chronic_disease

April 2, 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
        # Algorithms
        from sklearn import linear_model
        from sklearn.linear_model import LinearRegression

        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

                             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':'indicat
               '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':'
```

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','
                            axis = 1, inplace= True)
```

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

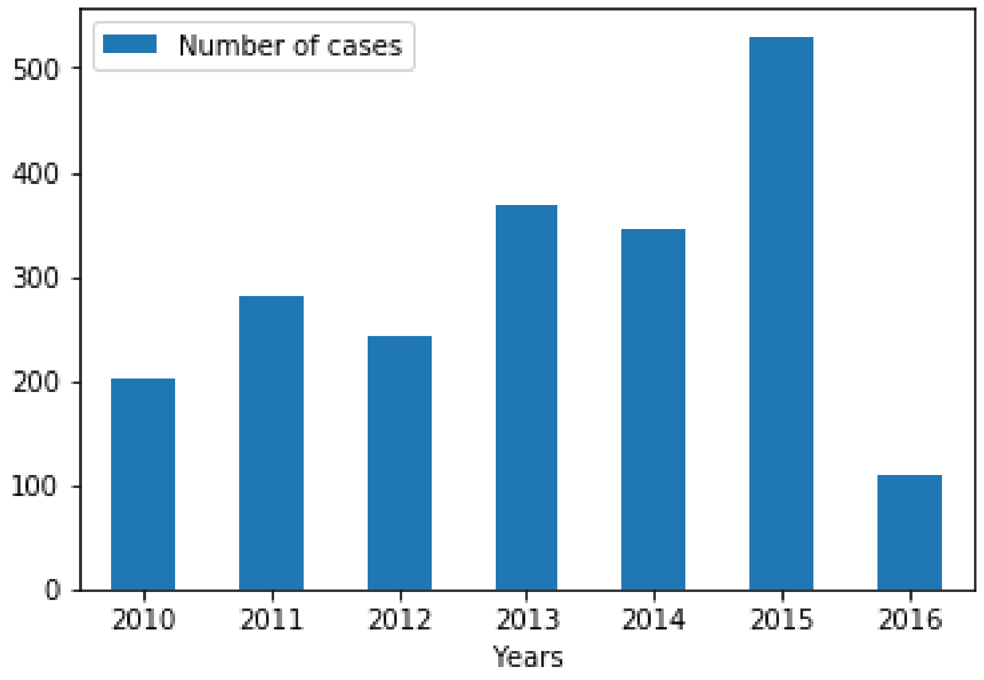
```
In [8]: chronic_dis_ds.dropna(axis=0, how='any',inplace= True)

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'],
                              'Number of cases':[c_year_2010_count, c_year_2011_count,c_year_20
                                            , c_year_2013_count,c_year_2014_count,c_year_2015_
         ax = fig1.plot.bar(x='Years', rot=0)
```

