Final Project, BAIT509 Winter 2023

Business Applications of Machine Learning [100 Marks]

Deadline: Thursday, February 9th @ 11:59pm

Academic Integrity

This is a group project. Do not share your code with other groups, or post any parts of your work online. You can only submit code that is produced by your group. If you use any online resource for developing parts of your code, you must explicitly acknowledge the source in a comment in your code. Students suspected of plagiarism on the project will be referred to the university for formal discipline according to the regulations.

Please note that late submissions receive a mark of 0 as per course outline and RHL regulations.

Please fill out the following:

• Full Names of all Group members: **Abhilash Yadav**

• Student Numbers of all Group member: 59925800

• Group number (from Canvas): Group 27

Two submission files are required per group:

For submitting this project, two files must be submitted on Canvas by the project deadline:

1) The complete Jupyter file (in .ipynb format) (that completely compiles on Google colab without any errors independent of the computer used.)

2) A self-contained and complete pdf printout of the same Jupyter file with all the output printed as well as all the code, text cells, comments, and figures.

Policy regarding the use of AI assistant tools

If you use ChatGPT (or a similar tool) to get ideas and/or partial answers for this project or to generate any text, you must declare that you have used it, with a couple sentences describing the extent to which it was used, and you must save any generated text from this tool in case it is requested.

You will not be penalized for using such AI assistant tools, but the TA or the instructor may ask you to provide the generated text in order to help with grading decisions. In this case, your (or your group's) original contributions will be evaluated. Failure to fully

declare the use of this tool will be considered "unauthorized" (See 3.b of the Vancouver Academic Calendar)

Part 0: Loading the libraries and the data [0 Marks]

In this project, we want to develop a statistical model for the mortality rate of lung cancer in the United States.

One of the parts overlooked in many machine learning projects is preprocessing. And a good way to learn it is by solving a lot of examples and test cases. A big part of this project is walking you through preprocessing, making informed decisions using your observations, and exploratory data analysis. Then we use supervised learning methods to construct models to predict the mortality rate of lung cancer using the features provided here.

In [56]:

```
# data wrangling tools
import pandas as pd
import numpy as np

# visualization
import matplotlib.pyplot as plt
import seaborn as sns

# statistical learning
import statsmodels.api as sm
import statsmodels.formula.api as smf
from statsmodels.stats.outliers_influence import variance_inflation_factor
```

Loading data

Load the three csv files as pandas dataframes directly from their URLs.

In [57]:

```
#import the required datasets
fulldf = pd.read_csv('https://saref.github.io/teaching/BAIT509/mydata.csv').drop(colum
data_dict = pd.read_csv('https://saref.github.io/teaching/BAIT509/descriptions.csv')
populationdf = pd.read_csv('https://saref.github.io/teaching/BAIT509/populations.csv')
```

Data set `mydata.csv` includes most of the data. Explanations on the meaning of each of the columns are included in `descriptions.csv`. Please take your time to understand the three dataframes before proceeding.

Part 1: Getting started [40 Marks]

Data cleaning

In this project, we go through specific data cleaning steps. Please read through the instructions carefully.

1.1 Convert `FIPS` column to correct format [5 Marks]

Federal Information Processing Standard or FIPS is a categorical variable. It is a code with five digits. The left two digits showing the state and the three right digits showing the county code. We recognize that desipite being a number, FIPS is actually a categorical variable. First, check the format of the `FIPS` column and convert them to the five digit format with type `np.object_` as seen in the county level section, here.

***Hint*: You can use apply to first convert the type and then use `str.pad` to format the values as five digit numbers.**

In [58]:
```
#understanding the data types of all the variables

fulldf.dtypes
```

Out[58]:
```
State                   object
AreaName                object
All_Poverty              int64
M_Poverty                int64
F_Poverty                int64
FIPS                     int64
Med_Income             float64
Med_Income_White       float64
Med_Income_Black       float64
Med_Income_Nat_Am      float64
Med_Income_Asian       float64
Med_Income_Hispanic    float64
M_With                   int64
M_Without                int64
F_With                   int64
F_Without                int64
All_With                 int64
All_Without              int64
Incidence_Rate          object
Avg_Ann_Incidence       object
Recent_Trend            object
Mortality_Rate          object
Avg_Ann_Deaths          object
dtype: object
```

In [59]:
```
#using the apply function to change the format of FIPS column

fulldf['FIPS'] = fulldf['FIPS'].apply(str)
fulldf['FIPS'] = fulldf['FIPS'].str.pad(width = 6,side = 'left',fillchar = '0')
```

In [60]:
```
#converting the data type to object

fulldf['FIPS'] = fulldf['FIPS'].astype(object)
```

In [61]:
```
fulldf.dtypes
```

Out[61]:
```
State                   object
AreaName                object
All_Poverty              int64
M_Poverty                int64
F_Poverty                int64
FIPS                    object
Med_Income             float64
Med_Income_White       float64
Med_Income_Black       float64
Med_Income_Nat_Am      float64
Med_Income_Asian       float64
Med_Income_Hispanic    float64
M_With                   int64
M_Without                int64
F_With                   int64
F_Without                int64
All_With                 int64
All_Without              int64
Incidence_Rate          object
Avg_Ann_Incidence       object
Recent_Trend            object
Mortality_Rate          object
Avg_Ann_Deaths          object
dtype: object
```

1.2 Check for null values [5 Marks]

Just check for null values and remove columns whenever the percentage of null values is greater than 20. Please briefly justify your choices w.r.t. the columns you have removed.

In [62]:
```
#creating a percent of nulls dataframe to calculate percentage of nulls

percent_of_nulls = pd.DataFrame(fulldf.isna().sum(), columns = ['nulls'])
percent_of_nulls["total_rows"] = len(fulldf.index)
percent_of_nulls["null_percentage"] = round((percent_of_nulls['nulls'] / percent_of_nu
```

In [63]:
```
percent_of_nulls
```

Out[63]:

	nulls	total_rows	null_percentage
State	0	3134	0.00
AreaName	0	3134	0.00
All_Poverty	0	3134	0.00
M_Poverty	0	3134	0.00
F_Poverty	0	3134	0.00
FIPS	0	3134	0.00
Med_Income	1	3134	0.03
Med_Income_White	2	3134	0.06
Med_Income_Black	1210	3134	38.61
Med_Income_Nat_Am	1660	3134	52.97
Med_Income_Asian	1757	3134	56.06
Med_Income_Hispanic	681	3134	21.73
M_With	0	3134	0.00
M_Without	0	3134	0.00
F_With	0	3134	0.00
F_Without	0	3134	0.00
All_With	0	3134	0.00
All_Without	0	3134	0.00
Incidence_Rate	0	3134	0.00
Avg_Ann_Incidence	0	3134	0.00
Recent_Trend	0	3134	0.00
Mortality_Rate	0	3134	0.00
Avg_Ann_Deaths	0	3134	0.00

In [64]:

```
#dropping the columns with more than 20% data missing

cols1= percent_of_nulls.loc[percent_of_nulls['null_percentage']>=20]
cols = pd.Series(cols1.index)
fulldf1= fulldf.drop(cols,axis = 1)
```

In [65]:

```
fulldf1.head()
```

Out[65]:

	State	AreaName	All_Poverty	M_Poverty	F_Poverty	FIPS	Med_Income	Med_Income_White
0	AK	Aleutians East Borough, Alaska	553	334	219	002013	61518.0	72639.0
1	AK	Aleutians West Census Area, Alaska	499	273	226	002016	84306.0	97321.0
2	AK	Anchorage Municipality, Alaska	23914	10698	13216	002020	78326.0	87235.0
3	AK	Bethel Census Area, Alaska	4364	2199	2165	002050	51012.0	92647.0
4	AK	Bristol Bay Borough, Alaska	69	33	36	002060	79750.0	88000.0

1.3 Check the format of columns [5 Marks]

Report the format of each column. List the columns that are in an unexpected format and state why you think that is the case.

