

cancer

April 1, 2019

Cancer Data Analysis

Cleaning Process

Following are the steps we followed for data analysis

1. Import the libraries

```
In [197]: #Import the Libraries
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt

%matplotlib inline

import seaborn as sns
import warnings
warnings.filterwarnings('ignore')
```

2. Load the dataset.

```
In [198]: dataset=pd.read_csv('data/data.csv')
```

```
In [199]: dataset.head(3)
```

```
Out[199]:
```

	Indicator Category \
0	Behavioral Health/Substance Abuse
1	Behavioral Health/Substance Abuse
2	Behavioral Health/Substance Abuse

	Indicator	Year	Sex \
0	Opioid-Related Unintentional Drug Overdose Mor...	2010	Both
1	Opioid-Related Unintentional Drug Overdose Mor...	2010	Both
2	Opioid-Related Unintentional Drug Overdose Mor...	2010	Both

	Race/Ethnicity	Value	Place \
0	All	1.7	Washington, DC
1	All	2.2	Fort Worth (Tarrant County), TX
2	All	2.3	Oakland (Alameda County), CA

	BCHC Requested Methodology \		Source \		Methods \		Notes \
0	Age-Adjusted rate of opioid-related mortality ...		D.C. Department of Health, Center for Policy, ...		NaN		This indicator is not exclusive of other drugs...
1	Age-adjusted rate of opioid-related mortality ...		National Center for Health Statistics		NaN		This indicator is not exclusive of other drugs...
2	Age-adjusted rate of opioid-related mortality ...		CDC Wonder				Data is for Alameda County. This indicator is ...

	90% Confidence Level - Low	90% Confidence Level - High \
0	NaN	NaN
1	NaN	NaN
2	NaN	NaN

	95% Confidence Level - Low	95% Confidence Level - High
0	NaN	NaN
1	1.5	3.0
2	1.6	3.2

Above we saw the column names and we might need to fix the spaces in the column names. In order to change that we need to first know what are the actual names of the columns. We do that using the pandas function `columns` to list all the columns

```
In [200]: dataset.columns
```

```
Out[200]: Index(['Indicator Category', 'Indicator', 'Year', 'Sex', 'Race/Ethnicity',
                'Value', 'Place', 'BCHC Requested Methodology', 'Source', 'Methods',
                'Notes', '90% Confidence Level - Low', '90% Confidence Level - High',
                '95% Confidence Level - Low', '95% Confidence Level - High'],
                dtype='object')
```

Now we rename the columns

```
In [201]: dataset.rename(columns={'Indicator Category':'indicator_category', 'Indicator':'indicator',
                                'Value':'value', 'Place':'place', 'BCHC Requested Methodology':'bchc_req_meth',
                                'Notes':'notes', '90% Confidence Level - Low':'90pc_con_lvl-low', '90% Confidence Level - High':'90pc_con_lvl-high',
                                '95% Confidence Level - Low':'95pc_con_lvl-low', '95% Confidence Level - High':'95pc_con_lvl-high'})
```

3. Now we need to filter the data according to the indicator category. We use one of the values "Cancer".

```
In [202]: cancer_ds = dataset.loc[dataset["indicator_category"] == "Cancer"]
```

4. And then we remove empty columns and unnecessary columns

```
In [203]: cancer_ds.drop(['indicator_category', 'bchc_req_meth', 'source', 'methods', 'notes', '90p
axis = 1, inplace= True)
```

5. Now we remove all the rows which has NaN or NA values

```
In [204]: cancer_ds.dropna(axis=0, how='any', inplace= True)
```

```
In [205]: cancer_ds.to_csv("data/cancer.csv")
```

```
In [206]: cancer_ds.head(3)
```

```
Out[206]:
```

			indicator	year	sex	\
1468	All Types of Cancer Mortality Rate (Age-Adjust...			2010	Both	
1469	All Types of Cancer Mortality Rate (Age-Adjust...			2010	Both	
1470	All Types of Cancer Mortality Rate (Age-Adjust...			2010	Both	

	race_ethnicity	value	place	95pc_con_lvl-low	\
1468	All	149.9	San Francisco, CA	145.3	
1469	All	156.7	Seattle, WA	146.5	
1470	All	159.9	San Antonio, TX	153.5	

	95pc_con_lvl-high
1468	154.6
1469	167.6
1470	166.4

Analysis

First we'll see how many patients have been reported for cancer in respective years from 2010 to 2016.

