Cancer death rate prediction

In [2]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
pd.pandas.set_option('display.max_columns',None)
```

In [3]:
```
data_frame=pd.read_csv('https://query.data.world/s/tsz7pgawspj35k6a
```

In [4]:
```
data_frame.head()
```

Out[4]:

	County	FIPS	Met Objective of 45.5? (1)	Age-Adjusted Death Rate	Lower 95% Confidence Interval for Death Rate	Upper 95% Confidence Interval for Death Rate	Average Deaths per Year	Recent Trend (2)	Recen 5-Yea Trenc (2) ir Deatl Rates
0	United States	0	No	46	45.9	46.1	157,376	falling	-2.4
1	Perry County, Kentucky	21193	No	125.6	108.9	144.2	43	stable	-0.6
2	Powell County, Kentucky	21197	No	125.3	100.2	155.1	18	stable	1.7
3	North Slope Borough, Alaska	2185	No	124.9	73	194.7	5	**	*
4	Owsley County, Kentucky	21189	No	118.5	83.1	165.5	8	stable	2.2

In [5]:
```
data_frame.columns=['County','FIPS','45.5_objective','Adj.Death_rat
                    'upper_death_rate','avg_deaths','recent_trend',
```

In [6]:
```
data_frame.head()
```

Out[6]:

	County	FIPS	45.5_objective	Adj.Death_rate	low_death_rate	upper_death_rate	avg_c
0	United States	0	No	46	45.9	46.1	1!
1	Perry County, Kentucky	21193	No	125.6	108.9	144.2	
2	Powell County, Kentucky	21197	No	125.3	100.2	155.1	
3	North Slope Borough, Alaska	2185	No	124.9	73	194.7	
4	Owsley County, Kentucky	21189	No	118.5	83.1	165.5	

In [7]:
```
#there are values like '*','**' in the series of data_frame. replac
for cols in data_frame.columns:
    print(cols)
    print(data_frame[cols].unique())
```

```
County
['United States' 'Perry County, Kentucky' 'Powell County, Kentucky
' ...
 'Zapata County, Texas' 'Zavala County, Texas'
 'Ziebach County, South Dakota']
FIPS
[    0 21193 21197 ... 48505 48507 46137]
45.5_objective
['No' 'Yes' '*']
Adj.Death_rate
['46' '125.6' '125.3' '124.9' '118.5' '113.5' '111.1' '110.3' '109
.1'
 '106' '104.6' '103.5' '103.3' '98.7' '98.5' '97.2' '96.5' '96.1'
'95.6'
 '95.3' '95.1' '94.9' '94.6' '92.7' '92.5' '92.3' '91.9' '90.8' '9
0.5'
 '90.2' '89.6' '89.3' '89.2' '89.1' '89' '88.9' '88' '87.9' '87.4'
'87.2'
 '87' '86.8' '86.6' '85.9' '85.4' '85.1' '84.8' '84.5' '84.3' '84.
```

In [8]:
```
for cols in data_frame.columns:
    for j in data_frame[cols]:
        if j=='*':
            data_frame[cols].replace('*',np.nan,inplace=True)
        elif j=='**':
            data_frame[cols].replace('**',np.nan,inplace=True)
```

In [9]:
```
data_frame.head()
```

Out[9]:

	County	FIPS	45.5_objective	Adj.Death_rate	low_death_rate	upper_death_rate	avg_c
0	United States	0	No	46	45.9	46.1	1!
1	Perry County, Kentucky	21193	No	125.6	108.9	144.2	
2	Powell County, Kentucky	21197	No	125.3	100.2	155.1	
3	North Slope Borough, Alaska	2185	No	124.9	73	194.7	
4	Owsley County, Kentucky	21189	No	118.5	83.1	165.5	

In [10]:
```
#getting the number of null values of features.
data_frame.isnull().sum()
```

Out[10]:
```
County                  0
FIPS                    0
45.5_objective        328
Adj.Death_rate        328
low_death_rate        328
upper_death_rate      328
avg_deaths            328
recent_trend          447
recent_5_year_trend   447
lower_trend           447
upper_trend           447
dtype: int64
```

In [11]:
```
#getting categorical features.
categorical_features=[]
for cols in data_frame.columns:
    if data_frame[cols].dtype=='O':
        categorical_features.append(cols)
```

In [12]:
```
data_frame[categorical_features].head()
```

Out[12]:

	County	45.5_objective	Adj.Death_rate	low_death_rate	upper_death_rate	avg_deaths
0	United States	No	46	45.9	46.1	157,376
1	Perry County, Kentucky	No	125.6	108.9	144.2	43
2	Powell County, Kentucky	No	125.3	100.2	155.1	18
3	North Slope Borough, Alaska	No	124.9	73	194.7	5
4	Owsley County, Kentucky	No	118.5	83.1	165.5	8

In [13]:
```
are some numerical features in the form of categorical type.
