life-expectancy

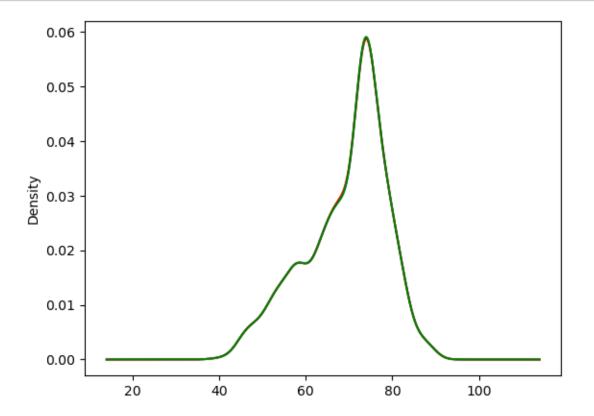
July 24, 2024

```
[1]: import pandas as pd
     import numpy as np
     import matplotlib.pyplot as plt
     import seaborn as sns
[3]: df = pd.read csv('data.csv')
     df.columns
[3]: Index(['Country', 'Year', 'Status', 'Life expectancy ', 'Adult Mortality',
            'infant deaths', 'Alcohol', 'percentage expenditure', 'Hepatitis B',
            'Measles ', ' BMI ', 'under-five deaths ', 'Polio', 'Total expenditure',
            'Diphtheria ', ' HIV/AIDS', 'GDP', 'Population',
            'thinness 1-19 years', 'thinness 5-9 years',
            'Income composition of resources', 'Schooling'],
           dtype='object')
[5]: df = df.drop(columns=['Country', 'Year', 'Status', 'percentage expenditure', 'BMI_

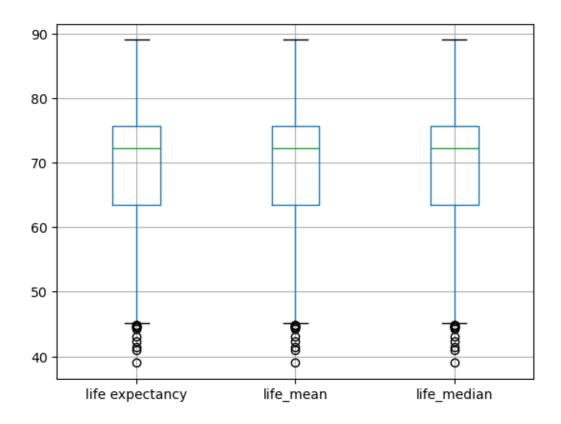
¬','Total expenditure','GDP','Population','Income composition of resources'])
[7]: df.columns
[7]: Index(['Life expectancy ', 'Adult Mortality', 'infant deaths', 'Alcohol',
            'Hepatitis B', 'Measles ', 'under-five deaths ', 'Polio', 'Diphtheria ',
            ' HIV/AIDS', ' thinness 1-19 years', ' thinness 5-9 years',
            'Schooling'],
           dtype='object')
[8]: df.rename(columns = {'Life expectancy ':'life expectancy', 'Adult Mortality':
      _{\hookrightarrow}'adult mortality' ,'Alcohol':'alcohol' , 'Hepatitis B':'hepatitis b'_{\sqcup}
      →,'Measles ':'measles' , 'under-five deaths ':'under five deaths' ,'Polio':
      _{\hookrightarrow}'polio' , 'Diphtheria ':'diphtheria' ,' HIV/AIDS':'hiv/aids' , ' thinness _{\sqcup}
      _{\ominus}1-19 years':'thinness 1-19 years' ,' thinness 5-9 years':'thinness 5-9_{\sqcup}
      →years' , 'Schooling':'schooling'} , inplace=True)
[9]: df.columns
```

```
[9]: Index(['life expectancy', 'adult mortality', 'infant deaths', 'alcohol',
             'hepatitis b', 'measles', 'under five deaths', 'polio', 'diphtheria',
             'hiv/aids', 'thinness 1-19 years', 'thinness 5-9 years', 'schooling'],
            dtype='object')
     Data Cleaning
[11]: df.duplicated().sum()
[11]: 0
[12]: df.isnull().sum()
[12]: life expectancy
                               6
     adult mortality
                               6
      infant deaths
                               0
     alcohol
                             136
                             370
     hepatitis b
     measles
                               0
     under five deaths
                               0
     polio
                              11
     diphtheria
                              11
     hiv/aids
                               0
      thinness 1-19 years
                              24
      thinness 5-9 years
                              24
      schooling
                             109
      dtype: int64
[13]: #-----life expectancy----
      df['life_mean'] = df['life expectancy'].fillna(df['life expectancy'].mean())
      df['life_median'] = df['life expectancy'].fillna(df['life expectancy'].median())
[14]: | print('life expectancy variance', df['life expectancy'].var())
      print('life mean variance',df['life mean'].var())
      print('life_median variance',df['life_median'].var())
     life expectancy variance 89.24759418633725
     life mean variance 88.98701726900484
     life_median variance 89.00991260757192
[15]: plt.subplot(111)
      df['life expectancy'].plot.kde()
      df['life_mean'].plot.kde(color='red')
      df['life_median'].plot.kde(color='green')
```

plt.show()

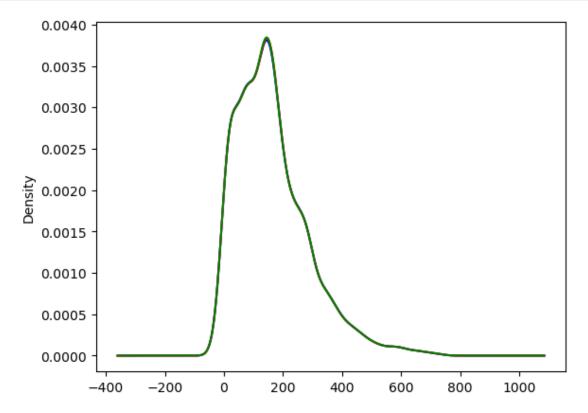


```
[16]: df[['life expectancy','life_mean','life_median']].boxplot()
    plt.show()
```

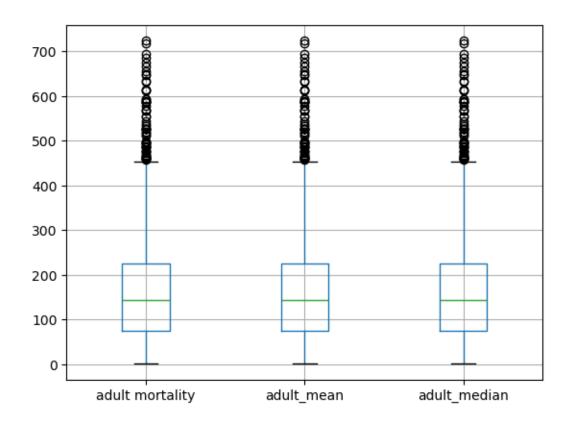


```
[17]: | df = df.drop(columns=['life_mean','life_median'])
[18]: #-
                       -----adult mortality------
      df['adult_mean'] = df['adult mortality'].fillna(df['adult mortality'].mean())
      df['adult_median'] = df['adult mortality'].fillna(df['adult mortality'].
       →median())
[27]: print('adult mortality variance', df['adult mortality'].var())
      print('adult_mean variance',df['adult_mean'].var())
      print('adult_median variance',df['adult_median'].var())
     adult mortality variance 15147.583834112995
     adult_mean variance 15103.357311969596
     adult_median variance 15104.486723091637
[31]: fig = plt.figure()
      ax = fig.add_subplot(111)
      df['adult mortality'].plot.kde(ax=ax , color='blue')
      df['adult_mean'].plot.kde(ax=ax , color='red')
```

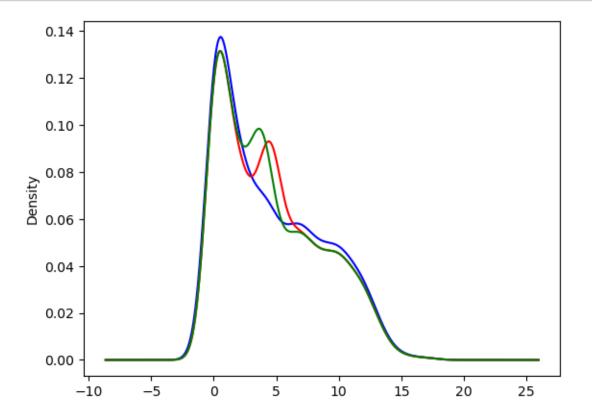
```
df['adult_median'].plot.kde(ax=ax , color='green')
plt.show()
```



