The purpose here is to share some very basic code useful for

unsupervised learning. Unsupervised learning is for when there is no target variable and the aim is to group, or cluster, the data into similar records. Yes, this data is a "textbook" example, being very small, and cherry-picked in such a way as to make it as intuitive for a person just starting to learn as possible. For a real-world problem set, the natural groups will not be as discernable on a scatterplot, and the data will probably have more features and observations. Nonetheless, the concepts and code (with just some minor tweaks) would still apply to a real-world problem set.

The data is stock data coming from Charles Schwab on 31mar2022.

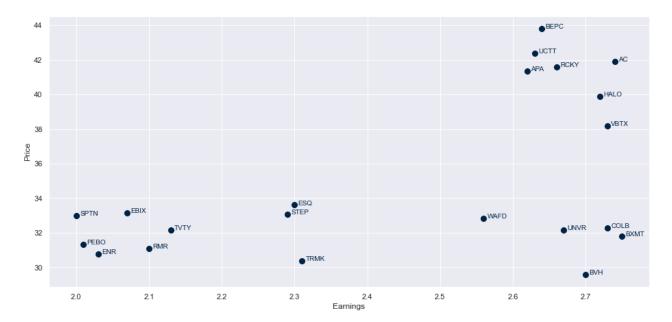
Import libraries

```
In [1]:
         import pandas as pd
         import numpy as np
         import matplotlib.pyplot as plt
         import seaborn as sns
         from sklearn.preprocessing import StandardScaler
         from scipy.cluster.hierarchy import linkage, dendrogram, fcluster
         from sklearn.cluster import KMeans
         from sklearn.pipeline import make pipeline
In [2]:
         #sns.set style('darkgrid')
         sns.set(rc={'figure.figsize':(15.7,7.27)})
In [3]:
         df1 = pd.read csv('clustering with dendrogram example.csv')
```

Display the first five rows of the dataframe and a scatterplot

```
In [4]:
         display(df1.head(5))
         sns.scatterplot(data = df1, x='Earnings', y='Price', s=100, color='#002244')
         for i in range(df1.shape[0]):
             plt.text(x=df1.Earnings.tolist()[i]+0.005,y=df1.Price.tolist()[i]+0.005,
                      s=df1.Symbol.tolist()[i],
                   fontdict=dict(color='#002244',size=10))
                   #bbox=dict(facecolor='yellow',alpha=0.5))
         plt.show()
```

	Symbol	Price	Earnings
0	AC	41.91	2.74
1	APA	41.33	2.62
2	BEPC	43.80	2.64
3	BVH	29.57	2.70
4	BXMT	31.79	2.75



Use the elbow method to determine the number of clusters:

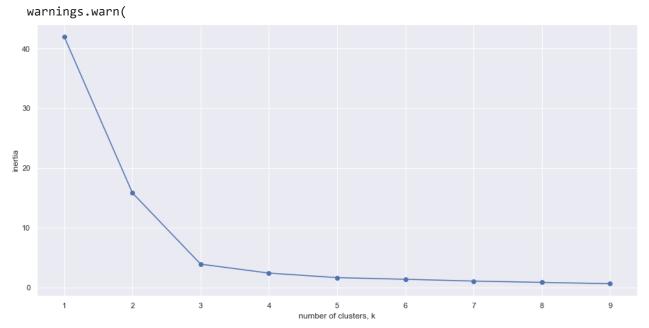
Inertia measures how spread out the clusters are (lower is better) or put differently, the distance from each sample to the centroid of its cluster. K-means attempts to minimize inertia when choosing clusters.

Use the Elbow method to determine the best number of clusters. That means, choosing the number of clusters corresponding to the "elbow" location in the line plot BELOW where inertia begins to decrease more slowly. Based on the scatter plot ABOVE, 3-4 appears to be the optimal number of clusters for k-means as it appears to be 3-4 natural groups in the scatterplot.

StandardScaler is a "preprocessing" step, that is crucial to use first with k-means. If not used, the algorithm will not group properly. MaxAbsScaler and Normalizer are also acceptable alternatives.

```
In [5]:
         samples = df1[['Price', 'Earnings']] #Hypothetically, df1[['Price', 'Earnings', 'Featur
         scaler = StandardScaler()
         scaler.fit(samples)
         samples scaled = scaler.transform(samples)
         ks = range(1, 10)
         inertias = []
         for k in ks:
             # Create a KMeans instance with k clusters: model
             model = KMeans(n clusters=k)
             # Fit model to samples
             model.fit(samples_scaled)
             # Append the inertia to the list of inertias
             inertias.append(model.inertia )
         # Plot ks vs inertias
         plt.plot(ks, inertias, '-o')
         plt.xlabel('number of clusters, k')
         plt.ylabel('inertia')
         plt.xticks(ks)
         plt.show()
```

C:\Users\henry\anaconda3\lib\site-packages\sklearn\cluster_kmeans.py:881: UserWarning: KMeans is known to have a memory leak on Windows with MKL, when there are less chunks th an available threads. You can avoid it by setting the environment variable OMP_NUM_THREA DS=1.



Using the elbow method with the chart above, 3 is the number of clusters I will choose. No surprise there based on the scatterplot.