_columns=['Adj.Death_rate','low_death_rate','upper_death_rate','rece
```

In [14]:
```
data_frame[num_cat_columns].head()
```

Out[14]:

	Adj.Death_rate	low_death_rate	upper_death_rate	recent_5_year_trend	lower_trend	uppe
0	46	45.9	46.1	-2.4	-2.6	
1	125.6	108.9	144.2	-0.6	-2.7	
2	125.3	100.2	155.1	1.7	0	
3	124.9	73	194.7	NaN	NaN	
4	118.5	83.1	165.5	2.2	-0.4	

In [15]:
```
#converting numeric string type values to numeric type values.
for cols in num_cat_columns:
    for j in data_frame[cols]:
        data_frame[cols].replace(j,float(j),inplace=True)
```

In [16]:
```
for cols in num_cat_columns:
    print(cols,data_frame[cols].dtype)
```

```
Adj.Death_rate float64
low_death_rate float64
upper_death_rate float64
recent_5_year_trend float64
lower_trend float64
upper_trend float64
```

In [17]:
```
data_frame['avg_deaths'].replace('157,376',157376,inplace=True)
```

In [18]:
```
for i in data_frame['avg_deaths'].unique():
    if type(i)==str:
        if ',' in i:
            data_frame['avg_deaths'].replace(i,i.replace(',',''),in
```

In [19]:
```
data_frame['avg_deaths']=data_frame['avg_deaths'].astype(float)
```

In [20]:
```
data_frame.head()
```

Out[20]:

	County	FIPS	45.5_objective	Adj.Death_rate	low_death_rate	upper_death_rate	avg_c
0	United States	0	No	46.0	45.9	46.1	157
1	Perry County, Kentucky	21193	No	125.6	108.9	144.2	
2	Powell County, Kentucky	21197	No	125.3	100.2	155.1	
3	North Slope Borough, Alaska	2185	No	124.9	73.0	194.7	
4	Owsley County, Kentucky	21189	No	118.5	83.1	165.5	

In [21]:
```
for cols in data_frame.columns:
    print(cols,data_frame[cols].dtype)
```

```
County object
FIPS int64
45.5_objective object
Adj.Death_rate float64
low_death_rate float64
upper_death_rate float64
avg_deaths float64
recent_trend object
recent_5_year_trend float64
lower_trend float64
upper_trend float64
```

In [22]:
```
#converting the values in 'County' feature to 'state'.
data_frame['State']=data_frame['County'].copy()
for values in data_frame['State']:
    data_frame['State'].replace(values,values.split(', ')[-1],inpla
```

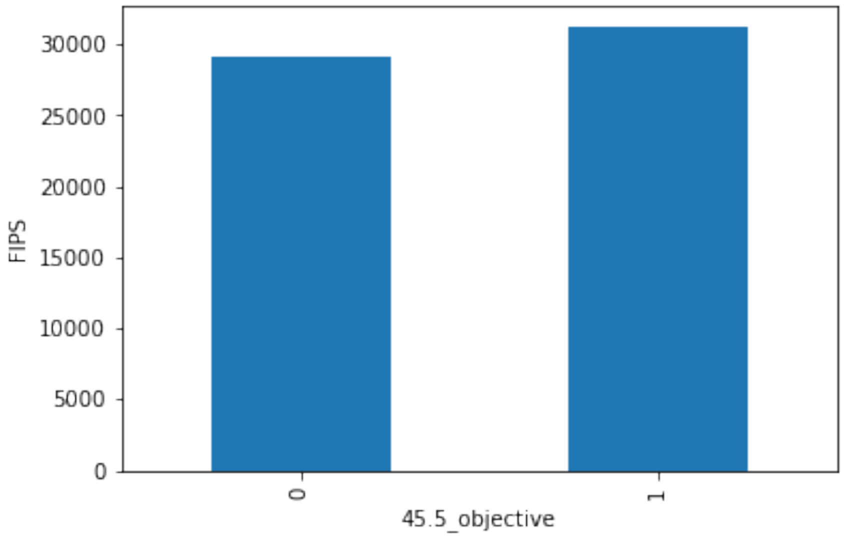
In [23]:
```
#taking out the real numerical and categorical features.
