2602063913_Bernardus Ignasio_Assignment 5 Machine Learning

June 28, 2024

1 Assignment 5 Machine Learning

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CLASS : LA01

Assignment Number: 5

```
[378]: import pandas as pd
       import matplotlib.pyplot as plt
       from sklearn.metrics import silhouette_score,␣
        ↪adjusted_rand_score,davies_bouldin_score
```

```
[379]: dataset=pd.read_csv('https://raw.githubusercontent.com/joh4nnes/MLData/main/
        ↪winequality-red.csv')
       dataset.head()
```

```
[379]:    fixed acidity  volatile acidity  citric acid  residual sugar  chlorides  \
       0            7.4              0.70         0.00             1.9      0.076
       1            7.8              0.88         0.00             2.6      0.098
       2            7.8              0.76         0.04             2.3      0.092
       3           11.2              0.28         0.56             1.9      0.075
       4            7.4              0.70         0.00             1.9      0.076

          free sulfur dioxide  total sulfur dioxide  density    pH  sulphates  \
       0                 11.0                  34.0   0.9978  3.51       0.56
       1                 25.0                  67.0   0.9968  3.20       0.68
       2                 15.0                  54.0   0.9970  3.26       0.65
       3                 17.0                  60.0   0.9980  3.16       0.58
       4                 11.0                  34.0   0.9978  3.51       0.56

          alcohol  quality
       0      9.4        5
       1      9.8        5
       2      9.8        5
       3      9.8        6
       4      9.4        5
```

[403]:

```
dataset.isna().sum()
```

[403]:

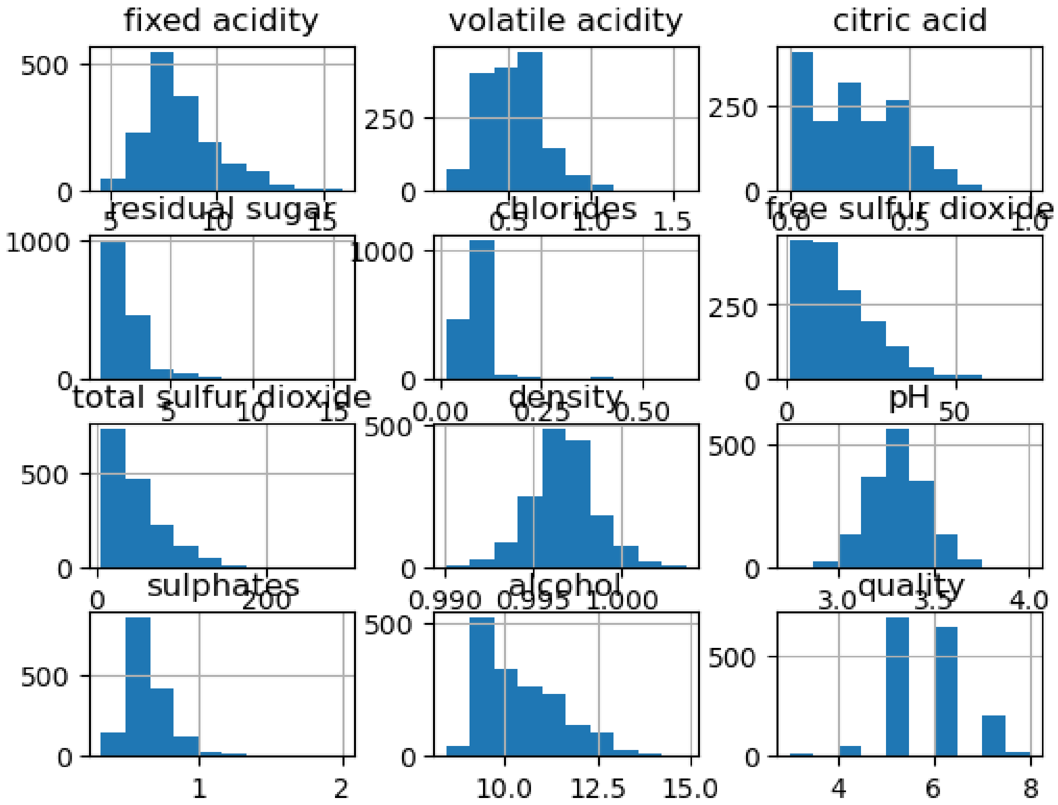
```
fixed acidity           0
volatile acidity        0
citric acid             0
residual sugar          0
chlorides               0
free sulfur dioxide     0
total sulfur dioxide    0
density                 0
pH                      0
sulphates               0
alcohol                 0
quality                 0
dtype: int64
```

