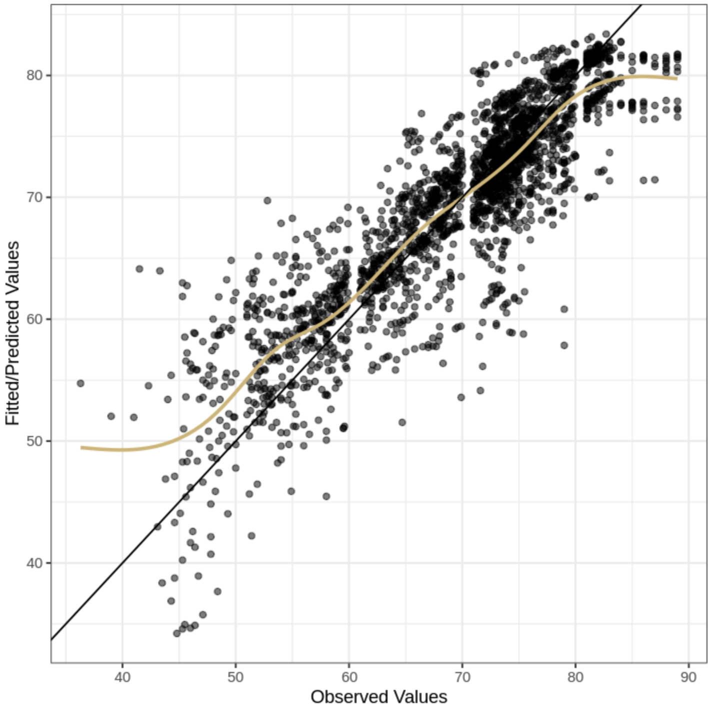
From the Q-Q plot, we can see that the points are coinciding with theoretical straight line in the middle and there are some deviations at the extremes in the plot. Though this not perfect normal, at the same time it is not serious enough to reject the normality of residuals.

From the residuals vs leverage plot, we can see that there are some influential points that might affect the model's preditctions. Removing these points might impact model's performance.

```
In [51]: df.diagnostics = data.frame(yhat = fitted(model_full), r = resid(model
         _full), y = train$Life.expectancy)
```

```
In [52]: options(repr.plot.width = 6, repr.plot.height = 6)
         ggplot(df.diagnostics, aes(x = y, y = yhat)) +
             geom_point(alpha = 0.5) +
             geom_smooth(se = F, col = "#CFB87C") +
             geom_abline(intercept = 0, slope = 1)+
             xlab("Observed Values") +
             ylab("Fitted/Predicted Values") +
             theme_bw()
```

```
`geom_smooth()` using method = 'gam' and formula = 'y ~ s(x, bs = "c
s")'
```



For lower values it is predicting more than expected. For higher values it is predicting less than the oberserved values. There might be a chance of bias.From backward selection, the regression is as follows: Life.expectancy ~ Status + Adult.Mortality + BMI + Diphtheria + HIV.AIDS + Income.composition.of.resources

Model Selection

In [53]:
```
install.packages("leaps")
library(leaps)
library(MASS)
```

```
Installing package into ‘/usr/local/lib/R/site-library’
(as ‘lib’ is unspecified)


Attaching package: ‘MASS’


The following object is masked from ‘package:dplyr’:

    select

```

In [54]:
```
n = dim(df)[1]
reg1 = regsubsets(Life.expectancy ~ Status + Adult.Mortality + Alcohol
+
    Hepatitis.B + BMI + under.five.deaths + Polio + Total.expenditure
+
    Diphtheria + HIV.AIDS + GDP + Income.composition.of.resources, dat
a = train, nvmax=12)
rs = summary(reg1)
rs$which
```

