chronic_disease

April 1, 2019

Chronic Diseases Data Analysis
Cleaning Process
Following are the steps we followed for data analysis

1. Import the libraries

```
In [1]: #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 [2]: dataset=pd.read_csv('data/data.csv')
```

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

```
Out[3]:                      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
```

1

```
                                BCHC Requested Methodology  \
0  Age-Adjusted rate of opioid-related mortality ...
1  Age-adjusted rate of opioid-related mortality ...
2  Age-adjusted rate of opioid-related mortality ...

                                              Source  \
0  D.C. Department of Health, Center for Policy, ...
1              National Center for Health Statistics
2                                          CDC Wonder

                                              Methods  \
0                                                  NaN
1                                                  NaN
2  Age-adjusted rate of opioid-related mortality ...

                                                Notes  \
0  This indicator is not exclusive of other drugs...
1  This indicator is not exclusive of other drugs...
2  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 [4]: dataset.columns

Out[4]: 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 [5]: dataset.rename(columns={'Indicator Category':'indicator_category','Indicator':'indicato
           'Value':'value', 'Place':'place', 'BCHC Requested Methodology':'bchc_req_meth',
           'Notes':'notes', '90% Confidence Level - Low':'90pc_con_lvl-low', '90% Confiden
           '95% Confidence Level - Low':'95pc_con_lvl-low','95% Confidence Level - High':'9
```

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

```
In [6]: chronic_dis_ds = dataset.loc[dataset["indicator_category"] == "Chronic Disease"]
```

4.And then we remove empty columns and unnecessary columns

```
In [7]: chronic_dis_ds.drop(['indicator_category','bchc_req_meth','source','methods','notes','9
                    axis = 1, inplace= True)
```

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

```
In [8]: chronic_dis_ds.dropna(axis=0, how='any',inplace= True)
```

```
In [9]: chronic_dis_ds.to_csv("data/chronic_disease.csv")
```

```
In [10]: chronic_dis_ds.head(3)
```

```
Out[10]:                                               indicator  year   sex  \
         4136  Asthma Emergency Department Visit Rate (Age-Ad...  2010  Both
         4137  Asthma Emergency Department Visit Rate (Age-Ad...  2010  Both
         4139  Asthma Emergency Department Visit Rate (Age-Ad...  2010  Both

               race_ethnicity  value                      place  95pc_con_lvl-low  \
         4136             All   99.4              Chicago, Il                 98.1
         4137             All  109.0  Las Vegas (Clark County), NV            107.5
         4139         Asian/PI   12.9             Chicago, Il                 10.8

               95pc_con_lvl-high
         4136              100.6
         4137              110.5
         4139               15.1
```

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 [11]: c_year_2010=chronic_dis_ds[chronic_dis_ds['year']==2010]
         c_year_2010_count=c_year_2010['year'].count()
```

```
In [12]: c_year_2010.shape
```

```
Out[12]: (201, 8)
```

```
In [13]: c_year_2011=chronic_dis_ds[chronic_dis_ds['year']==2011]
         c_year_2011_count=c_year_2011['year'].count()

