MACHINE LEARNING PROJECT

Project Name: Life Expectancy Prediction Using Machine Learning

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Abstract

Life Expectancy is an important metric to assess the health of a nation. This project presents a comparative analysis of life expectancy between developed and developing countries with the help of a Supervised Machine Learning model.

The prediction model is trained using three regression models, namely Random Forest Regressor, DecisionTreeRegressor, LinearRegression.

The selection of model is done on the basis of R 2 score & Mean Squared Error .

Random Forest Regressor is selected for the development of the prediction model for life expectancy, as it had R2 score as 0.99 and 0.95 on training & testing data respectively.

The study undertaken suggests that, developed countries have high life expectancy as compared to developing countries. India has high adult mortality as compared to considered developed countries because of the low expenditure on healthcare. The insights from this analysis can be used by Government and Healthcare sectors for the betterment of society.

1. Importing Required libraries

In [1]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import random
from scipy.stats.mstats import winsorize
from sklearn.preprocessing import LabelEncoder, MinMaxScaler
from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestRegressor
from sklearn.linear_model import LinearRegression
from sklearn.metrics import mean_absolute_error,r2_score
from sklearn.tree import DecisionTreeRegressor
from sklearn.metrics import mean_absolute_percentage_error as mape, mean_squared_error as mse
import warnings
warnings.filterwarnings('ignore')
```

2. Reading the Dataset

In [2]:
```
data=pd.read_csv('Life Expectancy Data.csv')
```

In [3]:
```
data.head()
```

Out[3]:

	Country	Year	Status	Life expectancy	Adult Mortality	infant deaths	Alcohol	percentage expenditure	Hepatitis B	Measles	...	Polio	Total expenditure	Diphtheria	HIV/AIDS	GD
0	Afghanistan	2015	Developing	65.0	263.0	62	0.01	71.279624	65.0	1154	...	6.0	8.16	65.0	0.1	584.2592
1	Afghanistan	2014	Developing	59.9	271.0	64	0.01	73.523582	62.0	492	...	58.0	8.18	62.0	0.1	612.6965
2	Afghanistan	2013	Developing	59.9	268.0	66	0.01	73.219243	64.0	430	...	62.0	8.13	64.0	0.1	631.7449
3	Afghanistan	2012	Developing	59.5	272.0	69	0.01	78.184215	67.0	2787	...	67.0	8.52	67.0	0.1	669.9590
4	Afghanistan	2011	Developing	59.2	275.0	71	0.01	7.097109	68.0	3013	...	68.0	7.87	68.0	0.1	63.5372

5 rows × 22 columns

In [4]:
```
data.shape
```

Out[4]:
```
(2938, 22)
```

Our Dataset contain 2938 rows and 22 columns

Columns Meaning

Country : Country

Year : Year

Status : Country Developed or Developing status

Life expectancy : Life expectancy in age

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

infant deaths : Number of Infant Deaths per 1000 population

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

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

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

Measles : Measles - number of reported cases per 1000 population

BMI : Average Body Mass Index of entire population

under-five deaths : Number of under-five deaths per 1000 population

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

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

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

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

GDP : Gross Domestic Product per capita (in USD)

Population : Population of the country

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

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

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

Schooling : Number of years of Schooling(years)

In [5]:
```
# A Quick information about the data

