Prediction of WHO Life Expectancy Data Using Multiple Linear Regression And Artificial Neural Network

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KEYWORDS

Life Expectancy
Multiple Linear Models
Artificial Neural Network
Machine Learning
R
Coefficient of Determination
Prediction
MSE
MAPE
Accuracy

ABSTRACT

Life expectancy is the key for assessing the population health. A lot of researches have already been done based on the factors of life expectancy data considering demographic variables, income composition and mortality rates. Researches on multiple linear regression based on a data set of one year for all the countries are available.

Now we can build a predictive model based on this data using multiple linear regression from the data set of 2000-2015 of all countries by dividing the whole dataset into two parts namely training and testing set in ratio 80:20. After fitting the model in training data and checking the model performance on both dataset we found that MLR is a very good fit for prediction, but it violates normality and homoscedasticity assumptions. To overcome this problem we fitted this data on ANN model in the same way like before which does not assume those assumptions. We found that ANN model performed even better than MLR. At last we compared their performances and tried to find pros and cons of both models.

I. INTRODUCTION

Life Expectancy is a statistical measure of the average time an organism is expected to live, based on the year of its birth, its current age and other demographic factors including gender. In other words, it is the statistical age that a person is expected to live until, based on actuarial data. Life expectancy at birth (LEB) is the most commonly used measure worldwide.

Assuming that a person maintains the minimum standard of hygiene, life expectancy may be the outcome of multiple factors such as Diet, Lifestyle, Heredity/genetic, Marital status, Local standard of healthcare and disease prevention, Access to clean water and fresh food supply, Community and social support, Absence of adverse environmental factors like pollution

To compute life expectancy it's a bit difficult & uses lot of different data sources for each country. Life expectancy is calculated through life table or life table calculator. The life table incorporates data with age specific death rates for the population in question which requires enumeration of data for the number of people & number of death at each age for that population. Most currently available life table or life expectancy calculators are based on a person's age, gender & race. According to actuarial science, life expectancy takes into account several individual-level as well as population-level factors to arrive at a figure.

The population of many rich developed countries has life expectancy around 80 years whereas the life expectancy of poor developing country has life expectancy around 50 to 60 years.

There are many uses for it in the financial world, including life insurance, pension planning, and Social security benefits. The most important use of life expectancy is in clinical researches. Life expectancy is used in pricing and underwriting life insurance and insurance products like annuities, as well as in retirement and pension planning.

II. DATA DESCRIPTION

The dataset we used for our project was provided by the Kaggle.com website. It is a free open source platform to all. The data was collected from WHO and United Nations website with the help of Deeksha Russell and Duan Wang. This dataset has usability rating 8.2. The data consists of 2938 rows and 22 columns. As the dataset is from WHO, we assume there is no error.
Dataset Link: *https://www.kaggle.com/kumarajarshi/life-expectancy-who*

Response Variable:

Y: Life expectancy – Life Expectancy in age

Regressors:

Country – Country

Year – Year

X1: Status – Developed or developing status

X2: Adult Mortality – Adult Mortality Rates of both sexes (probability of dying between 15 and 60 years per 1000 population)

X3: Infant deaths – Number of Infant Deaths per 1000 population

X4: Alcohol – Alcohol, recorded per capita (15+) consumption (in litres of pure alcohol)

X5: Percentage expenditure – Expenditure on health as a percentage of Gross Domestic Product per capita (%)

X6: Hepatitis B – Hepatitis B (HepB) immunization coverage among 1-year-olds (%)

X7: Measles – Number of reported Measles cases per 1000 population

X8: BMI – Average Body Mass Index of entire population

X9: Under-five deaths – Number of under-five deaths per 1000 population

X10: Polio – Polio (Pol3) immunization coverage among 1-year-olds (%)

X11: Total expenditure – General government expenditure on health as a percentage of total government expenditure (%)

X12: Diphtheria – Diphtheria tetanus toxoid and pertussis (DTP3) immunization coverage among 1-year-olds (%)

X13: HIV/AIDS – Deaths per 1 000 live births HIV/AIDS (0-4 years)

X14: GDP – Gross Domestic Product per capita (in USD)

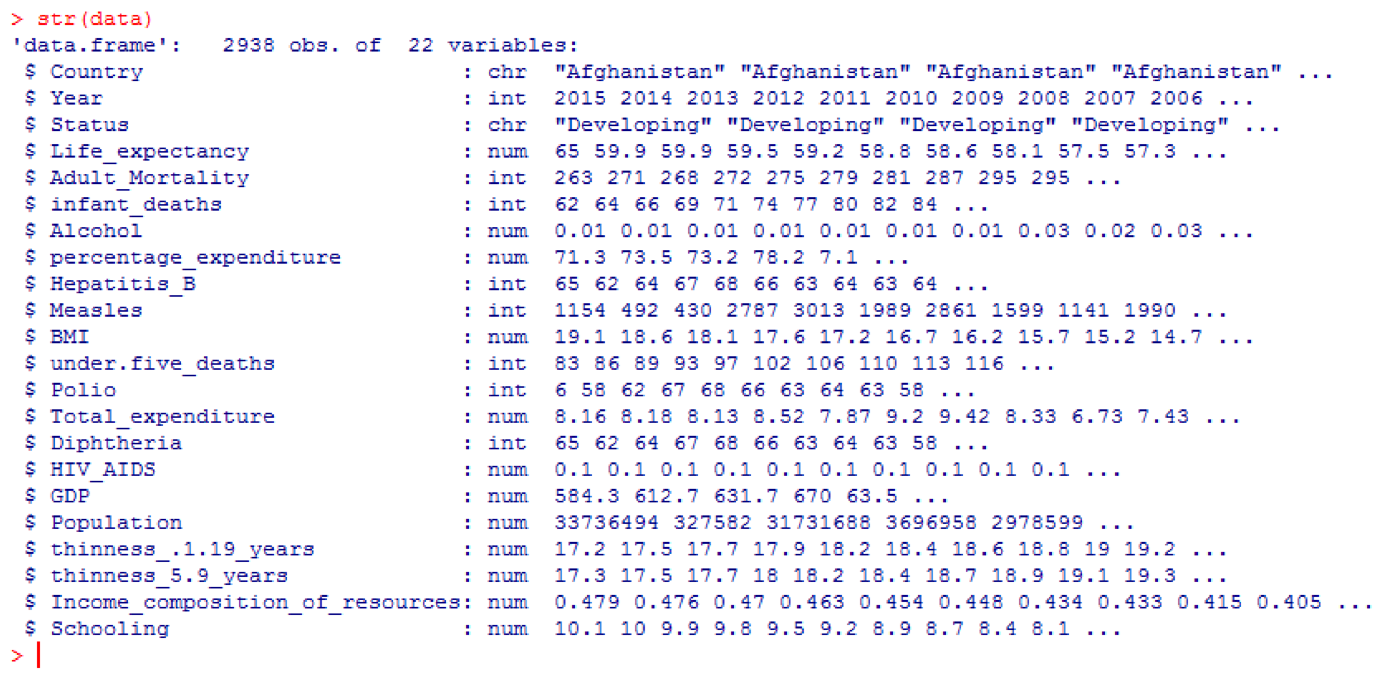
X15: Population – Population of the country

X16: Thinness 1-19 years – Prevalence of thinness among children and adolescents for Age 10 to 19 (%)

X17: Thinness 5-9 years – Prevalence of thinness among children for Age 5 to 9(%)

X18: Income composition of resources – Human Development Index in terms of income composition of resources (index ranging from 0 to 1)

X19: Schooling – Number of years of Schooling (years)



```
> str(data)
'data.frame':	2938 obs. of  22 variables:
 $ Country                        : chr  "Afghanistan" "Afghanistan" "Afghanistan" "Afghanistan" ...
 $ Year                           : int  2015 2014 2013 2012 2011 2010 2009 2008 2007 2006 ...
 $ Status                         : chr  "Developing" "Developing" "Developing" "Developing" ...
 $ Life_expectancy                : num  65 59.9 59.9 59.5 59.2 58.8 58.6 58.1 57.5 57.3 ...
 $ Adult_Mortality                : int  263 271 268 272 275 279 281 287 295 295 ...
 $ infant_deaths                  : int  62 64 66 69 71 74 77 80 82 84 ...
 $ Alcohol                        : num  0.01 0.01 0.01 0.01 0.01 0.01 0.01 0.03 0.02 0.03 ...
 $ percentage_expenditure         : num  71.3 73.5 73.2 78.2 7.1 ...
 $ Hepatitis_B                    : int  65 62 64 67 68 66 63 64 63 64 ...
 $ Measles                        : int  1154 492 430 2787 3013 1989 2861 1599 1141 1990 ...
 $ BMI                            : num  19.1 18.6 18.1 17.6 17.2 16.7 16.2 15.7 15.2 14.7 ...
 $ under.five_deaths              : int  83 86 89 93 97 102 106 110 113 116 ...
 $ Polio                          : int  6 58 62 67 68 66 63 64 63 58 ...
 $ Total_expenditure              : num  8.16 8.18 8.13 8.52 7.87 9.2 9.42 8.33 6.73 7.43 ...
 $ Diphtheria                     : int  65 62 64 67 68 66 63 64 63 58 ...
 $ HIV_AIDS                       : num  0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 ...
 $ GDP                            : num  584.3 612.7 631.7 670 63.5 ...
 $ Population                     : num  33736494 327582 31731688 3696958 2978599 ...
 $ thinness_.1.19_years           : num  17.2 17.5 17.7 17.9 18.2 18.4 18.6 18.8 19 19.2 ...
 $ thinness_5.9_years             : num  17.3 17.5 17.7 18 18.2 18.4 18.7 18.9 19.1 19.3 ...
 $ Income_composition_of_resources: num  0.479 0.476 0.47 0.463 0.454 0.448 0.434 0.433 0.415 0.405 ...
 $ Schooling                      : num  10.1 10 9.9 9.8 9.5 9.2 8.9 8.7 8.4 8.1 ...
> |
```

III. OBJECTIVE

The World Health Organization (WHO) keeps track of the health status and many others related factors for all countries, as well. This dataset for 193 countries has been collected from the WHO data. In this project we consider data from year 2000-2015 for 193 countries for analysis. As the dataset is from WHO there is no error in the data.

In the respective project we are going to find out the following factors:

- Whether the initially chosen predicting factors really affects the life expectancy or not & those predicting variables which actually affects the life expectancy.
- The type of correlation between life expectancy and other factors like smoking, exercise, lifestyles, alcohol consumptions etc.
- The impact of immunization coverage on life expectancy.
- Whether we can build a reliable predictive model to predict life expectancy in future or for any external dataset.

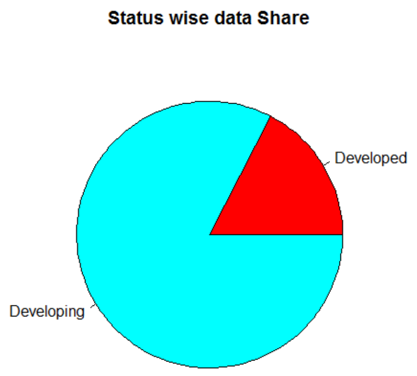
For doing the above we at first will build up a multiple linear regression model which is a supervised ML Model, based on Training data by dividing the whole data set in training set and test set randomly in ratio 80:20. Then we will check the multicollinearity, outliers, normality, and homoscedasticity. We will find out how well the model fits to the training data and how it predicts the test data by coefficient of determination along with MSE, MAPE and Accuracy. Then we will apply a Artificial Neural Network on the train data and check the model adequacy just like before. At last we will compare both models and conclude our findings accordingly.

IV. THE R ENVIRONMENT

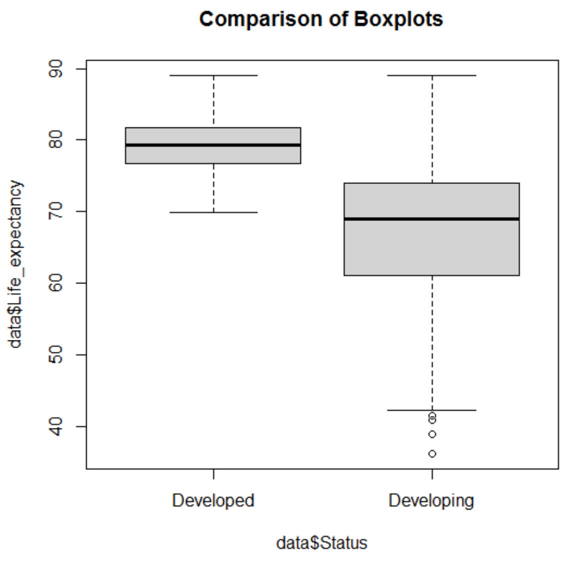
Here we are using R language for our analysis. R is a language and environment for statistical computing and graphics. R provides a wide variety of statistical (linear and nonlinear modeling, classical statistical tests, time-series analysis, classification, clustering …) and graphical techniques, and is highly extensible.