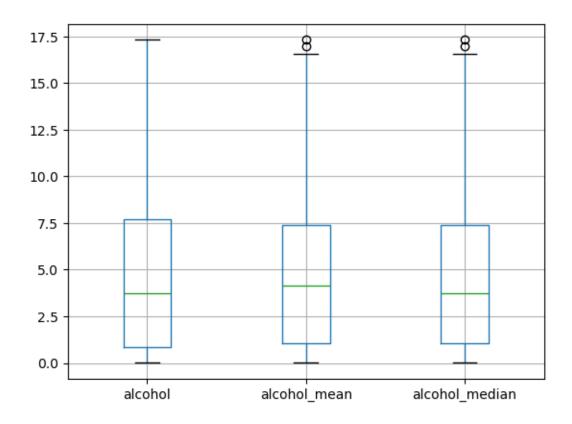
```
[32]: df[['adult mortality','adult_mean','adult_median']].boxplot()
plt.show()
```



plt.show()



[37]: df[['alcohol','alcohol_mean','alcohol_median']].boxplot()
plt.show()



```
[38]: df = df.drop(columns=['alcohol_mean','alcohol_median'])

[39]: # end of distribution imputation

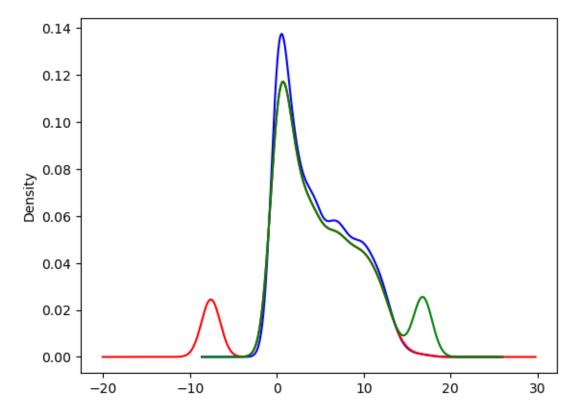
lower_alcohol = df['alcohol'].mean() - 3*df['alcohol'].std()
    upper_alcohol = df['alcohol'].mean() + 3*df['alcohol'].std()

df['alcohol_lower'] = df['alcohol'].fillna(lower_alcohol)
    df['alcohol_upper'] = df['alcohol'].var())
    print('alcohol_variance',df['alcohol_lower'].var())
    print('alcohol_lower variance',df['alcohol_lower'].var())

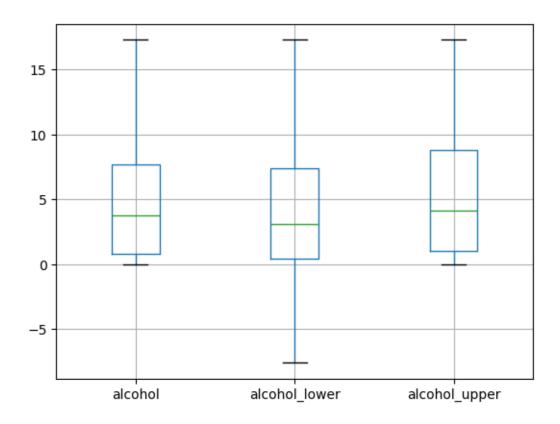
alcohol_variance 16.528493131839596
    alcohol_lower variance 24.62813858322042
    alcohol_upper variance 24.628138583220537

[41]: plt.subplot(111)
    df['alcohol'].plot.kde(color='blue')
```

```
df['alcohol_lower'].plot.kde(color='red')
df['alcohol_upper'].plot.kde(color='green')
plt.show()
```



```
[42]: df[['alcohol','alcohol_lower','alcohol_upper']].boxplot()
plt.show()
```



```
[43]: df = df.drop(columns = ['alcohol_lower', 'alcohol_upper'])

[44]: # second end of distribution imputation

q1_alcohol = df['alcohol'].quantile(0.25)
q3_alcohol = df['alcohol'].quantile(0.75)
iqr = q3_alcohol - q1_alcohol
lower_alcohol = q1_alcohol - 1.5*iqr
upper_alcohol = q3_alcohol + 1.5*iqr

df['alcohol_lower'] = df['alcohol'].fillna(lower_alcohol)
df['alcohol_upper'] = df['alcohol'].fillna(upper_alcohol)

[45]: print('alcohol_variance',df['alcohol'].var())
print('alcohol_lower_variance',df['alcohol_lower'].var())
print('alcohol_upper_variance',df['alcohol_upper'].var())
alcohol_variance 16.528493131839596
```

alcohol_lower variance 27.720696436327906 alcohol_upper variance 26.599053692711124

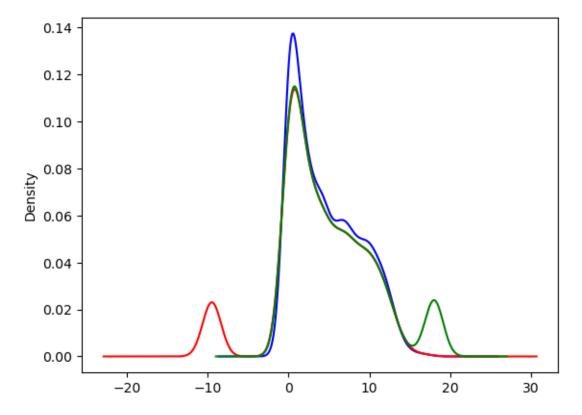
```
[46]: plt.subplot(111)

df['alcohol'].plot.kde(color='blue')

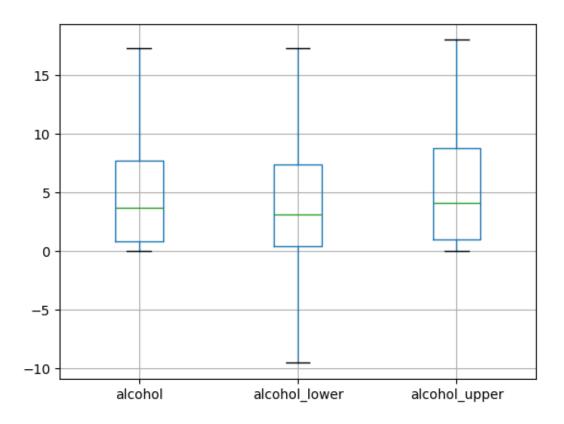
df['alcohol_lower'].plot.kde(color='red')

df['alcohol_upper'].plot.kde(color='green')

plt.show()
```

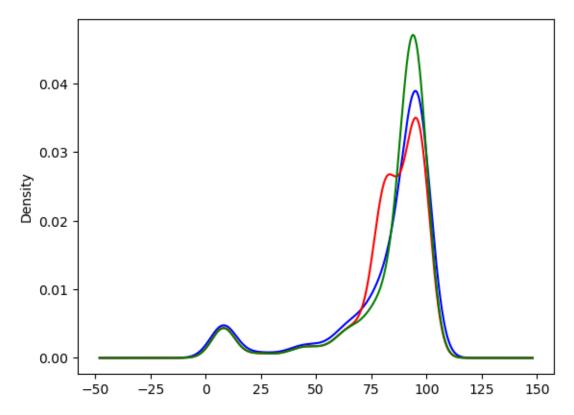


```
[47]: df[['alcohol', 'alcohol_lower', 'alcohol_upper']].boxplot()
plt.show()
```

