Estimation

In [1]:
```
import matplotlib.pyplot as plt
import numpy as np
import seaborn as sns
import altair as alt
import pandas as pd
import scipy.stats as ss
import statsmodels
```

Kernel density estimation

A useful density estimation technique. A "kernel" is a probability density function for a single data point. For instance, if we assume that, when we observe a single data point at x, the most likely underlying density distribution is $N(x, \sigma^2)$, then this normal distribution is our kernel. Once we have a kernel function defined, we can simply accumulate them for all data points.

Another way to think about is starting from a histogram. When we plot a histogram, we have to choose the bins. One simple way to avoid this choice is putting a box (with the area $\frac{1}{N}$, where N is the number of data points) centered at each data point. This is essentially a kernel density estimation with a rectangular kernel function.

When should we use KDE over histogram? There is no simple answer to this. As we can see in the construction of KDE from histogram, KDE resolves several issues with histogram (the sensitivity to the location of the bins and to the size of the bins) and it is in many cases a better inference method (esp. when using the Gaussian kernel). However, KDE can hide some important details (e.g., how sparse the data is) and it can mislead when the data is bounded. For instance, if data points are always non-negative and there are many data points at zero, the normal KDE will show probability distribution that stretches below 0, which is clearly inaccurate.

Import the IMDb data.

In [3]:
```
import vega_datasets

movies = vega_datasets.data.movies()
movies.head()
```

Out[3]:

	Title	US_Gross	Worldwide_Gross	US_DVD_Sales	Production_Budget	Release_Date	MPAA_Rating	Running_Time_min	Distributor	Source	Major_Genre	Creativ
0	The Land Girls	146083.0	146083.0	NaN	8000000.0	Jun 12 1998	R	NaN	Gramercy	None	None	
1	First Love, Last Rites	10876.0	10876.0	NaN	300000.0	Aug 07 1998	R	NaN	Strand	None	Drama	
2	I Married a Strange Person	203134.0	203134.0	NaN	250000.0	Aug 28 1998	None	NaN	Lionsgate	None	Comedy	
3	Let's Talk About Sex	373615.0	373615.0	NaN	300000.0	Sep 11 1998	None	NaN	Fine Line	None	Comedy	
4	Slam	1009819.0	1087521.0	NaN	1000000.0	Oct 09 1998	R	NaN	Trimark	Original Screenplay	Drama	Conter

In [4]:
```
vega_datasets.__version__
```

Out[4]:
```
'0.9.0'
```

Note: Please check your `vega_datasets` version using `vega_datasets.__version__` . If you have a version lower than `0.9.0` , you will need to check the column names in `movies.head()` and update it accordingly in the code cells below.

Q: Can you drop rows that have NaN value in either `IMDB_Rating` or `Rotten Tomatoes Rating` ?

In [ ]:
```
movies = movies.dropna(subset=['IMDB_Rating', 'Rotten_Tomatoes_Rating'])
movies.head()
```

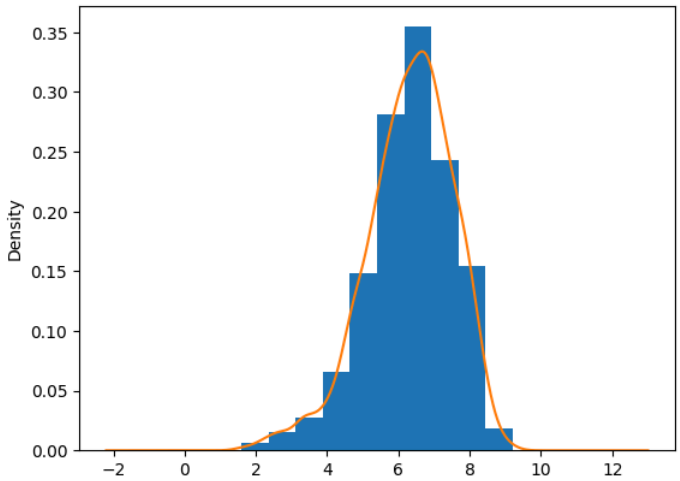
Out[ ]:

	Title	US_Gross	Worldwide_Gross	US_DVD_Sales	Production_Budget	Release_Date	MPAA_Rating	Running_Time_min	Distributor	Source	Major_Genre	Creati
4	Slam	1009819.0	1087521.0	NaN	1000000.0	Oct 09 1998	R	NaN	Trimark	Original Screenplay	Drama	Conte
8	Pirates	1641825.0	6341825.0	NaN	40000000.0	Jul 01 1986	R	NaN	None	None	None	
9	Duel in the Sun	20400000.0	20400000.0	NaN	6000000.0	Dec 31 2046	None	NaN	None	None	None	
10	Tom Jones	37600000.0	37600000.0	NaN	1000000.0	Oct 07 1963	None	NaN	None	None	None	
11	Oliver!	37402877.0	37402877.0	NaN	10000000.0	Dec 11 1968	None	NaN	Sony Pictures	None	Musical	

We can plot histogram and KDE using pandas:

In [6]:
```
movies['IMDB_Rating'].hist(bins=10, density=True)
movies['IMDB_Rating'].plot(kind='kde')
```

Out[6]:
```
<Axes: ylabel='Density'>
```

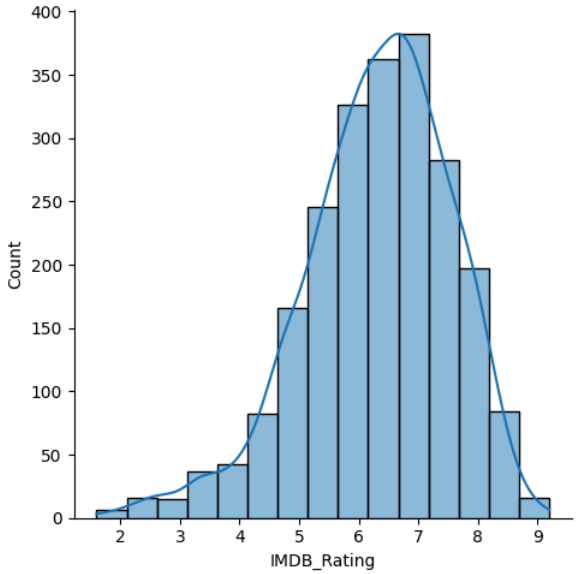


Or using seaborn:

We can use both `displot` and `histplot` to achieve this result:

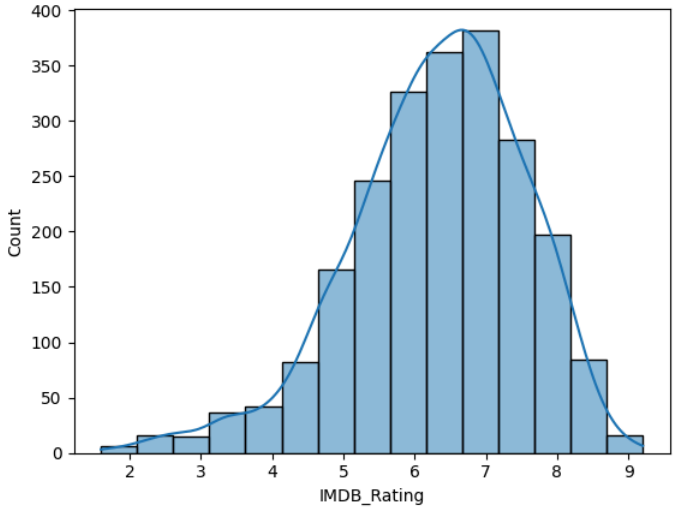
In [7]:
```
sns.displot(movies['IMDB_Rating'], bins=15, kde=True)
```

