

TP 2 – Clustering et classification

```
import pandas as pd
from sklearn.cluster import KMeans
import matplotlib.pyplot as plt
from sklearn.model_selection import train_test_split
from sklearn.cluster import DBSCAN
from sklearn.metrics import adjusted_rand_score

df=pd.read_csv('md_for_Python.csv',sep=';')
df.head()
```

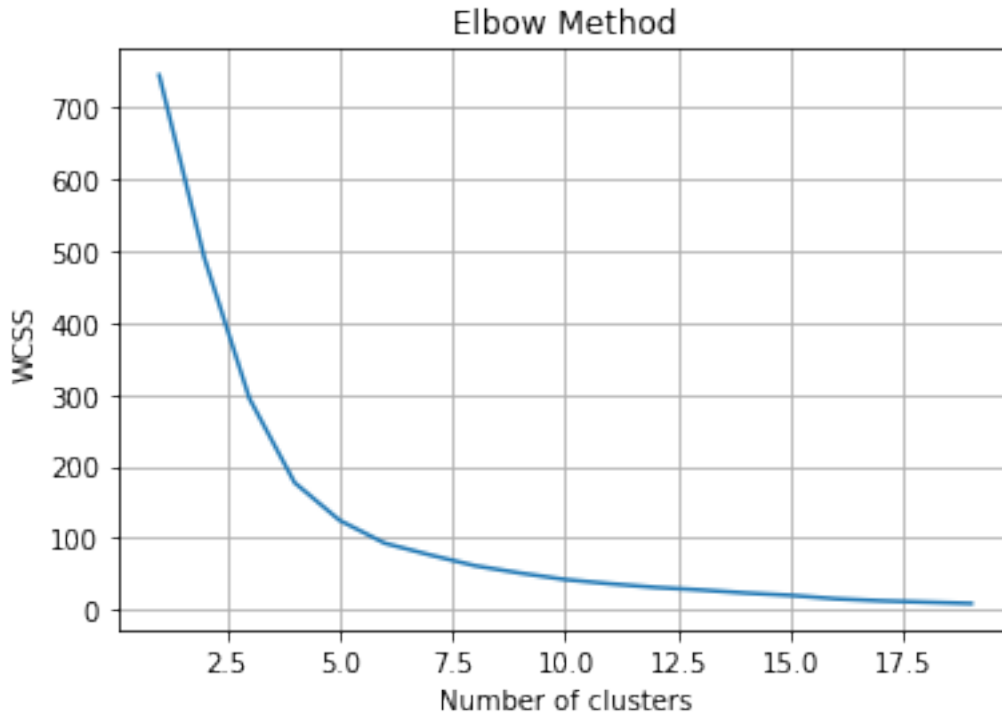
	name	top.i	bottom.i	top.c	bottom.c	top.pm
bottom.pm \						
0	Opossum	5	4	1	1	3
3						
1	Hairy tail mole	3	3	1	1	4
4						
2	Common mole	3	2	1	0	3
3						
3	Star nose mole	3	3	1	1	4
4						
4	Brown bat	2	3	1	1	3
3						

	top.m	bottom.m
0	4	4
1	3	3
2	3	3
3	3	3
4	3	3

```
df.shape
(66, 9)

wcss = []
for i in range(1, 20):
    kmeans = KMeans(n_clusters=i, init='k-means++', random_state=42)
    kmeans.fit(df.drop(['name'],axis=1))
    wcss.append(kmeans.inertia_)

# Plot the WCSS to see the elbow
plt.plot(range(1, 20), wcss)
plt.title('Elbow Method')
plt.xlabel('Number of clusters')
plt.ylabel('WCSS')
plt.grid(True)
plt.show()
```



```
# A list holds the silhouette coefficients for each k
silhouette_coefficients = []
# Notice you start at 2 clusters for silhouette coefficient
for k in range(2, 11):
    kmeans = KMeans(n_clusters=k, init='k-means++', random_state=42)
    kmeans.fit(df.drop(['name'],axis=1))
    score = silhouette_score(df.drop(['name'],axis=1), kmeans.labels_)
    silhouette_coefficients.append(score)
```