***Hint*: You can do this by either inspecting the dataframe or by writing a code snippet that tells you what cells cannot be reformatted to the correct format. The Titatinc Jupyter file that we covered in class may also give you some useful ideas.**

In [66]:

```
#check the format of all the columns

fulldf1.dtypes
```

Out[66]:

```
State                 object
AreaName              object
All_Poverty            int64
M_Poverty              int64
F_Poverty              int64
FIPS                  object
Med_Income           float64
Med_Income_White     float64
M_With                 int64
M_Without              int64
F_With                 int64
F_Without              int64
All_With               int64
All_Without            int64
Incidence_Rate        object
Avg_Ann_Incidence     object
Recent_Trend          object
Mortality_Rate        object
Avg_Ann_Deaths        object
dtype: object
```

Based on the below dictionary and the above data types, we need to make changes to Incidence_Rate, Avg_Ann_Incidence, Recent_Trend, Moratality_Rate, Avg_Ann_Deaths. All of the named columns are currently in object form, as we move forward we will have to define different data types based on exploratory data analysis

In [67]:
```
data_dict
```

Out[67]:

	Unnamed: 0	Feature	Definition	Notes
0	0	State	NaN	NaN
1	1	AreaName	NaN	NaN
2	2	All_Poverty	Both male and female reported below poverty li...	NaN
3	3	M_Poverty	Males below poverty (Raw)	NaN
4	4	F_Poverty	Females below poverty (Raw)	NaN
5	5	FIPS	State + County FIPS (Raw)	NaN
6	6	Med_Income	Med_Income all enthnicities (Raw)	NaN
7	7	Med_Income_White	Med_Income white (Raw)	NaN
8	8	Med_Income_Black	Med_Income black (Raw)	NaN
9	9	Med_Income_Nat_Am	Med_Income native American (Raw)	NaN
10	10	Med_Income_Asian	Med_Income Asian (Raw)	NaN
11	11	Med_Income_Hispanic	Med_Income Hispanic (Raw)	NaN
12	12	M_With	Males with health insurance (Raw)	NaN
13	13	M_Without	Males without health insurance (Raw)	NaN
14	14	F_With	Females with health insurance (Raw)	NaN
15	15	F_Without	Females without health insurance (Raw)	NaN
16	16	All_With	Males and Femaes with health ins. (Raw)	NaN
17	17	All_Without	Males an Females without health ins (Raw)	NaN
18	18	Incidence_Rate	Lung cancer incidence rate (per 100,000)	'*' = fewer that 16 reported cases
19	19	Avg_Ann_Incidence	Average lung cancer incidence rate (Raw)	NaN
20	20	Recent_Trend	Recent trend (incidence)	NaN
21	21	Mortality_Rate	Lung cancer mortality rate (per 100,000)	'*' = fewer that 16 reported cases
22	22	Avg_Ann_Deaths	Average lung cancer mortalities (Raw)	NaN

1.4 Merge the population data to the main dataframe [5 Marks]

You already know about FIPS. You can use the state and county columns in this dataset to construct a FIPS column in the population dataframe in the same format as the main dataframe. Then merge the population data to the main dataframe. It is up to you to decide the type of merge and whether it is done properly.

In [68]:
```
#adding 0 to the left of the state column
populationdf['STATE'] = populationdf['STATE'].apply(str)
populationdf['STATE'] = populationdf['STATE'].str.pad(width = 3,side = 'left',fillchar

#adding 0 to the left of the county column
populationdf['COUNTY'] = populationdf['COUNTY'].apply(str)
populationdf['COUNTY'] = populationdf['COUNTY'].str.pad(width = 3,side = 'left',fillch

#creating a FIPS column
populationdf['FIPS2'] = populationdf['STATE'] + populationdf['COUNTY']

#creating a merge dataset
merge_df = fulldf1.merge(populationdf,how = 'left',left_on='FIPS',right_on='FIPS2')
```

In [69]:
```
merge_df = merge_df.drop(['STATE','COUNTY','FIPS2'], axis = 1)
merge_df.head()
```

Out[69]:

	State	AreaName	All_Poverty	M_Poverty	F_Poverty	FIPS	Med_Income	Med_Income_White
0	AK	Aleutians East Borough, Alaska	553	334	219	002013	61518.0	72639.0
1	AK	Aleutians West Census Area, Alaska	499	273	226	002016	84306.0	97321.0
2	AK	Anchorage Municipality, Alaska	23914	10698	13216	002020	78326.0	87235.0
3	AK	Bethel Census Area, Alaska	4364	2199	2165	002050	51012.0	92647.0
4	AK	Bristol Bay Borough, Alaska	69	33	36	002060	79750.0	88000.0

1.5 Cleaning the output (response) column `Mortality_Rate` [10 Marks]

Using the file `descriptions.csv`, explain what the non-numerical values of `Mortality_Rate` mean.

Then, it is decision making time, we have to decide whether to remove the non-numerical values from `Mortality_Rate` or to assign a specific numerical value to them. This

decision is based on you inferring if the non-numerical values were caused by error in data gathering or not.

Note that if the observations are valid and are deleted, we are adding a bias to the model.

***Hint*: To get the full mark for this part, conduct multiple relevant exploratory data analyses. Then use them to support your decision on removing or modifying the non-numerical values. Your choice results in full mark if the supporting analysis and arguments are deemed adequate and convincing.**

Based on the desciptions available, mortality rate has been marked * where fewer than 16 cases have been reported per 100,000 people.

