# Project4_PDF

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## 1 Project 4 Report

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CS458

[ ]:
```
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import math
import pandas as pd
from sklearn import datasets
import pydotplus
from IPython.display import Image
import pydotplus
from sklearn.cluster import AgglomerativeClustering
from scipy.cluster.hierarchy import dendrogram, linkage
from scipy.spatial.distance import squareform
from sklearn.datasets import make_swiss_roll
from sklearn.neighbors import kneighbors_graph
from sklearn.cluster import DBSCAN
from sklearn.cluster import KMeans
from sklearn.metrics import accuracy_score
from sklearn.decomposition import PCA
from sklearn.preprocessing import scale
from sklearn.metrics import completeness_score
from sklearn.metrics import homogeneity_score
from sklearn.metrics import v_measure_score
```

### 1.1 P4-1. Hierarchical Clustering Dendrogram

**(a) Randomly generate the following data points: import numpy as np np.random.seed(0) X1 = np.random.randn(50,2)+[2,2] X2 = np.random.randn(50,2)+[6,10] X3 = np.random.randn(50,2)+[10,2] X = np.concatenate((X1,X2,X3))**

[ ]:
```
# Codes for P4-1(a)
np.random.seed(0)
X1 = np.random.randn(50,2)+[2,2]
```

```
X2 = np.random.randn(50,2)+[6,10]
X3 = np.random.randn(50,2)+[10,2]
X = np.concatenate((X1,X2,X3))
```

(b) Use **sklearn.cluster.AgglomerativeClustering** to cluster the points generated in (a). Plot your Dendrogram using different **linkage {"ward", "complete", "average", "single"}.**

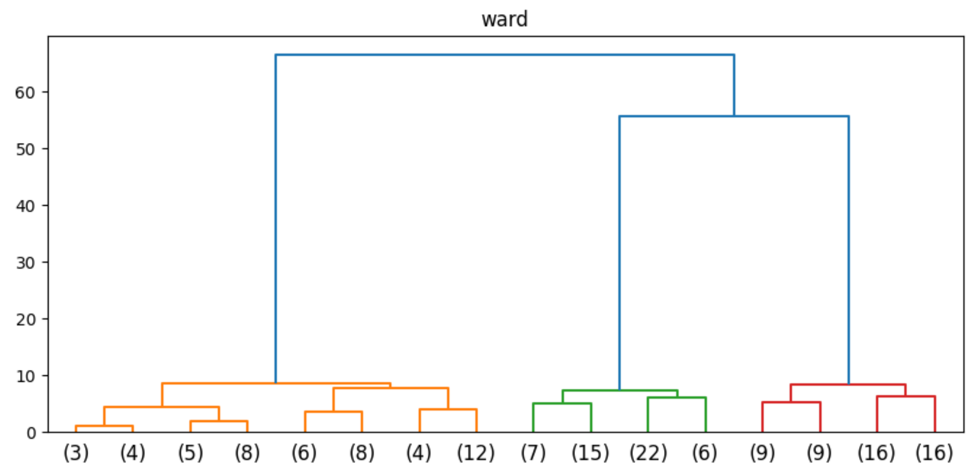
**Instructions:** Set **distance_threshold=0, n_clusters=None** in AgglomerativeClustering. The default metric used to compute the linkage is 'euclidean', so you do not need to change this parameter.

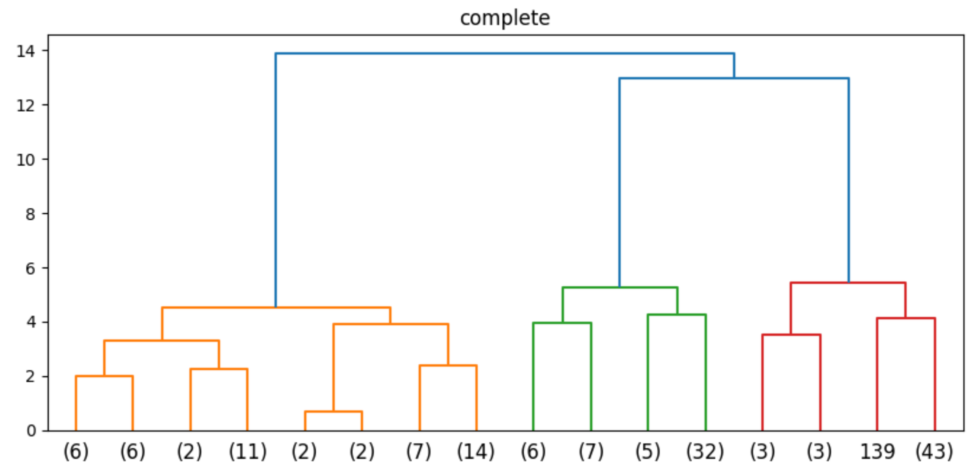
```
[ ]: def plot_dendrogram(model, **kwargs):
         # Create linkage matrix and then plot the dendrogram

         # create the counts of samples under each node
         counts = np.zeros(model.children_.shape[0])
         n_samples = len(model.labels_)
         for i, merge in enumerate(model.children_):
             current_count = 0
             for child_idx in merge:
                 if child_idx < n_samples:
                     current_count += 1  # leaf node
                 else:
                     current_count += counts[child_idx - n_samples]
             counts[i] = current_count

         linkage_matrix = np.column_stack(
             [model.children_, model.distances_, counts]
         ).astype(float)

         # Plot the corresponding dendrogram
         dendrogram(linkage_matrix, **kwargs)
```

