

# hiv\_aids

April 1, 2019

HIV/AIDS Data Analysis

Cleaning Process

Following are the steps we followed for data cleaning

## 1. Import the libraries

```
In [26]: #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 [27]: dataset=pd.read_csv('data/data.csv')
```

```
In [28]: dataset.head(3)
```

```
Out[28]:
```

	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 \		90% Confidence Level - Low	90% Confidence Level - High \		95% Confidence Level - Low	95% Confidence Level - High
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...		NaN	NaN		NaN	NaN
1	Age-adjusted rate of opioid-related mortality ...		National Center for Health Statistics		NaN		This indicator is not exclusive of other drugs...		NaN	NaN		1.5	3.0
2	Age-adjusted rate of opioid-related mortality ...		CDC Wonder				Data is for Alameda County. This indicator is ...		NaN	NaN		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 [29]: dataset.columns
```

```
Out[29]: 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 [30]: 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 [31]: hiv_ds = dataset.loc[dataset["indicator_category"] == "HIV/AIDS"]
```

4. And then we remove empty columns and unnecessary columns

```
In [32]: hiv_ds.drop(['indicator_category', 'bchc_req_meth', 'source', 'methods', 'notes', '90pc_con'],
                    axis = 1, inplace= True)
```

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

```
In [33]: hiv_ds.dropna(axis=0, how='any', inplace= True)
```

```
In [34]: hiv_ds.to_csv("data/hiv_aids.csv")
```

```
In [35]: hiv_ds.head(3)
```

```
Out[35]:
```

	indicator	year	sex	race_ethnicity	\
14189	AIDS Diagnoses Rate (Per 100,000 people)	2010	Both		All
14191	AIDS Diagnoses Rate (Per 100,000 people)	2010	Both		All
14194	AIDS Diagnoses Rate (Per 100,000 people)	2010	Both		All

	value	place	95pc_con_lvl-low	\
14189	2.3	Fort Worth (Tarrant County), TX	1.6	
14191	9.0	Oakland (Alameda County), CA	6.2	
14194	10.8	Las Vegas (Clark County), NV	9.4	

	95pc_con_lvl-high
14189	3.0
14191	12.5
14194	12.3

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 [15]: c_year_2010=hiv_ds[hiv_ds['year']==2010]
        c_year_2010_count=c_year_2010['year'].count()
```

```
In [37]: c_year_2010.shape
```

```
Out[37]: (134, 8)
```

```
In [38]: c_year_2011=hiv_ds[hiv_ds['year']==2011]
        c_year_2011_count=c_year_2011['year'].count()
```

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

```

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

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

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

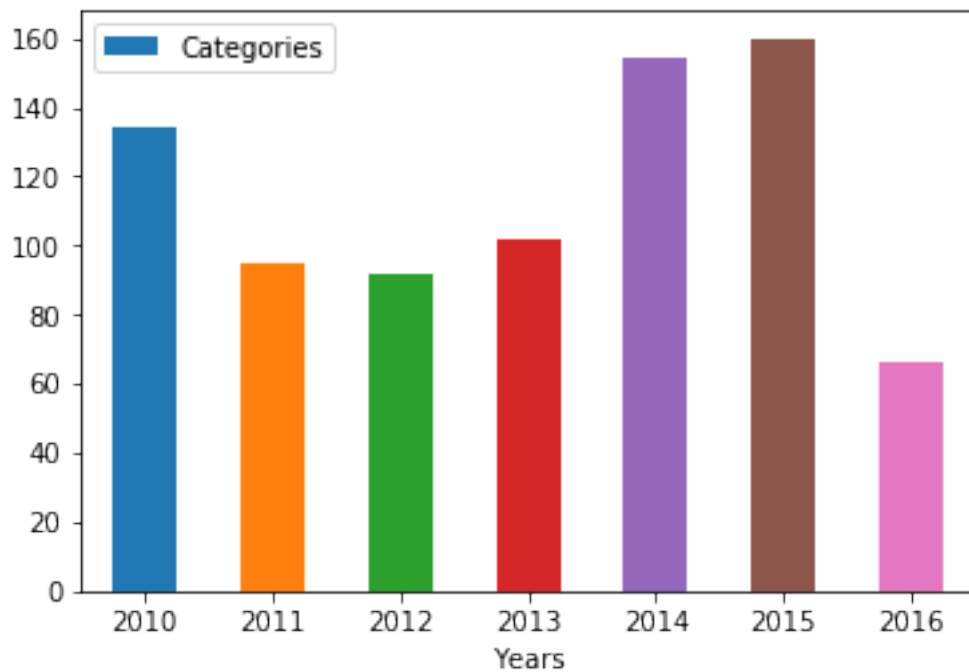
c_year_2016=hiv_ds[hiv_ds['year']==2016]
c_year_2016_count=c_year_2016['year'].count()

```

```

In [39]: fig1 = pd.DataFrame({'Years':['2010', '2011', '2012','2013','2014','2015','2016'], 'C
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 [40]: sorted_cancer = hiv_ds['indicator'].value_counts()
sorted_cancer