data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 2938 entries, 0 to 2937
Data columns (total 22 columns):
 #   Column                           Non-Null Count  Dtype  
---  ------                           --------------  -----  
 0   Country                          2938 non-null   object 
 1   Year                             2938 non-null   int64  
 2   Status                           2938 non-null   object 
 3   Life expectancy                  2928 non-null   float64
 4   Adult Mortality                  2928 non-null   float64
 5   infant deaths                    2938 non-null   int64  
 6   Alcohol                          2744 non-null   float64
 7   percentage expenditure           2938 non-null   float64
 8   Hepatitis B                      2385 non-null   float64
 9   Measles                          2938 non-null   int64  
 10   BMI                             2904 non-null   float64
 11  under-five deaths                2938 non-null   int64  
 12  Polio                            2919 non-null   float64
 13  Total expenditure                2712 non-null   float64
 14  Diphtheria                       2919 non-null   float64
 15   HIV/AIDS                        2938 non-null   float64
 16  GDP                              2490 non-null   float64
 17  Population                       2286 non-null   float64
 18   thinness  1-19 years            2904 non-null   float64
 19   thinness 5-9 years              2904 non-null   float64
 20  Income composition of resources  2771 non-null   float64
 21  Schooling                        2775 non-null   float64
dtypes: float64(16), int64(4), object(2)
memory usage: 505.1+ KB
```

There are some leading and trailing spaces in column names so i will remove them for further operations

In [6]:
```
data.rename(str.strip ,axis='columns' , inplace=True)
columns=data.columns
new_cols=[]
for i in columns:
    new_cols.append(i.strip().replace(' ','_'))
data.columns=new_cols
```

The columnnames are Now in understandable format without any spaces

In [7]:
```
# As this columnname must be corrected with 10 to 19 not 1 to 19
data.rename(columns={'thinness__1-19_years':'thinness_10_19_years'},inplace=True)
```

In [8]:
```
# Statistical information of all numerical columns
data.describe()
```

Out[8]:

	Year	Life_expectancy	Adult_Mortality	infant_deaths	Alcohol	percentage_expenditure	Hepatitis_B	Measles	BMI	under-five_deaths
count	2938.000000	2928.000000	2928.000000	2938.000000	2744.000000	2938.000000	2385.000000	2938.000000	2904.000000	2938.000000
mean	2007.518720	69.224932	164.796448	30.303948	4.602861	738.251295	80.940461	2419.592240	38.321247	42.035739
std	4.613841	9.523867	124.292079	117.926501	4.052413	1987.914858	25.070016	11467.272489	20.044034	160.445548
min	2000.000000	36.300000	1.000000	0.000000	0.010000	0.000000	1.000000	0.000000	1.000000	0.000000
25%	2004.000000	63.100000	74.000000	0.000000	0.877500	4.685343	77.000000	0.000000	19.300000	0.000000
50%	2008.000000	72.100000	144.000000	3.000000	3.755000	64.912906	92.000000	17.000000	43.500000	4.000000
75%	2012.000000	75.700000	228.000000	22.000000	7.702500	441.534144	97.000000	360.250000	56.200000	28.000000
max	2015.000000	89.000000	723.000000	1800.000000	17.870000	19479.911610	99.000000	212183.000000	87.300000	2500.000000

3. Missing Values Detection

In [5]:
```
data.describe().iloc[:,1:] #skipped the 'Year' feature
```

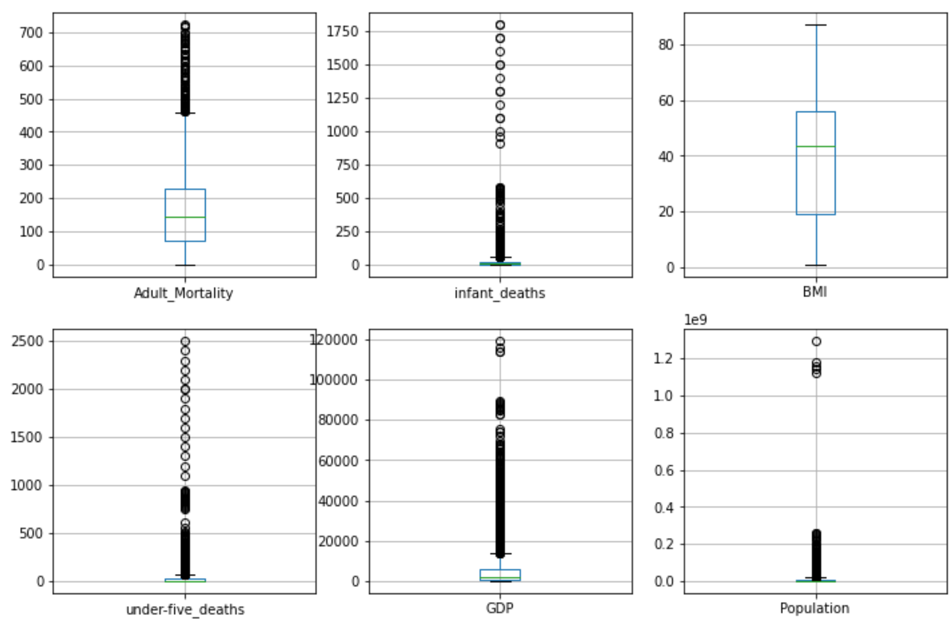
Out[5]:

	Life_expectancy	Adult_Mortality	infant_deaths	Alcohol	percentage_expenditure	Hepatitis_B	Measles	BMI	under-five_deaths	Polio
count	2928.000000	2928.000000	2938.000000	2744.000000	2938.000000	2385.000000	2938.000000	2904.000000	2938.000000	2919.000000
mean	69.224932	164.796448	30.303948	4.602861	738.251295	80.940461	2419.592240	38.321247	42.035739	82.550188
std	9.523867	124.292079	117.926501	4.052413	1987.914858	25.070016	11467.272489	20.044034	160.445548	23.428046
min	36.300000	1.000000	0.000000	0.010000	0.000000	1.000000	0.000000	1.000000	0.000000	3.000000
25%	63.100000	74.000000	0.000000	0.877500	4.685343	77.000000	0.000000	19.300000	0.000000	78.000000
50%	72.100000	144.000000	3.000000	3.755000	64.912906	92.000000	17.000000	43.500000	4.000000	93.000000
75%	75.700000	228.000000	22.000000	7.702500	441.534144	97.000000	360.250000	56.200000	28.000000	97.000000
max	89.000000	723.000000	1800.000000	17.870000	19479.911610	99.000000	212183.000000	87.300000	2500.000000	99.000000

Things that may not make sense from above:

- Adult mortality of 1? The adult mortality is the probability of death between age 15 to 60. This is likely an error in measurement, but what values make sense here? May need to change to null if under a certain threshold.
- Infant deaths as low as 0 per 1000? That just isn't plausible - I'm deeming those values to actually be null. Also on the other end 1800 is likely an outlier, but it is possible in a country with very high birthrates and perhaps a not very high population total - this can be dealt with later.
- BMI of 1 and 87.3? Pretty sure the whole population would not exist if that were the case. A BMI of 15 or lower is seriously underweight and a BMI of 40 or higher is morbidly obese, therefore a large number of these measurements just seem unrealistic...this variable might not be worth digging into at all.
- Under Five Deaths, similar to infant deaths just isn't likely (perhaps even impossible) to have values at zero.
- GDP per capita as low as 1.68 (USD) possible? Doubtful - but perhaps values this low are outliers.
- Population of 34 for an entire country?

In [9]:
```
plt.figure(figsize=(12,8))
for i, col in enumerate(['Adult_Mortality','infant_deaths','BMI','under-five_deaths','GDP','Population']):
    plt.subplot(2,3,i+1)
    data.boxplot(col)
```



There are a few of the above that could simply be outliers, but there are some that almost certainly have to be errors of some sort. Of the above variables, changes to null will be made for the following since these numbers don't make any sense:

1) Adult mortality rates lower than the 5th percentile

2) Infant deaths of 0

3) BMI less than 10 and greater than 50

4) Under Five deaths of 0

The features having some errors to be corrected to the certain threshold

In [10]:
```
# to replace null at the adult mortality of less than 5 percentile
mort_5_percentile = np.percentile(data.Adult_Mortality.dropna(), 5)
data.Adult_Mortality = data.apply(lambda x: np.nan if x.Adult_Mortality < mort_5_percentile else x.Adult_Mortality, axis=1)

# to replace the 0 infantdeaths with null
data.infant_deaths = data.infant_deaths.replace(0, np.nan)

#To replace the bmi less than 10 or greater than 50 with null
data.BMI = data.apply(lambda x: np.nan if (x.BMI < 10 or x.BMI > 50) else x.BMI, axis=1)

#replace 0s with null in under five deaths
data['under-five_deaths'] = data['under-five_deaths'].replace(0, np.nan)
```

In [11]:
```
# Checking for null/missing values
data.isnull().sum()
```

Out[11]:
```
Country                               0
Year                                  0
Status                                0
Life_expectancy                      10
Adult_Mortality                     155
infant_deaths                       848
Alcohol                             194
percentage_expenditure                0
Hepatitis_B                         553
Measles                               0
BMI                                1456
under-five_deaths                   785
Polio                                19
Total_expenditure                   226
Diphtheria                           19
HIV/AIDS                              0
GDP                                 448
Population                          652
thinness_10_19_years                 34
thinness_5-9_years                   34
Income_composition_of_resources     167
Schooling                           163
dtype: int64
```