Out[7]:
```
<seaborn.axisgrid.FacetGrid at 0x13f55ed3c10>
```



In [8]:
```
sns.histplot(movies['IMDB_Rating'], bins=15, kde=True)
```

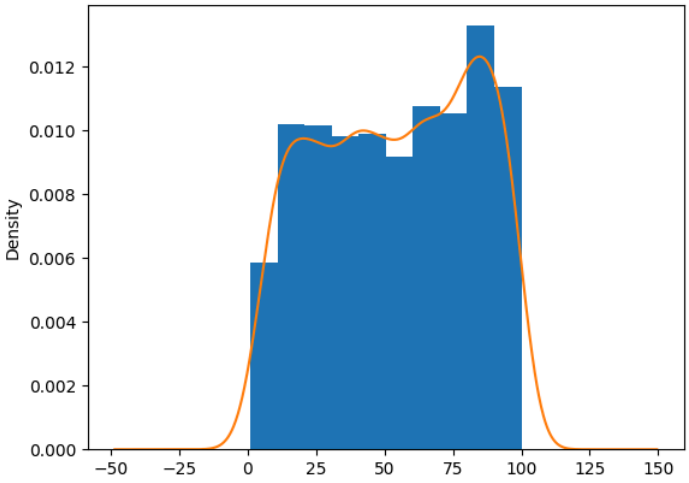
Out[8]:
```
<Axes: xlabel='IMDB_Rating', ylabel='Count'>
```



Q: Can you plot the histogram and KDE of the `Rotten Tomatoes Rating` ?

In [9]:
```
movies['Rotten_Tomatoes_Rating'].hist(bins=10, density=True)
movies['Rotten_Tomatoes_Rating'].plot(kind='kde')
```

Out[9]: <Axes: ylabel='Density'>

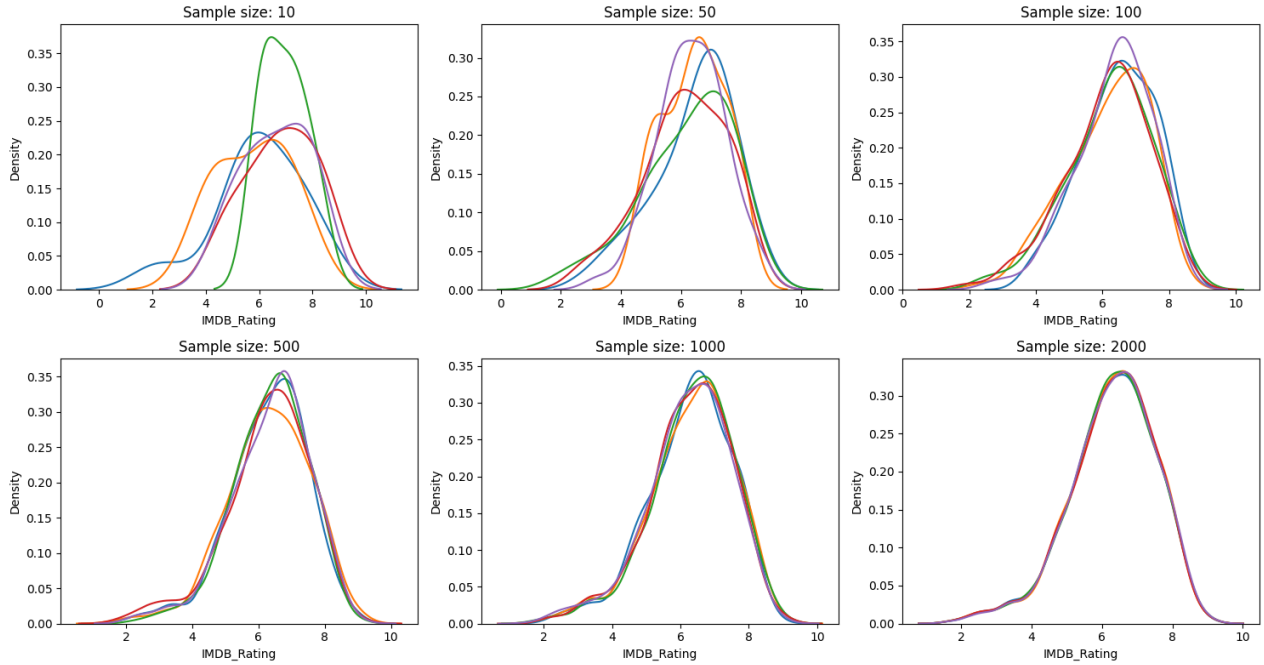


We can get a random sample using the pandas' **`sample()`** (http://pandas.pydata.org/pandas-docs/stable/generated/pandas.DataFrame.sample.html) function. The **`kdeplot()`** (https://stanford.edu/~mwaskom/software/seaborn/generated/seaborn.kdeplot.html) function in seaborn provides many options to do KDE. Let's sample some data points and see how does KDE plot changes with the size of the samples.

Seaborn recently deprecated the use of all non-gaussian kernel types and now only support Gaussian kernel.

In [11]:
```
f = plt.figure(figsize=(15,8))
plt.xlim(0, 10)

sample_sizes = [10, 50, 100, 500, 1000, 2000]
for i, N in enumerate(sample_sizes, 1):
    plt.subplot(2,3,i)
    plt.title("Sample size: {}".format(N))
    for j in range(5):
        s = movies['IMDB_Rating'].sample(N)
        sns.kdeplot(s, legend=False)
plt.tight_layout()
```

```
C:\Users\Stefan\AppData\Local\Temp\ipykernel_11448\918431562.py:6: MatplotlibDeprecationWarning: Auto-removal of overlapping axes is depr
ecated since 3.6 and will be removed two minor releases later; explicitly call ax.remove() as needed.
  plt.subplot(2,3,i)
```



We can also draw KDE plots using scikit-learn to change kernel functions

First, we need points to score across.

- Remember the np.linspace() function?
- IMDB scores are only between 1 and 10. Let's create 1000 points between 1 and 10.

In [15]:
```
X_vals = np.linspace(1,10,1000)
X_vals[:10]
```

Out[15]:
```
array([1.        , 1.00900901, 1.01801802, 1.02702703, 1.03603604,
       1.04504505, 1.05405405, 1.06306306, 1.07207207, 1.08108108])
```

In [16]:
```
X_vals.shape
```

Out[16]:
```
(1000,)
```

Our array needs to have 2 dimensions for score_samples() to work. Let's add another dimension to our array using np.newaxis.

In [17]:
```
X_plot = X_vals[:, np.newaxis]
X_plot[0:10]
```

Out[17]:
```
array([[1.        ],
       [1.00900901],
       [1.01801802],
       [1.02702703],
       [1.03603604],
       [1.04504505],
       [1.05405405],
       [1.06306306],
       [1.07207207],
       [1.08108108]])
```

In [18]:
```
X_plot.shape
```

Out[18]:
```
(1000, 1)
```

The KernelDensity function in scikit-learn needs a 2d array for the samples when we fit to the different kernels. Multidimensional scaling is deprecated for pandas series. We can cast the series to a numpy array before adding another dimension to solve this issue (if you're unfamiliar with casting, don't worry it's done for you below). You only need to implement code where instructed by the TODO.

NOTE: If you're unfamiliar with the term `cast` in regards to datatypes. It just means when we take some existing data of say type `x` and reinterpret the same data as a different type `y`. But we don't change the data itself, just how it's interpreted by the computer/compiler/interpreter.

