Aim: To implement different clustering algorithms.

Theory:
Clustering is an unsupervised machine learning technique used to group similar data points together. The objective is to discover natural groupings within a dataset without prior knowledge of class labels. Clustering is widely used in customer segmentation, anomaly detection, image segmentation, and bioinformatics.

Types of Clustering

1. Partition-based Clustering (e.g., K-Means)
    - Divides data into a predefined number of clusters.
    - Each data point belongs to exactly one cluster.
2. Density-based Clustering (e.g., DBSCAN)
    - Forms clusters based on dense regions in the data.
    - Can identify clusters of arbitrary shape and detect noise.
3. Hierarchical Clustering
    - Builds a tree of clusters using a bottom-up (agglomerative) or top-down (divisive) approach.
4. Model-based Clustering
    - Assumes data is generated by a mixture of underlying probability distributions (e.g., Gaussian Mixture Models).

K Means Clustering:
K-Means is a partition-based clustering algorithm that divides data into K clusters.

Algorithm Steps:

1. Choose the number of clusters, K.
2. Randomly initialize K centroids.
3. Assign each data point to the nearest centroid.
4. Update centroids by computing the mean of points in each cluster.
5. Repeat steps 3 & 4 until convergence (when centroids stop changing significantly).

Key Considerations:
Choosing K: The Elbow method and Silhouette Score help determine the optimal number of clusters.
Limitations: Sensitive to initial centroid placement and does not work well with non-spherical clusters or varying densities.
DBSCAN (Density-Based Spatial Clustering of Applications with Noise):
DBSCAN is a density-based clustering algorithm that groups points closely packed together while marking low-density points as noise.

Algorithm Steps:

1. Set parameters:
2. ε (epsilon): Maximum distance to be considered a neighbor.
3. MinPts: Minimum points required to form a dense region.
4. Choose an unvisited point and determine its ε-neighborhood.
5. If the point has at least MinPts neighbors, a new cluster is formed.
6. Expand the cluster by adding density-reachable points.
7. Repeat for all points, marking outliers as noise.

Advantages:

- Handles clusters of arbitrary shape.
- Automatically detects noise and outliers.
- No need to specify the number of clusters.

Disadvantages:

- Choosing optimal ε and MinPts is challenging.
- Struggles with varying density clusters.

Steps:

1. **Load and preprocess the dataset.**

	Gender	Customer Type	Age	Type of Travel	Class	Flight Distance	Inflight wifi service	Departure/Arrival time convenient	Ease of Online booking	Gate location	...	Inflight entertainment	On-board service	Leg room service	Baggage handling
0	1	0	13	1	2	460	3	4	3	1	...	5	4	3	4
1	1	1	25	0	0	235	3	2	3	3	...	1	1	5	3
2	0	0	26	0	0	1142	2	2	2	2	...	5	4	3	4
3	0	0	25	0	0	562	2	5	5	5	...	2	2	5	3
4	1	0	61	0	0	214	3	3	3	3	...	3	3	4	4

Checkin service	Inflight service	Cleanliness	Departure Delay in Minutes	Arrival Delay in Minutes	satisfaction
4	5	5	25	18.0	0
1	4	1	1	6.0	0
4	4	5	0	0.0	1
1	4	2	11	9.0	0
3	3	3	0	0.0	1

The dataset represents airline passenger satisfaction, containing demographic details (Gender, Age, Customer Type, Type of Travel), flight-related attributes (Class, Flight Distance, Gate Location), in-flight service ratings (Seat Comfort, Inflight WiFi, Entertainment, Food & Drink), and delay metrics (Departure/Arrival Delay). Satisfaction is labeled as 0 (Unsatisfied) or 1 (Satisfied), making it suitable for classification and clustering.

2. Elbow method for number of clusters

The Elbow Method plot helps determine the optimal number of clusters (K) in K-Means by plotting inertia (sum of squared distances to cluster centers) against different K values. The "elbow" point, where inertia reduction slows significantly, indicates the ideal K.

