# id5055-tutorial-3

## September 6, 2023

```
[1]: import pandas as pd
     import numpy as np
     import matplotlib.pyplot as plt
     import seaborn as sns
     import scipy.cluster.hierarchy as sho
     from sklearn import metrics
     from sklearn.datasets import make_blobs, make_circles, make_moons
     from sklearn.cluster import AgglomerativeClustering, DBSCAN, SpectralClustering
     from sklearn.preprocessing import StandardScaler
[2]: # Helper function to plot
     def plot_clusters(data, true_labels=None, cluster_labels=None, title_true="True_"
      ⇔clusters", title_cluster="Agglomerative Clustering"):
         fig, (ax1, ax2) = plt.subplots(1, 2, figsize=(12, 5))
         ax1.scatter(data[:, 0], data[:, 1], c=true_labels)
         ax1.set_title(title_true)
         if cluster labels is not None:
             ax2.scatter(data[:, 0], data[:, 1], c=cluster_labels)
             ax2.set title(title cluster)
         plt.show()
     # Example usage:
     # plot_clusters(blob_X, blob_true_labels, agglo_cluster.labels_,u
      ⇒title_cluster="Agglomerative Clustering")
```

#### 0.0.1 common

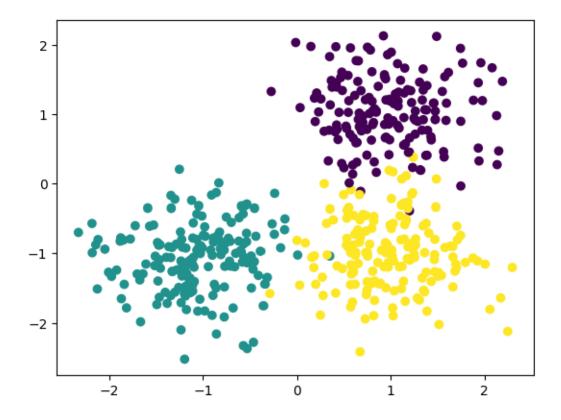
```
[3]: seed = 0
[4]: # blob data
centers = [[1, 1], [-1, -1], [1, -1]]
```

```
blob_X, blob_true_labels = make_blobs(n_samples=500, centers=centers,_u cluster_std=0.5, random_state=seed)

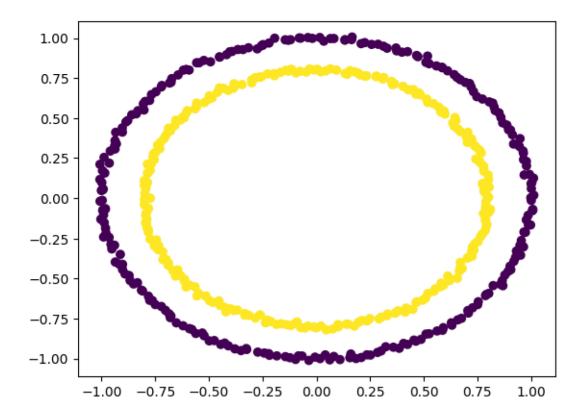
scaled_blob_X = StandardScaler().fit_transform(blob_X)

plt.scatter(blob_X[:, 0], blob_X[:, 1], c=blob_true_labels)
```

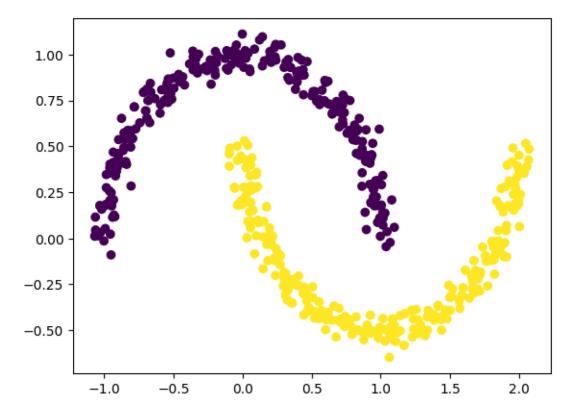
[4]: <matplotlib.collections.PathCollection at 0x7f58654156f0>



[5]: <matplotlib.collections.PathCollection at 0x7f586328a290>



[6]: <matplotlib.collections.PathCollection at 0x7f5861922da0>



[]:

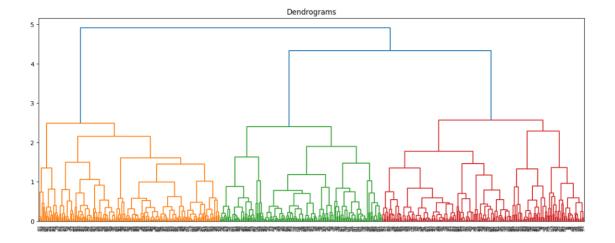
#### 0.0.2 Hierarchical Clustering

Unlike **K-means clustering**, tree-like morphologies are used to bunch the dataset, and dendrograms are used to create the hierarchy of the clusters.