In [26]:
```
sample = movies['IMDB_Rating'].sample(5)
print(sample)
print(type(sample))
print(sample.shape)
```

```
2539    6.4
2004    7.4
41      7.6
306     7.9
777     7.1
Name: IMDB_Rating, dtype: float64
<class 'pandas.core.series.Series'>
(5,)
```

In [27]:
```
# This is where we cast to a numpy array
sample = np.array(sample)
print(sample)
print(type(sample))
print(sample.shape)
```

```
[6.4 7.4 7.6 7.9 7.1]
<class 'numpy.ndarray'>
(5,)
```

In [28]:
```
sample = sample[:,np.newaxis]
sample
```

Out[28]:
```
array([[6.4],
       [7.4],
       [7.6],
       [7.9],
       [7.1]])
```

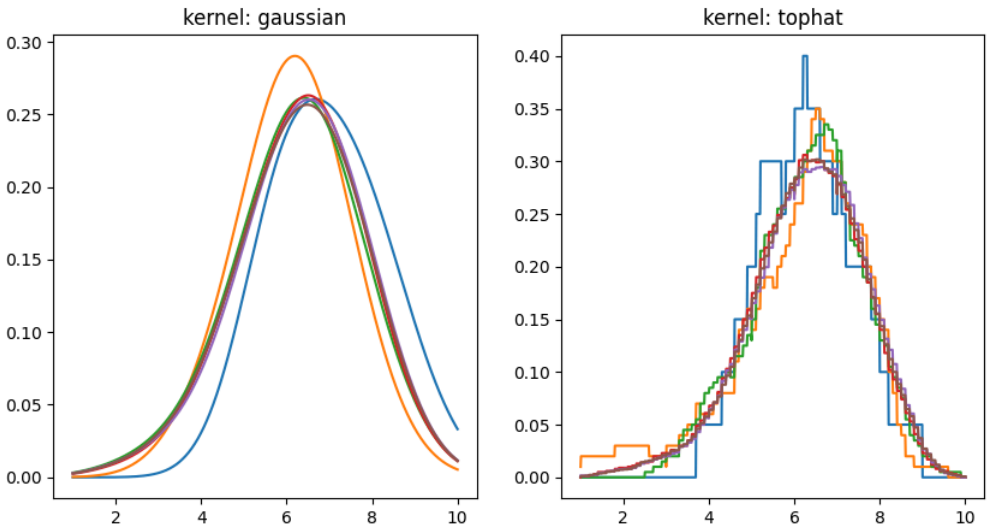
In [29]:
```
print(sample)
print(type(sample))
print(sample.shape)
```

```
[[6.4]
 [7.4]
 [7.6]
 [7.9]
 [7.1]]
<class 'numpy.ndarray'>
(5, 1)
```

Now, let's plot using the `tophat` and `gaussian` kernels using the different sample sizes we used before. We'll do this using scikit-learn's `KernelDensity()` function.

In [30]:
```
from sklearn.neighbors import KernelDensity
sample_sizes = [10, 50, 100, 500, 1000, 2000]

def plot_kde(X_plot, sample_sizes, movies, kernel='gaussian'):
    for sample_size in sample_sizes:
        sample = np.array(movies['IMDB_Rating'].sample(sample_size))[:, np.newaxis]
        kde = KernelDensity(kernel=kernel).fit(sample)
        log_density = kde.score_samples(X_plot)
        plt.plot(X_plot[:, 0], np.exp(log_density), '-')

fig, ax = plt.subplots(figsize=(10,5))

# Let's look at the gaussian kernel like before
# put it in the first spot on a 1x2 grid
plt.subplot(1,2,1)
plt.title("kernel: {}".format('gaussian'))
plot_kde(X_plot, sample_sizes, movies)
# Now let's look at the tophat kernel
# put it in the second spot on a 1x2 grid
plt.subplot(1,2,2)
plt.title("kernel: {}".format('tophat'))
plot_kde(X_plot, sample_sizes, movies, kernel='tophat')
```

```
C:\Users\Stefan\AppData\Local\Temp\ipykernel_11448\2345161141.py:15: MatplotlibDeprecationWarning: Auto-removal of overlapping axes is de
precated since 3.6 and will be removed two minor releases later; explicitly call ax.remove() as needed.
  plt.subplot(1,2,1)
```



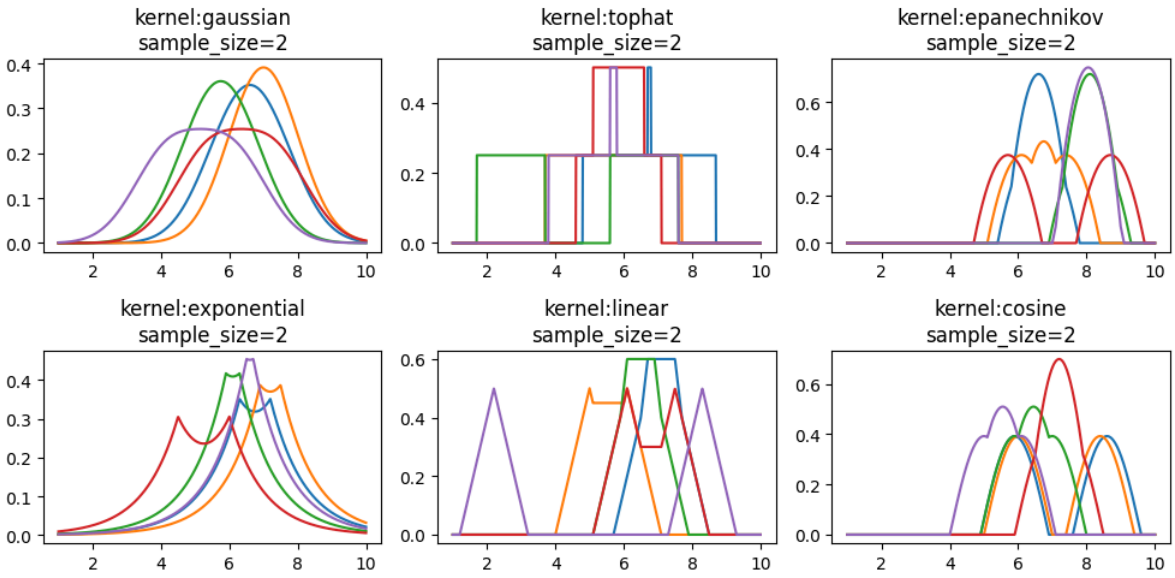
Let's try all kernel types using scikit-learn's `KernelDensity()` . Plot a 2x3 grid, however, instead of changing sample sizes like above, make each plot use the 6 different kernels supported by scikit-learn. Keep the sample size to 2 so we can more easily see the different distribution shapes. Also, draw a different sample (of 2) 5 times like the plots we drew with seaborn above.

Helpful links:

- https://scikit-learn.org/stable/modules/density.html (https://scikit-learn.org/stable/modules/density.html)
- https://scikit-learn.org/stable/modules/generated/sklearn.neighbors.KernelDensity.html#sklearn.neighbors.KernelDensity (https://scikit-learn.org/stable/modules/generated/sklearn.neighbors.KernelDensity.html#sklearn.neighbors.KernelDensity)
- https://scikit-learn.org/stable/auto_examples/neighbors/plot_kde_1d.html (https://scikit-learn.org/stable/auto_examples/neighbors/plot_kde_1d.html)

In [35]:
```
from sklearn.neighbors import KernelDensity
kernels = ['gaussian', 'tophat', 'epanechnikov', 'exponential', 'linear', 'cosine']
sample_sizes = [2]

def plot_kde(X_plot, sample_sizes, movies, kernel):
    for sample_size in sample_sizes:
        for i in range(5):
            sample = np.array(movies['IMDB_Rating'].sample(sample_size))[:, np.newaxis]
            kde = KernelDensity(kernel=kernel).fit(sample)
            log_density = kde.score_samples(X_plot)
            plt.plot(X_plot[:, 0], np.exp(log_density), '-')

fig, ax = plt.subplots(figsize=(10,5))

for i, kernel in enumerate(kernels):
    plt.subplot(2,3,i+1)
    plt.title(f"kernel:{kernel}\nsample_size=2")
    plot_kde(X_plot, sample_sizes, movies, kernel)
plt.tight_layout()
```