```
It appears that there are a decent amount of null values, may be of more use to break down the data into those that contain
nulls in order to take a closer look.
```

Nearly half of the BMI variable's values are null,, it is likely best to remove this variable altogether.

In [12]:
```
data.drop(columns='BMI', inplace=True) #As total rows are 2938 out of 1456 are null
```

Alright, so it looks like there are a lot of columns containing null values, since this is time series data assorted by country, the best course of action would be to interpolate the data by country. However, when attempting to interpolate by country it doesn't fill in any values as the countries' data for all the null values are null for each year, therefore imputation by year may be the best possible method here. Imputation of each year's mean is done below.

Replacing Null values with the median as there are some outliers in our data

In the following loop, the null values are filled with mean of the column where the year is same

In [13]:
```
imputed_data = []
for year in list(data.Year.unique()):
    year_data = data[data.Year == year].copy()
    for col in list(year_data.columns)[3:]:
        year_data[col] = year_data[col].fillna(year_data[col].dropna().median()).copy()
    imputed_data.append(year_data)
data = pd.concat(imputed_data).copy()
```

In [14]:
```
data.describe()
```

Out[14]:

	Year	Life_expectancy	Adult_Mortality	infant_deaths	Alcohol	percentage_expenditure	Hepatitis_B	Measles	under-five_deaths	Polio
count	2938.000000	2938.000000	2938.000000	2938.000000	2938.000000	2938.000000	2938.000000	2938.000000	2938.000000	2938.000000
mean	2007.518720	69.238462	171.768890	32.958816	4.637600	738.251295	82.644656	2419.592240	44.970558	82.605344
std	4.613841	9.510459	118.943766	117.316899	3.921306	1987.914858	22.881890	11467.272489	159.749128	23.362728
min	2000.000000	36.300000	13.000000	1.000000	0.010000	0.000000	1.000000	0.000000	1.000000	3.000000
25%	2004.000000	63.200000	84.000000	4.000000	1.082500	4.685343	82.000000	0.000000	4.000000	78.000000
50%	2008.000000	72.100000	148.000000	9.000000	4.100000	64.912906	91.000000	17.000000	11.000000	93.000000
75%	2012.000000	75.600000	227.000000	22.000000	7.390000	441.534144	96.000000	360.250000	28.000000	97.000000