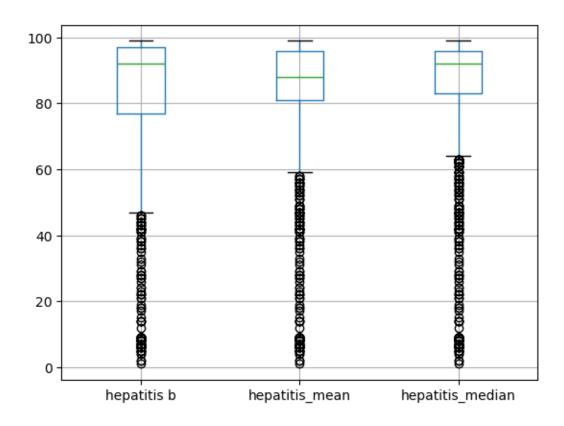


```
[48]: df = df.drop(columns = ['alcohol_lower', 'alcohol_upper'])
[49]:
     # alcohol->mean + 3*std
[50]:
                           -----hepatitis b-----
     df['hepatitis_mean'] = df['hepatitis b'].fillna(df['hepatitis b'].mean())
     df['hepatitis_median'] = df['hepatitis b'].fillna(df['hepatitis b'].median())
[51]: print('hepatitis variance',df['hepatitis b'].var())
     print('hepatitis_mean variance',df['hepatitis_mean'].var())
     print('hepatitis_median variance',df['hepatitis_median'].var())
     hepatitis variance 621.3171219785185
     hepatitis_mean variance 509.44980561255795
     hepatitis_median variance 526.8728106923436
[52]: plt.subplot(111)
     df['hepatitis b'].plot.kde(color='blue')
     df['hepatitis_mean'].plot.kde(color='red')
```

```
df['hepatitis_median'].plot.kde(color='green')
plt.show()
```



```
[53]: df[['hepatitis b','hepatitis_mean','hepatitis_median']].boxplot() plt.show()
```



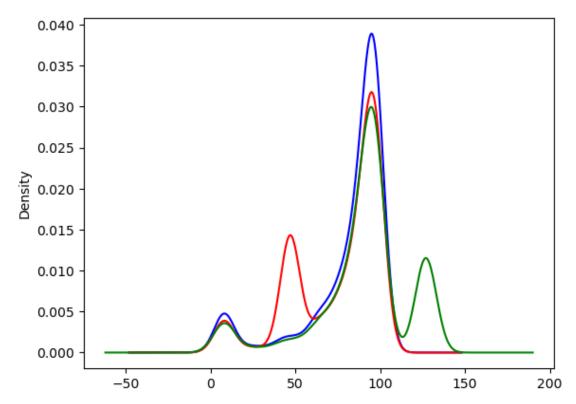
```
[54]: df = df.drop(columns=['hepatitis_mean', 'hepatitis_median'])
[55]: # end of distribution imputation
      q1_hep = df['hepatitis b'].quantile(0.25)
      q3_hep = df['hepatitis b'].quantile(0.75)
      iqr = q3_{hep} - q1_{hep}
      lower_hep = q1_hep - 1.5*iqr
      upper_hep = q3_hep + 1.5*iqr
      df['hepatitis_lower'] = df['hepatitis b'].fillna(lower_hep)
      df['hepatitis_upper'] = df['hepatitis b'].fillna(upper_hep)
[56]: print('hepatitis variance',df['hepatitis b'].var())
      print('hepatitis_lower variance',df['hepatitis_lower'].var())
      print('hepatitis_upper variance',df['hepatitis_upper'].var())
     hepatitis variance 621.3171219785185
     hepatitis_lower variance 681.5079891978423
     hepatitis_upper variance 820.012348878613
[57]: plt.subplot(111)
```

```
df['hepatitis b'].plot.kde(color='blue')

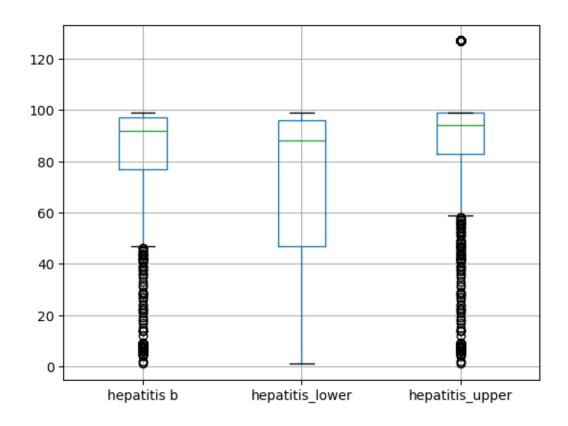
df['hepatitis_lower'].plot.kde(color='red')

df['hepatitis_upper'].plot.kde(color='green')

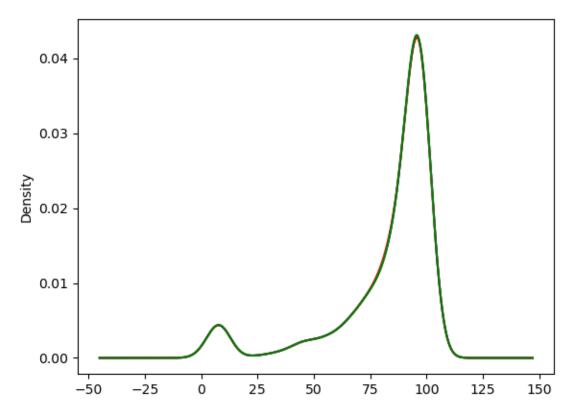
plt.show()
```



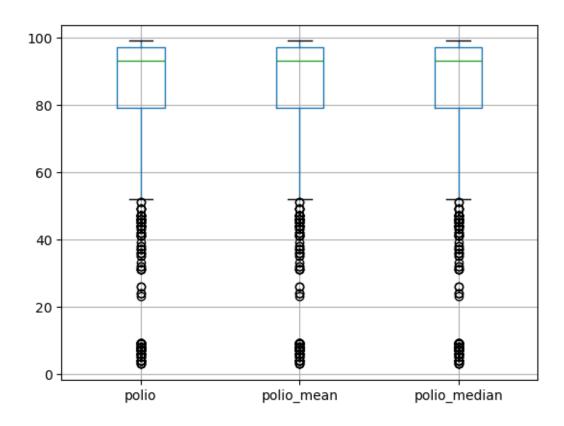
```
[58]: df[['hepatitis b','hepatitis_lower','hepatitis_upper']].boxplot() plt.show()
```



```
df['polio_median'].plot.kde(color='green')
plt.show()
```

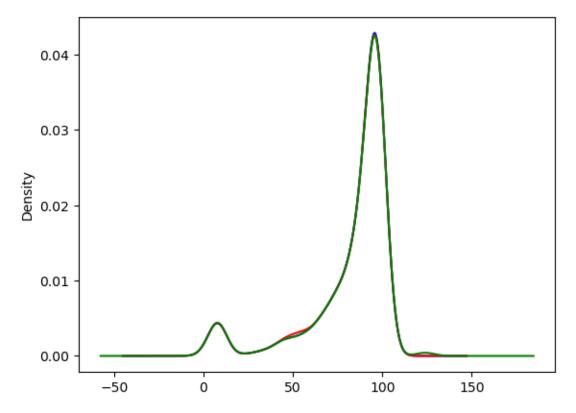


```
[63]: df[['polio','polio_mean','polio_median']].boxplot()
plt.show()
```

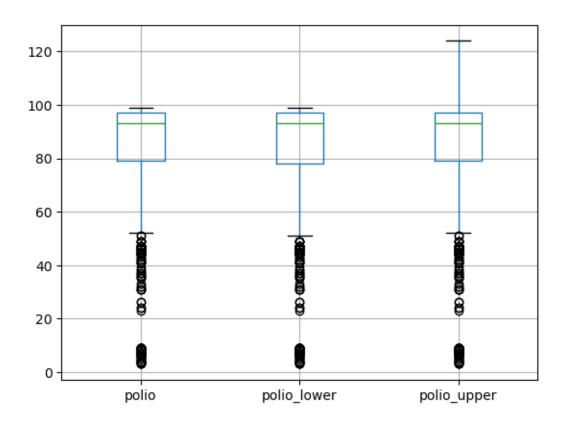


```
[64]: df = df.drop(columns=['polio_mean', 'polio_median'])
[65]: q1_polio = df['polio'].quantile(0.25)
      q3_polio = df['polio'].quantile(0.75)
      iqr = q3_polio - q1_polio
      lower_polio = q1_polio - 1.5*iqr
      upper_polio = q3_polio + 1.5*iqr
      df['polio_lower'] = df['polio'].fillna(lower_polio)
      df['polio_upper'] = df['polio'].fillna(upper_polio)
[66]: print('polio variance', df['polio'].var())
      print('polio_lower variance',df['polio_lower'].var())
      print('polio_upper variance',df['polio_upper'].var())
     polio variance 545.1439968612297
     polio_lower variance 547.274737519765
     polio_upper variance 551.2659670349411
[67]: plt.subplot(111)
      df['polio'].plot.kde(color='blue')
```

```
df['polio_lower'].plot.kde(color='red')
df['polio_upper'].plot.kde(color='green')
plt.show()
```