Following is the process to do the same

```
In [207]: c_year_2010=cancer_ds[cancer_ds['year']==2010]
c_year_2010_count=c_year_2010['year'].count()
```

```
In [208]: c_year_2010.shape
```

```
Out[208]: (138, 8)
```

```
In [209]: c_year_2011=cancer_ds[cancer_ds['year']==2011]
c_year_2011_count=c_year_2011['year'].count()
```

```
c_year_2012=cancer_ds[cancer_ds['year']==2012]
c_year_2012_count=c_year_2012['year'].count()
```

```

c_year_2013=cancer_ds[cancer_ds['year']==2013]
c_year_2013_count=c_year_2013['year'].count()

c_year_2014=cancer_ds[cancer_ds['year']==2014]
c_year_2014_count=c_year_2014['year'].count()

c_year_2015=cancer_ds[cancer_ds['year']==2015]
c_year_2015_count=c_year_2015['year'].count()

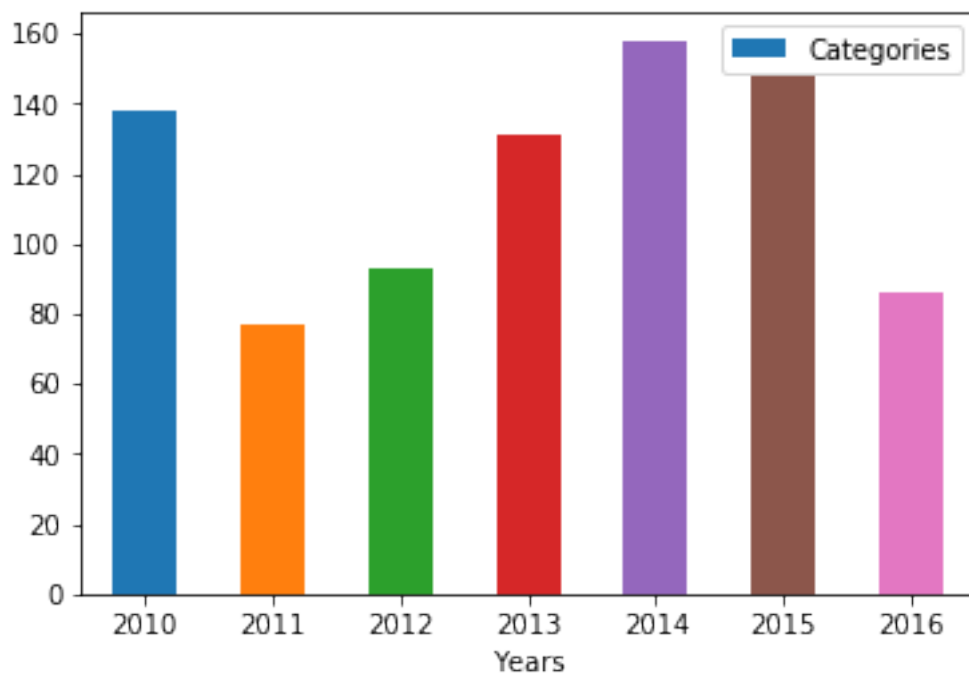
c_year_2016=cancer_ds[cancer_ds['year']==2016]
c_year_2016_count=c_year_2016['year'].count()

```

```

In [210]: fig1 = pd.DataFrame({'Years':['2010', '2011', '2012', '2013', '2014', '2015', '2016'], 'Categories': ['C1', 'C2', 'C3', 'C4', 'C5', 'C6', 'C7']})
ax = fig1.plot.bar(x='Years', y='Categories', rot=0)