max	2015.000000	89.000000	723.000000	1800.000000	17.870000	19479.911610	99.000000	212183.000000	2500.000000	99.000000

In [15]:
```
data.isnull().sum()
```

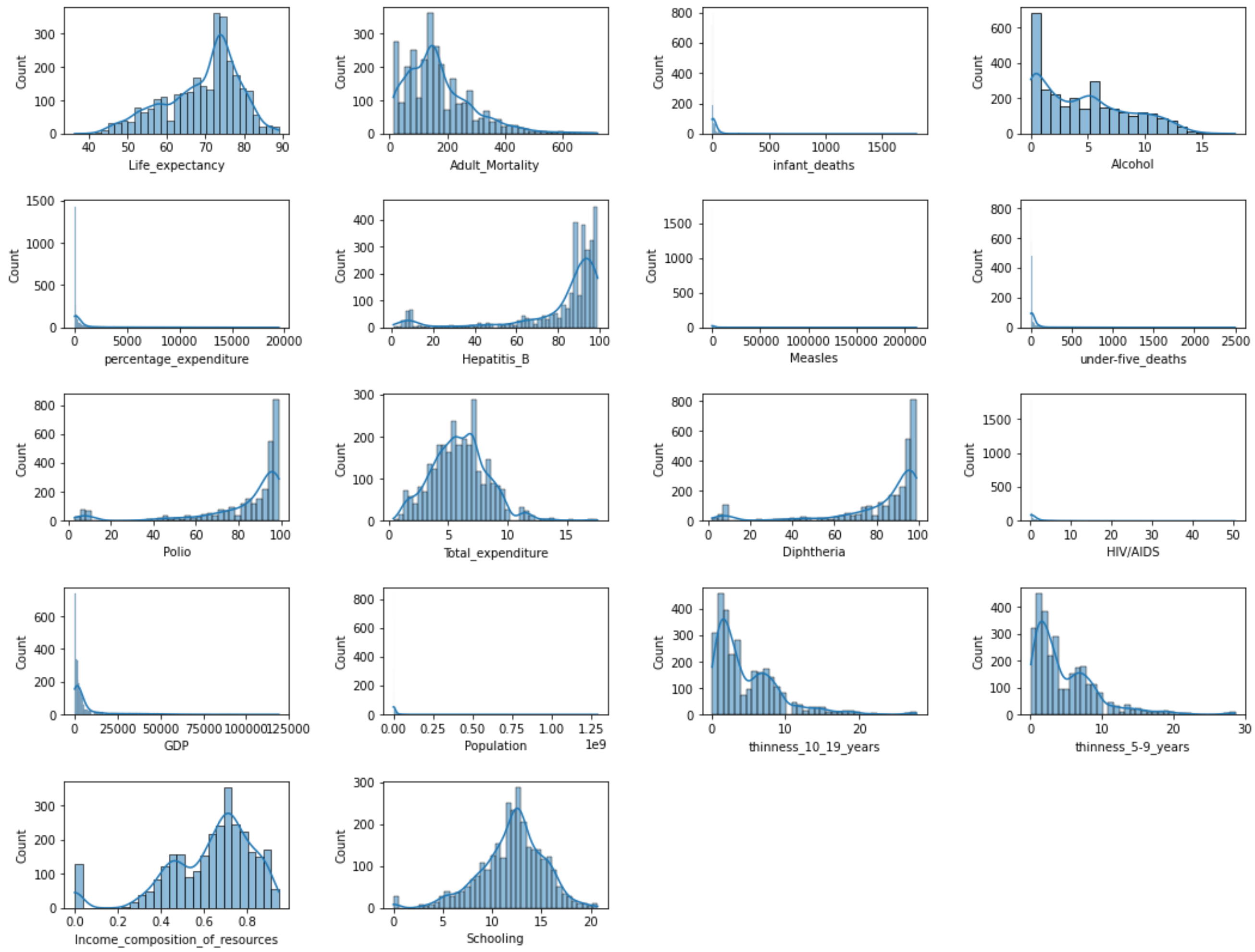
Out[15]:
```
Country                            0
Year                               0
Status                             0
Life_expectancy                    0
Adult_Mortality                    0
infant_deaths                      0
Alcohol                            0
percentage_expenditure             0
Hepatitis_B                        0
Measles                            0
under-five_deaths                  0
Polio                              0
Total_expenditure                  0
Diphtheria                         0
HIV/AIDS                           0
GDP                                0
Population                         0
thinness_10_19_years               0
thinness_5-9_years                 0
Income_composition_of_resources    0
Schooling                          0
dtype: int64
```

We have successfully replaced the missing values with medians

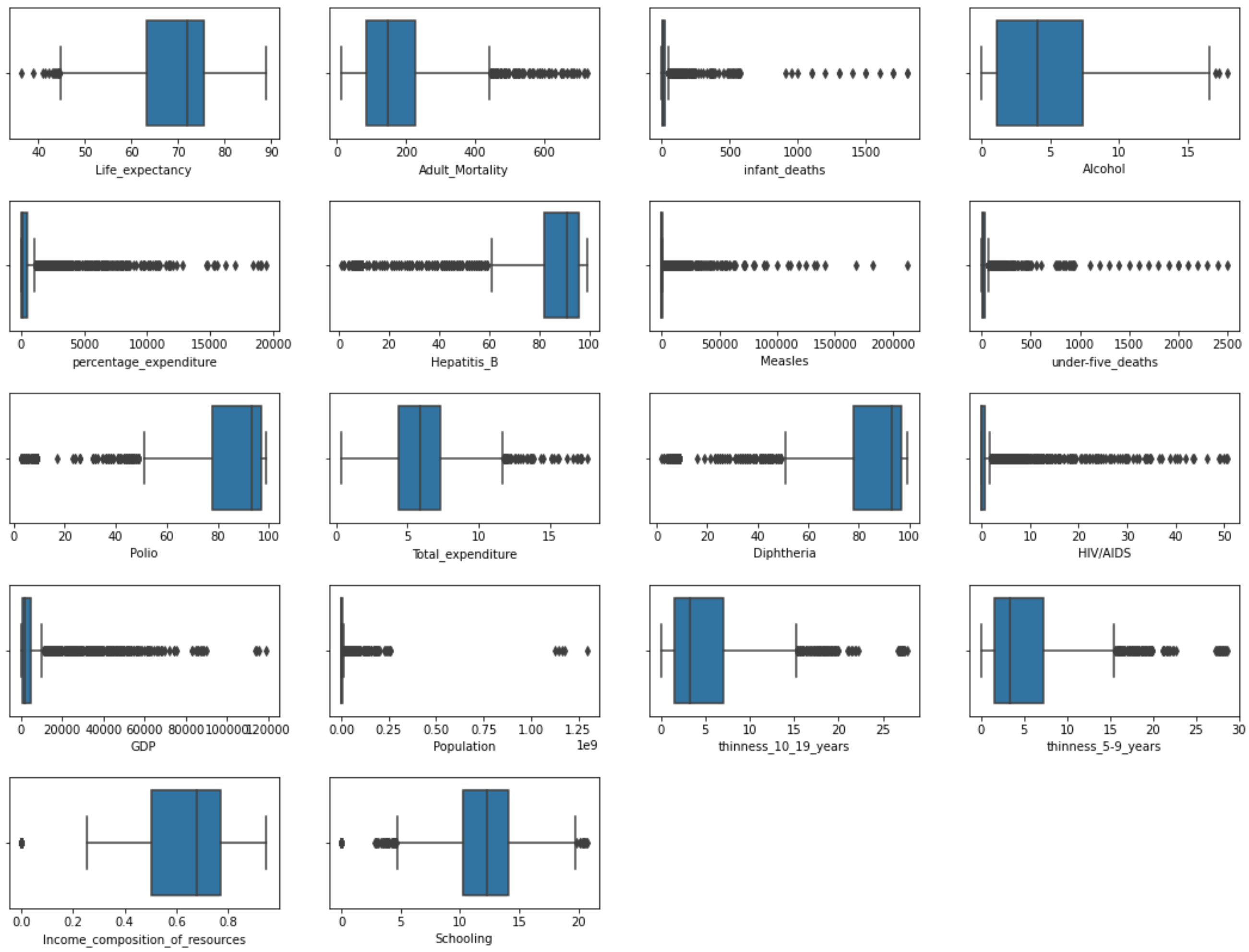
4. Outliers Detection

In [16]:
```
data_num=data.select_dtypes(exclude=object).columns.tolist()
data_num.remove('Year')
```

In [17]:
```
plt.figure(figsize=(15,20))
for i, col in enumerate(data_num):
    plt.subplot((len(data_num) + 1) // 2, 4, i+1 )
    sns.histplot(x=col,data=data,kde=True)
plt.tight_layout(pad = 2)
```



In [18]:
```
plt.figure(figsize=(15,20))
for i, col in enumerate(data_num):
    plt.subplot((len(data_num) + 1) // 2, 4, i+1 )
    sns.boxplot(x=col,data=data)
plt.tight_layout(pad = 2)
```



Visually, it is plain to see that there are a number of outliers for all of these variables - including the target variable, life expectancy. Firstly i am calculating the total outliers using IQR method. outliers being considered anything outside of 1.5 times the IQR.

In [19]:
```
outliersless = []
outliersgreat=[]
def detect_outliers_iqr(data):
    data = sorted(data)
    q1 = np.percentile(data, 25)
    q3 = np.percentile(data, 75)
    # print(q1, q3)
    IQR = q3-q1
    lwr_bound = q1-(1.5*IQR)
    upr_bound = q3+(1.5*IQR)
    # print(lwr_bound, upr_bound)
    for i in data:
        if i<lwr_bound:
            outliersless.append(i)
        if i>upr_bound:
            outliersgreat.append(i)