R is one of the major languages for data science. It provides excellent visualization features, which is essential to explore the data before submitting it to any automated learning, as well as assessing the results of the learning algorithm. Many R packages for machine learning are available off the shelf and many modern methods in statistical learning are implemented in R as part of their development.

V. DATA INSIGHTS



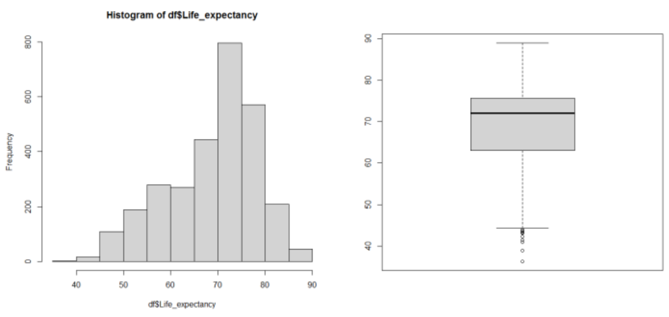
82.57318 % of total dataset comes from developing countries and 17.42682 % data comes from developed countries.



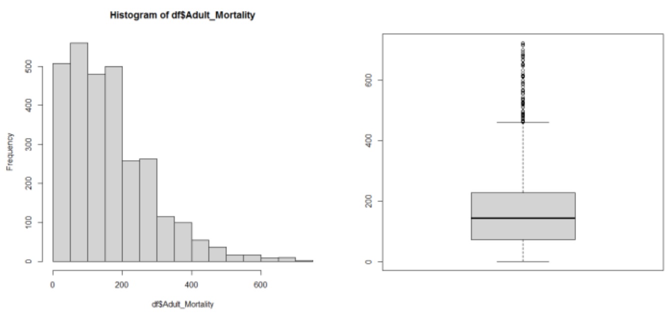
Note that avg. life expectancy in developed countries is around 80 years and spread is less compared to developing countries whereas in developing countries avg. life expectancy is around 70 years. There are some outliers in developing data points.

Now let us take a look into the data visualizations. Below we have histogram and boxplot of each variable