In [70]:
```
#first we are going look at the relationship between the different popluation paramete
import matplotlib.pyplot as plt

#creating a test set without the * markings
test_set = merge_df[(merge_df.Mortality_Rate!='*')].copy()
test_set['pop_rank'] = test_set.groupby('State')['POPESTIMATE2015'].rank(method = 'der
test_set['Mortality_Rate1'] = test_set['Mortality_Rate'].astype('float')
```

In [71]:
```
#creating a rank variable to account for the high varibility in population
merge_df['pop_rank'] = merge_df.groupby('State')['POPESTIMATE2015'].rank(method = 'der
```

In [72]:
```
merge_df['is_present'] = np.where(merge_df['Mortality_Rate'] !='*',1,0)
count_df = pd.DataFrame(merge_df.groupby(['State','is_present'])['Mortality_Rate'].cou
total_counts = pd.DataFrame(merge_df.groupby(['State'])['Mortality_Rate'].count().rese
```

In [73]:
```
# creating a percentage missing dataframe to get missing mortality rate data at state
percentage_missing = count_df.merge(total_counts,how='left',on = 'State', suffixes=('_
```

In [74]:
```
percentage_missing['percent_missing'] = percentage_missing['Mortality_Rate_left'] / (p
percentage_missing[percentage_missing['is_present'] == 0]
```

Out[74]:

	State	is_present	Mortality_Rate_left	Mortality_Rate_right	percent_missing
0	AK	0	11	23	0.323529
5	CA	0	3	58	0.049180
7	CO	0	24	64	0.272727
13	GA	0	8	159	0.047904
15	HI	0	1	5	0.166667
17	IA	0	2	99	0.019802
19	ID	0	15	44	0.254237
23	KS	0	36	105	0.255319
25	KY	0	1	120	0.008264
31	MI	0	1	83	0.011905
33	MN	0	5	87	0.054348
35	MO	0	1	115	0.008621
37	MS	0	1	82	0.012048
39	MT	0	21	56	0.272727
42	ND	0	30	53	0.361446
44	NE	0	37	93	0.284615
48	NM	0	7	33	0.175000
50	NV	0	5	17	0.227273
54	OK	0	5	77	0.060976
56	OR	0	3	36	0.076923
58	PA	0	1	67	0.014706
62	SD	0	31	65	0.322917
65	TX	0	56	254	0.180645
67	UT	0	12	29	0.292683
69	VA	0	3	132	0.022222
72	WA	0	2	39	0.048780
74	WI	0	1	72	0.013699
77	WY	0	2	23	0.080000

In [75]:

```
#cols for states with less than 10% data is missing
cols = percentage_missing[percentage_missing["percent_missing"]<=0.10]['State'].tolist
cols
```

Out[75]:
```
['CA',
 'GA',
 'IA',
 'KY',
 'MI',
 'MN',
 'MO',
 'MS',
 'OK',
 'OR',
 'PA',
 'VA',
 'WA',
 'WI',
 'WY']
```

Based on the above table, we can see that for some states very less data is missing and we can remove the rows with less than 10% data is missing. Now let's also look at the lowest values of population based on the missing mortality rate data and other

Now I am getting the minimum population for each of the states with missing and available mortality rates. Hypothesis is to remove all the missing mortality rate values rows of states which have population above the minimum of available mortaility population

In [76]:
```
def conditions(s):
    if ((s['State'] in ('CA','GA',
 'IA',
 'KY',
 'MI',
 'MN',
 'MO',
 'MS',
 'OK',
 'OR',
 'PA',
 'VA',
 'WA',
 'WI',
 'WY')) & (s['Mortality_Rate']=='*')) :
        return 1
    else:
        return 0
```

In [77]:
```
merge_df['remove_values'] = merge_df.apply(conditions, axis = 1)
```

In [78]:
```
test_df = merge_df.loc[merge_df.groupby(['State','is_present']).POPESTIMATE2015.idxmir
```

In [79]:
```
pd.set_option('display.max_rows', None)
test_df = test_df[["State","AreaName","POPESTIMATE2015","is_present","Mortality_Rate"]
test_df['mortality1'] = np.where(test_df['Mortality_Rate']!='*',test_df['Mortality_Rat
test_df['mortality1'] = test_df['mortality1'].astype('float')
test_df['mortality2'] = (test_df['mortality1']/100000)*test_df['POPESTIMATE2015']
```

In [80]:
```
test_df.head()
```

Out[80]:

	State	AreaName	POPESTIMATE2015	is_present	Mortality_Rate	mortality1	mortality2
0	AK	Yakutat City and Borough, Alaska	613	0	*	0.0	0.000000
1	AK	Sitka City and Borough, Alaska	8863	1	39.6	39.6	3.509748
2	AL	Greene County, Alabama	8479	1	34.5	34.5	2.925255
3	AR	Calhoun County, Arkansas	5229	1	70.2	70.2	3.670758
4	AZ	Greenlee County, Arizona	9529	1	41.8	41.8	3.983122

In [81]:
```
average = merge_df[merge_df['is_present']==1].copy()
average['Mortality_Rate1'] = average['Mortality_Rate'].astype('float')
median = pd.DataFrame(average.groupby(['State'])['Mortality_Rate1'].median().reset_inc
```

In [82]:
```
min_present_pop = test_df[test_df['is_present']==1]
min_present_pop = min_present_pop[["State","POPESTIMATE2015"]]
min_present_pop.rename(columns={'POPESTIMATE2015':'min_pop_state'}, inplace=True)
```

In [83]:
```
final_merge = merge_df.merge(min_present_pop,on = 'State',how = 'left')
```

In [84]:
```
final_merge['greater_than_min'] = np.where((final_merge['POPESTIMATE2015']>final_merge
                                            (final_merge['Mortality_Rate']=='*'),1,0)
```

In [85]:
```
#number of rows i am removing in total
x=final_merge[(final_merge['remove_values']==1) | (final_merge['greater_than_min']==1)
x['Mortality_Rate'].count()
```

Out[85]:
```
150
```

We will remove these 150 values from our datasets. This is based on 2 conditions: if a state has less than 10% data missing and if the row with missing mortality for population higher than the minimum value of the avialble mortality population

In [86]:
```
final_merge = final_merge[final_merge['Med_Income'].notna()]
```

In [87]:
```
final_merge_data = final_merge[(final_merge['remove_values']!=1) | (final_merge['great
final_merge_data.rename(columns={'Mortality_Rate_':'median_mortality_rate'}, inplace=T
```

In [88]:
```
final_merge_data = final_merge_data.merge(median,how = 'left',on= 'State')
final_merge_data.head()
```

Out[88]:

	State	AreaName	All_Poverty	M_Poverty	F_Poverty	FIPS	Med_Income	Med_Income_White
0	AK	Aleutians East Borough, Alaska	553	334	219	002013	61518.0	72639.0
1	AK	Aleutians West Census Area, Alaska	499	273	226	002016	84306.0	97321.0
2	AK	Anchorage Municipality, Alaska	23914	10698	13216	002020	78326.0	87235.0
3	AK	Bethel Census Area, Alaska	4364	2199	2165	002050	51012.0	92647.0
4	AK	Bristol Bay Borough, Alaska	69	33	36	002060	79750.0	88000.0

5 rows × 26 columns

In [89]:

```
final_merge_data['Mortality_Rate'] = np.where(final_merge_data['Mortality_Rate']=='*',
                                              final_merge_data['Mortality_Rate1'],fina
```