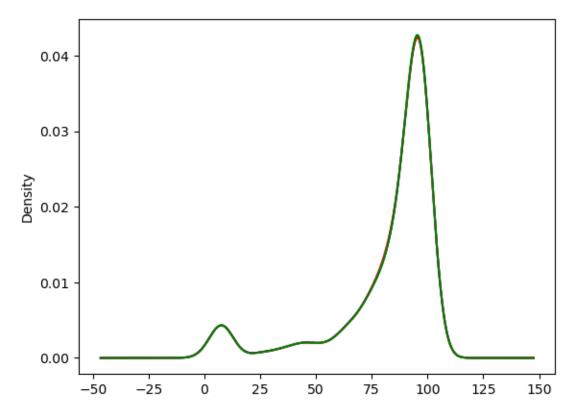


```
[68]: df[['polio','polio_lower','polio_upper']].boxplot()
plt.show()
```

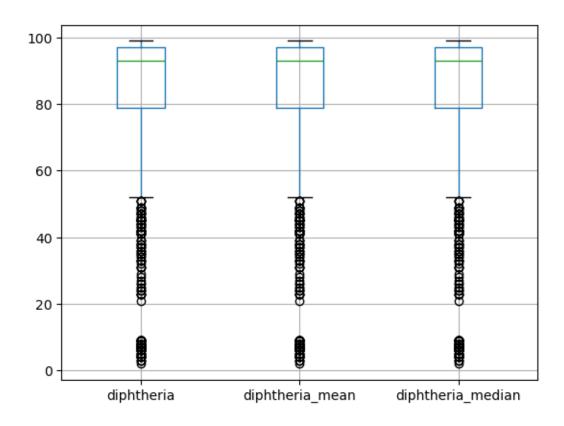


[69]: # polio-> mean

```
df['diphtheria_median'].plot.kde(color='green')
plt.show()
```

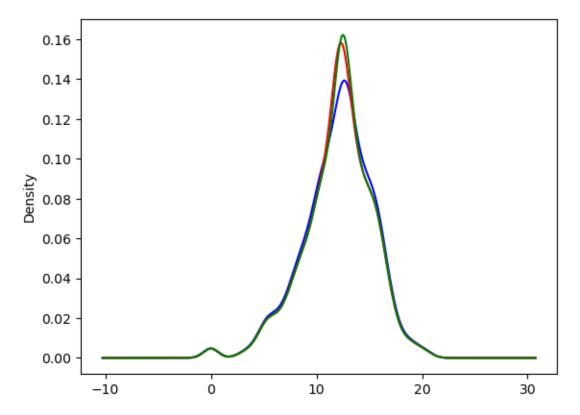


```
[73]: df[['diphtheria','diphtheria_mean','diphtheria_median']].boxplot()
plt.show()
```

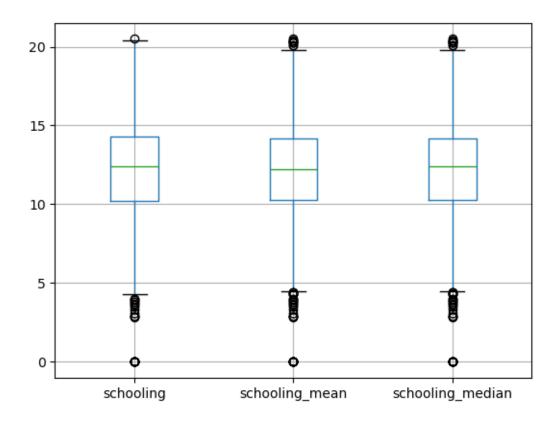


```
[74]: df = df.drop(columns=['diphtheria_mean', 'diphtheria_median'])
[75]:
     # diphtheria->mean
[76]:
                      -----schooling-----
     df['schooling_mean'] = df['schooling'].fillna(df['schooling'].mean())
     df['schooling_median'] = df['schooling'].fillna(df['schooling'].median())
     print('schooling variance',df['schooling'].var())
     print('schooling_mean variance',df['schooling_mean'].var())
     print('schooling_median variance',df['schooling_median'].var())
     schooling variance 10.996035738435486
     schooling_mean variance 10.41279102043574
     schooling_median variance 10.418979380272084
[77]: plt.subplot(111)
     df['schooling'].plot.kde(color='blue')
     df['schooling_mean'].plot.kde(color='red')
```

```
df['schooling_median'].plot.kde(color='green')
plt.show()
```



```
[78]: df[['schooling','schooling_mean','schooling_median']].boxplot() plt.show()
```



```
[79]: df = df.drop(columns=['schooling_mean', 'schooling_median'])
[80]: #end of distribution imputation

lower_schooling = df['schooling'].mean() - 3*df['schooling'].std()
    upper_schooling = df['schooling'].mean() + 3*df['schooling'].std()

df['schooling_lower'] = df['schooling'].fillna(lower_schooling)

df['schooling_upper'] = df['schooling'].fillna(upper_schooling)

[81]: print('schooling_variance',df['schooling'].var())
    print('schooling_lower_variance',df['schooling_lower'].var())

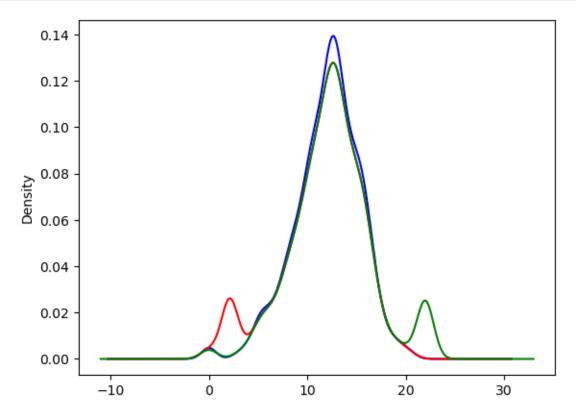
schooling_upper_variance is.383704052298354
    schooling_lower_variance is.383704052298318

[82]: plt.subplot(111)

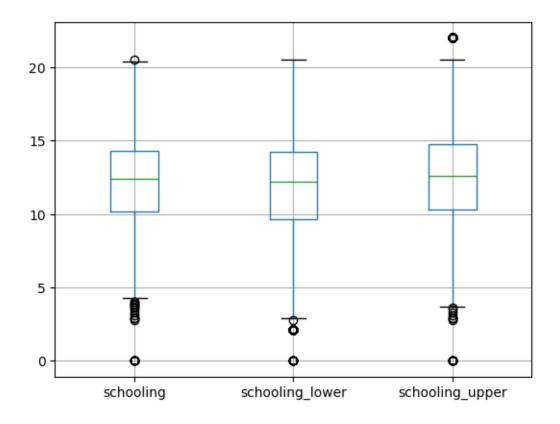
df['schooling'].plot.kde(color='blue')
```

```
df['schooling_lower'].plot.kde(color='red')

df['schooling_upper'].plot.kde(color='green')
plt.show()
```



```
[83]: df[['schooling','schooling_lower','schooling_upper']].boxplot()
plt.show()
```



```
[84]: # schooling-> mean - 3*std
[86]: df = df.drop(columns=['schooling_lower', 'schooling_upper'])
[87]: df = df.drop(columns=['thinness 5-9 years'])
[88]: df.isnull().sum()
[88]: life expectancy
                               6
      adult mortality
                               6
      infant deaths
                               0
      alcohol
                             136
      hepatitis b
                             370
      measles
                               0
      under five deaths
                               0
      polio
                              11
      diphtheria
                              11
      hiv/aids
                               0
      thinness 1-19 years
                              24
      schooling
                              109
      dtype: int64
```

```
[89]: from sklearn.compose import ColumnTransformer
     from sklearn.impute import SimpleImputer
     alcohol_upper = df['alcohol'].mean() + 3*df['alcohol'].std()
     q1_hep = df['hepatitis b'].quantile(0.25)
     q3_hep = df['hepatitis b'].quantile(0.75)
     iqr_hep = q3_hep - q1_hep
     hepatitis_lower = q1_hep - 1.5*iqr_hep
     schooling lower = df['schooling'].mean() - 3*df['schooling'].std()
     trf1 = ColumnTransformer([
         ('mean_impute',SimpleImputer(strategy='mean'),['life expectancy','adult⊔
      →mortality','polio','diphtheria']),
      ⇔('hepatitis_impute',SimpleImputer(strategy='constant',fill_value=hepatitis_lower),['hepatit
      →b¹]),
      →('schooling_impute',SimpleImputer(strategy='constant',fill_value=schooling_lower),['schooli
     ],remainder='passthrough')
[90]: df1 = trf1.fit_transform(df)
[93]: df1 = pd.DataFrame(df1)
[94]: df1.rename(columns = {0:'life expectancy',1:'adult mortality',2:'polio',3:

¬'diphtheria',4:'alcohol',5:'hepatitis b',6:'schooling',7:'infant deaths',8:
      →inplace=True)
[95]: df1.info()
    <class 'pandas.core.frame.DataFrame'>
    RangeIndex: 2056 entries, 0 to 2055
    Data columns (total 12 columns):
     #
        Column
                           Non-Null Count Dtype
     ___ ____
                           _____
     0
        life expectancy
                           2056 non-null
                                         float64
                           2056 non-null float64
     1
         adult mortality
                                         float64
     2
        polio
                           2056 non-null
     3
        diphtheria
                           2056 non-null float64
     4
         alcohol
                           2056 non-null
                                         float64
         hepatitis b
                           2056 non-null float64
         schooling
                           2056 non-null
                                         float64
```

