DSC 530 - Spring 2023

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Week 12 - Final Project

In [1]:
```
from os.path import basename, exists


def download(url):
    filename = basename(url)
    if not exists(filename):
        from urllib.request import urlretrieve

        local, _ = urlretrieve(url, filename)
        print("s " + local)

download("https://github.com/AllenDowney/ThinkStats2/raw/master/code/thinkst
download("https://github.com/AllenDowney/ThinkStats2/raw/master/code/thinkpl
```

In [2]:
```
import pandas as pd

covid_data = pd.read_csv('/Users/aaronbrown/Documents/ClassWork/DSC 530 -Dat
ranking_data = pd.read_csv('/Users/aaronbrown/Documents/ClassWork/DSC 530 -D
```

Statistical Question/Hypothesis

To find and determine key relationships between variables that infleuence the total number of cases in the United States, by state and counties.

About Our Data

covid_data: This is data taken from the peak COVID year of 2020. It contains key COVID-19 information, including variables of interest such as: state, county, cases, deaths, and date of the record.

ranking_data: contains variables from health status, and chronic conditions, like: percent_fair_or_poor_health percent_smokers percent_adults_with_obesity percent_excessive_drinking income_ratio percent_adults_with_diabetes

Data Cleaning/Preparation

Removing unneeded columns.

In [3]:
```
covid_county = covid_data.drop(columns = ['fips'])
covid_county
```

Out[3]:

	date	county	state	cases	deaths
0	2020-01-21	Snohomish	Washington	1	0
1	2020-01-22	Snohomish	Washington	1	0
2	2020-01-23	Snohomish	Washington	1	0
3	2020-01-24	Cook	Illinois	1	0
4	2020-01-24	Snohomish	Washington	1	0
...	...	...	...	...	...
185643	2020-05-28	Sweetwater	Wyoming	26	0
185644	2020-05-28	Teton	Wyoming	100	1
185645	2020-05-28	Uinta	Wyoming	12	0
185646	2020-05-28	Washakie	Wyoming	34	3
185647	2020-05-28	Weston	Wyoming	1	0

185648 rows × 5 columns

Two new variables will be created: peak_case and peak_deaths.

In [4]:
```
covid_county = covid_county.sort_values(['county','state','date'])
covid_county['peak_case'] = covid_county.groupby(['county','state'])['cases'
covid_county
```

Out[4]:

	date	county	state	cases	deaths	peak_case
5000	2020-03-19	Abbeville	South Carolina	1	0	0.0
5873	2020-03-20	Abbeville	South Carolina	1	0	0.0
6877	2020-03-21	Abbeville	South Carolina	1	0	0.0
7997	2020-03-22	Abbeville	South Carolina	1	0	0.0
9208	2020-03-23	Abbeville	South Carolina	1	0	0.0
...	...	...	...	...	...	...
173083	2020-05-24	Ziebach	South Dakota	1	0	0.0
176048	2020-05-25	Ziebach	South Dakota	1	0	0.0
179013	2020-05-26	Ziebach	South Dakota	1	0	0.0
181985	2020-05-27	Ziebach	South Dakota	1	0	0.0
184963	2020-05-28	Ziebach	South Dakota	1	0	0.0

185648 rows × 6 columns

Data is grouped by: County, State.

In [5]:
```
covid_county['peak_deaths'] = covid_county.groupby(['county','state'])['deat
covid_county
```

Out[5]:

	date	county	state	cases	deaths	peak_case	peak_deaths
5000	2020-03-19	Abbeville	South Carolina	1	0	0.0	0.0
5873	2020-03-20	Abbeville	South Carolina	1	0	0.0	0.0
6877	2020-03-21	Abbeville	South Carolina	1	0	0.0	0.0
7997	2020-03-22	Abbeville	South Carolina	1	0	0.0	0.0
9208	2020-03-23	Abbeville	South Carolina	1	0	0.0	0.0
...	...	...	...	...	...	...	...
173083	2020-05-24	Ziebach	South Dakota	1	0	0.0	0.0
176048	2020-05-25	Ziebach	South Dakota	1	0	0.0	0.0
179013	2020-05-26	Ziebach	South Dakota	1	0	0.0	0.0
181985	2020-05-27	Ziebach	South Dakota	1	0	0.0	0.0
184963	2020-05-28	Ziebach	South Dakota	1	0	0.0	0.0

185648 rows × 7 columns

Removes states from the rank_county data that have missing values in the "county" column.

In [6]:
```
rank_county = ranking_data[['county','state','percent_fair_or_poor_health' ,
                            'percent_adults_with_obesity' , 'percent_exce
                            'income_ratio', 'percent_adults_with_diabetes
rank_county.dropna()
```

Out[6]:

	county	state	percent_fair_or_poor_health	percent_smokers	percent_adults_v
1	Autauga	Alabama	20.882987	18.081557	
2	Baldwin	Alabama	17.509134	17.489033	
3	Barbour	Alabama	29.591802	21.999985	
4	Bibb	Alabama	19.439724	19.114200	
5	Blount	Alabama	21.745293	19.208672	
...	...	...	...	...	
3188	Sweetwater	Wyoming	14.813082	18.073422	
3189	Teton	Wyoming	11.914358	14.546369	
3190	Uinta	Wyoming	15.537464	17.212675	
3191	Washakie	Wyoming	15.955971	16.859400	
3192	Weston	Wyoming	13.934025	16.693134	

3140 rows × 8 columns

Combines data to help compare the number of cases and deaths with other mortality encouraging conditions (eg. smoking, obesity, drinking, and overall health status).

In [7]:
```
sample_data = covid_county[covid_county.date == '2020-05-28']
sample_data
```

Out[7]:

	date	county	state	cases	deaths	peak_case	peak_deaths
184868	2020-05-28	Abbeville	South Carolina	37	0	2.0	0.0
183742	2020-05-28	Acadia	Louisiana	401	22	4.0	4.0
185332	2020-05-28	Accomack	Virginia	807	12	27.0	0.0
183210	2020-05-28	Ada	Idaho	803	22	3.0	0.0
183436	2020-05-28	Adair	Iowa	8	0	0.0	0.0
...	...	...	...	...	...	...	...
182770	2020-05-28	Yuma	Arizona	822	11	40.0	1.0
182962	2020-05-28	Yuma	Colorado	20	0	1.0	0.0
185288	2020-05-28	Zapata	Texas	8	0	0.0	0.0
185289	2020-05-28	Zavala	Texas	11	0	0.0	0.0
184963	2020-05-28	Ziebach	South Dakota	1	0	0.0	0.0

2978 rows × 7 columns

In [8]:
```
health_totals = pd.merge(sample_data[['county','state','cases','deaths']], r
health_totals
```

Out[8]:

	county	state	cases	deaths	percent_fair_or_poor_health	percent_smokers	p
0	Abbeville	South Carolina	37	0	19.895036	17.323519	
1	Acadia	Louisiana	401	22	20.890035	21.534088	
2	Accomack	Virginia	807	12	20.089199	18.316929	
3	Ada	Idaho	803	22	11.474882	11.990701	
4	Adair	Iowa	8	0	13.854797	15.583571	
...	...	...	...	...	...	...	
2973	Yuma	Arizona	822	11	22.726376	13.327036	
2974	Yuma	Colorado	20	0	15.268202	14.277809	
2975	Zapata	Texas	8	0	35.610705	17.275488	
2976	Zavala	Texas	11	0	40.990687	19.871284	
2977	Ziebach	South Dakota	1	0	29.166512	32.021175	

2978 rows × 10 columns

Will exclude 160+ observations from the data due to missing values in cases/deaths. An additional 87 counties will be dropped to to missing health data values.

In [9]:
```
health_totals.dropna()
```

Out[9]:

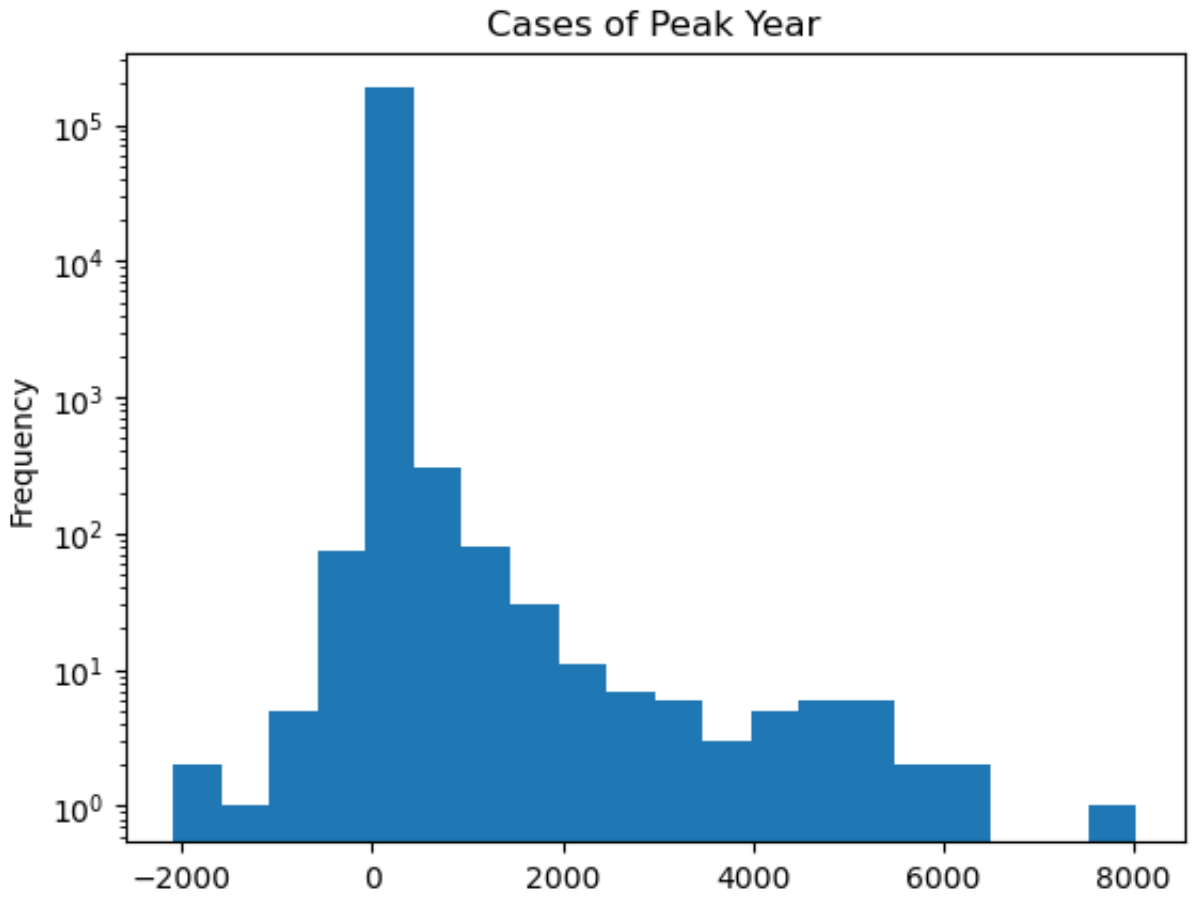
	county	state	cases	deaths	percent_fair_or_poor_health	percent_smokers	p
0	Abbeville	South Carolina	37	0	19.895036	17.323519	
1	Acadia	Louisiana	401	22	20.890035	21.534088	
2	Accomack	Virginia	807	12	20.089199	18.316929	
3	Ada	Idaho	803	22	11.474882	11.990701	
4	Adair	Iowa	8	0	13.854797	15.583571	
...	...	...	...	...	...	...	
2973	Yuma	Arizona	822	11	22.726376	13.327036	
2974	Yuma	Colorado	20	0	15.268202	14.277809	
2975	Zapata	Texas	8	0	35.610705	17.275488	
2976	Zavala	Texas	11	0	40.990687	19.871284	
2977	Ziebach	South Dakota	1	0	29.166512	32.021175	

