EwerDSC530FinalProject

August 5, 2024

[1]:
```
import statsmodels.formula.api as smf
import pandas as pd
import seaborn as sns
import numpy as np
import matplotlib.pyplot as plt
import thinkstats2
import thinkplot

import warnings
warnings.filterwarnings('ignore')

%matplotlib inline
```

[2]:
```
who_df = pd.read_csv('who_life_exp.csv')
who_df.head()
```

[2]:
```
  country country_code  region  year  life_expect  life_exp60  \
0  Angola          AGO  Africa  2000     47.33730    14.73400
1  Angola          AGO  Africa  2001     48.19789    14.95963
2  Angola          AGO  Africa  2002     49.42569    15.20010
3  Angola          AGO  Africa  2003     50.50266    15.39144
4  Angola          AGO  Africa  2004     51.52863    15.56860

   adult_mortality  infant_mort  age1-4mort  alcohol  …  che_gdp    une_pop  \
0         383.5583     0.137985    0.025695  1.47439  …  1.90860  16395.473
1         372.3876     0.133675    0.024500  1.94025  …  4.48352  16945.753
2         354.5147     0.128320    0.023260  2.07512  …  3.32946  17519.417
3         343.2169     0.122040    0.021925  2.20275  …  3.54797  18121.479
4         333.8711     0.115700    0.020545  2.41274  …  3.96720  18758.145

   une_infant  une_life  une_hiv  une_gni  une_poverty  une_edu_spend  \
0       122.2    46.522      1.0   2530.0         32.3        2.60753
1       118.9    47.059      1.1   2630.0          NaN            NaN
2       115.1    47.702      1.2   3180.0          NaN            NaN
3       110.8    48.440      1.3   3260.0          NaN            NaN
4       106.2    49.263      1.3   3560.0          NaN            NaN

   une_literacy  une_school
```

```
0          NaN         NaN
1     67.40542         NaN
2          NaN         NaN
3          NaN         NaN
4          NaN         NaN

[5 rows x 32 columns]
```

Data Cleanup

Remove missing data or impute values based on means

[3]:
```python
who_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 3111 entries, 0 to 3110
Data columns (total 32 columns):
 #   Column           Non-Null Count  Dtype
---  ------           --------------  -----
 0   country          3111 non-null   object
 1   country_code     3111 non-null   object
 2   region           3111 non-null   object
 3   year             3111 non-null   int64
 4   life_expect      3111 non-null   float64
 5   life_exp60       3111 non-null   float64
 6   adult_mortality  3111 non-null   float64
 7   infant_mort      3111 non-null   float64
 8   age1-4mort       3111 non-null   float64
 9   alcohol          3061 non-null   float64
 10  bmi              3077 non-null   float64
 11  age5-19thinness  3077 non-null   float64
 12  age5-19obesity   3077 non-null   float64
 13  hepatitis        2542 non-null   float64
 14  measles          3092 non-null   float64
 15  polio            3092 non-null   float64
 16  diphtheria       3092 non-null   float64
 17  basic_water      3079 non-null   float64
 18  doctors          1780 non-null   float64
 19  hospitals        130 non-null    float64
 20  gni_capita       2429 non-null   float64
 21  gghe-d           3011 non-null   float64
 22  che_gdp          2994 non-null   float64
 23  une_pop          3074 non-null   float64
 24  une_infant       3111 non-null   float64
 25  une_life         3111 non-null   float64
 26  une_hiv          2370 non-null   float64
 27  une_gni          2994 non-null   float64
 28  une_poverty      913 non-null    float64
```

```
 29   une_edu_spend     1825 non-null    float64
 30   une_literacy      571 non-null     float64
 31   une_school        805 non-null     float64
dtypes: float64(28), int64(1), object(3)
memory usage: 777.9+ KB
```

[4]:
```
# Drop the columns that have too many null values to imput
who_df.drop(['hepatitis', 'doctors', 'hospitals', 'une_poverty',␣
 ↪'une_literacy', 'une_school', 'une_edu_spend'], axis=1, inplace=True)

## rename gghe-d since that's a problem later
who_df.rename(columns={'gghe-d': 'health_expenditure', 'age5-19obesity':␣
 ↪'youth_obesity'}, inplace=True)
```

Correlation

Look at the correlation between continuous variables

[5]:
```
continuous_df = who_df.drop(['region', 'country', 'country_code'], axis=1)
continuous_df.corr()
```

[5]:

	year	life_expect	life_exp60	adult_mortality \
year	1.000000	0.190961	0.192872	-0.170946
life_expect	0.190961	1.000000	0.886159	-0.946419
life_exp60	0.192872	0.886159	1.000000	-0.775321
adult_mortality	-0.170946	-0.946419	-0.775321	1.000000
infant_mort	-0.195293	-0.930113	-0.769839	0.813210
age1-4mort	-0.191723	-0.864414	-0.661082	0.756230
alcohol	0.006428	0.399797	0.465785	-0.246530
bmi	0.170244	0.597996	0.458839	-0.517095
age5-19thinness	-0.081810	-0.565396	-0.556536	0.455205
youth_obesity	0.278359	0.621000	0.547764	-0.571792
measles	0.142717	0.640408	0.504875	-0.526185
polio	0.128699	0.646486	0.501654	-0.537973
diphtheria	0.141351	0.640473	0.503303	-0.529967
basic_water	0.109352	0.831099	0.680990	-0.732704
gni_capita	0.118967	0.585603	0.582539	-0.527650
health_expenditure	0.081852	0.609787	0.670995	-0.485836
che_gdp	0.112887	0.284920	0.388805	-0.198618
une_pop	0.016757	0.032126	0.004131	-0.061503
une_infant	-0.187952	-0.931899	-0.776510	0.814884
une_life	0.185664	0.991448	0.869439	-0.943640
une_hiv	-0.018294	-0.511821	-0.343894	0.680558
une_gni	0.147887	0.603019	0.602258	-0.544664