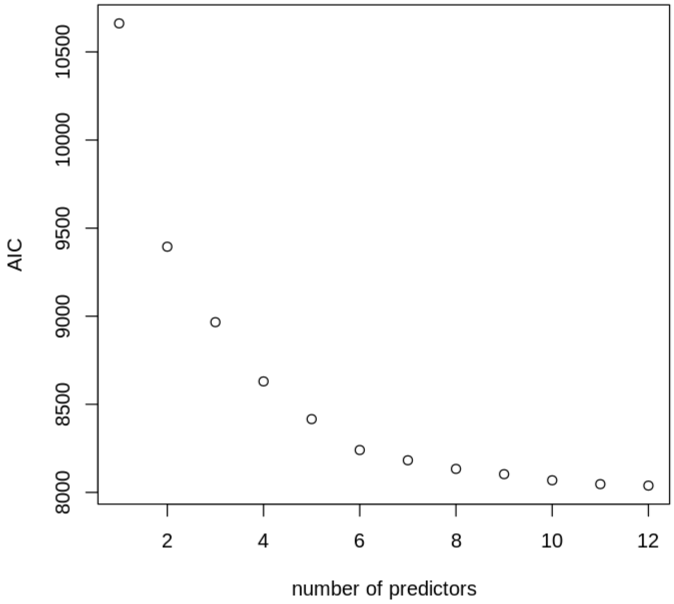
A matrix: 12 × 13 of type lgl

	(Intercept)	StatusDeveloping	Adult.Mortality	Alcohol	Hepatitis.B	BMI	under.five.deaths
1	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE	FALSE
2	TRUE	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
3	TRUE	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
4	TRUE	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
5	TRUE	FALSE	TRUE	FALSE	FALSE	TRUE	FALSE
6	TRUE	TRUE	TRUE	FALSE	FALSE	TRUE	FALSE
7	TRUE	TRUE	TRUE	FALSE	FALSE	TRUE	FALSE
8	TRUE	TRUE	TRUE	FALSE	FALSE	TRUE	FALSE
9	TRUE	TRUE	TRUE	FALSE	FALSE	TRUE	TRUE
10	TRUE	TRUE	TRUE	FALSE	TRUE	TRUE	TRUE
11	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
12	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE

The above table provides information of best model in terms of RSS of size K=1,2,3........,12.

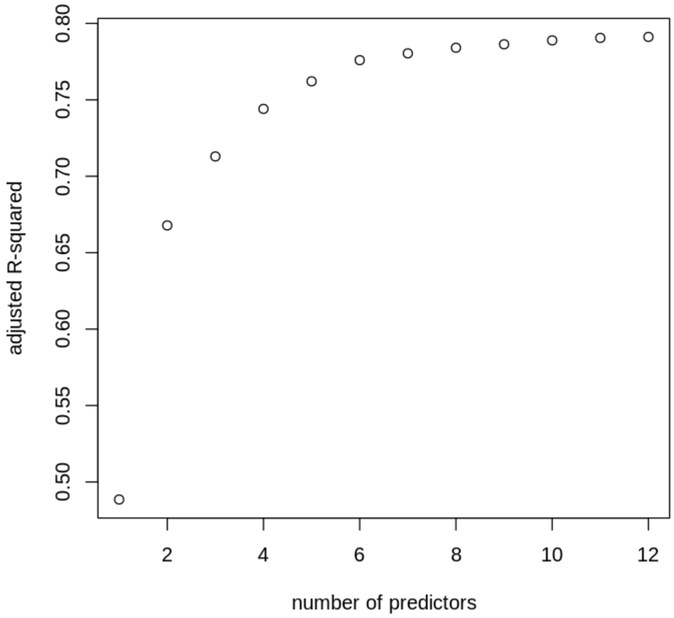
In [55]:

```r
AIC = 2*(2:13) + n*log(rs$rss/n)
plot(AIC ~ I(1:12), xlab = "number of predictors", ylab = "AIC")
```

