```python
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
import statsmodels.api as sm
from scipy import stats
```

Description:

Context:

This study analyzes life expectancy data from 2000-2015 from this dataset, focusing on factors such as immunization, mortality, economic, and social aspects. It uses a regression model based on mixed effects model and multiple linear regression, aiming to highlight key contributors to life expectancy. This will assist countries in identifying areas of focus to increase their populations' life expectancy.

Content:

Data for 193 countries is sourced from the Global Health Observatory (GHO) data repository (World Health Organization) and the United Nations. The dataset includes critical health-related factors observed over the past 15 years. After merging individual files and handling missing data (mostly population, Hepatitis B, and GDP data), the final dataset comprises 22 columns and 2938 rows, indicating 20 predicting variables. These predictors fall into categories: immunization-related, mortality, economical, and social factors.

Acknowledgements:

Data collection was facilitated by Deeksha Russell and Duan Wang from the WHO and United Nations websites.

```python
df = pd.read_csv("Life Expectancy Data.csv")
```

```python
df.shape
```

```
(2938, 22)
```

```python
df.head()
```

```
       Country  Year      Status  Life expectancy   Adult Mortality  \
0  Afghanistan  2015  Developing              65.0            263.0
1  Afghanistan  2014  Developing              59.9            271.0
2  Afghanistan  2013  Developing              59.9            268.0
3  Afghanistan  2012  Developing              59.5            272.0
4  Afghanistan  2011  Developing              59.2            275.0

   infant deaths  Alcohol  percentage expenditure  Hepatitis B
Measles   ...  \
0             62     0.01               71.279624         65.0
1154  ...
```

```
1              64     0.01               73.523582        62.0
492  ...
2              66     0.01               73.219243        64.0
430  ...
3              69     0.01               78.184215        67.0
2787  ...
4              71     0.01                7.097109        68.0
3013  ...

   Polio  Total expenditure  Diphtheria    HIV/AIDS         GDP
Population  \
0    6.0               8.16         65.0        0.1  584.259210
33736494.0
1   58.0               8.18         62.0        0.1  612.696514
327582.0
2   62.0               8.13         64.0        0.1  631.744976
31731688.0
3   67.0               8.52         67.0        0.1  669.959000
3696958.0
4   68.0               7.87         68.0        0.1   63.537231
2978599.0

    thinness  1-19 years   thinness 5-9 years  \
0                  17.2                 17.3
1                  17.5                 17.5
2                  17.7                 17.7
3                  17.9                 18.0
4                  18.2                 18.2

   Income composition of resources  Schooling
0                            0.479       10.1
1                            0.476       10.0
2                            0.470        9.9
3                            0.463        9.8
4                            0.454        9.5

[5 rows x 22 columns]
```

```
df.columns = df.columns.str.replace(' ', '_')
```

```
df.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
```

Q1: Our data contains missing values. Determine the percentage of missing data in each column. Is the missingness associated with any other variable? For example, could the data be more likely missing in specific years?

```python
missing_data = df.isnull().mean() * 100
print("Percentage of missing data in each column:")
print(missing_data)
```

```
Percentage of missing data in each column:
Country                             0.000000
Year                                0.000000
Status                              0.000000
Life_expectancy_                    0.340368
Adult_Mortality                     0.340368
infant_deaths                       0.000000
Alcohol                             6.603131
percentage_expenditure              0.000000
Hepatitis_B                        18.822328
Measles_                            0.000000
_BMI_                               1.157250
under-five_deaths_                  0.000000
Polio                               0.646698
Total_expenditure                   7.692308
Diphtheria_                         0.646698
_HIV/AIDS                           0.000000
GDP                                15.248468
Population                         22.191967
_thinness__1-19_years               1.157250
_thinness_5-9_years                 1.157250
```

```
Income_composition_of_resources     5.684139
Schooling                           5.547992
dtype: float64
```

```python
#H0 - there's no significant association between the missingness in
the column and 'year' (p>0.05)
#H1 - there's significant association between the missingness in the
column and 'year' (p<=0.05)

columns = df.columns.tolist()
columns.remove('Year')

for column in columns:
    df['is_missing'] = df[column].isnull()
    contingency_table = pd.crosstab(df['is_missing'], df['Year'])
    chi2, p, dof, expected = stats.chi2_contingency(contingency_table)
    print(f"\nChi-square test between missingness of {column} and
Year:")
    print(f"Chi2 value: {chi2}")
    print(f"P-value: {p}")
```

```
Chi-square test between missingness of Country and Year:
Chi2 value: 0.0
P-value: 1.0

Chi-square test between missingness of Status and Year:
Chi2 value: 0.0
P-value: 1.0

Chi-square test between missingness of Life_expectancy_ and Year:
Chi2 value: 142.71373056994818
P-value: 6.700969304769984e-23

Chi-square test between missingness of Adult_Mortality and Year:
Chi2 value: 142.71373056994818
P-value: 6.700969304769984e-23

Chi-square test between missingness of infant_deaths and Year:
Chi2 value: 0.0
P-value: 1.0

Chi-square test between missingness of Alcohol and Year:
Chi2 value: 2570.0865379816364
P-value: 0.0

Chi-square test between missingness of percentage_expenditure and
Year:
Chi2 value: 0.0
P-value: 1.0
```

```
Chi-square test between missingness of Hepatitis_B and Year:
Chi2 value: 442.4908142143988
P-value: 7.884609666510395e-85

Chi-square test between missingness of Measles_ and Year:
Chi2 value: 0.0
P-value: 1.0

Chi-square test between missingness of _BMI_ and Year:
Chi2 value: 1.5129038229150384
P-value: 0.999995479339797

Chi-square test between missingness of under-five_deaths_ and Year:
Chi2 value: 0.0
P-value: 1.0

Chi-square test between missingness of Polio and Year:
Chi2 value: 14.045100367382663
P-value: 0.522111393336138

Chi-square test between missingness of Total_expenditure and Year:
Chi2 value: 2287.22630878564
P-value: 0.0

Chi-square test between missingness of Diphtheria_ and Year:
Chi2 value: 14.045100367382663
P-value: 0.522111393336138

Chi-square test between missingness of _HIV/AIDS and Year:
Chi2 value: 0.0
P-value: 1.0

Chi-square test between missingness of GDP and Year:
Chi2 value: 0.9416982156500103
P-value: 0.9999998342217689

Chi-square test between missingness of Population and Year:
Chi2 value: 1.298405382595901
P-value: 0.9999984226955846

Chi-square test between missingness of _thinness__1-19_years and Year:
Chi2 value: 1.5129038229150384
P-value: 0.999995479339797

Chi-square test between missingness of _thinness_5-9_years and Year:
Chi2 value: 1.5129038229150384
P-value: 0.999995479339797
```

```
Chi-square test between missingness of Income_composition_of_resources
and Year:
Chi2 value: 3.760810494440295
P-value: 0.9984211730202514

Chi-square test between missingness of Schooling and Year:
Chi2 value: 0.5561305359420944
P-value: 0.9999999962196013
```

From the tests, we observe that:

- For most features, including Country, Year, Status, infant_deaths, percentage_expenditure, Measles_, BMI, under-five_deaths_, _HIV/AIDS, GDP, Population, _thinness__1-19_years, _thinness_5-9_years, Income_composition_of_resources, and Schooling, the p-value is nearly 1, suggesting the missingness in these features is not related to the 'Year'. Thus, these variables are Missing Completely At Random.