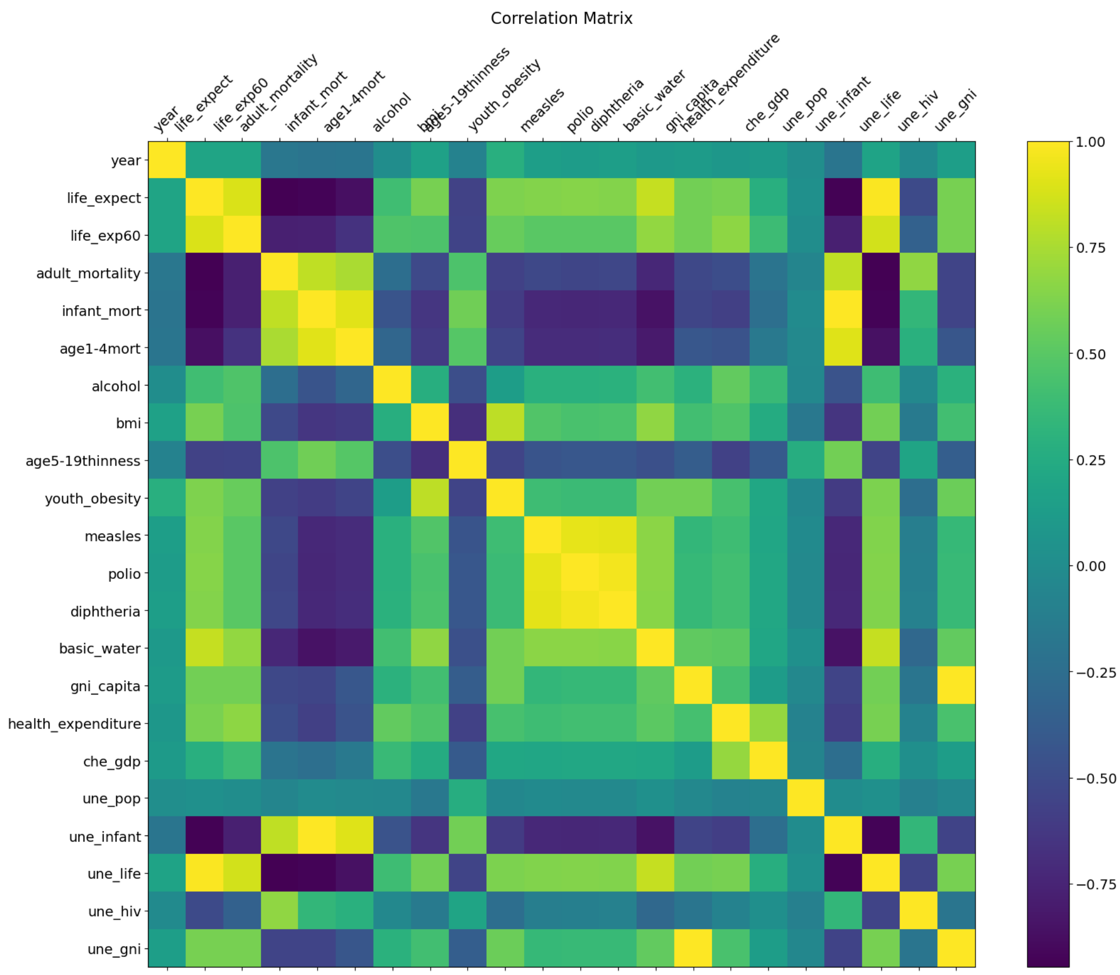
	infant_mort	age1-4mort	alcohol	bmi \
year	-0.195293	-0.191723	0.006428	0.170244
life_expect	-0.930113	-0.864414	0.399797	0.597996

```
life_exp60          -0.769839   -0.661082  0.465785  0.458839
adult_mortality      0.813210    0.756230 -0.246530 -0.517095
infant_mort          1.000000    0.909032 -0.444580 -0.641874
age1-4mort           0.909032    1.000000 -0.305744 -0.615242
alcohol             -0.444580   -0.305744  1.000000  0.272832
bmi                 -0.641874   -0.615242  0.272832  1.000000
age5-19thinness      0.578230    0.486846 -0.481989 -0.685819
youth_obesity       -0.602402   -0.544587  0.140611  0.807143
measles             -0.720169   -0.698573  0.291679  0.468788
polio               -0.728603   -0.700788  0.289802  0.441274
diphtheria          -0.720741   -0.694145  0.294311  0.446225
basic_water         -0.851514   -0.802324  0.407690  0.673261
gni_capita          -0.539514   -0.417762  0.304989  0.410808
health_expenditure  -0.576804   -0.447373  0.529580  0.461679
che_gdp             -0.238393   -0.162339  0.372205  0.248024
une_pop             -0.003967   -0.032953 -0.037812 -0.166194
une_infant           0.996975    0.902324 -0.449387 -0.644441
une_life            -0.926927   -0.855848  0.394807  0.587912
une_hiv              0.341615    0.292005 -0.038341 -0.154689
une_gni             -0.549928   -0.421805  0.296187  0.413644

                    age5-19thinness  youth_obesity  …  diphtheria  \
year                      -0.081810       0.278359  …    0.141351
life_expect               -0.565396       0.621000  …    0.640473
life_exp60                -0.556536       0.547764  …    0.503303
adult_mortality            0.455205      -0.571792  …   -0.529967
infant_mort                0.578230      -0.602402  …   -0.720741
age1-4mort                 0.486846      -0.544587  …   -0.694145
alcohol                   -0.481989       0.140611  …    0.294311
bmi                       -0.685819       0.807143  …    0.446225
age5-19thinness            1.000000      -0.548601  …   -0.418306
youth_obesity             -0.548601       1.000000  …    0.380033
measles                   -0.439146       0.399031  …    0.923205
polio                     -0.415575       0.376953  …    0.964453
diphtheria                -0.418306       0.380033  …    1.000000
basic_water               -0.474768       0.588918  …    0.651661
gni_capita                -0.370173       0.584749  …    0.355730
health_expenditure        -0.573455       0.432588  …    0.409616
che_gdp                   -0.396721       0.210695  …    0.224228
une_pop                    0.265009      -0.044698  …   -0.028161
une_infant                 0.586277      -0.606526  …   -0.721966
une_life                  -0.551026       0.613217  …    0.632861
une_hiv                    0.193470      -0.243627  …   -0.093512
une_gni                   -0.368289       0.565269  …    0.362230

                    basic_water  gni_capita  health_expenditure   che_gdp  \
year                   0.109352    0.118967            0.081852  0.112887
```

```
life_expect           0.831099   0.585603             0.609787  0.284920
life_exp60            0.680990   0.582539             0.670995  0.388805
adult_mortality      -0.732704  -0.527650            -0.485836 -0.198618
infant_mort          -0.851514  -0.539514            -0.576804 -0.238393
age1-4mort           -0.802324  -0.417762            -0.447373 -0.162339
alcohol               0.407690   0.304989             0.529580  0.372205
bmi                   0.673261   0.410808             0.461679  0.248024
age5-19thinness      -0.474768  -0.370173            -0.573455 -0.396721
youth_obesity         0.588918   0.584749             0.432588  0.210695
measles               0.659893   0.343571             0.397029  0.203850
polio                 0.662147   0.356950             0.412707  0.223872
diphtheria            0.651661   0.355730             0.409616  0.224228
basic_water           1.000000   0.521022             0.510005  0.205403
gni_capita            0.521022   1.000000             0.424780  0.127437
health_expenditure    0.510005   0.424780             1.000000  0.689880
che_gdp               0.205403   0.127437             0.689880  1.000000
une_pop               0.028914  -0.038913            -0.081169 -0.070979
une_infant           -0.850791  -0.547087            -0.588625 -0.246567
une_life              0.830581   0.581836             0.597990  0.275515
une_hiv              -0.287143  -0.190708            -0.086570  0.024850
une_gni               0.532326   0.995786             0.443471  0.136916

                     une_pop  une_infant  une_life   une_hiv   une_gni
year                0.016757   -0.187952  0.185664 -0.018294  0.147887
life_expect         0.032126   -0.931899  0.991448 -0.511821  0.603019
life_exp60          0.004131   -0.776510  0.869439 -0.343894  0.602258
adult_mortality    -0.061503    0.814884 -0.943640  0.680558 -0.544664
infant_mort        -0.003967    0.996975 -0.926927  0.341615 -0.549928
age1-4mort         -0.032953    0.902324 -0.855848  0.292005 -0.421805
alcohol            -0.037812   -0.449387  0.394807 -0.038341  0.296187
bmi                -0.166194   -0.644441  0.587912 -0.154689  0.413644
age5-19thinness     0.265009    0.586277 -0.551026  0.193470 -0.368289
youth_obesity      -0.044698   -0.606526  0.613217 -0.243627  0.565269
measles            -0.015849   -0.723022  0.634170 -0.110764  0.357171
polio              -0.029698   -0.729671  0.641438 -0.107839  0.367155
diphtheria         -0.028161   -0.721966  0.632861 -0.093512  0.362230
basic_water         0.028914   -0.850791  0.830581 -0.287143  0.532326
gni_capita         -0.038913   -0.547087  0.581836 -0.190708  0.995786
health_expenditure -0.081169   -0.588625  0.597990 -0.086570  0.443471
che_gdp            -0.070979   -0.246567  0.275515  0.024850  0.136916
une_pop             1.000000    0.000892  0.030840 -0.102309 -0.043031
une_infant          0.000892    1.000000 -0.928764  0.341339 -0.557588
une_life            0.030840   -0.928764  1.000000 -0.543800  0.598395
une_hiv            -0.102309    0.341339 -0.543800  1.000000 -0.190072
une_gni            -0.043031   -0.557588  0.598395 -0.190072  1.000000

[22 rows x 22 columns]
```

[6]:
```
figure = plt.figure(figsize=(19, 15))
plt.matshow(continuous_df.corr(), fignum=figure.number)
plt.xticks(range(continuous_df.select_dtypes(['number']).shape[1]),␣
 ↪continuous_df.select_dtypes(['number']).columns, fontsize=14, rotation=45)
plt.yticks(range(continuous_df.select_dtypes(['number']).shape[1]),␣
 ↪continuous_df.select_dtypes(['number']).columns, fontsize=14)
cb = plt.colorbar()
cb.ax.tick_params(labelsize=14)
plt.title('Correlation Matrix', fontsize=16)
```

[6]:
```
Text(0.5, 1.0, 'Correlation Matrix')
```



[7]:
```
# Find the correlations above a specific threshold
high_corr_pairs = continuous_df.corr().abs().unstack().
 ↪sort_values(kind="quicksort", ascending=False)
filtered_pairs = high_corr_pairs[high_corr_pairs > .6]
filtered_pairs = filtered_pairs[filtered_pairs < 1.0]
```

```
life_exp_high_correlation = filtered_pairs
print(filtered_pairs)
```

```
infant_mort    une_infant       0.996975
une_infant     infant_mort      0.996975
gni_capita     une_gni          0.995786
une_gni        gni_capita       0.995786
une_life       life_expect      0.991448
                                  …
une_gni        life_expect      0.603019
infant_mort    youth_obesity    0.602402
youth_obesity  infant_mort      0.602402
life_exp60     une_gni          0.602258
une_gni        life_exp60       0.602258
Length: 132, dtype: float64
```

[8]:
```
filtered_pairs.loc[lambda x: x.index.get_level_values(level=0).str.
 ↪startswith('life_expect')]
```

[8]:
```
life_expect  une_life              0.991448
             adult_mortality       0.946419
             une_infant            0.931899
             infant_mort           0.930113
             life_exp60            0.886159
             age1-4mort            0.864414
             basic_water           0.831099
             polio                 0.646486
             diphtheria            0.640473
             measles               0.640408
             youth_obesity         0.621000
             health_expenditure    0.609787
             une_gni               0.603019
dtype: float64
```

The following variables have high correlation with life_expect: - infant_mort - age1-4mort - age5-19obesity - gni_capita - une_life - une_infant - measles - polio - diptheria - basic_water - gni_capita - health_expenditure - une_life - une_gni

However, the variables related to mortality rates or expectancy rates are already self-describing, so I will ignore them for the purposes of this project. They will be useful later on to validate any assumptions made.