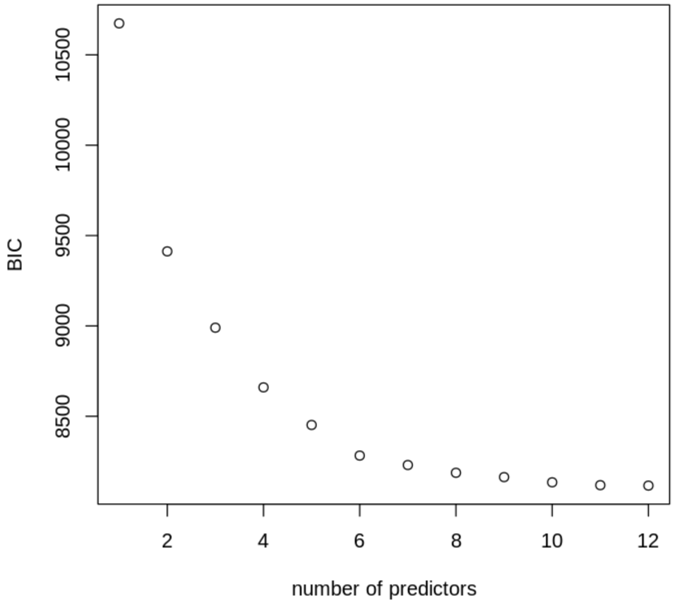


From the above plot we can see that model(k)=10, has the lowest AIC. From k=10 the curve looks almost flat, we can go with 10 predictors for linear regression model.

In [56]:
```
plot(1:12, rs$adjr2, xlab = "number of predictors", ylab = "adjusted R
-squared")
```



In [57]:
```
BIC = log(n)*(2:13) + n*log(rs$rss/n)
plot(BIC ~ I(1:12), xlab = "number of predictors", ylab = "BIC")
```



From the above plot we are getting the same model as AIC and R-squared with 10 predictors. Now, we will check the evidence of collinearity between our predictors using VIF.

```
In [58]: lm_aic = lm(Life.expectancy ~ Status + Adult.Mortality +Hepatitis.B+ B
         MI +under.five.deaths+Polio+Diphtheria + HIV.AIDS + GDP+Income.composi
         tion.of.resources,data = train)
         vif(lm_aic)
         kappa(lm_aic)
         cor(model.matrix(lm_aic)[,-1])
```

Status: 1.45138927110688 **Adult.Mortality:** 1.73359263884626 **Hepatitis.B:** 1.28783680204836 **BMI:** 1.44450712143028 **under.five.deaths:** 1.09694749121252 **Polio:** 1.92711527360719 **Diphtheria:** 2.12525216025418 **HIV.AIDS:** 1.42545500938298 **GDP:** 1.39429764410479 **Income.composition.of.resources:** 1.83430652665592

173420.363259154

A matrix: 10 × 10 of type dbl

	StatusDeveloping	Adult.Mortality	Hepatitis.B	BMI	unde
StatusDeveloping	1.0000000	0.31704038	-0.13044461	-0.3017484	
Adult.Mortality	0.3170404	1.00000000	-0.10836989	-0.3812972	
Hepatitis.B	-0.1304446	-0.10836989	1.00000000	0.1067408	
BMI	-0.3017484	-0.38129722	0.10674085	1.0000000	
under.five.deaths	0.1127362	0.07802194	-0.17827122	-0.2332971	
Polio	-0.2179678	-0.25872110	0.35705901	0.2878016	
Diphtheria	-0.2120589	-0.26962105	0.44693665	0.2893996	
HIV.AIDS	0.1503960	0.54105601	-0.06291413	-0.2525007	
GDP	-0.4596618	-0.27636965	0.07729116	0.2646855	
Income.composition.of.resources	-0.4613313	-0.44302642	0.11310767	0.4863720	