categorical_features=[]
numerical_features=[]
for cols in data_frame.columns:
    if data_frame[cols].dtype=='O':
        categorical_features.append(cols)
    else:
        numerical_features.append(cols)
```

In [24]:
```
print('categorical_features: ',categorical_features)
print('Numerical features: ',numerical_features)
```

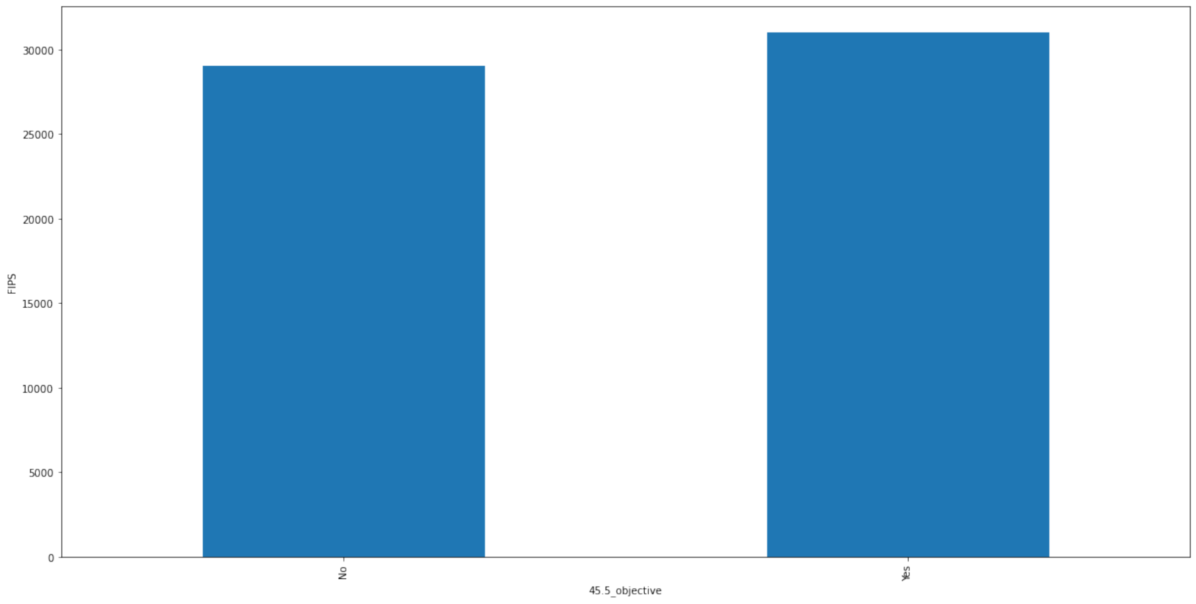
```
categorical_features:  ['County', '45.5_objective', 'recent_trend'
, 'State']
Numerical features:  ['FIPS', 'Adj.Death_rate', 'low_death_rate',
'upper_death_rate', 'avg_deaths', 'recent_5_year_trend', 'lower_tr
end', 'upper_trend']
```

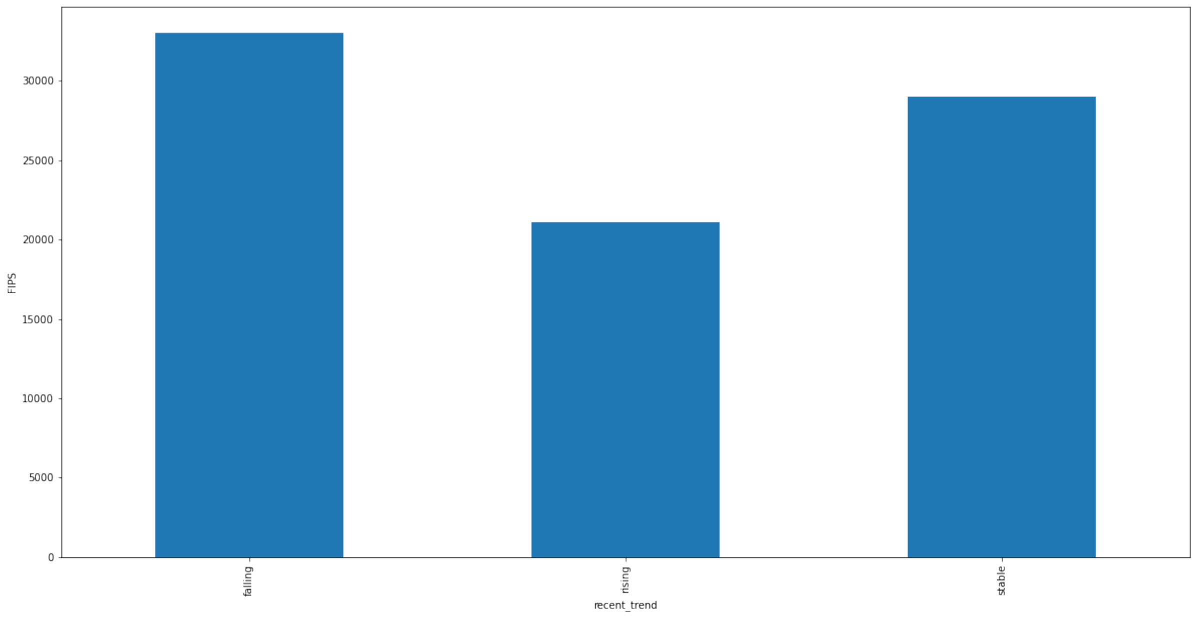
In [25]:
```
null_value_features=[]
for cols in data_frame.columns:
    percentage=(data_frame[cols].isnull().sum()/len(data_frame))*10
    if percentage>0:
        null_value_features.append(cols)
```

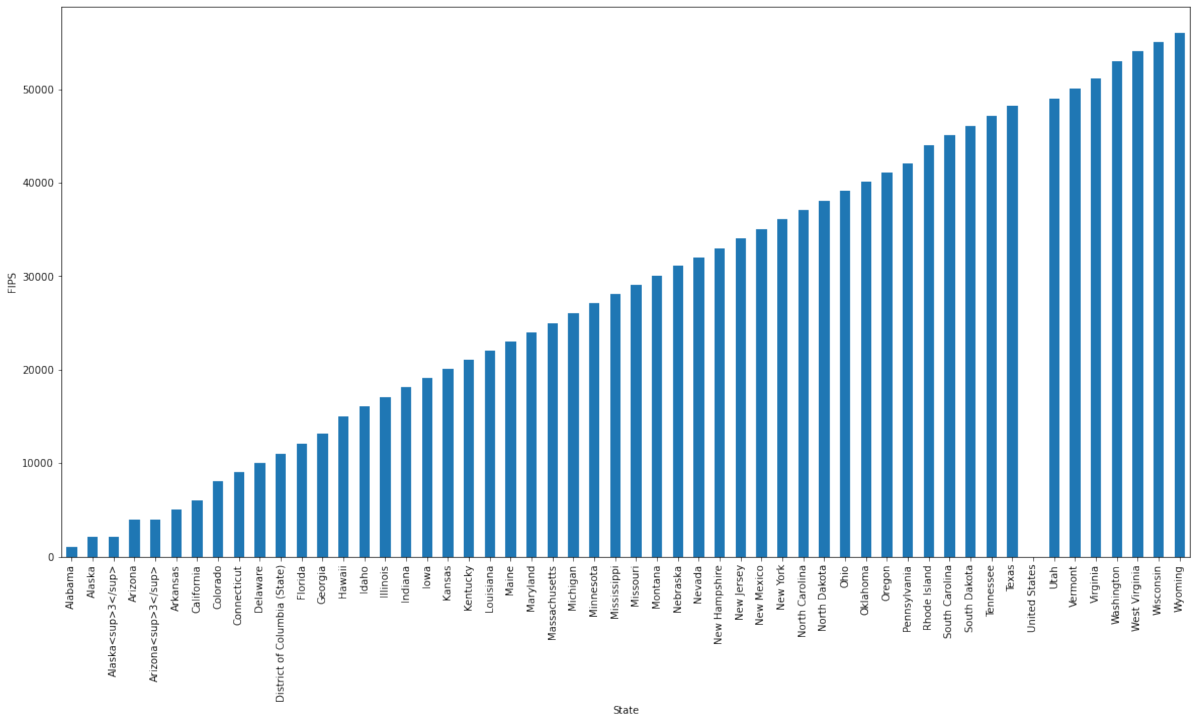
In [26]:
```
#finding the relationship between missing values features and depen
for cols in null_value_features:
    data=data_frame.copy()
    data[cols]=np.where(data[cols].isnull(),1,0)
    data.groupby(cols)['FIPS'].median().plot.bar()
    plt.ylabel('FIPS')
    plt.xlabel(cols)
    plt.show()
```



In [27]:
```
for cols in categorical_features:
    if cols!='County':
        data.groupby(cols)['FIPS'].median().plot.bar(figsize=(20,10
        plt.xlabel(cols)
        plt.ylabel('FIPS')
        plt.show()
```




FIPS
0
5000
10000
15000
20000
25000
30000
falling
rising
stable
recent_trend