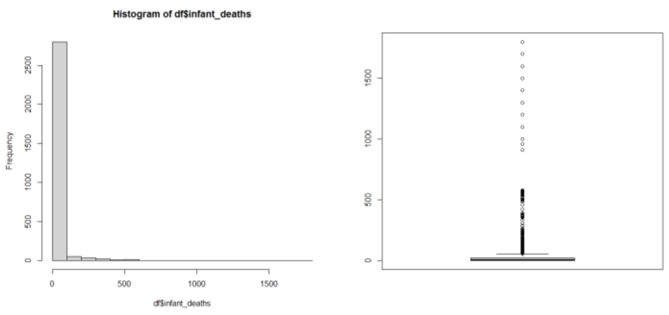
Y: Life expectancy



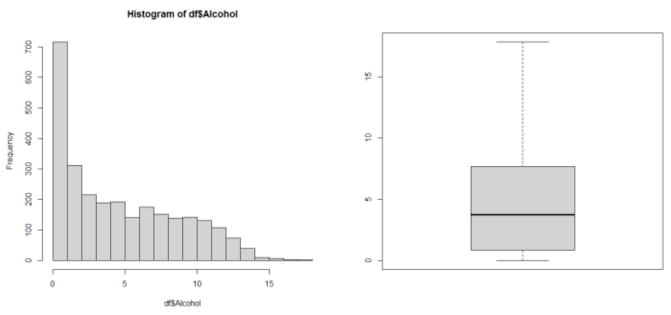
X2: Adult Mortality



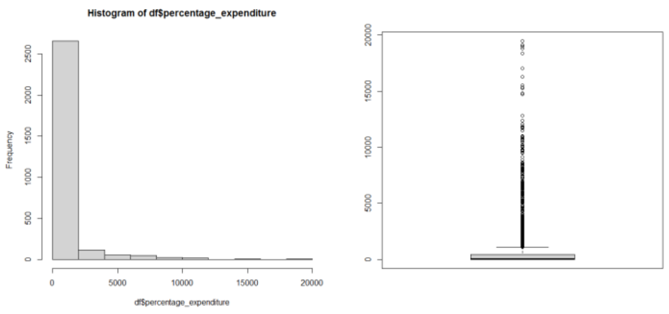
X3: Infant deaths



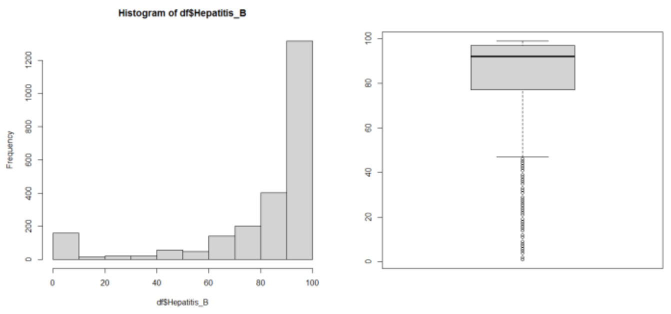
X4: Alcohol



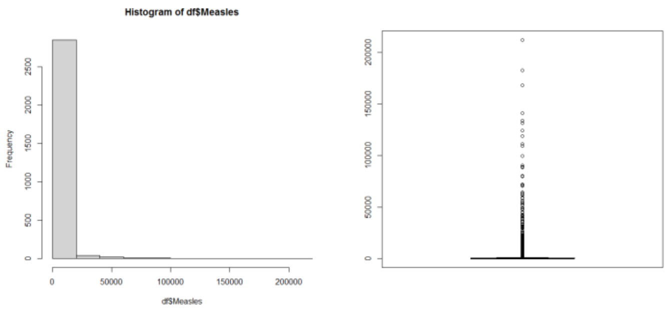
X5: Percentage expenditure



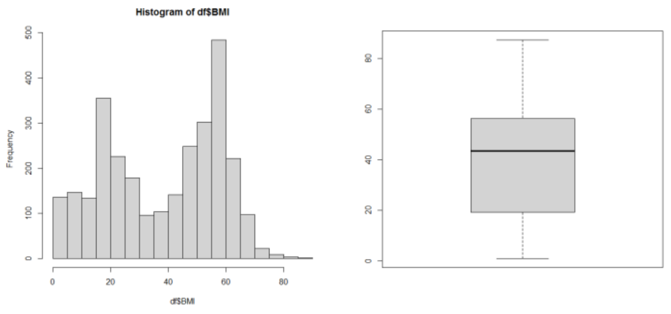
X6: Hepatitis B



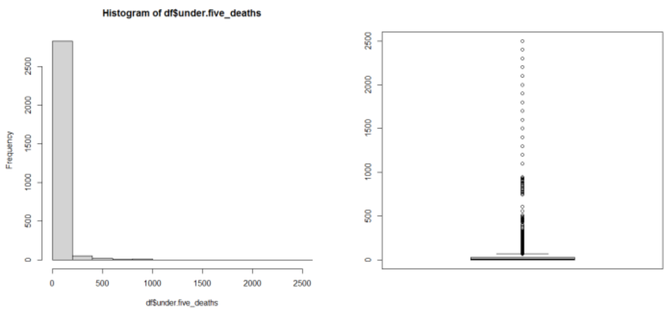
X7: Measles



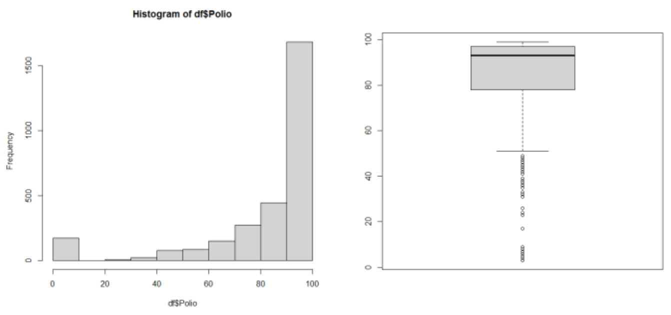
X8: BMI



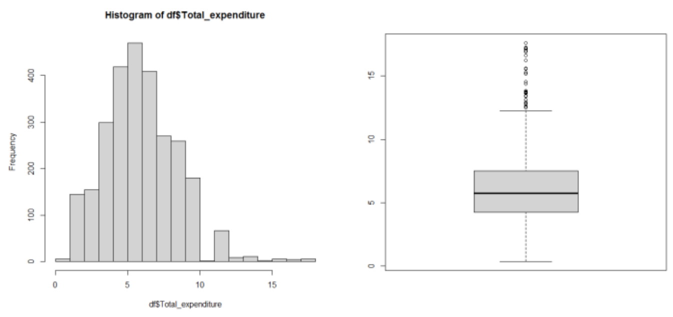
X9: Under-five deaths



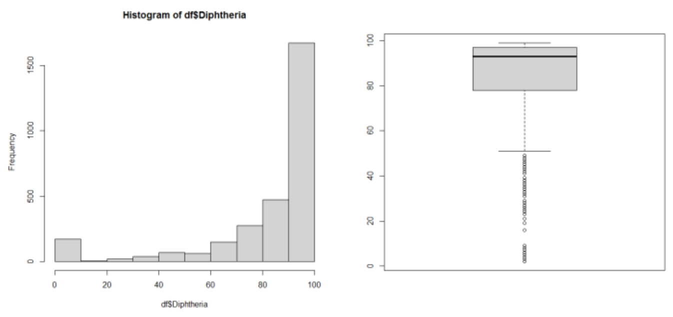
X10: Polio



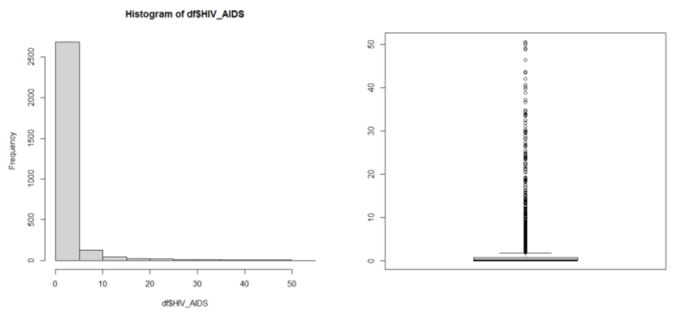
X11: Total expenditure



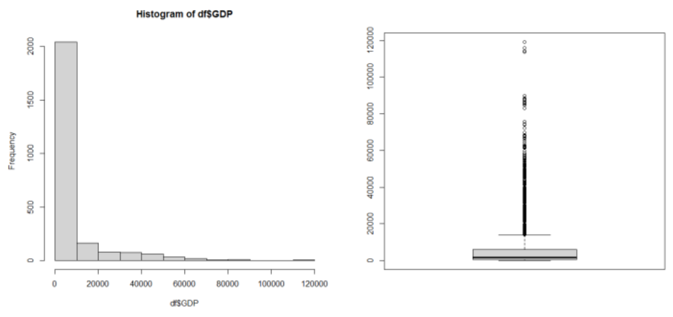
X12: Diphtheria



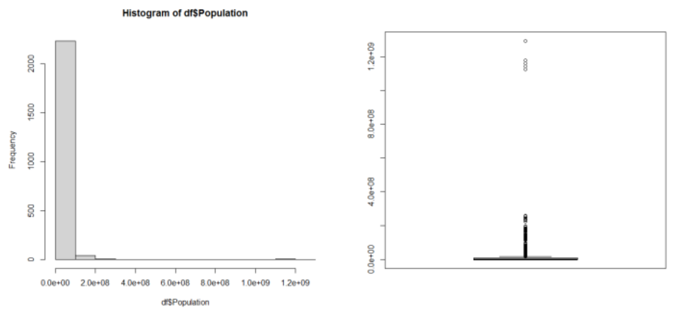
X13: HIV/AIDS



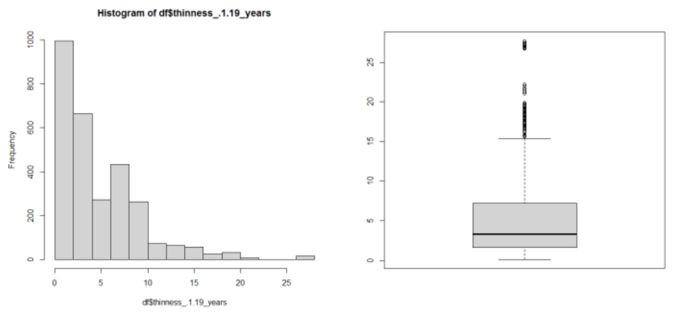
X14: GDP



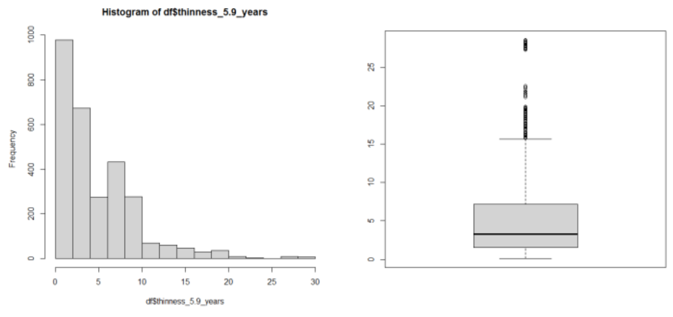
X15: Population



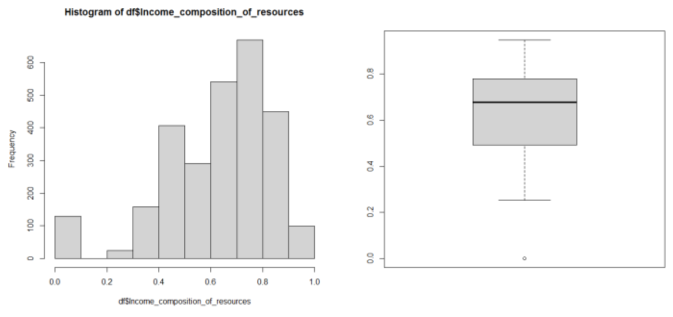
X16: Thinness 1-19 years



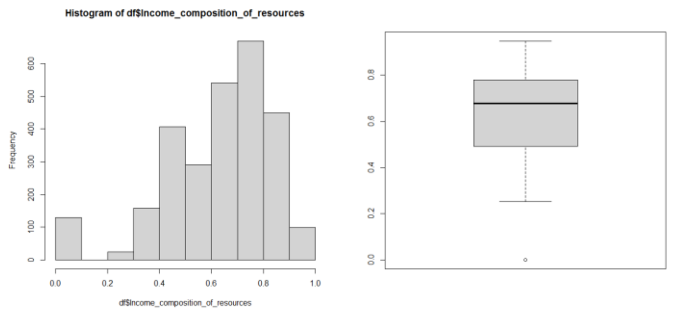
X17: Thinness 5-9 years



X18: Income composition of resources

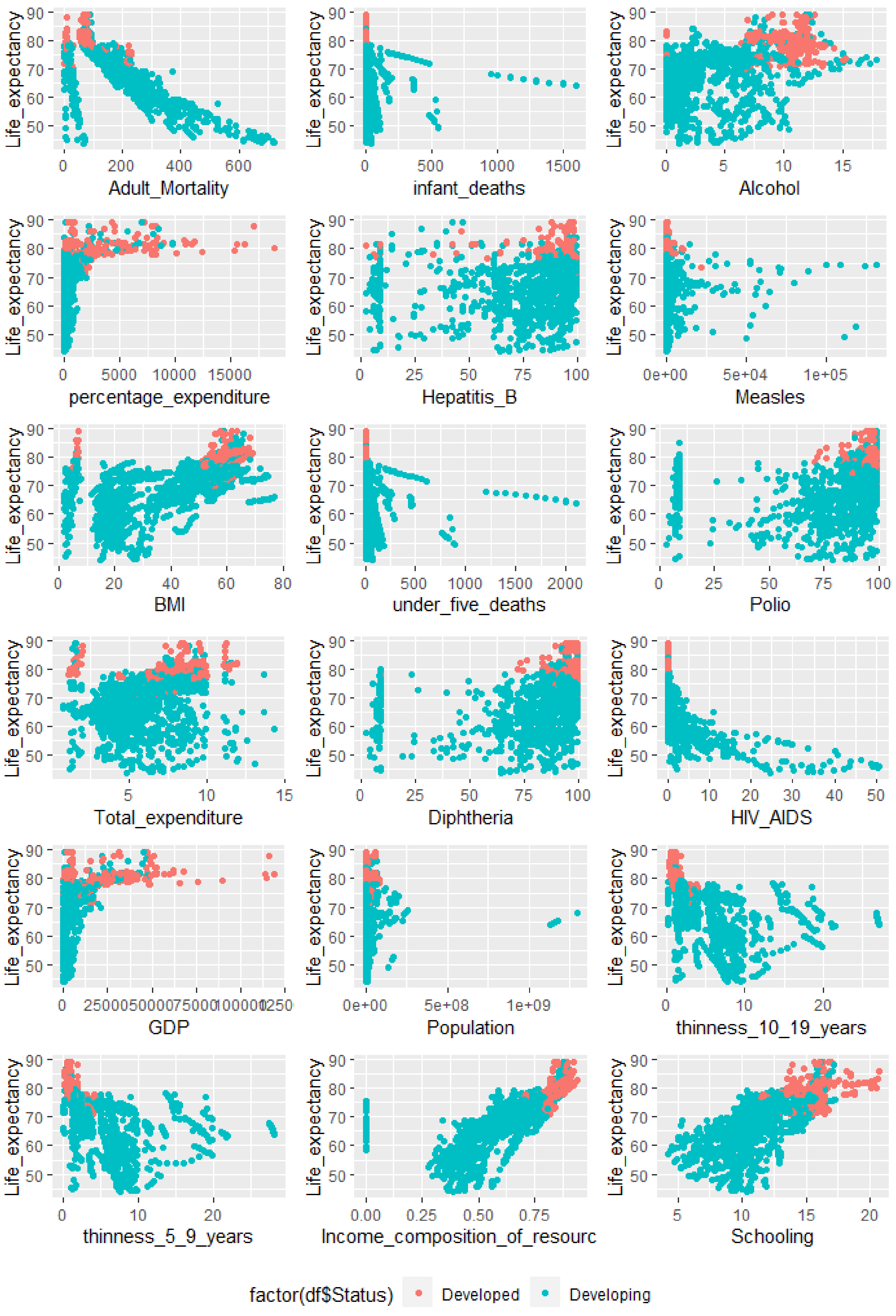


X19: Schooling



We can see most of the variables are highly skewed and contain too much outlier.

Now we will draw individual scatterplot to visualize the relationship of each regressor with the response variable. The blue points correspond to developing country and red points belong to developed country.



Life_expectancy
Adult_Mortality
infant_deaths
Alcohol
percentage_expenditure
Hepatitis_B
Measles
BMI
under_five_deaths
Polio
Total_expenditure
Diphtheria
HIV_AIDS
GDP
Population
thinness_10_19_years
thinness_5_9_years
Income_composition_of_resourc
Schooling
factor(df$Status)
Developed
Developing

VI. DATA PREPROCESSING

For machine learning algorithms to work it is necessary to convert the raw data into a clean data set and dataset must be converted to numeric data. You have to encode all the categorical labels to column vectors with binary values. Missing values or NaNs in the dataset is an annoying problem. You have to either drop the missing rows or fill them up with mean or interpolated values. Both the training data and test data must have same dimensions for the model.

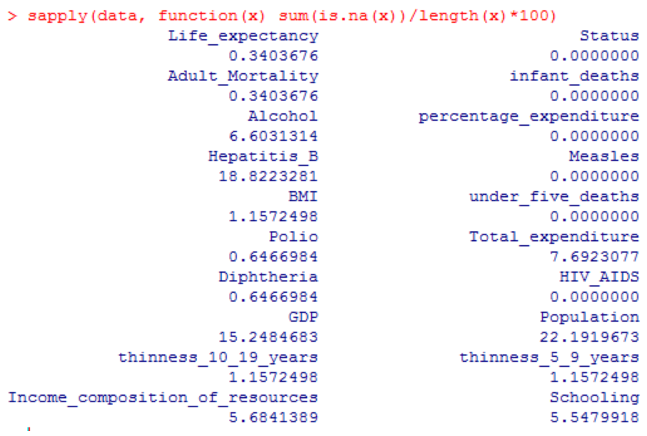
Dropping Columns which are not useful

At first step we will drop some of the columns which may not contribute much to our machine learning model such as Country, Year.

Renaming Columns

For ease of our study and modeling we have renamed a few columns such as: "Life.expectancy" to "Life_expectancy"; or "thinness..1.19.years" to "thinness_10_19_years" etc.

Dealing with Missing values



```
> sapply(data, function(x) sum(is.na(x))/length(x)*100)
           Life_expectancy                     Status
                 0.3403676                  0.0000000
           Adult_Mortality              infant_deaths
                 0.3403676                  0.0000000
                   Alcohol     percentage_expenditure
                 6.6031314                  0.0000000
               Hepatitis_B                    Measles
                18.8223281                  0.0000000
                       BMI          under_five_deaths
                 1.1572498                  0.0000000
                     Polio          Total_expenditure
                 0.6466984                  7.6923077
                Diphtheria                   HIV_AIDS
                 0.6466984                  0.0000000
                       GDP                 Population
                15.2484683                 22.1919673
      thinness_10_19_years           thinness_5_9_years
                 1.1572498                  1.1572498
Income_composition_of_resources              Schooling
                 5.6841389                  5.5479918
```

We can see that a lot of values are missing in this data. If we delete those rows completely we might lose a large amount of data. So instead of removing the null values completely, we have used data imputation technique. We have replaced the missing cells by interpolation technique. At last we have removed remaining null values.

VII. METHOD OF ANALYSIS

[A] MULTIPLE LINEAR REGRESSION

Here our multiple linear model is

$Y=X\beta+\varepsilon$

Where,

Y=vector of responses

X=Design matrix (Vector of Regressors)

β=vector of unknown parameters

ε = error of linear model

Assumptions:

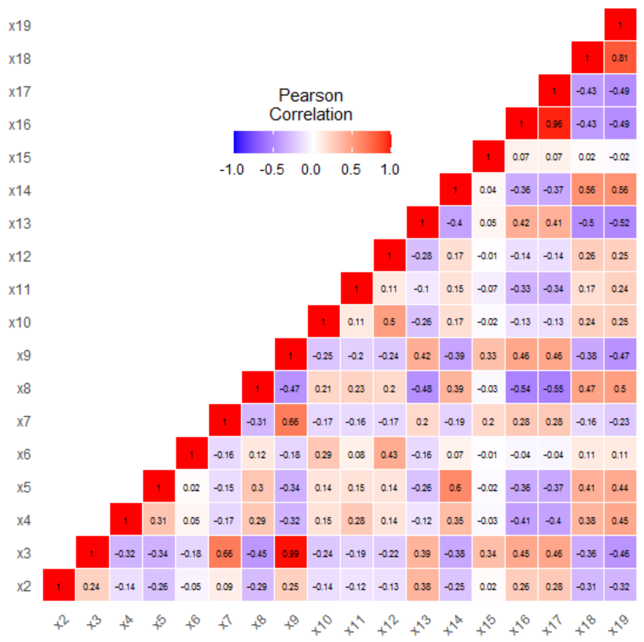
- Errors are i.i.d. distributed with E(ϵ)=0 & var(ϵ)= σ2In .
- Explanatory variables are independent i.e. X is of full column rank.

Data Transformation

From the Histogram and boxplot of the Regressors it is evident that most of them are highly skewed. Skewed data is cumbersome and common. Different features in the data set may have values in different ranges. Data transformation comes to our aid in such situations. Here we have used log transformation and cube root transformation for skewed data.

Heatmap & correlation Matrix

a good way to quickly check correlations among columns is by visualizing the correlation matrix as a heatmap.



We see there is high correlation between x18-x19, x16-x17& x3-x9. So we have removed x19, x16 & x9 from the data frame.

Detection and Removal of Outlier

In statistics, an outlier is defined as an observation which stands far away from the most of other observations. Often an outlier is present due to the measurements error. Therefore, one of the most important tasks in data analysis is to identify and (if is necessary) to remove the outliers. Outliers can occur by chance in any distribution, but they often indicate either measurement error or that the population has a heavy-tailed distribution. In the former case one wishes to discard them or use statistics that are robust to outliers, while in the latter case they indicate that the distribution has high skewness and that one should be very cautious in using tools or intuitions that assume a normal distribution. There is no rigid mathematical definition of what constitutes an outlier; determining whether or not an observation is an outlier is ultimately a subjective exercise. There are various methods of outlier detection.

Cook's Distance: Di is used in Regression Analysis to find the influential outliers in a set of predictor variables. In other words, it's a way to identify points that negatively affect your regression model. The measurement is a combination of each observation's leverage and residual values; the higher the leverage and residuals, the higher the Cook's distance.