In [59]:
```
summary(lm_aic)
```

```
Call:
lm(formula = Life.expectancy ~ Status + Adult.Mortality + Hepatitis.B
+
    BMI + under.five.deaths + Polio + Diphtheria + HIV.AIDS +
    GDP + Income.composition.of.resources, data = train)

Residuals:
     Min       1Q   Median       3Q      Max
-22.2864  -2.4829  -0.1242   2.3325  19.6660

Coefficients:
                                  Estimate Std. Error t value Pr(>|t|)
(Intercept)                      5.911e+01  6.770e-01  87.314  < 2e-16
***
StatusDeveloping                -2.864e+00  2.898e-01  -9.884  < 2e-16
***
Adult.Mortality                 -2.039e-02  9.573e-04 -21.304  < 2e-16
***
Hepatitis.B                     -2.401e-02  4.429e-03  -5.422 6.50e-08
***
BMI                              6.293e-02  5.467e-03  11.511  < 2e-16
***
under.five.deaths               -3.202e-03  5.654e-04  -5.663 1.67e-08
***
Polio                            3.861e-02  5.396e-03   7.154 1.12e-12
***
Diphtheria                       5.360e-02  5.533e-03   9.687  < 2e-16
***
HIV.AIDS                        -4.716e-01  2.164e-02 -21.793  < 2e-16
***
GDP                              5.087e-05  7.987e-06   6.369 2.28e-10
***
Income.composition.of.resources  1.344e+01  6.067e-01  22.157  < 2e-16
***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 4.408 on 2339 degrees of freedom
Multiple R-squared:  0.7898,    Adjusted R-squared:  0.7889
F-statistic: 878.8 on 10 and 2339 DF,  p-value: < 2.2e-16
```

From the above model, we can see that VIF value for each variable is less than 5, this suggests that there is no evidence of collinearity.

Now, let's calculate MSPE for the models done through backward selection and AIC,BIC, R-squared.

In [60]:
```
back_pred = predict(model_full, newdata=test)
```

In [61]:

```
squared_residuals <- (test$Life.expectancy - back_pred)^2
MSPE_back <- mean(squared_residuals)
MSPE_back
```

```
17.4380394865856
```

In [62]:

```
aic_pred = predict(lm_aic, newdata=test)
```

In [63]:

```
squared_residuals <- (test$Life.expectancy - aic_pred)^2
MSPE_aic <- mean(squared_residuals)
MSPE_aic
```

```
16.592518107029
```

On comparing the MSPE values we are seeing slight difference of 0.2 which in negligible on the test data.

GLM

In [64]:

```
glm_model <- glm(Life.expectancy ~ Status + Adult.Mortality + Alcohol + Hepatitis.B + Measles + BMI + under.five.deaths + Polio + Total.expenditure + Diphtheria + HIV.AIDS + GDP + Population + thinness..1.19.years + Income.composition.of.resources, data = df, family = "gaussian")
summary(glm_model)
```

```
Call:
glm(formula = Life.expectancy ~ Status + Adult.Mortality + Alcohol + 
    Hepatitis.B + Measles + BMI + under.five.deaths + Polio + 
    Total.expenditure + Diphtheria + HIV.AIDS + GDP + Population + 
    thinness..1.19.years + Income.composition.of.resources, family = 
"gaussian", 
    data = df)

Coefficients:
                                  Estimate Std. Error t value Pr(>|t|)
(Intercept)                      5.860e+01  6.762e-01  86.660  < 2e-16
***
StatusDeveloping                -1.863e+00  2.855e-01  -6.525 7.97e-11
***
Adult.Mortality                 -2.144e-02  8.393e-04 -25.543  < 2e-16
***
Alcohol                          1.068e-01  2.671e-02   3.996 6.59e-05
***
Hepatitis.B                     -2.047e-02  3.942e-03  -5.193 2.21e-07
***
Measles                         -1.936e-05  8.122e-06  -2.383 0.017217
*  
BMI                              5.510e-02  5.160e-03  10.679  < 2e-16
***
under.five.deaths               -2.712e-03  7.277e-04  -3.727 0.000198
***
Polio                            3.647e-02  4.712e-03   7.741 1.35e-14
***
Total.expenditure                1.038e-01  3.589e-02   2.893 0.003840
** 
Diphtheria                       5.037e-02  4.893e-03  10.296  < 2e-16
***
HIV.AIDS                        -4.750e-01  1.861e-02 -25.521  < 2e-16
***
GDP                              4.960e-05  7.031e-06   7.055 2.15e-12
***
Population                       4.144e-09  1.767e-09   2.346 0.019054
*  
thinness..1.19.years            -6.110e-02  2.529e-02  -2.417 0.015726
*  
Income.composition.of.resources  1.265e+01  5.292e-01  23.902  < 2e-16
***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for gaussian family taken to be 18.54471)

    Null deviance: 265573  on 2937  degrees of freedom
Residual deviance:  54188  on 2922  degrees of freedom
AIC: 16935

Number of Fisher Scoring iterations: 2
```

