METRO COLLEGE OF TECHNOLOGY

R - PROJECT

LIFE EXPECTANCY DATA SET FROM ‘W.H.O’ DATA REPOSITORY

From Kaggle.

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In this project we have considered data related to life expectancy, health factors from year 2000-2015 for 193 countries for the analysis.

The six phases of CRISP-DM include:

1. BUISNESS UNDERSTANDING
2. DATA UNDERSTANDING
3. DATA PREPARATION
4. MODELLING
5. EVALUATION
6. DEPLOYMENT

EXPLORATORY DATA ANALYSIS (EDA)

BUISNESS UNDERSTANDING :

This project is based on factors affecting life expectancy considering demographic variables, income composition and mortality rates

In a nutshell, this study will focus on immunization factors, mortality factors, economic factors, social factors and other health related factors as well.

Since the observations in this dataset are based on different countries, it will be easier for a country to determine the predicting factor which is contributing to lower the value of life expectancy.

This will help in suggesting a country which area should be given importance in order to efficiently improve the life expectancy of its population.

1. BUISNESS UNDERSTANDING :

Gone through the meta data for business understanding.
The insights of these kind of research done in the past gives deep understanding.

2. UNDERSTANDING THE DATA :

```
> dim(df1)                          # Checking the shape of the Data set
[1] 2938   22
```

```
> head(df1,3)                    # Checking  the head of the Data set
      Country Year     Status Life.expectancy Adult.Mortality infant.deaths Alcohol percentage.expenditure Hepatitis.B Measles  BMI under-five.deaths Polio
1 Afghanistan 2015 Developing            65.0             263            62    0.01               71.27962          65     1154 19.1                83     6
2 Afghanistan 2014 Developing            59.9             271            64    0.01               73.52358          62      492 18.6                86    58
3 Afghanistan 2013 Developing            59.9             268            66    0.01               73.21924          64      430 18.1                89    62
  Total.expenditure Diphtheria HIV/AIDS      GDP Population thinness.1-19.years thinness.5-9.years Income.composition.of.resources Schooling
1              8.16         65      0.1 584.2592   33736494                17.2               17.3                           0.479      10.1
2              8.18         62      0.1 612.6965     327582                17.5               17.5                           0.476      10.0
3              8.13         64      0.1 631.7450   31731688                17.7               17.7                           0.470       9.9
```

```
> tail(df1,3)                    # Checking the tail of the Data set
      Country Year     Status Life.expectancy Adult.Mortality infant.deaths Alcohol percentage.expenditure Hepatitis.B Measles  BMI under-five.deaths Polio
2936 Zimbabwe 2002 Developing            44.8              73            25    4.43                      0          73     304 26.3                40    73
2937 Zimbabwe 2001 Developing            45.3             686            25    1.72                      0          76     529 25.9                39    76
2938 Zimbabwe 2000 Developing            46.0             665            24    1.68                      0          79    1483 25.5                39    78
     Total.expenditure Diphtheria HIV/AIDS       GDP Population thinness.1-19.years thinness.5-9.years Income.composition.of.resources Schooling
2936              6.53         71     39.8  57.34834     125525                 1.2                1.3                           0.427      10.0
2937              6.16         75     42.1 548.58731   12366165                 1.6                1.7                           0.427       9.8
2938              7.10         78     43.5 547.35888   12222251                11.0               11.2                           0.434       9.8
```

```
> str(df1)                       # To visualize the structure of DATA
'data.frame':   2938 obs. of  22 variables:
 $ Country                        : chr  "Afghanistan" "Afghanistan" "Afghanistan" "Afghanistan" ...
 $ Year                           : num  2015 2014 2013 2012 2011 ...
 $ 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                : num  263 271 268 272 275 279 281 287 295 295 ...
 $ infant.deaths                  : num  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                    : num  65 62 64 67 68 66 63 64 63 64 ...
 $ Measles                        : num  1154 492 430 2787 3013 ...
 $ 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              : num  83 86 89 93 97 102 106 110 113 116 ...
 $ Polio                          : num  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                     : num  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 ...
>
```

Changing the column names which are not according to R standards :

```
colnames(df1)[c(12,16,19,20)]<-c("Under.five.deaths","HIV.AIDS","thinness.1_19.years","thinness.5_9.years")
```

Dropping Features : As we have no related information to extract meaningful data from it.

```
#dropping features as we don't have any knowledge to extract meaning full features from them

df1[,c("thinness.1_19.years","thinness.5_9.years")]<-NULL
```

Finding the Total number of duplicated data, This data set does not have any Duplicates

```
#How many duplicated data are there?
sum(duplicated((df1))) # gives total number of duplicate data values, NO DUPLICATES FOUND
r1<-which(duplicated(df1)) # gives row numbers of duplicate values
df1<-df1[-r1,]    # removing the rows with duplicate values.
```

Handling Missing values :

```
df1[df1==' ']<-NA               # assigning missing values with 'NA'
```

```
>
> sum(is.na(df1))               # To get total number of missing values
[1] 2563
>
```

To get the number of missing values column wise.

```
> colSums(is.na(df1))           # To get the number of missing values column wise
                        Country                       Year                Status
                              0                          0                     0
                Life.expectancy            Adult.Mortality         infant.deaths
                              0                          0                     0
                        Alcohol     percentage.expenditure           Hepatitis.B
                            193                          0                   553
                        Measles                        BMI     Under.five.deaths
                              0                         32                     0
                          Polio          Total.expenditure            Diphtheria
                             19                        226                    19
                       HIV.AIDS                        GDP            Population
                              0                        443                   644
Income.composition.of.resources                  Schooling        lifeExp.agegroup
                            160                        160                     0
>
```