In [90]:

```
final_merge_data.columns
```

Out[90]:

```
Index(['State', 'AreaName', 'All_Poverty', 'M_Poverty', 'F_Poverty', 'FIPS',
       'Med_Income', 'Med_Income_White', 'M_With', 'M_Without', 'F_With',
       'F_Without', 'All_With', 'All_Without', 'Incidence_Rate',
       'Avg_Ann_Incidence', 'Recent_Trend', 'Mortality_Rate', 'Avg_Ann_Deaths',
       'POPESTIMATE2015', 'pop_rank', 'is_present', 'remove_values',
       'min_pop_state', 'greater_than_min', 'Mortality_Rate1'],
      dtype='object')
```

In [ ]:

Approach: Replace with state median if the population is lower than minimum population of the available mortality rate values

The overall idea was to reduce the number of rows we have to remove from the data and get the best number to impute the values. I have taken state medians as there are high variation between medians of different states and it's better to account for that variation in some way. A high mortality rate in smaller population will hold more significance that raw lower raw numbers in the higher population, and hence it makes sense to remove that data. I took the minimum of available mortality rate population as my bandwidth to remove these values

(while minimum of available mortality rate population is a good parameter, i also tested if this is prone to being outliers and found no evidence for that in most of the states)

1.6 Reformat the rest of the columns specified in 1.3 to numerical [5 Marks]

In each column reformat all the cells that you can.

***Hint*: You can keep the cells that you cannot reformat until you decide if you want to use the specific column in the model. This is because you want to lose as least data as possible. So you can drop the associated rows if you want to use the column and keep them if the specific column is not used.**

For the below changes, i have followed these steps: make the required changes and replacements, replace the missing values with the median of the states if state median is available. If not, i am replacing that with overall median.

In [91]:
```
#making the required changes to incidence rate
final_merge_data['Incidence_Rate'] = final_merge_data['Incidence_Rate'].replace('*',np
final_merge_data['Incidence_Rate'] = final_merge_data['Incidence_Rate'].replace(['_','
final_merge_data['Incidence_Rate'] = final_merge_data['Incidence_Rate'].replace(' #',
final_merge_data['Incidence_Rate'] = final_merge_data['Incidence_Rate'].astype(float)
```

In [92]:
```
#Overall median
overall_incidence_median = final_merge_data['Incidence_Rate'].median()
```

In [93]:
```
#merge with the final data to get a column with the median at state level
median_incidence = pd.DataFrame(final_merge_data.groupby(['State'])['Incidence_Rate'].
final_merge_data = final_merge_data.merge(median_incidence,how = 'left',on= 'State')
```

In [94]:
```
#filling missing values with the required results
final_merge_data['Incidence_Rate_x'] = np.where(final_merge_data['Incidence_Rate_x']==
                                     final_merge_data['Incidence_Rate_y'],fir
final_merge_data['Incidence_Rate_x'].fillna(final_merge_data['Incidence_Rate_y'],inpla
final_merge_data['Incidence_Rate_x'].fillna(overall_incidence_median,inplace=True)
```

In [95]:
```
#a similar approach has been followed for Avg Ann Deaths
```

In [96]:
```
final_merge_data['Avg_Ann_Deaths'] = final_merge_data['Avg_Ann_Deaths'].replace('*',np
final_merge_data['Avg_Ann_Deaths'] = final_merge_data['Avg_Ann_Deaths'].replace(['_','
final_merge_data['Avg_Ann_Deaths'] = final_merge_data['Avg_Ann_Deaths'].replace(',', '
final_merge_data['Avg_Ann_Deaths'] = final_merge_data['Avg_Ann_Deaths'].astype(float)
```

In [97]:
```
overall_ann_death_median = final_merge_data['Avg_Ann_Deaths'].median()
```

In [98]:
```
median_ann_death = pd.DataFrame(final_merge_data.groupby(['State'])['Avg_Ann_Deaths'].
final_merge_data = final_merge_data.merge(median_ann_death,how = 'left',on= 'State')
```

In [99]:
```
final_merge_data['Avg_Ann_Deaths_x'] = np.where(final_merge_data['Avg_Ann_Deaths_x']==
                                     final_merge_data['Avg_Ann_Deaths_y'],fir
final_merge_data['Avg_Ann_Deaths_x'].fillna(final_merge_data['Avg_Ann_Deaths_y'],inpla
final_merge_data['Avg_Ann_Deaths_x'].fillna(overall_ann_death_median,inplace=True)
```

In [100…
```
#a similar approach has been followed for Avg Ann Incidence
```

In [101…
```
final_merge_data['Avg_Ann_Incidence'] = final_merge_data['Avg_Ann_Incidence'].replace(
final_merge_data['Avg_Ann_Incidence'] = final_merge_data['Avg_Ann_Incidence'].replace(
final_merge_data['Avg_Ann_Incidence'] = final_merge_data['Avg_Ann_Incidence'].astype(f
```

In [102…
```
overall_ann_inci_median = final_merge_data['Avg_Ann_Incidence'].median()
```

In [103…
```
median_ann_inci_death = pd.DataFrame(final_merge_data.groupby(['State'])['Avg_Ann_Inci
final_merge_data = final_merge_data.merge(median_ann_inci_death,how = 'left',on= 'Stat
```

In [104…
```
final_merge_data['Avg_Ann_Incidence_x'] = np.where(final_merge_data['Avg_Ann_Incidence
                                                final_merge_data['Avg_Ann_Incidence_y'],
final_merge_data['Avg_Ann_Incidence_x'].fillna(final_merge_data['Avg_Ann_Incidence_y']
final_merge_data['Avg_Ann_Incidence_x'].fillna(overall_ann_inci_median,inplace=True)
```

In [105…
```
#cols have been defined based on the data dictionary
cols = ['M_Poverty','F_Poverty','M_With','M_Without','F_Without','All_With','All_Witho
```

1.7 Make the numerical data useful [5 Marks]

We know we have many columns of data, some of them are dependent on the populations. As a *Hint*, convert all the raw data to per 100,000 persons rates (divide by population and multiply by 100,000).

In [106…
```
#create a for loop for apply the same formula to multiple columns
for col in final_merge_data[cols]:
    final_merge_data[col] = (final_merge_data[col]/final_merge_data['POPESTIMATE2015']
```

In [107…
```
final_merge_data['Mortality_Rate'] = final_merge_data['Mortality_Rate'].astype(float)
```

In [108…
```
final_merge_data.dtypes
```

Out[108]:
```
State                    object
AreaName                 object
All_Poverty               int64
M_Poverty               float64
F_Poverty               float64
FIPS                     object
Med_Income              float64
Med_Income_White        float64
M_With                  float64
M_Without               float64
F_With                    int64
F_Without               float64
All_With                float64
All_Without             float64
Incidence_Rate_x        float64
Avg_Ann_Incidence_x     float64
Recent_Trend             object
Mortality_Rate          float64
Avg_Ann_Deaths_x        float64
POPESTIMATE2015           int64
pop_rank                  int32
is_present                int32
remove_values             int64
min_pop_state             int64
greater_than_min          int32
Mortality_Rate1         float64
Incidence_Rate_y        float64
Avg_Ann_Deaths_y        float64
Avg_Ann_Incidence_y     float64
dtype: object
```