    return outliersless,outliersgreat # Driver code


for col in data_num:
    outliersless , outliersgreat = detect_outliers_iqr(data[col])
    print(f"Outliers of {col}: lessmin: {len(outliersless)} greatermax: {len(outliersgreat)}")
    outliersless.clear(),outliersgreat.clear()
```

```
Outliers of Life_expectancy: lessmin: 17 greatermax: 0
Outliers of Adult_Mortality: lessmin: 0 greatermax: 97
Outliers of infant_deaths: lessmin: 0 greatermax: 374
Outliers of Alcohol: lessmin: 0 greatermax: 3
Outliers of percentage_expenditure: lessmin: 0 greatermax: 389
Outliers of Hepatitis_B: lessmin: 322 greatermax: 0
Outliers of Measles: lessmin: 0 greatermax: 542
Outliers of under-five_deaths: lessmin: 0 greatermax: 418
Outliers of Polio: lessmin: 279 greatermax: 0
Outliers of Total_expenditure: lessmin: 0 greatermax: 51
Outliers of Diphtheria: lessmin: 298 greatermax: 0
Outliers of HIV/AIDS: lessmin: 0 greatermax: 542
Outliers of GDP: lessmin: 0 greatermax: 445
Outliers of Population: lessmin: 0 greatermax: 452
Outliers of thinness_10_19_years: lessmin: 0 greatermax: 100
Outliers of thinness_5-9_years: lessmin: 0 greatermax: 99
Outliers of Income_composition_of_resources: lessmin: 130 greatermax: 0
Outliers of Schooling: lessmin: 64 greatermax: 13
```

Since each variable has a unique amount of outliers and also has outliers on different sides of the data, the best route to take is probably replacing the values with 25 percentile and 75 percentile for each side of the data.

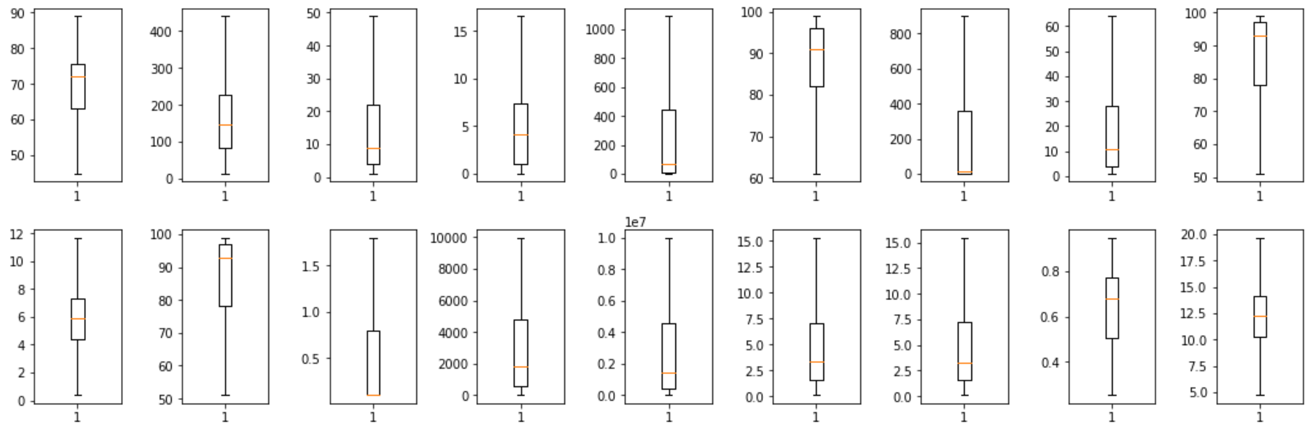
In [20]:
```
for col in data_num:
    outliersless , outliersgreat = detect_outliers_iqr(data[col])
    mi=np.percentile(data[col],25)
    ma=np.percentile(data[col],75)
    data[col].replace(to_replace=outliersless,value=mi,inplace=True)
    data[col].replace(to_replace=outliersgreat,value=ma,inplace=True)