```



Now we calculate the number of cases for each type of cancer. In order to that we will group according to the indicator and take the count.

```

In [211]: sorted_cancer = cancer_ds['indicator'].value_counts()
sorted_cancer

```

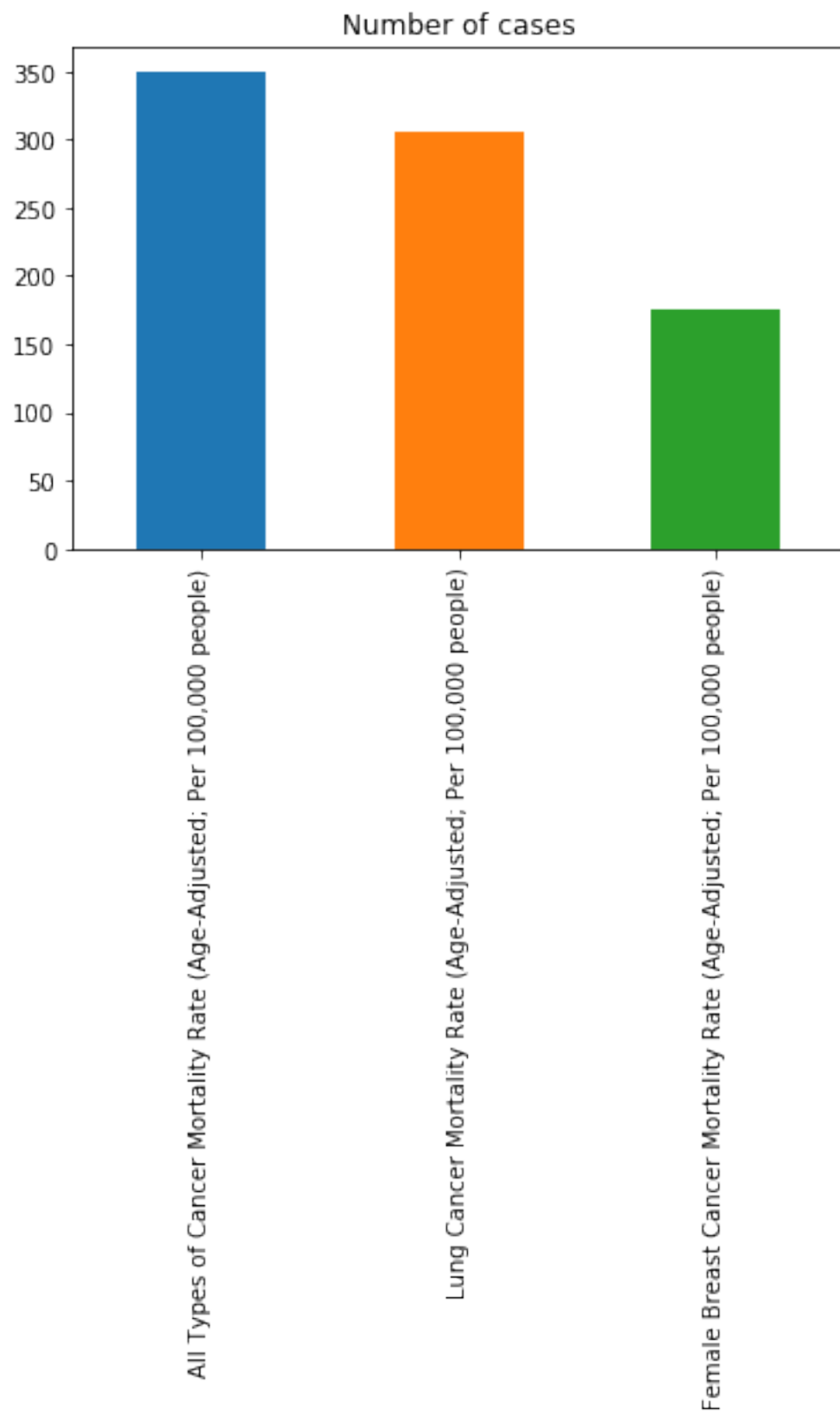
```

Out[211]: All Types of Cancer Mortality Rate (Age-Adjusted; Per 100,000 people)    350
Lung Cancer Mortality Rate (Age-Adjusted; Per 100,000 people)                    306
Female Breast Cancer Mortality Rate (Age-Adjusted; Per 100,000 people)            175
Name: indicator, dtype: int64

