# ASSIGNMENT 5 - CLUSTERING

## Objective

The objective of this assessment is to evaluate the understanding and application of clustering techniques on a real-world dataset.

## Dataset

The dataset used for this assignment is the **Iris dataset**, available in the `sklearn` library.

In [1]:
```
import warnings
import sys
if not sys.warnoptions:
    warnings.simplefilter("ignore")
```

#### 1. Loading and Preprocessing

In [15]:
```
from sklearn.datasets import load_iris
import pandas as pd

iris = load_iris()

df = pd.DataFrame(data=iris.data, columns=iris.feature_names)

df.head()
```

Out[15]:

| | sepal length (cm) | sepal width (cm) | petal length (cm) | petal width (cm) |
|---|---|---|---|---|
| **0** | 5.1 | 3.5 | 1.4 | 0.2 |
| **1** | 4.9 | 3.0 | 1.4 | 0.2 |
| **2** | 4.7 | 3.2 | 1.3 | 0.2 |
| **3** | 4.6 | 3.1 | 1.5 | 0.2 |
| **4** | 5.0 | 3.6 | 1.4 | 0.2 |

In [3]:
```
df['species'] = iris.target


df_without_species = df.drop(columns=['species'])


print(df_without_species.head())
```

```
   sepal length (cm)  sepal width (cm)  petal length (cm)  petal width (cm)
0                5.1               3.5                1.4               0.2
1                4.9               3.0                1.4               0.2
2                4.7               3.2                1.3               0.2
3                4.6               3.1                1.5               0.2
4                5.0               3.6                1.4               0.2
```

In [4]:
```
print("Dataset Info:")
df_without_species.info()
```

```
Dataset Info:
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 150 entries, 0 to 149
Data columns (total 4 columns):
 #   Column             Non-Null Count  Dtype  
---  ------             --------------  -----  
 0   sepal length (cm)  150 non-null    float64
 1   sepal width (cm)   150 non-null    float64
 2   petal length (cm)  150 non-null    float64
 3   petal width (cm)   150 non-null    float64
dtypes: float64(4)
memory usage: 4.8 KB
```

In [5]:
```
print("Statistical Summary:")
df_without_species.describe()
```

```
Statistical Summary:
```

Out[5]:

| | sepal length (cm) | sepal width (cm) | petal length (cm) | petal width (cm) |
|---|---|---|---|---|
| **count** | 150.000000 | 150.000000 | 150.000000 | 150.000000 |
| **mean** | 5.843333 | 3.057333 | 3.758000 | 1.199333 |
| **std** | 0.828066 | 0.435866 | 1.765298 | 0.762238 |
| **min** | 4.300000 | 2.000000 | 1.000000 | 0.100000 |
| **25%** | 5.100000 | 2.800000 | 1.600000 | 0.300000 |
| **50%** | 5.800000 | 3.000000 | 4.350000 | 1.300000 |
| **75%** | 6.400000 | 3.300000 | 5.100000 | 1.800000 |
| **max** | 7.900000 | 4.400000 | 6.900000 | 2.500000 |

In [6]:
```
print("Null values in each column:")
print(df_without_species.isnull().sum())
```

```
Null values in each column:
sepal length (cm)    0
sepal width (cm)     0
petal length (cm)    0
petal width (cm)     0
dtype: int64
```

In [7]:
```
df_without_species.duplicated().sum()
```

Out[7]:
```
np.int64(1)
```

In [8]:
```
df_without_species.shape
```

Out[8]:
```
(150, 4)
```

In [9]:
```
df_without_species.drop_duplicates(inplace=True)
```

In [10]:
```
df_without_species.shape
```

Out[10]: (149, 4)

In [11]:
```
from sklearn.preprocessing import StandardScaler
scaler = StandardScaler()
scaled_data = scaler.fit_transform(df_without_species)
scaled_df = pd.DataFrame(data=scaled_data, columns=iris.feature_names)
print(scaled_df.head())
```

```
   sepal length (cm)  sepal width (cm)  petal length (cm)  petal width (cm)
0          -0.898033          1.012401          -1.333255         -1.308624
1          -1.139562         -0.137353          -1.333255         -1.308624
2          -1.381091          0.322549          -1.390014         -1.308624
3          -1.501855          0.092598          -1.276496         -1.308624
4          -1.018798          1.242352          -1.333255         -1.308624
```

# 2. Clustering Algorithm Implementation

## A) KMeans Clustering

### Description of KMeans Clustering

KMeans is a widely used clustering algorithm that partitions data into **K clusters** by minimizing intra-cluster variance. The algorithm follows these steps:

1. **Initialize Centroids**: Randomly select K initial cluster centroids.
2. **Assign Points to Clusters**: Assign each data point to the nearest centroid based on a distance metric (e.g., Euclidean distance).
3. **Update Centroids**: Recalculate the centroids as the mean of all points assigned to each cluster.
4. **Iterate**: Repeat steps 2 and 3 until the centroids stabilize (i.e., no further changes) or the maximum number of iterations is reached.

