For project 8, we will plot proportional plots.

In [1]:
```
import pandas as pd
cvpd_read_csv("https://covid.ourworldindata.org/data/owid-covid-data.csv")
c.head()
```

Out[1]:

	iso_code	continent	location	date	total_cases	new_cases	new_cases_smoothed	total_deaths	new_deaths	new_deat
0	AFG	Asia	Afghanistan	2020-02-24	1.0	1.0	NaN	NaN	NaN	
1	AFG	Asia	Afghanistan	2020-02-25	1.0	0.0	NaN	NaN	NaN	
2	AFG	Asia	Afghanistan	2020-02-26	1.0	0.0	NaN	NaN	NaN	
3	AFG	Asia	Afghanistan	2020-02-27	1.0	0.0	NaN	NaN	NaN	
4	AFG	Asia	Afghanistan	2020-02-28	1.0	0.0	NaN	NaN	NaN	

5 rows × 59 columns

Now as this a very big data we will focus on the dataset of united states. As a result we will filter out all other data

In [2]:
```
#time series plot for USA
dat_USA = c[c['iso_code']=="USA"]
dat_USA.shape
dat_USA.head()
```

Out[2]:

	iso_code	continent	location	date	total_cases	new_cases	new_cases_smoothed	total_deaths	new_deaths	new_de
74954	USA	North America	United States	2020-01-22	1.0	NaN	NaN	NaN	NaN	
74955	USA	North America	United States	2020-01-23	1.0	0.0	NaN	NaN	NaN	
74956	USA	North America	United States	2020-01-24	2.0	1.0	NaN	NaN	NaN	
74957	USA	North America	United States	2020-01-25	2.0	0.0	NaN	NaN	NaN	
74958	USA	North America	United States	2020-01-26	5.0	3.0	NaN	NaN	NaN	

5 rows × 59 columns

In [3]:
```
dat_USA.columns
```

Out[3]:
```
Index(['iso_code', 'continent', 'location', 'date', 'total_cases', 'new_cases',
       'new_cases_smoothed', 'total_deaths', 'new_deaths',
       'new_deaths_smoothed', 'total_cases_per_million',
       'new_cases_per_million', 'new_cases_smoothed_per_million',
       'total_deaths_per_million', 'new_deaths_per_million',
       'new_deaths_smoothed_per_million', 'reproduction_rate', 'icu_patients',
       'icu_patients_per_million', 'hosp_patients',
       'hosp_patients_per_million', 'weekly_icu_admissions',
       'weekly_icu_admissions_per_million', 'weekly_hosp_admissions',
       'weekly_hosp_admissions_per_million', 'new_tests', 'total_tests',
       'total_tests_per_thousand', 'new_tests_per_thousand',
       'new_tests_smoothed', 'new_tests_smoothed_per_thousand',
       'positive_rate', 'tests_per_case', 'tests_units', 'total_vaccinations',
       'people_vaccinated', 'people_fully_vaccinated', 'new_vaccinations',
       'new_vaccinations_smoothed', 'total_vaccinations_per_hundred',
       'people_vaccinated_per_hundred', 'people_fully_vaccinated_per_hundred',
       'new_vaccinations_smoothed_per_million', 'stringency_index',
       'population', 'population_density', 'median_age', 'aged_65_older',
       'aged_70_older', 'gdp_per_capita', 'extreme_poverty',
       'cardiovasc_death_rate', 'diabetes_prevalence', 'female_smokers',
       'male_smokers', 'handwashing_facilities', 'hospital_beds_per_thousand',
       'life_expectancy', 'human_development_index'],
      dtype="object")
```

In [4]:
```
#We will convert date to index for variations with time
dat_USA['date'] = pd.to_datetime(dat_USA['date'], utc=True)
dat_USA_index = dat_USA.set_index('date')
dat_USA_index.head()
```

```
C:\Users\shams\AppData\Local\Continuum\anaconda3\lib\site-packages\ipykernel_launcher.py:2: S
ettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: http://pandas.pydata.org/pandas-docs/stable/user_guide/
indexing.html#returning-a-view-versus-a-copy
```