- In contrast, for Life_expectancy_, Adult_Mortality, Alcohol, Hepatitis_B, and Total_expenditure, the p-values are significantly less than 0.05, meaning the null hypothesis (H0: the data are MCAR) can be rejected. This suggests a significant association between the 'Year' and the missingness in these features, implying that the missingness in these variables is not random and might be dependent on 'Year'.

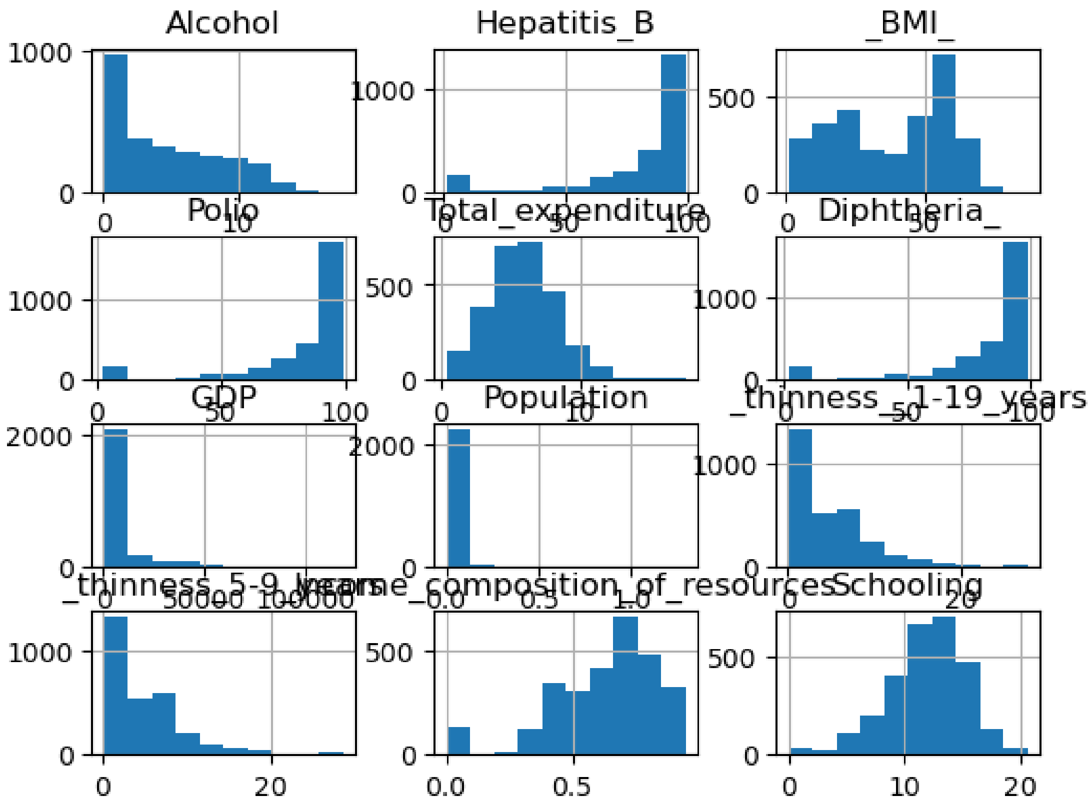
- For Polio and Diphtheria_, the p-value is above 0.05, suggesting that the missingness of these variables could be random with respect to 'Year'.

It may be necessary to employ more complex imputation strategies, like multiple imputation or predictive modeling, that consider the dependence on 'Year' but we will use mean, mode or median to fill that NaN values. Let's check their distributions.

```python
nan_features = ["Alcohol", "Hepatitis_B", "_BMI_", "Polio",
"Total_expenditure", "Diphtheria_",
                "GDP", "Population", "_thinness__1-19_years",
"_thinness_5-9_years",
                "Income_composition_of_resources", "Schooling"]

df[nan_features].hist()
```

```
array([[<AxesSubplot:title={'center':'Alcohol'}>,
        <AxesSubplot:title={'center':'Hepatitis_B'}>,
        <AxesSubplot:title={'center':'_BMI_'}>],
       [<AxesSubplot:title={'center':'Polio'}>,
        <AxesSubplot:title={'center':'Total_expenditure'}>,
        <AxesSubplot:title={'center':'Diphtheria_'}>],
       [<AxesSubplot:title={'center':'GDP'}>,
        <AxesSubplot:title={'center':'Population'}>,
        <AxesSubplot:title={'center':'_thinness__1-19_years'}>],
       [<AxesSubplot:title={'center':'_thinness_5-9_years'}>,
```

```
<AxesSubplot:title={'center':'Income_composition_of_resources'}>,
        <AxesSubplot:title={'center':'Schooling'}>]], dtype=object)
```



Only Total_expenditure and Schooling look like normal distributed features - we will use mean for NaN replacing of their variables. For all other features we will use median.

```python
# mean replacing
df["Total_expenditure"].fillna(df["Total_expenditure"].mean(),
inplace=True)
df["Schooling"].fillna(df["Schooling"].mean(), inplace=True)

#median replacing
nan_features = df.columns[df.isnull().any()].tolist()
for i in nan_features:
    if i not in ["Total_expenditure", "Schooling"]:
        df[i].fillna(df[i].median(), inplace=True)
```