Agglomerarive Clustering is based on the distance between groups, similar collections are merged based on the loss of the algorithm after one iteration. Again the loss value is calculated in the next iteration, where similar clusters are combined again. The process continues until we reach the minimum value of the loss.

**Dendogram Clustering Plot** A **Hierarchical clustering** is typically visualized as a **dendrogram** as shown in the following cell. Each merge is represented by a *horizontal line*. The y-coordinate of the horizontal line is the similarity of the two clusters that were merged, where cities are viewed as singleton clusters. By moving up from the bottom layer to the top node, a dendrogram allows us to reconstruct the history of merges that resulted in the depicted clustering.

```
[7]: plt.figure(figsize=(16, 6))
   plt.title("Dendrograms")
   Z = shc.linkage(scaled_blob_X, method="complete")
   dend = shc.dendrogram(Z)
```



Agglomerative Clustering The Agglomerative Clustering class will require two inputs:

- n\_clusters: The number of clusters to form as well as the number of centroids to generate.
   Value will be: 3
- linkage: Which linkage criterion to use. The linkage criterion determines which distance to use between sets of observation. The algorithm will merge the pairs of cluster that minimize this criterion.
  - Value will be: 'complete'

Hierarchical Agglomerative clustering starts with treating each observation as an individual cluster, and then iteratively merges clusters until all the data points are merged into a single cluster.

Clusters are merged based on the distance between them and to calculate the distance between the clusters we have different types of linkages.

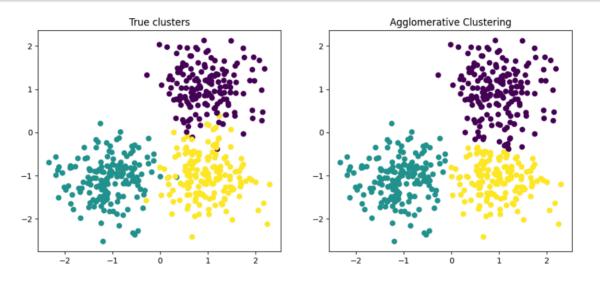
**Linkage Criteria**: It determines the distance between sets of observations as a function of the pairwise distance between observations.

- Single Linkage: the distance between two clusters is the minimum distance between members of the two clusters
- Complete Linkage: the distance between two clusters is the maximum distance between members of the two clusters
- Average Linkage: the distance between two clusters is the average of all distances between members of the two clusters
- Centroid Linkage: the distance between two clusters is is the distance between their centroids

At least  $O(n^2 \log n)$ , where 'n' is the number of data points.

#### For Blob Data

[8]: AgglomerativeClustering(linkage='complete', metric='euclidean', n\_clusters=3)



Silhouette Coefficient: 0.555 Adjusted Rand Index: 0.881

Adjusted Mutual Information: 0.863

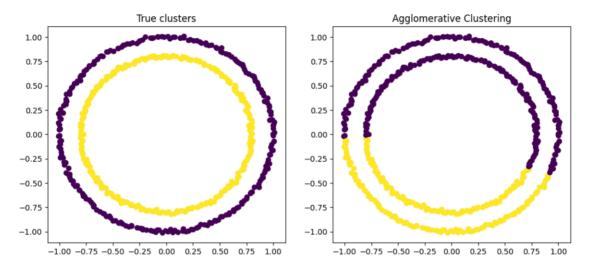
## [11]:

```
For Circular Data
```

```
[11]: agglo_cluster = AgglomerativeClustering(n_clusters=2, metric='euclidean', ⊔ ⇔linkage='complete')
```

```
agglo_cluster.fit(scaled_circle_X)
```

[11]: AgglomerativeClustering(linkage='complete', metric='euclidean')