Out[4]:

	iso_code	continent	location	total_cases	new_cases	new_cases_smoothed	total_deaths	new_deaths	new_d
date									
2020-01-22 00:00:00+00:00	USA	North America	United States	1.0	NaN	NaN	NaN	NaN	
2020-01-23 00:00:00+00:00	USA	North America	United States	1.0	0.0	NaN	NaN	NaN	
2020-01-24 00:00:00+00:00	USA	North America	United States	2.0	1.0	NaN	NaN	NaN	
2020-01-25 00:00:00+00:00	USA	North America	United States	2.0	0.0	NaN	NaN	NaN	
2020-01-26 00:00:00+00:00	USA	North America	United States	5.0	3.0	NaN	NaN	NaN	

5 rows × 58 columns

From the Pie chart we can see that patients with cardiovasc death rate is the highest, followed by smokers which indicates that the more vulnerable tun-gs is the more probability of being affected by Covid.

Now we will plot the distribution plot.

In [5]:
```
dat_USA_index['total_deaths'].resample('A').sum()
```

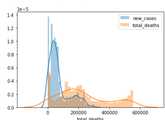
Out[5]:
```
date
2020-12-31 00:00:00+00:00    46921310.0
2021-12-31 00:00:00+00:00    43784455.0
Freq: A-DEC, Name: total_deaths, dtype: float64
```

Interestingly from the pie chart we can see that in 2021 there have been a huge amount of death just within four months, obvious enough that 2020 total death cases is more.

In [8]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
sns.distplot(dat_USA_index['new_cases'], bins=30, label='new_cases')
sns.distplot(dat_USA_index['total_deaths'], bins=30, label='total_deaths')
plt.legend()
```

```
C:\Users\shams\AppData\Local\Continuum\anaconda3\lib\site-packages\numpy\lib\histograms.py:82
4: RuntimeWarning: invalid value encountered in greater_equal
  keep = (tmp_a >= first_edge)
C:\Users\shams\AppData\Local\Continuum\anaconda3\lib\site-packages\numpy\lib\histograms.py:82
5: RuntimeWarning: invalid value encountered in less_equal
  keep &= (tmp_a <= last_edge)
C:\Users\shams\AppData\Local\Continuum\anaconda3\lib\site-packages\statsmodels\nonparametric
\kde.py:447: RuntimeWarning: invalid value encountered in greater
  X = X[np.logical_and(X > clip[0], X < clip[1])] # won't work for two columns.
C:\Users\shams\AppData\Local\Continuum\anaconda3\lib\site-packages\statsmodels\nonparametric
\kde.py:447: RuntimeWarning: invalid value encountered in less
  X = X[np.logical_and(X > clip[0], X < clip[1])] # won't work for two columns.
C:\Users\shams\AppData\Local\Continuum\anaconda3\lib\site-packages\numpy\lib\histograms.py:82
4: RuntimeWarning: invalid value encountered in greater_equal
  keep = (tmp_a >= first_edge)
C:\Users\shams\AppData\Local\Continuum\anaconda3\lib\site-packages\numpy\lib\histograms.py:82
5: RuntimeWarning: invalid value encountered in less_equal
  keep &= (tmp_a <= last_edge)
C:\Users\shams\AppData\Local\Continuum\anaconda3\lib\site-packages\statsmodels\nonparametric
\kde.py:447: RuntimeWarning: invalid value encountered in greater
  X = X[np.logical_and(X > clip[0], X < clip[1])] # won't work for two columns.
C:\Users\shams\AppData\Local\Continuum\anaconda3\lib\site-packages\statsmodels\nonparametric
\kde.py:447: RuntimeWarning: invalid value encountered in less
  X = X[np.logical_and(X > clip[0], X < clip[1])] # won't work for two columns.
```

Out[8]:
<matplotlib.legend.Legend at 0x257c4add588>

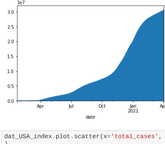


Here I plotted the distribution plot between new cases and total deaths. We can see the association between this two variables. Both the curves shows to bimodal indicating that there were two waves of covid death and cases.

In [9]:
```
dat_USA_index['total_cases'].plot(kind='area')
```