Q2: Does various predicting factors which has been chosen initially really affect the Life expectancy? What are the predicting variables actually affecting the life expectancy

```python
life_expectancy_df_corr = df.corr()["Life_expectancy_"][:-1]
golden_features_list =
life_expectancy_df_corr[abs(life_expectancy_df_corr) >
0.5].sort_values(ascending=False).iloc[1:]
print("There are {} high correlated features with Life expectancy:\
n{}".format(len(golden_features_list), golden_features_list))
```

```
There are 5 high correlated features with Life expectancy:
Schooling                             0.714358
Income_composition_of_resources       0.688662
_BMI_                                 0.556901
_HIV/AIDS                            -0.556703
Adult_Mortality                      -0.696390
Name: Life_expectancy_, dtype: float64
```

Q3: What is the average (mean) life expectancy across all countries in the dataset? How does it vary (standard deviation)? What are the minimum and maximum life expectancy values? (calculate for each year)

```
df[["Life_expectancy_", "Year"]].groupby(["Year"]).describe()
```

Life_expectancy_								
Year	count	mean	std	min	25%	50%	75%	max
2000	183.0	66.750273	10.295528	39.0	58.65	71.0	74.45	81.1
2001	183.0	67.128962	10.189630	41.0	59.00	71.2	74.90	82.0
2002	183.0	67.351366	10.062469	44.0	59.35	71.4	74.80	84.0
2003	183.0	67.433333	10.127681	41.5	59.75	71.1	74.70	87.0
2004	183.0	67.646448	10.126409	42.3	60.70	71.2	74.30	89.0
2005	183.0	68.209290	9.799516	43.3	63.50	71.6	74.95	88.0
2006	183.0	68.667760	9.815171	44.3	62.25	72.1	75.00	88.0
2007	183.0	69.036066	9.618584	45.3	62.05	72.4	75.15	89.0
2008	183.0	69.427869	9.202612	46.2	62.70	72.4	75.35	89.0
2009	183.0	69.938251	8.989124	47.1	64.45	72.6	76.00	89.0
2010	183.0	70.048634	9.302959	36.3	63.45	72.8	75.80	89.0
2011	183.0	70.654098	8.925040	48.9	63.90	73.3	76.10	88.0
2012	183.0	70.916940	8.562151	49.7	64.50	73.2	76.50	88.0
2013	193.0	71.280829	8.193983	49.9	66.00	72.8	76.20	87.0
2014	183.0	71.536612	8.560831	48.1	65.60	73.6	76.85	89.0

```
2015            183.0  71.616940   8.123706  51.0  65.75  73.9  76.95
88.0
```

From the results, we observe that:

- There is a general upward trend in life expectancy over the period from 2000 to 2015. The mean life expectancy increased from 66.75 years in 2000 to 71.61 years in 2015.
- The standard deviation, which measures the dispersion of data from its mean, has decreased over time. This indicates that life expectancy has become more uniform across different regions over these years.
- The minimum life expectancy has also shown a progressive increase from 39.0 in 2000 to 51.0 in 2015, suggesting improvements in countries with the lowest life expectancies.
- The maximum life expectancy has likewise increased over this period, from 81.1 in 2000 to 88.0 in 2015, indicating advances in the countries with the highest life expectancies.
- The interquartile ranges (from 25% to 75%), representing the middle 50% of the data, have also shown a general increase. This means that half of all countries have seen consistent growth in life expectancy over this period.

Overall, the table indicates global progress in increasing life expectancy between 2000 and 2015. The trend suggests improvements in healthcare, living conditions, and access to basic services over this period. However, disparities still exist, as shown by the continued variation in life expectancy across different regions.

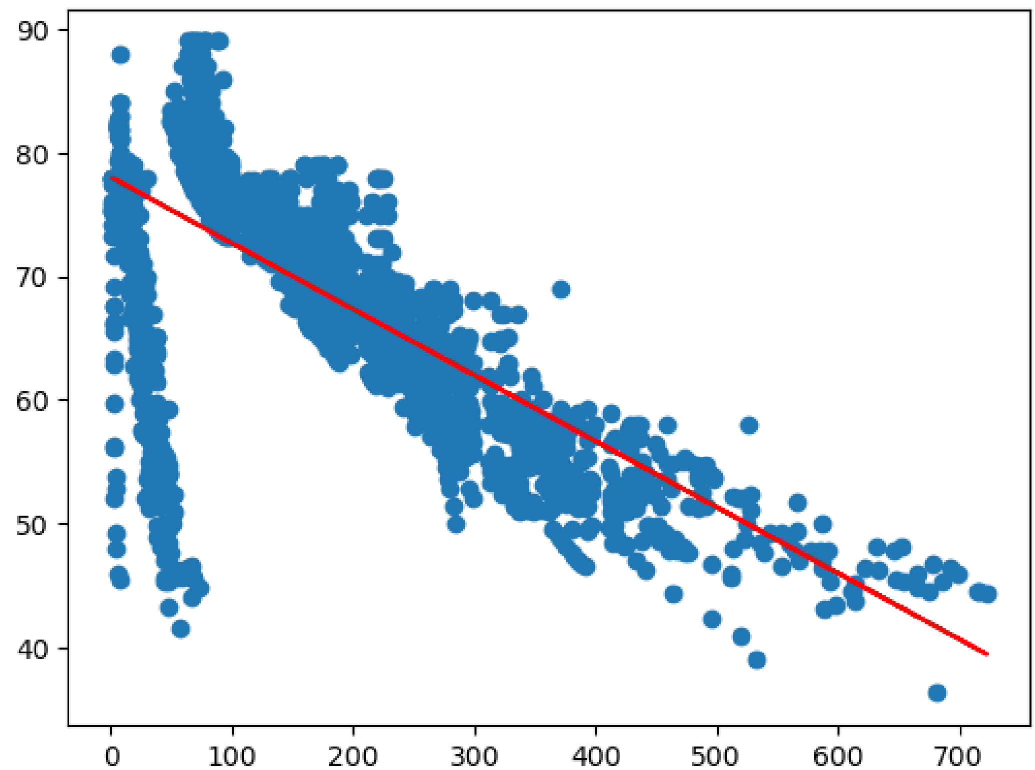
Q4: Can we predict life expectancy based on variables like Adult Mortality, Alcohol consumption, percentage expenditure, and schooling? How much of the variation in life expectancy can be explained by these variables?

```
am = list(df["Adult_Mortality"])
ac = list(df["Alcohol"])
te = list(df["Total_expenditure"])
s = list(df["Schooling"])

le = list(df["Life_expectancy_"])

X_am = sm.add_constant(am)
model_am = sm.OLS(le, am)
results_am = model_am.fit()

print(results_am.summary())

slope, intercept, r, p, std_err = stats.linregress(am, le)

lrmodel_am = [slope * x + intercept for x in am]
```

```
plt.scatter(am, le)
plt.plot(am, lrmodel_am, color="red")
plt.show()
```

```
                                 OLS Regression Results                                
=======================================================================================
Dep. Variable:                      y   R-squared (uncentered):                   0.539
Model:                            OLS   Adj. R-squared (uncentered):              0.539
Method:                 Least Squares   F-statistic:                              3438.
Date:                Wed, 14 Jun 2023   Prob (F-statistic):                        0.00
Time:                        10:45:30   Log-Likelihood:                         -15508.
No. Observations:                2938   AIC:                                  3.102e+04
Df Residuals:                    2937   BIC:                                  3.102e+04
Df Model:                           1                                                  
Covariance Type:            nonrobust                                                  
==============================================================================
                 coef    std err          t      P>|t|      [0.025      0.975]
------------------------------------------------------------------------------
x1             0.2489      0.004     58.634      0.000       0.241       0.257
==============================================================================
Omnibus:                      567.598   Durbin-Watson:                   0.329
Prob(Omnibus):                  0.000   Jarque-Bera (JB):             1014.186
Skew:                          -1.217   Prob(JB):                    5.92e-221
Kurtosis:                       4.536   Cond. No.                         1.00
==============================================================================

Notes:
[1] R² is computed without centering (uncentered) since the model does
```

```
not contain a constant.
[2] Standard Errors assume that the covariance matrix of the errors is
correctly specified.
```