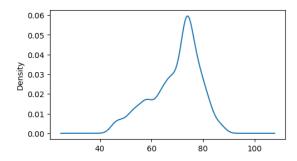
```
7
          infant deaths
                                 2056 non-null
                                                 float64
          measles
                                 2056 non-null
                                                 float64
          under five deaths
                                2056 non-null
                                                 float64
      10 hiv/aids
                                2056 non-null
                                                 float64
      11 thinness 1-19 years 2032 non-null
                                                 float64
     dtypes: float64(12)
     memory usage: 192.9 KB
[96]: df1 = df1.dropna(ignore_index=True)
[97]: df1.isnull().sum()
[97]: life expectancy
                              0
      adult mortality
                              0
      polio
                              0
                              0
      diphtheria
      alcohol
                              0
      hepatitis b
      schooling
      infant deaths
      measles
                              0
      under five deaths
                              0
      hiv/aids
                              0
      thinness 1-19 years
      dtype: int64
[98]: #----outlier remove for life_
       \hookrightarrow expectancy-----
      plt.figure(figsize=(12,3))
      plt.subplot(121)
      df1['life expectancy'].plot.kde()
      plt.subplot(122)
      df1[['life expectancy']].boxplot()
      plt.show()
            0.06
                                                    90
            0.05
            0.04
                                                    70
          Density
60.0
                                                    60
            0.02
                                                    50
            0.01
                                                    40
            0.00
                                                                  life expectancy
```

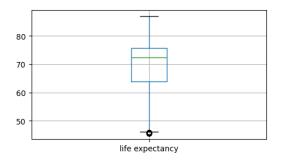
```
[99]: # using percentile method

lower_life = df1['life expectancy'].quantile(0.01)
upper_life = df1['life expectancy'].quantile(0.99)

df1['life expectancy'] = np.where(
          df1['life expectancy'] > upper_life,
          upper_life,
          np.where(
                df1['life expectancy'] < lower_life,
                lower_life,
                df1['life expectancy']
          )
)</pre>
```

```
[100]: plt.figure(figsize=(12,3))
   plt.subplot(121)
   df1['life expectancy'].plot.kde()
   plt.subplot(122)
   df1[['life expectancy']].boxplot()
   plt.show()
```

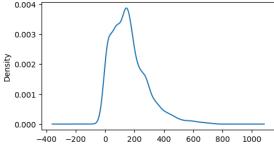


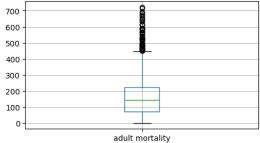


[101]: df1['life expectancy'].describe()

```
[101]: count
                2032.000000
                  69.522824
       mean
       std
                   9.334135
                  45.600000
       min
       25%
                  63.875000
       50%
                  72.300000
       75%
                  75.725000
                  87.000000
       max
```

Name: life expectancy, dtype: float64





```
[103]: df1['adult mortality'].skew()
```

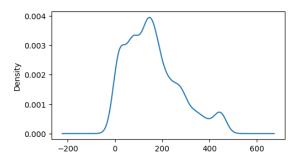
[103]: 1.2224880956072182

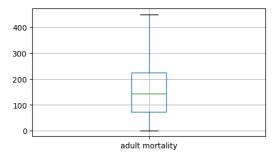
```
[104]: # using IQR method
q1_adult = df1['adult mortality'].quantile(0.25)
q3_adult = df1['adult mortality'].quantile(0.75)
iqr_adult = q3_adult - q1_adult
lower_adult = q1_adult - 1.5*iqr_adult
upper_adult = q3_adult + 1.5*iqr_adult
upper_adult
```

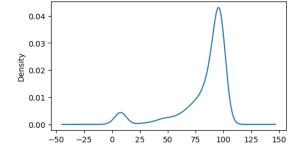
[104]: 449.375

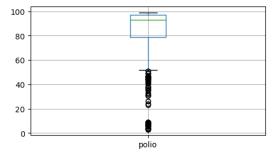
```
[106]: plt.figure(figsize=(12,3)) plt.subplot(121)
```

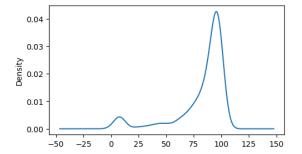
```
df1['adult mortality'].plot.kde()
plt.subplot(122)
df1[['adult mortality']].boxplot()
plt.show()
```











df1['diphtheria'] = np.where(

df1['diphtheria'] > upper_diphtheria,

```
100 80 60 40 20 diphtheria
```

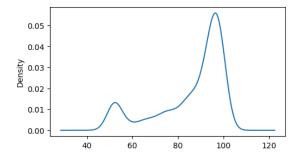
```
[108]: print(df1['polio'].skew())
       print(df1['diphtheria'].skew())
      -2.1450033377706332
      -2.1295534637143922
[109]: # using IQR method
       q1_polio = df1['polio'].quantile(0.25)
       q3_polio = df1['polio'].quantile(0.75)
       iqr_polio = q3_polio - q1_polio
       lower_polio = q1_polio - 1.5*iqr_polio
       upper_polio = q3_polio + 1.5*iqr_polio
       print(lower_polio)
       q1_diphtheria = df1['diphtheria'].quantile(0.25)
       q3_diphtheria = df1['diphtheria'].quantile(0.75)
       iqr_diphtheria = q3_diphtheria - q1_diphtheria
       lower_diphtheria = q1_diphtheria - 1.5*iqr_diphtheria
       upper_diphtheria = q3_diphtheria + 1.5*iqr_diphtheria
       print(lower_diphtheria)
      52.0
      52.0
[110]: df1['polio'] = np.where(
           df1['polio'] > upper_polio,
           upper_polio,
           np.where(
               df1['polio'] < lower_polio,</pre>
               lower_polio,
               df1['polio']
           )
       )
```

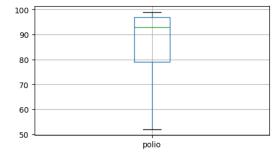
```
upper_diphtheria,
np.where(
    df1['diphtheria'] < lower_diphtheria,
    lower_diphtheria,
    df1['diphtheria']
)
)</pre>
```