Variables for analysis

(Descriptions are from the kaggle codebook)

life_expect (dependent): Life expectancy at birth measured in years

bmi: Mean BMI

youth_obesity(renamed from age5-19obesit‘): Prevalence of obesity among children and adolescents. Crude estimate percentage for children with BMI < (median - 2 stdev)

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

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

measles: Measles-containing-vaccine first-dose (MCV1) immunization coverage among 1-year-olds (%)

health_expenditure (renamed from gghe-d): Domestic general government health expenditure (GGHE-D) as percentage of gross domestic product (GDP)

[9]:
```
analysis_df = who_df[['life_expect', 'bmi', 'youth_obesity', 'polio',␣
↪'diphtheria', 'measles', 'health_expenditure', 'year']].copy()
```

Further cleanup

Find any rows that have na data to determine how to handle

[10]:
```
analysis_df[analysis_df.isna().any(axis=1)]
```

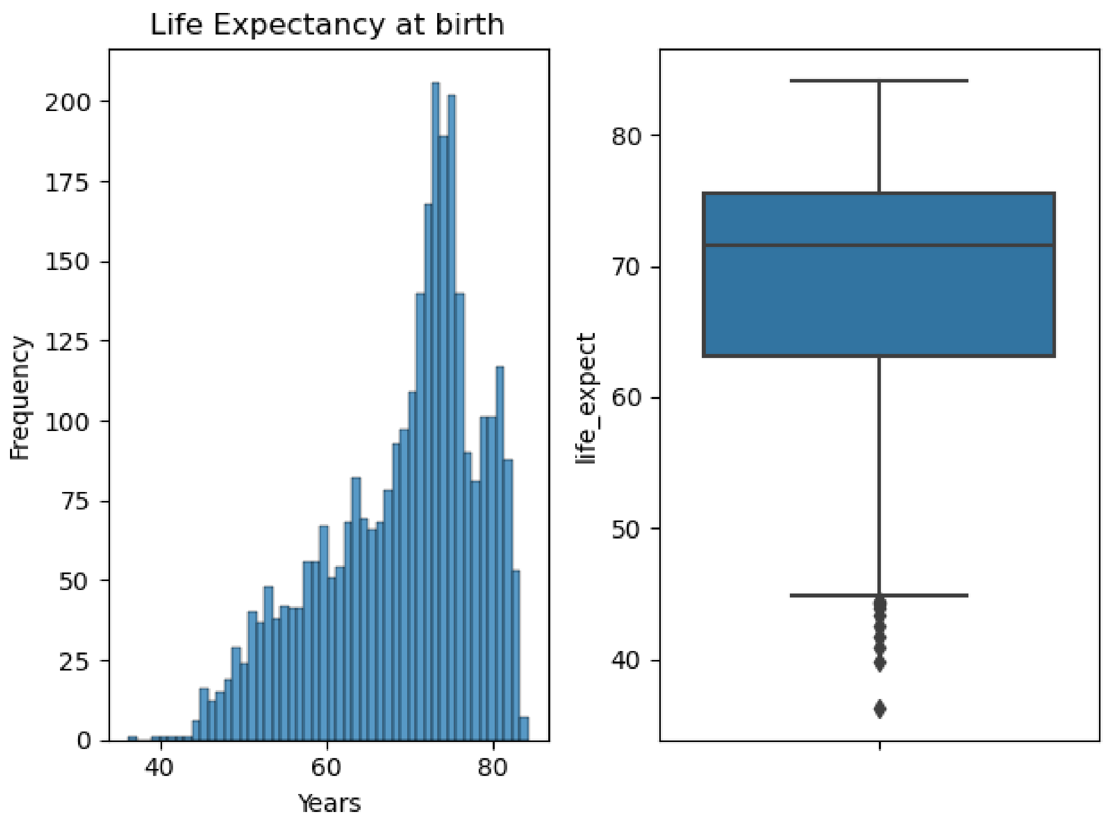
[10]:
```
      life_expect   bmi  youth_obesity  polio  diphtheria  measles  \
170      45.92585  23.3            0.8   78.0        78.0     75.0
171      45.39107  23.3            0.9   76.0        75.0     73.0
172      45.04528  23.3            1.0   73.0        71.0     70.0
173      44.94328  23.4            1.2   70.0        68.0     68.0
174      45.02172  23.4            1.3   67.0        65.0     66.0
…             …     …            …      …           …        …
2718     71.75651  24.0            8.1   99.0        96.0     98.0
2719     71.94337  24.1            8.5   99.0        96.0     99.0
2737     59.13620  19.9            0.9    NaN         NaN      NaN
2738     59.65171  20.0            1.0    NaN         NaN      NaN
2739     60.19300  20.0            1.1   38.0        54.0     56.0

      health_expenditure  year
170                  NaN  2000
171                  NaN  2001
172                  NaN  2002
173                  NaN  2003
174                  NaN  2004
…                    …     …
2718                 NaN  2015
2719                 NaN  2016
2737                 NaN  2000
2738                 NaN  2001
2739                 NaN  2002

[117 rows x 8 columns]
```

[11]:
```python
# Impute the mean for na continuous variables
analysis_df['health_expenditure'].fillna(analysis_df['health_expenditure'].
 ↪mean(), inplace=True)
analysis_df['bmi'].fillna(analysis_df['bmi'].mean(), inplace=True)
analysis_df['polio'].fillna(analysis_df['polio'].mean(), inplace=True)
analysis_df['diphtheria'].fillna(analysis_df['diphtheria'].mean(), inplace=True)
analysis_df['measles'].fillna(analysis_df['measles'].mean(), inplace=True)
```

[12]:
```python
def print_summary(series, title, x_title, y_title='Frequency', bins=50):
    print(series.describe())

    plt.subplot(1, 2, 1)
    sns.histplot(series, bins=bins)
    plt.title(title)
    plt.ylabel(y_title)
    plt.xlabel(x_title)

    plt.subplot(1, 2, 2)
    sns.boxplot(y=series)

    plt.tight_layout()
    plt.show()
```

[13]:
```python
life_expect = analysis_df['life_expect']
print_summary(life_expect, 'Life Expectancy at birth', 'Years')
```

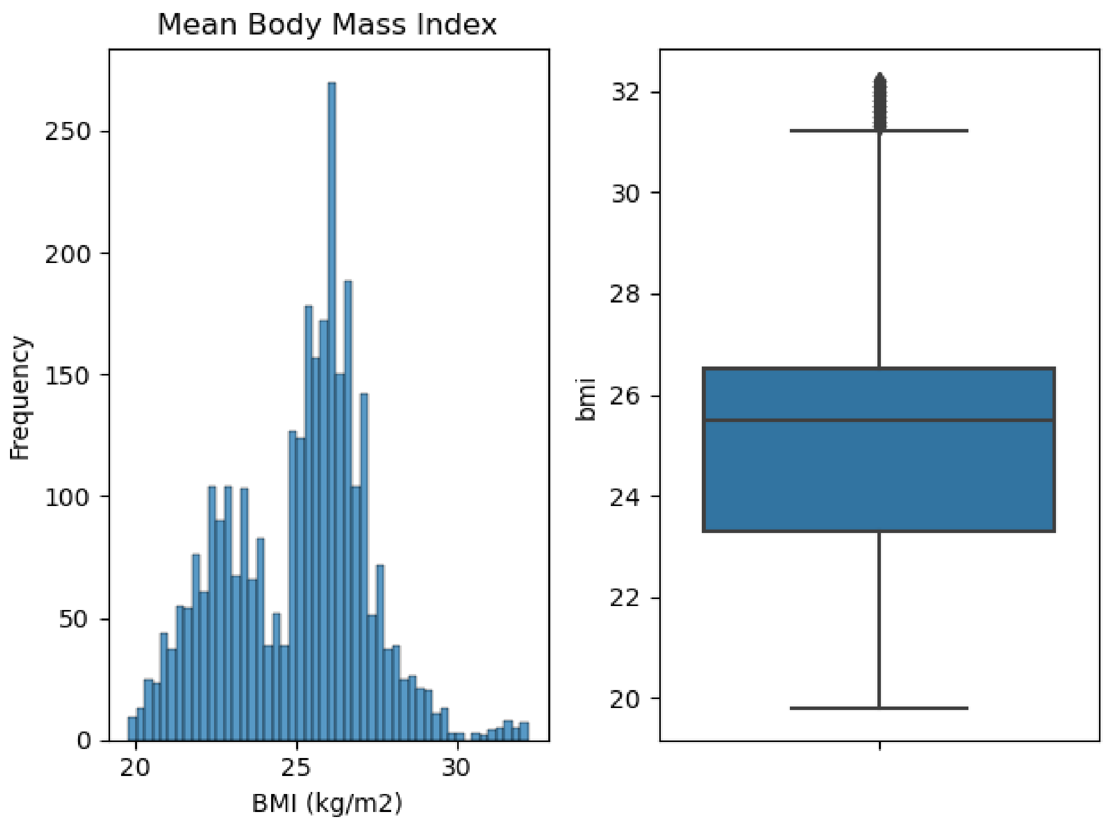
```
count    3111.000000
mean       69.146384
std         9.129761
min        36.227360
25%        63.200095
50%        71.597200
75%        75.537030
max        84.166160
Name: life_expect, dtype: float64
```



Life expectancy is left/negatively skewed with a long tail on the left side of the histogram.

[14]:
```
bmi = analysis_df['bmi']
print_summary(bmi, 'Mean Body Mass Index', 'BMI (kg/m2)')
```