    outliersless.clear(),outliersgreat.clear()
```

All the variables have now been replaced as little as possible in order to keep as much data in tact as possible while still being able to eliminate the outliers.

Finally, bellow boxplots will be shown for each variable's replaced data to show that the outliers have indeed been dealt with.

In [22]:
```
plt.figure(figsize=(15,5))
for i, col in enumerate(data_num, 1):
    plt.subplot(2, 9, i)
    plt.boxplot(data[col])
plt.tight_layout()
plt.show()
```

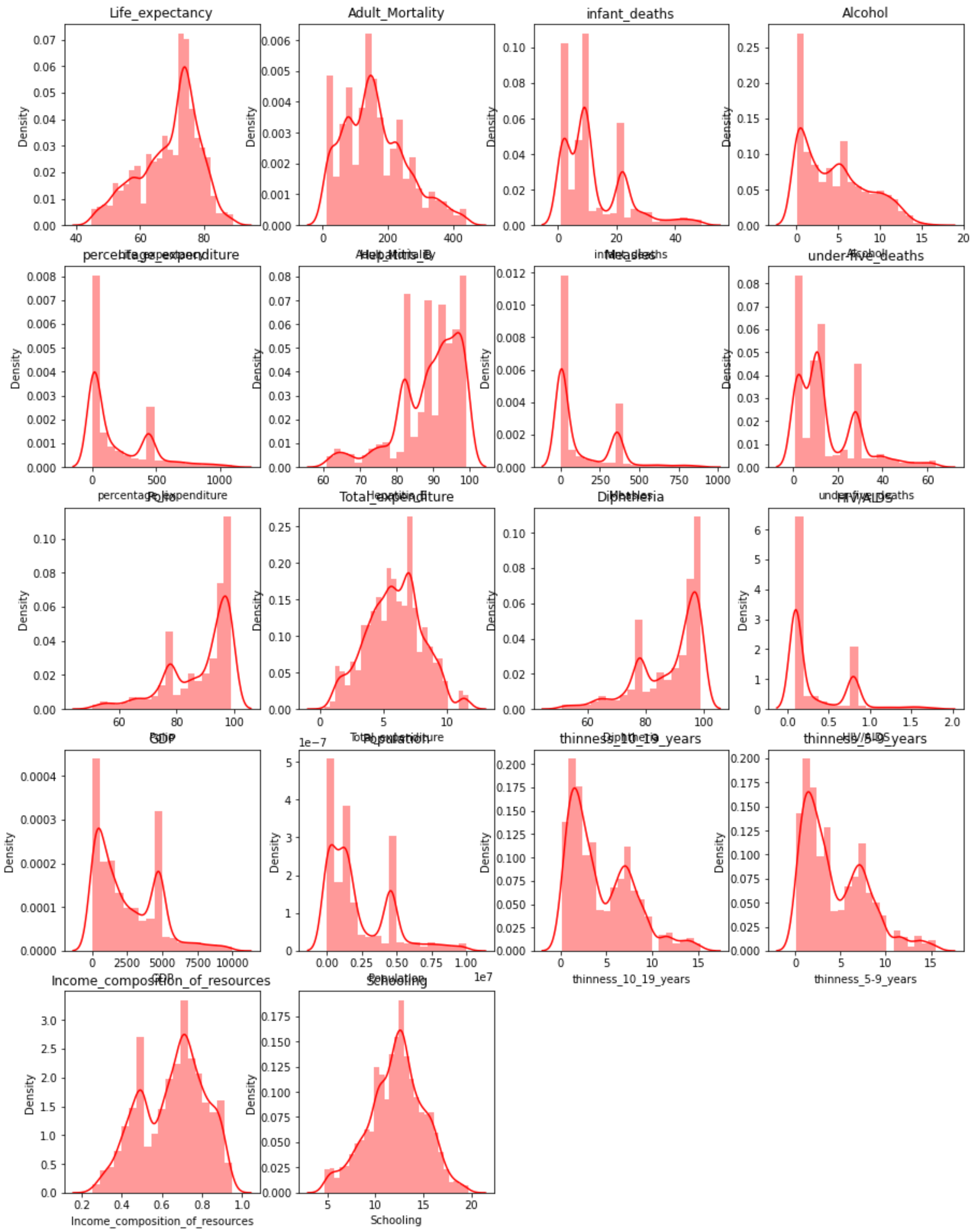


Now that the outliers have been dealt with, the data cleaning section is complete.

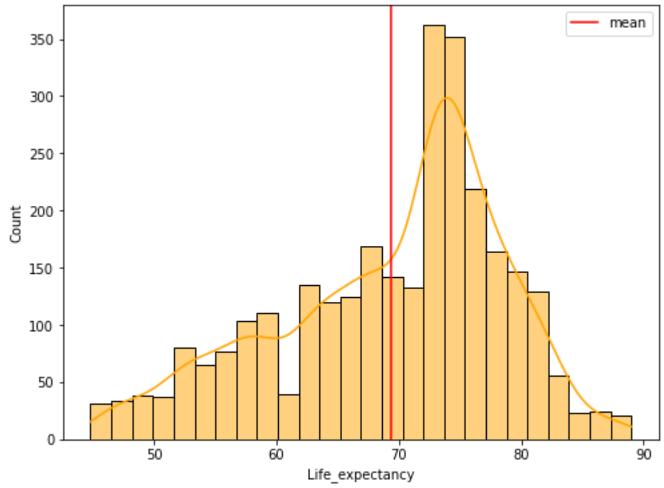
5. Data Exploration

The following histogram shows the distribution of each feature

In [23]:
```
plt.figure(figsize=(15,20))
for i ,col in enumerate(data_num,1):
    plt.subplot(5,4,i)
    sns.distplot(data[col],color='red')
    plt.title(col)
```



In [24]:
```
plt.figure(figsize=(8,6))
sns.histplot(data['Life_expectancy'],kde=True,color='orange')
plt.axvline(data['Life_expectancy'].mean(),color='red',label='mean')
plt.legend()
plt.show()
```



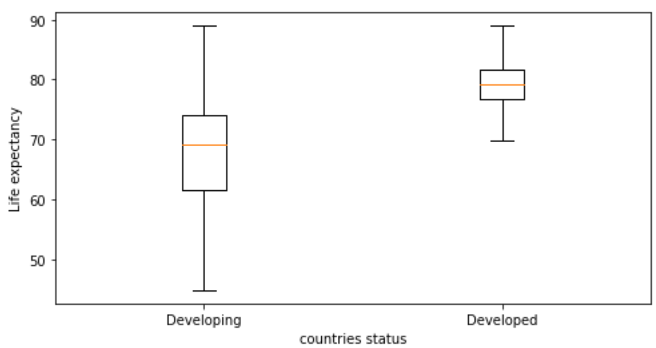
This above graph shows the distribution of **target column i.e. 'Life Expectancy' Most of the lifespan lies between 45 to 90 years, with an average lifespan of 69 years

In [25]:
```
data['Status'].value_counts()
```

Out[25]:
```
Developing    2426
Developed      512
Name: Status, dtype: int64
```

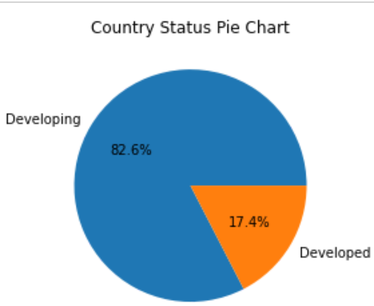
In [27]:
```
plt.figure(figsize=(8,4))
plt.boxplot([data[data['Status']=='Developing']['Life_expectancy'],data[data['Status']=='Developed']['Life_expectancy']],labels=[
plt.ylabel('Life expectancy')
plt.xlabel('countries status')