From the results, we observe that:

- Coefficient of Adult_Mortality: The coefficient of Adult_Mortality is positive (0.2489), indicating that there is a positive relationship between Adult_Mortality and the dependent variable Life_expectancy_. For each unit increase in Adult_Mortality, the expected value of Life_expectancy_ increases by 0.2489 units, holding all else constant.

- Significance of Adult_Mortality: The p-value for Adult_Mortality is 0.000, which is less than the commonly used significance level of 0.05. This means that the variable Adult_Mortality is statistically significant in explaining the variation in Life_expectancy_. The 95% confidence interval for the coefficient of Adult_Mortality (0.241 to 0.257) does not contain zero, further confirming its significance.

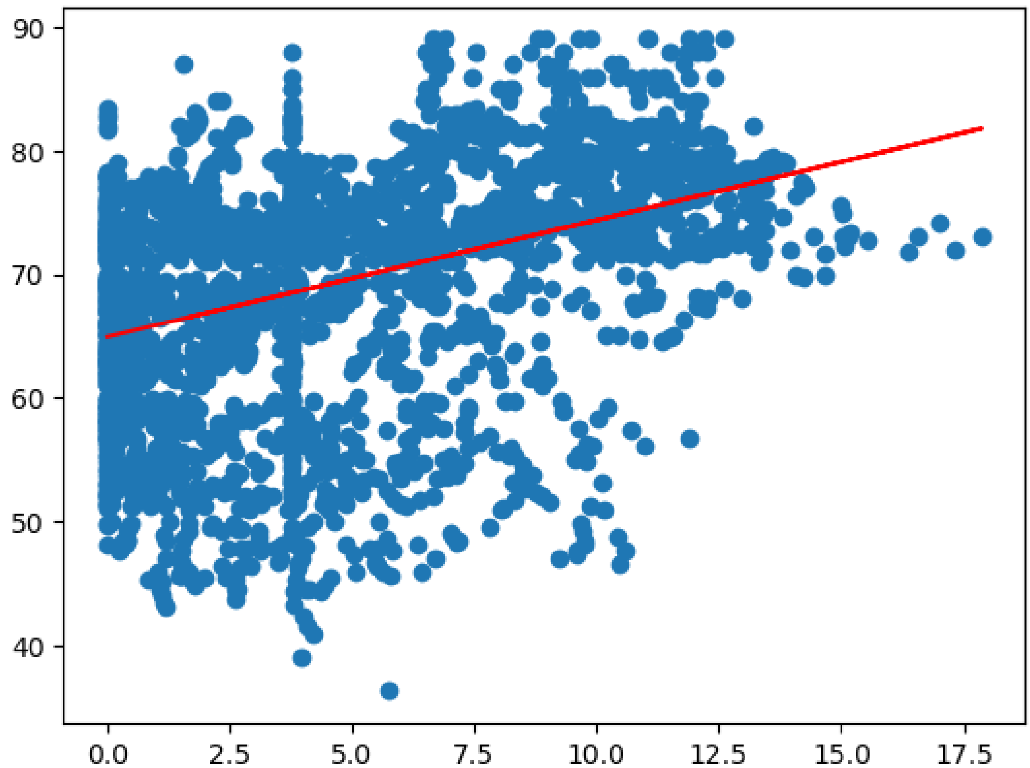
- Model Fit: The R-squared value is 0.539, which means that approximately 53.9% of the variation in the dependent variable Life_expectancy_ can be explained by the independent variable Adult_Mortality. The adjusted R-squared, which takes into account the number of predictors in the model, is also 0.539, suggesting that the model does not suffer from the inclusion of irrelevant predictors.

```
X_ac = sm.add_constant(ac)
model_ac = sm.OLS(le, ac)
```

```
results_ac = model_ac.fit()

print(results_ac.summary())

slope, intercept, r, p, std_err = stats.linregress(ac, le)

lrmodel_ac = [slope * x + intercept for x in ac]

plt.scatter(ac, le)
plt.plot(ac, lrmodel_ac, color="red")
plt.show()
```

```
                                 OLS Regression Results                                

=======================================================================================
Dep. Variable:                      y   R-squared (uncentered):                   0.616
Model:                            OLS   Adj. R-squared (uncentered):              0.616
Method:                 Least Squares   F-statistic:                              4710.
Date:                Wed, 14 Jun 2023   Prob (F-statistic):                        0.00
Time:                        10:45:31   Log-Likelihood:                         -15240.
No. Observations:                2938   AIC:                                  3.048e+04
Df Residuals:                    2937   BIC:                                  3.049e+04
Df Model:                           1                                                  

Covariance Type:            nonrobust                                                  

==============================================================================
                 coef    std err          t      P>|t|      [0.025      0.975]
------------------------------------------------------------------------------
x1             9.1344      0.133     68.626      0.000       8.873       9.395
==============================================================================
Omnibus:                      216.922   Durbin-Watson:                   0.142
Prob(Omnibus):                  0.000   Jarque-Bera (JB):              196.251
Skew:                          -0.566   Prob(JB):                     2.43e-43
```

```
Kurtosis:                       2.433   Cond. No.
1.00
======================================================================
========

Notes:
[1] R² is computed without centering (uncentered) since the model does
not contain a constant.
[2] Standard Errors assume that the covariance matrix of the errors is
correctly specified.
```



From the results, we observe that:

- Coefficient of Alcohol: The coefficient of Alcohol is positive (9.1344), indicating that there is a positive relationship between Alcohol and the dependent variable Life_expectancy_. For each unit increase in Alcohol, the expected value of Life_expectancy_ increases by approximately 9.1344 units, holding all else constant.