Silhouette Coefficient: 0.389 Adjusted Rand Index: -0.002

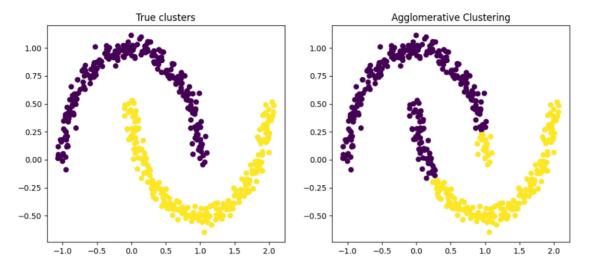
Adjusted Mutual Information: -0.001

#### For Moons Data

[14]: AgglomerativeClustering(metric='euclidean')

```
[15]: plot_clusters(moons_X, moons_true_labels, agglo_cluster.labels_,_

title_cluster="Agglomerative Clustering")
```



Silhouette Coefficient: 0.484 Adjusted Rand Index: 0.467

Adjusted Mutual Information: 0.390

[]:

## 0.0.3 DBSCAN

DBSCAN stands for Density-Based Spatial Clustering of Applications with Noise.

- It groups 'densely grouped' data points into a single cluster. The most exciting feature of DBSCAN clustering is that it is **robust to outliers**.
- It also does not require the number of clusters to be told beforehand, unlike K-Means, where we have to specify the number of centroids.

Two hyperparameters: - epsilon: Epsilon is the radius of the circle to be created around each data point to check the density. - minPoints: minPoints is the minimum number of data points required

inside that circle for that data point to be classified as a **Core** point.

In higher dimensions the circle becomes **hypersphere**, epsilon becomes the **radius** of that hypersphere, and minPoints is the minimum number of data points required inside that hypersphere.

If the number of points is less than minPoints, then it is classified as **Border Point**, and if there are no other data points around any data point within epsilon radius, then it treated as **Noise**.

For locating data points in space, DBSCAN uses **Euclidean distance**. It also needs to scan through the entire dataset once, whereas in other algorithms we have to do it multiple times.

The value of minPoints should be at least one greater than the number of dimensions of the dataset, i.e.,

minPoints>=Dimensions+1. Generally, it is twice the dimensions. (Domain Knowledge, in practice.)

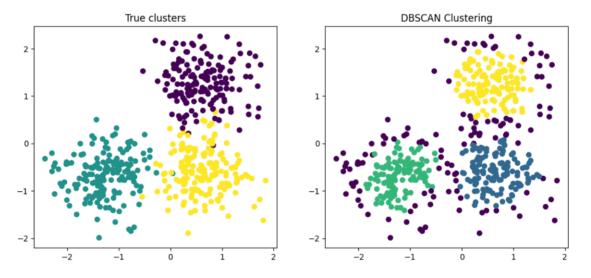
## For Blob Data

```
[17]: dbscan_cluster = DBSCAN(eps=0.3, min_samples=20)
dbscan_cluster.fit(scaled_blob_X)
```

[17]: DBSCAN(eps=0.3, min\_samples=20)

```
[18]: plot_clusters(scaled_blob_X, blob_true_labels, dbscan_cluster.labels_,__

stitle_cluster="DBSCAN Clustering")
```



Silhouette Coefficient: 0.369 Adjusted Rand Index: 0.589

Adjusted Mutual Information: 0.637

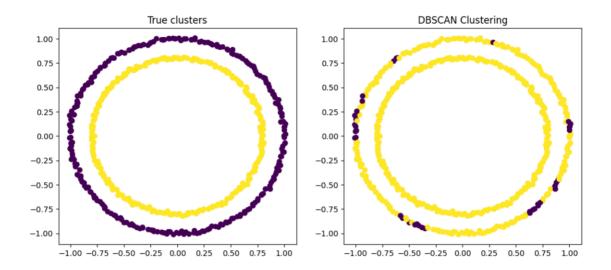
Terms: - Directly Density-Reachable - Density-Reachable - Density-Connected

- Directly Density-Reachable
- Density-Reachable
- Density-Connected

```
For Circular Data
```

```
[20]: dbscan_cluster = DBSCAN(eps=0.3, min_samples=20)
dbscan_cluster.fit(scaled_circle_X)
```

```
[20]: DBSCAN(eps=0.3, min_samples=20)
```



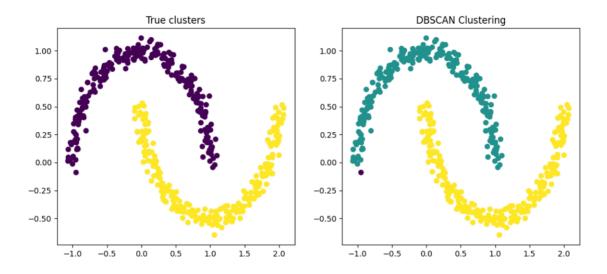
```
For Moons Data

[23]: dbscan_cluster = DBSCAN(eps=0.3, min_samples=20)
dbscan_cluster.fit(scaled_moons_X)
```