In [109…
```
#dropping extra columns we created
final_merge_data.drop(['Avg_Ann_Incidence_y', 'Avg_Ann_Deaths_y', 'Incidence_Rate_y',
                       'greater_than_min', 'min_pop_state','remove_values','is_present
```

Part 2: Exploratory analysis [15 Marks]

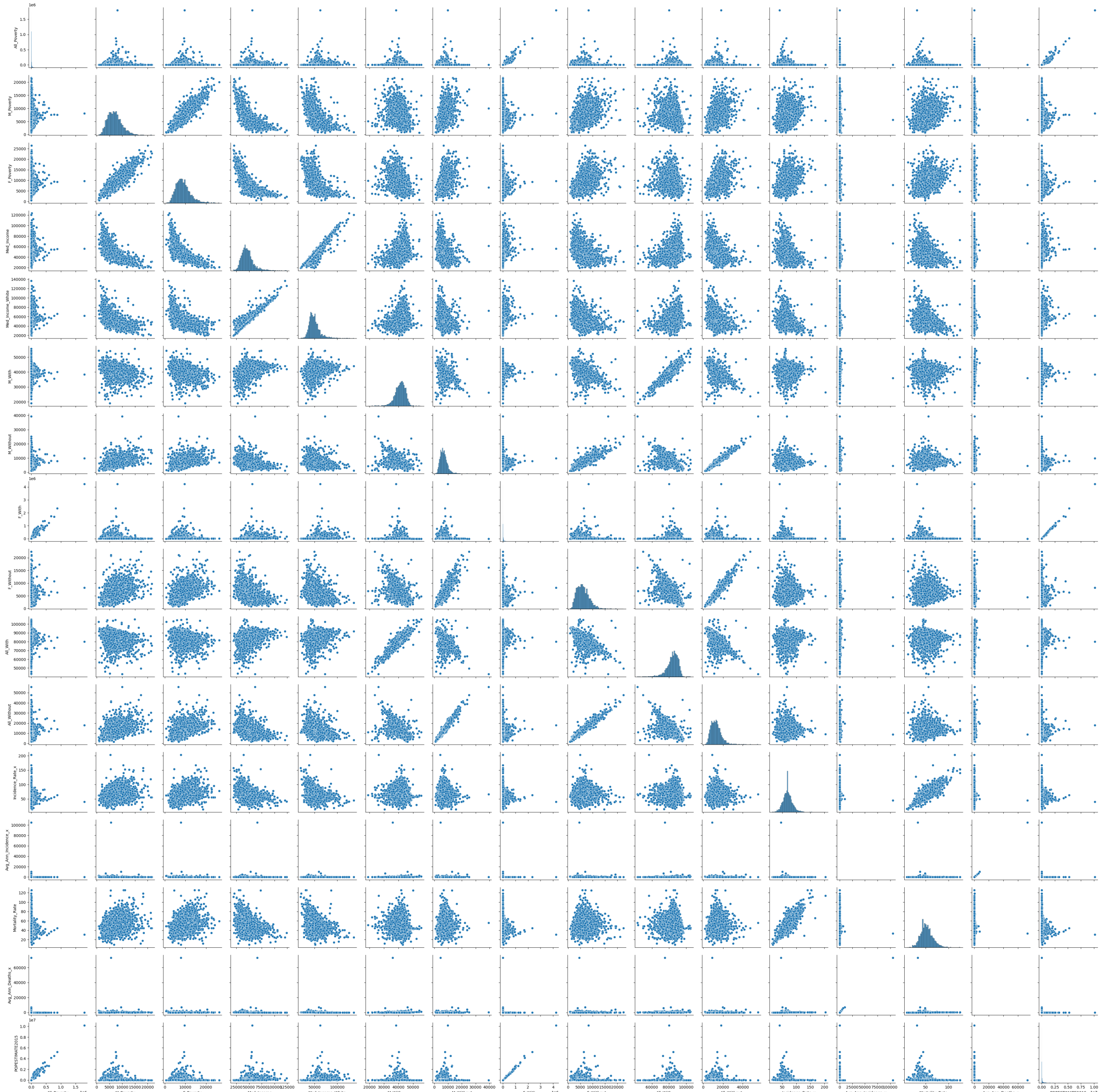
2.1 Visualizing different features [5 Marks]

Here, show different feature and how they change with respect to each other. *Hint*: A good function to use here is `sns.pairplot`. Remember to have the plots labeled properly so that they are self explanatory.

In [110…
```
sns.pairplot(final_merge_data)
```

Out[110]: <seaborn.axisgrid.PairGrid at 0x283a4c6bb50>

In [111…
```
plt.show()
```



2.2 Selecting the most important features [10 Marks]

In this step, we want to remove the redundant features.

***Hint*: This can be done by analyzing the correlation between the features and removing the highly correlated features. Remember, throughout the project, write down specific reasons for any desicion you make.**

In [112…

```
#removing extra Columns
final_merge_data.drop(['M_Poverty', 'F_Poverty', 'M_With', 'M_Without', 'F_With', 'F_W
```

The above columns have been removed as they are highly correlated with other variables such as M_poverty, F_poverty with All_Poverty, M_with and F_with with All_With and M_without and F_without with All_without

Part 3: Regression Model Construction [30 Marks]

3.1 Splitting the dataset [5 Marks]

Split the dataset to three parts: train, validation, and test. You choose the ratios for the three datasets and provide a one-sentence rationale on why you went with such ratios.

***Hint*: You can use the validation set approach from ch5 lab (google colab).**

In [131…

```
Auto = final_merge_data.sample(frac=1).reset_index(drop=True)
Auto_hold_out=Auto[int(0.75*len(Auto)):len(Auto)]

Auto=Auto[0:int(0.75*len(Auto))]

train = np.random.choice(Auto.shape[0], int(2*Auto.shape[0]/3), replace=False)
select = np.in1d(range(Auto.shape[0]), train)
len(select)
```

Out[131]:

```
2336
```

I have split the data into 3 sets - train(50%), validation(25%) and test (25%). we have used 25% for validation and test to get the best accuracy for our model. The rest 50% will be used for training the model.

3.2 Model training [15 Marks]

Create three different models, using different features (and optionally nonlinear transformations). The purpose of these models is to predict mortality rate of lung cancer with reasonably high R2 (at least exceeding 70%) using a carefully chosen and justified set of features. Use the visualizations from section 2.1 to inform the feature selection for each model.