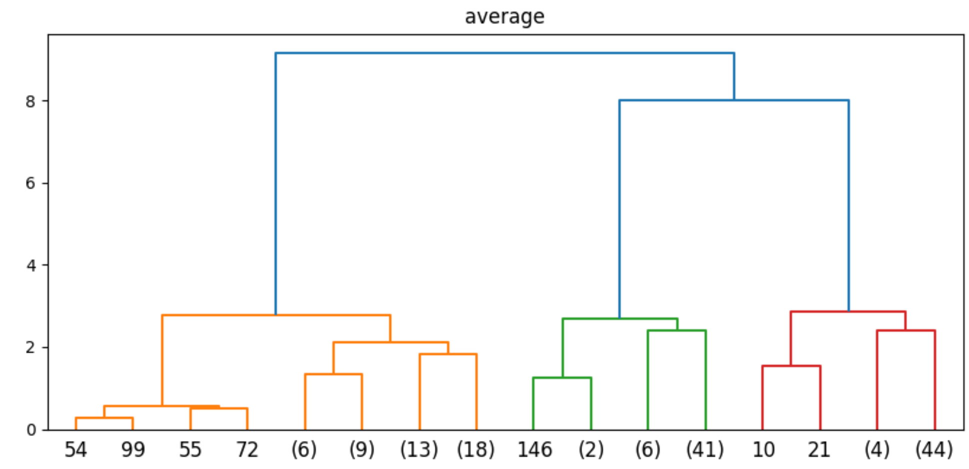
```
[ ]: # Codes for P4-1(b)
     fig, axs = plt.subplots(4, figsize=(10,20))

     cluster = AgglomerativeClustering(distance_threshold=0, n_clusters=None,␣
      ↪linkage="ward").fit(X)
     plot_dendrogram(cluster, truncate_mode="level", p=3, ax=axs[0])
     axs[0].set_title("ward")

     cluster = AgglomerativeClustering(distance_threshold=0, n_clusters=None,␣
      ↪linkage="complete").fit(X)
     plot_dendrogram(cluster, truncate_mode="level", p=3, ax=axs[1])
     axs[1].set_title("complete")

     cluster = AgglomerativeClustering(distance_threshold=0, n_clusters=None,␣
      ↪linkage="average").fit(X)
```

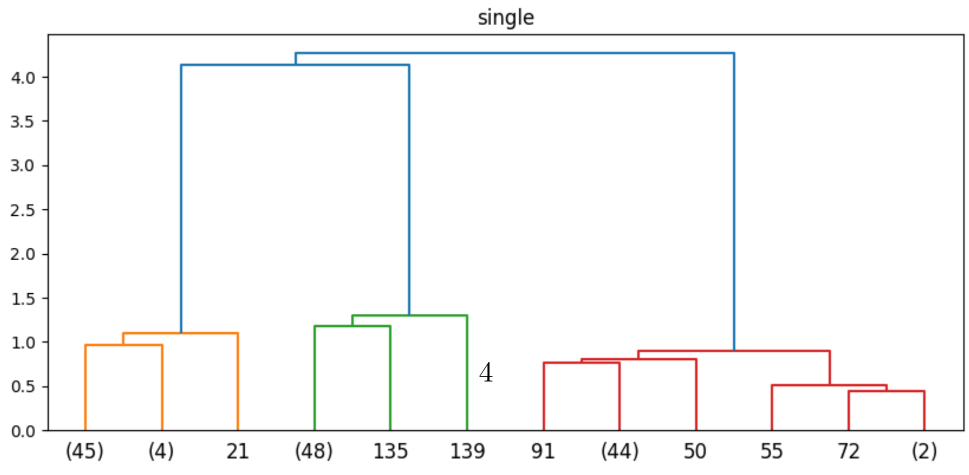
```
plot_dendrogram(cluster, truncate_mode="level", p=3, ax=axs[2])
axs[2].set_title("average")

cluster = AgglomerativeClustering(distance_threshold=0, n_clusters=None,␣
 ↪linkage="single").fit(X)
plot_dendrogram(cluster, truncate_mode="level", p=3, ax=axs[3])
axs[3].set_title("single")
```

```
[ ]: Text(0.5, 1.0, 'single')
```