- Silhouette Score:
- This method measures how similar an object is to its own cluster (cohesion) compared to other clusters (separation). The silhouette score ranges from -1 to 1, where a high value indicates that the object is well matched to its own cluster and poorly matched to neighboring clusters. If the graph of the silhouette score peaks at a certain number of clusters, this is considered the best number of clusters.

```
plt.style.use("fivethirtyeight")
plt.plot(range(2, 11), silhouette_coefficients)
plt.xticks(range(2, 11))
plt.xlabel("Number of Clusters")
plt.ylabel("Silhouette Coefficient")
plt.show()
```



```
k = 5 # for example, replace with the number of clusters you
determined
kmeans = KMeans(n_clusters=k, init='k-means++', random_state=42)
clusters = kmeans.fit_predict(df.drop(['name'],axis=1))
```

```
# Add the cluster data to the original dataframe
df['Cluster'] = clusters
```

```
# Now you can analyze the data based on clusters
print(df.head())
```

```
df
```

		name	top.i	bottom.i	top.c	bottom.c	top.pm
bottom.pm \	0	Opossum	5	4	1	1	3
	3						
	1	Hairy tail mole	3	3	1	1	4
	4						
	2	Common mole	3	2	1	0	3
	3						
	3	Star nose mole	3	3	1	1	4
	4						
	4	Brown bat	2	3	1	1	3
	3						

	..						

61	Antelope	0	4	0	0	3
3						
62	Bison	0	4	0	0	3
3						
63	Mountain goat	0	4	0	0	3
3						
64	Musk ox	0	4	0	0	3
3						
65	Mountain sheep	0	4	0	0	3
3						

	top.m	bottom.m	Cluster
0	4	4	5
1	3	3	5
2	3	3	5
3	3	3	5
4	3	3	4
..
61	3	3	0
62	3	3	0
63	3	3	0
64	3	3	0
65	3	3	0

[66 rows x 10 columns]

```
df1=pd.read_csv('md_for_Python.csv',sep=';')
df2=pd.read_csv('md_classes.csv',sep=';')
```

```
df2.columns
```

```
Index(['name', 'top.i', 'bottom.i', 'top.c', 'bottom.c', 'top.pm',
      'bottom.pm',
      'top.m', 'bottom.m', 'zoo.class'],
      dtype='object')
```

```
df2['zoo.class'].unique()
```

```
array([15, 14, 13, 12, 11, 10,  9,  8,  7,  6,  5,  4,  3,  2,  1],
      dtype=int64)
```

```
X=df.drop(['name'],axis=1)
```

```
# Instantiate k-means and dbscan algorithms
```

```
kmeans = KMeans(n_clusters=5)
```

```
dbscan = DBSCAN(eps=0.3)
```

```
# Fit the algorithms to the features
```

```
kmeans.fit(X)
```

```
dbscan.fit(X)
```

```
# Compute the silhouette scores for each algorithm
```

```

kmeans_silhouette = silhouette_score(X, kmeans.labels_).round(2)
dbscan_silhouette = silhouette_score(X, dbscan.labels_).round(2)

kmeans_silhouette

0.63

dbscan_silhouette

0.29

```

The silhouette coefficient is higher for the k-means algorithm. The DBSCAN algorithm appears to find more natural clusters according to the shape of the data:

```

kmeans.labels_

array([1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 4, 2, 2, 2, 2, 2, 2, 2, 2, 2,
2,
      2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 1, 1, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0,
0,
      0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 3, 3, 3, 3, 3, 3, 3, 3,
3])

df2=pd.read_csv('md_classes.csv',sep=';')

ari_kmeans = adjusted_rand_score(df2['zoo.class'].values,
kmeans.labels_)
ari_dbscan = adjusted_rand_score(df2['zoo.class'].values,
dbscan.labels_)

ari_kmeans

0.44662624439992393

ari_dbscan

0.1398676719495307

```

The ARI output values range between -1 and 1. A score close to 0.0 indicates random assignments, and a score close to 1 indicates perfectly labeled clusters.

```

ari_km=[]
silh_km=[]
for k in range(2,20):
    kmeans = KMeans(n_clusters=k)
    kmeans.fit(df.drop(['name', 'Cluster'],axis=1))
    ari_kmeans = adjusted_rand_score(df2['zoo.class'].values,
kmeans.labels_)
    ari_km.append(ari_kmeans)

```

```
silh_km.append(silhouette_score(df.drop(['name', 'Cluster'], axis=1),  
kmeans.labels_))
```

```
len(silh_km)
```