2891 rows × 10 columns

Histograms

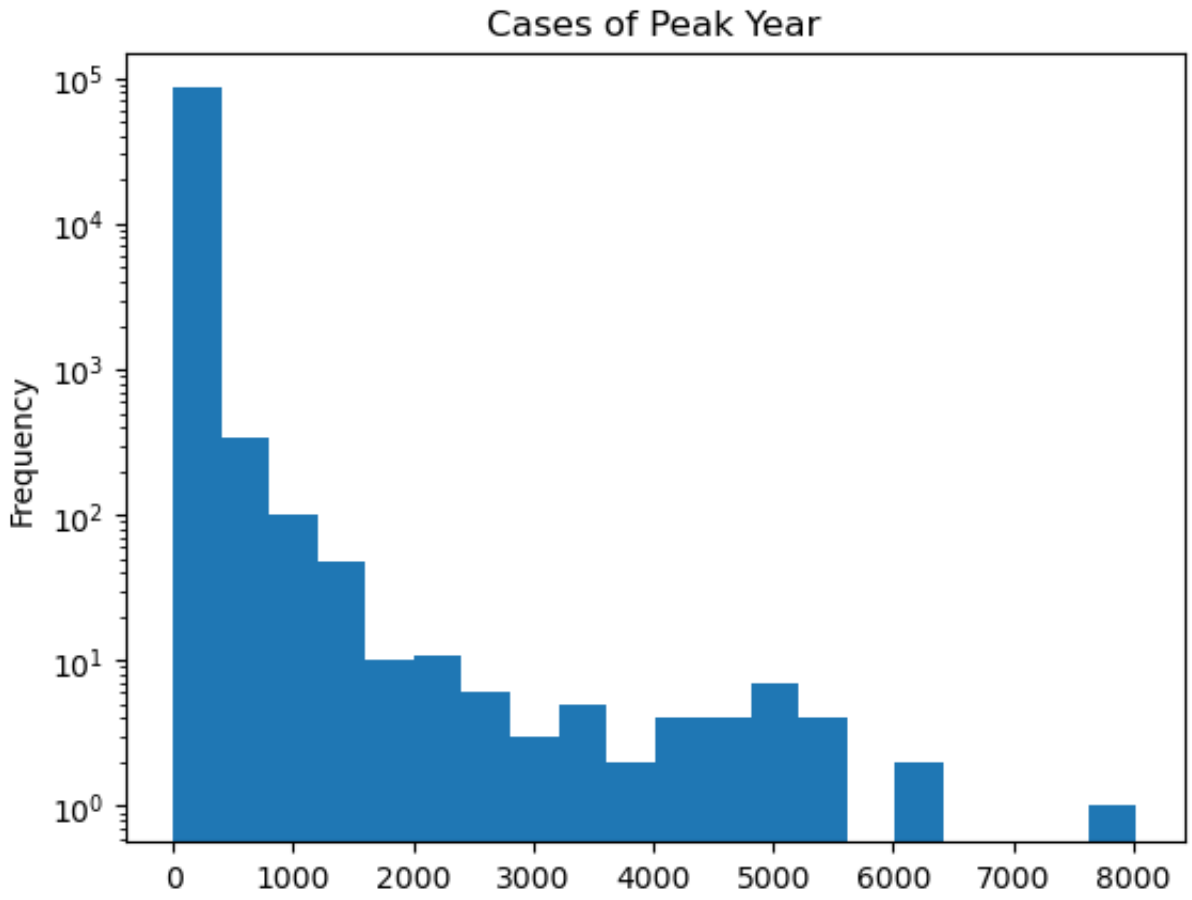
In [10]:
```
covid_county.peak_case.plot.hist(bins = 20, logy = True, title = 'Cases of P
```

Out[10]:
```
<AxesSubplot:title={'center':'Cases of Peak Year'}, ylabel='Frequency'>
```



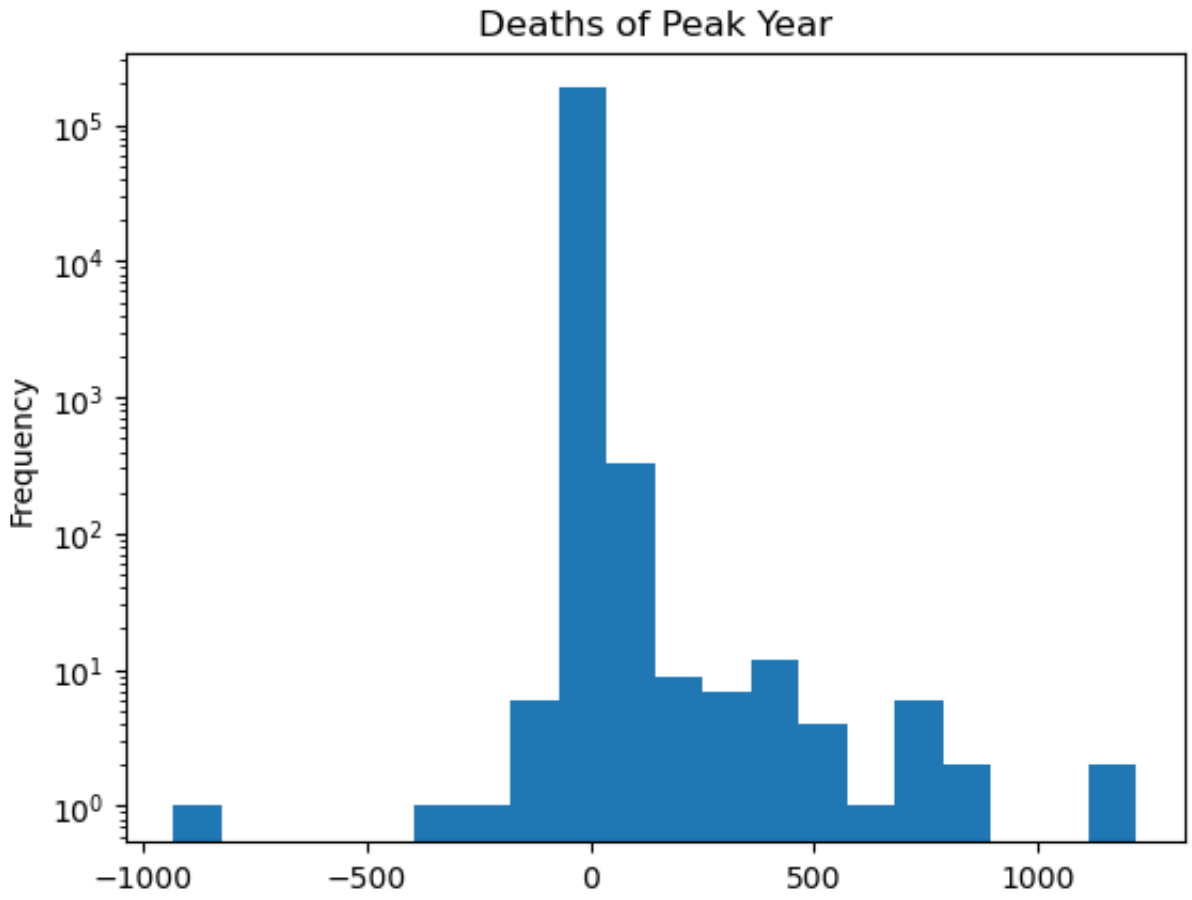
In [11]:
```
covid_county1 = covid_county.loc[covid_county['peak_case']>0]
covid_county1.peak_case.plot.hist(bins = 20,logy = True, title = 'Cases of P
```

Out[11]:
```
<AxesSubplot:title={'center':'Cases of Peak Year'}, ylabel='Frequency'>
```



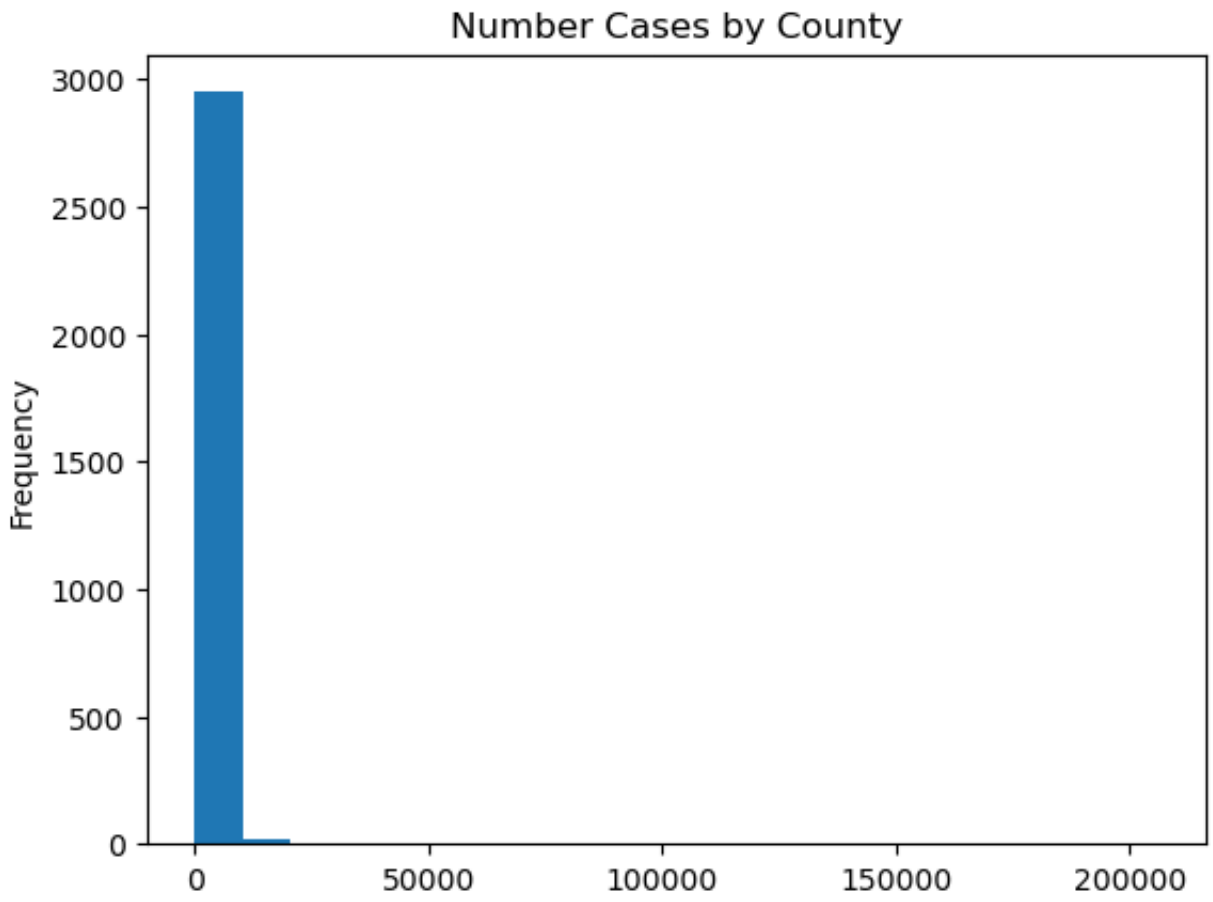
In [12]:
```
covid_county.peak_deaths.plot.hist(bins = 20,logy = True, title = 'Deaths of
```

Out[12]:
```
<AxesSubplot:title={'center':'Deaths of Peak Year'}, ylabel='Frequency'>
```



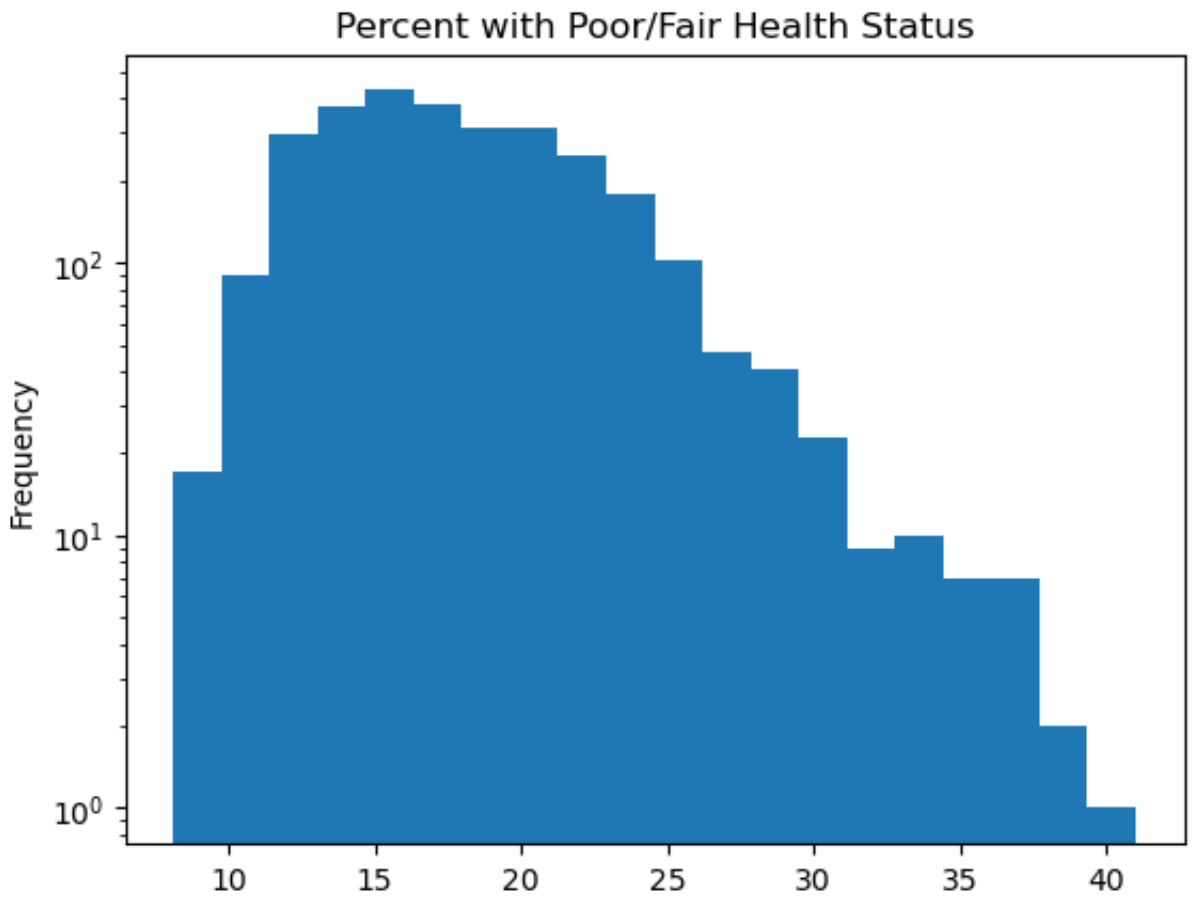
In [13]:
```
health_totals.cases.plot.hist(bins = 20, title = 'Number Cases by County')
```