```
C:\Users\shams\AppData\Local\Continuum\anaconda3\lib\site-packages\pandas\core\arrays\datetim
es.py:1269: UserWarning: Converting to PeriodArray/Index representation will drop timezone in
formation.
  UserWarning,
```

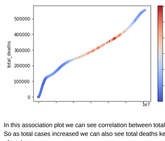
Out[9]:
<matplotlib.axes._subplots.AxesSubplot at 0x257c4b18dc8>



In [11]:
```
dat_USA_index.plot.scatter(x='total_cases', y='total_deaths', c='new_cases', cmap='coolwarm'
)
```

```
C:\Users\shams\AppData\Local\Continuum\anaconda3\lib\site-packages\pandas\plotting\_matplotli
b\tools.py:307: MatplotlibDeprecationWarning:
The rowNum attribute was deprecated in Matplotlib 3.2 and will be removed two minor releases
later. Use ax.get_subplotspec().rowspan.start instead.
  layout[ax.rowNum, ax.colNum] = ax.get_visible()
C:\Users\shams\AppData\Local\Continuum\anaconda3\lib\site-packages\pandas\plotting\_matplotli
b\tools.py:307: MatplotlibDeprecationWarning:
The colNum attribute was deprecated in Matplotlib 3.2 and will be removed two minor releases
later. Use ax.get_subplotspec().colspan.start instead.
  layout[ax.rowNum, ax.colNum] = ax.get_visible()
C:\Users\shams\AppData\Local\Continuum\anaconda3\lib\site-packages\pandas\plotting\_matplotli
b\tools.py:313: MatplotlibDeprecationWarning:
The rowNum attribute was deprecated in Matplotlib 3.2 and will be removed two minor releases
later. Use ax.get_subplotspec().rowspan.start instead.
  if not layout[ax.rowNum + 1, ax.colNum]:
C:\Users\shams\AppData\Local\Continuum\anaconda3\lib\site-packages\pandas\plotting\_matplotli
b\tools.py:313: MatplotlibDeprecationWarning:
The colNum attribute was deprecated in Matplotlib 3.2 and will be removed two minor releases
later. Use ax.get_subplotspec().colspan.start instead.
  if not layout[ax.rowNum + 1, ax.colNum]:
```

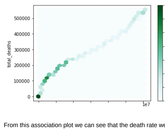
Out[11]:
<matplotlib.axes._subplots.AxesSubplot at 0x257c4f05448>



In this association plot we can see correlation between total death and new cases. Also the reddish points indicate new cases. So as total cases increased we can also see total deaths kept increasing, and there were new cases were active in the midst of total cases.

In [12]:
```
dat_USA_index.plot.hexbin(x='total_cases', y='total_deaths', gridsize=25)
```

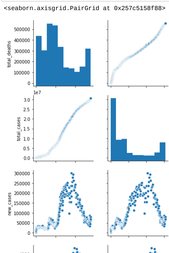
Out[12]:
<matplotlib.axes._subplots.AxesSubplot at 0x257c4fd648B>



From this association plot we can see that the death rate were dense during initial covid cases.

In [15]:
```
sns.pairplot(dat_USA_index[['total_deaths','total_cases','new_cases', 'new_deaths']])
```

Out[15]:
<seaborn.axisgrid.PairGrid at 0x257c5158f88>



I plotted the association plot for various variables. In this pair plot we can easily define the correlation between each pair of plots.