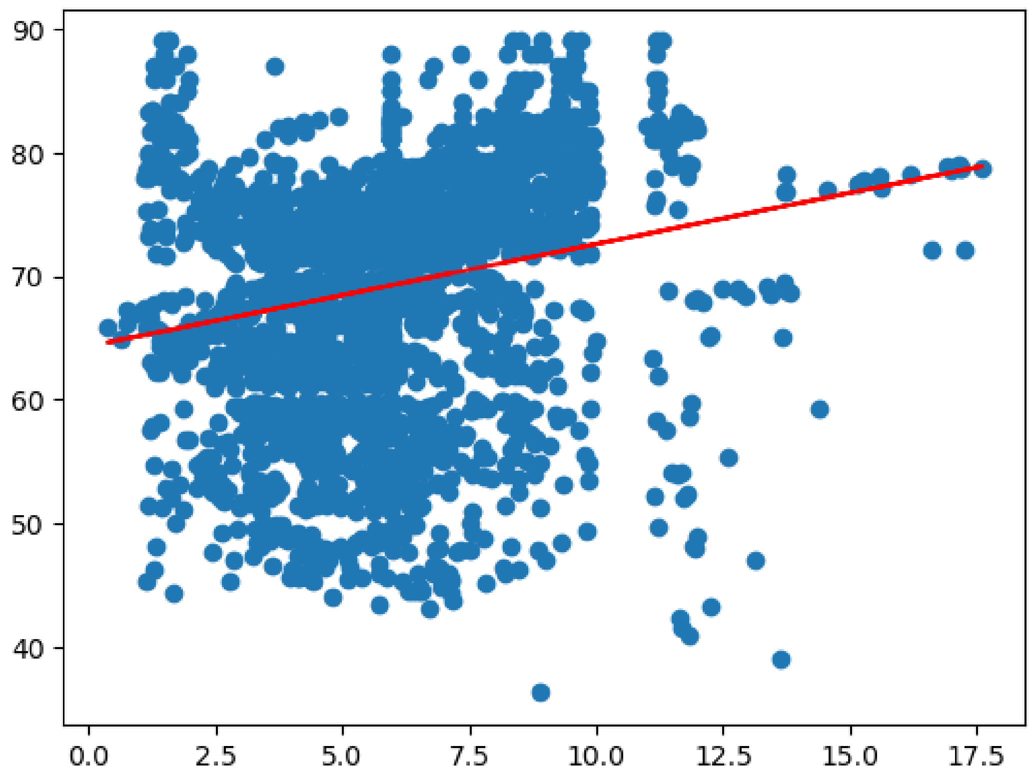
- Significance of Alcohol: The p-value for Alcohol is 0.000, which is less than the commonly used significance level of 0.05. This means that the variable Alcohol is statistically significant in explaining the variation in Life_expectancy_. The 95% confidence interval for the coefficient of Alcohol (8.873 to 9.395) does not contain zero, which further confirms its significance.

- Model Fit: The R-squared value is 0.616, which means that approximately 61.6% of the variation in the dependent variable Life_expectancy_ can be explained by the independent variable Alcohol. The adjusted R-squared, which takes into account the number of predictors in the model, is also 0.616, suggesting that the model does not suffer from the inclusion of irrelevant predictors.

```
X_te = sm.add_constant(te)
model_te = sm.OLS(le, te)
results_te = model_te.fit()

print(results_te.summary())

slope, intercept, r, p, std_err = stats.linregress(te, le)

lrmodel_te = [slope * x + intercept for x in te]

plt.scatter(te, le)
plt.plot(te, lrmodel_te, color="red")
plt.show()
```

```
                                 OLS Regression Results                                

=======================================================================================
Dep. Variable:                      y   R-squared (uncentered):                   
0.863
Model:                            OLS   Adj. R-squared (uncentered):              
0.863
Method:                 Least Squares   F-statistic:                              
1.856e+04
Date:                Wed, 14 Jun 2023   Prob (F-statistic):                       
0.00
Time:                        10:45:31   Log-Likelihood:                           
-13722.
No. Observations:                2938   AIC:                                      
2.745e+04
Df Residuals:                    2937   BIC:                                      
2.745e+04
Df Model:                           1                                                  

Covariance Type:            nonrobust                                                  

==============================================================================
========
                 coef    std err          t      P>|t|      [0.025      
0.975]
------------------------------------------------------------------------------
--------
x1          10.1385      0.074    136.229      0.000       9.993      
10.284
==============================================================================
========
```

```
Omnibus:                       229.597   Durbin-Watson:
0.552
Prob(Omnibus):                   0.000   Jarque-Bera (JB):
545.739
Skew:                           -0.471   Prob(JB):
3.12e-119
Kurtosis:                        4.889   Cond. No.
1.00
======================================================================
========

Notes:
[1] R² is computed without centering (uncentered) since the model does
not contain a constant.
[2] Standard Errors assume that the covariance matrix of the errors is
correctly specified.
```



From the results, we observe that:

- Coefficient of Total_expenditure: The coefficient of Total_expenditure is positive (10.1385), indicating that there is a positive relationship between Total_expenditure and the dependent variable Life_expectancy_. For each unit increase in Total_expenditure, the expected value of Life_expectancy_ increases by approximately 10.1385 units, holding all else constant.