Technically, Cook's Di is calculated by removing the ith data point from the model and recalculating the regression. It summarizes how much all the values in the regression model change when the ith observation is removed. The formula for Cook's distance is:

$$D_i = \frac{\sum_{j=1}^{n}(\widehat{Y}_j - \widehat{Y}_{j(i)})^2}{(p+1)\,\widehat{\sigma}^2}$$

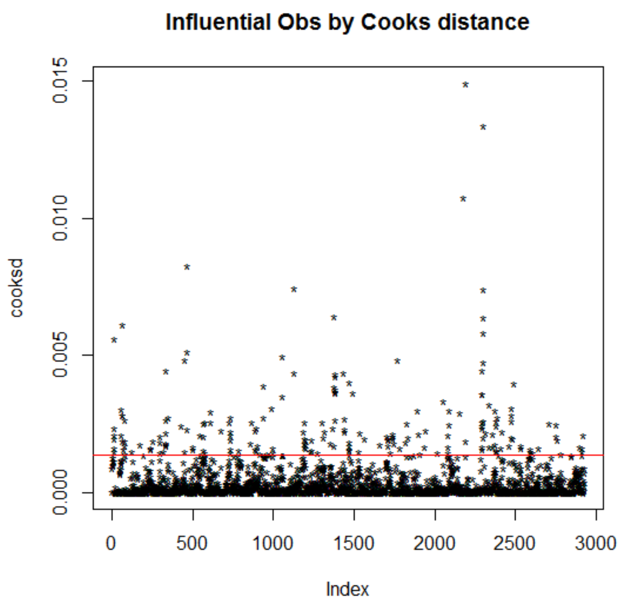
Where, Yj(i) is the fitted response value obtained when excluding i.

Decision Rule:

If (cook's distance) Di > 4/n

Then we conclude that point is outlier.

Where, n= no of rows in dataset.



The points above the red line are considered to be outliers.

After this we have divided the whole dataset in training and test set randomly in the ratio 80:20. Then we have deployed MLR on the training dataset.

Multicollinearity

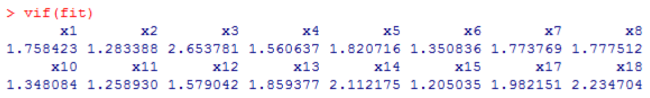
Variance Inflation Factor: Consider the following linear model with k independent variables:

Y = β0 + β1 X1 + β2 X2 + ... + βp Xp + ε.

VIF =1/(1-Rj2), for all j= 1 (1) p

Where, Rj2 is the coefficient of determination when Xj is regressed on the remaining regressor. High value of Rj2 suggests that Xj is well explained by the remaining set of regressor.

VIF > 2 is considered large & it suggests the presence of multicollinearity.



```
> vif(fit)
      x1       x2       x3       x4       x5       x6       x7       x8 
1.758423 1.283388 2.653781 1.560637 1.820716 1.350836 1.773769 1.777512 
     x10      x11      x12      x13      x14      x15      x17      x18 
1.348084 1.258930 1.579042 1.859377 2.112175 1.205035 1.982151 2.234704 
```

Variable Selection

Forward Backward & Stepwise Regression: The **stepwise regression** (or stepwise selection) consists of iteratively adding and removing predictors, in the predictive model, in order to find the subset of variables in the data set resulting in the best performing model that is a model that lowers prediction error.

There are three strategies of stepwise regression (James et al. 2014,P. Bruce and Bruce (2017)):

Forward selection, which starts with no predictors in the model, iteratively adds the most contributive predictors, and stops when the improvement is no longer statistically significant.

Backward selection (or **backward elimination**), which starts with all predictors in the model (full model), iteratively removes the least contributive predictors, and stops when you have a model where all predictors are statistically significant.

Stepwise selection (or sequential replacement), which is a combination of forward and backward selections. You start with no predictors, then sequentially add the most contributive predictors (like forward selection). After adding each new variable, remove any variables that no longer provide an improvement in the model fit (like backward selection).After stepwise selection, we will apply

Mellow Cp Statistic, AIC and adjusted R2 criterion for variable selection.

Mellow Cp statistic: In Mellow Cp statistic, we check the value of E(p) for different p(no. of regressor). A common method is to perform all possible regressions, then use Mallow's Cp to compare the results. The smaller Cp value is better as it indicate smaller amounts of unexplained error. We select the model of those p regressor for which **E (p) ≅p.**

AIC: The Akaike Information Criterion, or AIC for short, is a method for scoring and selecting a model. To use AIC for model selection, we simply choose the model giving smallest AIC over the set of models considered.

Output in Forward selection

```
> fit <- lm(y ~x1 + x2 + x4 + x5 + x6 + x7 + x8 + x10 +
+             x11 + x12 + x13 + x14 + x15 + x17,data=mlr_train)
> step_model_forward = stepAIC(fit ,direction="forward",trace=1)
Start:  AIC=5708.14
y ~ x1 + x2 + x4 + x5 + x6 + x7 + x8 + x10 + x11 + x12 + x13 +
    x14 + x15 + x17

> step_model_forward

Call:
lm(formula = y ~ x1 + x2 + x4 + x5 + x6 + x7 + x8 + x10 + x11 +
    x12 + x13 + x14 + x15 + x17, data = mlr_train)

Coefficients:
 (Intercept)  x1Developing            x2            x4            x5
    57.85164      -1.51952      -0.93520       1.06096       0.19285
          x6            x7            x8           x10           x11
    -0.02288      -0.07476       0.02849       0.66452       0.13929
         x12           x13           x14           x15           x17
     1.00246      -3.43951       0.35661      -0.01035      -0.73650
> best_subset_forward <-ols_step_best_subset(step_model_forward)
> best_subset_forward
                     Best Subsets Regression
------------------------------------------------------------------
Model Index    Predictors
------------------------------------------------------------------
     1         x13
     2         x5 x13
     3         x4 x5 x13
     4         x4 x5 x13 x17
     5         x2 x4 x5 x13 x17
     6         x2 x4 x5 x12 x13 x17
     7         x2 x4 x5 x7 x12 x13 x17
     8         x2 x4 x5 x7 x12 x13 x14 x17
     9         x1 x2 x4 x5 x7 x12 x13 x14 x17
    10         x1 x2 x4 x5 x7 x8 x12 x13 x14 x17
    11         x1 x2 x4 x5 x7 x8 x10 x12 x13 x14 x17
    12         x1 x2 x4 x5 x7 x8 x10 x11 x12 x13 x14 x17
    13         x1 x2 x4 x5 x7 x8 x10 x11 x12 x13 x14 x15 x17
    14         x1 x2 x4 x5 x6 x7 x8 x10 x11 x12 x13 x14 x15 x17
------------------------------------------------------------------
                                                       Subsets Regr
-------------------------------------------------------------------
                      Adj.        Pred
Model    R-Square    R-Square    R-Square      C(p)          AIC
-------------------------------------------------------------------
  1        0.6948      0.6947      0.6943    1978.1067    13300.3883
  2        0.7628      0.7626      0.7623    1053.4563    12751.8446
  3        0.7930      0.7927      0.7923     644.3261    12456.6826
  4        0.8063      0.8059      0.8054     465.3964    12313.8917
  5        0.8170      0.8166      0.8159     321.5698    12191.7727
  6        0.8248      0.8243      0.8236     217.5346    12098.8736
  7        0.8296      0.8291      0.8283     153.6494    12039.7598
  8        0.8333      0.8327      0.8318     106.0126    11994.5607
  9        0.8361      0.8354      0.8346      69.6374    11959.3575
 10        0.8385      0.8378      0.8369      38.2563    11928.4721
 11        0.8398      0.8390       0.838      22.7116    11912.9872
 12        0.8408      0.8399      0.8389      11.1269    11901.3520
 13        0.8408      0.8399      0.8388      13.0223    11903.2467
 14        0.8408      0.8398      0.8386      15.0000    11905.2242
-------------------------------------------------------------------
AIC: Akaike Information Criteria
 SBIC: Sawa's Bayesian Information Criteria
 SBC: Schwarz Bayesian Criteria
 MSEP: Estimated error of prediction, assuming multivariate normality
 FPE: Final Prediction Error
 HSP: Hocking's Sp
 APC: Amemiva Prediction Criteria
```

Here, the value of E(Cp) =13 corresponding the p(13), So, we select 13th subset model. Also, the value of adj. R2 correspond to 14th subset model is 0.8399 which is highest among all the subset models & AIC is minimum.

Output in Backward selection

```
> step_model_backward = stepAIC(fit ,direction="backward",trace=1)
Start:  AIC=5708.14
y ~ x1 + x2 + x4 + x5 + x6 + x7 + x8 + x10 + x11 + x12 + x13 +
    x14 + x15 + x17

       Df Sum of Sq   RSS    AIC
- x6    1         0 29423 5706.2
- x15   1         1 29424 5706.2
<none>              29423 5708.1
- x11   1       183 29606 5719.7
- x10   1       226 29649 5722.9
- x8    1       400 29822 5735.6
- x1    1       437 29860 5738.3
- x12   1       449 29872 5739.2
- x14   1       465 29888 5740.4
- x7    1       563 29986 5747.5
- x17   1       652 30075 5754.0
- x4    1       688 30111 5756.6
- x5    1      1176 30599 5791.7
- x2    1      1605 31027 5822.1
- x13   1     39445 68868 7562.6
Step:  AIC=5706.16
y ~ x1 + x2 + x4 + x5 + x7 + x8 + x10 + x11 + x12 + x13 + x14 +
    x15 + x17

       Df Sum of Sq   RSS    AIC
- x15   1         1 29425 5704.3
<none>              29423 5706.2
- x11   1       183 29606 5717.7
- x10   1       226 29649 5720.9
- x8    1       399 29823 5733.6
- x1    1       437 29860 5736.3
- x14   1       465 29888 5738.4
- x12   1       524 29947 5742.7
- x7    1       564 29987 5745.6
- x17   1       659 30083 5752.5
- x4    1       688 30111 5754.6
- x5    1      1180 30603 5790.0
- x2    1      1606 31029 5820.2
- x13   1     39487 68910 7561.9

Step:  AIC=5704.27
y ~ x1 + x2 + x4 + x5 + x7 + x8 + x10 + x11 + x12 + x13 + x14 +
    x17
Step:  AIC=5704.27
y ~ x1 + x2 + x4 + x5 + x7 + x8 + x10 + x11 + x12 + x13 + x14 +
    x17

       Df Sum of Sq   RSS    AIC
<none>              29425 5704.3
- x11   1       184 29609 5715.9
- x10   1       226 29651 5719.0
- x8    1       398 29823 5731.6
- x1    1       436 29860 5734.4
- x14   1       464 29888 5736.4
- x12   1       523 29947 5740.7
- x7    1       598 30023 5746.2
- x17   1       660 30085 5750.7
- x4    1       692 30116 5753.0
- x5    1      1190 30614 5788.8
- x2    1      1606 31031 5818.3
- x13   1     39693 69117 7566.5

> step_model_backward

Call:
lm(formula = y ~ x1 + x2 + x4 + x5 + x7 + x8 + x10 + x11 + x12 +
    x13 + x14 + x17, data = mlr_train)

Coefficients:
 (Intercept)  x1Developing            x2            x4            x5
    57.68485      -1.51624      -0.93552       1.06293       0.19341
          x7            x8           x10           x11           x12
    -0.07536       0.02837       0.66265       0.13963       0.99013
         x13           x14           x17
    -3.44054       0.35469      -0.73823
```

```
> best_subset_backward <-ols_step_best_subset(step_model_backward)
> best_subset_backward
                        Best Subsets Regression
------------------------------------------------------------
Model Index     Predictors
------------------------------------------------------------
     1          x13
     2          x5 x13
     3          x4 x5 x13
     4          x4 x5 x13 x17
     5          x2 x4 x5 x13 x17
     6          x2 x4 x5 x12 x13 x17
     7          x2 x4 x5 x7 x12 x13 x17
     8          x2 x4 x5 x7 x12 x13 x14 x17
     9          x1 x2 x4 x5 x7 x12 x13 x14 x17
    10          x1 x2 x4 x5 x7 x8 x12 x13 x14 x17
    11          x1 x2 x4 x5 x7 x8 x10 x12 x13 x14 x17
    12          x1 x2 x4 x5 x7 x8 x10 x11 x12 x13 x14 x17
------------------------------------------------------------
                                                           Subsets Regre
----------------------------------------------------------------------------
                        Adj.        Pred
Model    R-Square    R-Square    R-Square        C(p)            AIC
----------------------------------------------------------------------------
  1        0.6948      0.6947      0.6943    1981.6981     13300.3883
  2        0.7628      0.7626      0.7623    1056.2471     12751.8446
  3        0.7930      0.7927      0.7923     646.7618     12456.6826
  4        0.8063      0.8059      0.8054     467.6757     12313.8917
  5        0.8170      0.8166      0.8159     323.7232     12191.7727
  6        0.8248      0.8243      0.8236     219.5964     12098.8736
  7        0.8296      0.8291      0.8283     155.6542     12039.7598
  8        0.8333      0.8327      0.8318     107.9746     11994.5607
  9        0.8361      0.8354      0.8346      71.5662     11959.3575
 10        0.8385      0.8378      0.8369      40.1563     11928.4721
 11        0.8398      0.8390       0.838      24.5964     11912.9872
 12        0.8408      0.8399      0.8389      13.0000     11901.3520
----------------------------------------------------------------------------
AIC: Akaike Information Criteria
 SBIC: Sawa's Bayesian Information Criteria
 SBC: Schwarz Bayesian Criteria
 MSEP: Estimated error of prediction, assuming multivariate normality
 FPE: Final Prediction Error
 HSP: Hocking's Sp
 APC: Amemiya Prediction Criteria
```

Here, the value of E(Cp) =13 corresponding the p(12), So, we select 12th subset model. Also, the value of adj. R2 correspond to 14th subset model is 0.8399 which is highest among all the subset models & AIC is minimum.