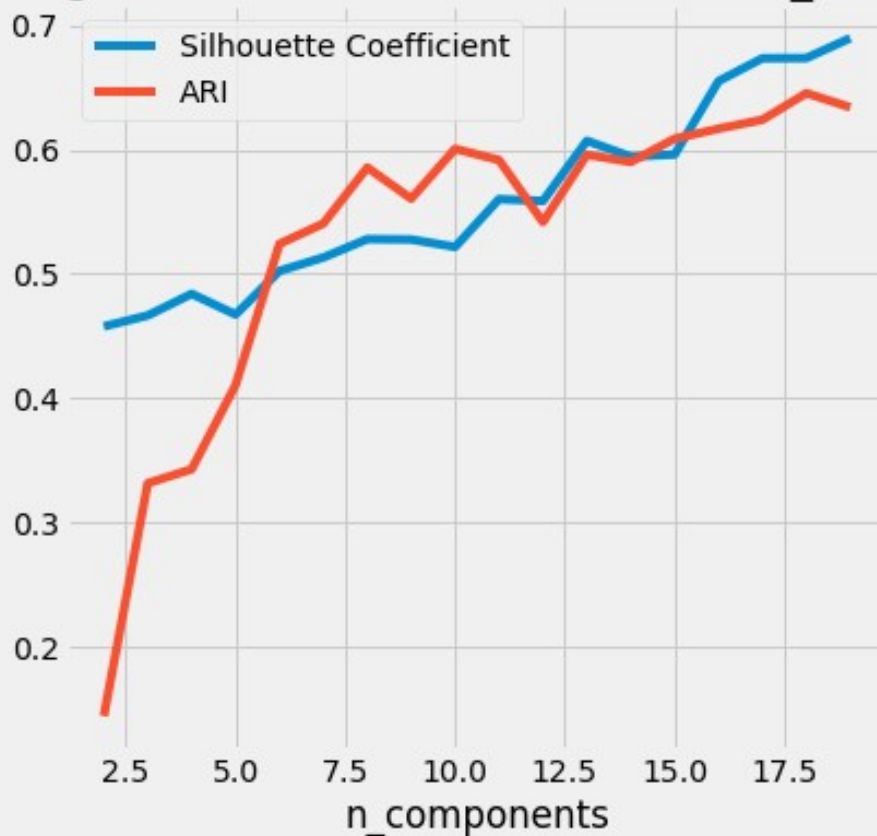
```
18
```

L'Adjusted Rand Index (ARI) est une mesure d'évaluation de la qualité d'un clustering qui compare les regroupements obtenus avec les regroupements réels (ou ground truth) ajustés pour le hasard. L'ARI varie de -1 à 1, où :

- 1 indique une correspondance parfaite entre les regroupements obtenus et les regroupements réels.
- 0 indique que les regroupements obtenus sont équivalents à ce que l'on pourrait obtenir par hasard.
- -1 indique une discordance totale entre les regroupements obtenus et les regroupements réels.

```
plt.style.use("fivethirtyeight")  
plt.figure(figsize=(6, 6))  
plt.plot(range(2, 20), silh_km, c="#008fd5", label="Silhouette  
Coefficient",)  
plt.plot(range(2, 20), ari_km, c="#fc4f30", label="ARI")  
plt.xlabel("n_components")  
plt.legend()  
plt.title("Clustering Performance as a Function of n_components")  
plt.tight_layout()  
plt.show()
```

Clustering Performance as a Function of n_components



```
dbscan.labels_
array([-1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1,  0,  0,
        0,  0,  0,  1,  1,  1,  1,  2,  2,  2,  2,  2,  1,  1, -1, -1,
       -1, -1, -1, -1, -1,  3,  3,  3, -1,  3,  3, -1, -1, -1, -1, -1,
       -1, -1, -1, -1, -1, -1, -1,  4,  4, -1,  4,  4,  4,  4,  4],
      dtype=int64)
```

Classification

```
data=pd.read_csv('md_classes.csv',sep=';')
```

```
data.head()
```

	name	top.i	bottom.i	top.c	bottom.c	top.pm
bottom.pm \						
0	Opossum	5	4	1	1	3
3						
1	Hairy tail mole	3	3	1	1	4
4						

```

2      Common mole      3      2      1      0      3
3
3      Star nose mole      3      3      1      1      4
4
4      Brown bat      2      3      1      1      3
3

```

```

      top.m  bottom.m  zoo.class
0         4         4         15
1         3         3         14
2         3         3         14
3         3         3         14
4         3         3         13