```

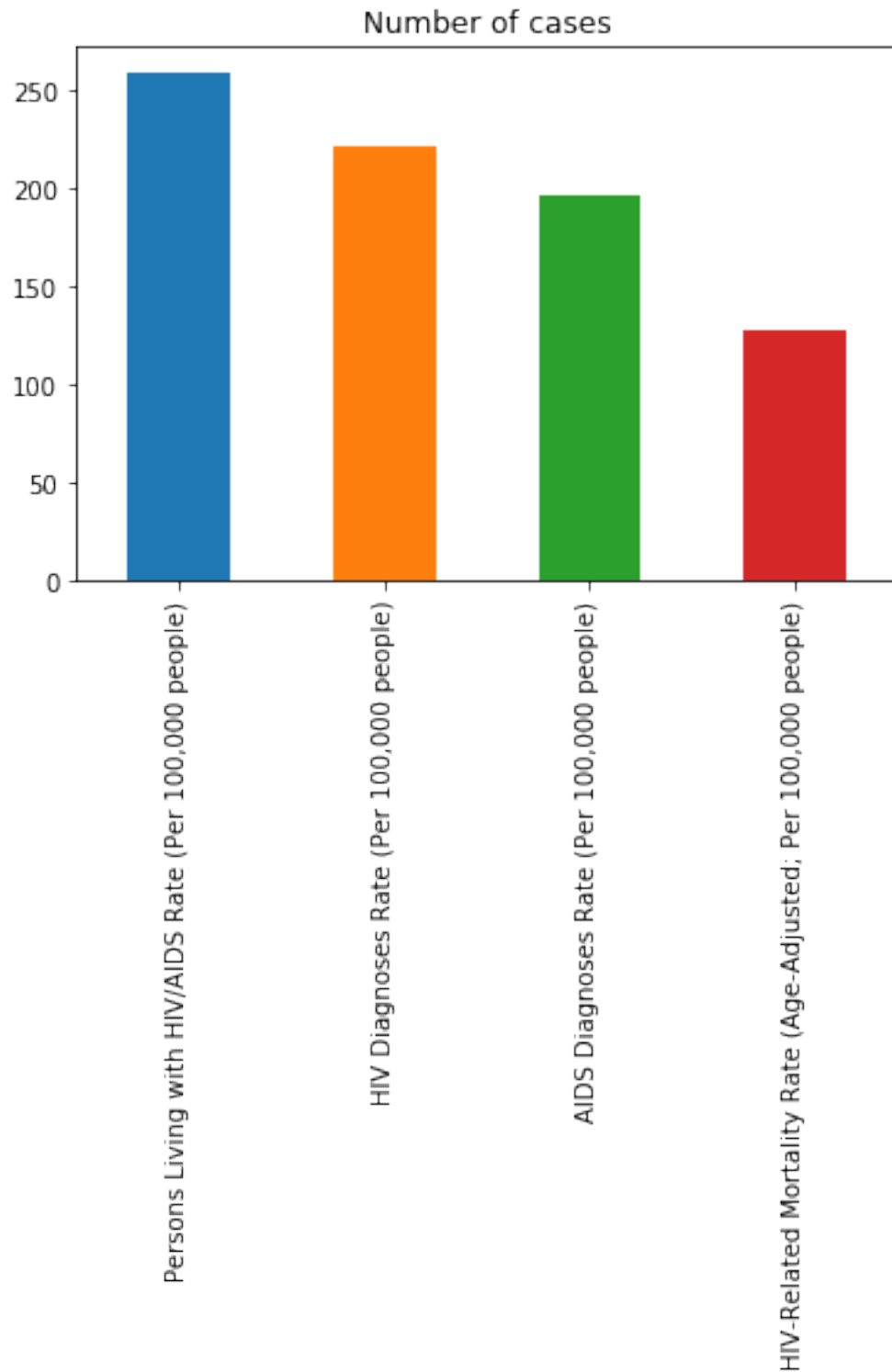
```

Out[40]: Persons Living with HIV/AIDS Rate (Per 100,000 people)      259
HIV Diagnoses Rate (Per 100,000 people)                             221
AIDS Diagnoses Rate (Per 100,000 people)                             196
HIV-Related Mortality Rate (Age-Adjusted; Per 100,000 people)       127
Name: indicator, dtype: int64

```

And we plot a histogram to see.

```
In [41]: labels=list(hiv_ds.columns)
sorted_cancer = hiv_ds['indicator'].value_counts().plot(title='Number of cases', kind=
plt.show()
#label=list(group.columns)
```



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

```
In [42]: all=hiv_ds[hiv_ds['race_ethnicity']=="All"]  
         all_count=all.race_ethnicity.count()
```

```

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

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

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

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

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

```

```

In [43]: fig2 = pd.DataFrame({'race_ethnicity':['All', 'Asian/PI', 'Black', 'Hispanic', 'Other',
ax = fig2.plot.bar(x='race_ethnicity', y='Count', rot=0)

```