Feature Engineering : I am adding Two categorical column to the data set to make it easy to handle.

```r
df1$lifeExp.agegroup<-NA
df1

f1=function(x){
  if (is.na(x)) "N/A"
  else if (x<25)     "< 25"
  else if (x<= 35) "25-35"
  else if (x<= 45) "36-45"
  else if (x<= 55) "46-55"
  else if (x<= 65) "56-65"
  else if (x<= 75) "66-75"
  else if (x<= 85) "76-85"
  else if (x<= 95) "86-95"
  else              "95+"
}
# applying the function to 'life expectancy' column using 'sapply'
df1$lifeExp.agegroup<-sapply(df1$Life.expectancy ,f1)
df1
```

```r
# Adding Another Categorical column to the Data S

df1$Year.groups<-NA
str(df1)

f2=function(x)  {
  if (x>=2000 && x<=2003) "2000-2003"
   else if (x>=2004 && x<=2007) "2004=2007"
    else if (x>=2008 && x<=2011) "2008-2011"
     else if (x>=2012 && x<=2015) "2012-2015"
}

df1$Year.groups<-sapply(df1$Year,f2)
str(df1)
df1
```

UNIVARIATE ANALYSIS for Categorical Variables : We have 4 categorical variables in this data set. 1. Country 2. Status 3. Life.Exp.agegroup 4. Year.groups

1. Country :

Summarization : table of frequency or percentage

Visualization : pie chart or bar chart

Making a copy of the data set before doing any changes.

```
df_org1<-df1                    # making a copy of the Data Set
```

```
#1.SUMMARIZING Categorical Variables
sum(is.na(df1$Country)) # No missing values found.

levels(as.factor(df1$Country)) # give levels (different values) for column 'Country'
                               # shows Names of 193 countries
tb1<-table(df1$Country) #Viewing the frequency of each 'Country' which should be 16 for all countries
tb1                     #as we are considering data for 16 years.
                        # But, found frequency of '1' for few (10) countries.
```

DATA CLEANING :

```
# Dropping the Rows with frequency '1'.

df1<-df1[-c(625,770,1651,1716,1813,1910,1959,2168,2217,2714), ]
```

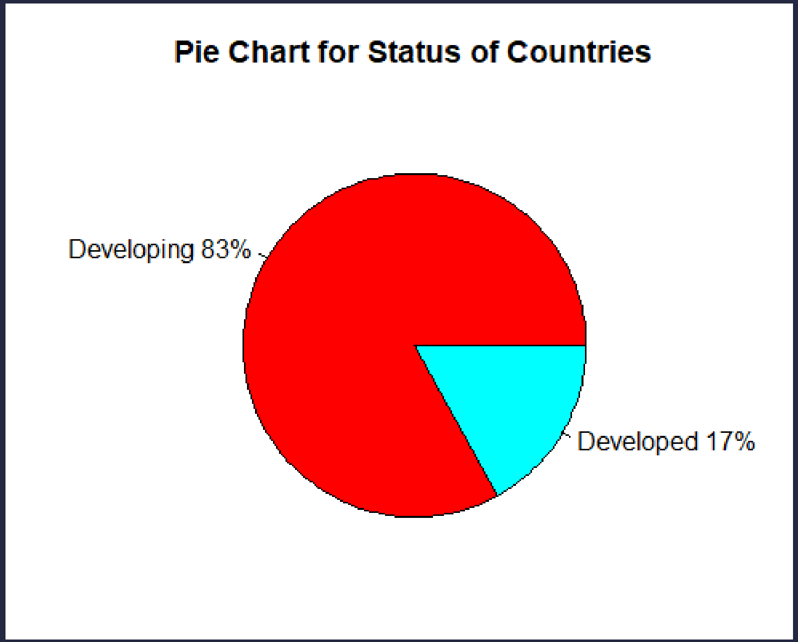
2. Status

```
levels(as.factor(df1$Status))  # gives 2 levels for column Status.
.] "Developed"  "Developing"
```

```
tb2<-table(df1$Status)    #Viewing the frequency of each level of 'Status'
tb2

Developed Developing
      512       2416
```

Visualization:




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

freq1 <- c(161,32)
pct <- round(freq1/sum(freq1)*100)
lbls <- c("Developing", "Developed")
lbls <- paste(lbls, pct) # add percents to labels
lbls <- paste(lbls,"%",sep="") # ad % to labels
pie(pct,labels = lbls, col=rainbow(length(lbls)),#length(lbls) = 5
    main="Pie Chart for Status of Countries")
```

3. Life.Exp.agegroup

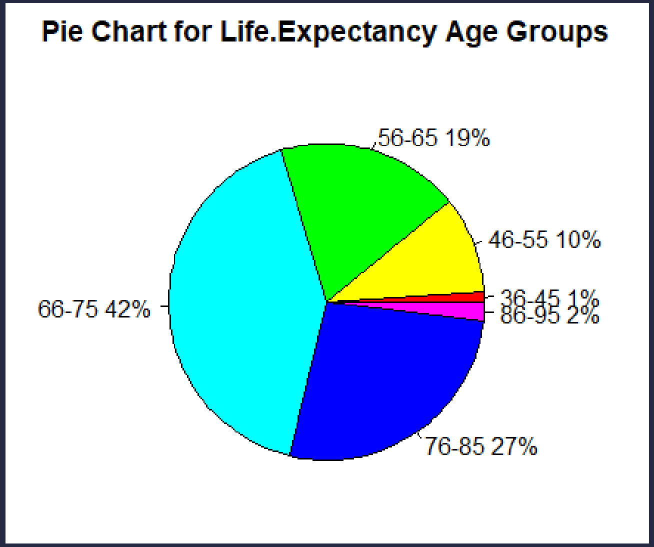
```
levels(as.factor(df1$lifeExp.agegroup))  # 6 levels are retured
1] "36-45" "46-55" "56-65" "66-75" "76-85" "86-95"
```

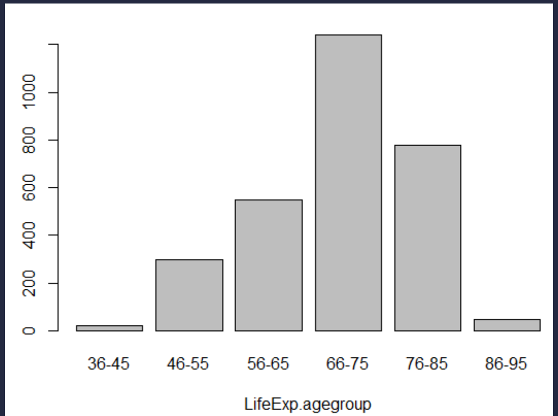
```
> tb5<-table(df1$lifeExp.agegroup)         # frequency of life expectancy of each agegroup
> tb5

36-45 46-55 56-65 66-75 76-85 86-95
   19   296   549  1240   779    45
```

```
# VISUALIZATION BY PIE CHART
par(mfrow = c(1, 1))

freq1 <- c(19,296,549,1240,779,45)
pct <- round(freq1/sum(freq1)*100)
lbls <- c("36-45","46-55","56-65","66-75","76-85","86-95")
lbls <- paste(lbls, pct) # add percents to labels
lbls <- paste(lbls,"%",sep="") # ad % to labels
pie(pct,labels = lbls, col=rainbow(length(lbls)),#length(lbls) = 5
    main="Pie Chart for Life.Expectancy Age Groups")
```





UNIVARIATE ANALYSIS FOR CONTINOUS (NUMERIC) VARIABLES :

Summarization : Central tendency(Mean, Median, Mode, Min, Max, 25th percentile, 75th percentile,Standard Deviation, Variance.

Visualization : Histogram, Densityplot, boxplot

Removing Categorical variables

```
str(df1)
dataset<-df1[,-c(1,3,21)]
str(dataset)
```

To check the Summary of all Numerical Variables.

```
      Year      Life.expectancy Adult.Mortality infant.deaths       Alcohol        percentage.expenditure
 Min.   :2000   Min.   :36.30   Min.   :  1.0   Min.   :   0.00   Min.   : 0.010   Min.   :    0.000
 1st Qu.:2004   1st Qu.:63.10   1st Qu.: 74.0   1st Qu.:   0.00   1st Qu.: 0.905   1st Qu.:    4.854
 Median :2008   Median :72.10   Median :144.0   Median :   3.00   Median : 3.770   Median :   65.611
 Mean   :2008   Mean   :69.22   Mean   :164.8   Mean   :  30.41   Mean   : 4.615   Mean   :  740.321
 3rd Qu.:2011   3rd Qu.:75.70   3rd Qu.:228.0   3rd Qu.:  22.00   3rd Qu.: 7.715   3rd Qu.:  442.614
 Max.   :2015   Max.   :89.00   Max.   :723.0   Max.   :1800.00   Max.   :17.870   Max.   :19479.912
                                                                  NA's   :193
```

```
  Hepatitis.B       Measles              BMI        Under.five.deaths      Polio      Total.expenditur
 Min.   : 1.00   Min.   :      0.0   Min.   : 1.00   Min.   :   0.00   Min.   : 3.00   Min.   : 0.37
 1st Qu.:77.00   1st Qu.:      0.0   1st Qu.:19.30   1st Qu.:   0.00   1st Qu.:78.00   1st Qu.: 4.26
 Median :92.00   Median :     17.0   Median :43.35   Median :   4.00   Median :93.00   Median : 5.75
 Mean   :80.96   Mean   :   2427.9   Mean   :38.24   Mean   :  42.18   Mean   :82.55   Mean   : 5.93
 3rd Qu.:97.00   3rd Qu.:    362.2   3rd Qu.:56.10   3rd Qu.:  28.00   3rd Qu.:97.00   3rd Qu.: 7.49
 Max.   :99.00   Max.   :212183.0   Max.   :77.60   Max.   :2500.00   Max.   :99.00   Max.   :17.60
 NA's   :553                         NA's   :32                         NA's   :19     NA's   :226
```

```
   Diphtheria       HIV.AIDS            GDP              Population         Income.composition.of.resources
 Min.   : 2.00   Min.   : 0.100   Min.   :     1.68   Min.   :3.400e+01   Min.   :0.0000
 1st Qu.:78.00   1st Qu.: 0.100   1st Qu.:   463.85   1st Qu.:1.967e+05   1st Qu.:0.4930
 Median :93.00   Median : 0.100   Median :  1764.97   Median :1.392e+06   Median :0.6770
 Mean   :82.32   Mean   : 1.748   Mean   :  7494.21   Mean   :1.276e+07   Mean   :0.6274
 3rd Qu.:97.00   3rd Qu.: 0.800   3rd Qu.:  5932.90   3rd Qu.:7.427e+06   3rd Qu.:0.7792
 Max.   :99.00   Max.   :50.600   Max.   :119172.74   Max.   :1.294e+09   Max.   :0.9480
 NA's   :19                       NA's   :443         NA's   :644         NA's   :160
```