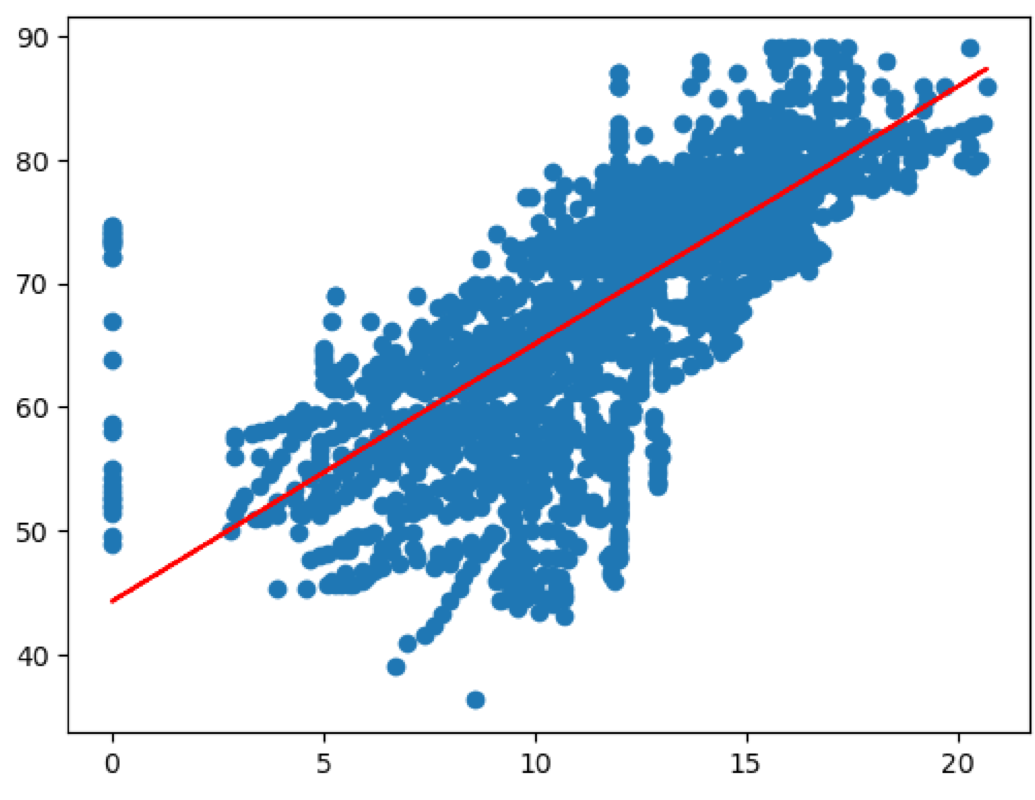
- Significance of Total_expenditure: The p-value for Total_expenditure is 0.000, which is less than the commonly used significance level of 0.05. This means that the variable Total_expenditure is statistically significant in explaining the variation in Life_expectancy_. The 95% confidence interval for the coefficient of Total_expenditure (9.993 to 10.284) does not contain zero, which further confirms its significance.

- Model Fit: The R-squared value is 0.863, which means that approximately 86.3% of the variation in the dependent variable Life_expectancy_ can be explained by the independent variable Total_expenditure. The adjusted R-squared, which takes into account the number of predictors in the model, is also 0.863, suggesting that the model does not suffer from the inclusion of irrelevant predictors.

```
X_s = sm.add_constant(s)
model_s = sm.OLS(le, s)
results_s = model_s.fit()

print(results_s.summary())

slope, intercept, r, p, std_err = stats.linregress(s, le)

lrmodel_s = [slope * x + intercept for x in s]

plt.scatter(s, le)
plt.plot(s, lrmodel_s, color="red")
plt.show()
```

```
                                 OLS Regression Results

======================================================================
=================
Dep. Variable:                      y   R-squared (uncentered):
0.963
Model:                            OLS   Adj. R-squared (uncentered):
0.963
Method:                 Least Squares   F-statistic:
7.699e+04
Date:                Wed, 14 Jun 2023   Prob (F-statistic):
0.00
Time:                        10:45:31   Log-Likelihood:
-11793.
No. Observations:                2938   AIC:
2.359e+04
Df Residuals:                    2937   BIC:
2.359e+04
Df Model:                           1

Covariance Type:            nonrobust
```

```
======================================================================
========
                 coef    std err          t      P>|t|      [0.025
0.975]
----------------------------------------------------------------------
--------
x1             5.5184      0.020    277.470      0.000       5.479
5.557
======================================================================
========
Omnibus:                      691.995   Durbin-Watson:
0.268
Prob(Omnibus):                  0.000   Jarque-Bera (JB):
2724.632
Skew:                           1.109   Prob(JB):
0.00
Kurtosis:                       7.164   Cond. No.
1.00
======================================================================
========

Notes:
[1] R² is computed without centering (uncentered) since the model does
not contain a constant.
[2] Standard Errors assume that the covariance matrix of the errors is
correctly specified.
```



From the results, we observe that:

- Coefficient of Schooling: The coefficient of Schooling is positive (5.5184), indicating that there is a positive relationship between Schooling and the dependent variable Life_expectancy_. For each unit increase in Schooling, the expected value of Life_expectancy_ increases by approximately 5.5184 units, holding all else constant.

- Significance of Schooling: The p-value for Schooling is 0.000, which is less than the commonly used significance level of 0.05. This means that the variable Schooling is statistically significant in explaining the variation in Life_expectancy_. The 95% confidence interval for the coefficient of Schooling (5.479 to 5.557) does not contain zero, which further confirms its significance.

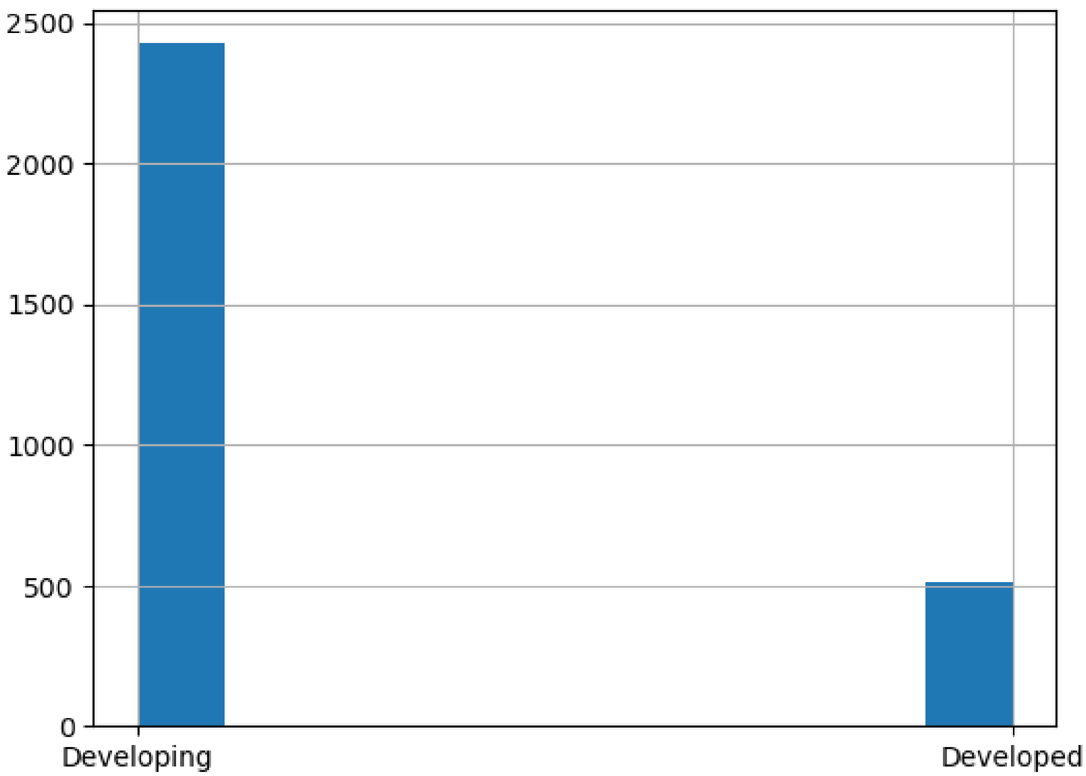
- Model Fit: The R-squared value is 0.963, which means that approximately 96.3% of the variation in the dependent variable Life_expectancy_ can be explained by the independent variable Schooling. The adjusted R-squared, which takes into account the number of predictors in the model, is also 0.963, suggesting that the model does not suffer from the inclusion of irrelevant predictors.