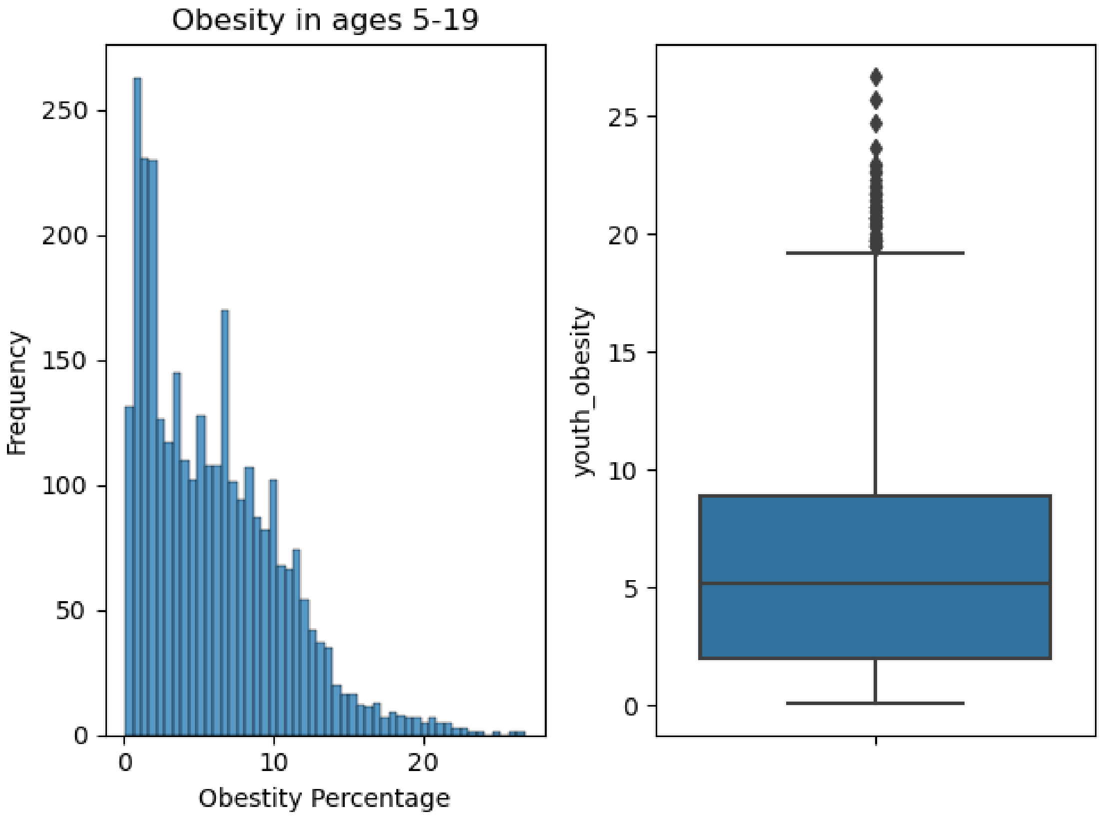
```
count    3111.000000
mean       25.052714
std         2.181422
min        19.800000
25%        23.300000
50%        25.500000
75%        26.500000
max        32.200000
Name: bmi, dtype: float64
```



BMI has a bimodal distribution, with two peaks occuring around 22-24 and at 26.

[15]:
```
youth_obesity = analysis_df['youth_obesity']
print_summary(youth_obesity, 'Obesity in ages 5-19', 'Obestity Percentage')
```

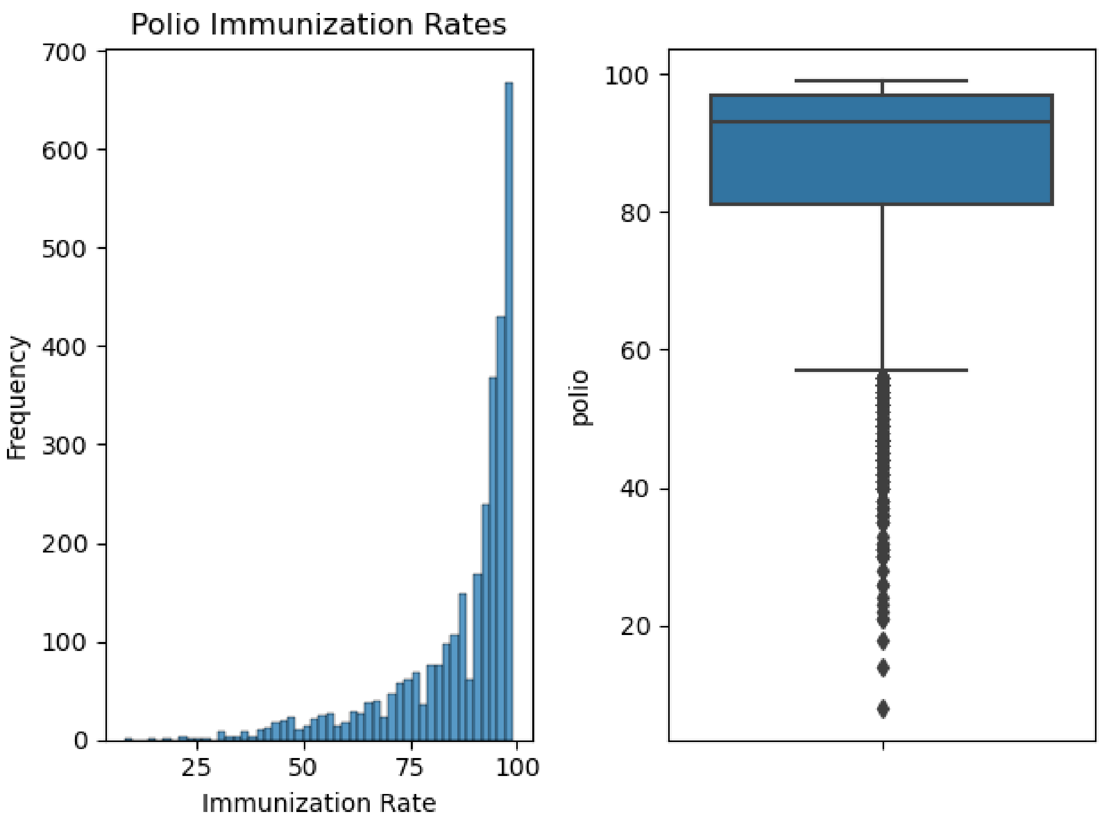
```
count    3077.000000
mean        5.972278
std         4.530812
min         0.100000
25%         2.000000
50%         5.200000
75%         8.900000
max        26.700000
Name: youth_obesity, dtype: float64
```



Obesity in younger children and teenagers is heavily right/positively skewed with a very long tail above 15%

[16]:
```
polio = analysis_df['polio']
print_summary(polio, 'Polio Immunization Rates', 'Immunization Rate')
```

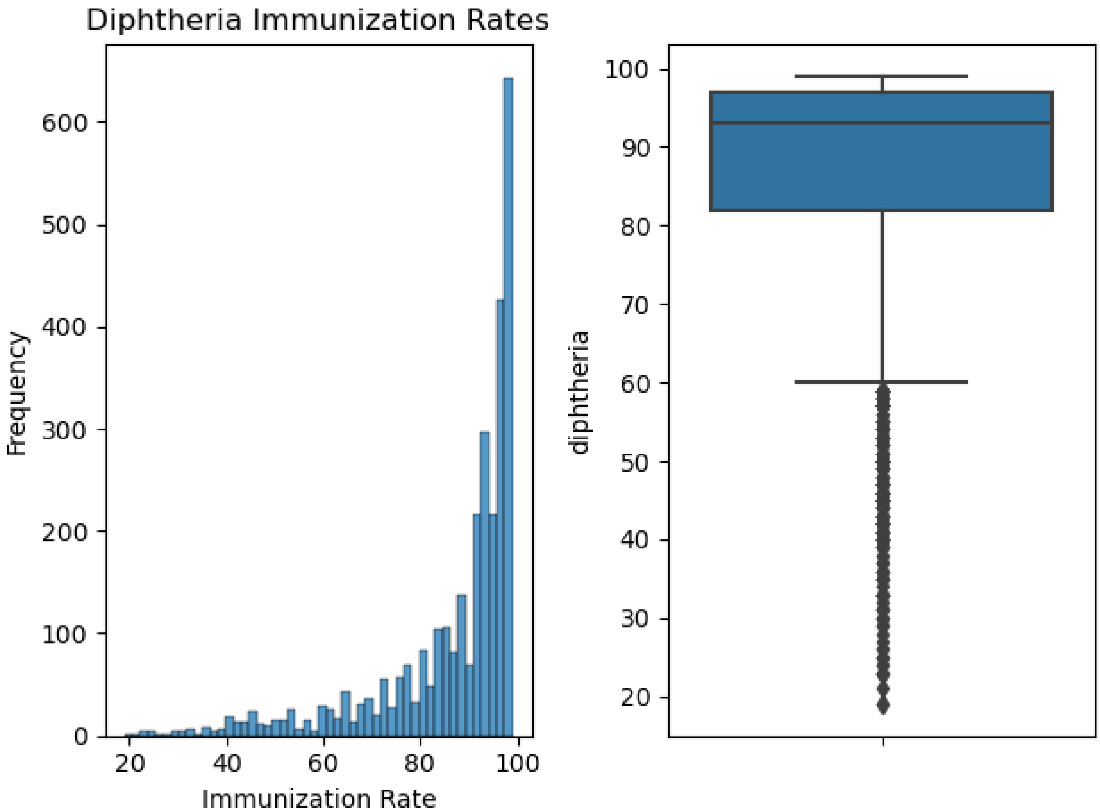
```
count    3111.000000
mean       86.608991
std        14.897509
min         8.000000
25%        81.000000
50%        93.000000
75%        97.000000
max        99.000000
Name: polio, dtype: float64
```



Immunization for polio is very left/negatively skewed with a very long tail on the right.

