Title -

IMPLEMENTATION OF CLUSTERING TECHNIQUES

1. K-MEANS
2. HIERARCHICAL CLUSTERING
3. DBSCAN
4. EXPECTATION MAXIMIZATION ALGORITHM

THEORY:

1. K-means Clustering: Objective: Partition the data into k clusters, where each data point belongs to the cluster with the nearest mean. How it works: Randomly initialize k cluster centroids. Assign each data point to the nearest centroid. Recalculate the centroid of each cluster. Repeat the assignment and recalculation steps until convergence or a specified number of iterations.Key Parameters: Number of clusters (k): The user must specify the number of clusters to form. Initialization: The method used to initialize the centroids.

2. Hierarchical Clustering: Objective: Build a hierarchy of clusters. The result is a tree-like structure called a dendrogram. How it works: Treat each data point as a single cluster. Merge the two closest clusters at each step until only one cluster remains. The dendrogram visually represents the hierarchy of clusters, and you can cut it at a certain height to obtain a specific number of clusters. Key Parameters: Linkage Method: Determines the distance between clusters. Dendrogram Cut Height: Specifies the level at which to cut the dendrogram.

3. DBSCAN (Density-Based Spatial Clustering of Applications with Noise): Objective: Identify clusters based on dense regions in the data space, and it can find clusters of arbitrary shapes. How it works: Define a neighborhood around each data point within a specified distance (eps). If a point has at least a minimum number of points (min_samples) within its neighborhood, it's considered a core point. Expand clusters by connecting core points that are close enough to each other. Points that are not core points or part of any cluster are considered outliers or noise. Key Parameters: Epsilon (eps): Maximum distance between two samples for one to be considered as being in the neighborhood of the other. Min_samples: The minimum number of samples in a neighborhood for a point to be considered as a core point.

4. EXPECTATION MAXIMIZATION ALGORITHM: The Expectation-Maximization (EM) algorithm is defined as the combination of various unsupervised machine learning algorithms, which is used to determine the local maximum likelihood estimates (MLE) or maximum a posteriori estimates (MAP) for unobservable variables in statistical models. Further, it is a technique to find maximum likelihood estimation when the latent variables are present. It is also referred to as the latent variable model.

```
import pandas as pd
from sklearn.preprocessing import StandardScaler
from sklearn.cluster import KMeans, DBSCAN
from sklearn.preprocessing import StandardScaler
from scipy.cluster.hierarchy import dendrogram, linkage
from sklearn.metrics import silhouette_score
import numpy as np
from sklearn.cluster import DBSCAN
from sklearn.impute import SimpleImputer
from sklearn.metrics import silhouette_score, adjusted_rand_score
from sklearn.mixture import GaussianMixture
import matplotlib.pyplot as plt
import seaborn as sns
```

```
file = pd.read_csv('/content/Gender_classification_dataset.csv')
file.head(20)
```

	long_hair	forehead_width_cm	forehead_height_cm	nose_wide	nose_long	lips_thin	distance_nose_to_lip_long	gender
0	1	11.8	6.1	1	0	1	1	1
1	0	14.0	5.4	0	0	1	0	0
2	0	11.8	6.3	1	1	1	1	1
3	0	14.4	6.1	0	1	1	1	1
4	1	13.5	5.9	0	0	0	0	0
5	1	13.0	6.8	1	1	1	1	1
6	1	15.3	6.2	1	1	1	0	1
7	0	13.0	5.2	0	0	0	0	0
8	1	11.9	5.4	1	0	1	1	0

```
file.isna().sum()
```

```
long_hair                    0
forehead_width_cm            0
forehead_height_cm           0
nose_wide                    0
nose_long                    0
lips_thin                    0
distance_nose_to_lip_long    0
gender                       0
dtype: int64
```

15 0 12.5 5.2 1 1 1 1 1

```
file.columns
```

```
Index(['long_hair', 'forehead_width_cm', 'forehead_height_cm', 'nose_wide',
       'nose_long', 'lips_thin', 'distance_nose_to_lip_long', 'gender'],
      dtype='object')
```