In [65]:

```
glm_pred = predict(glm_model, newdata=test)
```

In [66]:

```
squared_residuals <- (test$Life.expectancy - glm_pred)^2
MSPE_back <- mean(squared_residuals)
MSPE_back
```

16.1634724232781

From the above we can say that MSPE is less for GLM model.

In [67]:

```
glm_reduced <- glm(Life.expectancy ~ Status + Adult.Mortality + Alcohol + Hepatitis.B + Measles + BMI + under.five.deaths + Polio + Total.expenditure + Diphtheria + HIV.AIDS + GDP + Population + thinness..1.19.years, data = df, family = "gaussian")
summary(glm_reduced)
```

```
Call:
glm(formula = Life.expectancy ~ Status + Adult.Mortality + Alcohol + 
    Hepatitis.B + Measles + BMI + under.five.deaths + Polio + 
    Total.expenditure + Diphtheria + HIV.AIDS + GDP + Population + 
    thinness..1.19.years, family = "gaussian", data = df)

Coefficients:
                       Estimate Std. Error t value Pr(>|t|)    
(Intercept)           6.544e+01  6.696e-01  97.737  < 2e-16 ***
StatusDeveloping     -2.759e+00  3.094e-01  -8.916  < 2e-16 ***
Adult.Mortality      -2.505e-02  9.026e-04 -27.751  < 2e-16 ***
Alcohol               1.966e-01  2.891e-02   6.801 1.26e-11 ***
Hepatitis.B          -2.724e-02  4.298e-03  -6.336 2.71e-10 ***
Measles              -2.335e-05  8.877e-06  -2.630 0.008580 ** 
BMI                   8.127e-02  5.512e-03  14.743  < 2e-16 ***
under.five.deaths    -2.728e-03  7.955e-04  -3.430 0.000612 ***
Polio                 4.409e-02  5.139e-03   8.580  < 2e-16 ***
Total.expenditure     3.938e-02  3.913e-02   1.006 0.314294    
Diphtheria            6.568e-02  5.303e-03  12.386  < 2e-16 ***
HIV.AIDS             -4.833e-01  2.034e-02 -23.754  < 2e-16 ***
GDP                   8.676e-05  7.496e-06  11.575  < 2e-16 ***
Population            5.439e-09  1.930e-09   2.817 0.004875 ** 
thinness..1.19.years -9.707e-02  2.759e-02  -3.518 0.000442 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for gaussian family taken to be 22.16283)

    Null deviance: 265573  on 2937  degrees of freedom
Residual deviance:  64782  on 2923  degrees of freedom
AIC: 17458

Number of Fisher Scoring iterations: 2
```

In [68]:

```
glm_red = predict(glm_reduced, newdata=test)
```

In [69]:

```
squared_residuals <- (test$Life.expectancy - glm_red)^2
MSPE_back <- mean(squared_residuals)
MSPE_back
```

```
19.647774434057
```

By comparing the two MSPE's it is evident that the model with all variables has the least MSPE.

ANOVA

Null Hypothesis: H_0 = Reduced model is sufficient
Alternative Hypothesis: H_1 = Reduced model is not sufficient

In [70]:

```
anova(glm_reduced,glm_model)
```

A anova: 2 × 6

	Resid. Df	Resid. Dev	Df	Deviance	F	Pr(>F)
	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
1	2923	64781.94	NA	NA	NA	NA
2	2922	54187.64	1	10594.31	571.2847	1.800701e-115

From the above ANOVA table, we can see the output of F-statistic and p-value. It suggests we are rejecting the null hypothesis. We are concluding that reduced model is not sufficient.