Out[13]:
```
<AxesSubplot:title={'center':'Number Cases by County'}, ylabel='Frequency'>
```



In [14]:
```
health_totals.percent_fair_or_poor_health.plot.hist(bins = 20,
                title = 'Percent with Poor/Fair Health Status', logy = True)
```

Out[14]:
```
<AxesSubplot:title={'center':'Percent with Poor/Fair Health Status'}, ylabel
='Frequency'>
```



In [15]:
```
health_totals_1 = pd.DataFrame()
health_totals_1['mean'] = health_totals.mean()
health_totals_1['median'] = health_totals.median()
health_totals_1['var'] = health_totals.var()
health_totals_1['std'] = health_totals.std()
health_totals_1
```

```
/var/folders/8g/4dlsnvvj5l7738w04p6b2xk80000gn/T/ipykernel_89579/3720952239.
py:2: FutureWarning: Dropping of nuisance columns in DataFrame reductions (w
ith 'numeric_only=None') is deprecated; in a future version this will raise
TypeError.  Select only valid columns before calling the reduction.
  health_totals_1['mean'] = health_totals.mean()
/var/folders/8g/4dlsnvvj5l7738w04p6b2xk80000gn/T/ipykernel_89579/3720952239.
py:3: FutureWarning: Dropping of nuisance columns in DataFrame reductions (w
ith 'numeric_only=None') is deprecated; in a future version this will raise
TypeError.  Select only valid columns before calling the reduction.
  health_totals_1['median'] = health_totals.median()
/var/folders/8g/4dlsnvvj5l7738w04p6b2xk80000gn/T/ipykernel_89579/3720952239.
py:4: FutureWarning: Dropping of nuisance columns in DataFrame reductions (w
ith 'numeric_only=None') is deprecated; in a future version this will raise
TypeError.  Select only valid columns before calling the reduction.
  health_totals_1['var'] = health_totals.var()
/var/folders/8g/4dlsnvvj5l7738w04p6b2xk80000gn/T/ipykernel_89579/3720952239.
py:5: FutureWarning: Dropping of nuisance columns in DataFrame reductions (w
ith 'numeric_only=None') is deprecated; in a future version this will raise
TypeError.  Select only valid columns before calling the reduction.
  health_totals_1['std'] = health_totals.std()
```

Out[15]:

	mean	median	var	std
cases	581.075890	43.000000	2.089346e+07	4570.936959
deaths	34.123909	1.000000	1.686084e+05	410.619516
percent_fair_or_poor_health	18.034635	17.343802	2.234296e+01	4.726834
percent_smokers	17.532791	17.087545	1.255117e+01	3.542763
percent_adults_with_obesity	33.026591	33.300000	2.948427e+01	5.429942
percent_excessive_drinking	17.483325	17.559710	1.008055e+01	3.174989
income_ratio	4.520333	4.411360	5.491752e-01	0.741064
percent_adults_with_diabetes	12.237759	11.700000	1.635616e+01	4.044275

In [16]:
```
covid_county2 = pd.DataFrame()
covid_county2['mean'] = covid_county1[['peak_case','peak_deaths']].mean()
covid_county2['median'] = covid_county1[['peak_case','peak_deaths']].median(
covid_county2['var'] = covid_county1[['peak_case','peak_deaths']].var()
covid_county2['std'] = covid_county1[['peak_case','peak_deaths']].std()
covid_county2
```

Out[16]:

	mean	median	var	std
peak_case	20.504134	3.0	14241.769449	119.338885
peak_deaths	1.165234	0.0	158.266400	12.580397

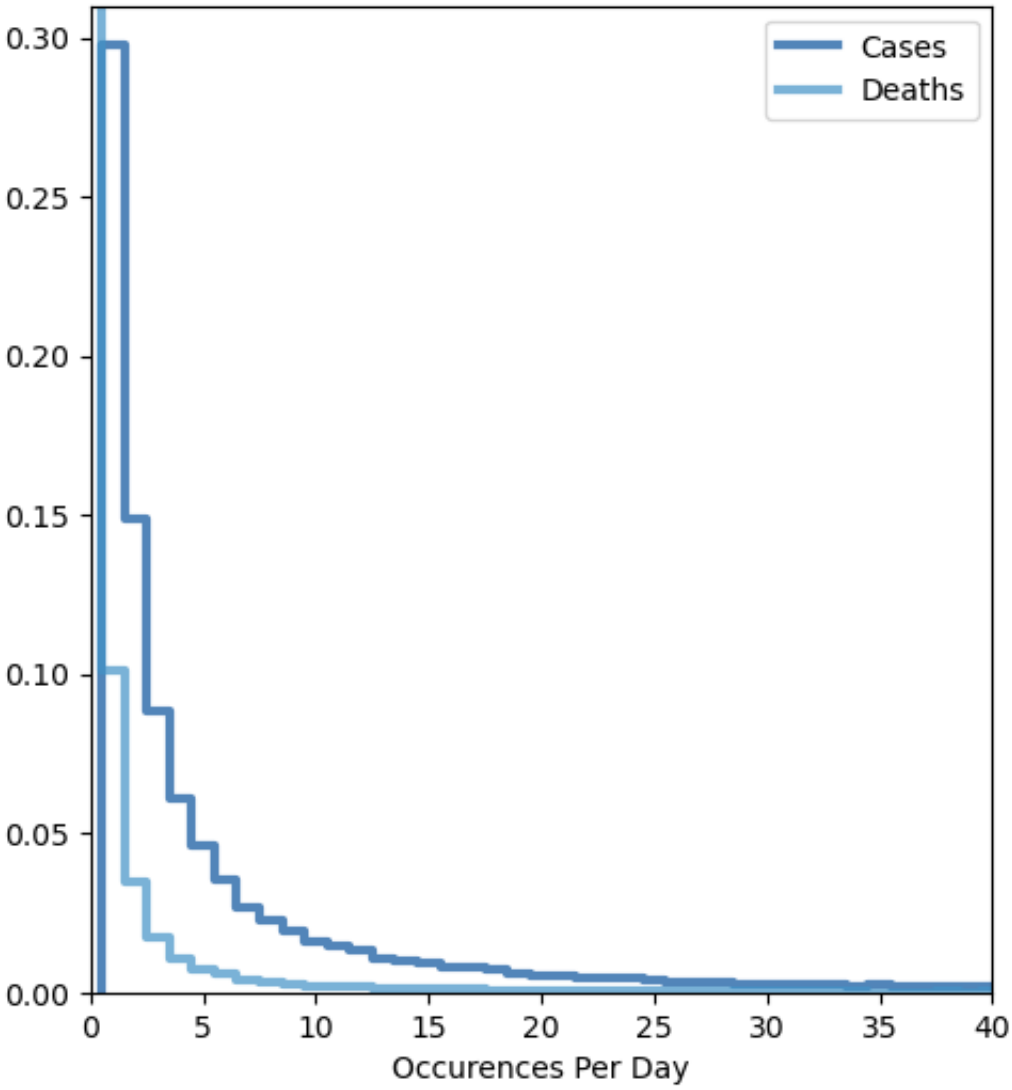
In [17]:
```
import thinkstats2
import thinkplot
```

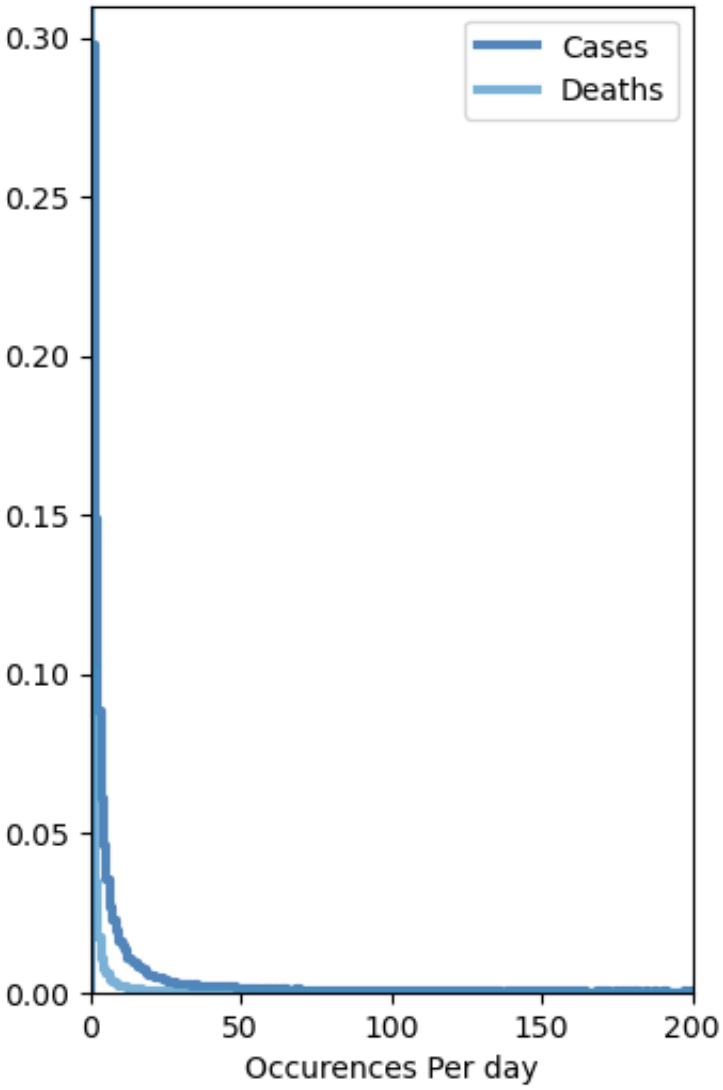
Probability Mass Function (PMF)

In [18]:
```
pmf_peak_cases = thinkstats2.Pmf(covid_county1['peak_case'], label = 'Cases'
pmf_peak_deaths = thinkstats2.Pmf(covid_county1['peak_deaths'], label = 'Dea
pmf_peak_cases.Normalize()
pmf_peak_deaths.Normalize()
```

Out[18]:
```
0.9999999999999943
```

In [19]:
```
thinkplot.PrePlot(2,cols = 2)
thinkplot.Pmfs([pmf_peak_cases,pmf_peak_deaths])
thinkplot.Show(xlabel = 'Occurences Per Day',axis = [0,40,0,0.31])
thinkplot.PrePlot(2)
thinkplot.SubPlot(2)
thinkplot.Pmfs([pmf_peak_cases,pmf_peak_deaths])
thinkplot.Show(xlabel = 'Occurences Per day',axis = [0,200,0,0.31])
```


Cases
Deaths
0.30
0.25
0.20
0.15
0.10
0.05
0.00
0
5
10
15
20
25
30
35
40
Occurences Per Day