```

And we plot a histogram to see.

```
In [212]: labels=list(cancer_ds.columns)
          sorted_cancer = cancer_ds['indicator'].value_counts().plot(title='Number of cases',
          plt.show()
          #label=list(group.columns)
```



Now we find out the distribution of cancer patients with respect to the race and ethnicity.

```
In [215]: all=cancer_ds[cancer_ds['race_ethnicity']=="All"]
          all_count=all.race_ethnicity.count()

          asian=cancer_ds[cancer_ds['race_ethnicity']=="Asian/PI"]
          asian_count=asian.race_ethnicity.count()

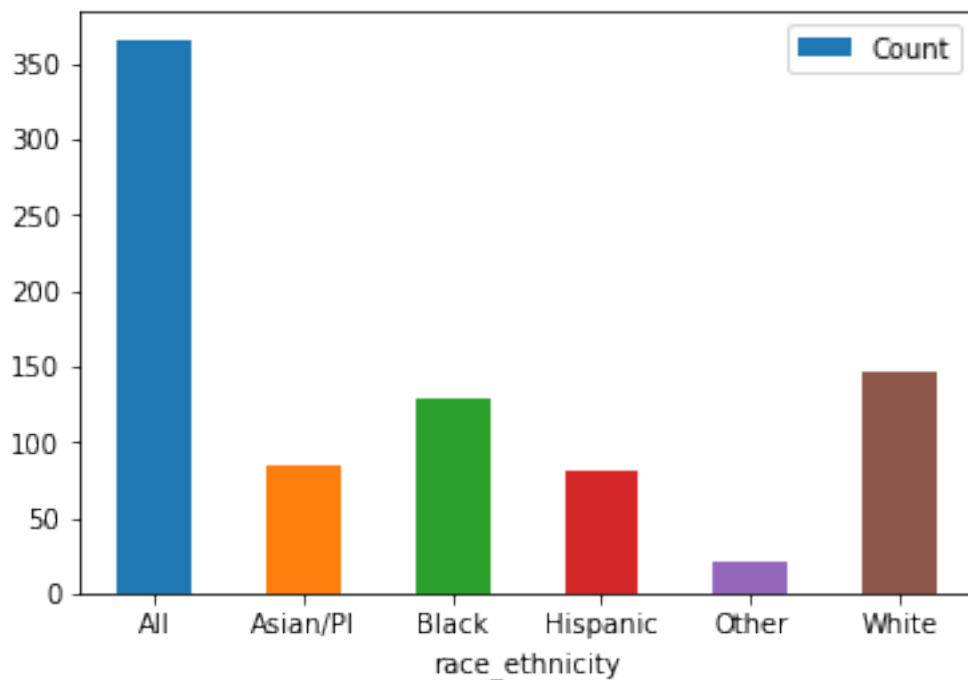
          black=cancer_ds[cancer_ds['race_ethnicity']=="Black"]
          black_count=black.race_ethnicity.count()

          hispanic=cancer_ds[cancer_ds['race_ethnicity']=="Hispanic"]
          hispanic_count=hispanic.race_ethnicity.count()

          other=cancer_ds[cancer_ds['race_ethnicity']=="Other"]
          other_count=other.race_ethnicity.count()

          white=cancer_ds[cancer_ds['race_ethnicity']=="White"]
          white_count=white.race_ethnicity.count()

In [216]: fig2 = pd.DataFrame({'race_ethnicity':['All', 'Asian/PI', 'Black', 'Hispanic', 'Other', 'White'],
                               'Count': [all_count, asian_count, black_count, hispanic_count, other_count, white_count]})
          ax = fig2.plot.bar(x='race_ethnicity', y='Count', rot=0)
```



```
In [ ]:
```

```
In [ ]:
```