Output in Stepwise selection

```
> step_model_both = stepAIC(fit ,direction="both",trace=1)
Start:  AIC=5708.14
y ~ x1 + x2 + x4 + x5 + x6 + x7 + x8 + x10 + x11 + x12 + x13 + 
    x14 + x15 + x17

       Df Sum of Sq   RSS    AIC
- x6    1         0 29423 5706.2
- x15   1         1 29424 5706.2
<none>              29423 5708.1
- x11   1       183 29606 5719.7
- x10   1       226 29649 5722.9
- x8    1       400 29822 5735.6
- x1    1       437 29860 5738.3
- x12   1       449 29872 5739.2
- x14   1       465 29888 5740.4
- x7    1       563 29986 5747.5
- x17   1       652 30075 5754.0
- x4    1       688 30111 5756.6
- x5    1      1176 30599 5791.7
- x2    1      1605 31027 5822.1
- x13   1     39445 68868 7562.6

Step:  AIC=5706.16
y ~ x1 + x2 + x4 + x5 + x7 + x8 + x10 + x11 + x12 + x13 + x14 + 
    x15 + x17

       Df Sum of Sq   RSS    AIC
- x15   1         1 29425 5704.3
<none>              29423 5706.2
+ x6    1         0 29423 5708.1
- x11   1       183 29606 5717.7
- x10   1       226 29649 5720.9
- x8    1       399 29823 5733.6
- x1    1       437 29860 5736.3
- x14   1       465 29888 5738.4
- x12   1       524 29947 5742.7
- x7    1       564 29987 5745.6
- x17   1       659 30083 5752.5
- x4    1       688 30111 5754.6
- x5    1      1180 30603 5790.0
- x2    1      1606 31029 5820.2
- x13   1     39487 68910 7561.9
```

```
Step:  AIC=5704.27
y ~ x1 + x2 + x4 + x5 + x7 + x8 + x10 + x11 + x12 + x13 + x14 + 
    x17

       Df Sum of Sq   RSS    AIC
<none>              29425 5704.3
+ x15   1         1 29423 5706.2
+ x6    1         0 29424 5706.2
- x11   1       184 29609 5715.9
- x10   1       226 29651 5719.0
- x8    1       398 29823 5731.6
- x1    1       436 29860 5734.4
- x14   1       464 29888 5736.4
- x12   1       523 29947 5740.7
- x7    1       598 30023 5746.2
- x17   1       660 30085 5750.7
- x4    1       692 30116 5753.0
- x5    1      1190 30614 5788.8
- x2    1      1606 31031 5818.3
- x13   1     39693 69117 7566.5


> step_model_both

Call:
lm(formula = y ~ x1 + x2 + x4 + x5 + x7 + x8 + x10 + x11 + x12 + 
    x13 + x14 + x17, data = mlr_train)

Coefficients:
 (Intercept)  x1Developing           x2           x4           x5  
    57.68485      -1.51624     -0.93552      1.06293      0.19341  
          x7            x8          x10          x11          x12  
    -0.07536       0.02837      0.66265      0.13963      0.99013  
         x13           x14          x17  
    -3.44054       0.35469     -0.73823  
```

```
> best_subset_both <-ols_step_best_subset(step_model_both)
> best_subset_both
                        Best Subsets Regression
------------------------------------------------------------
Model Index     Predictors
------------------------------------------------------------
     1          x13
     2          x5 x13
     3          x4 x5 x13
     4          x4 x5 x13 x17
     5          x2 x4 x5 x13 x17
     6          x2 x4 x5 x12 x13 x17
     7          x2 x4 x5 x7 x12 x13 x17
     8          x2 x4 x5 x7 x12 x13 x14 x17
     9          x1 x2 x4 x5 x7 x12 x13 x14 x17
    10          x1 x2 x4 x5 x7 x8 x12 x13 x14 x17
    11          x1 x2 x4 x5 x7 x8 x10 x12 x13 x14 x17
    12          x1 x2 x4 x5 x7 x8 x10 x11 x12 x13 x14 x17
------------------------------------------------------------

                                                           Subsets Regre
----------------------------------------------------------------------------
                        Adj.        Pred
Model    R-Square    R-Square    R-Square        C(p)            AIC
----------------------------------------------------------------------------
  1        0.6948      0.6947      0.6943    1981.6981     13300.3883
  2        0.7628      0.7626      0.7623    1056.2471     12751.8446
  3        0.7930      0.7927      0.7923     646.7618     12456.6826
  4        0.8063      0.8059      0.8054     467.6757     12313.8917
  5        0.8170      0.8166      0.8159     323.7232     12191.7727
  6        0.8248      0.8243      0.8236     219.5964     12098.8736
  7        0.8296      0.8291      0.8283     155.6542     12039.7598
  8        0.8333      0.8327      0.8318     107.9746     11994.5607
  9        0.8361      0.8354      0.8346      71.5662     11959.3575
 10        0.8385      0.8378      0.8369      40.1563     11928.4721
 11        0.8398      0.8390       0.838      24.5964     11912.9872
 12        0.8408      0.8399      0.8389      13.0000     11901.3520
----------------------------------------------------------------------------
AIC: Akaike Information Criteria
 SBIC: Sawa's Bayesian Information Criteria
 SBC: Schwarz Bayesian Criteria
 MSEP: Estimated error of prediction, assuming multivariate normality
 FPE: Final Prediction Error
 HSP: Hocking's Sp
 APC: Amemiya Prediction Criteria
```

Here, the value of E(Cp) =13 corresponding the p(12), So, we select 12th subset model.
Also, the value of adj. R2 correspond to 14th subset model is 0.8399 which is highest among all the subset models & AIC is minimum.

Final Model

After, variable selection we lead to the final model which is:

y = (β1 x1 + β2x2 + β4 x4 + β5 x5 + β7 x7 + β8 x8 + β10 x10 + β11 x11 + β12 x12 + β13 x13 + β14 x14 + β17 x17)

```
> fit1 <- lm(y ~x1 + x2 + x4 + x5 + x7 + x8 + x10 +
+             x11 + x12 + x13 + x14 + x17,data=mlr_train)
> summary(fit1)

Call:
lm(formula = y ~ x1 + x2 + x4 + x5 + x7 + x8 + x10 + x11 + x12 +
    x13 + x14 + x17, data = mlr_train)

Residuals:
    Min      1Q  Median      3Q     Max
-12.986  -2.226  -0.027   2.326  11.484

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  57.684851   1.063049  54.264  < 2e-16 ***
x1Developing -1.516242   0.267458  -5.669 1.63e-08 ***
x2           -0.935517   0.085957 -10.884  < 2e-16 ***
x4            1.062930   0.148813   7.143 1.24e-12 ***
x5            0.193408   0.020648   9.367  < 2e-16 ***
x7           -0.075356   0.011346  -6.642 3.91e-11 ***
x8            0.028366   0.005236   5.418 6.70e-08 ***
x10           0.662648   0.162202   4.085 4.56e-05 ***
x11           0.139625   0.037866   3.687 0.000232 ***
x12           0.990132   0.159480   6.209 6.39e-10 ***
x13          -3.440537   0.063591 -54.104  < 2e-16 ***
x14           0.354689   0.060643   5.849 5.70e-09 ***
x17          -0.738233   0.105801  -6.978 3.97e-12 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 3.682 on 2170 degrees of freedom
Multiple R-squared:  0.8408,    Adjusted R-squared:  0.8399
F-statistic: 955.2 on 12 and 2170 DF,  p-value: < 2.2e-16
```

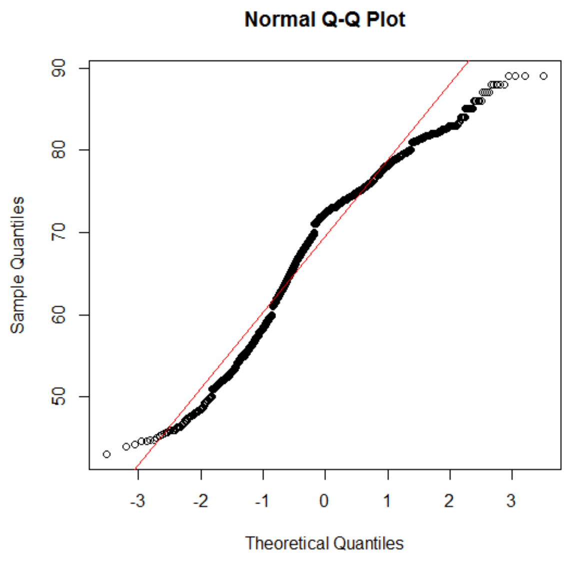
Test for Normality

Shapiro – Wilk Test

The Shapiro – Wilk test is a test of normality of a random sample.
H0: Sample comes from normally distributed population
HA: Sample does not come from normal population
Test Statistic:

$$W = \frac{\left(\sum_{i=1}^{n} a_i x_{(i)}\right)^2}{\sum_{i=1}^{n}(x_i - \overline{x})^2}$$

Where, xi's are the ordered random sample values.
ai's are the constant generated from the covariance, variances and means of the sample (size n) from a normally distributed sample.
Decision Rule :
We reject Ho if W < Wα,at α % level of significance otherwise accept Ho



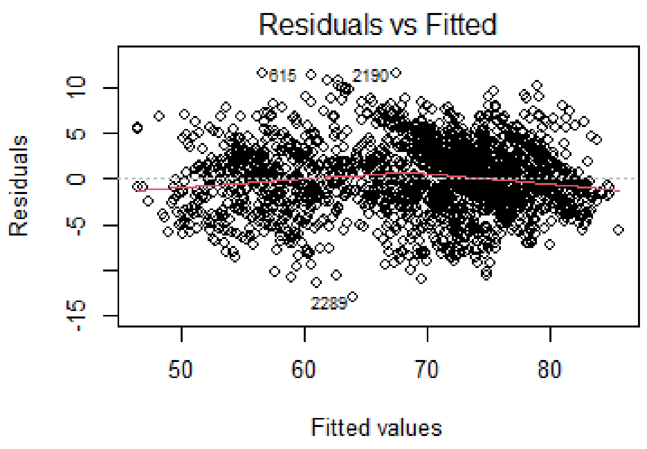
```
> qqnorm(mlr_train$y)
> qqline(mlr_train$y,col="red")
> shapiro.test(mlr_train$y)

        Shapiro-Wilk normality test

data:  mlr_train$y
W = 0.94986, p-value < 2.2e-16
```

Since, p-value < 0.05 thus, we reject the null hypothesis at 5% level of significance. Hence, data is non-normal.

Homoscedasticity
H0: the residual is homoscedastic
H1 : the residual is heteroscedastic
Residual Plot:



```
> #Breusch-Pagan test
> bptest(fit1)

        studentized Breusch-Pagan test

data:  fit1
BP = 59.712, df = 12, p-value = 2.548e-08
```

Since, p-value < 0.01 thus, we reject the null hypothesis at 1% level of significance. Hence, Training data is **Heteroskedastic.**

Auto correlation

H0: there is no serial correlation

H1 : there is serial correlation

```
> dwt(fit1)
 lag Autocorrelation D-W Statistic p-value
   1     -0.01266898      2.021858   0.552
 Alternative hypothesis: rho != 0
```

Since, p-value> 0.01 thus, we fail to reject the null hypothesis at 1% level of significance. Hence, there is no serial autocorrelation.

Model Performance

It is important to appropriately estimate the prediction error of a model, since (a) it provides insight into its accuracy; (b) it allows comparison of different models, and (c) it is used to define warning thresholds. In order to facilitate the analysis of final calculation results, different performance evaluation functions are adopted in this paper, that is, mean square error (MSE), maximum absolute percentage error (MAPE).