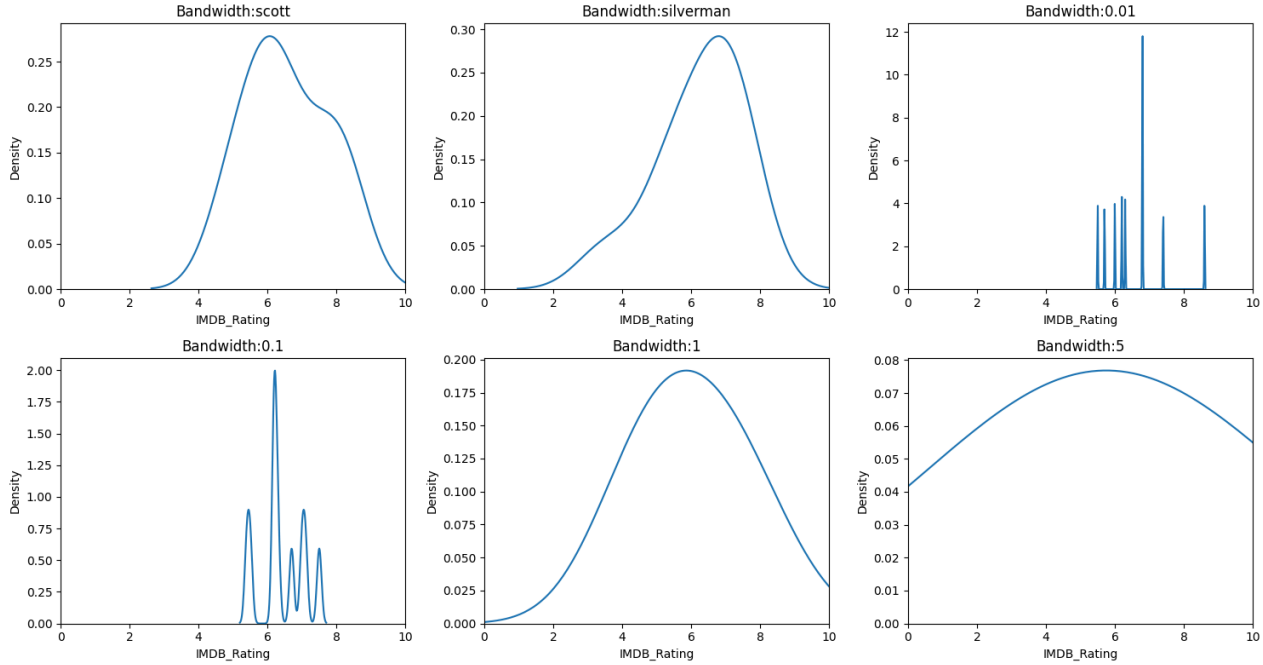
```
C:\Users\Stefan\AppData\Local\Temp\ipykernel_11448\2267816964.py:16: MatplotlibDeprecationWarning: Auto-removal of overlapping axes is de
precated since 3.6 and will be removed two minor releases later; explicitly call ax.remove() as needed.
  plt.subplot(2,3,i+1)
```



Q: Let's use Seaborn again. We can play with the bandwidth option. Make sure to set the `xlim` so that all plots have the same x range, so that we can compare.

In [44]:
```
bw_method = ['scott', 'silverman', 0.01, 0.1, 1, 5]
sample_size = 10

fig, ax = plt.subplots(figsize=(15,8))

for i in range(6):
    plt.subplot(2,3,i+1)
    plt.title(f"Bandwidth:{bw_method[i]}")
    sns.kdeplot(movies['IMDB_Rating'].sample(sample_size), bw_method=bw_method[i])
    plt.xlim(0, 10)
plt.tight_layout()
```

```
C:\Users\Stefan\AppData\Local\Temp\ipykernel_11448\1001762512.py:7: MatplotlibDeprecationWarning: Auto-removal of overlapping axes is dep
recated since 3.6 and will be removed two minor releases later; explicitly call ax.remove() as needed.
  plt.subplot(2,3,i+1)
```



Q: What's your takeaway? Explain how bandwidth affects the result of your visualization.

- A smaller bandwidth = rough curbe, can identify peaks
- A larger bandwidth = produces too smooth results, hiding the modality of the distribution

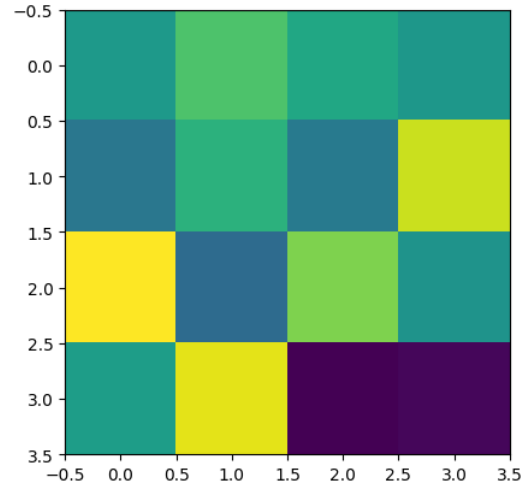
Interpolation

One area where interpolation is used a lot is image processing. Play with it!

https://matplotlib.org/examples/images_contours_and_fields/interpolation_methods.html (https://matplotlib.org/examples/images_contours_and_fields/interpolation_methods.html)

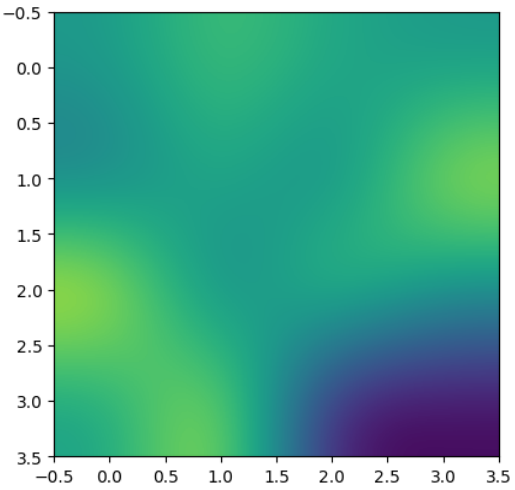
In [45]:
```
methods = [None, 'none', 'nearest', 'bilinear', 'bicubic', 'spline16',
           'spline36', 'hanning', 'hamming', 'hermite', 'kaiser', 'quadric',
           'catrom', 'gaussian', 'bessel', 'mitchell', 'sinc', 'lanczos']
np.random.seed(0)
grid = np.random.rand(4, 4)

plt.imshow(grid, interpolation=None, cmap='viridis')
```

Out[45]:
```
<matplotlib.image.AxesImage at 0x13f67f42710>
```



In [46]:
```
plt.imshow(grid, interpolation='bicubic', cmap='viridis')
```

Out[46]:
```
<matplotlib.image.AxesImage at 0x13f70d4b250>
```



Let's look at some time series data.

In [47]:
```
co2 = vega_datasets.data.co2_concentration()
co2.head()
```

Out[47]:

	Date	CO2
0	1958-03-01	315.70
1	1958-04-01	317.46
2	1958-05-01	317.51
3	1958-07-01	315.86
4	1958-08-01	314.93

Note: If your `vega_datasets` version is below `0.9.0`, you may notice another column named `adjusted CO2` in the output above. If yes, please remove this column by uncommenting the code cell below.

In [ ]:
```
# co2.drop(['adjusted CO2'], axis=1, inplace=True)
```

In [48]:
```
co2.Date.dtype
```

Out[48]:
```
dtype('O')
```

The `Date` colume is stored as strings. Let's convert it to `datetime` so that we can manipulate.