```
   Schooling
 Min.   : 0.0
 1st Qu.:10.1
 Median :12.3
 Mean   :12.0
 3rd Qu.:14.3
 Max.   :20.7
 NA's   :160
```

Interpretation :

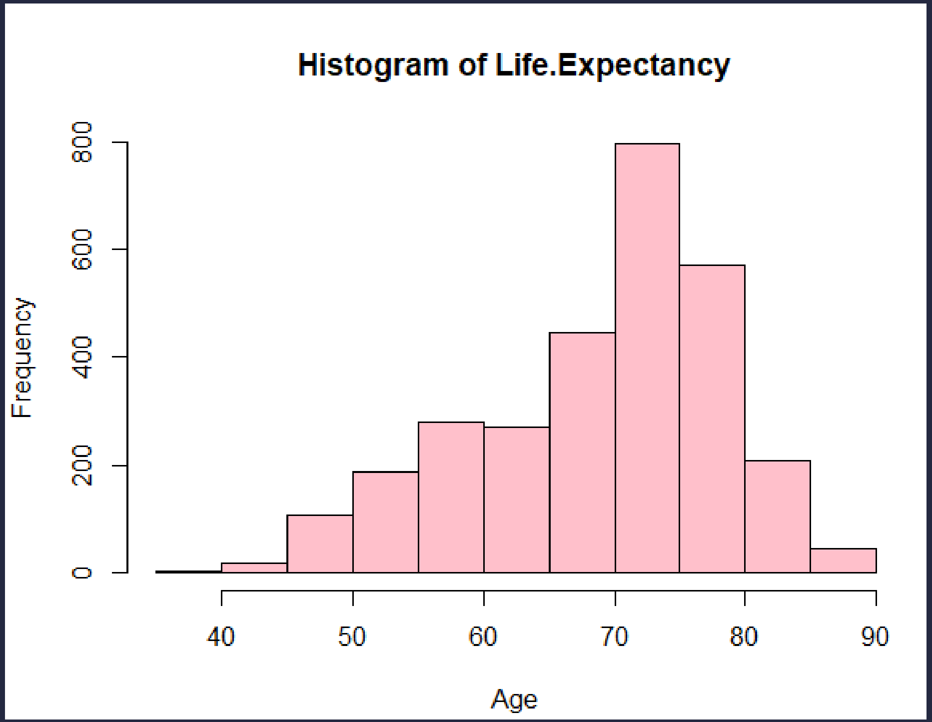
- We have 2930 observations and 22 Variables (columns)
- Life.Expectancy is the Target (Response) variable which is Continuous (Numeric) data type.
- Adult.Mortality is our second Target variable which is Continuous (Numeric) data type.
- And all other variables

Status, Year , GDP, Schooling, Hepatitis, Alcohol…are predicting variables.

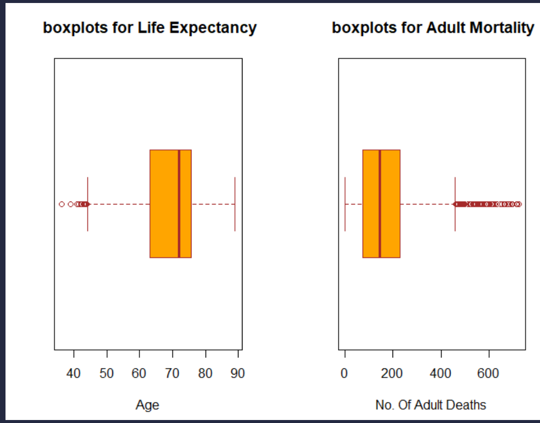
- In some variables like Adult.Mortality, infant deaths, percentage.expenditure, measels, under-five deaths there is a huge difference between the 3rd quartile and the maximum value.
- Which can be considered as OUTLIERS, But, I am not considering them as outliers as the data belong to 183 different countries and each country have its own factors affecting these values.

1. What is the distribution of Target variable Life Expectancy