Report

Introduction and Background:

Life expectancy is very crucial indicator for a country well-being. My interest in this area has started during my under-grad final semester. During my under-grad I have done some research on health care predictive analytics. At that time I was curious about how socioeconomic and environmental factors influence public health outcomes. I have explored more public health policies that can provide some information about differences in health outcomes.

Significant research has been done in this topic, highlighting various factors that influence life expectancy. Some studies suggests that longer life expectancy correlates with higher income due to better access of health care system. Moreover, a research conducted by the World Health Organization shows that preventive health care and regular health checkups can improve the life expectancy outcomes. Also, in some parts of the past research was done considering multiple linear regression on the test set for a span of one year. This gives me the motivation to implement multiple linear regression from 2000 to 2015 years for all countries. This will help for a country in suggesting which area should be given importance to improve the life expectancy.

Further Reading:

Life expectancy is defined as the average number of years a person who can survive at current mortality rates and other factors in the country at the time of birth. It is a vital metric used by health care officals, policy makers to measure overall health of the population.

This data was collected from WHO and United Nations website with the help of Deeksha Russell and Duan Wang. In-depth research of this topic is found here here (https://www.irjet.net/archives/V8/i7/IRJET-V8I7785.pdf). In this project my aim is to know how long people live in different countries and want to learn what factor affects.I plan to test hypothesis about life expectancy around the world. Additionally I will construct a model which predicts life expectancy considering factors such as mortality rate etc. The performance of this model will be evaluated by using metrics such as AIC, BIC, and adjusted R-squared.

Implementation of Methods:

This data is obtained from Kaggle website can be found here here (https://www.kaggle.com/datasets/kumarajarshi/life-expectancy-who). The methodology is as follows:

1. Data Cleaning and visualisation: There are missing values in the dataset. Box plots were drawn for better understanding. Missing values are replaced with a boxplots containing more outilers with mean and the box plots containing less outliers are replaced with median.
2. Analysis:

   Validation of Hypothesis statements: I have carried out t-test to see the life expectancy across developed and developing countries. I have done another hypothesis test to see the impact of alochol on life expectancy.

   F-Test: This test is conducted to see if there is atleast any predictor which is significantly contributing to prediction of output. This can be known by doing full F-test.

   Regression Modelling: I have used MLR and choosed features using backward selection process. I repeated the process for few times like 8-9 iterations, until my model included only the most important predictors. After that I have chosen the best model.

   Diagnosis Plots: I have plotted diagnostics to check whether the model fits the data well. The satisfactory conditions of assumptions which I got in above plots reflects that model fits linearity assumption. In fitted and observed values graph it showed that the model, for lower values it is predicting more than expected. For higher values it is predicting less than the oberserved values.

   Selection of Model based on metrics (AIC, BIC, R_a^2): `regsubsets()` is used to identify best model at each size of n. The output shows the best combination of features in every row and indicated as TRUE. Then again models with different number of predictors can't be compared by using R^2. So, AIC, BIC, adj R-sq plots were drawn to identify best model.

   Generalized Linear Modeling: It is carried out when the response variables have error distribution models other than guassian distribution.It shows that the GLM model is the best fit model.
3. Discussion of results:

Hypothesis test 1: We will reject the null hypothesis and conclude that here is a significant difference in life expectancy between developed and developing countries, with developed countries having a higher life expectancy. Below is the snippet of the result.