[404]:

```
dataset.hist()
```

[404]:

```
array([[<Axes: title={'center': 'fixed acidity'}>,
        <Axes: title={'center': 'volatile acidity'}>,
        <Axes: title={'center': 'citric acid'}>],
       [<Axes: title={'center': 'residual sugar'}>,
        <Axes: title={'center': 'chlorides'}>,
        <Axes: title={'center': 'free sulfur dioxide'}>],
       [<Axes: title={'center': 'total sulfur dioxide'}>,
        <Axes: title={'center': 'density'}>,
        <Axes: title={'center': 'pH'}>],
       [<Axes: title={'center': 'sulphates'}>,
        <Axes: title={'center': 'alcohol'}>,
        <Axes: title={'center': 'quality'}>]], dtype=object)
```



Extracting matrix of features

[381]:
```
x=dataset.iloc[:,:11].values
x
```

[381]:
```
array([[ 7.4  ,  0.7  ,  0.   , …,  3.51 ,  0.56 ,  9.4  ],
       [ 7.8  ,  0.88 ,  0.   , …,  3.2  ,  0.68 ,  9.8  ],
       [ 7.8  ,  0.76 ,  0.04 , …,  3.26 ,  0.65 ,  9.8  ],
       …,
       [ 6.3  ,  0.51 ,  0.13 , …,  3.42 ,  0.75 , 11.   ],
       [ 5.9  ,  0.645,  0.12 , …,  3.57 ,  0.71 , 10.2  ],
       [ 6.   ,  0.31 ,  0.47 , …,  3.39 ,  0.66 , 11.   ]])
```

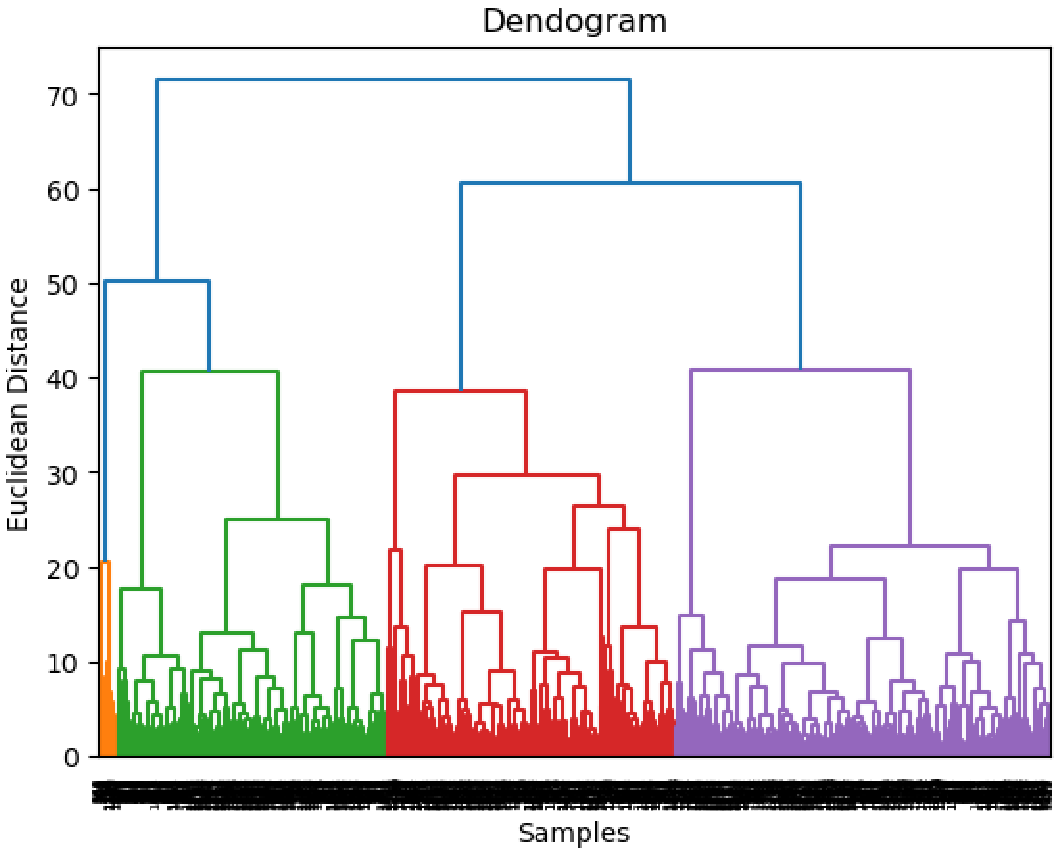
[382]:
```
from sklearn.preprocessing import StandardScaler

scale=StandardScaler()
x=scale.fit_transform(x)
x
```