[55]:
```
diphtheria = analysis_df['diphtheria']
print_summary(diphtheria, 'Diphtheria Immunization Rates', 'Immunization Rate')
```

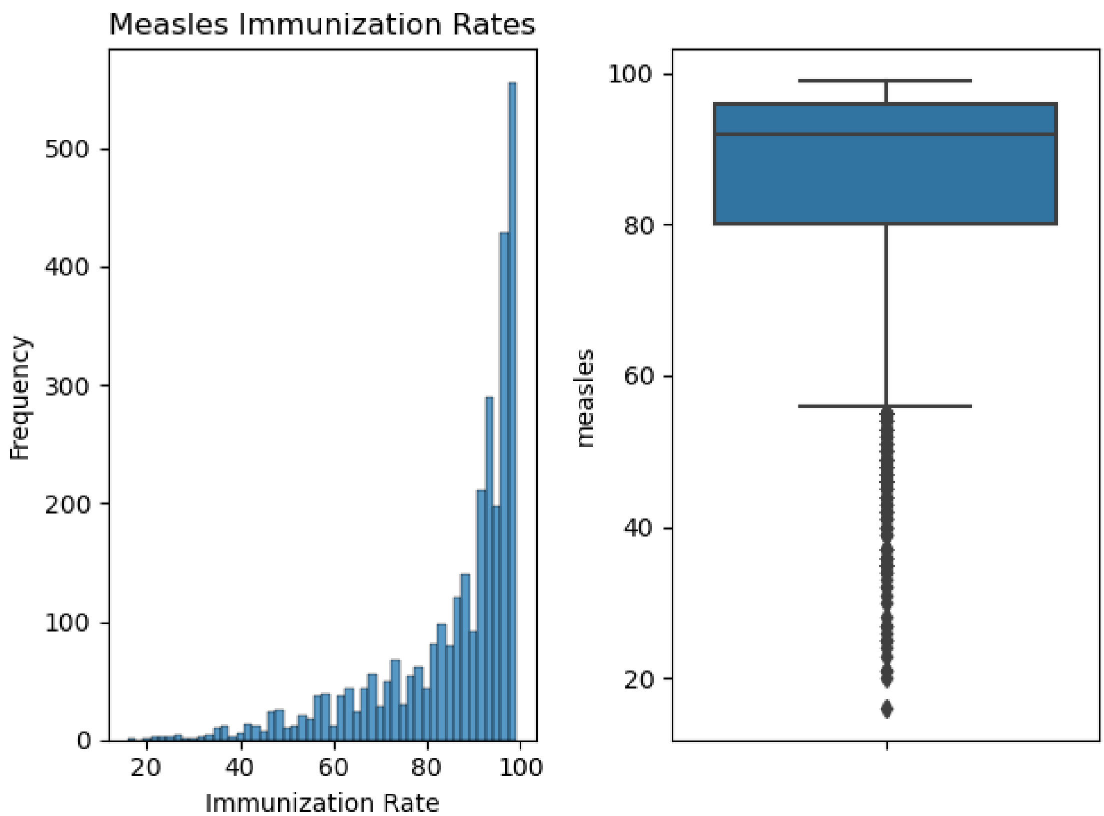
```
count    3111.000000
mean       86.420116
std        15.285254
min        19.000000
25%        82.000000
50%        93.000000
75%        97.000000
max        99.000000
Name: diphtheria, dtype: float64
```



This distribution (and the variable's mode and mean) are identical to that of polio. This leads me to believe that polio and diphtheria immunizations are given together.

[56]:
```
measles = analysis_df['measles']
print_summary(measles, 'Measles Immunization Rates', 'Immunization Rate')
```

```
count    3111.000000
mean       85.540427
std        15.235493
min        16.000000
25%        80.000000
50%        92.000000
75%        96.000000
max        99.000000
Name: measles, dtype: float64
```

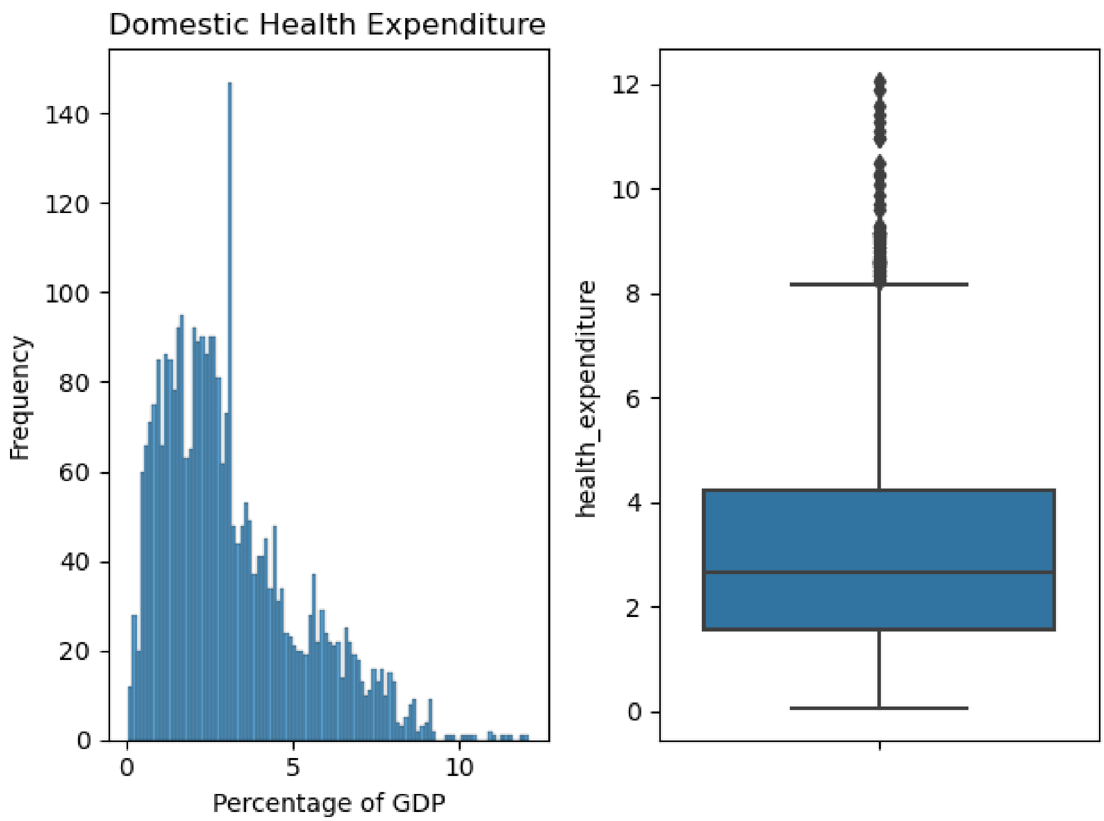


As seen above, this distribution (and the variable's mode and mean) are identical to that of polio and diphtheria. After doing more research, these vaccines are typically given together in a DTaP vaccine containing all three vaccines.

Given that discovery, I will only use one of the variables in further analysis.

[19]:
```
health_expenditure = analysis_df['health_expenditure']
print_summary(health_expenditure, 'Domestic Health Expenditure', 'Percentage of␣
↪GDP', 'Frequency', bins=100)
```

```
count    3111.000000
mean        3.122935
std         2.057816
min         0.062360
25%         1.568265
50%         2.662370
75%         4.219620
max        12.062730
Name: health_expenditure, dtype: float64
```



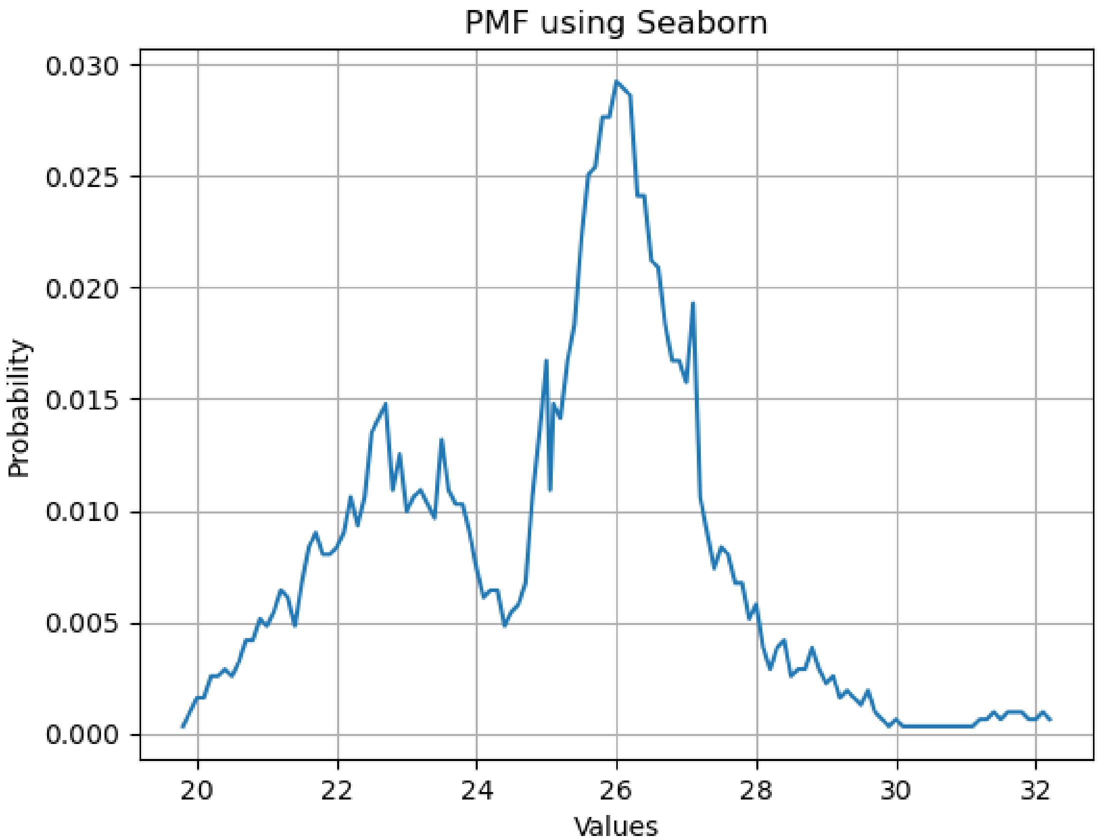
This distribution is right/positively skewed, with a shorter tail. I couldn't tell if it was also bimodal since there seems to be a slight hump around the 6% mark. However, when increasing or reducing the number of bins, I think this distribution is still typically asymmetrical.