Formula to calculate:

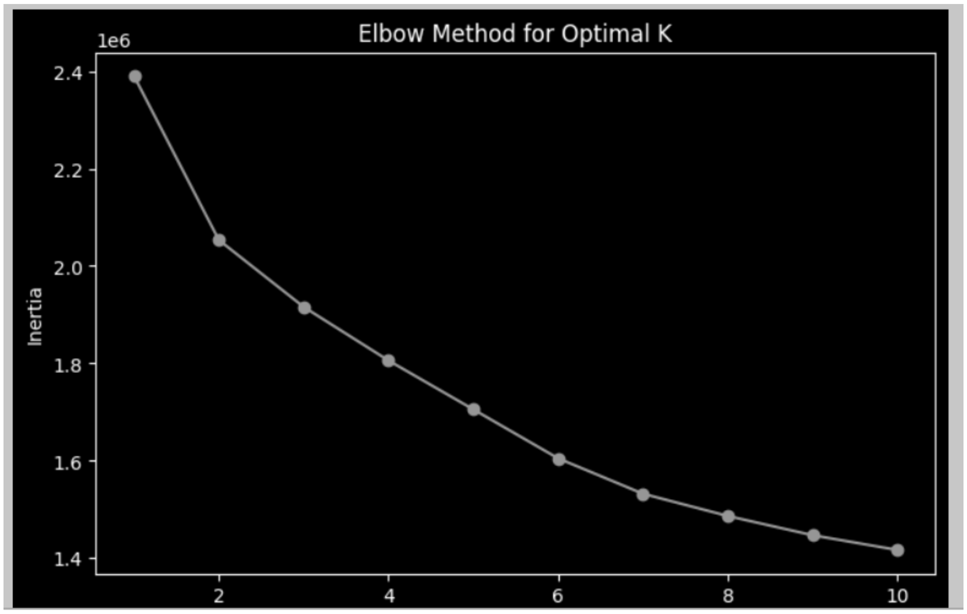
$$WCSS = \sum_{i=1}^{K} \sum_{x \in C_i} ||x - \mu_i||^2$$

where,

- Ci = Cluster i
- μi = Centroid of cluster Ci
- || xi - μi $||^2$ = Squared Euclidean distance between a point and its cluster centroid

The **elbow point** is where the WCSS starts decreasing at a slower rate.

```
# Determine optimal clusters using Elbow Method
inertia = []
k_values = range(1, 11)
for k in k_values:
    kmeans = KMeans(n_clusters=k, random_state=42, n_init=10)
    kmeans.fit(df_scaled)
    inertia.append(kmeans.inertia_)

# Plot the Elbow Method
plt.figure(figsize=(8, 5))
plt.plot(k_values, inertia, marker='o')
plt.xlabel("Number of Clusters")
plt.ylabel("Inertia")
plt.title("Elbow Method for Optimal K")
plt.show()
```



In this plot, the elbow appears around K = 4 or 5.The dataset likely has 4 or 5 naturally distinct groups, and choosing K balances segmentation quality and computational efficiency

3. **K means clustering**

```
# Apply K-Means with optimal K (assume 3 based on elbow method)
kmeans = KMeans(n_clusters=4, random_state=42, n_init=10)
df['Cluster'] = kmeans.fit_predict(df_scaled)

# Display cluster distribution
print(df['Cluster'].value_counts())
```

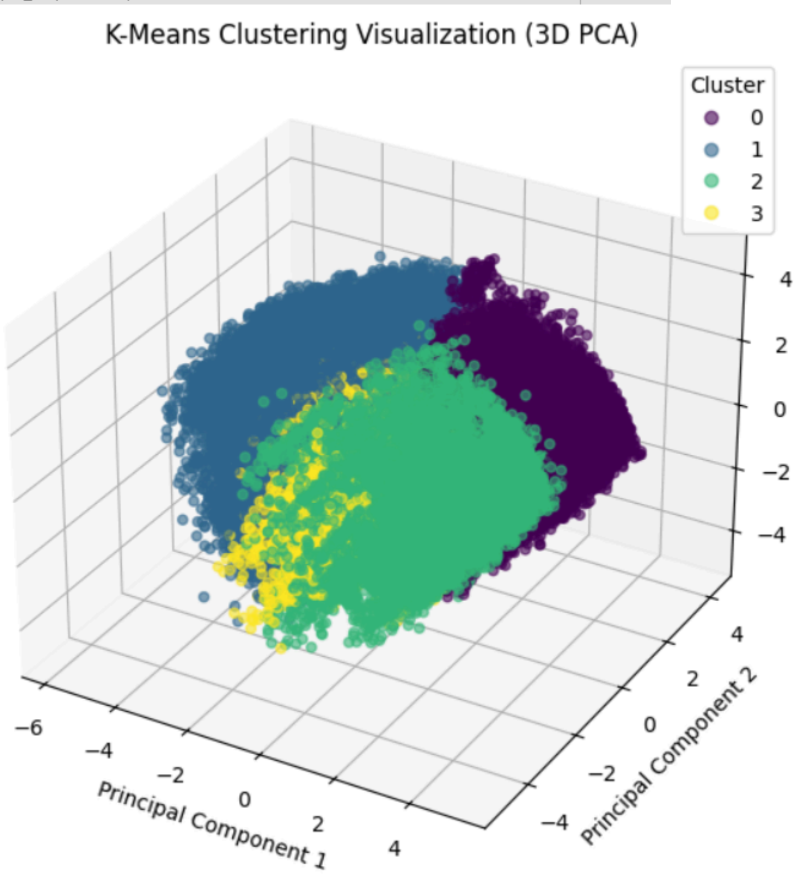
```
Cluster
1    35729
3    25697
0    22216
2    20262
Name: count, dtype: int64
```