```
# 1. Problem : What is the distribution of Target (Numerical) variable
# Answer : By seeing the Histogram we can say that it is Normal with positive Kurtosis.
hist(df1$Life.expectancy,br=14,col="pink",xlab="Age",ylab="Frequency",
     freq=TRUE,main="Histogram of Life.Expectancy")
```



By seeing the Histogram we can say that it is Normal with positive kurtosis.



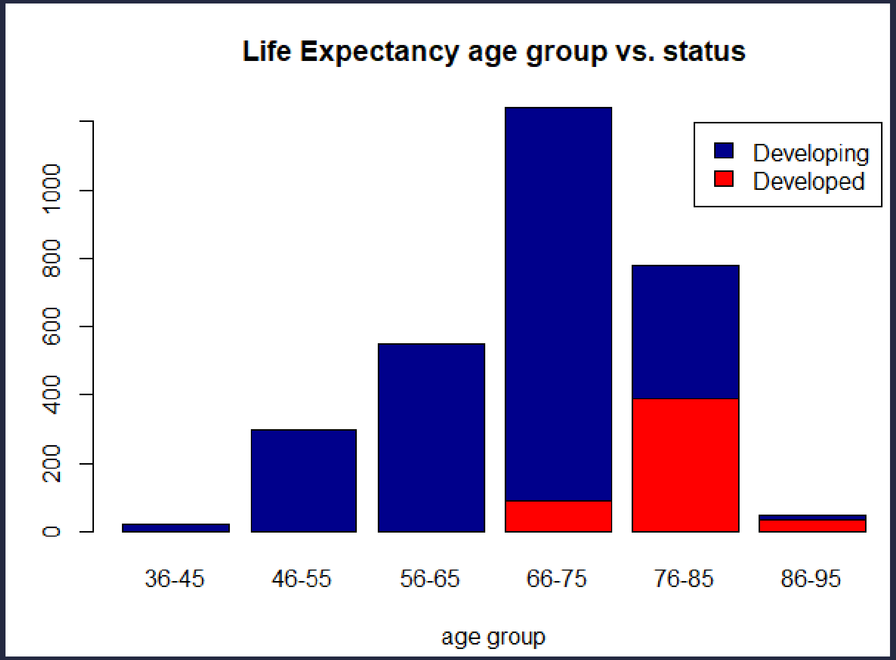
BIVARIATE ANALYSIS : CATEGORICAL VS. CATEGORICAL

Summarizing : using Contingency Table

```
> tbl_ag_S<-xtabs(~ lifeExp.agegroup + Status, data=df1)
> tbl_ag_S
                Status
lifeExp.agegroup Developed Developing
           36-45         0         19
           46-55         0        296
           56-65         0        549
           66-75        90       1150
           76-85       387        392
           86-95        35         10
```

```
> tbl_ag_S.t<-t(tbl_ag_S)   # transpose tbl_ag_S
> tbl_ag_S.t
            lifeExp.agegroup
Status        36-45 46-55 56-65 66-75 76-85 86-95
  Developed       0     0     0    90   387    35
  Developing     19   296   549  1150   392    10
```

VISUALIZATION : Stacked bar plot



2. Is there any relationship between the above 2 categorical variables. We need chisquare test for finding this.

HO : No relation between 'lifeExp.agegroup' and 'Status'

```
> chisq.test(tbl_ag_S)

        Pearson's Chi-squared test

data:  tbl_ag_S
X-squared = 945.91, df = 5, p-value < 2.2e-16
```

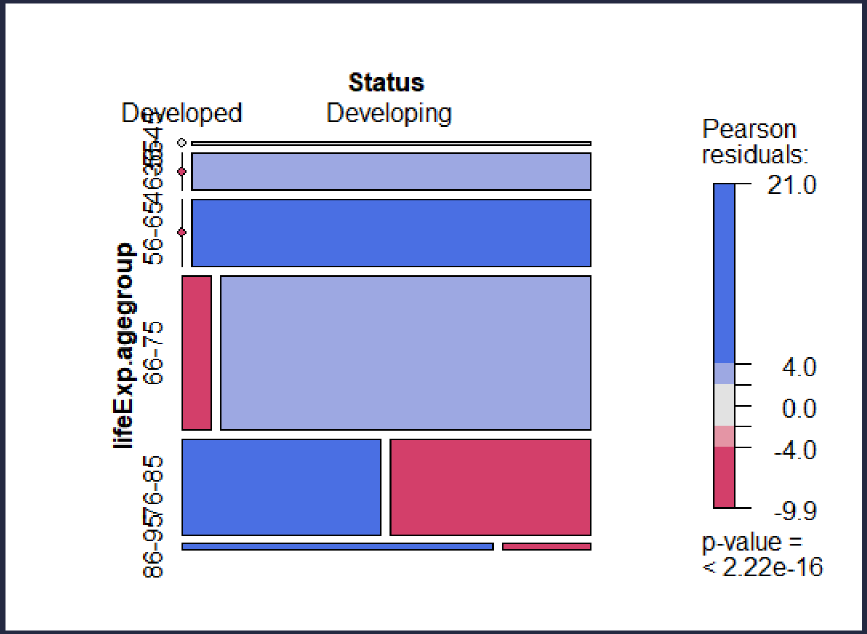
Since p-value is less than 0.05 significance level. We reject the NULL hypothesis.

There is a relation between 'lifeExp.agegroup' and 'Status'

```
> prop.table(table(df1$lifeExp.agegroup, df1$Status))#calculates  probability of frequenc

        Developed  Developing
 36-45 0.000000000 0.006489071
 46-55 0.000000000 0.101092896
 56-65 0.000000000 0.187500000
 66-75 0.030737705 0.392759563
 76-85 0.132172131 0.133879781
 86-95 0.011953552 0.003415301
```