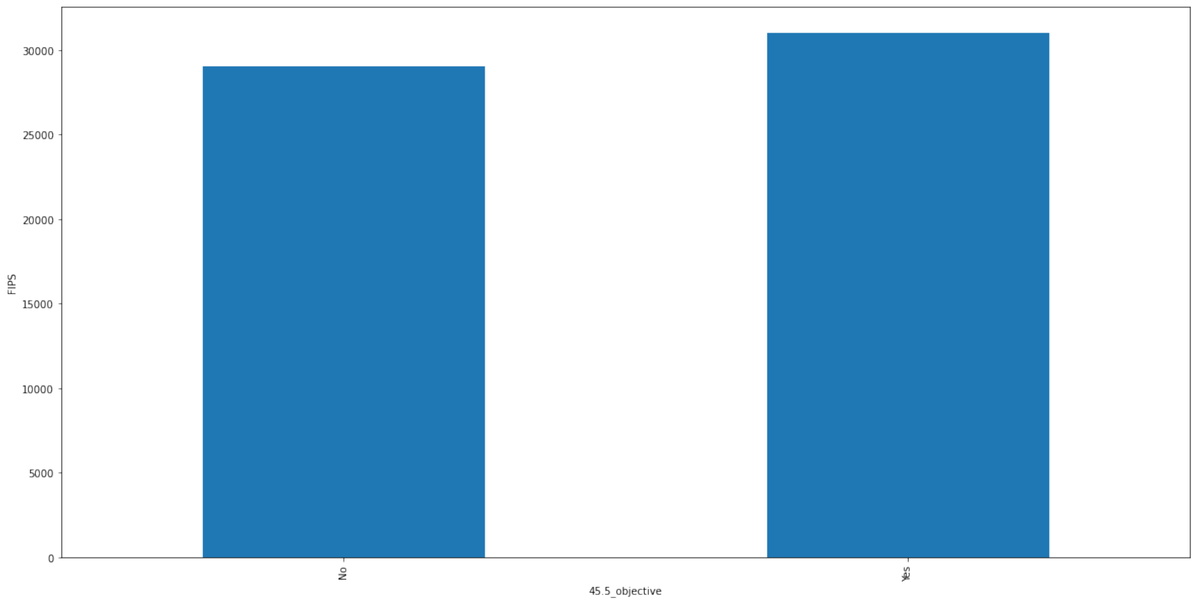

FIPS
State
Alabama
Alaska
Alaska³
Arizona
Arizona³
Arkansas
California
Colorado
Connecticut
Delaware
District of Columbia (State)
Florida
Georgia
Hawaii
Idaho
Illinois
Indiana
Iowa
Kansas
Kentucky
Louisiana
Maine
Maryland
Massachusetts
Michigan
Minnesota
Mississippi
Missouri
Montana
Nebraska
Nevada
New Hampshire
New Jersey
New Mexico
New York
North Carolina
North Dakota
Ohio
Oklahoma
Oregon
Pennsylvania
Rhode Island
South Carolina
South Dakota
Tennessee
Texas
United States
Utah
Vermont
Virginia
Washington
West Virginia
Wisconsin
Wyoming

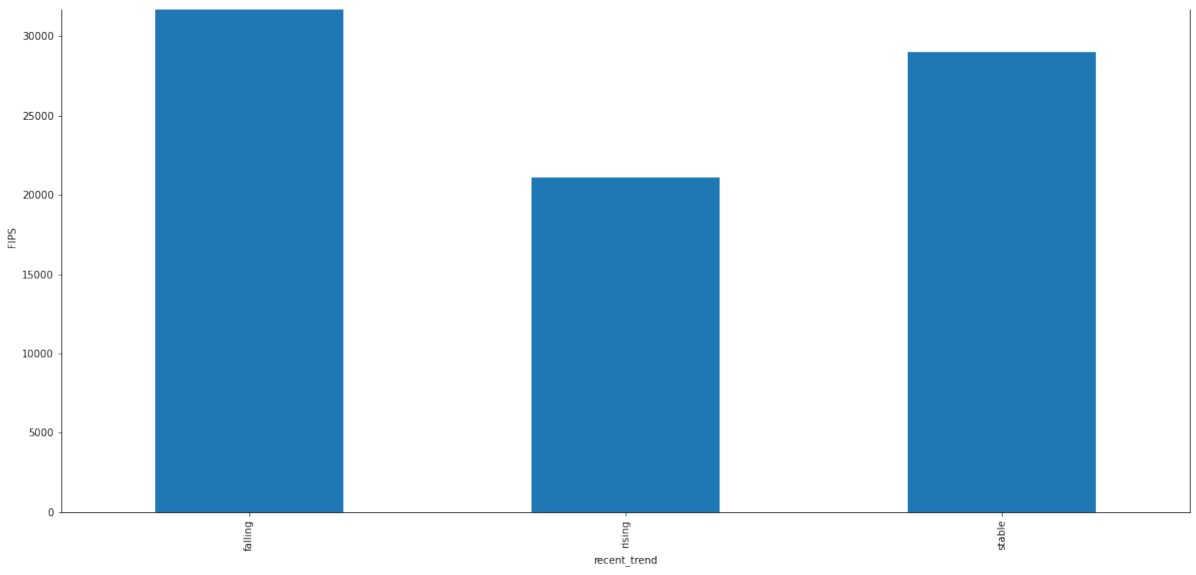
In [28]:
```
#there are few wrong categories in State feature.
data_frame['State'].unique()
```