ward
0
10
20
30
40
50
60
(3) (4) (5) (8) (6) (8) (4) (12) (7) (15) (22) (6) (9) (9) (16) (16)


complete
0
2
4
6
8
10
12
14
(6) (6) (2) (11) (2) (2) (7) (14) (6) (7) (5) (32) (3) (3) 139 (43)


average
0
2
4
6
8
54 99 55 72 (6) (9) (13) (18) 146 (2) (6) (41) 10 21 (4) (44)


single
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
4.0
(45) (4) 21 (48) 135 139 91 (44) 50 55 72 (2)

## 2 P4-2. Clustering structured dataset

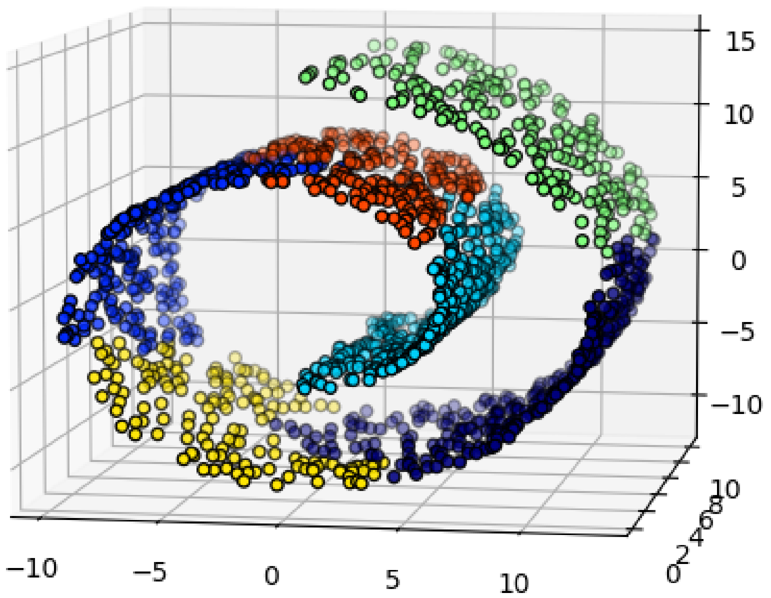
**(a) Generate a swiss roll dataset: from sklearn.datasets import make_swiss_roll # Generate data (swiss roll dataset) n_samples = 1500 noise = 0.05 X, _ = make_swiss_roll(n_samples, noise=noise) # Make it thinner X[:, 1] *= .5**

[ ]:
```
# Codes for P4-2(a)
# Generate data (swiss roll dataset)
n_samples = 1500
noise = 0.05
X, _ = make_swiss_roll(n_samples, noise=noise)
# Make it thinner
X[:, 1] *= .5
```

**(b) Use sklearn.cluster.AgglomerativeClustering to cluster the points generated in (a), where you set the parameters as n_clusters=6, connectivity=connectivity, linkage='ward', where**
**from sklearn.neighbors import kneighbors_graph connectivity = kneighbors_graph(X, n_neighbors=10, include_self=False)**