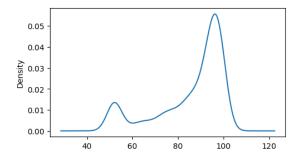
```
[111]: plt.figure(figsize=(12,3))
   plt.subplot(121)
   df1['polio'].plot.kde()
   plt.subplot(122)
   df1[['polio']].boxplot()

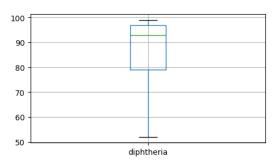
   plt.figure(figsize=(12,3))
   plt.subplot(121)
   df1['diphtheria'].plot.kde()
   plt.subplot(122)
   df1[['diphtheria']].boxplot()

   plt.show()
```









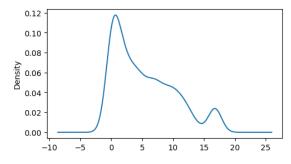
```
[112]: #------alcohol & hepatitis<sub>L</sub>
```

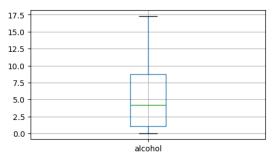
```
df1.isnull().sum()

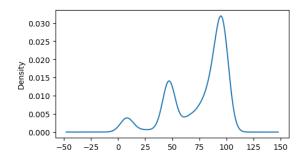
plt.figure(figsize=(12,3))
plt.subplot(121)
df1['alcohol'].plot.kde()
plt.subplot(122)
df1[['alcohol']].boxplot()

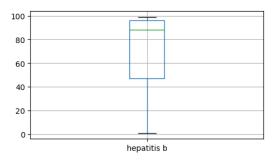
plt.figure(figsize=(12,3))
plt.subplot(121)
df1['hepatitis b'].plot.kde()
plt.subplot(122)
df1[['hepatitis b']].boxplot()

plt.show()
```



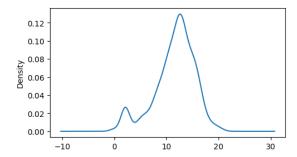


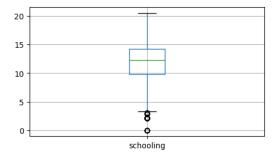




```
plt.figure(figsize=(12,3))
plt.subplot(121)
df1['schooling'].plot.kde()
plt.subplot(122)
df1[['schooling']].boxplot()
```

[113]: <Axes: >





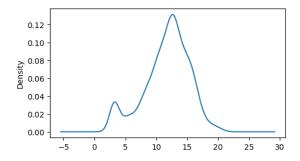
```
[114]: # using IQR method
q1_schooling = df1['schooling'].quantile(0.25)
q3_schooling = df1['schooling'].quantile(0.75)
iqr_schooling = q3_schooling - q1_schooling
lower_schooling = q1_schooling - 1.5*iqr_schooling
upper_schooling = q3_schooling + 1.5*iqr_schooling
lower_schooling
```

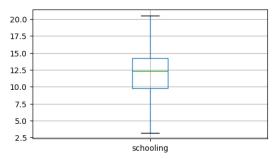
[114]: 3.200000000000003

```
[115]: df1['schooling'] = np.where(
    df1['schooling'] > upper_schooling,
    upper_schooling,
    np.where(
        df1['schooling'] < lower_schooling,
        lower_schooling,
        df1['schooling']
    )
)</pre>
```

```
[116]: plt.figure(figsize=(12,3))
   plt.subplot(121)
   df1['schooling'].plot.kde()
   plt.subplot(122)
   df1[['schooling']].boxplot()
```

[116]: <Axes: >



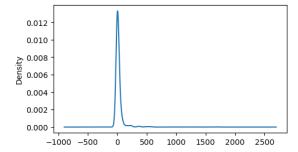


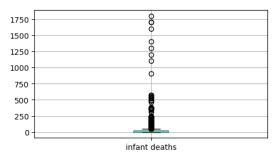
```
[117]: df1['schooling'].describe()
[117]: count
               2032.000000
      mean
                  11.683366
       std
                  3.666156
      min
                  3.200000
       25%
                  9.800000
      50%
                 12.300000
      75%
                  14.200000
                 20.500000
      max
       Name: schooling, dtype: float64
[118]: \#-----infant deaths ,measles ealso under \ five_{\sqcup}
        ⇔deaths ,hiv/aids,thinness 1-19 years ----
       plt.figure(figsize=(12,3))
       plt.subplot(121)
       df1['infant deaths'].plot.kde()
       plt.subplot(122)
       df1[['infant deaths']].boxplot()
       plt.figure(figsize=(12,3))
       plt.subplot(121)
       df1['measles'].plot.kde()
       plt.subplot(122)
       df1[['measles']].boxplot()
       plt.figure(figsize=(12,3))
       plt.subplot(121)
       df1['under five deaths'].plot.kde()
       plt.subplot(122)
       df1[['under five deaths']].boxplot()
       plt.figure(figsize=(12,3))
       plt.subplot(121)
```

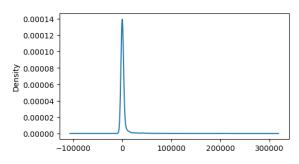
```
df1['hiv/aids'].plot.kde()
plt.subplot(122)
df1[['hiv/aids']].boxplot()

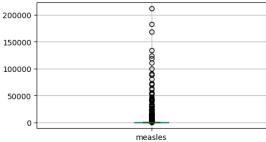
plt.figure(figsize=(12,3))
plt.subplot(121)
df1['thinness 1-19 years'].plot.kde()
plt.subplot(122)
df1[['thinness 1-19 years']].boxplot()

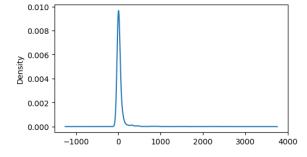
plt.show()
```

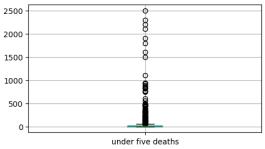


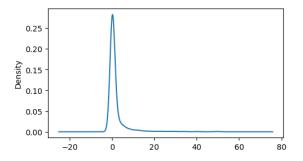


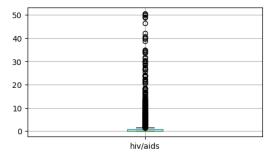


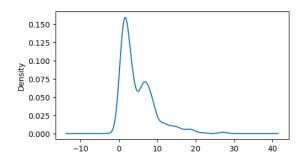


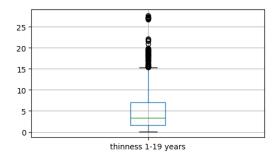












```
[202]: print(df1['infant deaths'].skew())
    print(df1['measles'].skew())
    print(df1['under five deaths'].skew())
    print(df1['hiv/aids'].skew())
    print(df1['thinness 1-19 years'].skew())
```