Comparison using a Probability Mass Function

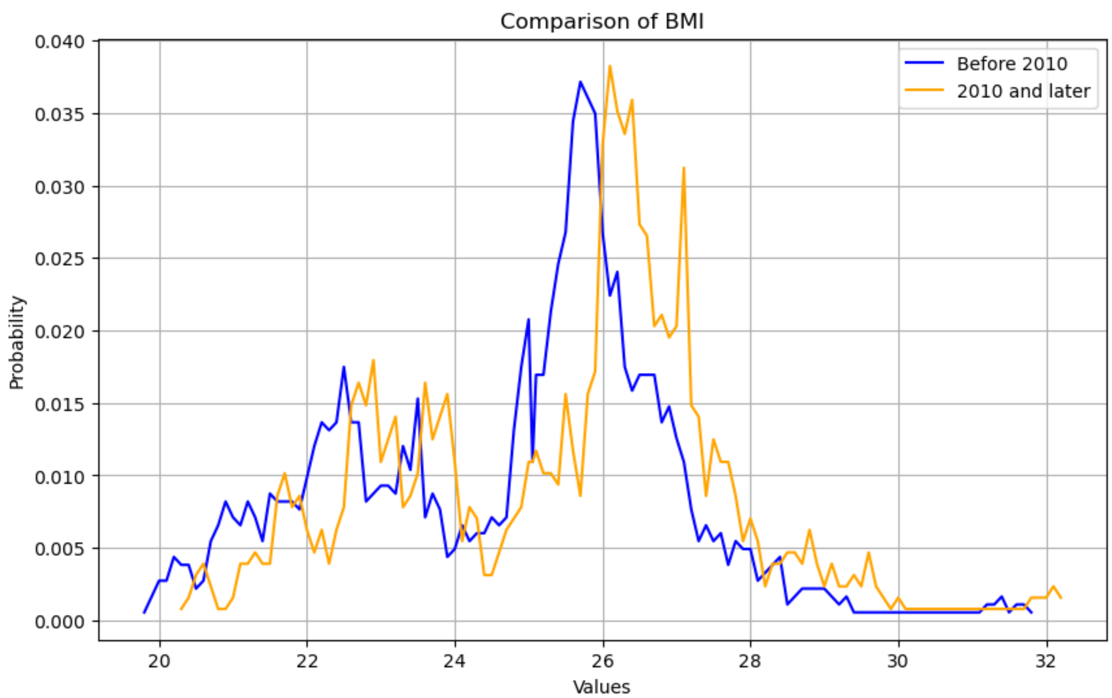
I was trying to find some sort of consistent value to filter data on, but `year` seemed like the only thing that would work, so the comparisons will segment data by year and use that for comparisons for a single variable.

[20]:
```
bmi_pmf = bmi.value_counts(normalize=True).sort_index()
```

[21]:
```
sns.lineplot(x=bmi_pmf.index, y=bmi_pmf.values)
plt.xlabel('Values')
plt.ylabel('Probability')
plt.title('PMF using Seaborn')
plt.grid(True)
plt.show()
```

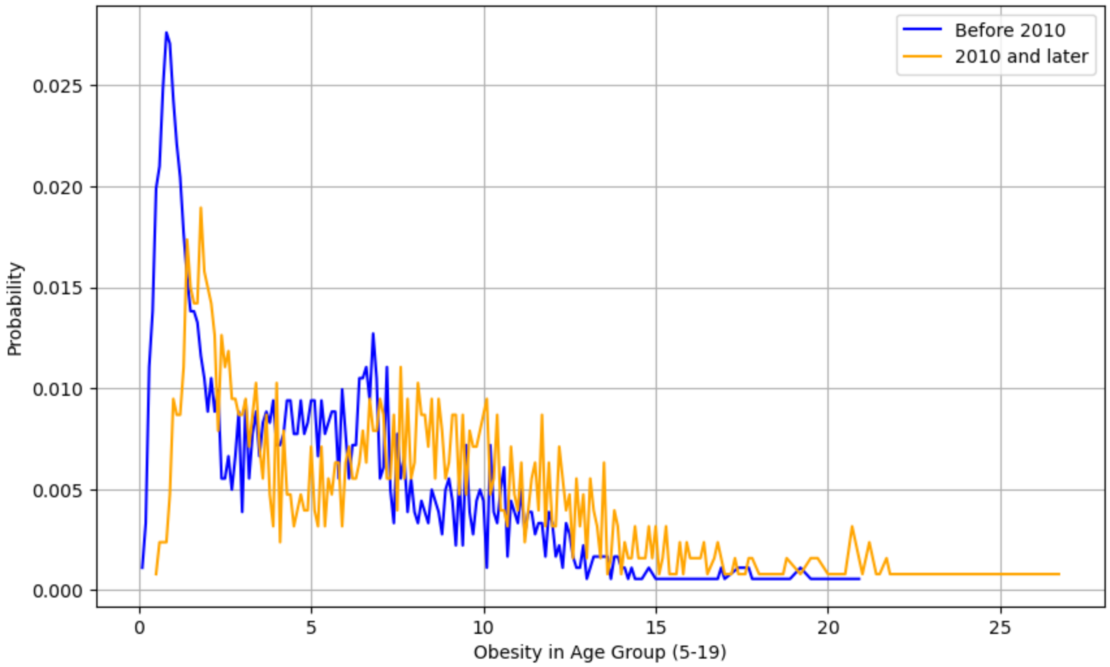


[22]:
```
pre_2010 = analysis_df[analysis_df['year'] < 2010]
pre_2010_pmf = pre_2010['bmi'].value_counts(normalize=True)

after_including_2010 = analysis_df.loc[analysis_df['year'] >= 2010]
after_including_2010_pmf = after_including_2010['bmi'].
 ↪value_counts(normalize=True)

# Plot the PMFs side by side
plt.figure(figsize=(10, 6))
sns.lineplot(x=pre_2010_pmf.index, y=pre_2010_pmf.values, color='blue',␣
 ↪label='Before 2010')
sns.lineplot(x=after_including_2010_pmf.index, y=after_including_2010_pmf.
 ↪values, color='orange', label='2010 and later')
plt.xlabel('Values')
plt.ylabel('Probability')
plt.title('Comparison of BMI')
plt.grid(True)
plt.legend()
plt.show()
```



Interesting to note that there is a clear increase in BMI for reports after 2010.

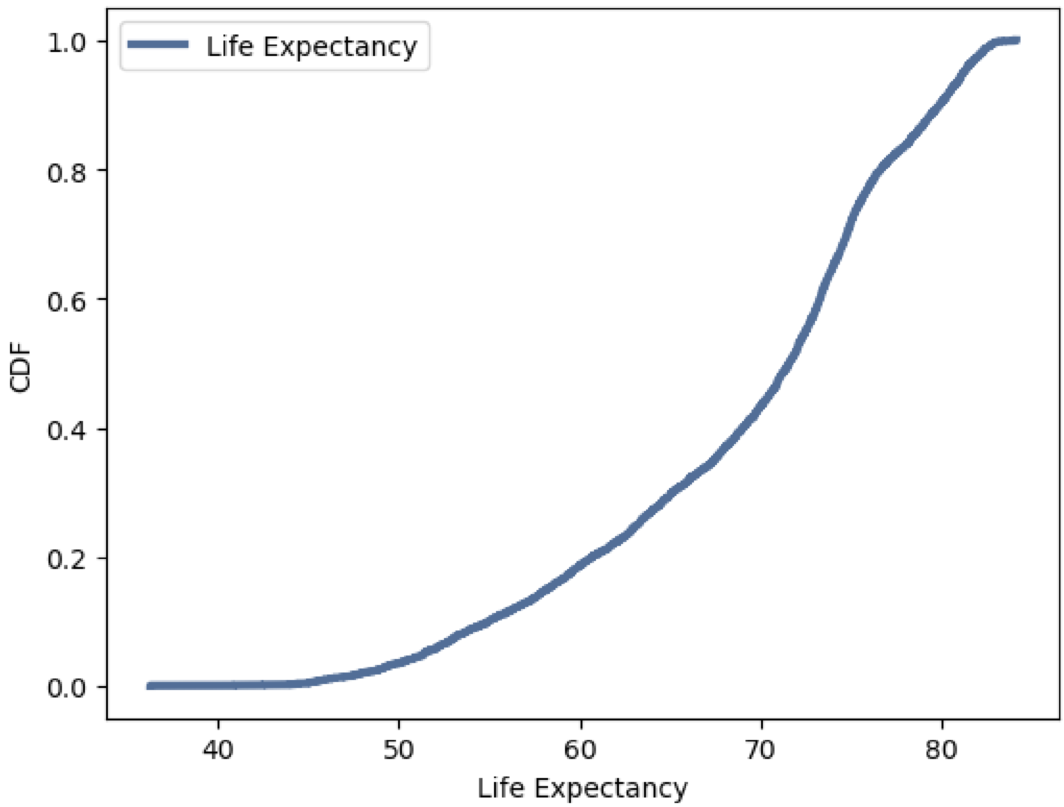
[23]:
```
# This was such an interesting comparison, I did the same thing for teenage␣
↪obesity levels
# to see if the same effect was in a smaller sample of the population
pre_2010 = analysis_df[analysis_df['year'] < 2010]
pre_2010_pmf = pre_2010['youth_obesity'].value_counts(normalize=True)

after_including_2010 = analysis_df.loc[analysis_df['year'] >= 2010]
after_including_2010_pmf = after_including_2010['youth_obesity'].
↪value_counts(normalize=True)

# Plot the PMFs side by side
plt.figure(figsize=(10, 6))
sns.lineplot(x=pre_2010_pmf.index, y=pre_2010_pmf.values, color='blue',␣
↪label='Before 2010')
sns.lineplot(x=after_including_2010_pmf.index, y=after_including_2010_pmf.
↪values, color='orange', label='2010 and later')
plt.ylabel('Probability')
plt.xlabel("Obesity in Age Group (5-19)")
plt.legend()
plt.grid(True)
plt.show()
```



Again, we see a similar trend in a different group of the population. Note in the years after and including 2010, the distribution has become less positively skewed and the tail has grown when compared to the sample before 2010.