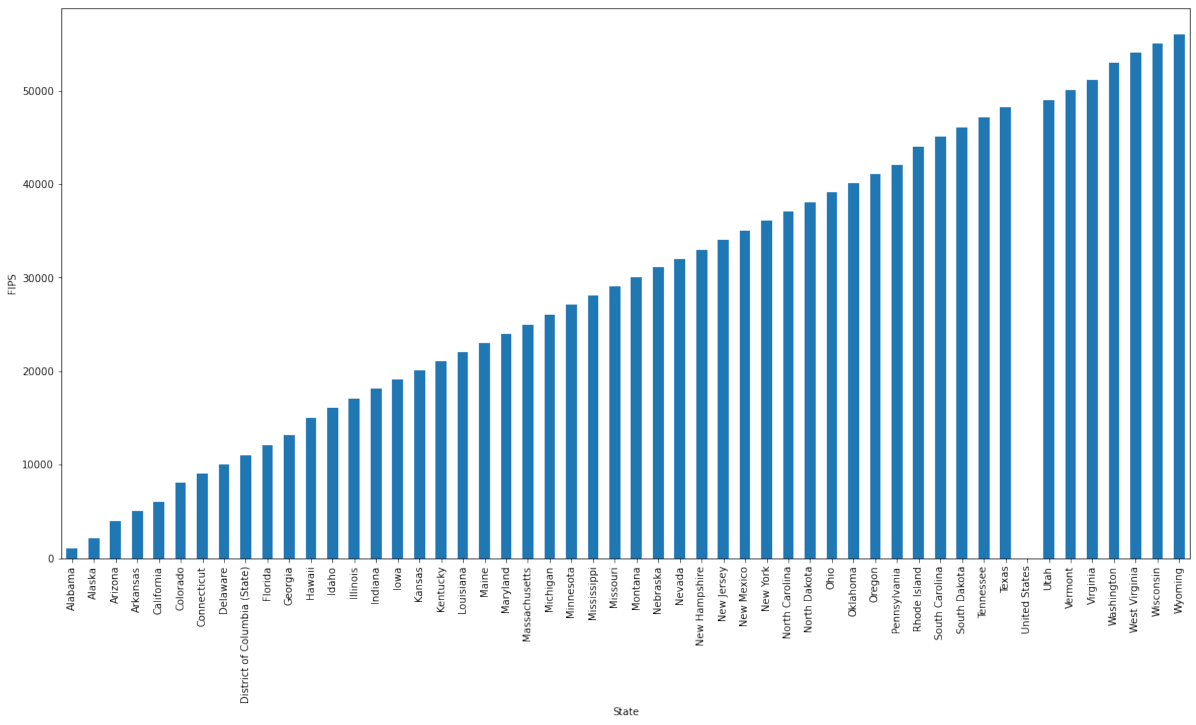
Out[28]:
```
array(['United States', 'Kentucky', 'Alaska', 'Florida', 'Arkansas
',
       'Tennessee', 'Missouri', 'West Virginia', 'Texas', 'Mississ
ippi',
       'Georgia', 'Virginia', 'Michigan', 'Minnesota', 'Oklahoma',
       'Indiana', 'Illinois', 'Kansas', 'Alabama', 'Louisiana',
       'North Dakota', 'North Carolina', 'Ohio', 'Idaho',
       'South Carolina', 'Wisconsin', 'Iowa', 'Maryland', 'Pennsyl
vania',
       'Nevada', 'Montana', 'Nebraska', 'New York', 'South Dakota'
,
       'Oregon', 'Washington', 'Maine', 'Wyoming', 'California',
       'Arizona', 'Vermont', 'Colorado', 'Delaware', 'New Jersey',
       'New Hampshire', 'Rhode Island', 'New Mexico', 'Massachuset
ts',