plt.show()
```



In [28]:
```
plt.pie(data['Status'].value_counts(),labels=data['Status'].value_counts().index,autopct='%1.1f%%')
plt.title('Country Status Pie Chart')

plt.show()
```



This **boxplot** and **pieplot** shows that developed countries are stable because the range of the live expectancy age of developed countries is short, also the developing countries may have very different life expenctacy rates

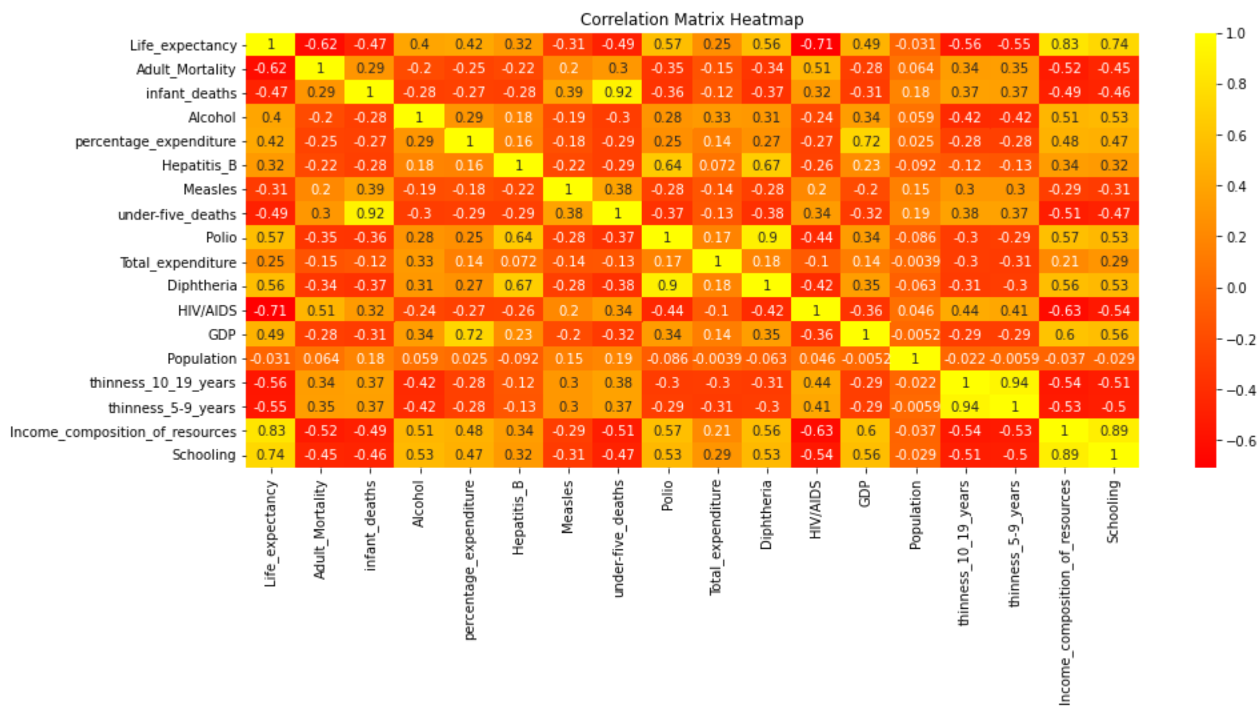
6. Data Visualization

In [29]:
```
data[data_num].corr()
```

Measles	-0.309690	0.202378	0.391352	-0.189626	-0.178267	-0.216784	1.000000	0.382211	-0.2
under-five_deaths	-0.485480	0.300587	0.919662	-0.298072	-0.286503	-0.286027	0.382211	1.000000	-0.3
Polio	0.565206	-0.347217	-0.358004	0.283874	0.249592	0.641416	-0.276787	-0.368972	1.0
Total_expenditure	0.247272	-0.152735	-0.123044	0.325135	0.144441	0.071548	-0.136789	-0.126643	0.1
Diphtheria	0.563065	-0.341228	-0.369474	0.307505	0.269671	0.672338	-0.280304	-0.382251	0.8
HIV/AIDS	-0.706526	0.506421	0.323561	-0.238150	-0.272929	-0.264480	0.200192	0.339920	-0.4
GDP	0.490669	-0.284599	-0.305174	0.341216	0.724438	0.231572	-0.204359	-0.318383	0.3
Population	-0.030806	0.064195	0.175365	0.059358	0.024857	-0.092461	0.149775	0.189046	-0.0
thinness_10_19_years	-0.556720	0.341977	0.369103	-0.423848	-0.275578	-0.123449	0.303943	0.378097	-0.3
thinness_5-9_years	-0.552063	0.347734	0.366175	-0.416844	-0.275418	-0.129564	0.302578	0.373590	-0.2
Income_composition_of_resources	0.825853	-0.522314	-0.486980	0.508111	0.483094	0.343759	-0.288798	-0.507937	0.5
Schooling	0.737758	-0.448980	-0.463912	0.531858	0.468559	0.322454	-0.312215	-0.474732	0.5

Above table shows the correlation

In [30]:
```
plt.figure(figsize=(15,6))
sns.heatmap(data[data_num].corr(), annot=True, cmap='autumn')
plt.title('Correlation Matrix Heatmap')
plt.show()
```



The above heatmap is very useful! It very easily displays a number of important correlations between variables. Some general takeaways from the graphic above:

• Life Expectancy (target variable) appears to be relatively highly correlated (negatively or positively) with:

• Adult Mortality (negative)

• HIV/AIDS (negative)

• Income Composition of Resources (positive)

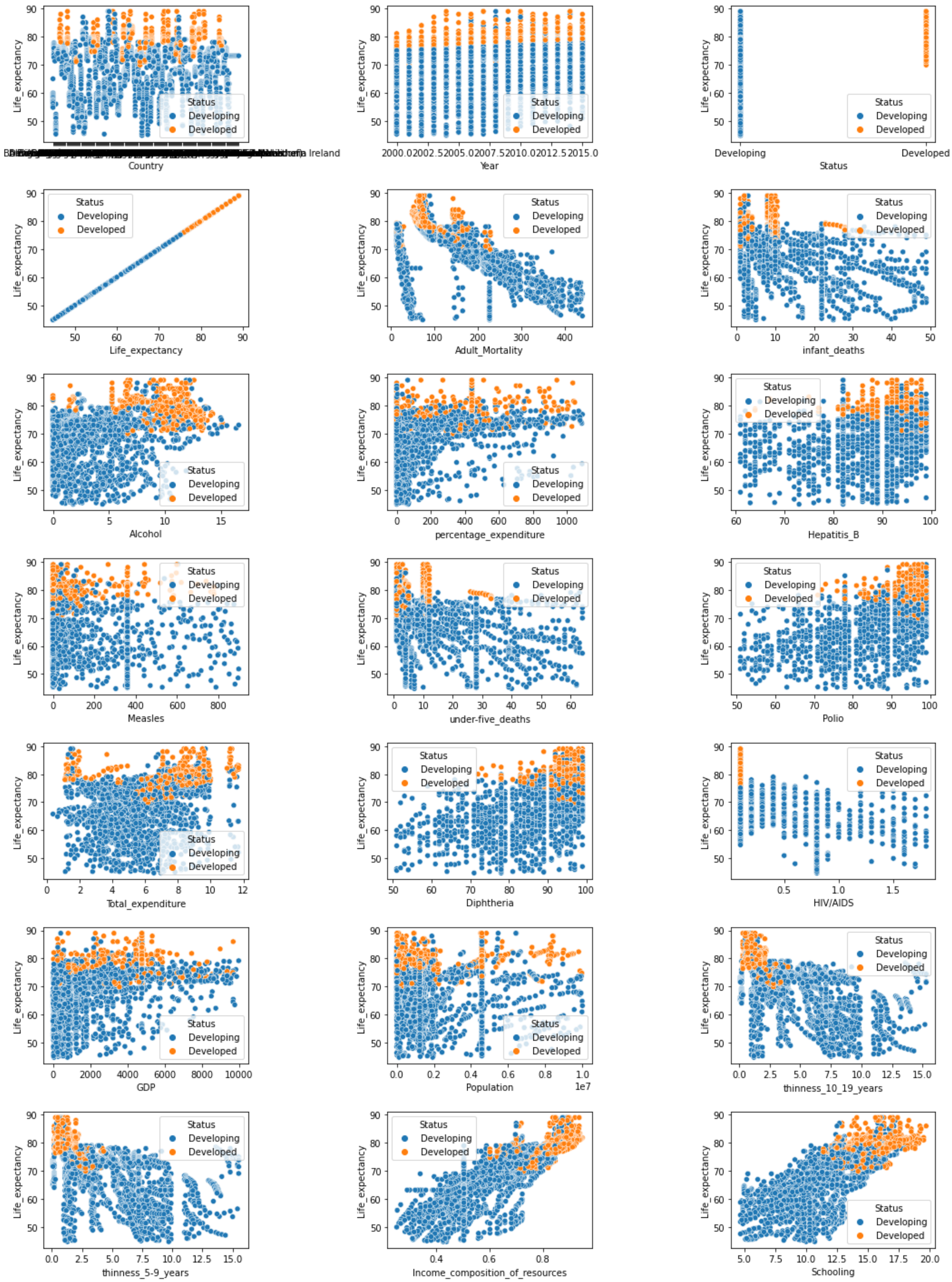
• Schooling (positive)

• Life expectancy (target variable) is extremely lowly correlated to population (nearly no correlation at all)

- Infant deaths and Under Five deaths are extremely highly correlated
- Percentage Expenditure and GDP are relatively highly correlated
- Hepatitis B vaccine rate is relatively positively correlated with Polio and Diphtheria vaccine rates
- Polio vaccine rate and Diphtheria vaccine rate are very positively correlated
- HIV/AIDS is relatively negatively correlated with Income Composition of Resources
- Thinness of 5-9 Year olds rate and Thinness of 10-15 Year olds rate is extremely highly correlated
- Income Composition of Resources and Schooling are very highly correlated

In [32]:
```
plt.figure(figsize=(15,20))
for i ,col in enumerate(data,1):