10.29218941757014

10.212825152688037

9.951003455406692

5.458571920430973

1.6749200084152065

```
[204]: #using IQR method

q1_infant = df1['infant deaths'].quantile(0.25)
q3_infant = df1['infant deaths'].quantile(0.75)
iqr_infant = q3_infant - q1_infant
lower_infant = q1_infant - 1.5*iqr_infant
upper_infant = q3_infant + 1.5*iqr_infant
print(upper_infant)

q1_measles = df1['measles'].quantile(0.25)
q3_measles = df1['measles'].quantile(0.75)
iqr_measles = q3_measles - q1_measles
```

```
lower_measles = q1_measles - 1.5*iqr_measles
       upper_measles = q3_measles + 1.5*iqr_measles
       print(upper_measles)
       q1_under = df1['under five deaths'].quantile(0.25)
       q3_under = df1['under five deaths'].quantile(0.75)
       iqr_under = q3_under - q1_under
       lower_under = q1_under - 1.5*iqr_under
       upper_under = q3_under + 1.5*iqr_under
       print(upper_under)
       q1_hiv = df1['hiv/aids'].quantile(0.25)
       q3_hiv = df1['hiv/aids'].quantile(0.75)
       iqr_hiv = q3_hiv - q1_hiv
       lower_hiv = q1_hiv - 1.5*iqr_hiv
       upper_hiv = q3_hiv + 1.5*iqr_hiv
       print(upper_hiv)
       q1_thinness = df1['thinness 1-19 years'].quantile(0.25)
       q3_thinness = df1['thinness 1-19 years'].quantile(0.75)
       iqr_thinness = q3_thinness - q1_thinness
       lower_thinness = q1_thinness - 1.5*iqr_thinness
       upper_thinness = q3_thinness + 1.5*iqr_thinness
       print(upper_thinness)
      50.0
      930.0
      60.0
      1.599999999999999
      15.35
[206]: df1['infant deaths'] = np.where(
           df1['infant deaths'] > upper_infant,
           upper_infant,
           np.where(
               df1['infant deaths'] < lower_infant,</pre>
               lower_infant,
               df1['infant deaths']
           )
       )
       df1['measles'] = np.where(
           df1['measles'] > upper_measles,
           upper_measles,
           np.where(
               df1['measles'] < lower_measles,</pre>
               lower_measles,
```

```
df1['measles']
    )
)
df1['under five deaths'] = np.where(
    df1['under five deaths'] > upper_under,
    upper_under,
    np.where(
        df1['under five deaths'] < lower_under,</pre>
        lower_under,
        df1['under five deaths']
    )
)
df1['hiv/aids'] = np.where(
    df1['hiv/aids'] > upper_hiv,
    upper_hiv,
    np.where(
        df1['hiv/aids'] < lower_hiv,</pre>
        lower_hiv,
        df1['hiv/aids']
    )
)
df1['thinness 1-19 years'] = np.where(
    df1['thinness 1-19 years'] > upper_thinness,
    upper_thinness,
    np.where(
        df1['thinness 1-19 years'] < lower_thinness,</pre>
        lower_thinness,
        df1['thinness 1-19 years']
    )
)
```

```
[208]: plt.figure(figsize=(12,3))
  plt.subplot(121)
  df1['infant deaths'].plot.kde()
  plt.subplot(122)
  df1[['infant deaths']].boxplot()

  plt.figure(figsize=(12,3))
  plt.subplot(121)
  df1['measles'].plot.kde()
  plt.subplot(122)
  df1[['measles']].boxplot()

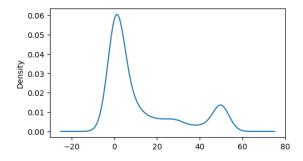
  plt.figure(figsize=(12,3))
```

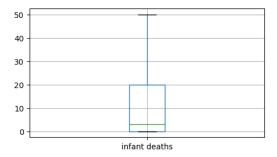
```
plt.subplot(121)
df1['under five deaths'].plot.kde()
plt.subplot(122)
df1[['under five deaths']].boxplot()

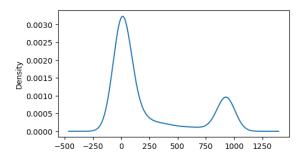
plt.figure(figsize=(12,3))
plt.subplot(121)
df1['hiv/aids'].plot.kde()
plt.subplot(122)
df1[['hiv/aids']].boxplot()

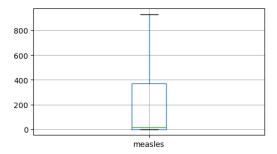
plt.figure(figsize=(12,3))
plt.subplot(121)
df1['thinness 1-19 years'].plot.kde()
plt.subplot(122)
df1[['thinness 1-19 years']].boxplot()

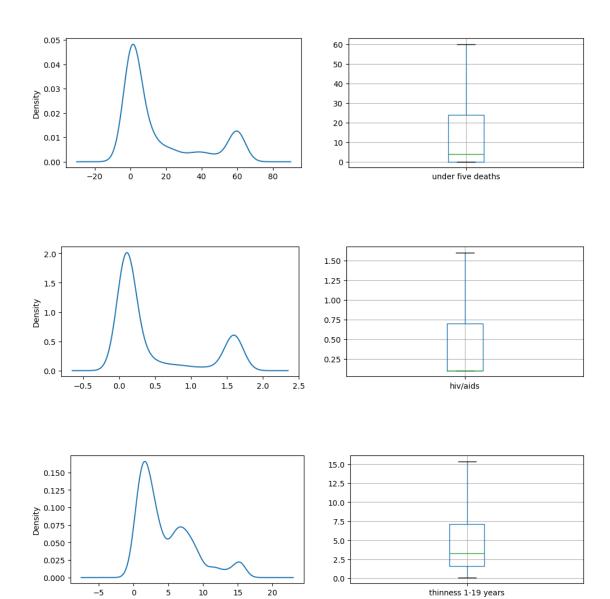
plt.show()
```







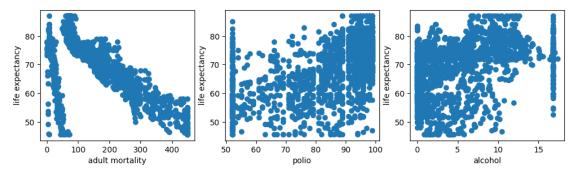




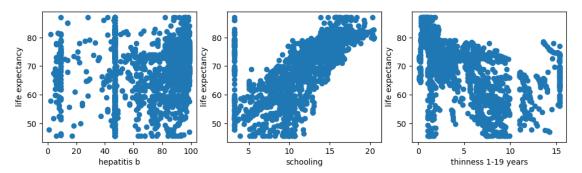
EDA

```
[211]: plt.figure(figsize=(12,3))
   plt.subplot(131)
   plt.scatter(df1['adult mortality'],df1['life expectancy'])
   plt.xlabel('adult mortality')
   plt.ylabel('life expectancy')
   plt.subplot(132)
   plt.scatter(df1['polio'],df1['life expectancy'])
   plt.xlabel('polio')
   plt.ylabel('life expectancy')
   plt.subplot(133)
   plt.scatter(df1['alcohol'],df1['life expectancy'])
```

```
plt.xlabel('alcohol')
plt.ylabel('life expectancy')
plt.show()
```



```
[212]: plt.figure(figsize=(12,3))
    plt.subplot(131)
    plt.scatter(df1['hepatitis b'],df1['life expectancy'])
    plt.xlabel('hepatitis b')
    plt.ylabel('life expectancy')
    plt.subplot(132)
    plt.scatter(df1['schooling'],df1['life expectancy'])
    plt.xlabel('schooling')
    plt.ylabel('life expectancy')
    plt.subplot(133)
    plt.scatter(df1['thinness 1-19 years'],df1['life expectancy'])
    plt.xlabel('thinness 1-19 years')
    plt.ylabel('life expectancy')
    plt.show()
```