       'Connecticut', 'Utah', 'District of Columbia (State)',
       'Arizona<sup>3</sup>', 'Hawaii', 'Alaska<sup>3</sup>'],
      dtype=object)
```

In [29]:
```
#replacing those wrong categories.
data_frame['State'].replace('Arizona<sup>3</sup>','Arizona',inplace
data_frame['State'].replace('Alaska<sup>3</sup>','Alaska',inplace=T
```

In [30]:
```
for cols in categorical_features:
    if cols!='County':
        data=data_frame.copy()
        data.groupby(cols)['FIPS'].median().plot.bar(figsize=(20,10
        plt.xlabel(cols)
        plt.ylabel('FIPS')
        plt.show()
```





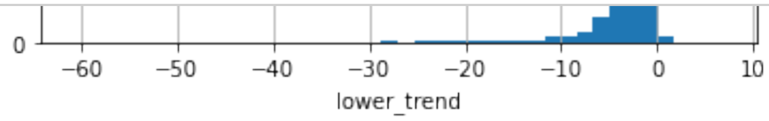


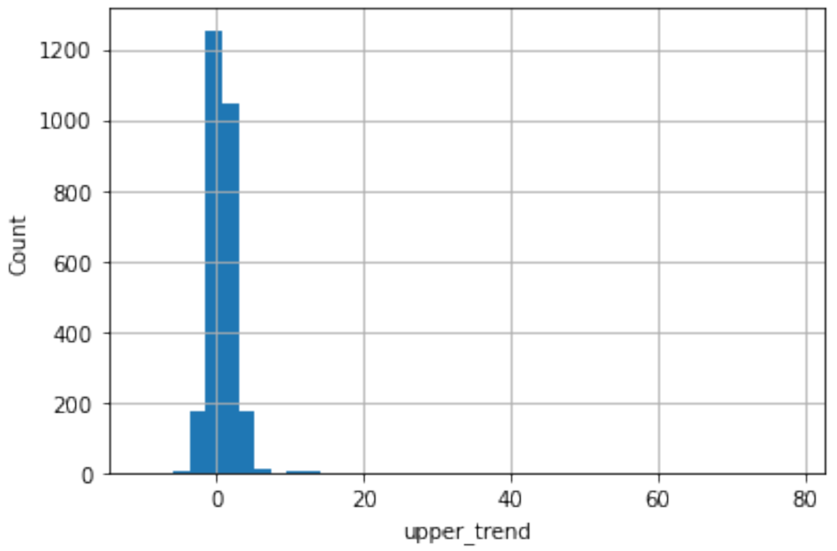
```
In [31]: #visualizing the numerical variables
         #getting the discrete and continous variables.