Q5: Is there a significant difference in the mean life expectancy between developed and developing countries (as indicated by the 'Status' column)?

We could use a t-test for this if the distributions are approximately normal, or a Mann-Whitney U test if they are not.

```
df["Status"].hist()
```

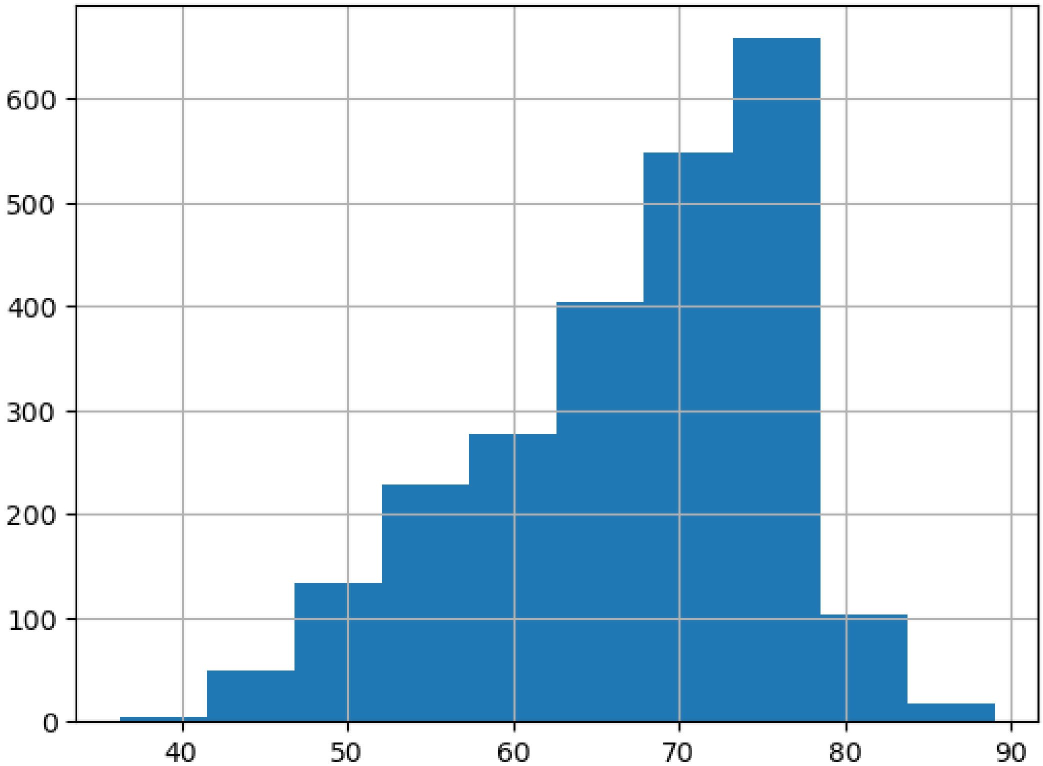
```
<AxesSubplot:>
```



We can see the high difference between the quantity of developing and developed countries.

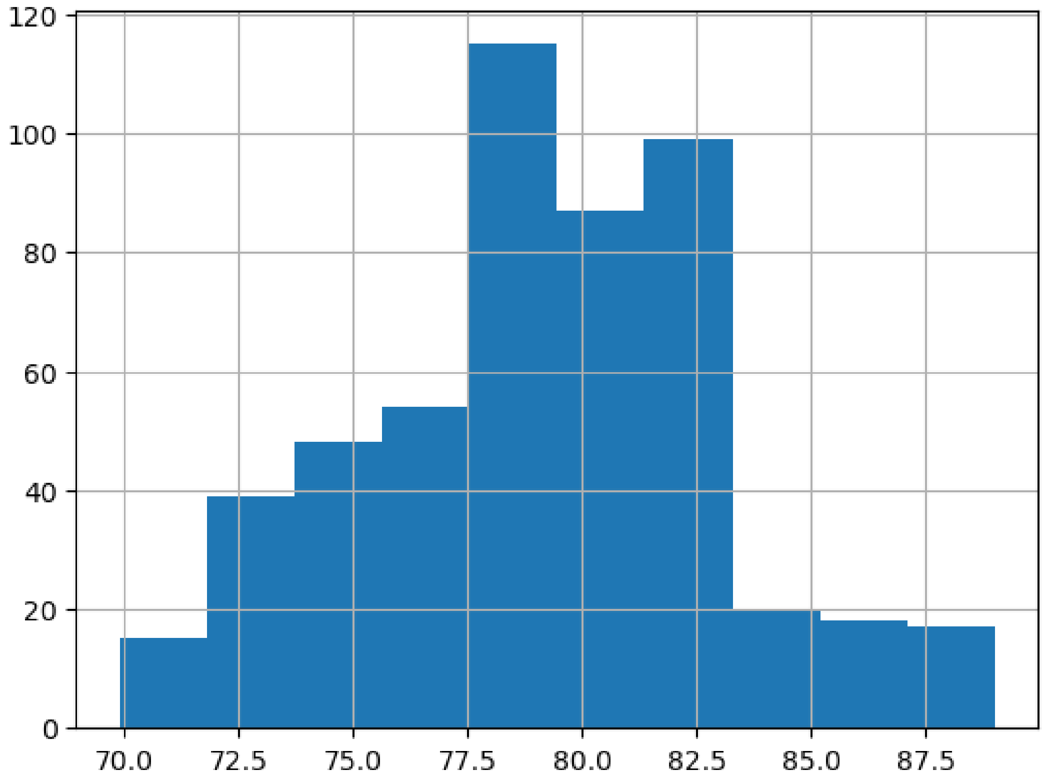
```
df[df["Status"] == "Developing"]["Life_expectancy_"].hist()
```

```
<AxesSubplot:>
```




```
df[df["Status"] == "Developed"]["Life_expectancy_"].hist()
```