For Model training and validation, i have used 3 different approches: Forward Selection, Backward Selection and Non Linear transformations

1. Forward Selection

(note: I have shown the first and the last model i arrived at for each of the methods)

In [132…

```
#inital forward selection model
import statsmodels.formula.api as smf
lm1 = smf.ols('Mortality_Rate~Incidence_Rate_x', data = Auto[select]).fit()
print(lm1.summary())
preds = lm1.predict(Auto)
square_error = (Auto['Mortality_Rate'] - preds)**2
print('--------Validation MSE for regression model--------')
print('MSE:',np.mean(square_error[~select]))
```

```
                            OLS Regression Results
==============================================================================
Dep. Variable:         Mortality_Rate   R-squared:                       0.723
Model:                            OLS   Adj. R-squared:                  0.723
Method:                 Least Squares   F-statistic:                     4063.
Date:                Thu, 09 Feb 2023   Prob (F-statistic):               0.00
Time:                        21:58:43   Log-Likelihood:                -5316.0
No. Observations:                1557   AIC:                         1.064e+04
Df Residuals:                    1555   BIC:                         1.065e+04
Df Model:                           1
Covariance Type:            nonrobust
====================================================================================
                       coef    std err          t      P>|t|      [0.025      0.975]
------------------------------------------------------------------------------------
Intercept            4.6774      0.770      6.072      0.000       3.166       6.188
Incidence_Rate_x     0.6952      0.011     63.738      0.000       0.674       0.717
==============================================================================
Omnibus:                       98.098   Durbin-Watson:                   2.039
Prob(Omnibus):                  0.000   Jarque-Bera (JB):              289.428
Skew:                           0.291   Prob(JB):                     1.42e-63
Kurtosis:                       5.030   Cond. No.                         292.
==============================================================================

Notes:
[1] Standard Errors assume that the covariance matrix of the errors is correctly spec
ified.
--------Validation MSE for regression model--------
MSE: 50.75248376609169
```

In [133…

```
#final forward selection model
lm3 = smf.ols ('Mortality_Rate~Incidence_Rate_x + All_Without + Med_Income', data = Au
print(lm3.summary())
preds = lm3.predict(Auto)
square_error = (Auto['Mortality_Rate'] - preds)**2
print('--------Validation MSE for regression model--------')
print('MSE:',square_error[~select].mean())
```

```
                            OLS Regression Results                            
==============================================================================
Dep. Variable:         Mortality_Rate   R-squared:                       0.746
Model:                            OLS   Adj. R-squared:                  0.745
Method:                 Least Squares   F-statistic:                     1518.
Date:                Thu, 09 Feb 2023   Prob (F-statistic):               0.00
Time:                        21:58:45   Log-Likelihood:                -5249.9
No. Observations:                1557   AIC:                         1.051e+04
Df Residuals:                    1553   BIC:                         1.053e+04
Df Model:                           3                                         
Covariance Type:            nonrobust                                         
====================================================================================
                       coef    std err          t      P>|t|      [0.025      0.975]
------------------------------------------------------------------------------------
Intercept            9.0957      1.553      5.856      0.000       6.049      12.142
Incidence_Rate_x     0.6668      0.011     59.417      0.000       0.645       0.689
All_Without          0.0002   3.77e-05      5.673      0.000       0.000       0.000
Med_Income          -0.0001   1.71e-05     -6.641      0.000      -0.000   -7.99e-05
==============================================================================
Omnibus:                       85.465   Durbin-Watson:                   2.006
Prob(Omnibus):                  0.000   Jarque-Bera (JB):              267.515
Skew:                           0.201   Prob(JB):                     8.13e-59
Kurtosis:                       4.990   Cond. No.                     4.32e+05
==============================================================================

Notes:
[1] Standard Errors assume that the covariance matrix of the errors is correctly spec
ified.
[2] The condition number is large, 4.32e+05. This might indicate that there are
strong multicollinearity or other numerical problems.
--------Validation MSE for regression model--------
MSE: 48.96518447146005
```

2. Backward Selection

In [134…

```
all_columns = "+".join(Auto.columns)
all_columns
#https://stackoverflow.com/questions/22388498/statsmodels-linear-regression-patsy-forn
```

Out[134]:

```
'State+AreaName+All_Poverty+FIPS+Med_Income+Med_Income_White+All_With+All_Without+Inc
idence_Rate_x+Avg_Ann_Incidence_x+Recent_Trend+Mortality_Rate+Avg_Ann_Deaths_x+POPEST
IMATE2015'
```

In [135…

```
#initial backward selection model
lmb1 = smf.ols('Mortality_Rate~All_Poverty+Med_Income+Med_Income_White+All_With+All_Wi
print(lmb1.summary())
preds = lmb1.predict(Auto)
square_error = (Auto['Mortality_Rate'] - preds)**2
print('--------Validation MSE for regression model--------')
print('MSE:',np.mean(square_error[~select]))
```

```
                            OLS Regression Results
==============================================================================
Dep. Variable:         Mortality_Rate   R-squared:                       0.752
Model:                            OLS   Adj. R-squared:                  0.750
Method:                 Least Squares   F-statistic:                     520.0
Date:                Thu, 09 Feb 2023   Prob (F-statistic):               0.00
Time:                        21:58:52   Log-Likelihood:                -5231.8
No. Observations:                1557   AIC:                         1.048e+04
Df Residuals:                    1547   BIC:                         1.054e+04
Df Model:                           9
Covariance Type:            nonrobust
================================================================================
==
                          coef    std err          t      P>|t|      [0.025      0.97
5]
--------------------------------------------------------------------------------
--
Intercept               1.0354      4.047      0.256      0.798      -6.902       8.9
73
All_Poverty         -1.813e-05   1.48e-05     -1.224      0.221   -4.72e-05    1.09e-
05
Med_Income             -0.0002   4.43e-05     -3.471      0.001      -0.000    -6.7e-
05
Med_Income_White     4.647e-05   4.04e-05      1.149      0.251   -3.29e-05       0.0
00
All_With             8.475e-05   3.86e-05      2.193      0.028    8.94e-06       0.0
00
All_Without             0.0003   5.31e-05      5.216      0.000       0.000       0.0
00
Incidence_Rate_x        0.6671      0.011     59.712      0.000       0.645       0.6
89
Avg_Ann_Incidence_x    -0.0079      0.002     -4.376      0.000      -0.011      -0.0
04
Avg_Ann_Deaths_x        0.0097      0.002      4.052      0.000       0.005       0.0
14
POPESTIMATE2015      6.637e-07   2.48e-06      0.267      0.789    -4.2e-06    5.53e-
06
==============================================================================
Omnibus:                       92.190   Durbin-Watson:                   1.997
Prob(Omnibus):                  0.000   Jarque-Bera (JB):              313.283
Skew:                           0.197   Prob(JB):                     9.36e-69
Kurtosis:                       5.162   Cond. No.                     6.99e+06
==============================================================================

Notes:
[1] Standard Errors assume that the covariance matrix of the errors is correctly spec
ified.
[2] The condition number is large, 6.99e+06. This might indicate that there are
strong multicollinearity or other numerical problems.
--------Validation MSE for regression model--------
MSE: 48.638238632852136
```