In [49]:
```
pd.to_datetime(co2.Date).head()
```

Out[49]:
```
0   1958-03-01
1   1958-04-01
2   1958-05-01
3   1958-07-01
4   1958-08-01
Name: Date, dtype: datetime64[ns]
```

In [50]:
```
co2.Date = pd.to_datetime(co2.Date)
```

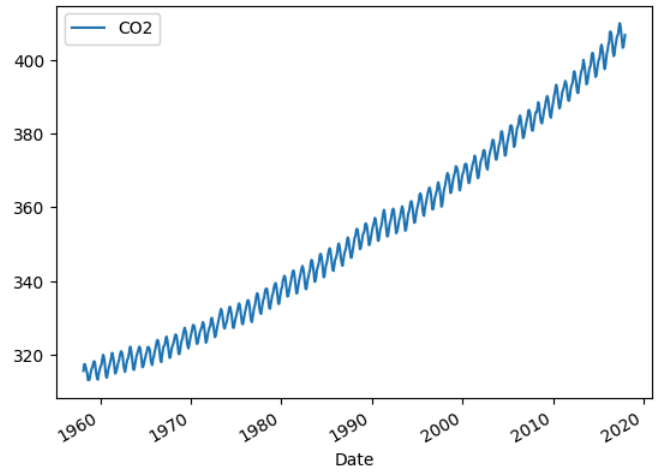
In [51]:
```
co2.set_index('Date', inplace=True)
co2.head()
```

Out[51]:

	CO2
Date	
1958-03-01	315.70
1958-04-01	317.46
1958-05-01	317.51
1958-07-01	315.86
1958-08-01	314.93

In [52]:
```
co2.plot()
```

Out[52]: <Axes: xlabel='Date'>

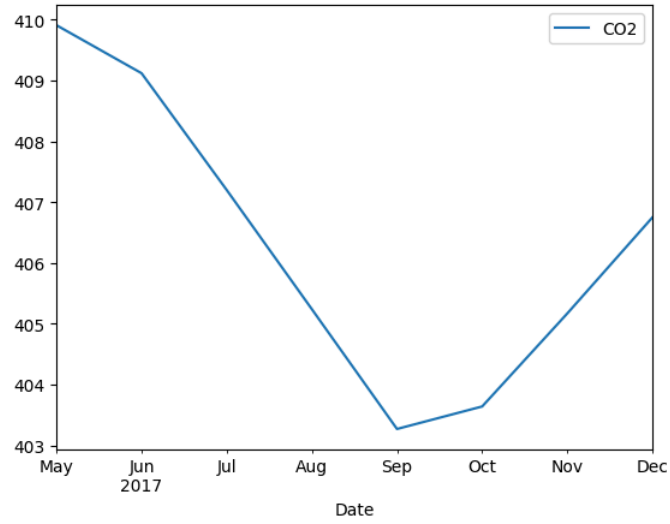


:(...

In [53]:
```
recent_co2 = co2.tail(8)
```

In [54]:
```
recent_co2.plot()
```

Out[54]: <Axes: xlabel='Date'>



This standard line chart above can be considered as a chart with linear interpolation between data points.

The data contains measurements at the resolution of about a month. Let's up-sample the data. This process create new rows that fill the gap between data points. We can use `interpolate()` function to fill the gaps.

In [55]:
```
upsampled = recent_co2.resample('D')
upsampled.interpolate().head()
```

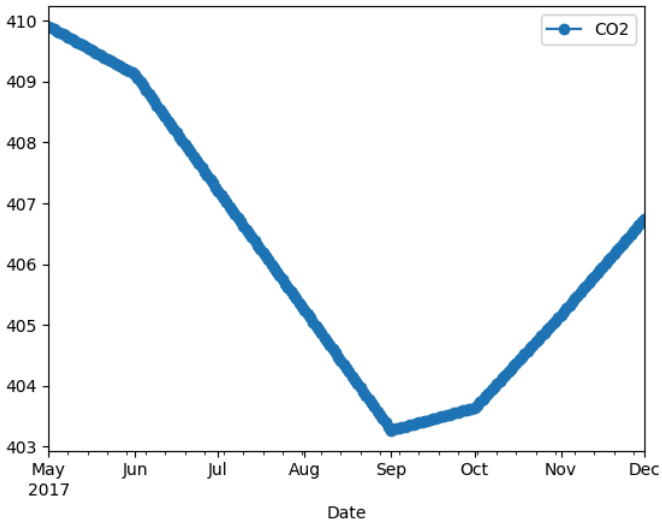
Out[55]:

	CO2
Date	
2017-05-01	409.910000
2017-05-02	409.884516
2017-05-03	409.859032
2017-05-04	409.833548
2017-05-05	409.808065

If we do `linear` interpolation, we get more or less the same plot, but just with more points.

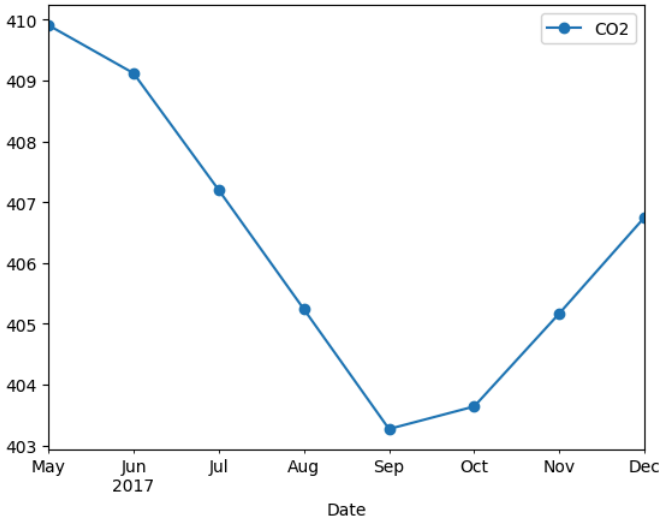
In [56]:
```
recent_co2.resample('D').interpolate(method='linear').plot(style='o-')
```

Out[56]: <Axes: xlabel='Date'>



In [57]:
```
recent_co2.plot(style='o-')
```

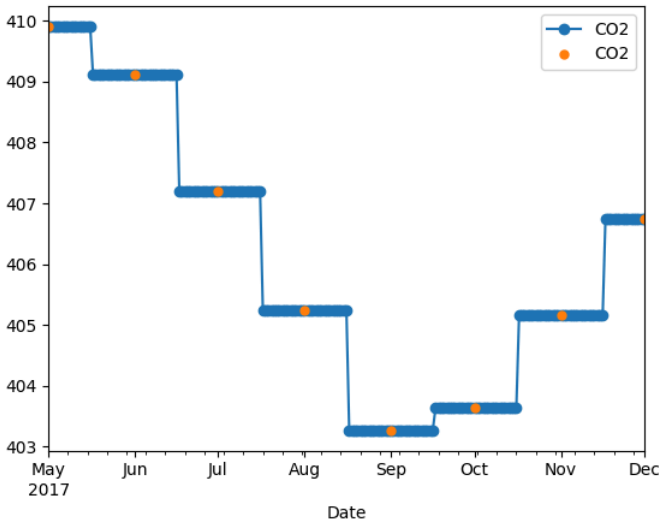
Out[57]: <Axes: xlabel='Date'>



`Nearest` interpolation is just a process of assigning the nearest value to each missing rows.

In [58]:
```
ax = recent_co2.resample('D').interpolate(method='nearest').plot(style='o-')
recent_co2.plot(ax=ax, style='o', ms=5)
```

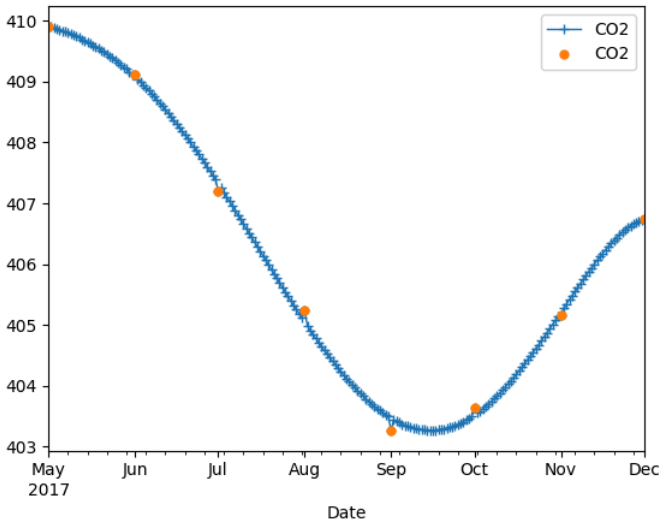
Out[58]: <Axes: xlabel='Date'>



Let's try a spline too.