We try out clusters for k = 4 and 5. With k = 5, we find that cluster size of last cluster is very small as compared to the other clusters formed. So we use k = 4, we can observe that the clusters formed are similar in size. The four cluster formed are:

0 - 22216
1 - 35729
2 - 20262
3 - 25697

Visualization of clusters:

```
from mpl_toolkits.mplot3d import Axes3D
from sklearn.decomposition import PCA

# Reduce dimensions to 3
pca_3d = PCA(n_components=3)
df_pca_3d = pca_3d.fit_transform(df_scaled)

df_plot_3d = pd.DataFrame(df_pca_3d, columns=['PC1', 'PC2', 'PC3'])
df_plot_3d['Cluster'] = df['Cluster']

# 3D scatter plot
fig = plt.figure(figsize=(10, 7))
ax = fig.add_subplot(111, projection='3d')

# Scatter plot with cluster colors
scatter = ax.scatter(df_plot_3d['PC1'], df_plot_3d['PC2'], df_plot_3d['PC3'],
                     c=df_plot_3d['Cluster'], cmap='viridis', alpha=0.6)

ax.set_title('K-Means Clustering Visualization (3D PCA)')
ax.set_xlabel('Principal Component 1')
ax.set_ylabel('Principal Component 2')
ax.set_zlabel('Principal Component 3')

plt.legend(*scatter.legend_elements(), title='Cluster')
plt.show()

# Ensure feature names match df_scaled
feature_names = df.select_dtypes(include=[np.number]).columns.tolist()[:df_scaled.shape[1]]

# Create PCA components DataFrame
pca_components = pd.DataFrame(pca_3d.components_, columns=feature_names,
                              index=['PC1', 'PC2', 'PC3'])

# Display how features contribute to each principal component
print(pca_components.T)
```



To visualize the clusters we perform **Principal Component Analysis (PCA)** to reduce the dataset dimensions to three, making it easier to visualize the clusters obtained from K-Means

clustering. The **3D scatter plot** visualizes the clusters in the transformed feature space, where different colors represent different clusters. The clusters appear to be well-defined, indicating that the K-Means algorithm successfully grouped similar data points.
The PCA components **help analyze the contribution** of original features to the new principal components, providing insights into how data is distributed across clusters.

4. **DBSCAN clustering**

DBSCAN is an unsupervised clustering algorithm that groups together densely packed points while marking outliers as noise. Unlike K-Means, it does not require specifying the number of clusters in advance and is useful for identifying arbitrarily shaped clusters.
1. Defines Two Parameters:
- ε (epsilon): The radius to consider neighboring points.
- MinPts: Minimum number of points required in an ε-neighborhood to form a cluster.

2. Classifies Points as:
- Core Points: Points with at least MinPts neighbors within ε.
- Border Points: Points within ε of a core point but with fewer than MinPts neighbors.
- Noise Points: Points that are neither core nor border (outliers).

3.Clustering Process:
- Starts with an unvisited point.
- Expands a cluster if it's a core point, connecting all reachable points.

Repeats until all points are classified.