```
> mosaic(tbl_ag_S, shade=TRUE, legend=TRUE)
```



Since, the probability of contingency table is ‘0’. The 2 variables are DEPENDENT

A mosaic plot is a visual representation of the association between two variables.

BIVARIATE ANALYSIS : NUMERIC Vs. CATEGORICAL

Summarizing : Using aggregate function

Here The life Expectancy in Developed countries is 79 years and Developing countries is 67 years.

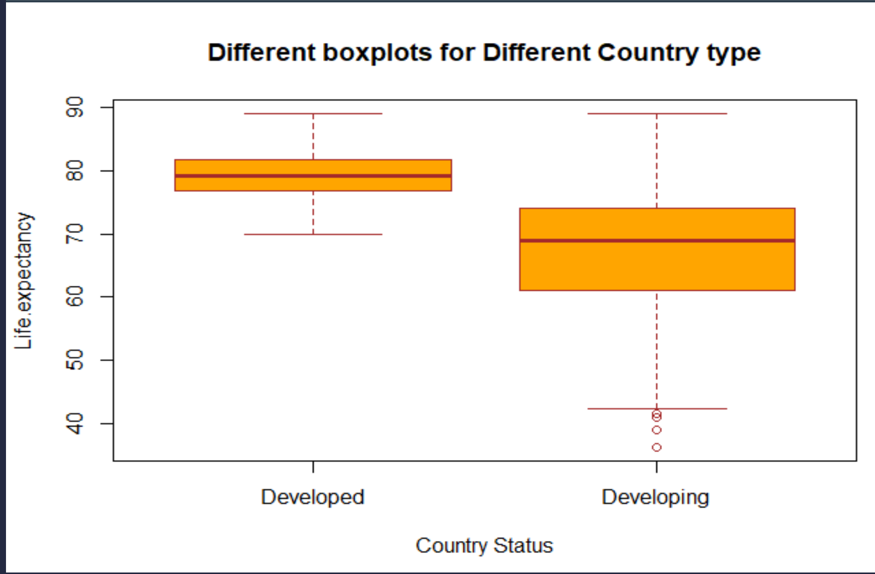
Number of Adult deaths is less in Developed countries than Developing countries

```
> tbba1<-aggregate(Life.expectancy~Status, data=df1, FUN=mean)
> tbba1
     Status Life.expectancy
1  Developed        79.19785
2 Developing        67.11147
>
```

```
tbba2<-aggregate(Adult.Mortality~Status, data=df1, FUN=mean)
tbba2
     Status Adult.Mortality
 Developed        79.68555
Developing       182.83320
```

```
# 2. VISUALIZING USING GROUP BOX PLOT

boxplot(Life.expectancy~Status,
        data=df1,
        main="Different boxplots for Different Country type",
        xlab="Country Status",
        ylab="Life.expectancy",
        col="orange",
        border="brown"
)
```




```
# t-test
t.test(Life.expectancy~Status, data = df1, alternative = "greater")
```

Ho: The mean of 2 groups is equal

```
> t.test(Life.expectancy~Status, data = df1, alternative = "greater")

	Welch Two Sample t-test

data:  Life.expectancy by Status
t = 47.868, df = 1807, p-value < 2.2e-16
alternative hypothesis: true difference in means is greater than 0
95 percent confidence interval:
 11.67086      Inf
sample estimates:
 mean in group Developed mean in group Developing
                79.19785                 67.11147
```

CHECKING Relationship(independence) USING T-TEST Since we have only 2 levels

The NULL Hypothesis is False. We Reject the Hypothesis.

Since p-value is < 0.05(5%) significance level .

The mean of 2 groups is statistically different from each other.

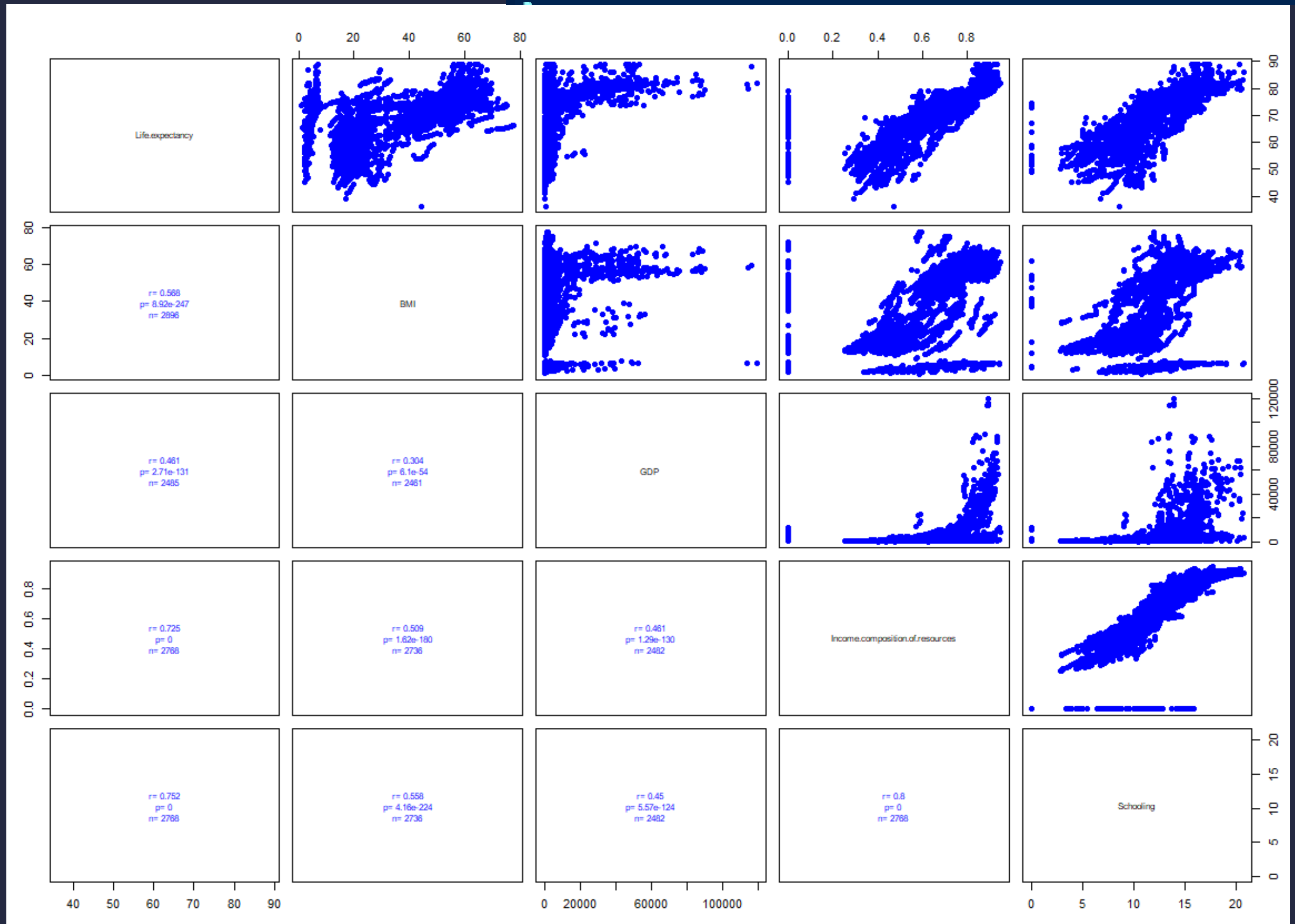
3. Which predicting features are positively co-related To Target