The mean absolute percentage error (MAPE) is a statistical measure of how accurate a forecast system is. It measures this accuracy as a percentage, and can be calculated as the average absolute percent error for each time period minus actual values divided by actual values. Where A_t is the actual value and F_t is the forecast value, this is given by:

$$M = \frac{1}{n}\sum_{t=1}^{n}\left|\frac{A_t - F_t}{A_t}\right|$$

The mean squared error (MSE) tells you how close a regression line is to a set of points. It does this by taking the distances from the points to the regression line (these distances are the "errors") and squaring them. The squaring is necessary to remove any negative signs. It also gives more weight to larger differences. It's called the mean squared error as you're finding the average of a set of errors.

```
> MSE_train
[1] 13.47896
> MSE_test
[1] 14.57727
> train_Mape
[1] 4.304494
> test_Mape
[1] 4.458779
> accuracy_train
[1] 99.68379
> accuracy_test
[1] 99.94273
```

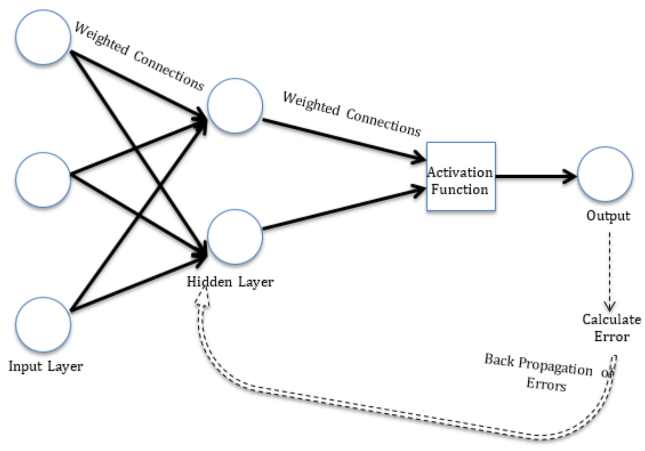
Multiple Linear regression Equation

(Life_expectancy) = 57.684851 + (-1.516242)*(Status) + (-0.935517)*(Adult_Mortality) + (1.062930)*(Alcohol) + (0.193408)*(percentage_expenditure) + (-0.075356)*(Measles) + (0.028366)*(BMI) + (0.662648)*(Polio) + (0.139625)*(Total_expenditure) + (0.990132)*(Diphtheria) + (-3.440537)*(HIV_AIDS) + (0.354689)*(GDP) + (-0.738233) *(thinness_5_9_years)

Even though MLR performs extremely well in this data for model Building and Prediction, but it violates homoscadasticity and normality assumptions. This encourages us to go for another algorithm that does not take into consideration normality.

[B] ARTIFICIAL NEURAL NETWORK

It has the ability to learn by examples. ANN is an information processing model inspired by the biological neuron system. It is composed of a large number of highly interconnected processing elements known as the neuron to solve problems. It follows the non-linear path and process information in parallel throughout the nodes. A neural network is a complex adaptive system. Adaptive means it has the ability to change its internal structure by adjusting weights of inputs.



A neural network consists of:

1. *Input layers:* Layers that take inputs based on existing data. Here we have 7 input variables.

2. *Hidden layers:* Layers that use back propagation to optimize the weights of the input variables in order to improve the predictive power of the model.

3. *Output layers:* Output of predictions based on the data from the input and hidden layers.

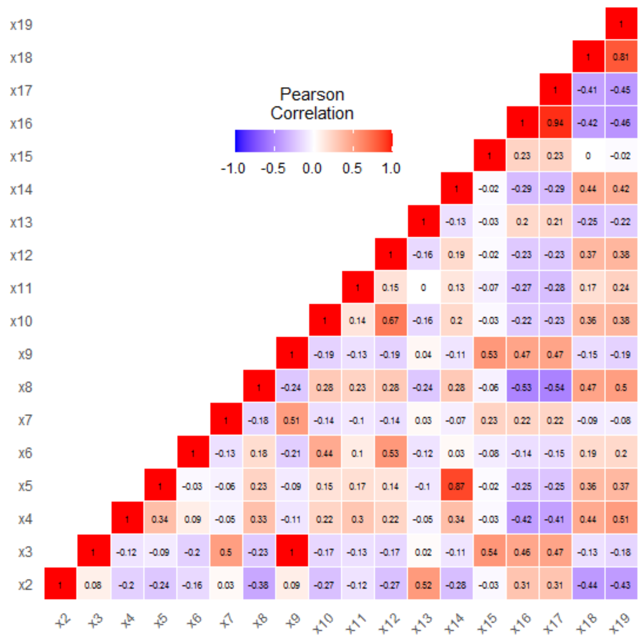
Before fitting a neural network, some preparation needs to be done. Neural networks are not that easy to train and tune. As a *first step*, we are going to address data preprocessing. In this case also we removed unnecessary columns, renamed them, and imputed missing values by interpolation.

Data Normalization

One of the most important procedures when forming a neural network is data normalization. This involves adjusting the data to a common scale so as to accurately compare predicted and actual values. Failure to normalize the data will typically result in the prediction value remaining the same across all observations, regardless of the input values. Most of the times the algorithm will not converge before the number of maximum iterations allowed. You can choose different methods to scale the data (z-normalization, min-max scale, etc…). I chose to use the min-max method and scale the data in the interval [0, 1]

Heatmap & correlation Matrix

A good way to quickly check correlations among columns is by visualizing the correlation matrix as a heatmap.



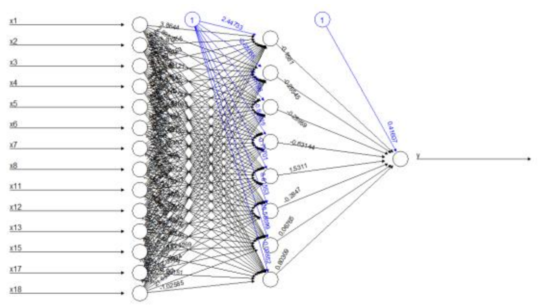
We see there is high correlation between x18-x19, x16-x17,x5-x14, x10-x12 & x3-x9. So we have removed x19, x16, x10, x14 & x9 from the data frame to avoid over fitting.

After this we have divided the whole dataset in training and test set randomly in the ratio 80:20. Then we have deployed MLR on the training dataset.

Parameter Setting

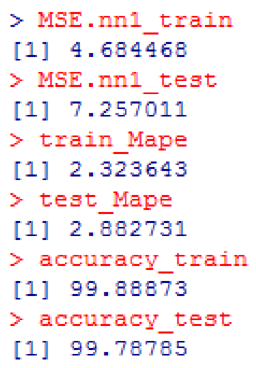
There is no fixed rule as to how many layers and neurons to use although there are several more or less accepted rules of thumb. Usually, if at all necessary, one hidden layer is enough for a vast numbers of applications. As far as the number of neurons is concerned, it should be between the input layer size and the output layer size, usually 2/3 of the input size. Here we have 1 response and 14 regressors so we used 8 neurons in the only hidden layer. The configuration of our neural network is (14:8:1)

This is the graphical representation of the model with the weights on each connection:



Predicting using the neural network

Now we can try to predict the values for the both train & test set and calculate the MSE, MAPE & Accuracy. Remember that the net will output a normalized prediction, so we need to scale it back in order to make a meaningful comparison (or just a simple prediction).



```
> MSE.nn1_train
[1] 4.684468
> MSE.nn1_test
[1] 7.257011
> train_Mape
[1] 2.323643
> test_Mape
[1] 2.882731
> accuracy_train
[1] 99.88873
> accuracy_test
[1] 99.78785
```

VIII. PERFORMACE OF THE ALGORITHMS

To compare the performance of these two algorithms we will use MSE, MAPE & accuracy of the both models on both training data and test data.

Statistical performance of the MLR and ANN

	MLR		ANN	
	Training	Testing	Training	Testing
MSE	13.47896	14.57727	4.684468	7.257011
MAPE	4.304494	4.458779	2.323643	2.882731
Accuracy	99.68379	99.94273	99.88873	99.78785

IX. CONCLUSION

In both the models we can see that all the Regressors are not contributing in predicting Life Expectancy. We had to drop few Regressors due to multicollinearity.

MLR model indicates that Alcohol, BMI, Polio, Total_expenditure, Diphtheria, GDP and percentage_expenditure have positive impact on Life Expectancy. On the other hand Measles, HIV_AIDS and thinness_5_9_years have negative impact on Life Expectancy.It is evident that immunization coverage improves life expectancy.

Both the models have performed exceptionally in predicting Life Expectancy. But neural networks usually outperform linear regression as they deal with non-linearity automatically with large number of inputs, whereas in linear regression you need to mention explicitly. Here also MAPE and MSE suggest that neural network has performed better than MLR in Prediction Life Expectancy.

FUTURE WORK

- There are many scopes in future with this data. We can run cross validation models to check if we can improve results.
- We can include the year column to do time series analysis, but for that we need more data.
- We can deploy other algorithms such as k means or decision tree according to our requirements.
- We can divide the whole dataset into two parts. One for developed country, another for developing country, and then we can again run MLR on that.

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###### R CODE

#Pie Chart

```
setwd("C:\\Users\\user\\Desktop\\GD project")
data<- read.csv("Life_Expectancy_Data.csv")

data <- data[ c(3,4) ]
data$Status <- as.factor(data$Status)

data1 <- data[data$Status == "Developed", ]
data2 <- data[data$Status == "Developing",]

a<-nrow(data1)/(nrow(data1)+nrow(data2))*100
b<-nrow(data2)/(nrow(data1)+nrow(data2))*100

Developed_LE <- data1[ 2 ]
Developing_LE <- data2[ 2 ]

# Create data for the graph.
x <- c(a, b)
labels <- c("Developed", "Developing")

# Plot the chart with title and rainbow color pallet.

pie(x, labels, main = "Status wise data Share",
    col = rainbow(length(x)))
```

#Use new R-script
#Histogram & Boxplot

```
library(boot)
library(car)
library(lmtest)
library(MASS)
library(ggplot2)
library(questionr)
library(e1071)
library(reshape2)
#load data

setwd("C:\\Users\\user\\Desktop\\GD project")
data<- read.csv("Life_Expectancy_Data.csv")

df <- data[ -c(1,2) ]
df <- df[,c(2,1,3:19,20)]
df$Status<-as.factor(df$Status)

df<-rename.variable(df,"Life.expectancy","Life_expectancy")
df<-rename.variable(df,"Adult.Mortality","Adult_Mortality")
df<-rename.variable(df,"infant.deaths","infant_deaths")
df<-rename.variable(df,"percentage.expenditure","percentage_expenditure")
df<-rename.variable(df,"Hepatitis.B","Hepatitis_B")
```

```
df<-rename.variable(df,"under.five.deaths","under_five_deaths")
df<-rename.variable(df,"Total.expenditure","Total_expenditure")
df<-rename.variable(df,"HIV.AIDS","HIV_AIDS")
df<-rename.variable(df,"thinness.5.9.years","thinness_5_9_years")
df<-rename.variable(df,"thinness..1.19.years","thinness_10_19_years")
df<-
rename.variable(df,"Income.composition.of.resources","Income_composition_of_res
ources")
```

#comparison of boxplots of life expectancy due to status

```
plot(df$Life_expectancy,, main, xlab, ylab, xlim, ylim, axes)
boxplot(df$Life_expectancy ~ df$Status, data = df, main = "Comparison of
Boxplots")
```

#Histogram and boxplot of regressors

```
par(mfrow=c(1,2))

hist(df$Life_expectancy)
boxplot(df$Life_expectancy)

hist(df$Life_expectancy)
boxplot(df$Adult_Mortality)

hist(df$infant_deaths)
boxplot(df$infant_deaths)

hist(df$Alcohol)
boxplot(df$Alcohol)

hist(df$percentage_expenditure)
boxplot(df$percentage_expenditure)

hist(df$Hepatitis_B)
boxplot(df$Hepatitis_B)

hist(df$Measles)
boxplot(df$Measles)

hist(df$BMI)
boxplot(df$BMI)

hist(df$under_five_deaths)
boxplot(df$under_five_deaths)

hist(df$Polio)
boxplot(df$Polio)

hist(df$Total_expenditure)
boxplot(df$Total_expenditure)

hist(df$Diphtheria)
boxplot(df$Diphtheria)
```

```
hist(df$HIV_AIDS )
boxplot(df$HIV_AIDS )

hist(df$GDP)
boxplot(df$GDP)

hist(df$Population)
boxplot(df$Population)

hist(df$thinness_10_19_years)
boxplot(df$thinness_10_19_years)

hist(df$thinness_5_9_years)
boxplot(df$thinness_5_9_years)

hist(df$Income_composition_of_resources)
boxplot(df$Income_composition_of_resources)

hist(df$Schooling)
boxplot(df$Schooling)
```