[382]:
```
array([[-0.52835961,  0.96187667, -1.39147228, …,  1.28864292,
        -0.57920652, -0.96024611],
       [-0.29854743,  1.96744245, -1.39147228, …, -0.7199333 ,
         0.1289504 , -0.58477711],
       [-0.29854743,  1.29706527, -1.18607043, …, -0.33117661,
        -0.04808883, -0.58477711],
       …,
       [-1.1603431 , -0.09955388, -0.72391627, …,  0.70550789,
         0.54204194,  0.54162988],
       [-1.39015528,  0.65462046, -0.77526673, …,  1.6773996 ,
         0.30598963, -0.20930812],
       [-1.33270223, -1.21684919,  1.02199944, …,  0.51112954,
         0.01092425,  0.54162988]])
```

Find Optimal number of cluster with dendogram

[383]:

```python
import scipy.cluster.hierarchy as shc
dendro=shc.dendrogram(shc.linkage(x,method='ward'))
plt.title('Dendogram')
plt.xlabel('Samples')
plt.ylabel('Euclidean Distance')
plt.show()
```



by slicing horizontally, optimal number of cluster is between 3 and 4

Clustering Dataset with agglomerative clustering and optimal cluster

[384]:

```
from sklearn.cluster import AgglomerativeClustering
hc=AgglomerativeClustering(n_clusters=4,affinity='euclidean',linkage='ward')
y_predict=hc.fit_predict(x)
y_predict
```

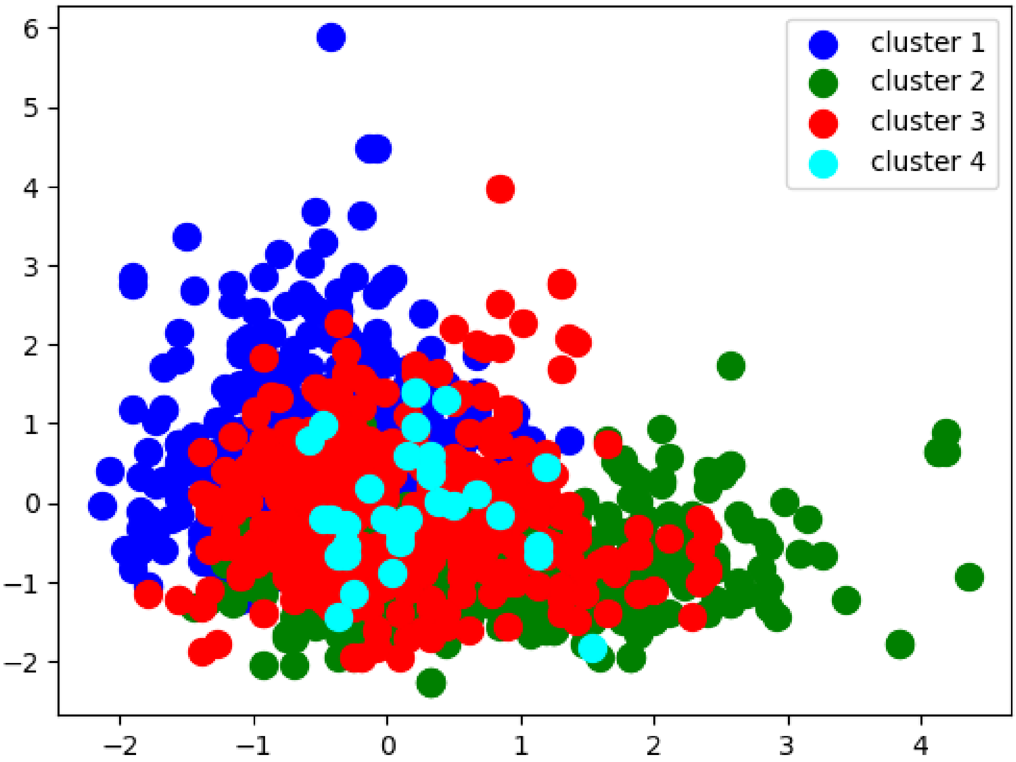
```
C:\Users\Ignas\anaconda3\Lib\site-
packages\sklearn\cluster\_agglomerative.py:1005: FutureWarning: Attribute
`affinity` was deprecated in version 1.2 and will be removed in 1.4. Use
`metric` instead
  warnings.warn(
```