In [136…

```
#Final backward selection model
lmb1 = smf.ols('Mortality_Rate~Med_Income+All_Without+Incidence_Rate_x', data = Auto[s
print(lmb1.summary())
preds = lmb1.predict(Auto)
square_error = (Auto['Mortality_Rate'] - preds)**2
print('--------Validation MSE for regression model--------')
print('MSE:',np.mean(square_error[~select]))
```

```
                            OLS Regression Results
==============================================================================
Dep. Variable:         Mortality_Rate   R-squared:                       0.746
Model:                            OLS   Adj. R-squared:                  0.745
Method:                 Least Squares   F-statistic:                     1518.
Date:                Thu, 09 Feb 2023   Prob (F-statistic):               0.00
Time:                        21:58:55   Log-Likelihood:                -5249.9
No. Observations:                1557   AIC:                         1.051e+04
Df Residuals:                    1553   BIC:                         1.053e+04
Df Model:                           3
Covariance Type:            nonrobust
====================================================================================
                       coef    std err          t      P>|t|      [0.025      0.975]
------------------------------------------------------------------------------------
Intercept            9.0957      1.553      5.856      0.000       6.049      12.142
Med_Income          -0.0001   1.71e-05     -6.641      0.000      -0.000   -7.99e-05
All_Without          0.0002   3.77e-05      5.673      0.000       0.000       0.000
Incidence_Rate_x     0.6668      0.011     59.417      0.000       0.645       0.689
==============================================================================
Omnibus:                       85.465   Durbin-Watson:                   2.006
Prob(Omnibus):                  0.000   Jarque-Bera (JB):              267.515
Skew:                           0.201   Prob(JB):                     8.13e-59
Kurtosis:                       4.990   Cond. No.                     4.32e+05
==============================================================================

Notes:
[1] Standard Errors assume that the covariance matrix of the errors is correctly spec
ified.
[2] The condition number is large, 4.32e+05. This might indicate that there are
strong multicollinearity or other numerical problems.
--------Validation MSE for regression model--------
MSE: 48.96518447145871
```

We arrive at the same model using backward selection as well. We do minor changes in R squared due to some variables, but small changes are not worth cost of increasing multiple data. This could be due to the way i have imputed the missing information. Not removing certain variables such as Average Annual Incidence has a minor effect on our model and should not be considered in the model

In [ ]:

3. Transformations

Based on the previous model we can try interaction terms and quadratic forms in order get a better Rsquared and MSE

In [137…

```
#initial transformation model
lmb1 = smf.ols('Mortality_Rate~Med_Income+ I(All_Without ** 2.0) + I(All_Without ** 3.
print(lmb1.summary())
preds = lmb1.predict(Auto)
square_error = (Auto['Mortality_Rate'] - preds)**2
print('--------Validation MSE for regression model--------')
print('MSE:',np.mean(square_error[~select]))
```

```
                            OLS Regression Results
==============================================================================
Dep. Variable:         Mortality_Rate   R-squared:                       0.750
Model:                            OLS   Adj. R-squared:                  0.749
Method:                 Least Squares   F-statistic:                     929.1
Date:                Thu, 09 Feb 2023   Prob (F-statistic):               0.00
Time:                        21:58:59   Log-Likelihood:                -5237.6
No. Observations:                1557   AIC:                         1.049e+04
Df Residuals:                    1551   BIC:                         1.052e+04
Df Model:                           5
Covariance Type:            nonrobust
==============================================================================
====
                            coef    std err          t      P>|t|      [0.025      0.
975]
------------------------------------------------------------------------------
----
Intercept                 1.7397      2.319      0.750      0.453      -2.810
6.289
Med_Income             -9.31e-05   1.74e-05     -5.336      0.000      -0.000   -5.89
e-05
I(All_Without ** 2.0) -5.125e-08   1.67e-08     -3.064      0.002   -8.41e-08   -1.84
e-08
I(All_Without ** 3.0)  5.937e-13   2.68e-13      2.215      0.027    6.79e-14    1.12
e-12
All_Without               0.0013      0.000      4.370      0.000       0.001
0.002
Incidence_Rate_x          0.6629      0.011     59.339      0.000       0.641
0.685
==============================================================================
Omnibus:                       89.037   Durbin-Watson:                   2.000
Prob(Omnibus):                  0.000   Jarque-Bera (JB):              262.647
Skew:                           0.248   Prob(JB):                     9.26e-58
Kurtosis:                       4.950   Cond. No.                     9.11e+13
==============================================================================

Notes:
[1] Standard Errors assume that the covariance matrix of the errors is correctly spec
ified.
[2] The condition number is large, 9.11e+13. This might indicate that there are
strong multicollinearity or other numerical problems.
--------Validation MSE for regression model--------
MSE: 48.8185041047003
```

While the above transformation produces a better R squared and MSE also increases but we risk falling into the curse of dimensionality.

In [ ]:

3.3 Model selection [10 Marks]

Using different model selection criteria and validation dataset, choose the single best perfoming model among the three models.

Based on the above we will choose the model we arrived at using additive method in regression modelling.

In [138…
```
lm3 = smf.ols ('Mortality_Rate~Incidence_Rate_x + All_Without + Med_Income', data = Au
print(lm3.summary())
preds = lm3.predict(Auto)
square_error = (Auto['Mortality_Rate'] - preds)**2
print('--------Validation MSE for regression model--------')
print('MSE:',square_error[~select].mean())
```

```
                            OLS Regression Results
==============================================================================
Dep. Variable:         Mortality_Rate   R-squared:                       0.746
Model:                            OLS   Adj. R-squared:                  0.745
Method:                 Least Squares   F-statistic:                     1518.
Date:                Thu, 09 Feb 2023   Prob (F-statistic):               0.00
Time:                        21:59:04   Log-Likelihood:                -5249.9
No. Observations:                1557   AIC:                         1.051e+04
Df Residuals:                    1553   BIC:                         1.053e+04
Df Model:                           3
Covariance Type:            nonrobust
====================================================================================
                       coef    std err          t      P>|t|      [0.025      0.975]
------------------------------------------------------------------------------------
Intercept            9.0957      1.553      5.856      0.000       6.049      12.142
Incidence_Rate_x     0.6668      0.011     59.417      0.000       0.645       0.689
All_Without          0.0002   3.77e-05      5.673      0.000       0.000       0.000
Med_Income          -0.0001   1.71e-05     -6.641      0.000      -0.000   -7.99e-05
==============================================================================
Omnibus:                       85.465   Durbin-Watson:                   2.006
Prob(Omnibus):                  0.000   Jarque-Bera (JB):              267.515
Skew:                           0.201   Prob(JB):                     8.13e-59
Kurtosis:                       4.990   Cond. No.                     4.32e+05
==============================================================================

Notes:
[1] Standard Errors assume that the covariance matrix of the errors is correctly spec
ified.
[2] The condition number is large, 4.32e+05. This might indicate that there are
strong multicollinearity or other numerical problems.
--------Validation MSE for regression model--------
MSE: 48.96518447146005
```

Part 4: Model diagnostics [10 marks]

Explore model collinearity with `variance_inflation_factor`. Larger values of VIF indicate multicollinearity. Remove the problematic features and refit the model. Report how model R-squared is affected.