#Use R studio

#Scatterplot

```
install.packages("gridExtra",dependencies=T)
library(gridExtra)
library(ggplot2)
library(questionr)

setwd("C:\\Users\\user\\Desktop\\GD project")
data<- read.csv("Life_Expectancy_Data.csv")

df <- data[ -c(1,2) ]
data <- df[,c(2,1,3:19,20)]
data$Status<-as.factor(df$Status)
data<-na.omit(data)

str(data)

data<-rename.variable(data,"Life.expectancy","Life_expectancy")
data<-rename.variable(data,"Adult.Mortality","Adult_Mortality")
data<-rename.variable(data,"infant.deaths","infant_deaths")
data<-rename.variable(data,"percentage.expenditure","percentage_expenditure")
data<-rename.variable(data,"Hepatitis.B","Hepatitis_B")
data<-rename.variable(data,"under.five.deaths","under_five_deaths")
data<-rename.variable(data,"Total.expenditure","Total_expenditure")
data<-rename.variable(data,"HIV.AIDS","HIV_AIDS")
data<-rename.variable(data,"thinness.5.9.years","thinness_5_9_years")
data<-rename.variable(data,"thinness..1.19.years","thinness_10_19_years")
data<-
rename.variable(data,"Income.composition.of.resources","Income_composition_of_r
esources")
```

```
g1<- ggplot(data, aes(x = Adult_Mortality, y = Life_expectancy)) +
  geom_point(aes(color = factor(Status ))) +  theme(legend.position="none")


g2 <- ggplot(data, aes(x = infant_deaths, y = Life_expectancy)) +
  geom_point(aes(color = factor(Status ))) + theme(legend.position="none")


g3 <-ggplot(data, aes(x = Alcohol, y = Life_expectancy)) +
  geom_point(aes(color = factor(Status ))) + theme(legend.position="none")


g4 <- ggplot(data, aes(x = percentage_expenditure, y = Life_expectancy)) +
  geom_point(aes(color = factor( Status ))) + theme(legend.position="none")


g5 <- ggplot(data, aes(x = Hepatitis_B, y = Life_expectancy)) +
  geom_point(aes(color = factor( Status ))) + theme(legend.position="none")


g6 <- ggplot(data, aes(x = Measles, y = Life_expectancy)) +
  geom_point(aes(color = factor(Status ))) + theme(legend.position="none")


g7 <- ggplot(data, aes(x = BMI, y = Life_expectancy)) +
  geom_point(aes(color = factor( Status ))) + theme(legend.position="none")


g8<-ggplot(data, aes(x = under_five_deaths, y = Life_expectancy)) +
  geom_point(aes(color = factor(Status ))) + theme(legend.position="none")


g9<-ggplot(data, aes(x = Polio, y = Life_expectancy)) +
  geom_point(aes(color = factor( Status ))) + theme(legend.position="none")


g10<-ggplot(data, aes(x = Total_expenditure, y = Life_expectancy)) +
  geom_point(aes(color = factor( Status ))) + theme(legend.position="none")


g11<-ggplot(data, aes(x = Diphtheria, y = Life_expectancy)) +
  geom_point(aes(color = factor( Status ))) + theme(legend.position="none")


g12<-ggplot(data, aes(x = HIV_AIDS, y = Life_expectancy)) +
  geom_point(aes(color = factor( Status ))) + theme(legend.position="none")


g13<-ggplot(data, aes(x = GDP, y = Life_expectancy)) +
  geom_point(aes(color = factor( Status ))) + theme(legend.position="none")


g14<-ggplot(data, aes(x = Population, y = Life_expectancy)) +
  geom_point(aes(color = factor( Status ))) + theme(legend.position="none")


g15<-ggplot(data, aes(x = thinness_10_19_years, y = Life_expectancy)) +
  geom_point(aes(color = factor( Status ))) + theme(legend.position="none")


g16<-ggplot(data, aes(x = thinness_5_9_years, y = Life_expectancy)) +
  geom_point(aes(color = factor( Status ))) + theme(legend.position="none")


g17<-ggplot(data, aes(x = Income_composition_of_resources, y =
Life_expectancy)) +
  geom_point(aes(color = factor( Status ))) + theme(legend.position="none")


g18<-ggplot(data, aes(x = Schooling, y = Life_expectancy)) +
  geom_point(aes(color = factor(Status ))) + theme(legend.position="none")

grid.arrange(g1, g2,g3,g4,g5,g6,g7,g8,g9, nrow = 3)
grid.arrange(g10,g11,g12,g13,g14,g15,g16,g17,g18, nrow = 3)
```

#### R CODE FOR MULTIPLE LINEAR REGRESSION ####
#### USE A NEW R-SCRIPT ####

```
#Installing Required packages

install.packages("questionr",dependencies=TRUE)
install.packages("dplyr",dependencies=TRUE)
install.packages("car",dependencies=TRUE)
install.packages("boot",dependencies=TRUE)
install.packages("QuantPsyc",dependencies=TRUE)
install.packages("lmtest",dependencies=TRUE)
install.packages("sandwich",dependencies=TRUE)
install.packages("vars",dependencies=TRUE)
install.packages("MASS",dependencies=TRUE)
install.packages("nortest",dependencies=TRUE)
install.packages("ggplot2",dependencies=TRUE)
install.packages("imputeTS",dependencies=TRUE)
install.packages("perturb",dependencies=TRUE)
install.packages("leaps",dependencies=TRUE)
install.packages("olsrr",dependencies=TRUE)
install.packages("e1071",dependencies=TRUE)
install.packages("reshape2",dependencies=TRUE)
```

# Calling the liabraries

```
library(boot)
library(car)
library(QuantPsyc)
library(lmtest)
library(sandwich)
library(vars)
library(nortest)
library(MASS)
library(ggplot2)
library(imputeTS)
library(perturb)
library(leaps)
library(olsrr)
library(e1071)
library(reshape2)
library(questionr)
```

#load data

```
setwd("C:\\Users\\user\\Desktop\\GD project")
data<- read.csv("Life_Expectancy_Data.csv")
str(data)
```

# Dropping year and country column

```
data <- data[ -c(1,2) ]
data <- data[,c(2,1,3:19,20)]
data$Status<-as.factor(data$Status)

# structure and summary of dataset
str(data)
summary(data)

#Renaming the columns

colnames(data)
data<-rename.variable(data,"Life.expectancy","Life_expectancy")
data<-rename.variable(data,"Adult.Mortality","Adult_Mortality")
data<-rename.variable(data,"infant.deaths","infant_deaths")
data<-rename.variable(data,"percentage.expenditure","percentage_expenditure")
data<-rename.variable(data,"Hepatitis.B","Hepatitis_B")
data<-rename.variable(data,"under.five.deaths","under_five_deaths")
data<-rename.variable(data,"Total.expenditure","Total_expenditure")
data<-rename.variable(data,"HIV.AIDS","HIV_AIDS")
data<-rename.variable(data,"thinness.5.9.years","thinness_5_9_years")
data<-rename.variable(data,"thinness..1.19.years","thinness_10_19_years")
data<-
rename.variable(data,"Income.composition.of.resources","Income_composition_of_r
esources")

#Checking for missing values and data imputation by interpolation

sapply(data, function(x) sum(is.na(x))/length(x)*100)

data$Adult_Mortality <- na_interpolation(data$Adult_Mortality )
data$Alcohol<-na_interpolation(data$Alcohol)
data$Hepatitis_B<-na_interpolation(data$Hepatitis_B)
data$BMI<-na_interpolation(data$BMI)
data$Polio<-na_interpolation(data$Polio)
data$Total_expenditure<-na_interpolation(data$Total_expenditure)
data$Diphtheria<-na_interpolation(data$Diphtheria)
data$GDP<-na_interpolation(data$GDP)
data$Population<-na_interpolation(data$Population)
data$thinness_10_19_years<-na_interpolation(data$thinness_10_19_years)
data$thinness_5_9_years<-na_interpolation(data$thinness_5_9_years)
data$Income_composition_of_resources<-
na_interpolation(data$Income_composition_of_resources)
data$Schooling<-na_interpolation(data$Schooling)

#omitting Null rows
data <- na.omit(data)
str(data)
summary(data)

#Checking Skewness
skewness(data$Life_expectancy)
skewness(data$thinness_5_9_years)
skewness(data$thinness_10_19_years)
skewness(data$Population)
skewness(data$Income_composition_of_resources)
skewness(data$GDP)
skewness(data$HIV_AIDS)
skewness(data$Diphtheria)
skewness(data$Total_expenditure)
skewness(data$Polio)
skewness(data$under_five_deaths)
skewness(data$BMI)
skewness(data$Measles)
skewness(data$Hepatitis_B)
skewness(data$percentage_expenditure)
skewness(data$Alcohol)
skewness(data$infant_deaths)
skewness(data$Adult_Mortality)
skewness(data$Schooling)

#Response Variable
y <- data$Life_expectancy

#Regressor Variables
x1 <- data$Status
x2 <- data$Adult_Mortality
x3 <- data$infant_deaths
x4 <- data$Alcohol
x5 <- data$percentage_expenditure
x6 <- data$Hepatitis_B
x7 <- data$Measles
x8 <- data$BMI
x9 <- data$under_five_deaths
x10 <- data$Polio
x11 <- data$Total_expenditure
x12 <- data$Diphtheria
x13 <- data$HIV_AIDS
x14 <- data$GDP
x15 <- data$Population
x16 <- data$thinness_10_19_years
x17 <- data$thinness_5_9_years
x18 <- data$Income_composition_of_resources
x19 <- data$Schooling

# Data Normalization/Standardization
y <- data$Life_expectancy
x1 <- data$Status
x2 <- log(data$Adult_Mortality)
x3 <- (data$infant_deaths)^(1/3)
x4 <- data$Alcohol^(1/3)
x5 <- (data$percentage_expenditure)^(1/3)
x6 <- log(data$Hepatitis_B)
x7 <- (data$Measles)^(1/3)
x8 <- data$BMI
x9 <- (data$under_five_deaths)^(1/3)
x10 <- log(data$Polio)
x11 <- data$Total_expenditure
```

```
x12 <- log(data$Diphtheria)
x13 <- log(data$HIV_AIDS)
x14 <- log(data$GDP)
x15 <- log(data$Population)
x16 <- log(data$thinness_10_19_years)
x17 <- log(data$thinness_5_9_years)
x18 <- data$Income_composition_of_resources
x19 <- data$Schooling

# Creating new dataframe
data1 <- data.frame(y,x1,x2,x3,x4,x5,x6,x7,x8,x9,x10,
x11,x12,x13,x14,x15,x16,x17,x18,x19)

head(data1)
nrow(data1)
str(data1)
summary(data1)

#########################################
#Heatmap & correlation Matrix to visualize Multicolinearity

df2 <- data1[ -c(1,2) ]
cormat <- round(cor(df2),2)

melted_cormat <- melt(cormat)
head(melted_cormat)
# Get upper triangle of the correlation matrix
 get_upper_tri <- function(cormat){
    cormat[lower.tri(cormat)]<- NA
    return(cormat)
  }
upper_tri <- get_upper_tri(cormat)
# Melt the correlation matrix
library(reshape2)
melted_cormat <- melt(upper_tri, na.rm = TRUE)
# Heatmap
library(ggplot2)
ggheatmap <- ggplot(data = melted_cormat, aes(Var2, Var1, fill = value))+
 geom_tile(color = "white")+
 scale_fill_gradient2(low = "blue", high = "red", mid = "white",
   midpoint = 0, limit = c(-1,1), space = "Lab",
   name="Pearson\nCorrelation") +
  theme_minimal()+
 theme(axis.text.x = element_text(angle = 45, vjust = 1,
    size = 8, hjust = 1))+
 coord_fixed()


ggheatmap +
geom_text(aes(Var2, Var1, label = value), color = "black", size = 2) +
theme(
  axis.title.x = element_blank(),
  axis.title.y = element_blank(),
  panel.grid.major = element_blank(),
  panel.border = element_blank(),
  panel.background = element_blank(),
  axis.ticks = element_blank(),
  legend.justification = c(1, 0),
  legend.position = c(0.6, 0.7),
  legend.direction = "horizontal")+
  guides(fill = guide_colorbar(barwidth = 7, barheight = 1,
              title.position = "top", title.hjust = 0.5))

############################################################

#removing unnecessery variables
data1 <- data.frame(y,x1,x2,x3,x4,x5,x6,x7,x8,x10,
x11,x12,x13,x14,x15,x17,x18)

#Outlier Detection (Cook's Distance)
sapply(data1, function(x) sum(is.na(x))/length(x)*100)
model <- lm(y ~ x1 + x2 + x3 + x4 + x5 + x6 + x7 + x8 + x10 +
x11 + x12 + x13 + x14 + x15 + x17 + x18,data=data1)

cooksd <- cooks.distance(model)

# Plot the Cook's Distance using the traditional 4/(n=sample zize) criterion
sample_size <- nrow(data1)
# plot cook's distance
plot(cooksd, pch="*", cex=1, main="Influential Obs by Cooks distance")
# add cutoff line
abline(h = (4/(sample_size)), col="red")

# Removing Outliers
# influential row numbers
influential <- as.numeric(names(cooksd)[(cooksd > (4/(sample_size-19-1)))])

data <- data1[-influential, ]

# Training and Test Data
index <- sample(1:nrow(data),round(0.8*nrow(data)))
mlr_train <- data [index,]
mlr_test <- data [-index,]

head(mlr_train)
nrow(mlr_train)

# Fitting Multiple Linear Regression Model on training data
fit <- lm(y ~x1 + x2 + x3 + x4 + x5 + x6 + x7 + x8 + x10 +
            x11 + x12 + x13 + x14 + x15 + x17 + x18,data=mlr_train)


fit <- lm(y ~x1 + x2 + x4 + x5 + x6 + x7 + x8 + x10 +
            x11 + x12 + x13 + x14 + x15 + x17,data=mlr_train)
```

```
# Summary of Model
#P value of independent variable (p value should be less than .05)
summary(fit)
#Again Checking Multicolinearity vif>2 means presence of multicollinearity
vif(fit)

#Stepwise regression
fit <- lm(y ~x1 + x2 + x4 + x5 + x6 + x7 + x8 + x10 +
            x11 + x12 + x13 + x14 + x15 + x17,data=mlr_train)

summary(fit )

#Forward Selection
step_model_forward = stepAIC(fit ,direction="forward",trace=1)
step_model_forward

best_subset_forward <-ols_step_best_subset(step_model_forward)
best_subset_forward

#Backward Elimination
step_model_backward = stepAIC(fit ,direction="backward",trace=1)
step_model_backward

best_subset_backward <-ols_step_best_subset(step_model_backward)
best_subset_backward

#Stepwise Regression
step_model_both = stepAIC(fit ,direction="both",trace=1)
step_model_both

best_subset_both <-ols_step_best_subset(step_model_both)
best_subset_both

#Final MOdel
fit1 <- lm(y ~x1 + x2 + x4 + x5 + x7 + x8 + x10 +
            x11 + x12 + x13 + x14 + x17,data=mlr_train)
summary(fit1)

# Test for Normality
qqnorm(mlr_train$y)
qqline(mlr_train$y,col="red")

shapiro.test(mlr_train$y)
ad.test(mlr_train$y)

#Breusch-Pagan test
par(mfrow = c(2,2))
plot(fit1)
bptest(fit1)

#Autocorrelation
dwt(fit1)
```

```
## Get the predicted or fitted values on training data
train_pred<-fitted(fit1)

#Validation on train set
attach(mlr_train)

train_Mape<-(sum((abs(mlr_train$y-
train_pred))/mlr_train$y))/nrow(mlr_train)*100
MSE_train <- sum((train_pred - mlr_train$y)^2)/nrow(mlr_train)
deviation_train=((mlr_train$y-train_pred)/mlr_train$y)
accuracy_train=(1-abs(mean(deviation_train)))*100

## Get the predicted or fitted values on training data
test_pred <- predict(fit1,mlr_test)

#Validation on test set
attach(mlr_test)

test_Mape<-(sum((abs(mlr_test$y-test_pred))/mlr_test$y))/nrow(mlr_test)*100
MSE_test <- sum((test_pred - mlr_test$y)^2)/nrow(mlr_test)
deviation_test=((mlr_test$y-test_pred)/mlr_test$y)
accuracy_test=(1-abs(mean(deviation_test)))*100


MSE_train
MSE_test
train_Mape
test_Mape
accuracy_train
accuracy_test
```