In [59]:
```
ax = recent_co2.resample('D').interpolate(method='spline', order=5).plot(style='+-', lw=1)
recent_co2.plot(ax=ax, style='o', ms=5)
```

Out[59]: <Axes: xlabel='Date'>



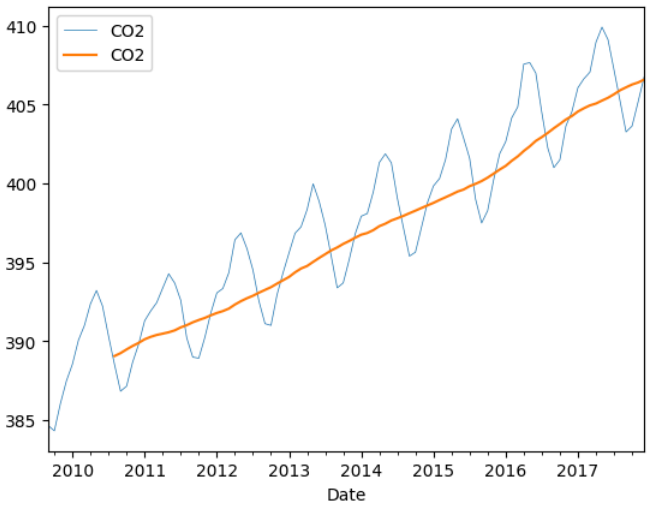
Moving average

Pandas has a nice method called `rolling()` : https://pandas.pydata.org/pandas-docs/stable/generated/pandas.DataFrame.rolling.html (https://pandas.pydata.org/pandas-docs/stable/generated/pandas.DataFrame.rolling.html)

It lets you do operations on the `rolling` windows. For instance, if you want to calculate the moving average, you can simply

In [60]:
```
ax = co2[-100:].plot(lw=0.5)
co2[-100:].rolling(12).mean().plot(ax=ax)
```

Out[60]: <Axes: xlabel='Date'>

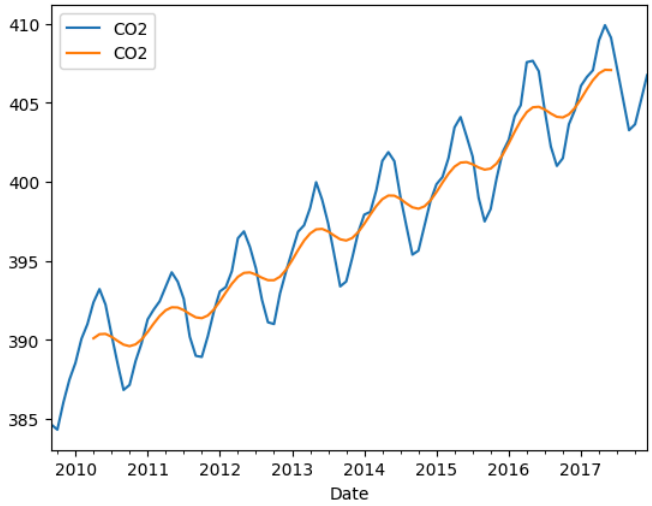


By default, it consider every data point inside each window equally (`win_type=None`) but there are many window types supported by `scipy` . Also by default, the mean value is put at the right end of the window (trailing average).

Q: can you create a plot with `triang` window type and centered average?

In [66]:
```
ax = co2[-100:].plot()
co2[-100:].rolling(14, win_type='triang', center=True).mean().plot(ax=ax)
```

Out[66]:
```
<Axes: xlabel='Date'>
```



Examining relationsips

Let's look at the data set Anscombe's quartet (https://en.wikipedia.org/wiki/Anscombe%27s_quartet)? Actually, the dataset is not only included in `vega_datasets` but also in `seaborn`.

In [67]:
```
df = sns.load_dataset("anscombe")
df.head()
```

Out[67]:

	dataset	x	y
0	I	10.0	8.04
1	I	8.0	6.95
2	I	13.0	7.58
3	I	9.0	8.81
4	I	11.0	8.33

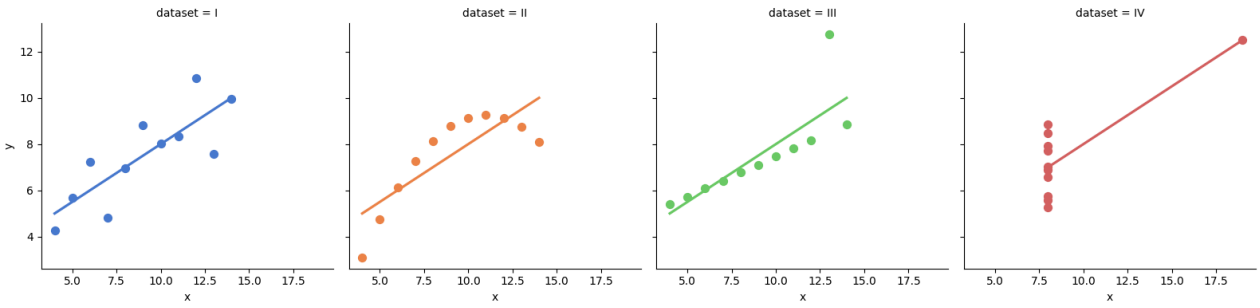
All four datasets are in this single data frame and the 'dataset' indicator is one of the columns. This is a form often called tidy data (http://vita.had.co.nz/papers/tidy-data.pdf), which is easy to manipulate and plot. In tidy data, each row is an observation and columns are the properties of the observation. Seaborn makes use of the tidy form. Using seaborn's `lmplot`, you can very quickly examine relationships between variables, separated by some facets of the dataset.

https://seaborn.pydata.org/generated/seaborn.lmplot.html (https://seaborn.pydata.org/generated/seaborn.lmplot.html)

Q: Can you produce the plot below using `lmplot()` ?

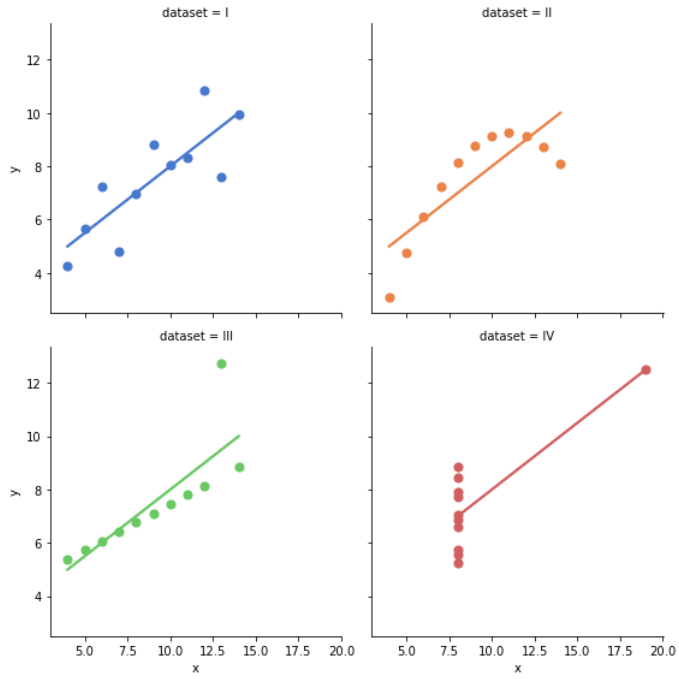
In [ ]:
```
# plotting parameters you can use
palette = "muted"
scatter_kws={"s": 50, "alpha": 1}
ci=None
height=4

sns.lmplot(df, x="x",y="y", hue="dataset", col="dataset", palette=palette, scatter_kws=scatter_kws, ci=ci, height=height)
```

Out[ ]:
```
<seaborn.axisgrid.FacetGrid at 0x13f73be3250>
```



In [ ]:
```
# plotting parameters you can use
palette = "muted"
scatter_kws={"s": 50, "alpha": 1}
ci=None
height=4

# TODO: Implement
```

Out[ ]:
```
<seaborn.axisgrid.FacetGrid at 0x7fc6c9f90d10>
```



Q: Let's look at the relationship between `IMDB_Rating` and `Rotten Tomatoes Rating` in the `movies` dataset, separated with respect to `MPAA Rating` . Put 4 plots in a row.