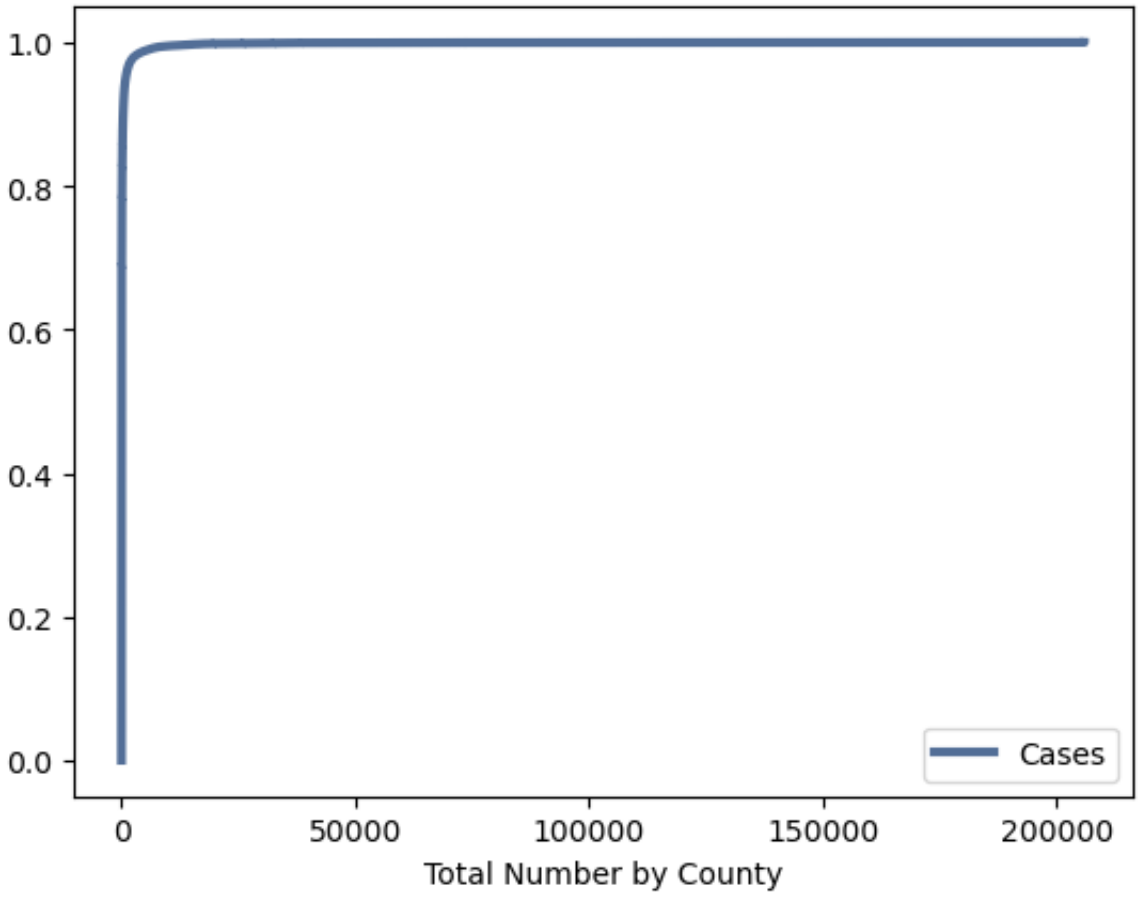

```
<Figure size 800x600 with 0 Axes>
```

Initially was working with a filter to compare the data between the State of New York and the rest of the USA. Yet I realized that sinze Deaths are dependent on Cases, you can think of it as a subset with an unfortunate categorical variable. The data continues outside the scope of the graph but to be able to see the nuances I decided to cut off the tail end. The Light blue graph represents the probability of the number of people to die on a certain day due to coronavirus. The darker blue represents the probability of the number of cases that will happen on a certain day.

Cumulative Distribution Function (CDF)

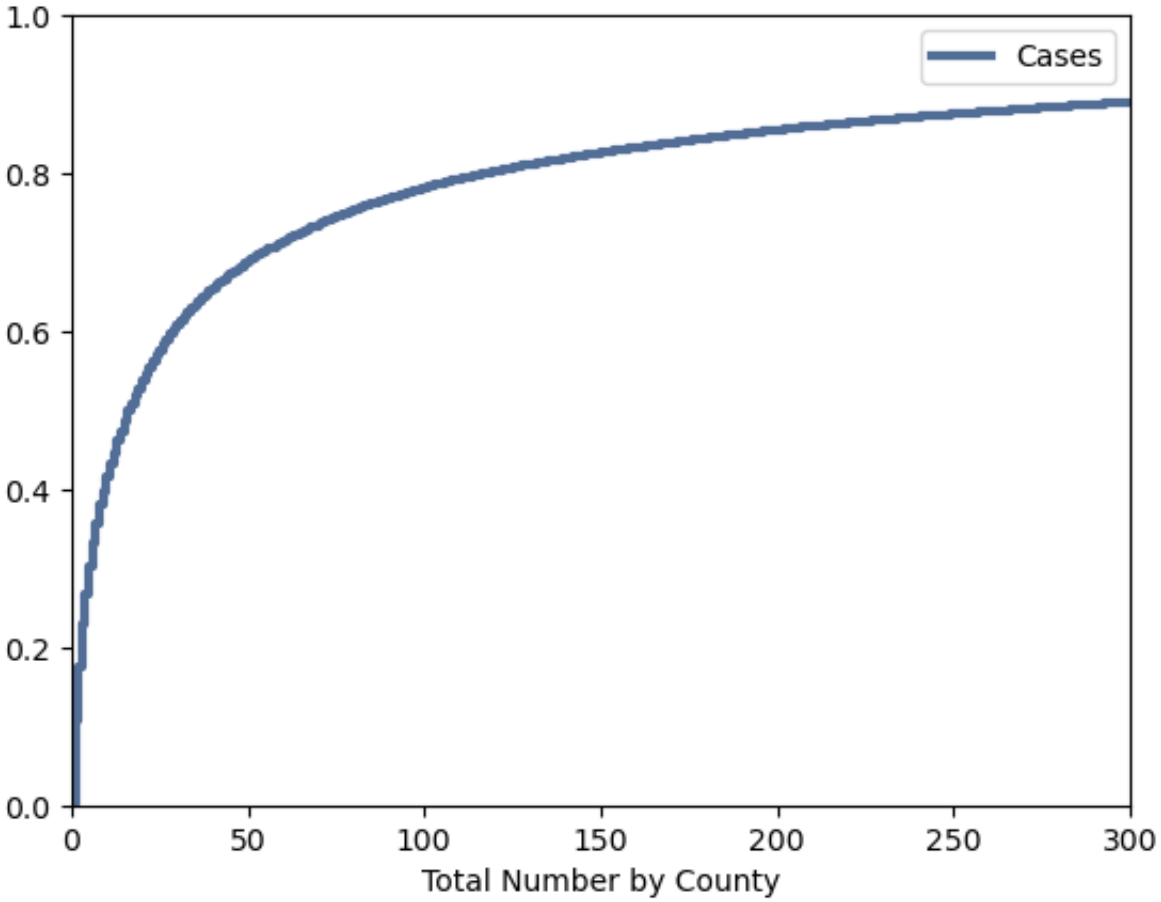
Caculation and plot of the CDF - Number of Cases by County.

In [20]:
```
cdf = thinkstats2.Cdf(covid_county.cases, label = 'Cases')
thinkplot.Cdf(cdf)
thinkplot.Show(xlabel = 'Total Number by County', y = 'CDF')
```




```
<Figure size 800x600 with 0 Axes>
```

In [21]:
```
thinkplot.Cdf(cdf)
thinkplot.Show(xlabel = 'Total Number by County', y = 'CDF',axis = [0,300,0,
```




```
<Figure size 800x600 with 0 Axes>
```

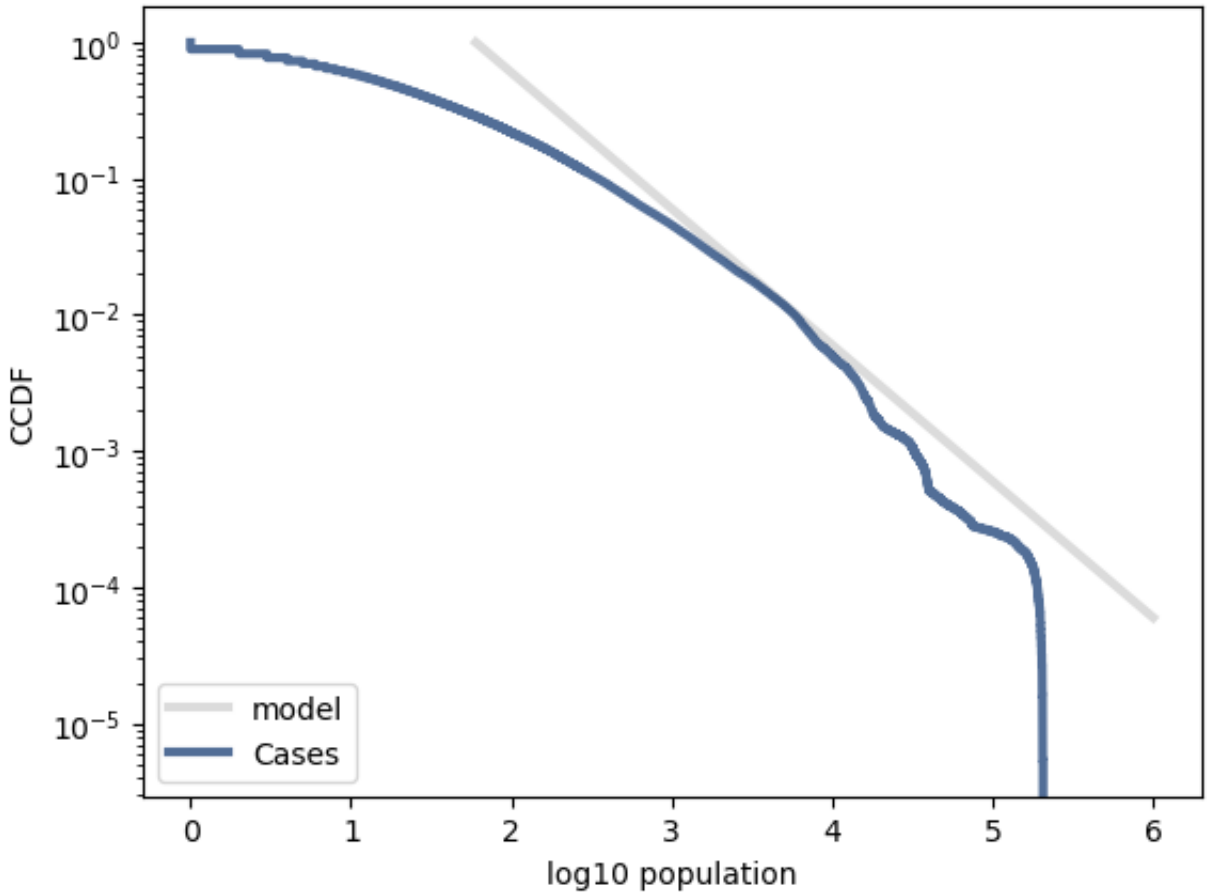
The slope produced by graphing the CDF indicated that about 70% of all US counties fall within 0-50 cases. To account for outliers, we appropriated 90% of the data.

Distribution of the Data

Since the CDF graph above looks very similar to a pareto distribution, we will log transform to see if a straight line is produced, suggesting a good fit.