Set n_clusters = 3 and preform k-means clustering on the data:

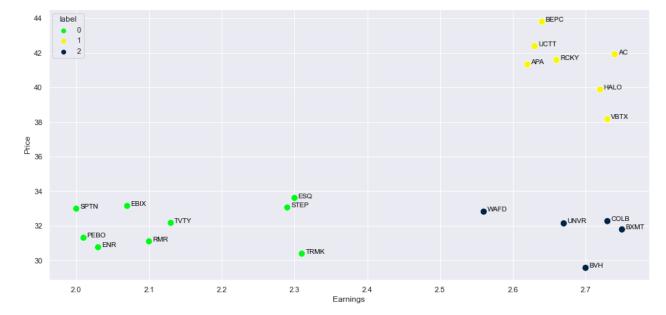
```
In [6]:
         scaler = StandardScaler()
         kmeans = KMeans(n_clusters=3) #set n_cluster=n right here
         pipeline = make pipeline(scaler, kmeans)
         pipeline.fit(samples)
         labels = pipeline.predict(samples)
         df1['label'] = labels
```

View the dataframe:

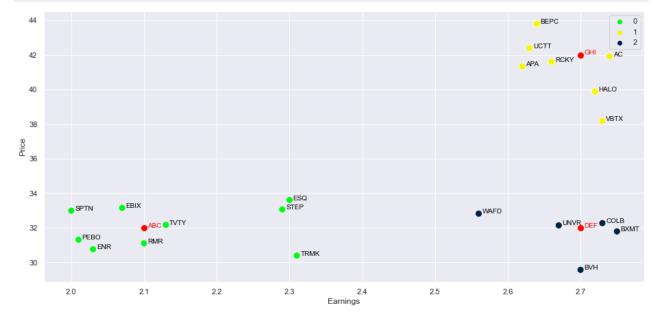
```
df1.sort values(by='label').head(21)
```

	diffisor c_values(by= facet)				
Out[7]:		Symbol	Price	Earnings	label
	10	PEBO	31.31	2.01	0
	16	TVTY	32.17	2.13	0
	15	TRMK	30.39	2.31	0
	14	STEP	33.06	2.29	0
	13	SPTN	32.99	2.00	0
	6	EBIX	33.15	2.07	0
	7	ENR	30.76	2.03	0
	8	ESQ	33.61	2.30	0
	12	RMR	31.10	2.10	0
	17	UCTT	42.39	2.63	1
	11	RCKY	41.59	2.66	1
	0	AC	41.91	2.74	1
	9	HALO	39.88	2.72	1
	2	BEPC	43.80	2.64	1
	1	APA	41.33	2.62	1
	19	VBTX	38.17	2.73	1
	5	COLB	32.27	2.73	2
	4	BXMT	31.79	2.75	2
	3	BVH	29.57	2.70	2
	18	UNVR	32.14	2.67	2
	20	WAFD	32.82	2.56	2

View the data with a scatterplot utilizing the "hue" option. This will color each cluster according to its value.



Create some fictitious data and plot it with the other data points. Color the new points red:



If k-means assigned a label "0" to "ABC", "2" to "DEF" and "1" to "GHI" it would make sense, and indeed it does, verified by the code below:

```
In [10]:
    new_labels = pipeline.predict(df_fictious_data[['Price', 'Earnings']])
    df_fictious_data['label'] = new_labels
    df_fictious_data.head()
```

Out[10]:		Symbol	Price	Earnings	label
	0	ABC	32.0	2.1	0
	1	DEF	32.0	2.7	2
	2	GHI	42.0	27	1

Visualizing data with a dendrogram is common with clustering.

Disclaimer: With a larger, more realistic dataframe, the dendrogram will look cluttered and messy.

The higher up on the dendrogram where a join happens, the more dissimilarity. Eq. HALO, and STEP are in separate groups at different corners of the scatter plot and do not join until a height of about 2.75, which is high. BXMT and COLB on the other hand, are deemed similar and join at a much lower height of approximately 0.25.

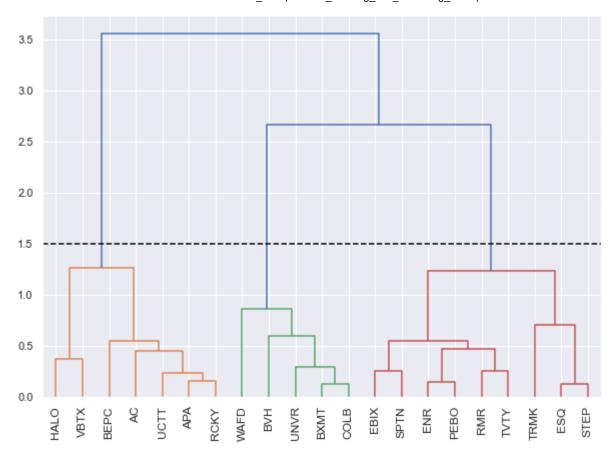
A word regarding the X-axis of the dendrogram:

The proximity of two labels on the X-axis of the dendrogram matters if the labels are in the same group (color). Outside the same group, the proximity of two labels on the X does not matter. For example, BXMT and COLB are both in the same group and are in close proximity in the scatterplot, thus they are close together on the dendrogram's X-axis.

COLB and EBIX are also close together on the dendrogram's X axis, however they are of different groups (colors), so that does not mean they are deemed just as similar.

I placed a black horizontal line on the dendrogram with a y-intercept of 1.5 to help illustrate that at a level of 1.5, there are three clusters as the black horizontal line crosses three vertical lines. At different levels, there would be a different amount of clusters.

```
In [11]:
          scaler = StandardScaler()
          scaler.fit(samples)
          StandardScaler(copy=True, with mean=True, with std=True)
          samples scaled = scaler.transform(samples)
          Symbol = df1.Symbol.tolist()
          plt.figure(figsize=(10, 7))
          mergings = linkage(samples scaled, method='complete')
          dendrogram(mergings,
          labels=Symbol,
          leaf_rotation=90,
          leaf_font_size=6)
          plt.axhline(y=1.5, color='black', linestyle='--')
          plt.xticks(fontsize= 12)
          plt.show()
```



How to extract the labels of the clusters at a level n (1.5)

```
In [12]:
          labels = fcluster(mergings, 1.5, criterion='distance')
          print(labels)
```