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

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

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

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

c_year_2016=chronic_dis_ds[chronic_dis_ds['year']==2016]
c_year_2016_count=c_year_2016['year'].count()
```
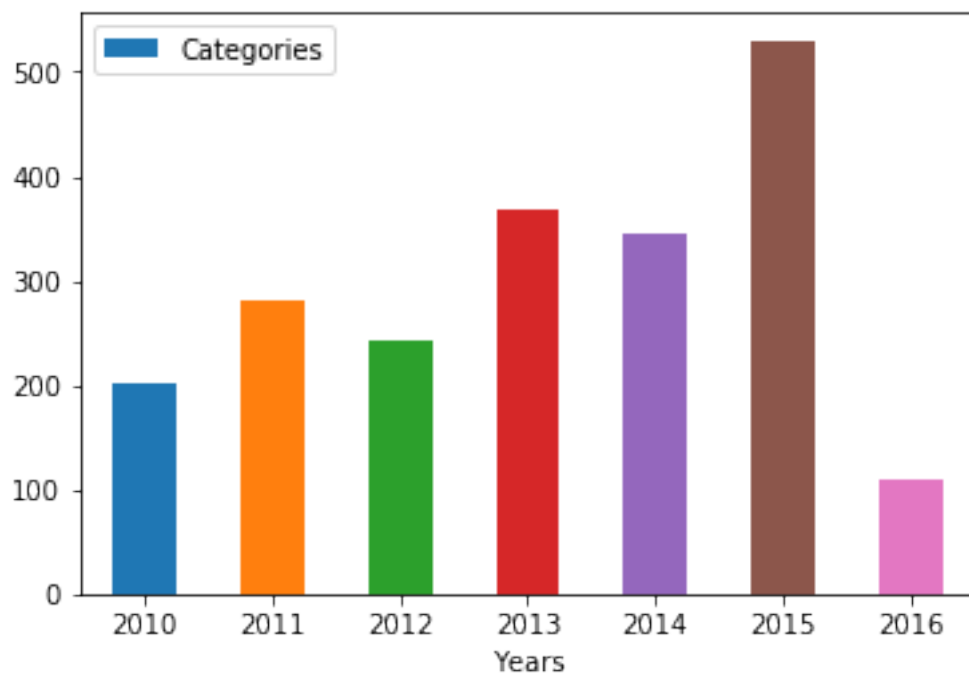
In [14]:
```
fig1 = pd.DataFrame({'Years':['2010', '2011', '2012','2013','2014','2015','2016'], 'Ca
ax = fig1.plot.bar(x='Years', y='Categories', rot=0)
```


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 [15]:
```
sorted_cd = chronic_dis_ds['indicator'].value_counts()
sorted_cd
```
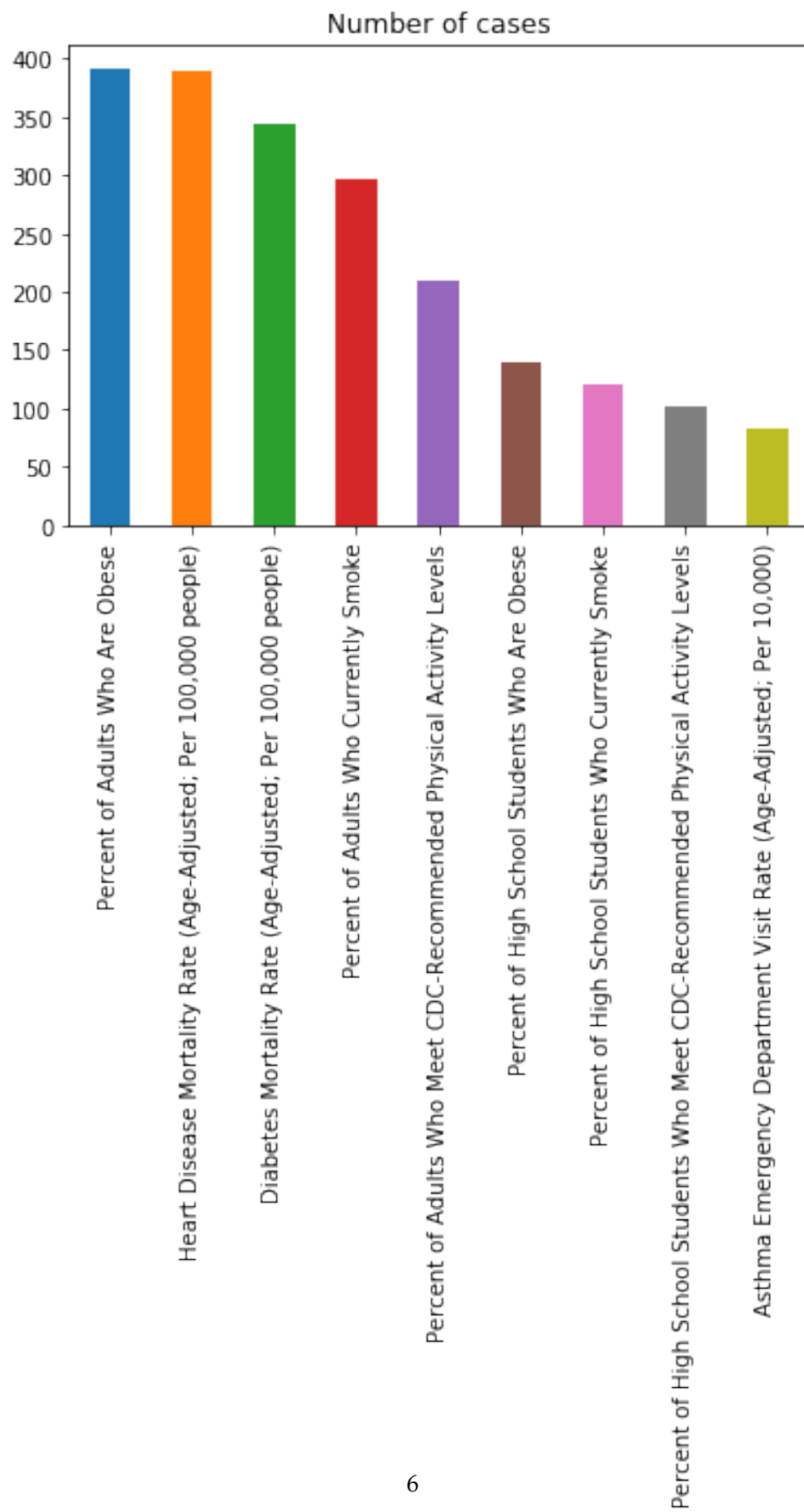
Out[15]:
```
Percent of Adults Who Are Obese                                 3
Heart Disease Mortality Rate (Age-Adjusted; Per 100,000 people) 3
Diabetes Mortality Rate (Age-Adjusted; Per 100,000 people)      3
Percent of Adults Who Currently Smoke                           2
```

4