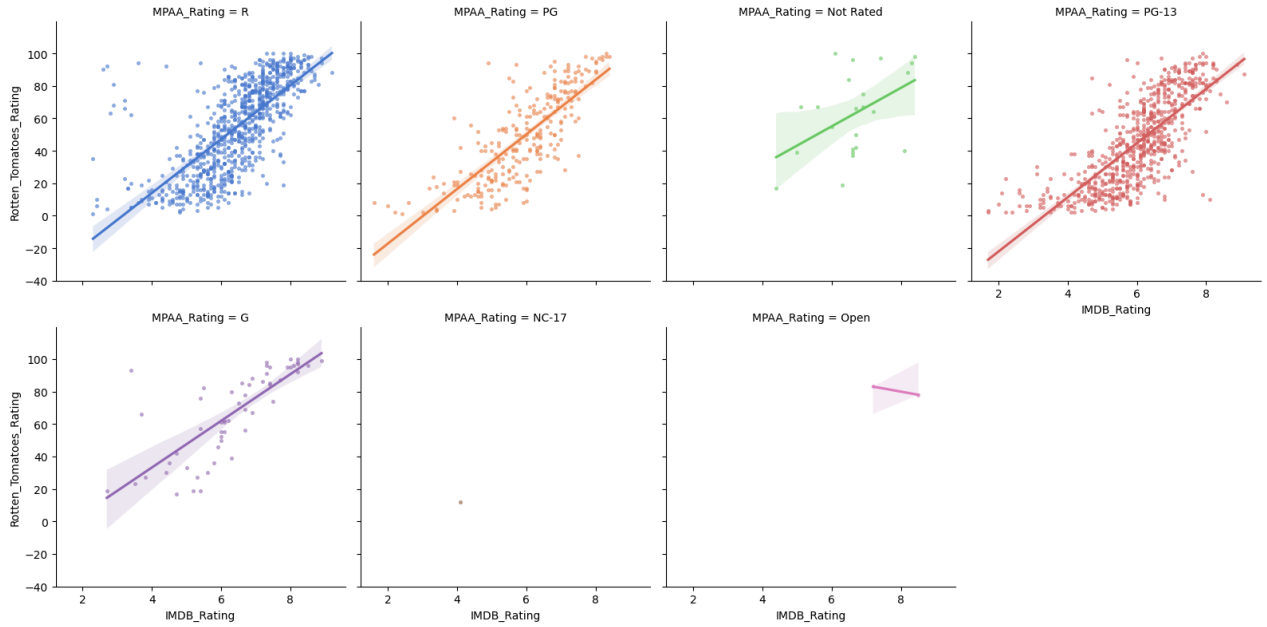
In [3]:
```
import vega_datasets
movies = vega_datasets.data.movies()
movies = movies.dropna(subset=['IMDB_Rating', 'Rotten_Tomatoes_Rating', 'MPAA_Rating'])
movies.head()
```

Out[3]:

	Title	US_Gross	Worldwide_Gross	US_DVD_Sales	Production_Budget	Release_Date	MPAA_Rating	Running_Time_min	Distributor	Source	Major_Genre	Cr
4	Slam	1009819.0	1087521.0	NaN	1000000.0	Oct 09 1998	R	NaN	Trimark	Original Screenplay	Drama	C
8	Pirates	1641825.0	6341825.0	NaN	40000000.0	Jul 01 1986	R	NaN	None	None	None	
21	1776	0.0	0.0	NaN	4000000.0	Nov 09 1972	PG	NaN	Sony/Columbia	Based on Play	Drama	
28	Twin Falls Idaho	985341.0	1027228.0	NaN	500000.0	Jul 30 1999	R	NaN	Sony Pictures Classics	Original Screenplay	Drama	C
31	3 Ninjas Kick Back	11744960.0	11744960.0	NaN	20000000.0	May 06 1994	PG	NaN	Walt Disney Pictures	Original Screenplay	Action	C

In [10]:
```
palette = "muted"
scatter_kws={"s": 7, "alpha": 0.5}
ci=None
height=4
sns.lmplot(movies, x="IMDB_Rating",y="Rotten_Tomatoes_Rating",
           hue="MPAA_Rating", col="MPAA_Rating", col_wrap=4, palette=palette,
           scatter_kws=scatter_kws, height=height)
```

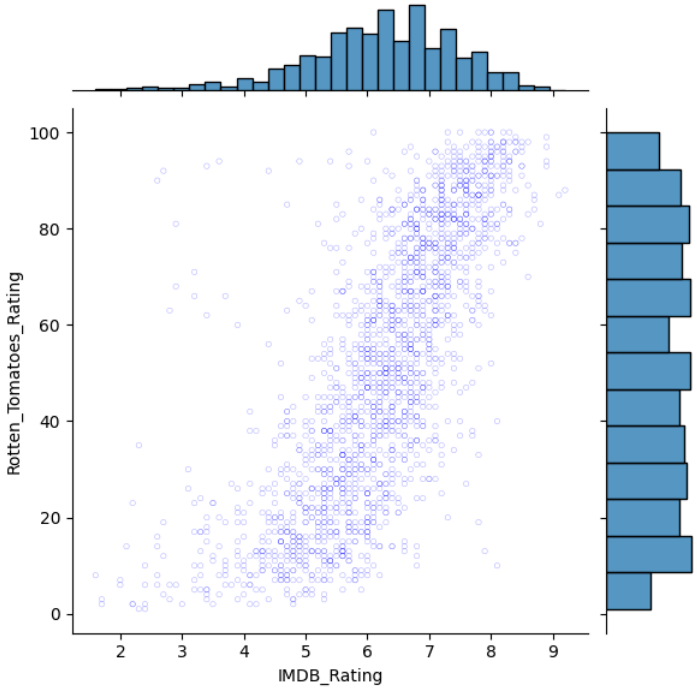
Out[10]:
```
<seaborn.axisgrid.FacetGrid at 0x1b84f525810>
```



It may be interesting to dig up what are the movies that have high Rotten Tomatoes rating and low IMDB rating (and vice versa)!

Another useful method for examining relationships is **`jointplot()`** (http://seaborn.pydata.org/generated/seaborn.jointplot.html), which produces a scatter plot with two marginal histograms.

In [11]:
```
g = sns.jointplot(x = movies['IMDB_Rating'], y = movies['Rotten_Tomatoes_Rating'], s=10, alpha=0.4, facecolors='none', edgecolor='b')
```



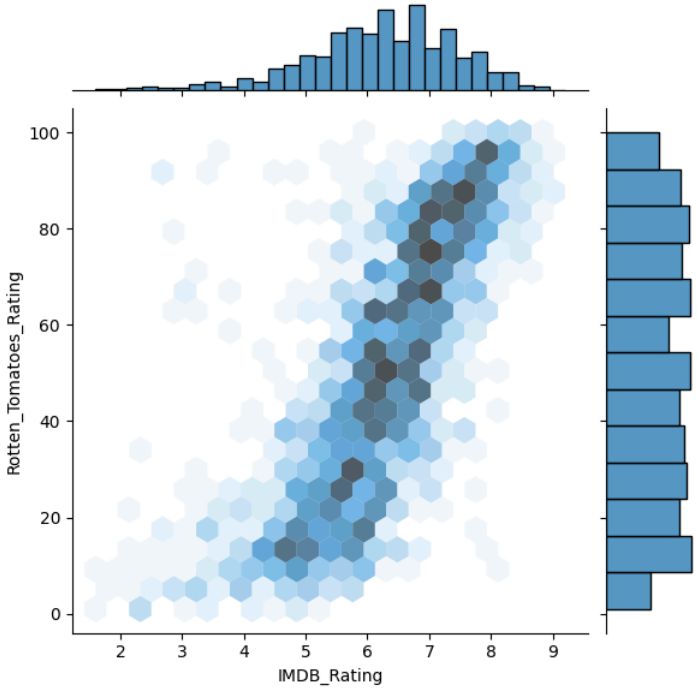
Hexbin density plot

In 2D, *heatmap* can be considered as a color-based histogram. You divide the space into bins and show the frequency with colors. A common binning method is the hexagonal bin.