[384]:

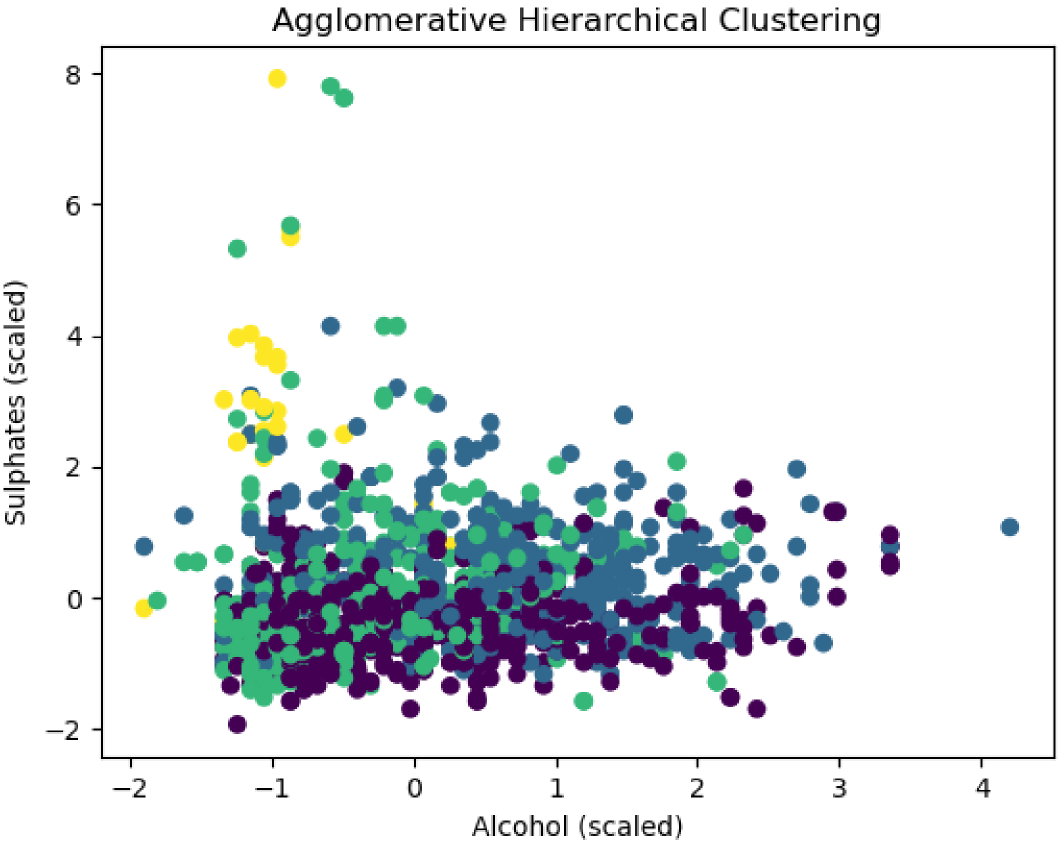
```
array([0, 0, 0, …, 2, 2, 1], dtype=int64)
```

[385]:

```
plt.scatter(x[y_predict==0,0],x[y_predict==0,1], s=100,c='blue',label='cluster␣
  ↪1')
plt.scatter(x[y_predict==1,0],x[y_predict==1,1], s=100,c='green',label='cluster␣
  ↪2')
plt.scatter(x[y_predict==2,0],x[y_predict==2,1], s=100,c='red',label='cluster␣
  ↪3')
plt.scatter(x[y_predict==3,0],x[y_predict==3,1], s=100,c='cyan',label='cluster␣
  ↪4')
#plt.scatter(x[y_predict==4,0],x[y_predict==4,1],␣
  ↪s=100,c='magenta',label='cluster 5')

plt.legend()
plt.show()
```