#### R CODE FOR ARTIFICIAL NEURAL NETWORK
#### USE A NEW R-SCRIPT

```
install.packages("car",dependencies=TRUE)
install.packages("boot",dependencies=TRUE)
install.packages("QuantPsyc",dependencies=TRUE)
install.packages("lmtest",dependencies=TRUE)
install.packages("sandwich",dependencies=TRUE)
install.packages("vars",dependencies=TRUE)
install.packages("MASS",dependencies=TRUE)
install.packages("nortest",dependencies=TRUE)
install.packages("ggplot2",dependencies=TRUE)
install.packages("imputeTS",dependencies=TRUE)
install.packages("perturb",dependencies=TRUE)
install.packages("leaps",dependencies=TRUE)
install.packages("olsrr",dependencies=TRUE)
install.packages("e1071",dependencies=TRUE)
install.packages("reshape2",dependencies=TRUE)
```

#Required Libraries

```
library(boot)
library(car)
library(QuantPsyc)
library(lmtest)
library(sandwich)
library(vars)
library(nortest)
library(MASS)
library(ggplot2)
library(imputeTS)
library(perturb)
library(leaps)
library(olsrr)
library(e1071)
library(reshape2)
```

#load data

```
setwd("C:\\Users\\user\\Desktop\\GD project")
data<- read.csv("Life_Expectancy_Data.csv")
str(data)

summary(data)

data <- data[ -c(1,2) ]
data <- data[,c(2,1,3:19,20)]
data$Status<-as.factor(data$Status)
data$Status <- ifelse(data$Status == "Developing",0,1)
```

#Renaming the columns

```
colnames(data)
```

```
data<-rename.variable(data,"Life.expectancy","Life_expectancy")
data<-rename.variable(data,"Adult.Mortality","Adult_Mortality")
data<-rename.variable(data,"infant.deaths","infant_deaths")
data<-rename.variable(data,"percentage.expenditure","percentage_expenditure")
data<-rename.variable(data,"Hepatitis.B","Hepatitis_B")
data<-rename.variable(data,"under.five.deaths","under_five_deaths")
data<-rename.variable(data,"Total.expenditure","Total_expenditure")
data<-rename.variable(data,"HIV.AIDS","HIV_AIDS")
data<-rename.variable(data,"thinness.5.9.years","thinness_5_9_years")
data<-rename.variable(data,"thinness..1.19.years","thinness_10_19_years")
data<-
rename.variable(data,"Income.composition.of.resources","Income_composition_of_r
esources")

# Checking for missing values and data imputation by interpolation
sapply(data, function(x) sum(is.na(x))/length(x)*100)

data$Adult_Mortality <- na_interpolation(data$Adult_Mortality )
data$Alcohol<-na_interpolation(data$Alcohol)
data$Hepatitis_B<-na_interpolation(data$Hepatitis_B)
data$BMI<-na_interpolation(data$BMI)
data$Polio<-na_interpolation(data$Polio)
data$Total_expenditure<-na_interpolation(data$Total_expenditure)
data$Diphtheria<-na_interpolation(data$Diphtheria)
data$GDP<-na_interpolation(data$GDP)
data$Population<-na_interpolation(data$Population)
data$thinness_10_19_years<-na_interpolation(data$thinness_10_19_years)
data$thinness_5_9_years<-na_interpolation(data$thinness_5_9_years)
data$Income_composition_of_resources<-
na_interpolation(data$Income_composition_of_resources)
data$Schooling<-na_interpolation(data$Schooling)

# omitting Null rows
data <- na.omit(data)

sapply(data, function(x) sum(is.na(x))/length(x)*100)

str(data)
summary(data)

#Response Variable
y <- data$Life_expectancy

#Regressor Variables
x1 <- data$Status
x2 <- data$Adult_Mortality
x3 <- data$infant_deaths
x4 <- data$Alcohol
x5 <- data$percentage_expenditure
x6 <- data$Hepatitis_B
x7 <- data$Measles
x8 <- data$BMI
x9 <- data$under_five_deaths
```

```
x10 <- data$Polio
x11 <- data$Total_expenditure
x12 <- data$Diphtheria
x13 <- data$HIV_AIDS
x14 <- data$GDP
x15 <- data$Population
x16 <- data$thinness_10_19_years
x17 <- data$thinness_5_9_years
x18 <- data$Income_composition_of_resources
x19 <- data$Schooling

data <- data.frame(y,x1,x2,x3,x4,x5,x6,x7,x8,x9,x10,
x11,x12,x13,x14,x15,x16,x17,x18,x19)

#Scaling dataset

maxs <- apply(data, 2, max)
mins <- apply(data, 2, min)
scaled <- as.data.frame(scale(data, center = mins, scale = maxs - mins))

summary(scaled )
str(scaled )

scaled$x19 <- NULL
scaled$x16 <- NULL
scaled$x10 <- NULL
scaled$x9 <- NULL
scaled$x14 <- NULL

#########################################

#Heatmap & correlation Matrix

df2 <- scaled [ -c(1,2) ]
cormat <- round(cor(df2),2)

melted_cormat <- melt(cormat)
head(melted_cormat)
# Get upper triangle of the correlation matrix
 get_upper_tri <- function(cormat){
    cormat[lower.tri(cormat)]<- NA
    return(cormat)
  }
upper_tri <- get_upper_tri(cormat)
# Melt the correlation matrix
library(reshape2)
melted_cormat <- melt(upper_tri, na.rm = TRUE)
# Heatmap
library(ggplot2)
ggheatmap <- ggplot(data = melted_cormat, aes(Var2, Var1, fill = value))+
 geom_tile(color = "white")+
 scale_fill_gradient2(low = "blue", high = "red", mid = "white",
   midpoint = 0, limit = c(-1,1), space = "Lab",
    name="Pearson\nCorrelation") +
   theme_minimal()+
  theme(axis.text.x = element_text(angle = 45, vjust = 1,
     size = 8, hjust = 1))+
  coord_fixed()


ggheatmap +
geom_text(aes(Var2, Var1, label = value), color = "black", size = 2) +
theme(
  axis.title.x = element_blank(),
  axis.title.y = element_blank(),
  panel.grid.major = element_blank(),
  panel.border = element_blank(),
  panel.background = element_blank(),
  axis.ticks = element_blank(),
  legend.justification = c(1, 0),
  legend.position = c(0.6, 0.7),
  legend.direction = "horizontal")+
  guides(fill = guide_colorbar(barwidth = 7, barheight = 1,
                title.position = "top", title.hjust = 0.5))

#########################################

sapply(scaled, function(x) sum(is.na(x))/length(x)*100)

# Training and Test Data
index <- sample(1:nrow(scaled),round(0.8*nrow(scaled)))
ann_train <- scaled[index,]
ann_test <- scaled [-index,]

summary(ann_train)
summary(ann_test)

install.packages("neuralnet",dependencies=T)
library(neuralnet)

n <- names(ann_train)
f <- as.formula(paste("y ~", paste(n[!n %in% "y"], collapse = " + ")))

## model1
set.seed(123)

nn1 <- neuralnet(f,data=ann_train,hidden=8,linear.output=T)

plot(nn1)
nn1$result.matrix
summary(nn1)
nrow(ann_train)
b <- ann_train[,2:15]
head(b)
pr.nn1_test <- compute(nn1,ann_test[,2:15])
pr.nn1_test <- pr.nn1_test$net.result*(max(data$y)-min(data$y))+min(data$y)
```

```
test.r <- (ann_test$y)*(max(data$y)-min(data$y))+min(data$y)
MSE.nn1_test <- sum((test.r - pr.nn1_test)^2)/nrow(ann_test)
test_Mape<-(sum((abs(test.r-pr.nn1_test))/test.r))/nrow(ann_test)*100

pr.nn1_train <- compute(nn1,b)
pr.nn1_train <- pr.nn1_train$net.result*(max(data$y)-min(data$y))+min(data$y)
train.r <- (ann_train$y)*(max(data$y)-min(data$y))+min(data$y)
MSE.nn1_train <- sum((train.r - pr.nn1_train)^2)/nrow(ann_train)
train_Mape<-(sum((abs(train.r-pr.nn1_train))/train.r))/nrow(ann_train)*100

## Accuracy

predicted_train=results_train$prediction
actual_train=results_train$actual
deviation_train=((actual_train-predicted_train)/actual_train)
comparison_train=data.frame(predicted_train,actual_train,deviation_train)
accuracy_train=(1-abs(mean(deviation_train)))*100

results_test <- data.frame(actual = test.r, prediction = pr.nn1_test)
results_test

predicted_test=results_test$prediction
actual_test=results_test$actual
deviation_test=((actual_test-predicted_test)/actual_test)
comparison_test=data.frame(predicted_test,actual_test,deviation_test)
accuracy_test=(1-abs(mean(deviation_test)))*100


MSE.nn1_train
MSE.nn1_test
train_Mape
test_Mape
accuracy_train
accuracy_test
```