Cumulative Distribution Function (CDF)

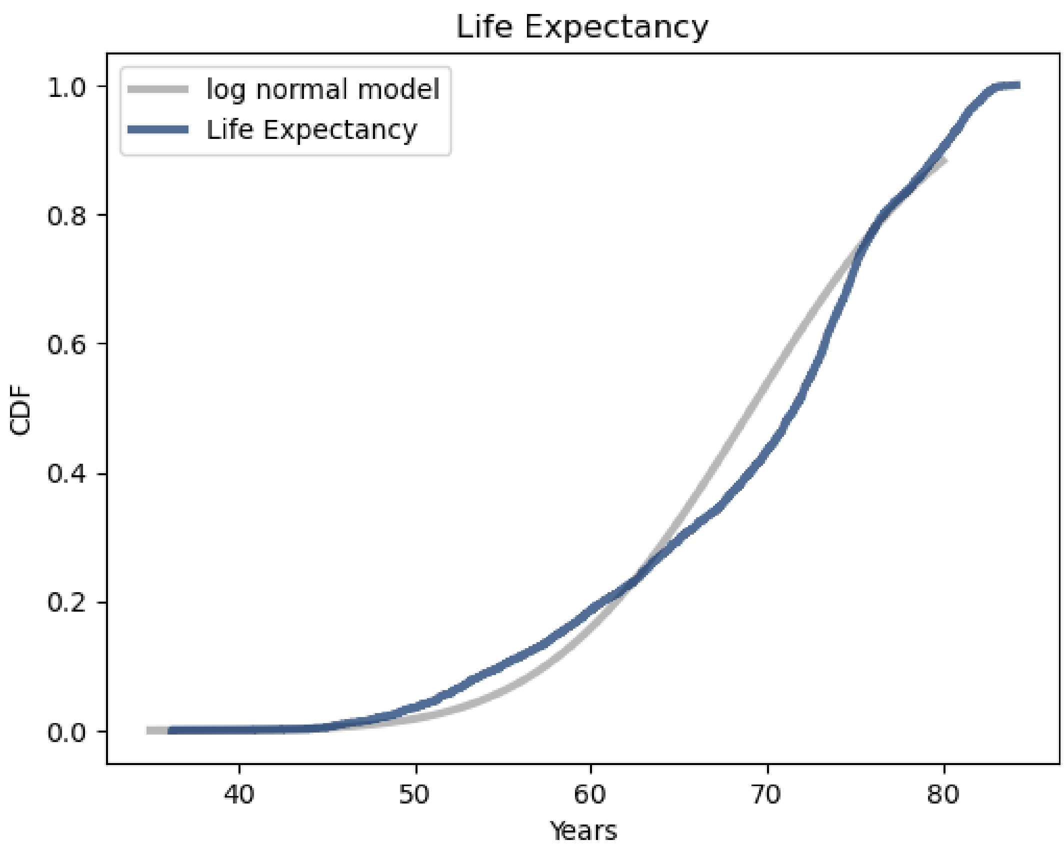
[24]:
```
life_expect_cdf = thinkstats2.Cdf(analysis_df['life_expect'], label = "Life␣
↪Expectancy")
thinkplot.Cdf(life_expect_cdf)
thinkplot.Show(xlabel = "Life Expectancy", ylabel = "CDF")
```



<Figure size 800x600 with 0 Axes>

[25]:
```
#Log CDF compared to log normal

life_expect_mean = analysis_df['life_expect'].mean()
life_expect_var = analysis_df['life_expect'].var()
life_expect_sig = np.sqrt(life_expect_var)
print(life_expect_mean, life_expect_var, life_expect_sig)

xs, ps = thinkstats2.RenderNormalCdf(life_expect_mean, life_expect_sig, low =␣
 ↪35, high = 80)

life_expect_cdf = thinkstats2.Cdf(analysis_df['life_expect'], label = "Life␣
 ↪Expectancy")

thinkplot.Plot(xs, ps, label = "log normal model", color = "0.6")
thinkplot.Cdf(life_expect_cdf)
thinkplot.Config(title = "Life Expectancy",
                xlabel = "Years",
                ylabel = "CDF")
```

```
69.1463837833494 83.35253040642105 9.129760698201299
```

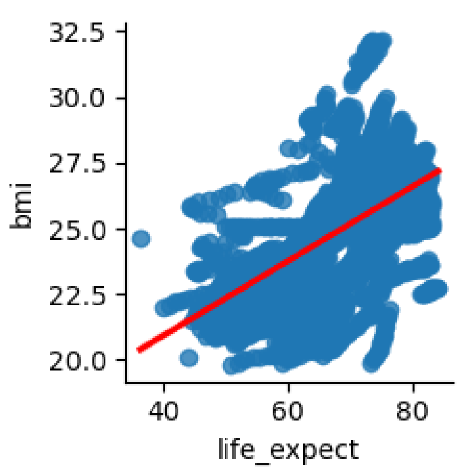


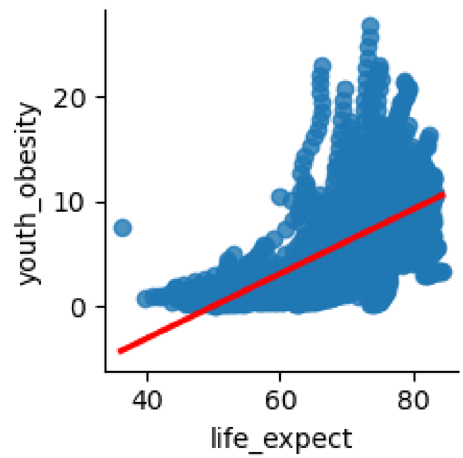
Analytical Distribution

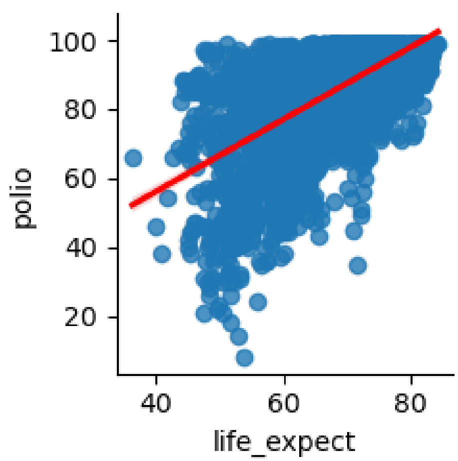
[37]:
```
mean, stdev = thinkstats2.TrimmedMeanVar(analysis_df['life_expect'], p=0.01)

print('Mean, Var', mean, stdev)

# plot the analytic model
sigma = np.sqrt(stdev)
print('Sigma', sigma)
xs, ps = thinkstats2.RenderNormalCdf(mean, sigma, low=20, high=100)

thinkplot.Plot(xs, ps, label='model', color ='0.6')
thinkplot.Config(title = 'Analytical Distribution of Life Expectancy',
                 xlabel = 'Year)',
                 ylabel = 'CDF')
```

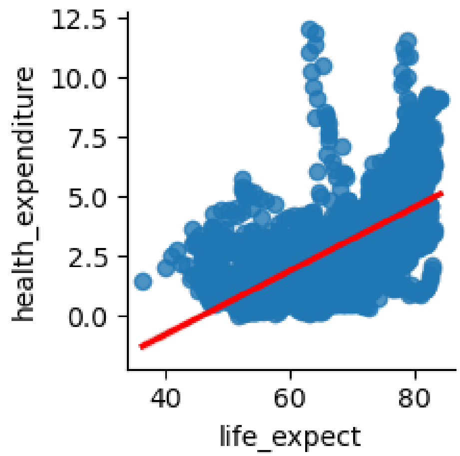
```
Mean, Var 69.25796309281732 76.72990397157666
Sigma 8.759560717957074
```

[54]:
```
for i in [1, 2, 3, 6]:
    sns.pairplot(data=analysis_df,
            kind="reg",
            y_vars=analysis_df.columns[i],
            x_vars=['life_expect'],
            plot_kws={'line_kws':{'color':'red'}})
```