19 1 14.4 5.6 1 0 1 1 1

```
imputer = SimpleImputer(strategy='most_frequent')
numeric_features = ['long_hair', 'forehead_width_cm', 'forehead_height_cm', 'nose_wide','nose_long', 'lips_thin', 'distance_nose_to_lip_
file[numeric_features] = imputer.fit_transform(file[numeric_features])
```

```
file[numeric_features] = file[numeric_features].apply(pd.to_numeric, errors='coerce')
```

```
file.dropna(inplace=True)
```

```
features = file[numeric_features]
```

```
numeric_features = ['long_hair', 'forehead_width_cm', 'forehead_height_cm', 'nose_wide','nose_long', 'lips_thin', 'distance_nose_to_lip_
```

```
scaler = StandardScaler()
scaled_features = scaler.fit_transform(features)
```

```
kmeans = KMeans(n_clusters=3, random_state=42)
kmeans_labels = kmeans.fit_predict(scaled_features)
```

```
/usr/local/lib/python3.10/dist-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change fro
  warnings.warn(
```

```
from sklearn.cluster import AgglomerativeClustering

hierarchical = AgglomerativeClustering(n_clusters=3)
hierarchical_labels = hierarchical.fit_predict(scaled_features)
```

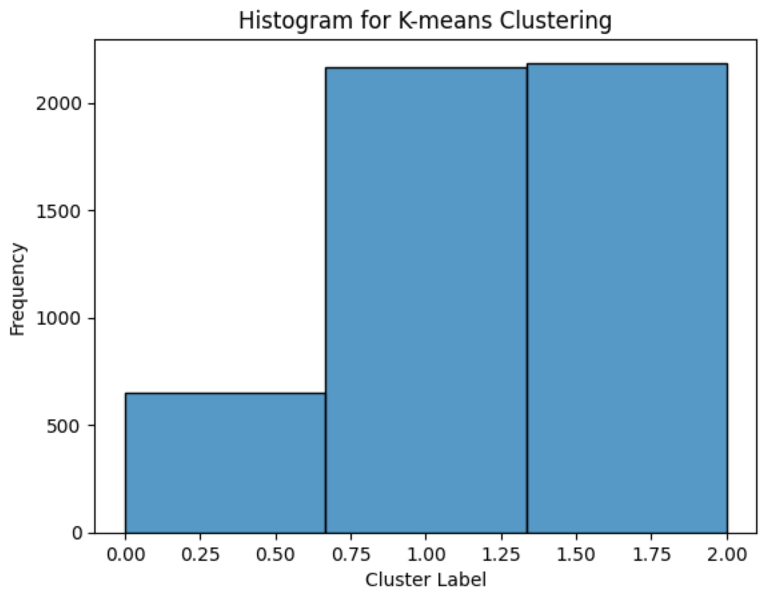
```
from sklearn.cluster import DBSCAN
from sklearn.metrics import silhouette_score

# Adjust DBSCAN parameters
dbscan = DBSCAN(eps=1.0, min_samples=5)  # Adjust parameters accordingly
dbscan_labels = dbscan.fit_predict(scaled_features)

# Check for multiple clusters
n_clusters = len(set(dbscan_labels)) - (1 if -1 in dbscan_labels else 0)

if n_clusters > 1:
    silhouette_dbscan = silhouette_score(scaled_features, dbscan_labels)
    print(f"DBSCAN Silhouette Score: {silhouette_dbscan}")
else:
    print("DBSCAN resulted in only one cluster or noise points.")
```

```
DBSCAN Silhouette Score: 0.34004545794222907
```