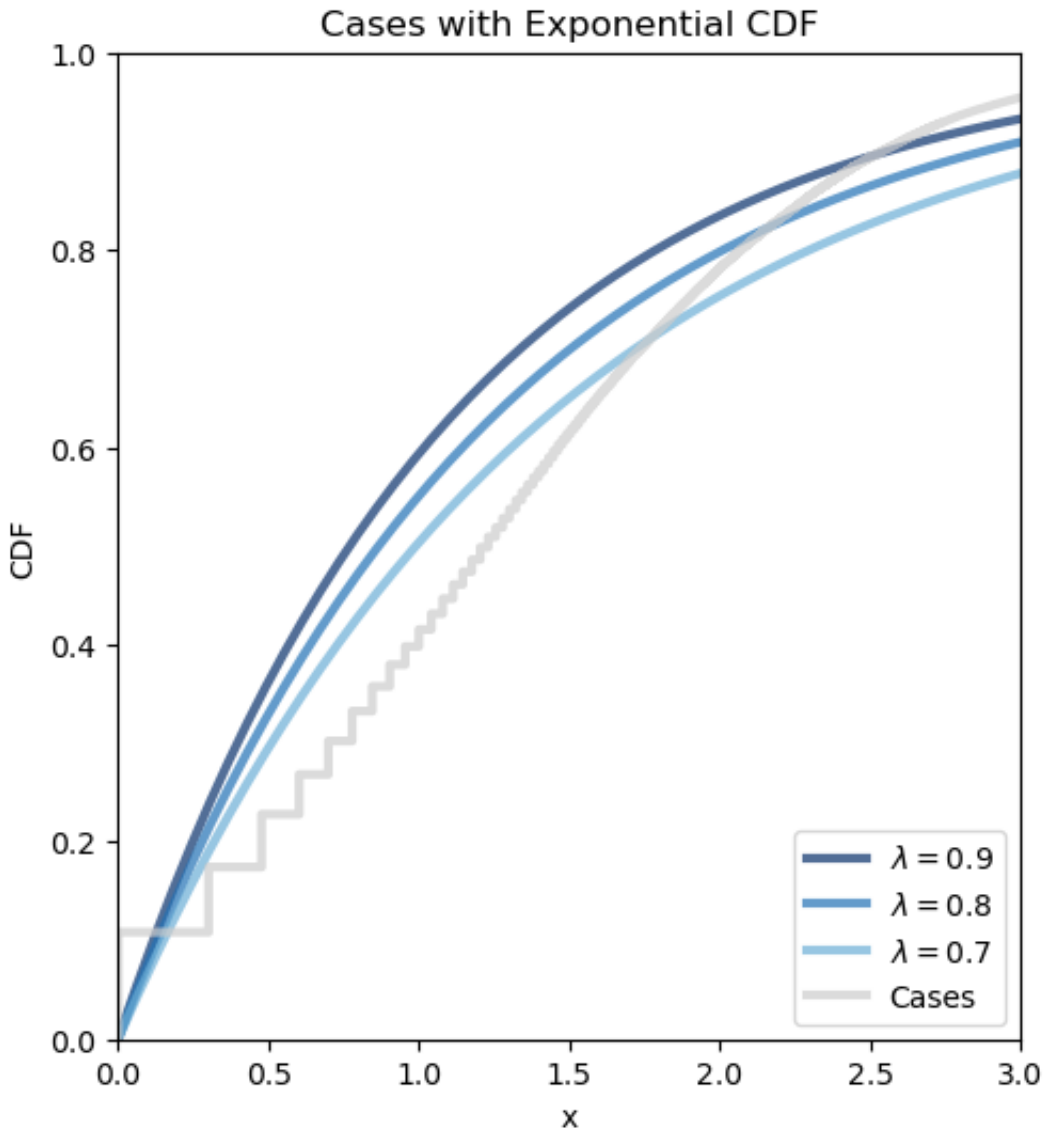
In [22]:
```
import numpy as np
cases_log = np.log10(covid_county.cases)
cdf_log = thinkstats2.Cdf(cases_log, label = 'Cases')

xs, ys = thinkstats2.RenderParetoCdf(xmin=60, alpha=1, low=0, high=1e6)
thinkplot.Plot(np.log10(xs), 1-ys, label='model', color='0.8')

thinkplot.Cdf(cdf_log, complement=True)
thinkplot.Config(xlabel='log10 population',
                 ylabel='CCDF',
                 yscale='log', loc='lower left')
```

```
/Users/aaronbrown/opt/anaconda3/lib/python3.9/site-packages/pandas/core/arra
ylike.py:397: RuntimeWarning: divide by zero encountered in log10
  result = getattr(ufunc, method)(*inputs, **kwargs)
```



A straight line is not produced here, which suggests that the Pareto Distribution is not a great fit either.

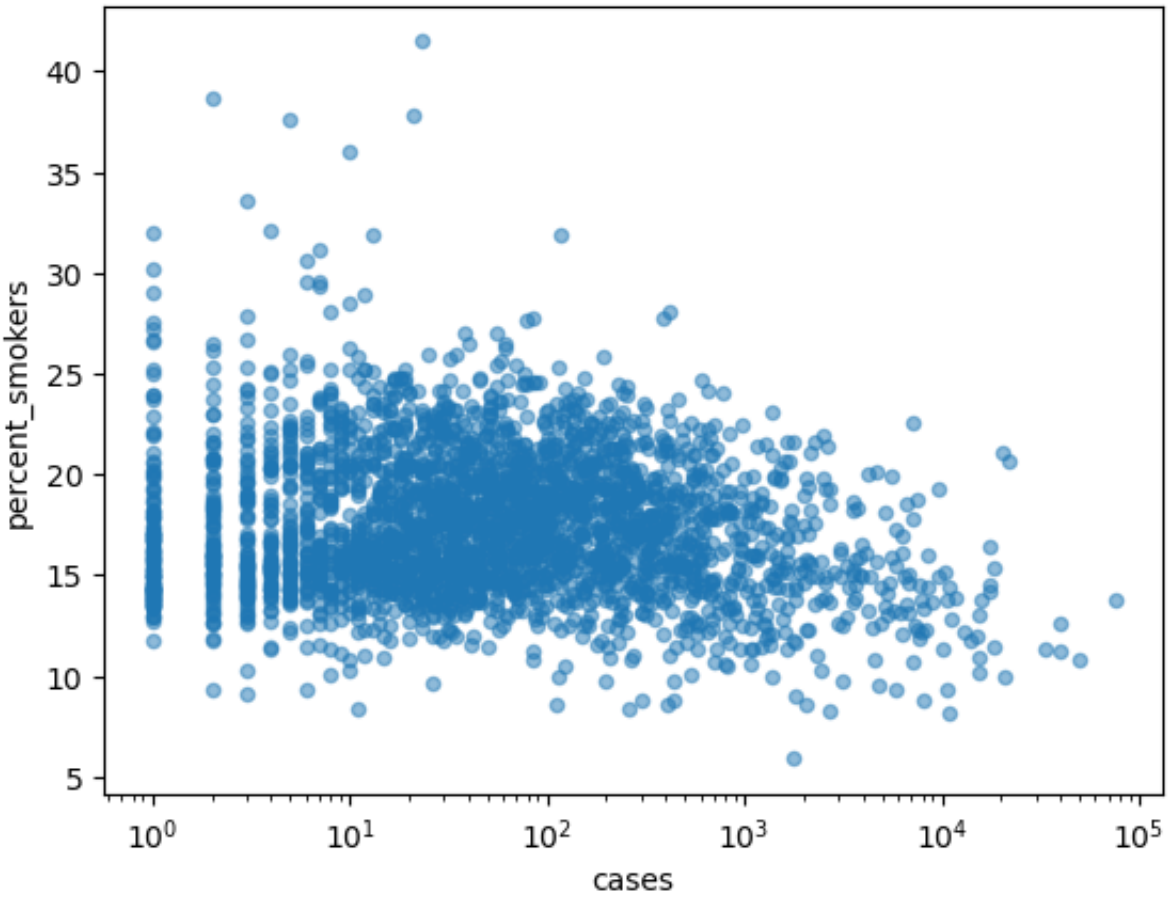
In [23]:
```
thinkplot.PrePlot(3, cols = 2)
for lam in [.9,.8,0.7]:
    xs, ps = thinkstats2.RenderExpoCdf(lam, 0, 3.0, 50)
    label = r'$\lambda=%g$' % lam
    thinkplot.Plot(xs, ps, label=label)
thinkplot.Cdf(cdf_log, color='0.8', yscale = 'log')
thinkplot.Config(title='Cases with Exponential CDF', xlabel='x', ylabel='CDF
                 loc='lower right',axis = [0,3,0,1])
```



The Exponential Distribution does not appear to be a good estimate of the log-log CDF of the total number of cases by county.

In [24]:
```
health_totals.plot(x= 'cases', y = 'percent_smokers', kind = 'scatter', logx
```

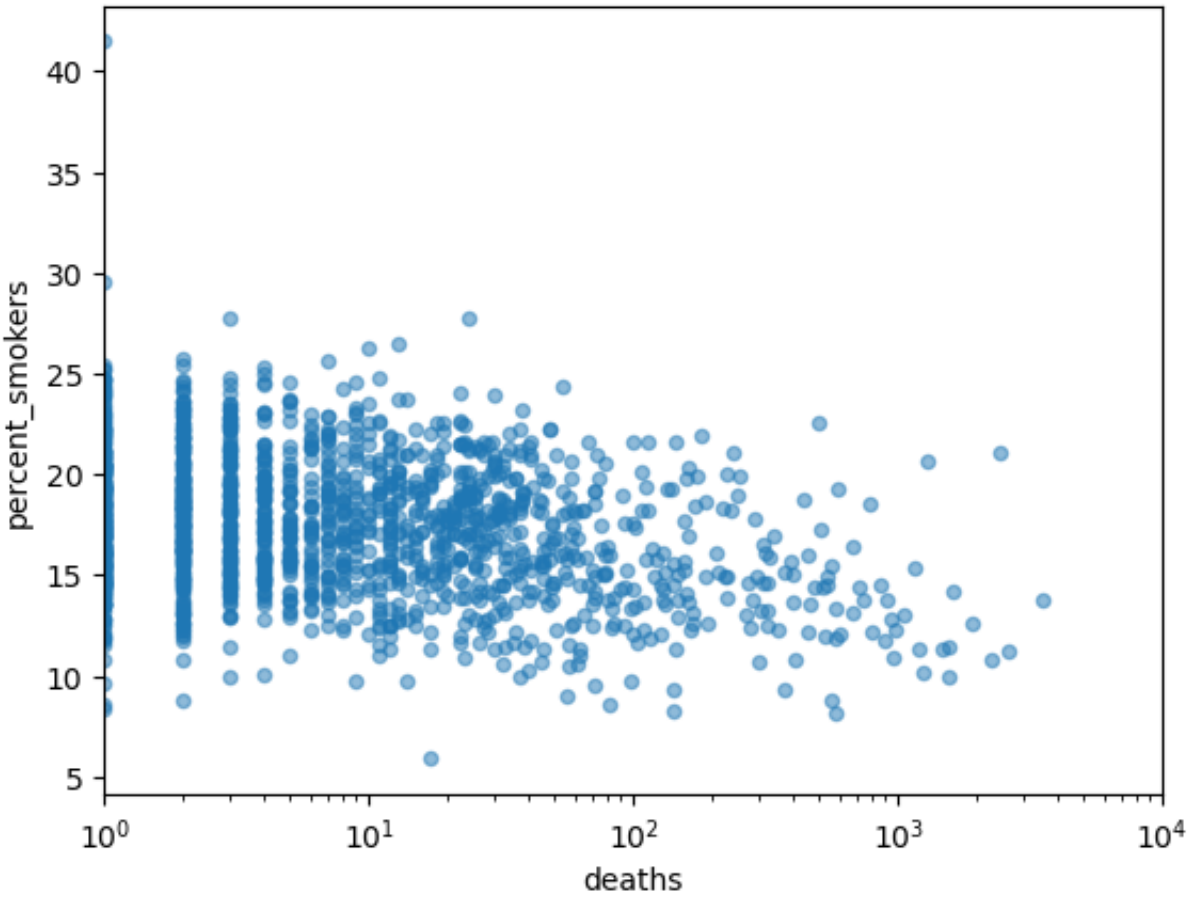
Out[24]:
```
<AxesSubplot:xlabel='cases', ylabel='percent_smokers'>
```



Here, the "number of cases" by "percent of smokers" is plotted; smoking does not directly relate to the number of COVID cases, as we see above. The number of cases does not seem to increase (or decrease) with increased smoking percentages.

In [25]:
```
health_totals.plot(x= 'deaths', y = 'percent_smokers', kind = 'scatter', log
```

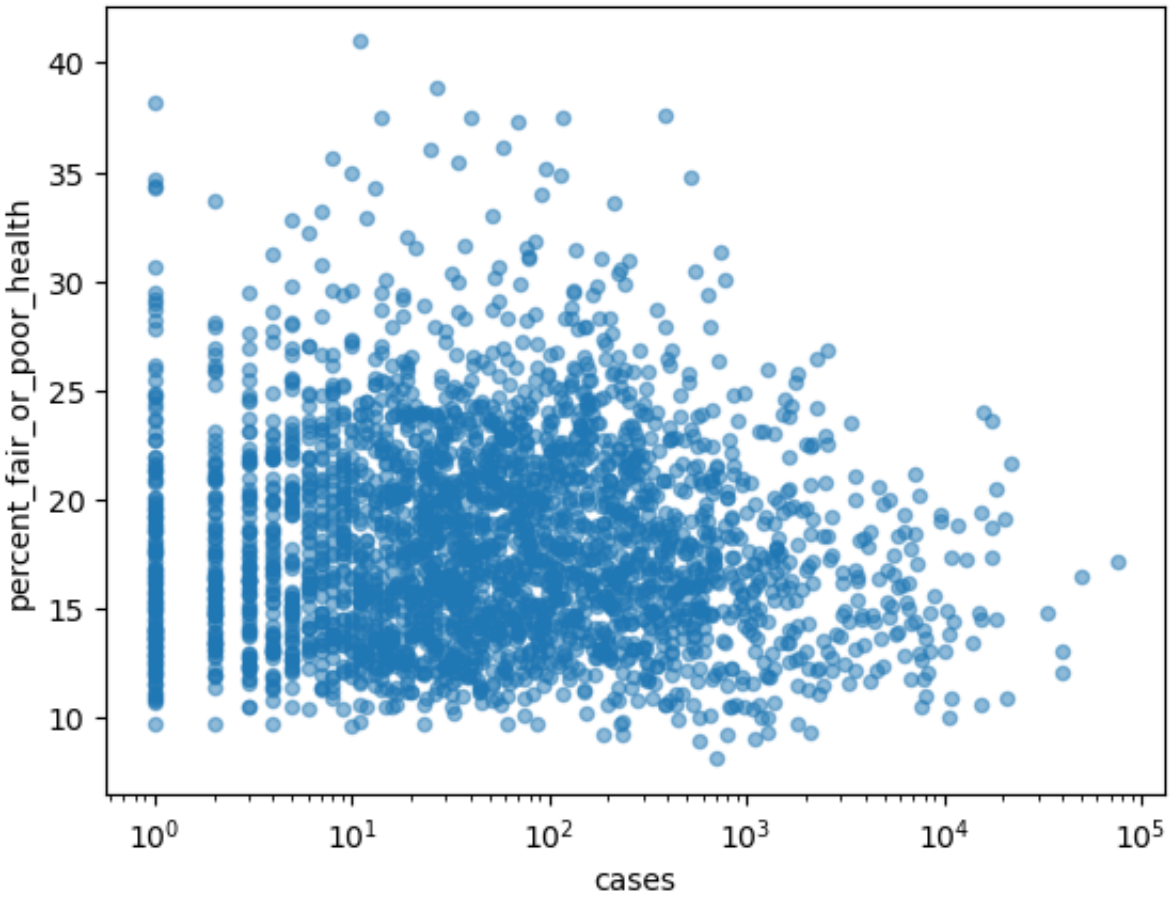
Out[25]:
```
<AxesSubplot:xlabel='deaths', ylabel='percent_smokers'>
```



Contrary to what was expected, the number of deaths did not seem to increase with increasing smoking perscentages. Seeing that COVID-19 is a respiratory disease, a more obvious relationship was expected between the two variables.