```

```
import seaborn as sns
```

```
data[data['zoo.class']==2]
```

```

      name  top.i  bottom.i  top.c  bottom.c  top.pm  bottom.pm
top.m \
56 Peccary      2      3      1      1      3      3
3

```

```

      bottom.m  zoo.class
56          3          2

```

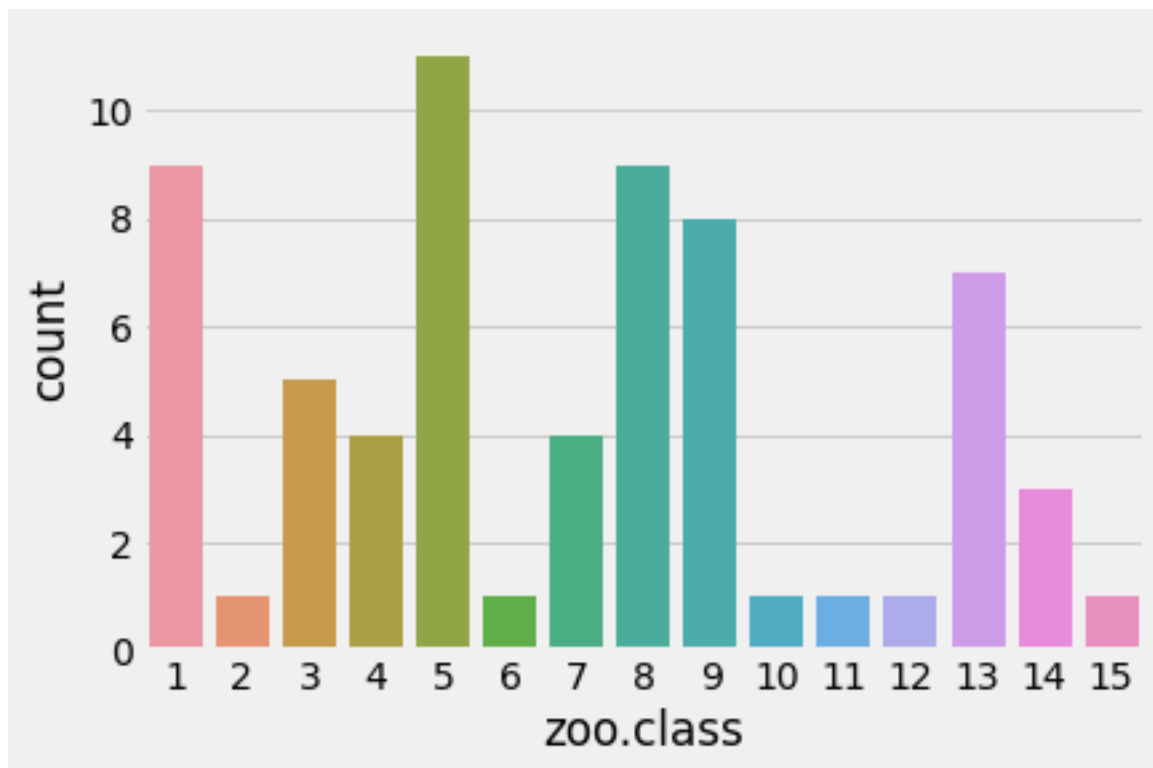
```
sns.countplot(data['zoo.class'])
```

```

C:\Users\user\AppData\Roaming\Python\Python310\site-packages\seaborn\
_decorators.py:36: FutureWarning: Pass the following variable as a
keyword arg: x. From version 0.12, the only valid positional argument
will be `data`, and passing other arguments without an explicit
keyword will result in an error or misinterpretation.
  warnings.warn(

```

```
<AxesSubplot:xlabel='zoo.class', ylabel='count'>
```

```
data['zoo.class'].value_counts()
```

```
5      11
```

```
8       9
```

```
1       9
```

```
9       8
```

```
13      7
```

```
3       5
```

```
7       4
```

```
4       4
```

```
14      3
```

```
15      1
```

```
12      1
```

```
11      1
```

```
10      1
```

```
6       1
```

```
2       1
```

```
Name: zoo.class, dtype: int64
```

```
data = data[~data['zoo.class'].isin([15, 12, 11, 10, 6, 2])]
```

```
data.head()
```

	name	top.i	bottom.i	top.c	bottom.c	top.pm
bottom.pm \						
1	Hairy tail mole	3	3	1	1	4

```
4
```