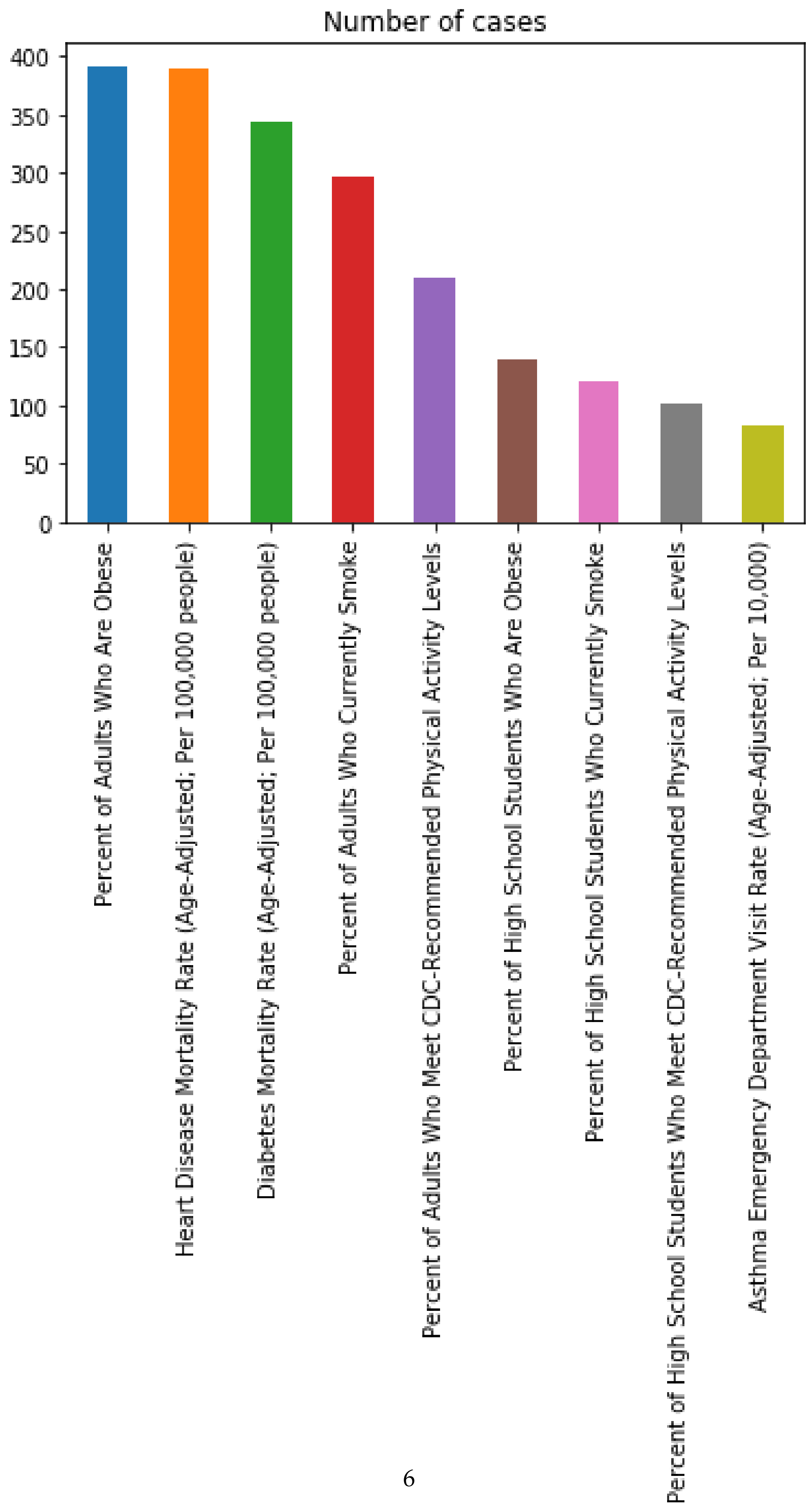


Now we calculate the number of cases for each type of cancer. In order to that we will group according to the indicator and take the count.

```
In [15]: sorted_cd = chronic_dis_ds['indicator'].value_counts()
         sorted_cd

Out[15]: Percent of Adults Who Are Obese
         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)
         Name: indicator, dtype: int64
```

And we plot a histogram to see.

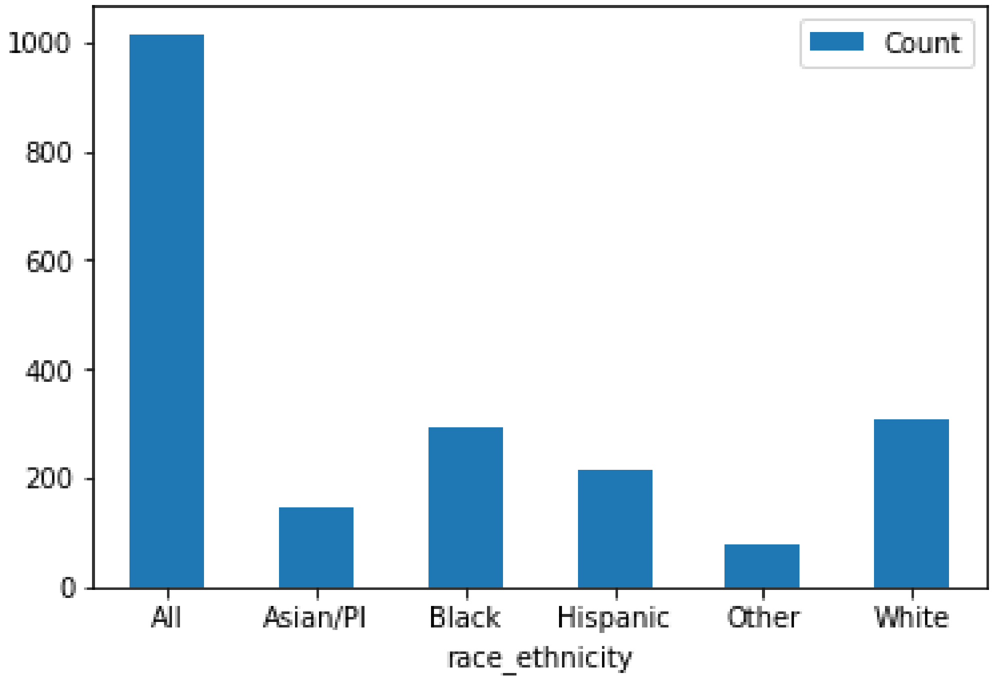
```
In [16]: labels=list(chronic_dis_ds.columns)
         sorted_cd = chronic_dis_ds['indicator'].value_counts().plot(title='Number of cases',
         plt.show()
         #label=list(group.columns)
```