In [26]:
```
health_totals.plot(x= 'cases', y = 'percent_fair_or_poor_health', kind = 'sc
```

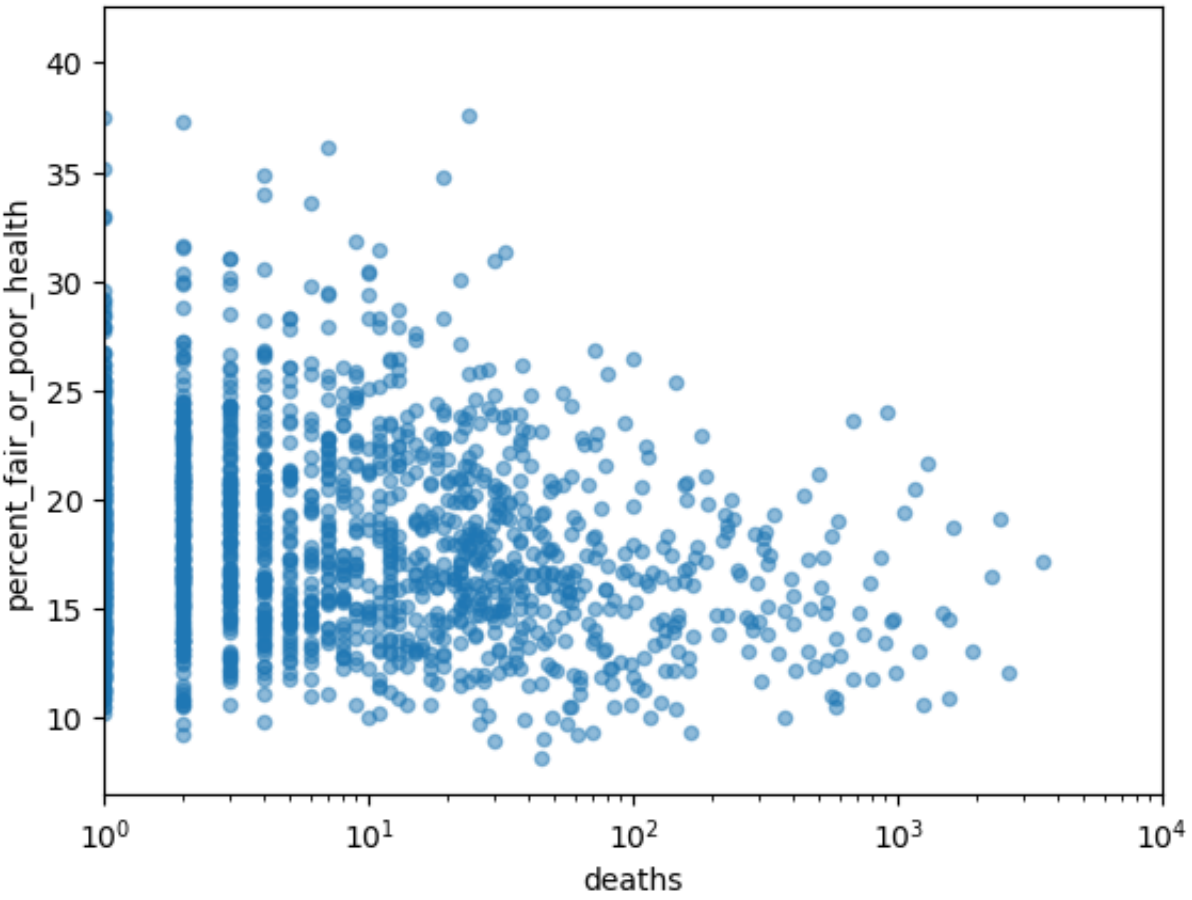
Out[26]:
```
<AxesSubplot:xlabel='cases', ylabel='percent_fair_or_poor_health'>
```



No significant relationship can be seen between the number of cases, and poor/fair overall health (above). A relationship between the number of deaths, and poor/fair overall health also seems to be nonexistant (below).

In [27]:
```
health_totals.plot(x= 'deaths', y = 'percent_fair_or_poor_health', kind = 's
```

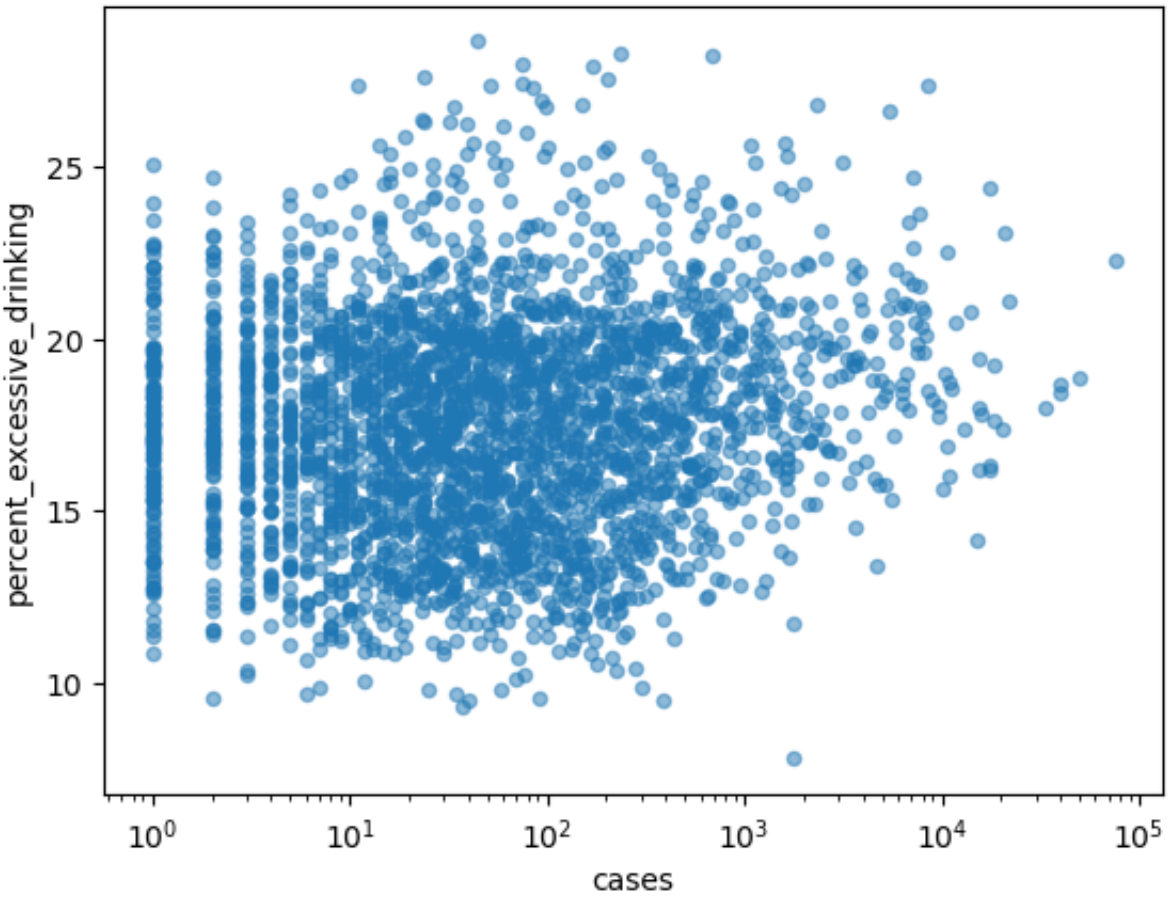
Out[27]:
```
<AxesSubplot:xlabel='deaths', ylabel='percent_fair_or_poor_health'>
```



Below are the plots for "percent excessive drinking" vs the number of cases, and the number of deaths.

In [28]:
```
health_totals.plot(x= 'cases', y = 'percent_excessive_drinking', kind = 'sca
```

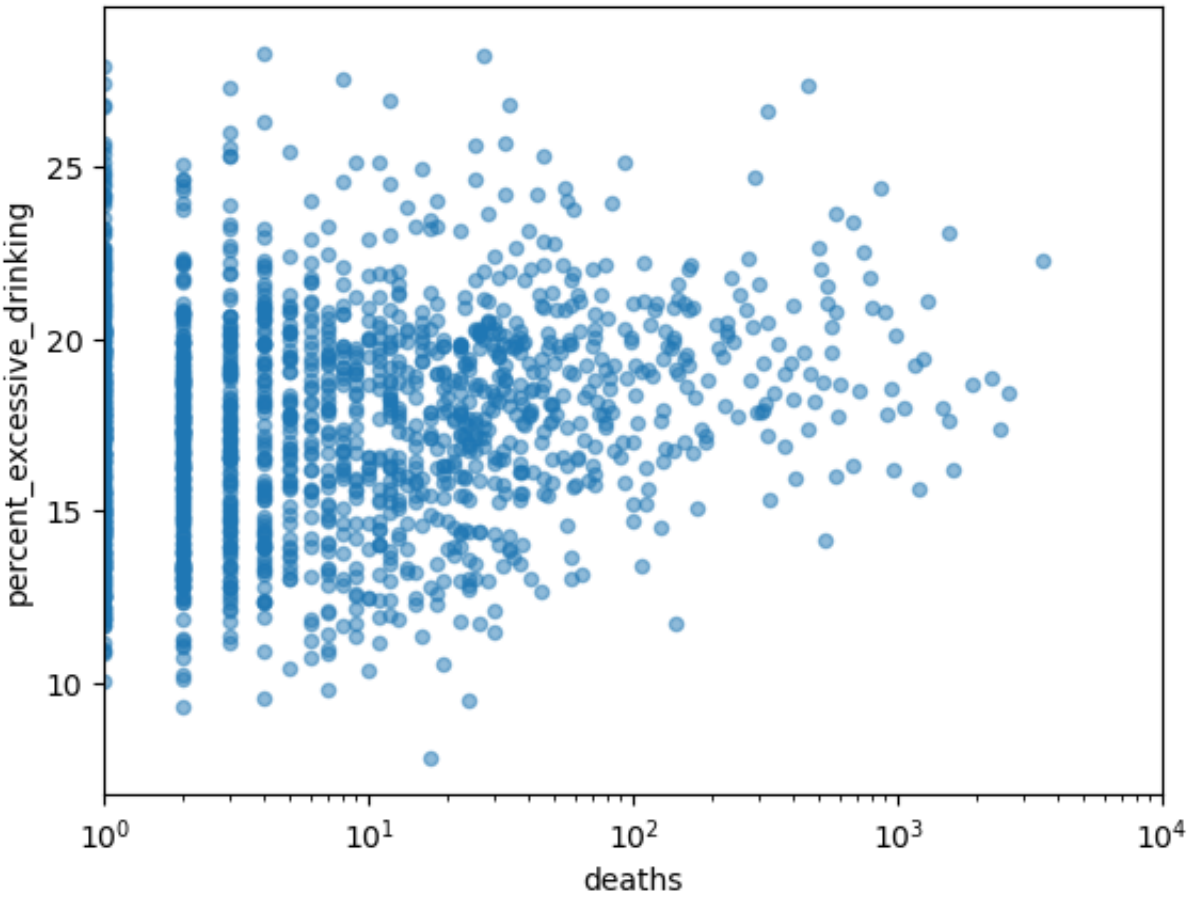
Out[28]:
```
<AxesSubplot:xlabel='cases', ylabel='percent_excessive_drinking'>
```



No obvious relationship can be determined between percent_excessive_drinking and cases.