### Suitability for the Iris Dataset

The Iris dataset contains three well-defined clusters that correspond to the three species: **Setosa**, **Versicolor**, and **Virginica**. KMeans clustering is particularly suitable for this dataset because:

- It is designed to partition data into compact clusters.
- The dataset's four numerical features (sepal length, sepal width, petal length, and petal width) provide a clear structure for clustering.
- KMeans efficiently identifies natural groupings in the data, making it an ideal choice for exploring the inherent structure of the Iris dataset.

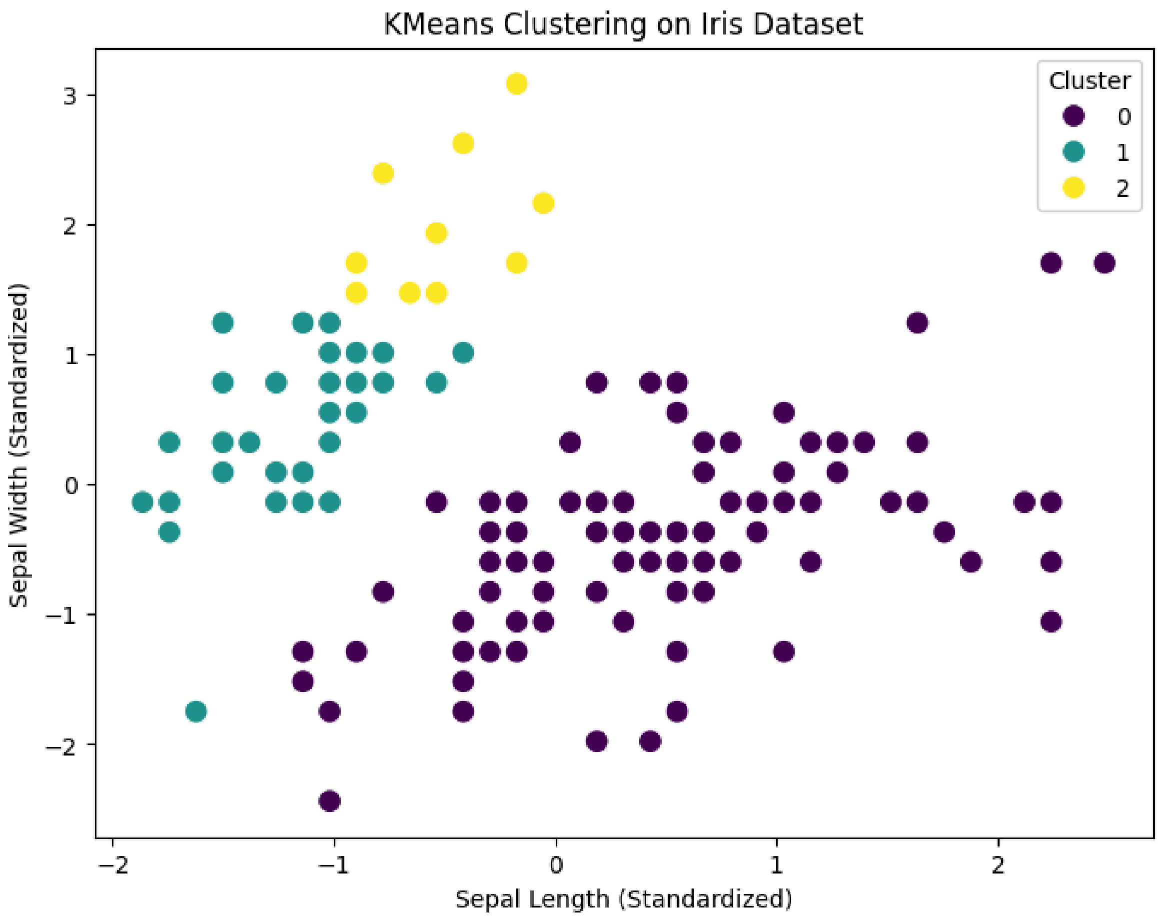
### Implementation

- Apply KMeans clustering to the preprocessed Iris dataset.
- Visualize the resulting clusters using scatter plots.

The clustering results will highlight how well the algorithm separates the data into meaningful groups.