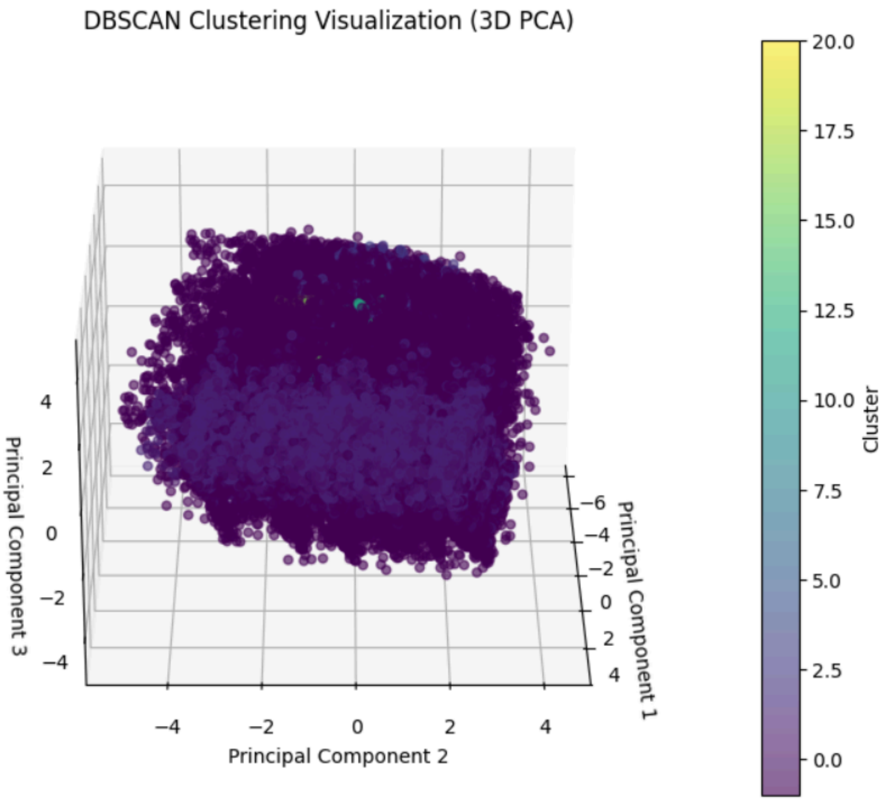
```
from sklearn.cluster import DBSCAN

# Apply DBSCAN clustering
dbscan = DBSCAN(eps=2, min_samples=50)  # Adjust eps and min_samples as needed
clusters = dbscan.fit_predict(df_scaled)

# Add cluster labels to the dataset
df["Cluster"] = clusters

# Display cluster distribution
print(df['Cluster'].value_counts())
```

```
Cluster
-1     70501
 1     11596
 0     11462
 2      4136
 3      3677
 4       695
 13      259
 11      219
 8       202
 5       178
 7       162
 14      129
 15      113
 6       107
 12      100
 10       75
 9        52
 19       51
 20       50
 16       49
 17       47
 18       44
Name: count, dtype: int64
```

We apply **DBSCAN clustering** with **eps=2** and **min_samples=50**, grouping data points based on density. It assigns cluster labels using dbscan.fit_predict(df_scaled) and stores them in the dataset. The output shows that **most points (70501)** are classified as **noise (-1)**, while the remaining data forms multiple clusters of varying sizes.

The **high number of noise points (-1)** in the output suggests that the chosen eps=2 is **too small to form dense clusters**, causing many points to be classified as outliers. Additionally, min_samples=50 requires at least 50 points in a neighborhood to form a cluster, which may be too restrictive for some regions of the dataset. As a result, only a few dense clusters are detected, while most points remain unclustered.

Visualization:



The DBSCAN clustering visualization in 3D PCA space shows that the majority of points are assigned to cluster -1 (noise) with only a few points belonging to distinct smaller clusters. This suggests that DBSCAN's parameters (epsilon and min_samples) may not be well-tuned for clear separation, leading to most points being grouped together while only a few scattered regions are identified as separate clusters.

<u>Inference from both the clustering:</u>

Overall we can see that the performance of **K means** is **better** than DBSCAN for clustering the dataset.

K-Means was a better choice for this dataset because the data is well-distributed without high-density regions, and clusters can be separated by distance rather than density.

DBSCAN struggled due to high dimensionality and the lack of naturally dense clusters, causing excessive noise detection.

Conclusion:

In all, we come to know that K-Means and DBSCAN analyze airline passenger satisfaction data. K-Means (K=4) successfully grouped data into well-separated clusters, confirmed by the Elbow Method and PCA visualization, though it is sensitive to outliers. DBSCAN, however, struggled with this dataset, classifying many points as noise due to a lack of well-defined dense regions, making it less effective for this case.