Number of cases
400
350
300
250
200
150
100
50
0
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', rot=0)
```



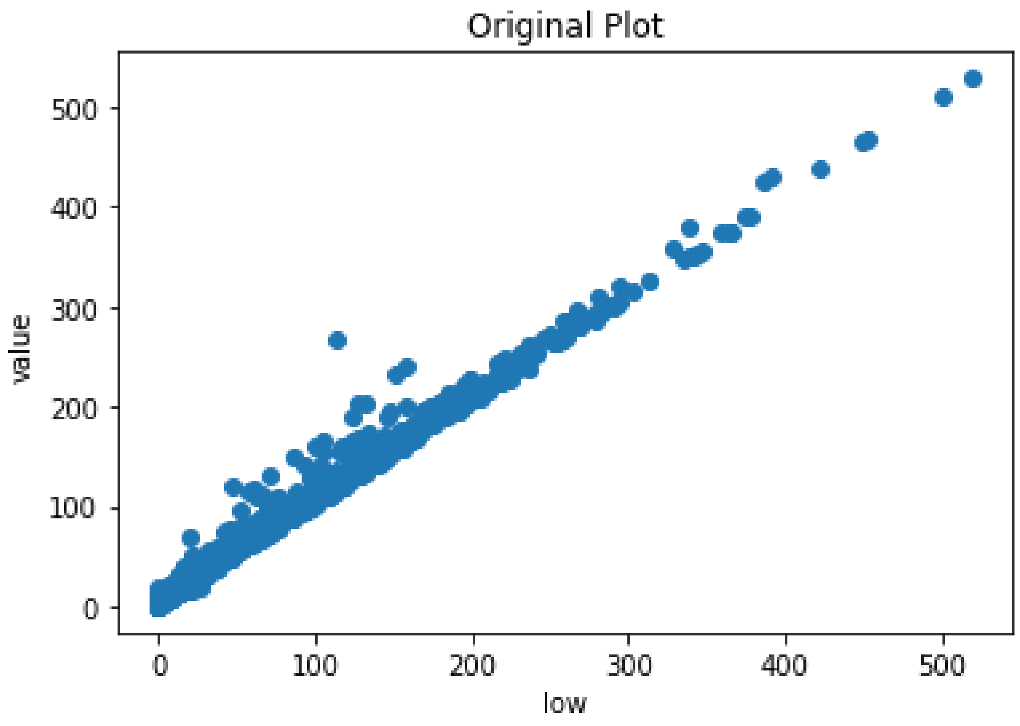
```
In [19]: chronic_dis_ds=chronic_dis_ds.rename(columns={'95pc_con_lvl-low':'low','95pc_con_lvl-I
```

```
In [24]: ds=chronic_dis_ds.drop(['indicator','year','sex','race_ethnicity'
                        ,'place'],
                            axis = 1)
```