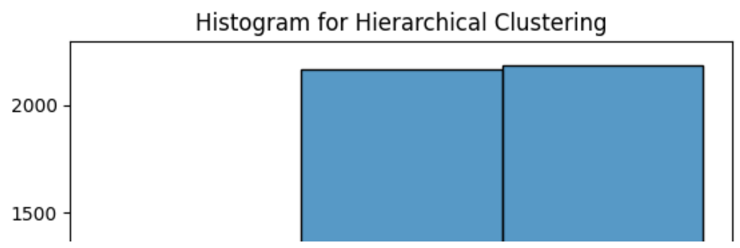
```
silhouette_kmeans = silhouette_score(scaled_features, kmeans_labels)
silhouette_hierarchical = silhouette_score(scaled_features, hierarchical_labels)
print("Silhouette Score - K-means:", silhouette_kmeans)
print("Silhouette Score - Hierarchical:", silhouette_hierarchical)
```

```
Silhouette Score - K-means: 0.39849039077126874
Silhouette Score - Hierarchical: 0.3887326841275086
```

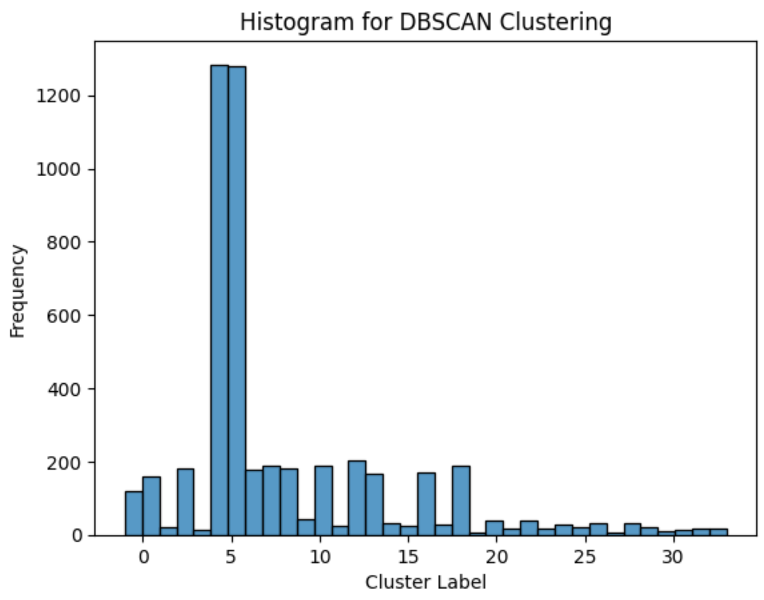
```
sns.histplot(data=kmeans_labels, bins=len(set(kmeans_labels)), kde=False)
plt.title('Histogram for K-means Clustering')
plt.xlabel('Cluster Label')
plt.ylabel('Frequency')
plt.show()
```



```
sns.histplot(data=hierarchical_labels, bins=len(set(hierarchical_labels)), kde=False)
plt.title('Histogram for Hierarchical Clustering')
plt.xlabel('Cluster Label')
plt.ylabel('Frequency')
plt.show()
```



```
sns.histplot(data=dbscan_labels, bins=len(set(dbscan_labels)), kde=False)
plt.title('Histogram for DBSCAN Clustering')
plt.xlabel('Cluster Label')
plt.ylabel('Frequency')
plt.show()
```