```
panel.cor1 <- function(x, y, cex.cor = 0.8, metho
  options(warn = -1)                          # Turn off
  usr <- par("usr"); on.exit(par(usr)) # Saves cu
  par(usr = c(0, 1, 0, 1))                    # Set plot
  r <- cor(x, y, method = method, use = "pair")
  p <- cor.test(x, y, method = method)$p.val
  n <- sum(complete.cases(x, y))
  txt <- format(r, digits = 3)
  txt1 <- format(p, digits = 3)
  txt2 <- paste0("r= ", txt, '\n', "p= ", txt1, '
  text(0.5, 0.5, txt2, cex = cex.cor, ...)
  options(warn = 0)
```

After visualizing the scatter plots of Life Expectancy with all other Continuous

Variables using “pairs()” came to a conclusion that

```
pairs(df1[,c(4,11,17,19,20)], pch=19, col="blue",lower.panel = panel.cor1)
```



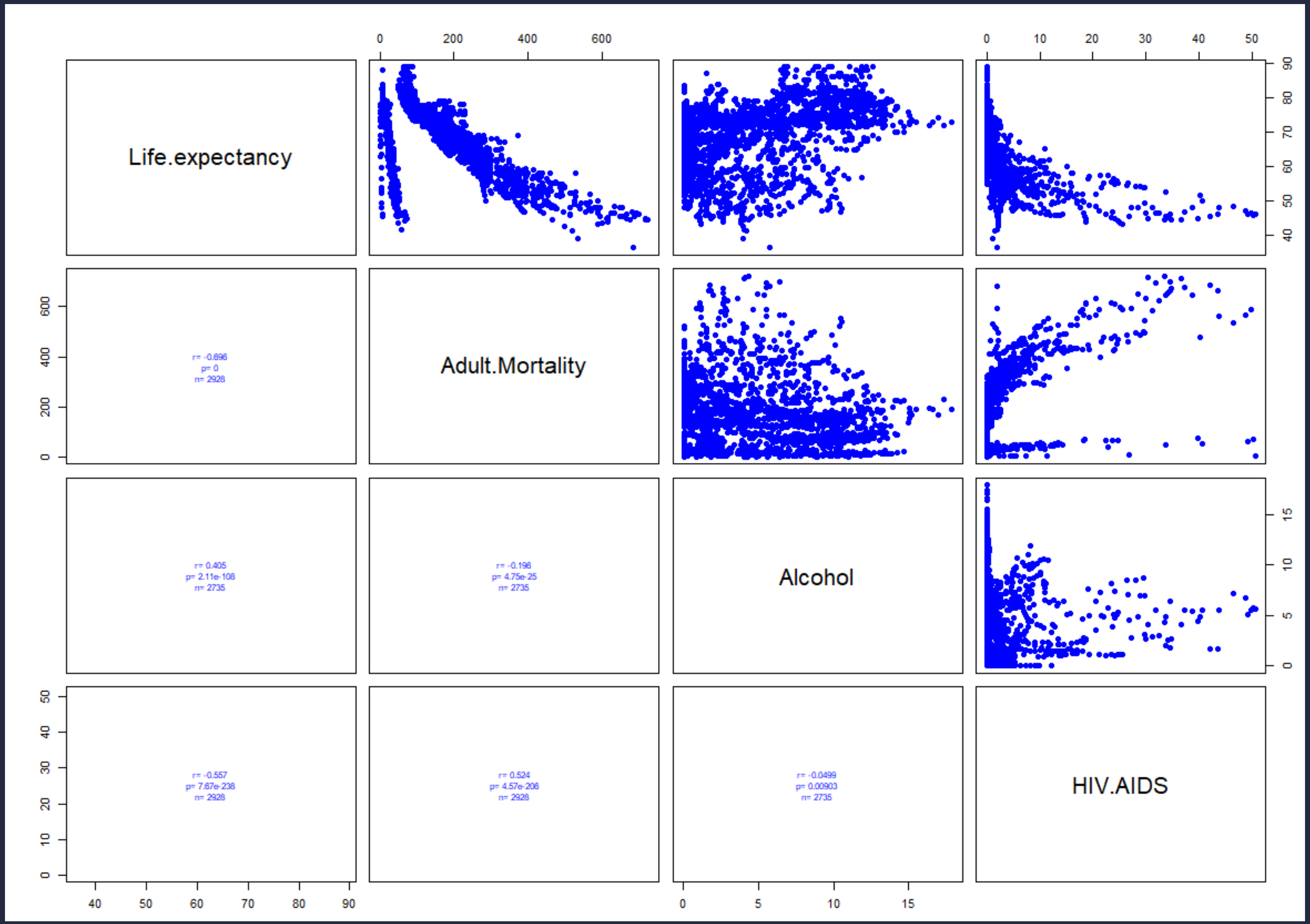
Life.Expectancy has positive co-relation with

- GDP,
- Income.composition.of Resources
- Schooling
- BMI

4. Q: Which features are negatively co-related to Target.