    plt.subplot(7,3,i)
    sns.scatterplot(x= data[col], y= data['Life_expectancy'], hue=data.Status)
    plt.xlabel(col)
    plt.ylabel('Life_expectancy')
plt.tight_layout(pad = 2)
```



Observation: Life_Expectancy has somewhat Negative relationship with AdultMortality. Life_Expectancy has positive relationship with Income_Comp_Of_Resources and Schooling.

7. Label Encoding

Now we have to do label encoding on the categorical features

In [33]:
```
data_cat=data.select_dtypes(object).columns
```

In [34]:
```
from sklearn.preprocessing import LabelEncoder, MinMaxScaler
```

In [35]:
```
# create object from labelencoder
le = LabelEncoder()
for column in data_cat:
    data[column]=le.fit_transform(data[column])
```

8. Feature selection

separate the target column and independent variables

In [36]:
```
x=data.drop('Life_expectancy',axis=1)
```

In [37]:
```
y=data['Life_expectancy']
```

9. Split the Training and Testing data for the Model training

In [38]:
```
from sklearn.model_selection import train_test_split
```

In [39]:
```
# spliting data to train and test
xtrain, xtest, ytrain, ytest =  train_test_split(x,y, test_size = 0.2, random_state = 42)
```

10. Model Training and Testing

In [40]:
```
alg= [RandomForestRegressor(),DecisionTreeRegressor(), LinearRegression()]
for i in alg:
    model= i
    model.fit(xtrain, ytrain)
    ypredtestdata= model.predict(xtest)
    ypredtraindata= model.predict(xtrain)
    print(i, "Train Root Mean Squared error:", np.sqrt(mse(ytrain, ypredtraindata)))
    print(i, "Train Accuracy:", (r2_score(ytrain, ypredtraindata))*100)
    print("*"*50)
    print(i, "Test Root Mean Squared error:", np.sqrt(mse(ytest, ypredtestdata)))
    print(i, "Test Accuracy:", (r2_score(ytest, ypredtestdata))*100)
    print("="*70)
```

```
RandomForestRegressor() Train Root Mean Squared error: 0.8176879431301571
RandomForestRegressor() Train Accuracy: 99.22452351690009
**************************************************
RandomForestRegressor() Test Root Mean Squared error: 2.1884115352508666
RandomForestRegressor() Test Accuracy: 94.55594113815172
======================================================================
DecisionTreeRegressor() Train Root Mean Squared error: 3.5903095795213697e-16
DecisionTreeRegressor() Train Accuracy: 100.0
**************************************************
DecisionTreeRegressor() Test Root Mean Squared error: 3.1193002442223228
DecisionTreeRegressor() Test Accuracy: 88.93938743321449
======================================================================
LinearRegression() Train Root Mean Squared error: 4.159638678597001
LinearRegression() Train Accuracy: 79.93197378958395
**************************************************
LinearRegression() Test Root Mean Squared error: 4.368581242821021
LinearRegression() Test Accuracy: 78.30569932357476
======================================================================
```

In [41]:
```
alg= [RandomForestRegressor(),DecisionTreeRegressor(), LinearRegression()]
tsscore=[]
trscore=[]
msescore=[]
for index,i in enumerate(alg):
    model= i
    model.fit(xtrain, ytrain)
    y_pred= model.predict(xtest)
    accts_score=r2_score(ytest,y_pred) #test score
    tsscore.append(accts_score*100)
    ypredtr= model.predict(xtrain)
    acctr_score=r2_score(ytrain,ypredtr) #train score
    trscore.append(acctr_score*100)
    ms=np.sqrt(mse(ytest, y_pred)) #mse score
    msescore.append(ms)
```

In [42]:
```
alg= ['RandomForestRegressor()', 'DecisionTreeRegressor()', 'LinearRegression()']
df=pd.DataFrame({'Model':alg,'test_acc_score':tsscore,'train_acc_score':trscore,'MSE_score':msescore})
df
```

Out[42]:

	Model	test_acc_score	train_acc_score	MSE_score
0	RandomForestRegressor()	94.755602	99.231146	2.147907
1	DecisionTreeRegressor()	89.233280	100.000000	3.077580
2	LinearRegression()	78.305699	79.931974	4.368581

From the above results, we can see that almost all the models are giving best accuracy

Random Forest algorithm giving us best accuracy score i.e. 96.16%

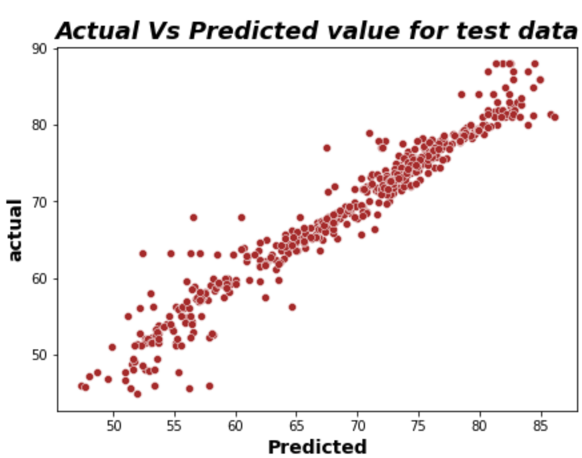
In [44]:
```
from sklearn.ensemble import RandomForestRegressor
rf= RandomForestRegressor()
rf.fit(xtrain, ytrain)
y_pred= rf.predict(xtest)
y_pred2= rf.predict(xtrain)
test_score=r2_score(ytest,y_pred)
print("Test Root Mean Squared error:", round(np.sqrt(mse(ytest, y_pred)),2))

print('R2_score:',test_score*100)
print("Mean Absolute Percentage Error:", round(mape(ytest, y_pred)*100),2)
```

```
Test Root Mean Squared error: 2.18
R2_score: 94.57967060302359
Mean Absolute Percentage Error: 2 2
```

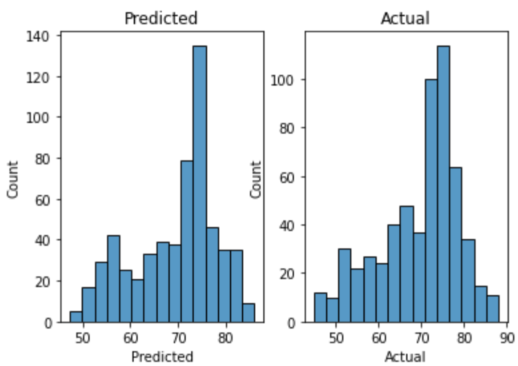
In [45]:
```
plt.figure(figsize= [7,5])
sns.scatterplot(y=ytest, x= y_pred,color= "brown")
plt.title("Actual Vs Predicted value for test data", fontsize= 18,fontweight="bold", fontstyle="italic")
plt.ylabel("actual", fontsize= 14, fontweight="bold")
plt.xlabel("Predicted", fontsize=14, fontweight="bold")
```

Out[45]: Text(0.5, 0, 'Predicted')



In [46]:
```
plt.subplot(1,2,1)
sns.histplot(y_pred)
plt.title("Predicted")
plt.xlabel("Predicted")
plt.subplot(1,2,2)
sns.histplot(ytest)
plt.title("Actual")
plt.xlabel("Actual")
```

Out[46]:
```
Text(0.5, 0, 'Actual')
```



The above graph shows the predicted and actual life expectancy distribution

From the above results, we can see that almost all the models are giving best accuracy

Random Forest algorithm giving us best accuracy score/ R2 score i.e. 94.5%