```
In [25]: ds.head()
```

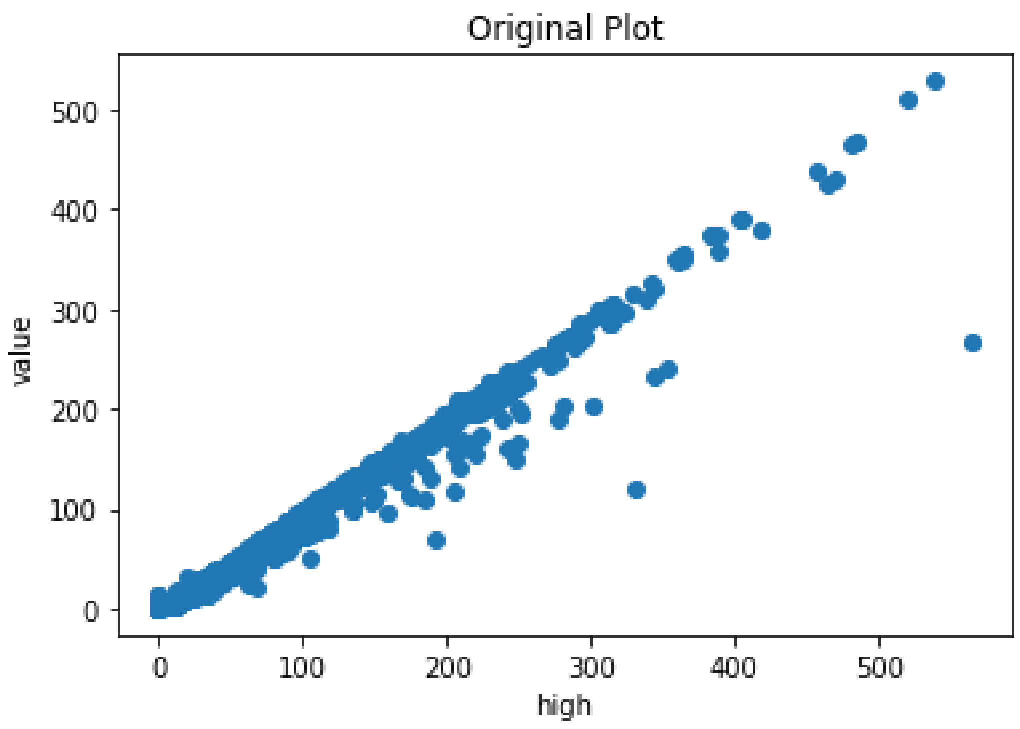
```
Out[25]:        value    low   high
         4136    99.4   98.1  100.6
         4137   109.0  107.5  110.5
         4139    12.9   10.8   15.1
         4141    47.4   44.0   50.7
         4143   226.9  223.6  230.1
```

```
In [26]: #very simple plotting
         fig = plt.figure(1)
         ax1 = fig.add_subplot(111)
         ax1.set_xlabel('low')
         ax1.set_ylabel('value')
         ax1.set_title('Original Plot')
         ax1.scatter('low', 'value', data = ds);
```



Linear Regression with high values

In [27]:
```
#very simple plotting with high value
fig = plt.figure(1)
ax1 = fig.add_subplot(111)
ax1.set_xlabel('high')
ax1.set_ylabel('value')
ax1.set_title('Original Plot')
ax1.scatter('high', 'value', data = ds);
```



In [28]:
```
x_y = np.array(ds)
x, y = x_y[:,0], x_y[:,1]

# Reshaping
x, y = x.reshape(-1,1), y.reshape(-1, 1)

# Linear Regression Object
lin_regression = LinearRegression()

# Fitting linear model to the data
lin_regression.fit(x,y)

# Get slope of fitted line
m = lin_regression.coef_

# Get y-Intercept of the Line
```

```
         b = lin_regression.intercept_

         # Get Predictions for original x values
         # you can also get predictions for new data
         predictions = lin_regression.predict(x)

         # following slope intercept form
         print ("formula: y = {0}x + {1}".format(m, b) )
```

```
formula: y = [[0.93916792]]x + [-4.02478764]
```

```
In [ ]: plt.scatter(x, y,  color='red')
        plt.plot(x, predictions, color='blue',linewidth=3)
        plt.show()
```

```
In [ ]:
```