2	Common mole	3	2	1	0	3
3	Star nose mole	3	3	1	1	4
4	Brown bat	2	3	1	1	3
5	Silver hair bat	2	3	1	1	2

	top.m	bottom.m	zoo.class
1	3	3	14
2	3	3	14
3	3	3	14
4	3	3	13
5	3	3	13

```

data['zoo.class'].value_counts().index
Int64Index([5, 8, 1, 9, 13, 3, 7, 4, 14], dtype='int64')

from sklearn.preprocessing import LabelEncoder
label_encoder = LabelEncoder()
data['zoo.class'] = label_encoder.fit_transform(data['zoo.class'])

data['zoo.class'].unique()

array([8, 7, 6, 5, 4, 3, 2, 1, 0], dtype=int64)

from sklearn.neighbors import KNeighborsClassifier
from sklearn.model_selection import cross_val_score
import numpy as np

# Assuming 'X' contains your features and 'y' contains the target
variable
X = data.drop(['zoo.class', 'name'], axis=1)
y = data['zoo.class']

# Create a list of possible n_neighbors values to try
neighbors = list(range(1, 21))

# Calculate cross-validation scores for each value of n_neighbors
cv_scores = []
for k in neighbors:
    knn = KNeighborsClassifier(n_neighbors=k)
    scores = cross_val_score(knn, X, y, cv=5, scoring='accuracy') #
    You can use a different scoring metric if needed
    cv_scores.append(np.mean(scores))

# Plotting the cross-validation scores for different values of
n_neighbors
import matplotlib.pyplot as plt

```

```
plt.plot(neighbors, cv_scores)
plt.xlabel('Number of Neighbors (n_neighbors)')
plt.ylabel('Cross-Validation Accuracy')
plt.title('Optimal Number of Neighbors')
plt.show()
```

```
C:\Users\user\AppData\Roaming\Python\Python310\site-packages\sklearn\
model_selection\_split.py:676: UserWarning: The least populated class
in y has only 3 members, which is less than n_splits=5.
```

```
warnings.warn(
```

```
C:\Users\user\AppData\Roaming\Python\Python310\site-packages\sklearn\
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```

```
warnings.warn(
```

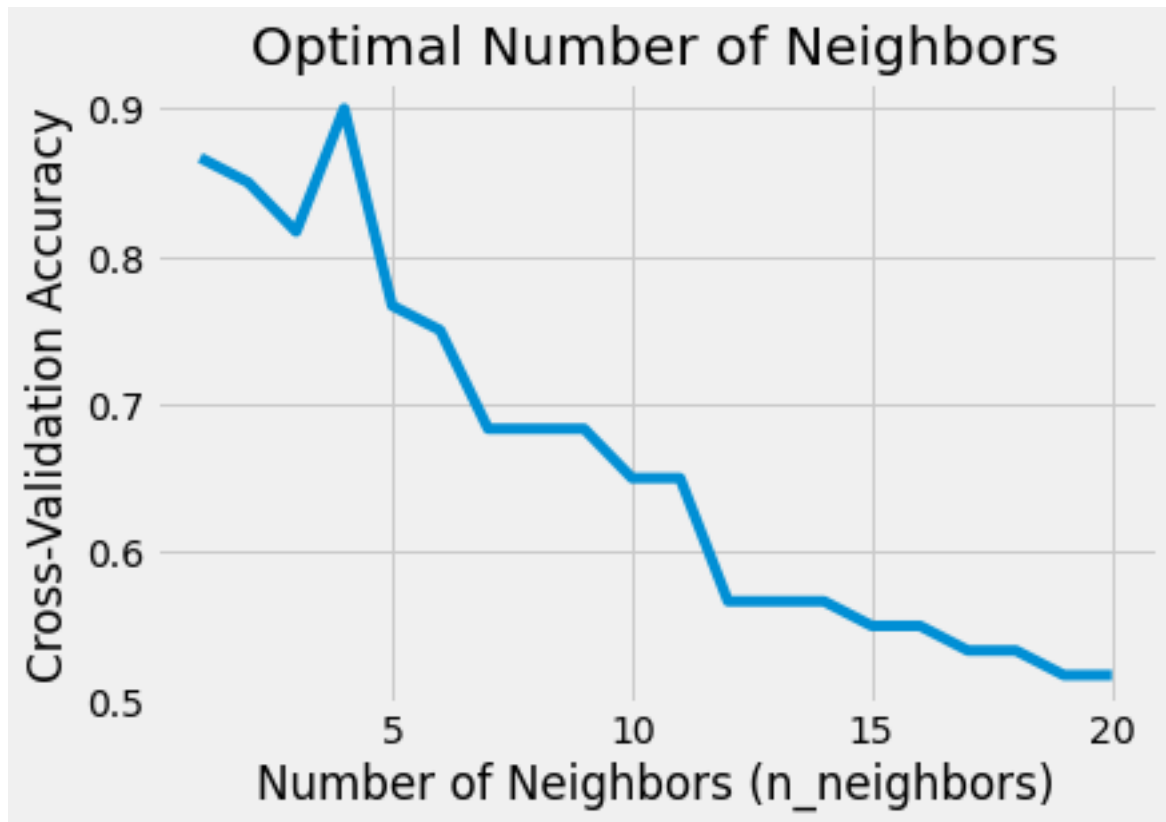
```
C:\Users\user\AppData\Roaming\Python\Python310\site-packages\sklearn\
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```

```
warnings.warn(
```

```
C:\Users\user\AppData\Roaming\Python\Python310\site-packages\sklearn\
model_selection\_split.py:676: UserWarning: The least populated class
in y has only 3 members, which is less than n_splits=5.
```

```
warnings.warn(
```