         discrete=[]
         continous=[]
         for cols in numerical_features:
             if len(data_frame[cols].unique())>25:
                 continous.append(cols)
             else:
                 discrete.append(cols)
```

In [32]:
```
print('Discrete: ',discrete)
print('Continous: ',continous)
```

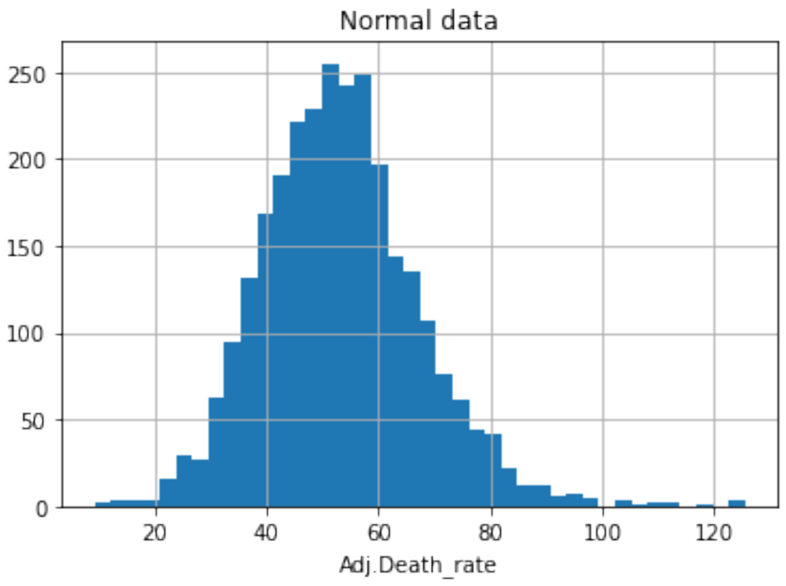
```
Discrete:  []
Continous:  ['FIPS', 'Adj.Death_rate', 'low_death_rate', 'upper_de
ath_rate', 'avg_deaths', 'recent_5_year_trend', 'lower_trend', 'up
per_trend']
```

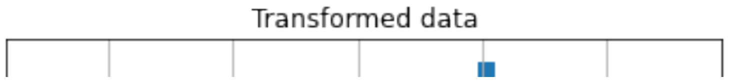
In [33]:
```
#there are no discrete features.
for cols in continous:
    data=data_frame.copy()
    data[cols].hist(bins=40)
    plt.xlabel(cols)
    plt.ylabel('Count')
    plt.show()
```



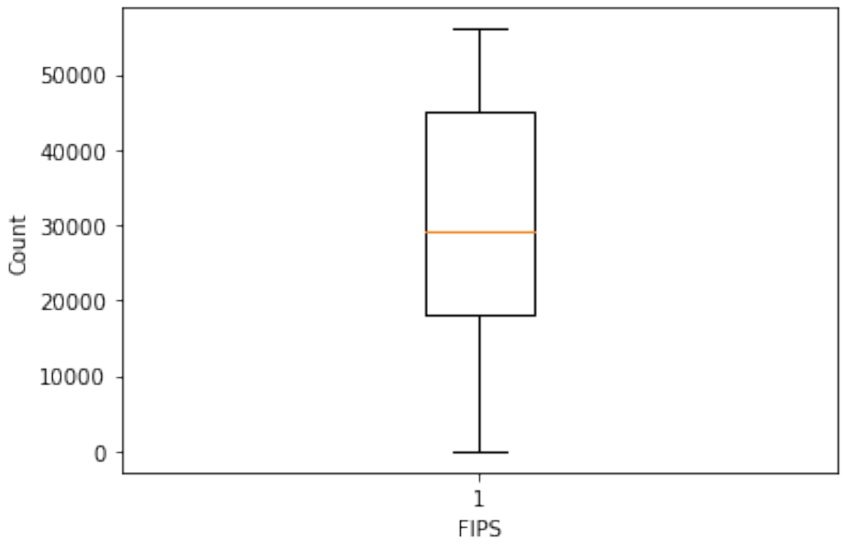


In [34]:
```
#some features are getting skewed more after transformation.
for cols in continous:
    data=data_frame.copy()
    if 0 in data[cols].unique():
        pass
    else:
        plt.title('Normal data')
        data[cols].hist(bins=40)
        plt.xlabel(cols)
        plt.show()
        plt.title('Transformed data')
        data[cols]=np.log(data[cols])
        data[cols].hist(bins=40)
        plt.xlabel(cols)
        plt.show()
```





In [35]:
```
#finding the outliers for the continous features.
for cols in continous:
    plt.boxplot(data_frame[cols])
    plt.xlabel(cols)
    plt.ylabel('Count')
    plt.show()
```



In [36]:
```
#looks that there's no outliers in the continous features.
```

In [37]:
```
#saving the dataframe to a file.
data_frame.to_csv('cancer_dataset.csv',index=False)
```