```
       Percent of Adults Who Meet CDC-Recommended Physical Activity Levels
       Percent of High School Students Who Are Obese
       Percent of High School Students Who Currently Smoke
       Percent of High School Students Who Meet CDC-Recommended Physical Activity Levels
       Asthma Emergency Department Visit Rate (Age-Adjusted; Per 10,000)
       Name: indicator, dtype: int64
```

And we plot a histogram to see.

```python
In [16]: labels=list(chronic_dis_ds.columns)
         sorted_cd = chronic_dis_ds['indicator'].value_counts().plot(title='Number of cases', 
         plt.show()
         #label=list(group.columns)
```

Number of cases

- Percent of Adults Who Are Obese
- Heart Disease Mortality Rate (Age-Adjusted; Per 100,000 people)
- Diabetes Mortality Rate (Age-Adjusted; Per 100,000 people)
- Percent of Adults Who Currently Smoke
- Percent of Adults Who Meet CDC-Recommended Physical Activity Levels
- Percent of High School Students Who Are Obese
- Percent of High School Students Who Currently Smoke
- Percent of High School Students Who Meet CDC-Recommended Physical Activity Levels
- Asthma Emergency Department Visit Rate (Age-Adjusted; Per 10,000)

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

```
In [17]: all=chronic_dis_ds[chronic_dis_ds['race_ethnicity']=="All"]
         all_count=all.race_ethnicity.count()

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

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

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

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

         white=chronic_dis_ds[chronic_dis_ds['race_ethnicity']=="White"]
         white_count=white.race_ethnicity.count()
In [18]: fig2 = pd.DataFrame({'race_ethnicity':['All', 'Asian/PI', 'Black','Hispanic','Other',
         ax = fig2.plot.bar(x='race_ethnicity', y='Count', rot=0)
```
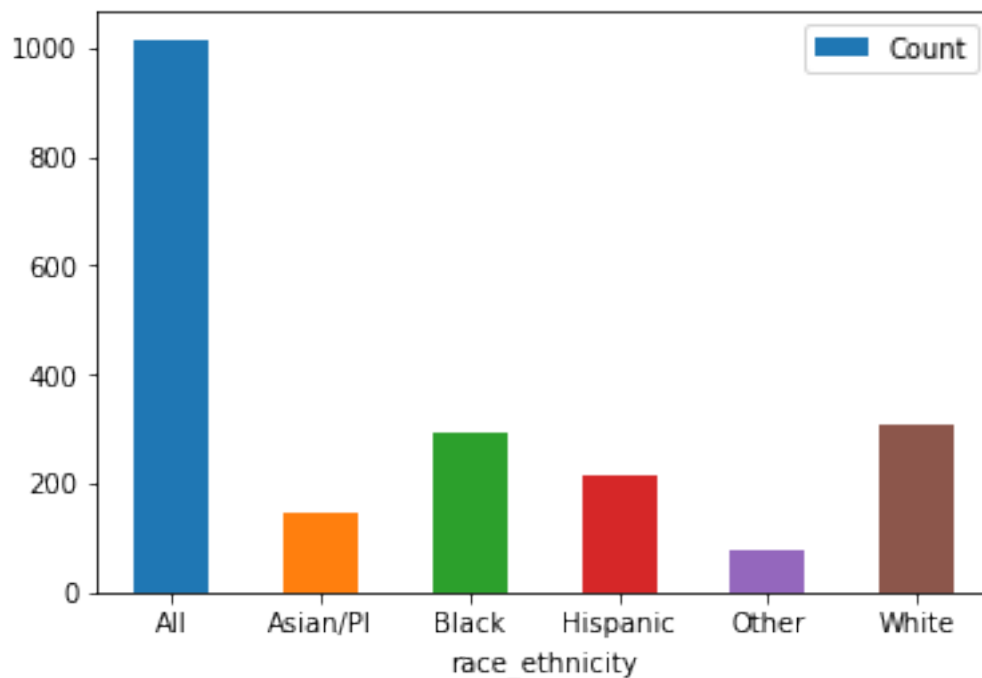


```
In [ ]:
```