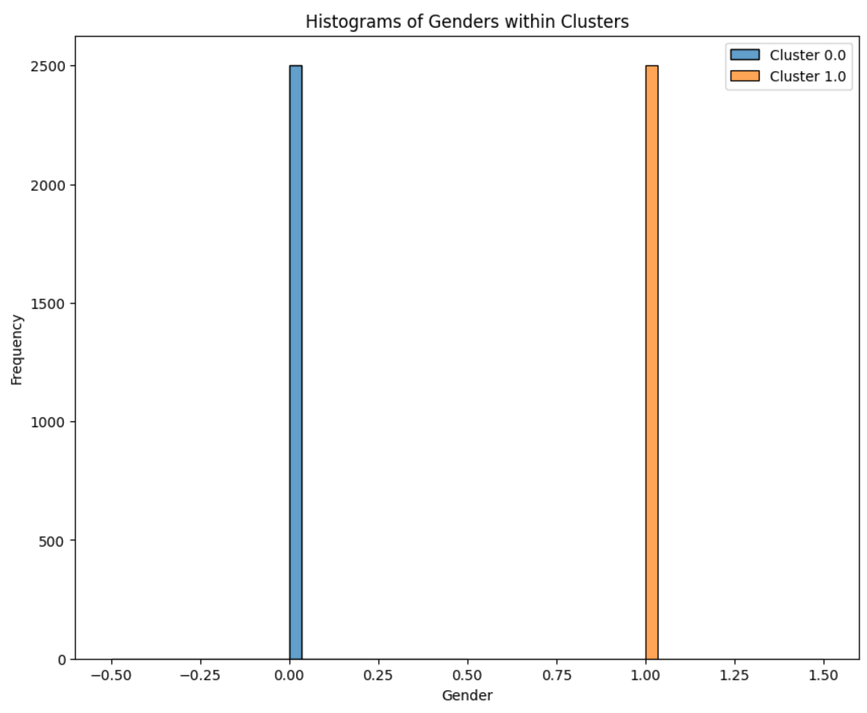


```
n_components = 3 # Adjust the number of components/clusters based on your analysis
gmm = GaussianMixture(n_components=n_components, random_state=42)
file['em_cluster'] = gmm.fit_predict(scaled_features)



silhouette_em = silhouette_score(scaled_features, file['em_cluster'])



print("\nAfter Expectation-Maximization (GMM):")
print(f"Silhouette Score (EM): {silhouette_em}")
print(file[['long_hair', 'forehead_width_cm', 'forehead_height_cm', 'nose_wide','nose_long', 'lips_thin', 'distance_nose_to_lip_long',
```

```
After Expectation-Maximization (GMM):
Silhouette Score (EM): 0.3065178986514508
      long_hair  forehead_width_cm  forehead_height_cm  nose_wide  nose_long  \
0           1.0               11.8                 6.1        1.0        0.0   
1           0.0               14.0                 5.4        0.0        0.0   
2           0.0               11.8                 6.3        1.0        1.0   
3           0.0               14.4                 6.1        0.0        1.0   
4           1.0               13.5                 5.9        0.0        0.0   
...         ...                ...                 ...        ...        ...   
4996        1.0               13.6                 5.1        0.0        0.0   
4997        1.0               11.9                 5.4        0.0        0.0   
4998        1.0               12.9                 5.7        0.0        0.0   
4999        1.0               13.2                 6.2        0.0        0.0   
5000        1.0               15.4                 5.4        1.0        1.0   

      lips_thin  distance_nose_to_lip_long  gender  
0           1.0                        1.0     1.0  
1           1.0                        0.0     0.0  
2           1.0                        1.0     1.0  
3           1.0                        1.0     1.0  
4           0.0                        0.0     0.0  
...         ...                        ...     ...  
4996        0.0                        0.0     0.0  
4997        0.0                        0.0     0.0  
4998        0.0                        0.0     0.0  
4999        0.0                        0.0     0.0  
5000        1.0                        1.0     1.0  
```

```
    [5001 rows x 8 columns]
```

```
import matplotlib.pyplot as plt
import seaborn as sns

plt.figure(figsize=(10, 8))

# Iterate over each cluster
for cluster in sorted(file['gender'].unique()):
    # Select data for the current cluster
    cluster_data = file[file['gender'] == cluster]

    # Plot histogram for 'gender'
    sns.histplot(cluster_data['gender'], bins=30, kde=True, label=f'Cluster {cluster}', alpha=0.7)

plt.title('Histograms of Genders within Clusters')
plt.xlabel('Gender')
plt.ylabel('Frequency')
plt.legend()
plt.show()
```


Histograms of Genders within Clusters
Cluster 0.0
Cluster 1.0
Frequency
Gender