***Hint:* Consider VIF > 10 as an indicator of multicollinearity. If the VIF for all your features is below 10, it is a positive indication that the level of collinearity is acceptably low without any changes to the model needed in this step.**

In [139…
```
from statsmodels.stats.outliers_influence import variance_inflation_factor


# the independent variables set
X = Auto[['Incidence_Rate_x', 'All_Without', 'Med_Income']]
```

```
# VIF dataframe
vif_data = pd.DataFrame()
vif_data["feature"] = X.columns

# calculating VIF for each feature
vif_data["VIF"] = [variance_inflation_factor(X.values, i)
                                                          for i in range(len(X.columns))]

print(vif_data)

#https://www.geeksforgeeks.org/detecting-multicollinearity-with-vif-python/
```

```
           feature       VIF
0  Incidence_Rate_x  9.313784
1       All_Without  5.564555
2        Med_Income  6.697614
```

As all the VIF values are below 10, the features are acceptable in our model

Part 5: Reporting test performance [5 marks]

Report the MSE of the final regression model using the test set.

In [140…

```
preds_test = lm3.predict(Auto_hold_out)
square_error = (Auto_hold_out['Mortality_Rate'] - preds_test)**2
print('--------Test MSE for regression model--------')
print('MSE:',square_error.mean())
```

```
--------Test MSE for regression model--------
MSE: 53.280495022678174
```

Part 6: Alternative predictive model (optional): [20 bonus points up to the maximum mark]

Use one other supervised learning model to outperform the regression model from part 5 (in terms of MSE) on the same hold-out test set. Document, justify, and explain all your decision w.r.t. the implementation of this alternative predictive model.

This part is deliberately designed without clear instructions as bonus points for efforts of groups in completing a very common ML task without a walkthrough or instrcutions.

I have tried 2 different models below-regression tree and Baggeed decision trees. I have also reported the MSE's for both the models to evaluate their performance against our linear regression model.

First I will try to fit a regression tree and check the MSE for the same

In [141…

```
#improting the required libraries
from sklearn.tree import DecisionTreeClassifier, export_graphviz, DecisionTreeRegresso
from sklearn.ensemble import RandomForestRegressor, GradientBoostingRegressor
from sklearn.metrics import confusion_matrix, accuracy_score, mean_squared_error
```

```
from sklearn import tree
import matplotlib.pyplot as plt
```

In [142…

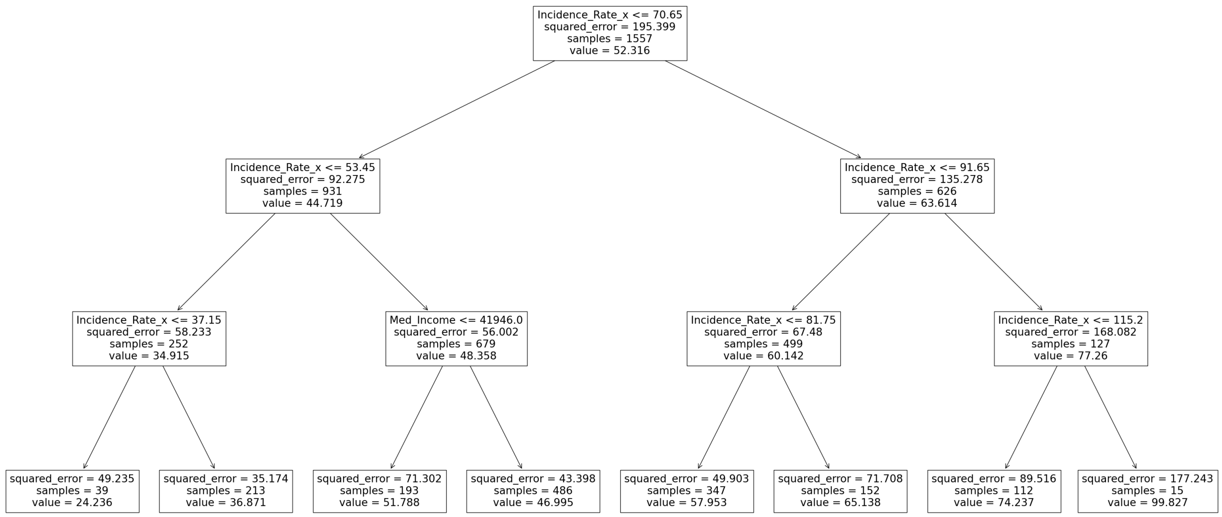
```
regr_tree = DecisionTreeRegressor(max_depth=3)
regr_tree.fit(Auto[['Incidence_Rate_x', 'All_Without', 'Med_Income']][select],Auto[['M
```

Out[142]:

```
DecisionTreeRegressor(max_depth=3)
```

In [143…

```
plt.figure(figsize=(40,20))  # customize according to the size of your tree
plot_tree(regr_tree, feature_names = Auto[['Incidence_Rate_x', 'All_Without', 'Med_Inc
plt.show()
```



In [144…

```
y_pred = regr_tree.predict(Auto[['Incidence_Rate_x', 'All_Without', 'Med_Income']][~se
print(mean_squared_error(Auto[['Mortality_Rate']][~select], y_pred))
```

```
53.08768430640933
```

In [145…

```
y_pred = regr_tree.predict(Auto_hold_out[['Incidence_Rate_x', 'All_Without', 'Med_Inco
print(mean_squared_error(Auto_hold_out[['Mortality_Rate']], y_pred))
```

```
65.74058989264995
```

Seems like regression tree is not the best method for us. lets try bagged decision tree

In [146…

```
all_features = Auto[['Incidence_Rate_x', 'All_Without', 'Med_Income']][select].shape[1
regr_bagging = RandomForestRegressor(max_features=all_features, random_state=2)
regr_bagging.fit(Auto[['Incidence_Rate_x', 'All_Without', 'Med_Income']][select], Auto
```

```
C:\Users\stati\AppData\Local\Temp\ipykernel_24668\262138268.py:3: DataConversionWarni
ng: A column-vector y was passed when a 1d array was expected. Please change the shap
e of y to (n_samples,), for example using ravel().
  regr_bagging.fit(Auto[['Incidence_Rate_x', 'All_Without', 'Med_Income']][select], A
uto[['Mortality_Rate']][select])
```

Out[146]:

```
RandomForestRegressor(max_features=3, random_state=2)
```

In [147…

```
#MSE for the validation set
y_pred = regr_bagging.predict(Auto[['Incidence_Rate_x', 'All_Without', 'Med_Income']][
```

```
print(mean_squared_error(Auto[['Mortality_Rate']][~select], y_pred))
```

```
52.257337223684225
```

In [148…

```
#getting MSE for the test set
y_pred = regr_bagging.predict(Auto_hold_out[['Incidence_Rate_x', 'All_Without', 'Med_I
print(mean_squared_error(Auto_hold_out[['Mortality_Rate']], y_pred))
```

```
57.64299663799748
```

even though bagged trees perform better than regression trees, it still does not perform better than the linear regression method