In [29]:
```
health_totals.plot(x= 'deaths', y = 'percent_excessive_drinking', kind = 'sc
                   logx = True, alpha = .5, xlim = (1,1e4))
```

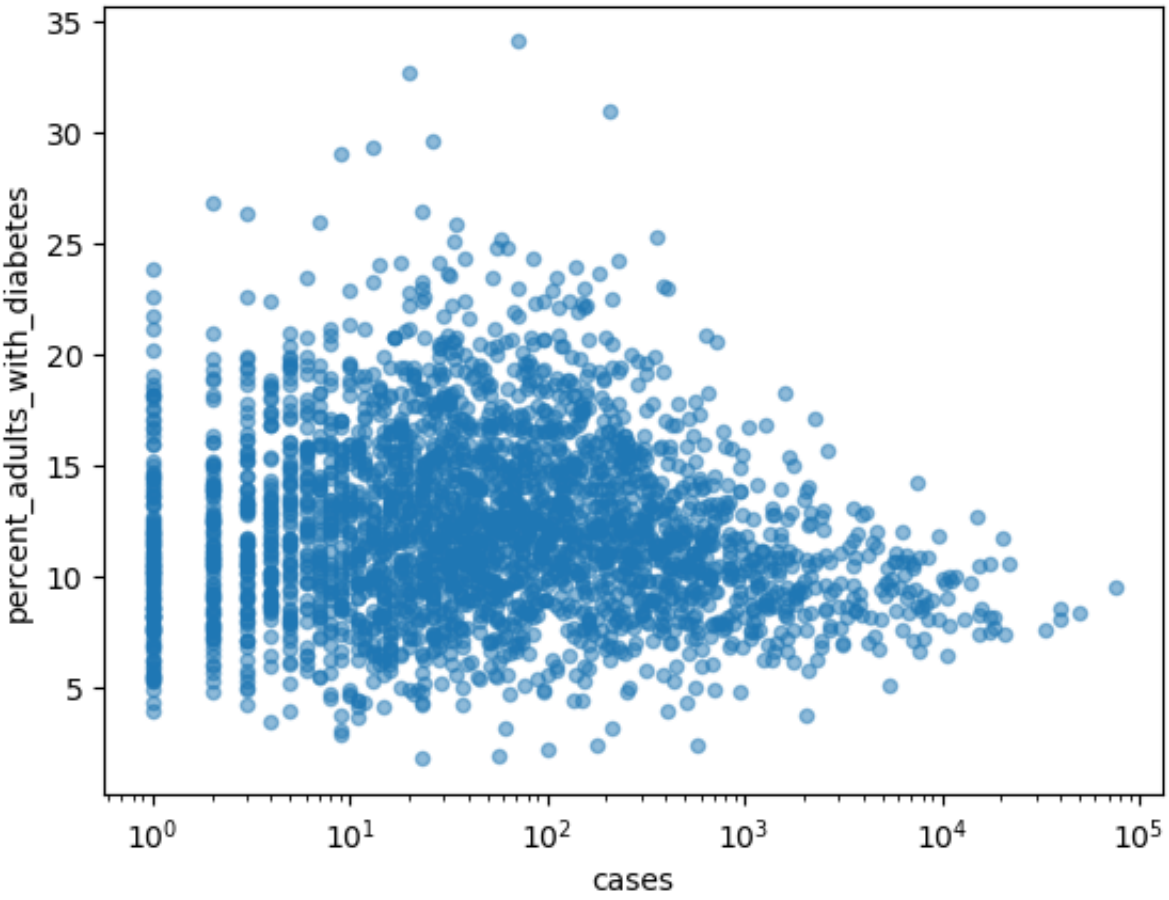
Out[29]:
```
<AxesSubplot:xlabel='deaths', ylabel='percent_excessive_drinking'>
```



In this case, the relationship between percent_excessive_drinking and deaths seems do direct in an upward trend.

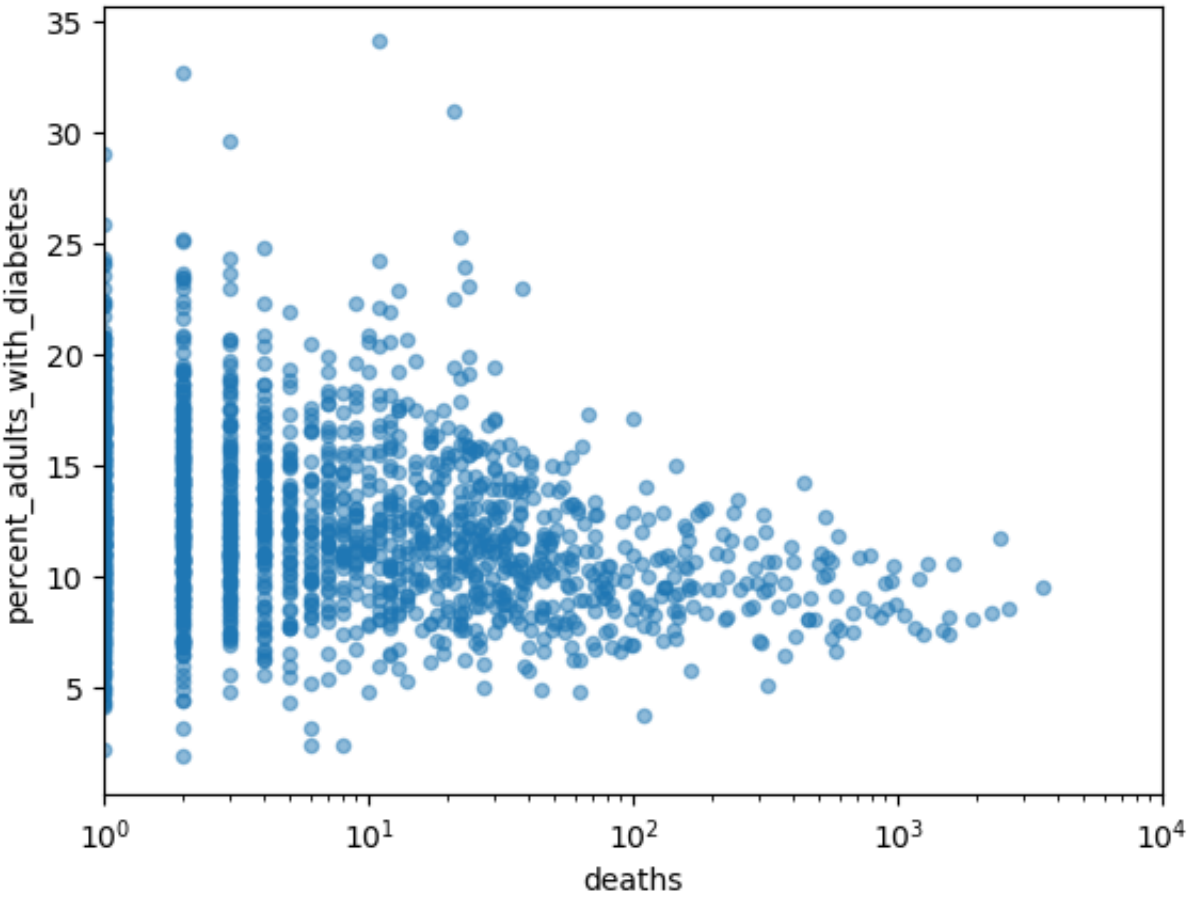
In [30]:
```
health_totals.plot(x= 'cases', y = 'percent_adults_with_diabetes', kind = 's
```

Out[30]:
```
<AxesSubplot:xlabel='cases', ylabel='percent_adults_with_diabetes'>
```



In [31]:
```
health_totals.plot(x= 'deaths', y = 'percent_adults_with_diabetes', kind = '
                   logx = True, alpha = .5, xlim = (1,1e4))
```

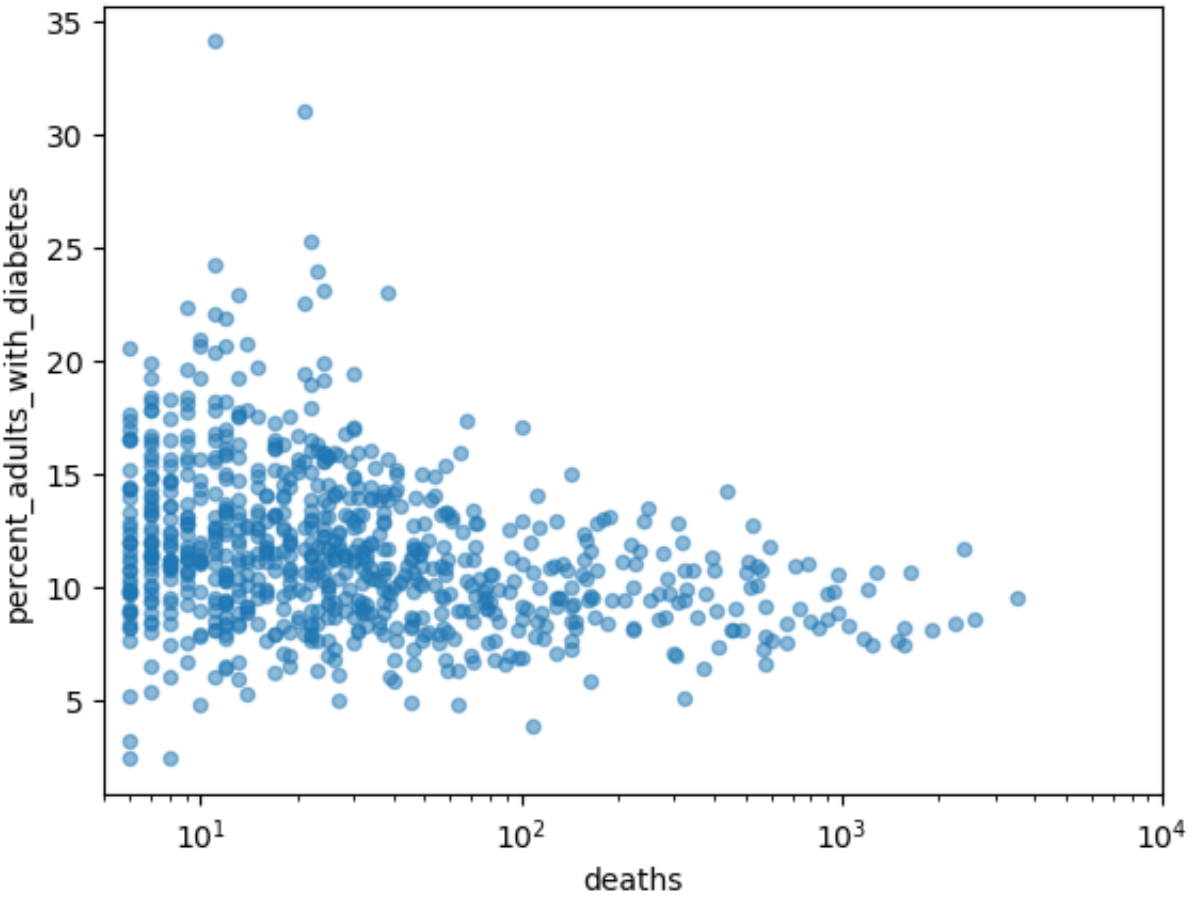
Out[31]:
```
<AxesSubplot:xlabel='deaths', ylabel='percent_adults_with_diabetes'>
```