[386]:
```
plt.scatter(x[:,10], x[:,9], c=y_predict,cmap='viridis',marker='o')
plt.title('Agglomerative Hierarchical Clustering')
plt.xlabel('Alcohol (scaled)')
plt.ylabel('Sulphates (scaled)')
plt.show()
```



[387]:

```
print(f"Silhouette Score: {silhouette_score(x,hc.labels_,metric='euclidean')}")
print(f"Davies Bouldin Index (DBI): {davies_bouldin_score(x,hc.labels_)}")
```

```
Silhouette Score: 0.17141826625204853
Davies Bouldin Index (DBI): 1.6648528437215329
```

from the visualization and evaluation metrics, we can see that the clustering is still poorly matched and the distance between every cluster cannot be seen, clusters are spreading and combining together which indicates poor clustering quality

Enhancing quality with PCA

[388]:

```
from sklearn.decomposition import PCA
pca=PCA(n_components=2)
x=pca.fit_transform(x)
x
```

[388]:

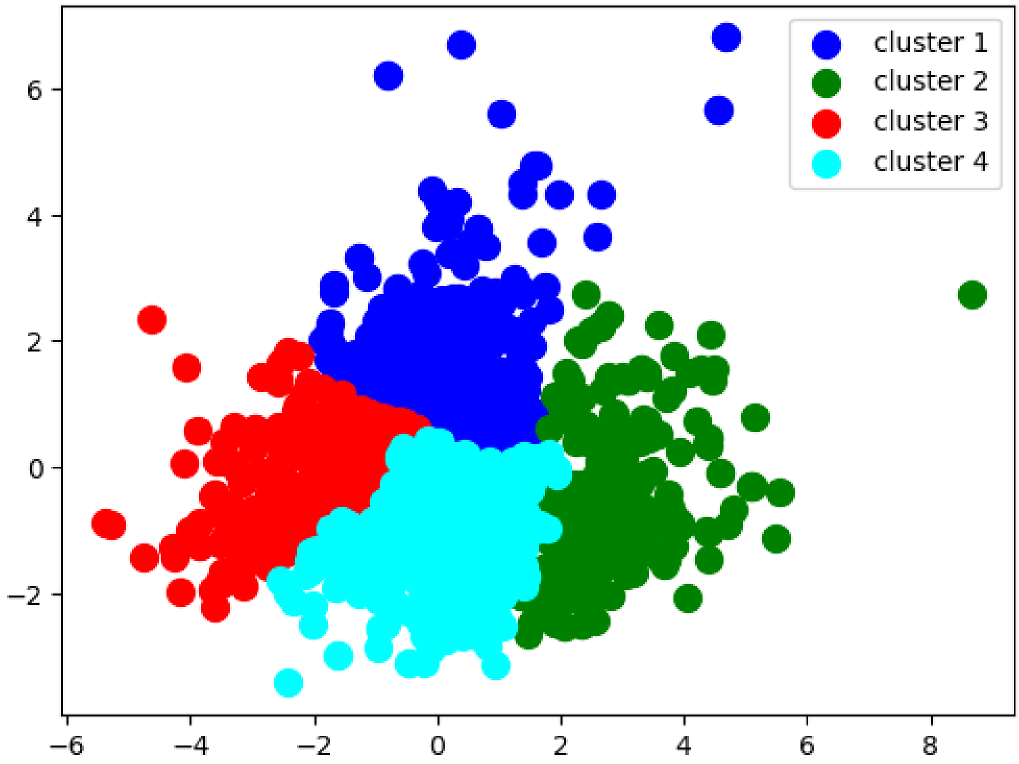
```
array([[-1.61952988,  0.45095009],
       [-0.79916993,  1.85655306],
       [-0.74847909,  0.88203886],
       …,
       [-1.45612897,  0.31174559],
       [-2.27051793,  0.97979111],
       [-0.42697475, -0.53669021]])
```

[389]:
```
hc=AgglomerativeClustering(n_clusters=4,affinity='euclidean',linkage='ward')
y_predict=hc.fit_predict(x)
y_predict
```