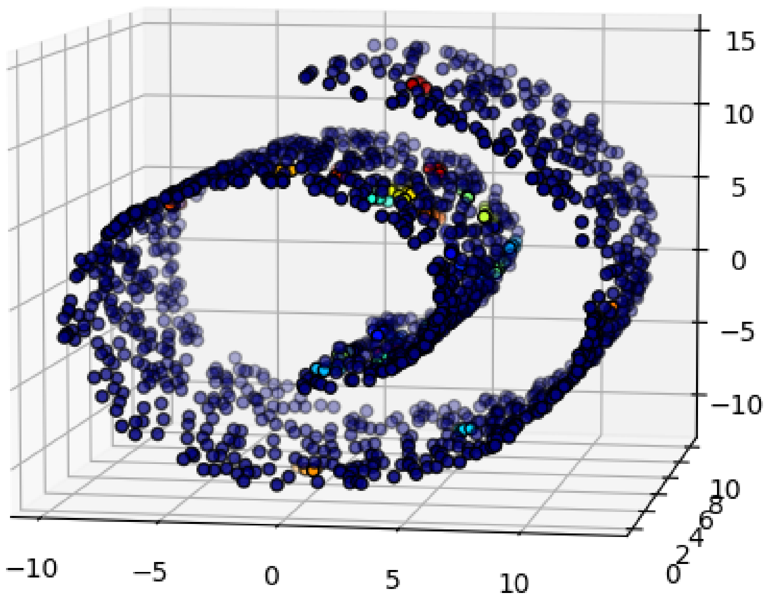
Plot the clustered data in a 3D figure and use different colors for different clusters in your figure.

[ ]:
```
# Codes for P4-2(b)
connectivity = kneighbors_graph(X, n_neighbors=10, include_self=False)
cluster = AgglomerativeClustering(connectivity=connectivity, n_clusters=6,␣
 ↪linkage = "ward").fit(X)

label = cluster.labels_

fig1 = plt.figure()
ax1 = fig1.add_subplot(111, projection="3d", elev=7, azim=-80)
ax1.set_position([0, 0, 0.95, 1])
for l in np.unique(label):
    ax1.scatter(
        X[label == l, 0],
        X[label == l, 1],
        X[label == l, 2],
        color=plt.cm.jet(float(l) / np.max(label + 1)),
        s=20,
        edgecolor="k",
    )
```



(c) Use **sklearn.cluster.DBSCAN** to cluster the points generated in (a). Plot the clustered data in a 3D figure and use different colors different clusters in your figure. Discuss and compare the results of DBSCAN with the results in (b).

[ ]:
```
cluster = DBSCAN().fit(X)

label = cluster.labels_

fig1 = plt.figure()
ax1 = fig1.add_subplot(111, projection="3d", elev=7, azim=-80)
ax1.set_position([0, 0, 0.95, 1])
for l in np.unique(label):
    ax1.scatter(
        X[label == l, 0],
        X[label == l, 1],
        X[label == l, 2],
        color=plt.cm.jet(float(l) / np.max(label + 1)),
        s=20,
        edgecolor="k",
    )
```



Based on the results of these cluster algorithms and results, k-neightbor is much more effective in clustering in the case of the swiss dataset. The DBSCAN cluster is only going for the closely knitted points which leads to random areas being designated as a cluster in terms of x.

## 3 P4-3. Clustering the handwritten digits data

```
[ ]: data, labels = datasets.load_digits(return_X_y=True)
     (n_samples, n_features), n_digits = data.shape, np.unique(labels).size

     pca = PCA()
     reducedData = pca.fit_transform(data)
```

**(a) Use the following methods to cluster the data: K-Means (sklearn.cluster.KMeans) DBSCAN (sklearn.cluster.DBSCAN) Optimize the parameters of these methods.**

```
[ ]: # Codes for P4-3(a)
     kmeans = KMeans(init="random", n_clusters=n_digits, n_init=4).fit(reducedData)

     DBscan = DBSCAN().fit(reducedData)
```

**(b) Evaluate these methods based on the labels of the data and discuss which method gives you the best results in terms of accuracy.**

```
[ ]: # Codes for P4-3(b)
     kmeanPred = kmeans.labels_
     print("KMeans homogeneity - ", homogeneity_score(kmeanPred, labels))
     print("KMeans completeness - ", completeness_score(kmeanPred, labels))
     print("KMeans v_measure - ", v_measure_score(kmeanPred, labels))


     DBscanPred = DBscan.labels_
     print("DBSCAN homogeneity - ", homogeneity_score(DBscanPred, labels))
     print("DBSCAN completeness - ", completeness_score(DBscanPred, labels))
     print("DBSCAN v_measure - ", v_measure_score(DBscanPred, labels))
```

```
KMeans homogeneity -  0.74339671889979
KMeans completeness -  0.7353879680410089
KMeans v_measure -  0.7393706567127246
DBSCAN homogeneity -  1.0
DBSCAN completeness -  0.0
DBSCAN v_measure -  0.0
```

There is an error with the DBSCAN in which the points are being designated as -1, which the algorithm deems as too noisy. The KMeans algorithm is better in this case due to elimination as DBSCAN is unable to handle this dataset.