<AxesSubplot:>



We can check the normality of distributions by Shapiro-Wilk test.

```
#H0 - the distribution is normal (p>0.05)
#H1 - the distribution isn't normal (p<=0.05)

shapiro_test = stats.shapiro(df[df["Status"] == "Developing"]
["Life_expectancy_"])
shapiro_test
```

```
ShapiroResult(statistic=0.9493448138237, pvalue=3.6954844884224 36e-28)
```

```
#H0 - the distribution is normal (p>0.05)
#H1 - the distribution isn't normal (p<=0.05)

shapiro_test = stats.shapiro(df[df["Status"] == "Developed"]
["Life_expectancy_"])
shapiro_test
```

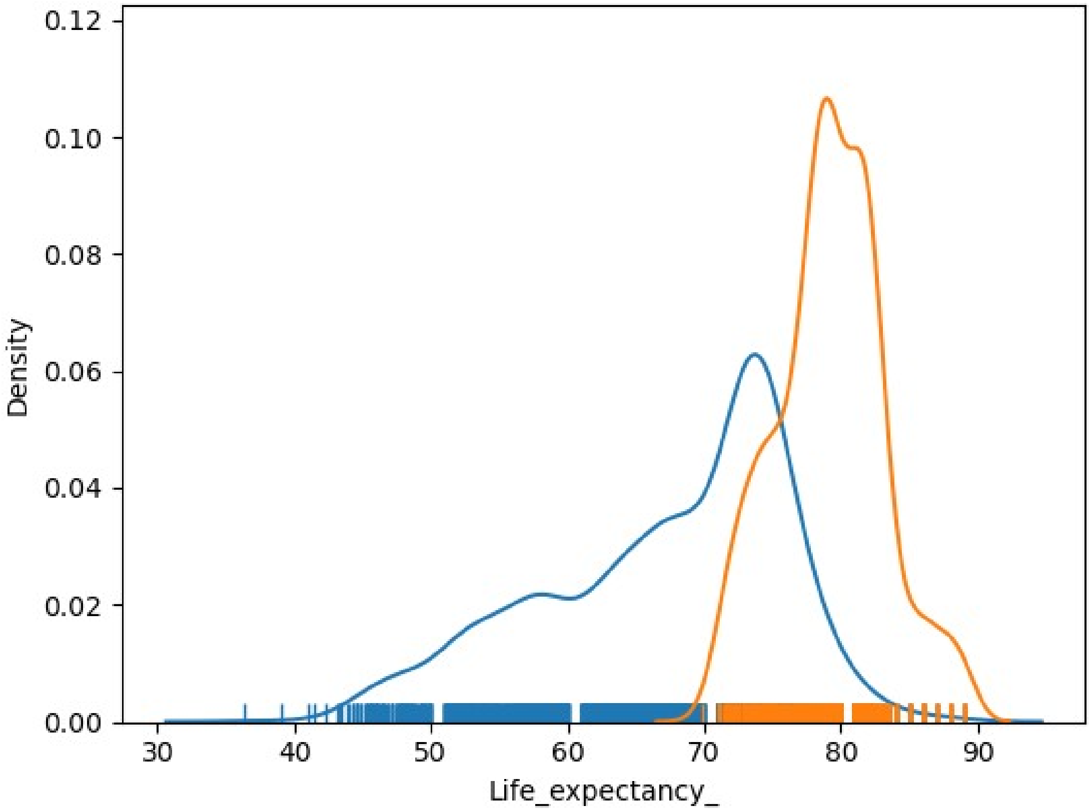
```
ShapiroResult(statistic=0.984403133392334, pvalue=2.6695464839576744e-
05)
```

We can reject H0 => Both distributions aren't normal. We will use Mann-Whitney U test.

```
developing = df[df["Status"] == "Developing"]["Life_expectancy_"]
developed = df[df["Status"] == "Developed"]["Life_expectancy_"]
```

```
sns.distplot(developing, hist=False, rug=True)
sns.distplot(developed, hist=False, rug=True)

plt.show()
```

```
/home/pcubu/anaconda3/lib/python3.9/site-packages/seaborn/
distributions.py:2619: FutureWarning: `distplot` is a deprecated
function and will be removed in a future version. Please adapt your
code to use either `displot` (a figure-level function with similar
flexibility) or `kdeplot` (an axes-level function for kernel density
plots).
  warnings.warn(msg, FutureWarning)
/home/pcubu/anaconda3/lib/python3.9/site-packages/seaborn/distribution
s.py:2103: FutureWarning: The `axis` variable is no longer used and
will be removed. Instead, assign variables directly to `x` or `y`.
  warnings.warn(msg, FutureWarning)
/home/pcubu/anaconda3/lib/python3.9/site-packages/seaborn/distribution
s.py:2619: FutureWarning: `distplot` is a deprecated function and will
be removed in a future version. Please adapt your code to use either
`displot` (a figure-level function with similar flexibility) or
`kdeplot` (an axes-level function for kernel density plots).
  warnings.warn(msg, FutureWarning)
/home/pcubu/anaconda3/lib/python3.9/site-packages/seaborn/distribution
s.py:2103: FutureWarning: The `axis` variable is no longer used and
will be removed. Instead, assign variables directly to `x` or `y`.
  warnings.warn(msg, FutureWarning)
```




```
#H0 -  There is no significant difference in the mean life expectancy
between developed and developing countries. (p>0.05)
#H1 - There is a significant difference in the mean life expectancy
between developed and developing countries. (p<=0.05)

u_stat, u_p_val = stats.mannwhitneyu(developed, developing)
print(f'Mann-Whitney U test p-value: {u_p_val}')
```

```
Mann-Whitney U test p-value: 6.6411125328204414e-192
```

We can reject H0 => There is a significant difference in the mean life expectancy between developed and developing countries.