Feature Engineering

```
[215]: X = df1.drop(columns=['life expectancy'])
y = df1['life expectancy']
```

```
[218]: from sklearn.preprocessing import StandardScaler
       scale = StandardScaler()
       X_trf = scale.fit_transform(X)
[224]: from sklearn.model_selection import train_test_split,cross_val_score
       X_train, X_test, y_train, y_test = train_test_split(X_trf, y, test_size=0.
        →2,random_state=3)
[226]: X_train.shape, X_test.shape
[226]: ((1625, 11), (407, 11))
      Linear Regression
[327]: from sklearn.linear_model import LinearRegression
       from sklearn.metrics import r2_score,mean_squared_error
       lr = LinearRegression()
       lr.fit(X_train,y_train)
       y_pred_lr = lr.predict(X_test)
       print('Linear Regression :')
       print('r2_score',r2_score(y_test,y_pred_lr))
       print('RMSE',np.sqrt(mean_squared_error(y_test,y_pred_lr)))
       print('cross_val_score', np.mean(cross_val_score(lr , X_trf , y , scoring='r2'u
        \rightarrow cv=10)))
      Linear Regression:
      r2 score 0.8120599518050007
      RMSE 4.066513909886408
      cross_val_score 0.8083447901641605
[331]: from sklearn.linear_model import LinearRegression
       from sklearn.preprocessing import PolynomialFeatures
       poly = PolynomialFeatures(degree=2,include_bias=True)
       X_trf_trans = poly.fit_transform(X_trf)
       X_train_trans = poly.fit_transform(X_train)
       X_test_trans = poly.fit_transform(X_test)
       lr = LinearRegression()
       lr.fit(X_train_trans,y_train)
       y_pred_lr = lr.predict(X_test_trans)
       print('Linear Regression :')
       print('r2_score',r2_score(y_test,y_pred_lr))
```

```
print('RMSE',np.sqrt(mean_squared_error(y_test,y_pred_lr)))
       print('cross_val_score', np.mean(cross_val_score(lr , X_trf_trans , y ,__

scoring='r2' , cv=10)))
      Linear Regression:
      r2 score 0.8924020062619413
      RMSE 3.0769092119461248
      cross_val_score 0.8917250304592474
      SGDRegressor
[295]: from sklearn.model_selection import RandomizedSearchCV
       param = {
           'penalty':['11','12'],
           'max_iter':[50,100,1000,2000,2500],
           'learning rate':['constant','invscaling'],
           'eta0': [0.2,0.1,0.01,0.001,0.05,0.005]
       }
       search = RandomizedSearchCV(estimator=sgd , param_distributions=param , cv=5)
       search.fit(X_train,y_train)
       print(search.best_score_)
       print(search.best_params_)
      0.8043305238705546
      {'penalty': '12', 'max_iter': 1000, 'learning_rate': 'invscaling', 'eta0': 0.01}
[335]: from sklearn.linear_model import SGDRegressor
       sgd = SGDRegressor(max_iter=1000, random_state=13)
       sgd.fit(X_train_trans,y_train)
       y_pred_sgd = sgd.predict(X_test_trans)
       print('SGDRegressor :')
       print('r2_score',r2_score(y_test,y_pred_sgd))
       print('RMSE',np.sqrt(mean_squared_error(y_test,y_pred_sgd)))
       print('cross_val_score', np.mean(cross_val_score(sgd , X_trf_trans , y ,__

scoring='r2' , cv=10)))
      SGDRegressor :
      r2_score 0.8856137922354794
      RMSE 3.172483896460241
      cross_val_score 0.8892192244103597
      {\bf Decision Tree Regressor}
[363]: from sklearn.tree import DecisionTreeRegressor
        DecisionTreeRegressor(criterion='squared_error',splitter='best',max_depth=8,max_features=No
```

```
dt.fit(X_train_trans,y_train)
       y_pred_dt = dt.predict(X_test_trans)
       print('DecisionTreeRegressor :')
       print('r2_score',r2_score(y_test,y_pred_dt))
       print('RMSE',np.sqrt(mean_squared_error(y_test,y_pred_dt)))
       print('cross_val_score', np.mean(cross_val_score(dt , X_trf_trans , y ,__
        ⇔scoring='r2' , cv=10)))
      DecisionTreeRegressor :
      r2 score 0.9023841089054837
      RMSE 2.9307100715434813
      cross val score 0.8900189201024997
      RandomForestRegressor
[438]: from sklearn.ensemble import RandomForestRegressor
       rf = RandomForestRegressor(n estimators=100, max depth=8, max samples=0.
        →9,bootstrap=True,max_features=None)
       rf.fit(X_train,y_train)
       y_pred_rf = rf.predict(X_test)
       print('RandomForestRegressor :')
       print('r2_score',r2_score(y_test,y_pred_rf))
       print('RMSE',np.sqrt(mean_squared_error(y_test,y_pred_rf)))
       print('cross_val_score', np.mean(cross_val_score(rf , X_trf , y , scoring='r2'u
        \hookrightarrow, cv=5)))
      RandomForestRegressor :
      r2_score 0.9441796929735596
      RMSE 2.2161987505068974
      cross_val_score 0.9423499641077168
      GradientBoostingRegressor
[399]: from sklearn.ensemble import GradientBoostingRegressor
       gbr = GradientBoostingRegressor(max_leaf_nodes=8, n_estimators=500, __
        →max_depth=8 , learning_rate=0.2)
       gbr.fit(X_train,y_train)
       y_pred_gbr = gbr.predict(X_test)
       print('GradientBoostingRegressor :')
       print('r2_score',r2_score(y_test,y_pred_gbr))
       print('RMSE',np.sqrt(mean_squared_error(y_test,y_pred_gbr)))
       print('cross_val_score', np.mean(cross_val_score(gbr , X_trf , y , scoring='r2'u
        \hookrightarrow, cv=5)))
```

GradientBoostingRegressor :
r2_score 0.9514828667819136

```
[393]: | from sklearn.model_selection import RandomizedSearchCV
      param = {
           'n_estimators':[100,500,1000],
           'max_depth': [1,3,5,7,8,9],
           'max leaf nodes': [1,3,5,8,10,13,15],
           'learning_rate': [0.2,0.1,0.3,0.4,0.5,0.6]
      }
      search = RandomizedSearchCV(estimator=gbr , param_distributions=param , cv=5)
      search.fit(X_train,y_train)
      print(search.best_score_)
      print(search.best_params_)
      D:\ProgramData\anaconda3\Lib\site-
      packages\sklearn\model_selection\_validation.py:378: FitFailedWarning:
      15 fits failed out of a total of 50.
      The score on these train-test partitions for these parameters will be set to
      If these failures are not expected, you can try to debug them by setting
      error_score='raise'.
      Below are more details about the failures:
      15 fits failed with the following error:
      Traceback (most recent call last):
        File "D:\ProgramData\anaconda3\Lib\site-
      packages\sklearn\model_selection\_validation.py", line 686, in _fit_and_score
          estimator.fit(X_train, y_train, **fit_params)
        File "D:\ProgramData\anaconda3\Lib\site-packages\sklearn\ensemble\_gb.py",
      line 420, in fit
          self._validate_params()
        File "D:\ProgramData\anaconda3\Lib\site-packages\sklearn\base.py", line 600,
      in _validate_params
          validate_parameter_constraints(
        File "D:\ProgramData\anaconda3\Lib\site-
      packages\sklearn\utils\_param_validation.py", line 97, in
      validate parameter constraints
          raise InvalidParameterError(
      sklearn.utils. param validation.InvalidParameterError: The 'max leaf nodes'
      parameter of GradientBoostingRegressor must be an int in the range [2, inf) or
      None. Got 1 instead.
        warnings.warn(some_fits_failed_message, FitFailedWarning)
      D:\ProgramData\anaconda3\Lib\site-
```

```
packages\sklearn\model_selection\_search.py:952: UserWarning: One or more of the
      test scores are non-finite: [0.92136897
                                                      nan 0.92530872 0.91639196
      0.92914027 0.94696278
       0.93268475
                         nan 0.84332804
                                                nanl
        warnings.warn(
      0.9469627812273324
      {'n_estimators': 500, 'max_leaf_nodes': 8, 'max_depth': 8, 'learning_rate': 0.2}
      SVR
[422]: from sklearn.svm import SVR
       svr = SVR(kernel='rbf')
       svr.fit(X_train,y_train)
       y_pred_svr = svr.predict(X_test)
       print('SupportVectorRegressor :')
       print('r2_score',r2_score(y_test,y_pred_svr))
       print('RMSE',np.sqrt(mean_squared_error(y_test,y_pred_svr)))
       print('cross_val_score', np.mean(cross_val_score(svr , X_trf , y , scoring='r2'u
        \hookrightarrow, cv=5)))
      SupportVectorRegressor :
      r2 score 0.8567371842375759
      RMSE 3.550416773129694
      cross_val_score 0.8542595126196586
      XGBoost
[435]: import xgboost as xgb
       xgbr = xgb.XGBRegressor(booster='dart',learning_rate=0.1,max_depth=8 ,__
        →random state=13)
       xgbr.fit(X_train,y_train)
       y_pred_xgbr = xgbr.predict(X_test)
       print('XGBRegressor :')
       print('r2_score',r2_score(y_test,y_pred_xgbr))
       print('RMSE',np.sqrt(mean_squared_error(y_test,y_pred_xgbr)))
       print('cross_val_score', np.mean(cross_val_score(xgbr , X_trf , y ,__
        ⇔scoring='r2' , cv=5)))
      XGBRegressor :
      r2_score 0.9533352053540002
      RMSE 2.026316471537876
      cross_val_score 0.9478619213421512
      VotingRegressor
[440]: from sklearn.ensemble import VotingRegressor
```