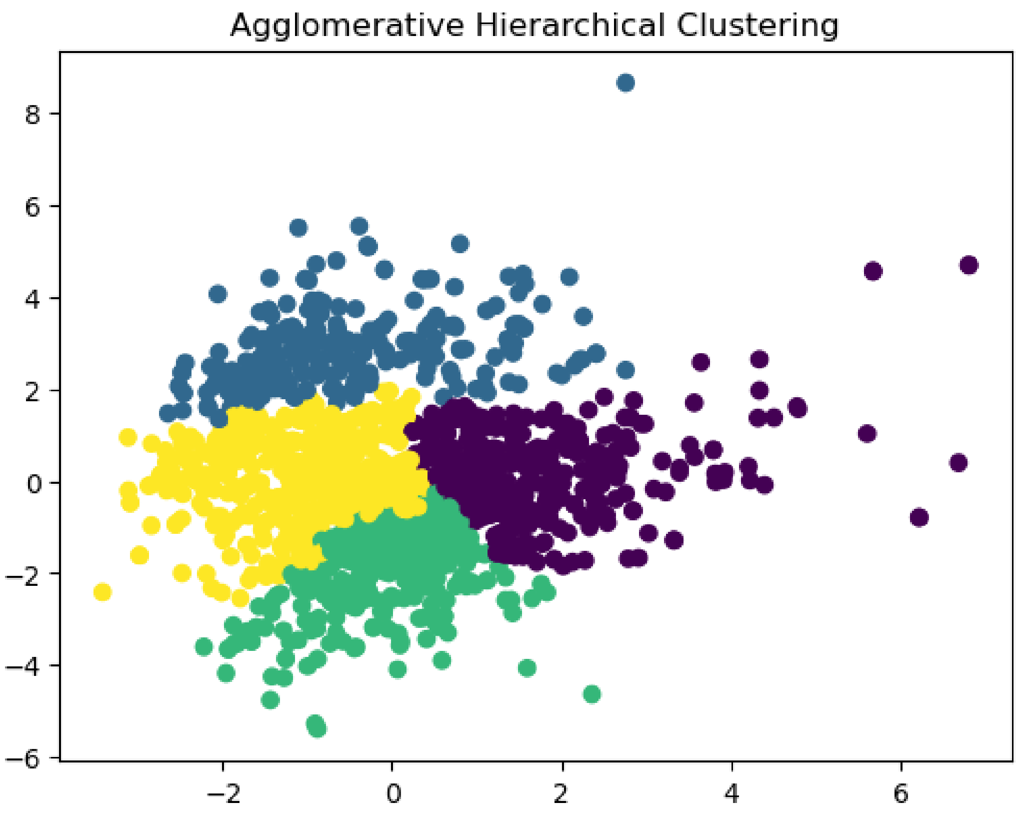
```
C:\Users\Ignas\anaconda3\Lib\site-
packages\sklearn\cluster\_agglomerative.py:1005: FutureWarning: Attribute
`affinity` was deprecated in version 1.2 and will be removed in 1.4. Use
`metric` instead
  warnings.warn(
```

[389]:
```
array([2, 0, 0, …, 2, 2, 3], dtype=int64)
```

[390]:
```
plt.scatter(x[y_predict==0,0],x[y_predict==0,1], s=100,c='blue',label='cluster␣
 ↪1')
plt.scatter(x[y_predict==1,0],x[y_predict==1,1], s=100,c='green',label='cluster␣
 ↪2')
plt.scatter(x[y_predict==2,0],x[y_predict==2,1], s=100,c='red',label='cluster␣
 ↪3')
plt.scatter(x[y_predict==3,0],x[y_predict==3,1], s=100,c='cyan',label='cluster␣
 ↪4')
#plt.scatter(x[y_predict==4,0],x[y_predict==4,1],␣
 ↪s=100,c='magenta',label='cluster 5')

plt.legend()
plt.show()
```



[391]:
```
plt.scatter(x[:,1], x[:,0], c=y_predict,cmap='viridis',marker='o')
plt.title('Agglomerative Hierarchical Clustering')
plt.show()
```



[392]:
```
print(f"Silhouette Score: {silhouette_score(x,hc.labels_,metric='euclidean')}")
print(f"Davies Bouldin Index (DBI): {davies_bouldin_score(x,hc.labels_)}")
```

```
Silhouette Score: 0.3413983711219637
Davies Bouldin Index (DBI): 0.9068520999649691
```

after implementing pca and reducting columns until 2 columns left, we can see that the clusters separation can be seen clearly although there's no gap/distance betweeen the clusters. also the evaluation metrics is better, indicating that the clustering is improving