In [32]:
```
hat_filter = health_totals[health_totals.deaths > 5]
```

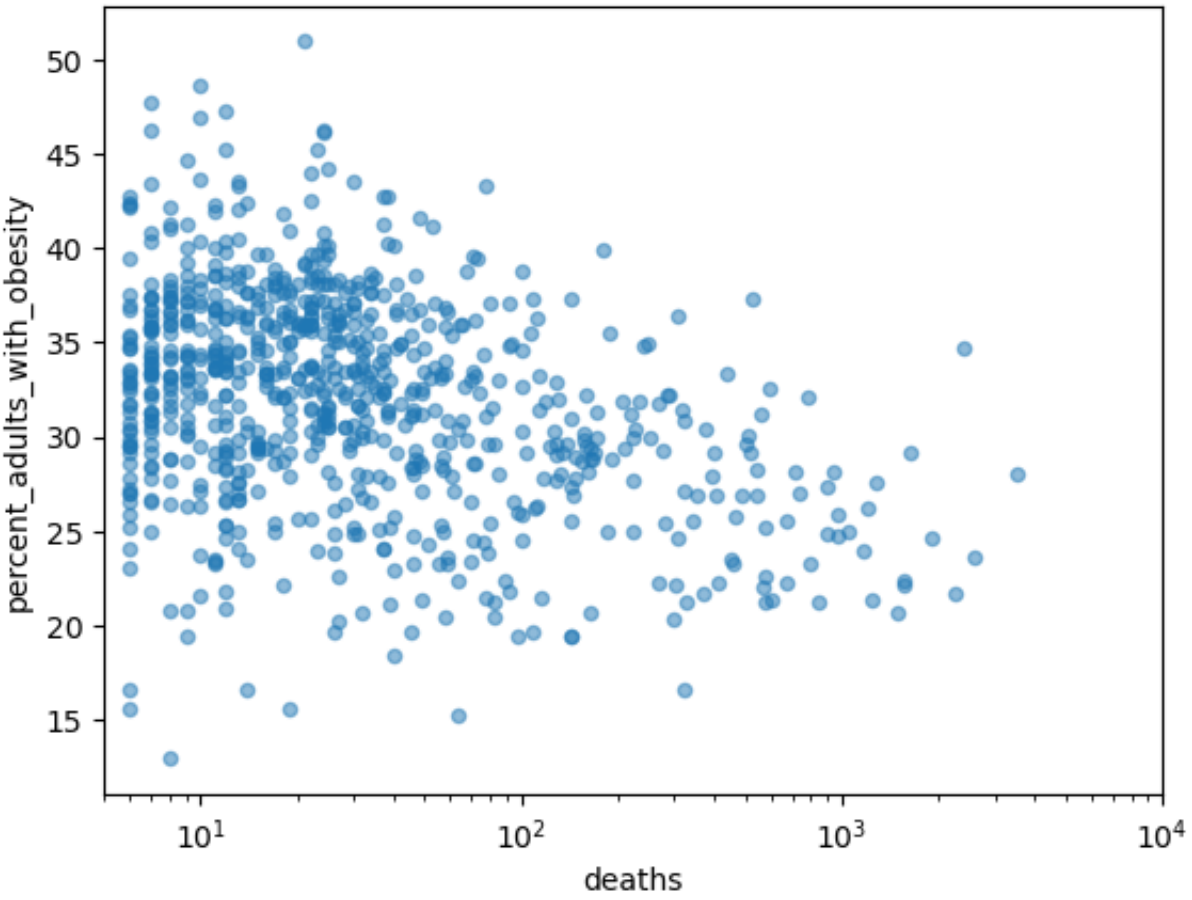
In [33]:
```
hat_filter.plot(x= 'deaths', y = 'percent_adults_with_diabetes', kind = 'sca
                logx = True, alpha = .5, xlim = (5,1e4))
```

Out[33]:
```
<AxesSubplot:xlabel='deaths', ylabel='percent_adults_with_diabetes'>
```



In [34]:
```
hat_filter.plot(x= 'deaths', y = 'percent_adults_with_obesity', kind = 'scat
                logx = True, alpha = .5, xlim = (5,1e4))
```

Out[34]:
```
<AxesSubplot:xlabel='deaths', ylabel='percent_adults_with_obesity'>
```



In [35]:
```
health_totals.corr()
```

Out[35]:

	cases	deaths	percent_fair_or_poor_health	percent_sn
cases	1.000000	0.961989	-0.067480	-0.1
deaths	0.961989	1.000000	-0.075720	-0.
percent_fair_or_poor_health	-0.067480	-0.075720	1.000000	0.7
percent_smokers	-0.153402	-0.143611	0.733166	1.0
percent_adults_with_obesity	-0.174721	-0.171740	0.437596	0.5
percent_excessive_drinking	0.092551	0.090817	-0.663194	-0.4
income_ratio	0.105900	0.117204	0.548911	0.4
percent_adults_with_diabetes	-0.115397	-0.107484	0.485468	0.4

In [36]:
```
hat_filter = health_totals[health_totals.deaths > 5]
hat_filter.corr()
```

Out[36]:

	cases	deaths	percent_fair_or_poor_health	percent_sr
cases	1.000000	0.962790	-0.110231	-0.2
deaths	0.962790	1.000000	-0.127434	-0.2
percent_fair_or_poor_health	-0.110231	-0.127434	1.000000	0.1
percent_smokers	-0.260420	-0.240905	0.733144	1.0
percent_adults_with_obesity	-0.275905	-0.270842	0.593747	0.6
percent_excessive_drinking	0.132584	0.131229	-0.661982	-0.4
income_ratio	0.150393	0.170120	0.513058	0.3
percent_adults_with_diabetes	-0.196161	-0.182626	0.586522	0.6

Here, we can see that there is a pretty obvious relationship between cases and deaths, likely since you have to have a case of COVID prior to dying from COVID. This chart also provides some additional insight to the realtionship between cases/deaths and our vaiables of interest. As we saw in previous graphs, our comparisons so far have been weak in terms of relationship strength, but the chart does shed light on other possible relationships between variables, for instance, a positive relationship is shown between "percent_smokers" and "percent_fair_or_poor_health", this is common knowledge, but interesting to see in our data.

Hypothesis Testing

To ensure that the relationships shown above are statistically reinforced, and that the probability that any effects are not occuring by chance, hypothesis testing is performed.

In [37]:
```
class HypothesisTest(object):

    def __init__(self, data):
        self.data = data
        self.MakeModel()
        self.actual = self.TestStatistic(data)

    def PValue(self, iters=1000):
        self.test_stats = [self.TestStatistic(self.RunModel())
                           for _ in range(iters)]

        count = sum(1 for x in self.test_stats if x >= self.actual)
        return count / iters

    def TestStatistic(self, data):
        raise UnimplementedMethodException()

    def MakeModel(self):
        pass

    def RunModel(self):
        raise UnimplementedMethodException()
```

In [38]:
```
class CorrelationPermute(thinkstats2.HypothesisTest):

    def TestStatistic(self, data):
        xs, ys = data
        test_stat = abs(thinkstats2.Corr(xs, ys))
        return test_stat

    def RunModel(self):
        xs, ys = self.data
        xs = np.random.permutation(xs)
        return xs, ys
```

Correlation: percent_adults_with_obesity

In [39]:
```
data = hat_filter.deaths, hat_filter.percent_adults_with_obesity
ht = CorrelationPermute(data)
pvalue = ht.PValue()
pvalue
```

Out[39]:
```
0.0
```

Our P-value in this case is less than 0.001.

In [40]:
```
import statsmodels.api as sm
hat_filter = hat_filter.dropna()

y = hat_filter.deaths
X = hat_filter.percent_adults_with_obesity
model = sm.OLS(y, X).fit()
predictions = model.predict(X)
model.summary()
```

Out[40]:

OLS Regression Results

Dep. Variable:	deaths	**R-squared (uncentered):**	0.081
Model:	OLS	**Adj. R-squared (uncentered):**	0.080
Method:	Least Squares	**F-statistic:**	69.22
Date:	Sat, 03 Jun 2023	**Prob (F-statistic):**	3.89e-16
Time:	19:34:55	**Log-Likelihood:**	-5553.7
No. Observations:	786	**AIC:**	1.111e+04
Df Residuals:	785	**BIC:**	1.111e+04
Df Model:	1		
Covariance Type:	nonrobust		

	coef	std err	t	P>|t|	[0.025	0.975]
percent_adults_with_obesity	2.5794	0.310	8.320	0.000	1.971	3.188

Omnibus:	966.975	**Durbin-Watson:**	1.927
Prob(Omnibus):	0.000	**Jarque-Bera (JB):**	91329.898
Skew:	6.295	**Prob(JB):**	0.00
Kurtosis:	54.286	**Cond. No.**	1.00

Notes:
[1] R^2 is computed without centering (uncentered) since the model does not contain a constant.
[2] Standard Errors assume that the covariance matrix of the errors is correctly specified.

With a p-value < .05, we can assume that for every 1% of the county's populatio that is obese, 2.58 deaths can be expected.

In [41]:

```
y = hat_filter.deaths
X = hat_filter[['percent_adults_with_obesity', 'percent_smokers']]
model = sm.OLS(y, X).fit()
predictions = model.predict(X)
model.summary()
```

Out[41]:

OLS Regression Results

Dep. Variable:	deaths	**R-squared (uncentered):**	0.082
Model:	OLS	**Adj. R-squared (uncentered):**	0.079
Method:	Least Squares	**F-statistic:**	34.80
Date:	Sat, 03 Jun 2023	**Prob (F-statistic):**	3.31e-15
Time:	19:34:55	**Log-Likelihood:**	-5553.5
No. Observations:	786	**AIC:**	1.111e+04
Df Residuals:	784	**BIC:**	1.112e+04
Df Model:	2		
Covariance Type:	nonrobust		

	coef	std err	t	P>|t|	[0.025	0.975]
percent_adults_with_obesity	1.2392	2.056	0.603	0.547	-2.796	5.274
percent_smokers	2.5691	3.895	0.660	0.510	-5.077	10.215

Omnibus:	967.787	**Durbin-Watson:**	1.925
Prob(Omnibus):	0.000	**Jarque-Bera (JB):**	91746.810
Skew:	6.303	**Prob(JB):**	0.00
Kurtosis:	54.406	**Cond. No.**	16.0

Notes:
[1] R^2 is computed without centering (uncentered) since the model does not contain a constant.
[2] Standard Errors assume that the covariance matrix of the errors is correctly specified.

High p-values in this case suggests no relationship between deaths and percent_adults_with_obesity and percent_smokers.

In [42]:

```
y = hat_filter.deaths
X = hat_filter[['percent_adults_with_obesity', 'percent_adults_with_diabetes
model = sm.OLS(y, X).fit()
predictions = model.predict(X)
model.summary()
```

Out[42]:

OLS Regression Results

Dep. Variable:	deaths	**R-squared (uncentered):**	0.083
Model:	OLS	**Adj. R-squared (uncentered):**	0.080
Method:	Least Squares	**F-statistic:**	35.27
Date:	Sat, 03 Jun 2023	**Prob (F-statistic):**	2.15e-15
Time:	19:34:55	**Log-Likelihood:**	-5553.1
No. Observations:	786	**AIC:**	1.111e+04
Df Residuals:	784	**BIC:**	1.112e+04
Df Model:	2		
Covariance Type:	nonrobust		

	coef	std err	t	P>|t|	[0.025	0.975]
percent_adults_with_obesity	4.1786	1.435	2.911	0.004	1.361	6.996
percent_adults_with_diabetes	-4.4038	3.860	-1.141	0.254	-11.980	3.173

Omnibus:	967.428	**Durbin-Watson:**	1.921
Prob(Omnibus):	0.000	**Jarque-Bera (JB):**	91513.372
Skew:	6.300	**Prob(JB):**	0.00
Kurtosis:	54.338	**Cond. No.**	14.1

Notes:
[1] R^2 is computed without centering (uncentered) since the model does not contain a constant.
[2] Standard Errors assume that the covariance matrix of the errors is correctly specified.

In [43]:

```
y = hat_filter.deaths
X = hat_filter[['percent_adults_with_obesity', 'percent_fair_or_poor_health'
model = sm.OLS(y, X).fit()
predictions = model.predict(X)
model.summary()
```

Out[43]:

OLS Regression Results

Dep. Variable:	deaths	**R-squared (uncentered):**	0.087
Model:	OLS	**Adj. R-squared (uncentered):**	0.085
Method:	Least Squares	**F-statistic:**	37.39
Date:	Sat, 03 Jun 2023	**Prob (F-statistic):**	3.08e-16
Time:	19:34:55	**Log-Likelihood:**	-5551.1
No. Observations:	786	**AIC:**	1.111e+04
Df Residuals:	784	**BIC:**	1.112e+04
Df Model:	2		
Covariance Type:	nonrobust		

	coef	std err	t	P>|t|	[0.025	0.975]
percent_adults_with_obesity	-0.8618	1.540	-0.560	0.576	-3.885	2.161
percent_fair_or_poor_health	6.3026	2.763	2.281	0.023	0.879	11.726

Omnibus:	964.791	**Durbin-Watson:**	1.925
Prob(Omnibus):	0.000	**Jarque-Bera (JB):**	91146.118
Skew:	6.268	**Prob(JB):**	0.00
Kurtosis:	54.244	**Cond. No.**	11.6

Notes:
[1] R^2 is computed without centering (uncentered) since the model does not contain a constant.
[2] Standard Errors assume that the covariance matrix of the errors is correctly specified.

Other than in the simple regression model (death*percent_adults_with_obesity), the P-values above suggest no relationship between our dependent variable (death) and our entered variables. The Simple Linear Regression Model appears to be the best fit for our data.

Resources

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