> Null Hypothesis (H0): The mean life expectancy is the same in developed and developing countries.
>
> Alternative Hypothesis (H1): The mean life expectancy differs between developed and developing countries.

```
Welch Two Sample t-test
data:  life_expectancy_developed and life_expectancy_developing
t = 47.875, df = 1800.5, p-value < 2.2e-16
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
11.57153 12.56012
sample estimates:
mean of x mean of y
79.19785  67.13203
```

Hypothesis test 2: We will reject the null hypothesis and conclude that there is a significant difference in life expectancy between groups with high alcohol consumption and lower alcohol consumption, where higher alcohol consumption is associated with a lower life expectancy. The snippet of the result is as follows:

> Null Hypothesis (H0): There is no difference in mean life expectancy between countries with high alcohol consumption and those with low or moderate alcohol consumption.
>
> Alternative Hypothesis (H1): Countries with high alcohol consumption have a different mean life expectancy compared to those with low or moderate alcohol consumption.

```
Welch Two Sample t-test
data:  high_alcohol and low_alcohol
t = 18.483, df = 2928.5, p-value < 2.2e-16
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
5.488386 6.791058
sample estimates:
mean of x mean of y
72.31503  66.17531
```

F-test: We reject null hypothesis and conclude that atleast one among all predictors is required for predicting target variable. The snippet of the result is as follows:

> Null Hypothesis: H_0 = Reduced model is sufficient
> Alternative Hypothesis: H_1 = Reduced model is not sufficient

```
A anova: 2 × 6
Res.Df  RSS Df  Sum of Sq   F   Pr(>F)
<dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>
1   2937    265573.14   NA  NA  NA  NA
2   2922    54187.64    15  211385.5    759.9131    0
```

MLR:

The best model is:

$$\text{Life expectancy} = 58.442 - 3.421 \times \text{Status (Developing)} - 0.021 \times \text{Adult Mortality} + 0.071 \times \text{BMI} + 0.06 \\ + 15.047 \times \text{Income Composition of Resources}$$

> For every one unit increase in adult mortality rate, life expectancy decreases by 0.0208 years, all other variables are constant.

Diagnostics: From the plots that are drawn above the model suggests that homoscedasticity and linearity are met.

Using AIC, BIC, $R_a^2: All the metrics have suggested the model with 10 predictors. The equation is as follows:

$$\text{Life expectancy} = 59.11 - 2.864 \times \text{Status} - 0.02039 \times \text{Adult Mortality} - 0.02401 \times \text{Hepatitis B} + 0.06293 \\ \times \text{under.five.deaths} + 0.03861 \times \text{Polio} + 0.05360 \times \text{Diphtheria} - 0.4716 \times \text{HIV/AIDS} + 0.00005087 \times \\ \times \text{Income Composition of Resources}$$

GLM: After comparing two models using ANOVA — one without income and another with income the results shows that income is a important predictor for GLM model. The equation is as follows:

$ \text{Life expectancy} = 58.60

- 1.863 \times \text{Status}
- 0.02144 \times \text{Adult Mortality}
- 0.1068 \times \text{Alcohol}
- 0.02047 \times \text{Hepatitis B}
- 0.00001936 \times \text{Measles}
- 0.0551 \times \text{BMI}
- 0.002712 \times \text{under.five.deaths}
- 0.03647 \times \text{Polio}
- 0.1038 \times \text{Total expenditure}
- 0.05037 \times \text{Diphtheria}
- 0.4750 \times \text{HIV/AIDS}
- 0.0000496 \times \text{GDP}
- 0.000000004144 \times \text{Population}
- 0.0611 \times \text{thinness 1-19 years}
- 12.65 \times \text{Income Composition of Resources} $

Final Word:

- People consuming more alcohol have relatively lesser life expectancies than people who don't/low alcohol. This means consumption of alcohol rates has impacted life expectancy.

- Life expectancy of people living in developed countries is not same as that of people those who are living in developing countries. This shows the real picture of contrasting life styles between developed and developing countries. This may be attributed to the fact that people from developed countries have access to better health care infrastructure facilities. Further research in these lines would help us understand root cause and can pave way for equal quality of life.
- Performance of GLM is better when compared to linear models because GLM's allows the response variable to have other distributions such as binomial,poisson and GLM's are robust to outliers.

Learnings:

- I believe that GLM will perform better than other regression models.