20
10
0
youth_obesity
40
60
80
life_expect

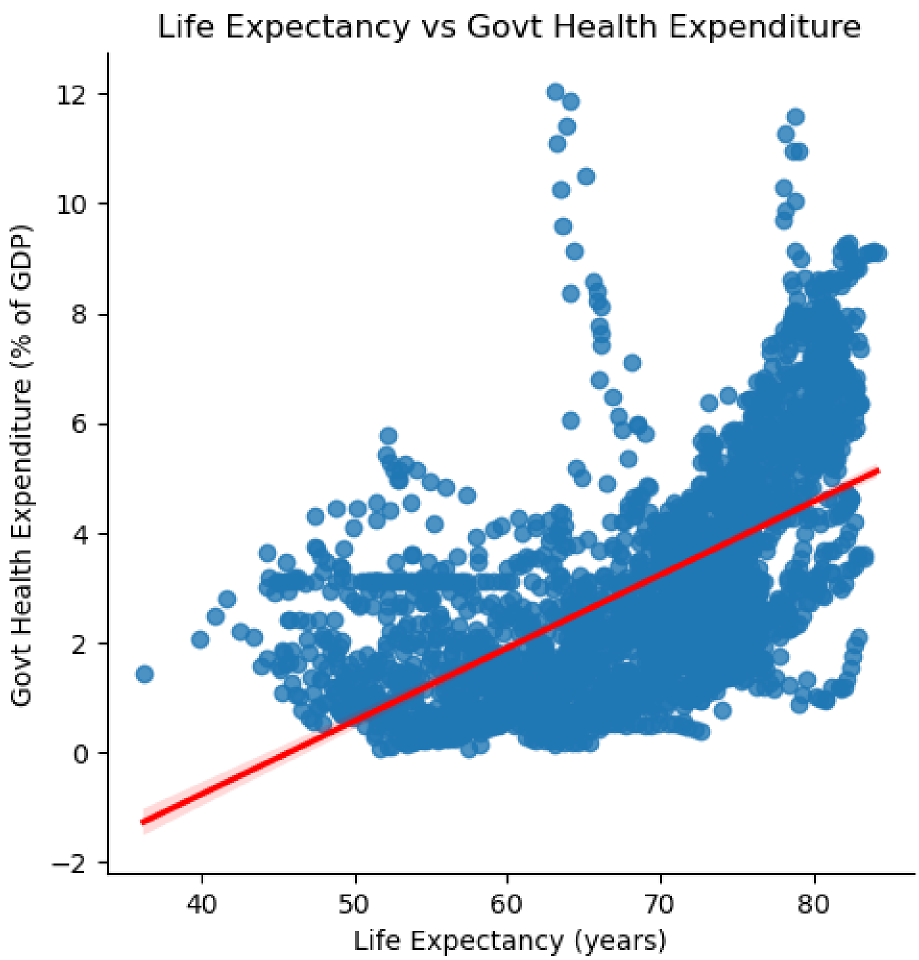

100
80
60
40
20
polio
40
60
80
life_expect



Scatter Plots comparing two variables

I will compare life expectancy to the expenditure of government money on health

[560]:
```
sns.lmplot(x='life_expect', y='health_expenditure', data=analysis_df,␣
 ↪line_kws={'color':"red"})
plt.xlabel('Life Expectancy (years)')
plt.ylabel('Govt Health Expenditure (% of GDP)')
plt.title('Life Expectancy vs Govt Health Expenditure')
plt.show()
```



As expected, there is a positive correlation between life expectancy and the health expenditure of a government. This is confirmed by an analysis of the spearman and pearson correlations between the values.

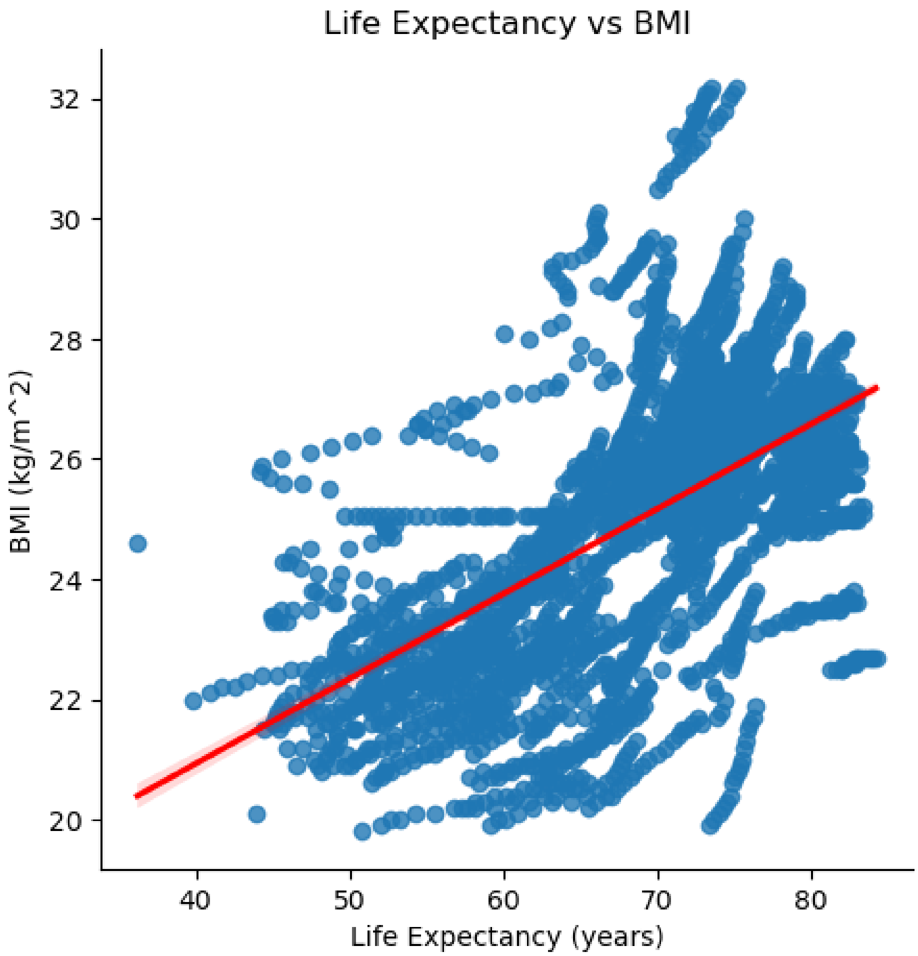
[562]:
```
rho, _ = spearmanr(analysis_df['life_expect'],␣
↪analysis_df['health_expenditure'])
print(f"Spearman correlation: {rho:.4f}")
print(f"Pearson correlation coefficient: {analysis_df['life_expect'].
↪corr(analysis_df['health_expenditure']):.4f}")
```

```
Spearman correlation: 0.6671
Pearson correlation coefficient: 0.5911
```

And a similar comparison between life expectancy and BMI

[565]:
```
sns.lmplot(x='life_expect', y='bmi', data=analysis_df, line_kws={'color':"red"})
plt.xlabel('Life Expectancy (years)')
plt.ylabel('BMI (kg/m^2)')
```

```
plt.title('Life Expectancy vs BMI')
plt.show()
```



[453]:
```
rho, _ = spearmanr(analysis_df['life_expect'], analysis_df['bmi'])
print(f"Spearman correlation: {rho:.4f}")
print(f"Pearson correlation coefficient: {analysis_df['life_expect'].
  ↪corr(analysis_df['bmi']):.4f}")
```

```
Spearman correlation: 0.5834
Pearson correlation coefficient: 0.5924
```

The correlation between life expectancy and BMI is still positive, but only slightly.

Hypothesis Test

Hypothesis: Governmental health expenditure is causitive to higher life expectancy

[473]:
```python
# Borrowed these helpers from thinkstats
class CorrelationPermute(thinkstats2.HypothesisTest):

    def TestStatistic(self, data):
        xs, ys = data
        test_stat = abs(thinkstats2.Corr(xs, ys))
        return test_stat

    def RunModel(self):
        xs, ys = self.data
        xs = np.random.permutation(xs)
        return xs, ys
```

[567]:
```python
life_expectancy_health_expenditure = analysis_df['life_expect'].values[:500],␣
 ↪analysis_df['health_expenditure'].values[:500]

health_expenditure_hypothesis =␣
 ↪CorrelationPermute(life_expectancy_health_expenditure)
p_value = health_expenditure_hypothesis.PValue(1000)

print('P Value of test:', round(p_value, 3))
print(health_expenditure_hypothesis.actual, health_expenditure_hypothesis.
 ↪MaxTestStat())
```

```
P Value of test: 0.003
0.13041427947150694 0.14684206051170612
```

The low p-value shows that, while there is some correlation between life expectancy and govermental health expenditure, it is not large enough to be statistically significant. Let's try again with the other variable.

[570]:
```python
life_expectancy_bmi = analysis_df['life_expect'].values[:500],␣
 ↪analysis_df['bmi'].values[:500]

bmi_hypothesis = CorrelationPermute(life_expectancy_bmi)
p_value = bmi_hypothesis.PValue(1000)

print('P Value of test:', round(p_value, 3))
print(bmi_hypothesis.actual, bmi_hypothesis.MaxTestStat())
```

```
P Value of test: 0.0
0.3956565748216251 0.14343644069932132
```

With an even lower p Value, it is safe to say that the correlation between BMI and life expectancy is not satistically significant either.

Regression Analysis

[610]:
```
formula = 'life_expect ~ bmi + health_expenditure + diphtheria + polio +␣
  ↪youth_obesity'
logit = smf.ols(formula, data=analysis_df)
results = logit.fit()
results.summary()
```

[610]:

Dep. Variable:	life_expect	**R-squared:**	0.644
Model:	OLS	**Adj. R-squared:**	0.643
Method:	Least Squares	**F-statistic:**	1080.
Date:	Fri, 02 Aug 2024	**Prob (F-statistic):**	0.00
Time:	16:34:50	**Log-Likelihood:**	-9282.0
No. Observations:	2994	**AIC:**	1.858e+04
Df Residuals:	2988	**BIC:**	1.861e+04
Df Model:	5		
Covariance Type:	nonrobust		

	coef	**std err**	**t**	**P> |t|**	**[0.025**	**0.975]**
Intercept	38.2642	1.765	21.674	0.000	34.803	41.726
bmi	0.0990	0.079	1.248	0.212	-0.056	0.254
health_expenditure	1.2767	0.055	23.142	0.000	1.169	1.385
diphtheria	0.0553	0.026	2.138	0.033	0.005	0.106
polio	0.1835	0.026	6.942	0.000	0.132	0.235
youth_obesity	0.6491	0.037	17.652	0.000	0.577	0.721

Omnibus:	640.778	**Durbin-Watson:**	0.179
Prob(Omnibus):	0.000	**Jarque-Bera (JB):**	1510.310
Skew:	-1.186	**Prob(JB):**	0.00
Kurtosis:	5.546	**Cond. No.**	2.29e+03

Notes:
[1] Standard Errors assume that the covariance matrix of the errors is correctly specified.
[2] The condition number is large, 2.29e+03. This might indicate that there are
strong multicollinearity or other numerical problems.

Reviewing the results from the regression analysis, we can conclude:

- The R-squared value is greater than 0.5 so it is better than random, though not a large amount. An r-squared value that approaches 1 is a better fit.
- The Durbin-Watson measures homoscedasticity, and a low number of 0.179 implies a strong positive serial correlation in the residuals.
- The kurtosis value of 5.5 implies that there are more extreme values in the distribution that would be a normal distribution. Therefore, there must be significant outliers or extreme values.