```
pairs(df1[,c(4,5,7,16)], pch=19, col="blue", lower.panel = panel.cor1)
```

Life.Expectancy shows strong negatively linear co-relation with Adult.Mortality and HIV.AIDS .

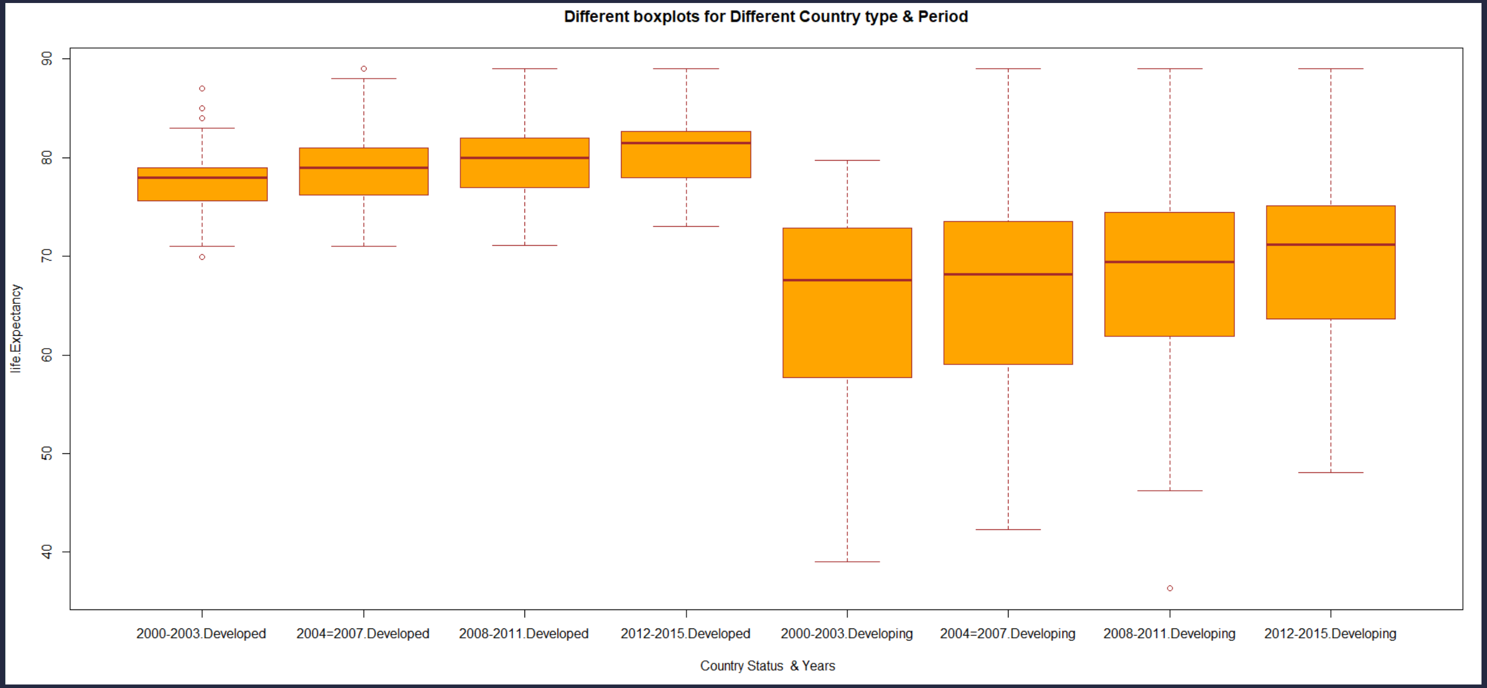


Q : 5 . What do you interpret regarding the Target Life Expectancy as the Years Pass by.

```
# Bivariate Analysis of Target(numerical) and Year.groups & (categorical)
# 1.SUMMARIZING
aggregate(Life.expectancy~Status+Year.groups, data=df1, FUN=mean)  # group
 str(df1)
 # 2. VISUALIZING
 boxplot(Life.expectancy~Year.groups+Status,
         data=df1,
         main="Different boxplots for Different Country type & Age group",
         xlab=" Country Status  & Years",
         ylab="life.Expectancy",
         col="orange",
         border="brown"
 )
```

Answer: The Range of Life.Expectancy for Developed countries is less than the Developing Countries.It is in increasing order from 2000 to 2015.

But, when we compare the Developed and Developing Countries, Life Expectancy of Developed countries is Higher than Developing Countries.



Conclusion:

By focusing on factors that are contributing for positive co-relation on Life-Expectancy, Developing Countries can focus on them and try to improve those factors in order to improve their Life-Expectancy and by focusing on factors that are negatively co-related, countries can try and take measures to mitigate their effect.