[23]: DBSCAN(eps=0.3, min\_samples=20)

```
[24]: plot_clusters(moons_X, moons_true_labels, dbscan_cluster.labels_,__

stitle_cluster="DBSCAN Clustering")
```



Silhouette Coefficient: 0.250 Adjusted Rand Index: 0.996

Adjusted Mutual Information: 0.991

[]:

## 0.0.4 Spectral Clustering

```
For Blob Data
```

```
[26]: spectral_cluster = SpectralClustering(n_clusters=3, □

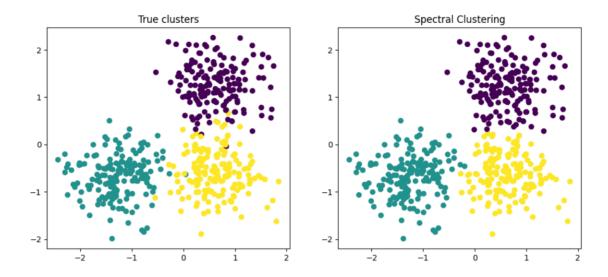
→affinity='nearest_neighbors')

spectral_cluster.fit(scaled_blob_X)
```

[26]: SpectralClustering(affinity='nearest\_neighbors', n\_clusters=3)

```
[27]: plot_clusters(scaled_blob_X, blob_true_labels, spectral_cluster.labels_,u

stitle_cluster="Spectral Clustering")
```



Silhouette Coefficient: 0.566 Adjusted Rand Index: 0.918 Adjusted Mutual Information: 0.880

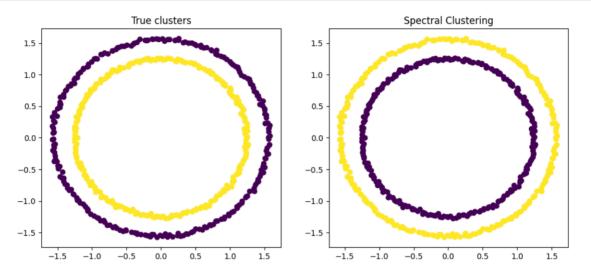
[]:

```
For Circular Data
```

/usr/local/lib/python3.10/distpackages/sklearn/manifold/\_spectral\_embedding.py:274: UserWarning: Graph is not fully connected, spectral embedding may not work as expected. warnings.warn(

[29]: SpectralClustering(affinity='nearest\_neighbors', n\_clusters=2)

```
[30]: plot_clusters(scaled_circle_X, circle_true_labels, spectral_cluster.labels_, u title_cluster="Spectral Clustering")
```



Silhouette Coefficient: 0.019 Adjusted Rand Index: 1.000

Adjusted Mutual Information: 1.000

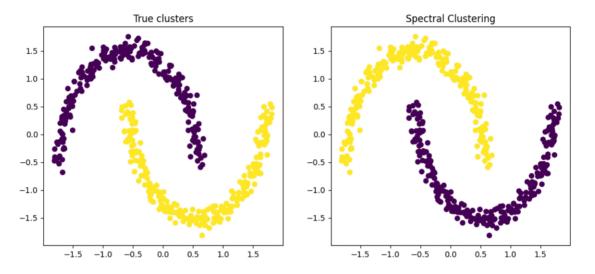
#### For Moons Data

```
/usr/local/lib/python3.10/dist-
packages/sklearn/manifold/_spectral_embedding.py:274: UserWarning: Graph is not
fully connected, spectral embedding may not work as expected.
warnings.warn(
```

```
[34]: SpectralClustering(affinity='nearest_neighbors', n_clusters=2)
```

```
[35]: plot_clusters(scaled_moons_X, moons_true_labels, spectral_cluster.labels_,⊔

→title_cluster="Spectral Clustering")
```



Silhouette Coefficient: 0.387 Adjusted Rand Index: 1.000

Adjusted Mutual Information: 1.000

[]:

# 1 Question

```
[]: # Explore and Compare Linkage Techniques (Optional).

# Using the given test data report best rand index and mutual information score

→ \

# for all the above discussed algorithms, along with the silhouette score.

# Explain the ambiguity in Silhoutte Scores.
```