[illegible]



```
# Find the optimal value of n_neighbors with the highest cross-
validation score
optimal_k = neighbors[np.argmax(cv_scores)]
print(f"The optimal value for n_neighbors is {optimal_k}")

The optimal value for n_neighbors is 4

from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score, classification_report,
confusion_matrix

# Assuming 'X' contains your features and 'y' contains the target
variable
X_train, X_test, y_train, y_test = train_test_split(X, y,
test_size=0.3, random_state=42)

# Train the K-nearest neighbors classifier with the optimal
n_neighbors
knn = KNeighborsClassifier(n_neighbors=4)
knn.fit(X_train, y_train)

# Make predictions on the test set
y_pred = knn.predict(X_test)

# Evaluate the performance
```

```

accuracy = accuracy_score(y_test, y_pred)
print(f"Accuracy: {accuracy}")

# Display the confusion matrix
conf_matrix = confusion_matrix(y_test, y_pred)
print("Confusion Matrix:")
print(conf_matrix)

# Display the classification report
class_report = classification_report(y_test, y_pred)
print("Classification Report:")
print(class_report)

```

Accuracy: 0.6666666666666666

Confusion Matrix:

```

[[3 0 0 0 0 0 0 0 0]
 [0 0 1 2 0 0 0 0 0]
 [0 0 1 0 0 0 0 0 0]
 [0 0 0 2 1 0 0 0 0]
 [0 0 0 0 0 0 0 0 0]
 [0 0 0 0 0 0 0 0 0]
 [0 0 0 0 0 1 2 0 0]
 [0 0 0 0 0 0 0 4 0]
 [0 0 0 0 1 0 0 0 0]]

```

Classification Report:

	precision	recall	f1-score	support
0	1.00	1.00	1.00	3
1	0.00	0.00	0.00	3
2	0.50	1.00	0.67	1
3	0.50	0.67	0.57	3
4	0.00	0.00	0.00	0
5	0.00	0.00	0.00	0
6	1.00	0.67	0.80	3
7	1.00	1.00	1.00	4
8	0.00	0.00	0.00	1
accuracy			0.67	18
macro avg	0.44	0.48	0.45	18
weighted avg	0.67	0.67	0.65	18

C:\Users\user\AppData\Roaming\Python\Python310\site-packages\sklearn\metrics_classification.py:1318: UndefinedMetricWarning: Precision and F-score are ill-defined and being set to 0.0 in labels with no predicted samples. Use `zero_division` parameter to control this behavior.

```
_warn_prf(average, modifier, msg_start, len(result))
```

C:\Users\user\AppData\Roaming\Python\Python310\site-packages\sklearn\metrics_classification.py:1318: UndefinedMetricWarning: Recall and F-

```
score are ill-defined and being set to 0.0 in labels with no true
samples. Use `zero_division` parameter to control this behavior.
    _warn_prf(average, modifier, msg_start, len(result))
C:\Users\user\AppData\Roaming\Python\Python310\site-packages\sklearn\
metrics\_classification.py:1318: UndefinedMetricWarning: Precision and
F-score are ill-defined and being set to 0.0 in labels with no
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predicted samples. Use `zero_division` parameter to control this
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samples. Use `zero_division` parameter to control this behavior.
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```