We can again use the **`jointplot()`** (http://stanford.edu/~mwaskom/software/seaborn/generated/seaborn.jointplot.html) and setting the `kind` to be `hex`.

Q: Can you create one?

In [17]:
```
g = sns.jointplot(x = movies['IMDB_Rating'], y = movies['Rotten_Tomatoes_Rating'], alpha=0.7, edgecolor='None', kind='hex')
```

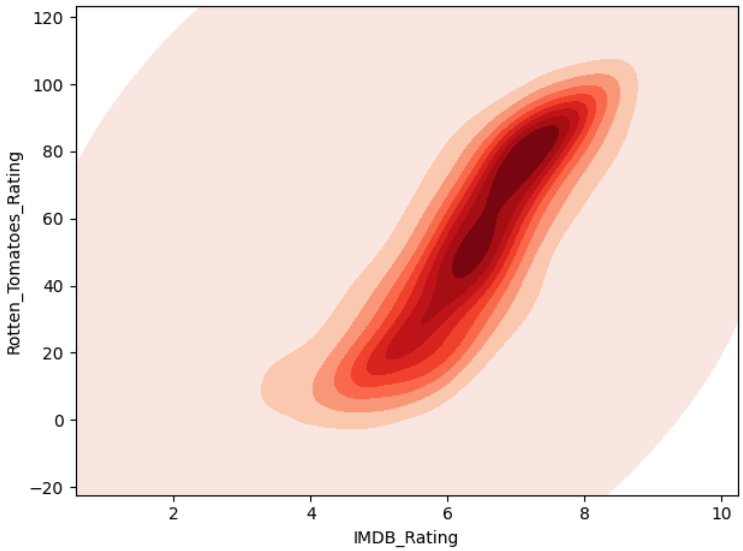


2D KDE

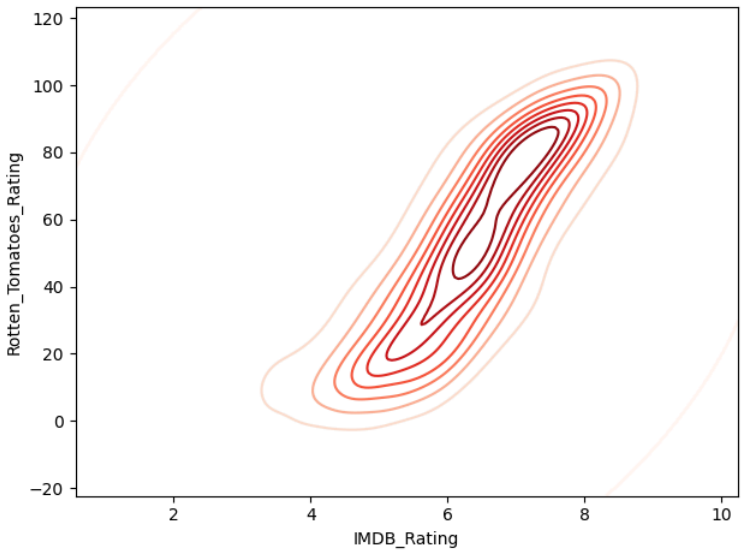
We can also do 2D KDE using seaborn's **`kdeplot()`** (https://stanford.edu/~mwaskom/software/seaborn/generated/seaborn.kdeplot.html) function.

Q: Can you draw one like this?

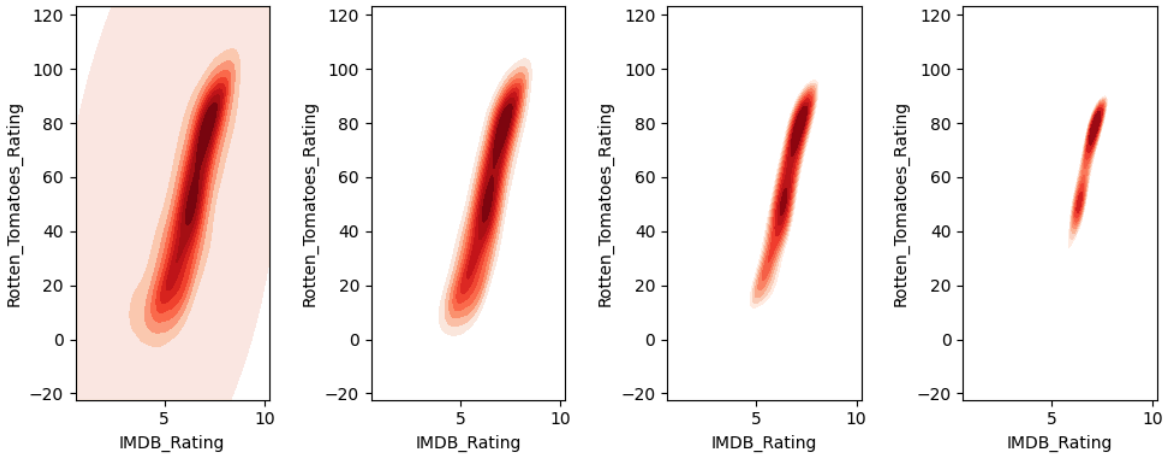
In [ ]:
```
cmap = "Reds"
# !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
# deprecated, use fill=True
# !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
shade = True          # what happens if you change this?
thresh = 0            # what happens if you change this?

sns.kdeplot(movies, x='IMDB_Rating', y='Rotten_Tomatoes_Rating', cmap="Reds", fill=True, thresh=0)
plt.tight_layout()
```



In [ ]:
```
sns.kdeplot(movies, x='IMDB_Rating', y='Rotten_Tomatoes_Rating', cmap="Reds", fill=False, thresh=0)
plt.tight_layout()
# it only shows contour levels instead of relief/heatmap
```



In [ ]:
```
plt.figure(figsize=(10,4))

for i,th in enumerate([0, 0.2, 0.5, 0.8]):
    plt.subplot(1, 4, i+1)
    sns.kdeplot(movies, x='IMDB_Rating', y='Rotten_Tomatoes_Rating', cmap="Reds", fill=True, thresh=th)
    plt.tight_layout()

# Once threshold increases, the plot becomes less and less detailed since more lower values are filtered out
```



Or again using **`jointplot()`** (http://stanford.edu/~mwaskom/software/seaborn/generated/seaborn.jointplot.html) by setting the `kind` parameter. Look, we also have the 1D marginal KDE plots!

Q: create jointplot with KDE The Y axis should be the IMDB Rating and the X axis should be the number of votes in log-scale. This means you just need to take the natural log of the values within the series. You can do so with numpy's log function. numpy log (https://numpy.org/doc/stable/reference/generated/numpy.log.html)

EXAMPLE: Get natural log of each item in a series

```
import numpy as np
np.log(WATEVER SERIES YOU WANT HERE)
```

NOTE: Depending on the version of seaborn you have installed, you'll either need to use the `shade_lowest` or the `thresh` parameter. Newer versions use `thresh`.

In [44]:
```
x = np.log(movies['IMDB_Votes'].values)
y = movies['IMDB_Rating'].values

sns.jointplot(x=x, y=y, kind='kde', fill=True, thresh=1e-5)
```

Out[44]: <seaborn.axisgrid.JointGrid at 0x1b85dbf5480>