In [12]:

```
from sklearn.cluster import KMeans
import matplotlib.pyplot as plt
import seaborn as sns
kmeans = KMeans(n_clusters=3, random_state=42)
kmeans.fit(scaled_df)
cluster_labels = kmeans.labels_
scaled_df['cluster'] = cluster_labels
plt.figure(figsize=(8, 6))
sns.scatterplot(
    x=scaled_df.iloc[:, 0],  # sepal length
    y=scaled_df.iloc[:, 1],  # sepal width
    hue=scaled_df['cluster'],  # color by cluster
    palette='viridis',
    s=100
)
plt.title('KMeans Clustering on Iris Dataset')
plt.xlabel('Sepal Length (Standardized)')
plt.ylabel('Sepal Width (Standardized)')
plt.legend(title='Cluster')
plt.show()
```




## B) Hierarchical Clustering

### Description of Hierarchical Clustering

Hierarchical clustering is a clustering technique that builds a hierarchy of clusters through one of two approaches:

- **Agglomerative (Bottom-Up)**: Starts with each data point as its own cluster and merges clusters iteratively.
- **Divisive (Top-Down)**: Starts with all data points in a single cluster and splits them iteratively.

Steps of Agglomerative Hierarchical Clustering:

1. **Treat Each Data Point as a Cluster**: Initially, each data point is considered its own cluster.
2. **Compute Distances**: Calculate pairwise distances between clusters using a linkage criterion (e.g., single linkage, complete linkage, average linkage).
3. **Merge Clusters**: Merge the two closest clusters based on the chosen distance metric.
4. **Repeat**: Continue merging clusters until all points are combined into a single cluster or a stopping criterion is reached.

### Suitability for the Iris Dataset

Hierarchical clustering is suitable for the Iris dataset because:

- It reveals **hierarchical relationships** among data points, which may naturally exist in the dataset.
- Unlike KMeans, it doesn't require specifying the number of clusters upfront, allowing exploration of different groupings.
- The dendrogram provides a visual representation of the clustering hierarchy, making it easier to analyze the cluster structure and relationships among data points.

### Implementation

- Apply agglomerative hierarchical clustering to the preprocessed Iris dataset.
- Visualize the clusters using dendrograms and scatter plots to analyze the results.

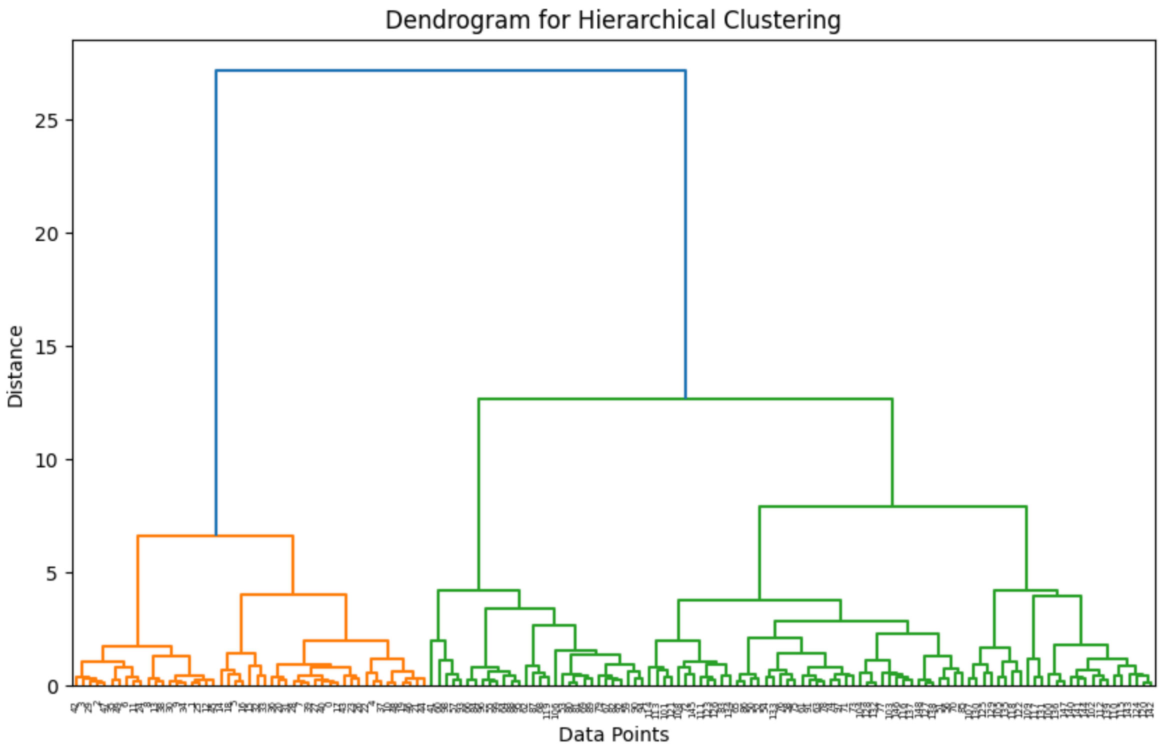
This method helps in identifying meaningful cluster structures and provides insights into the dataset's hierarchical nature.

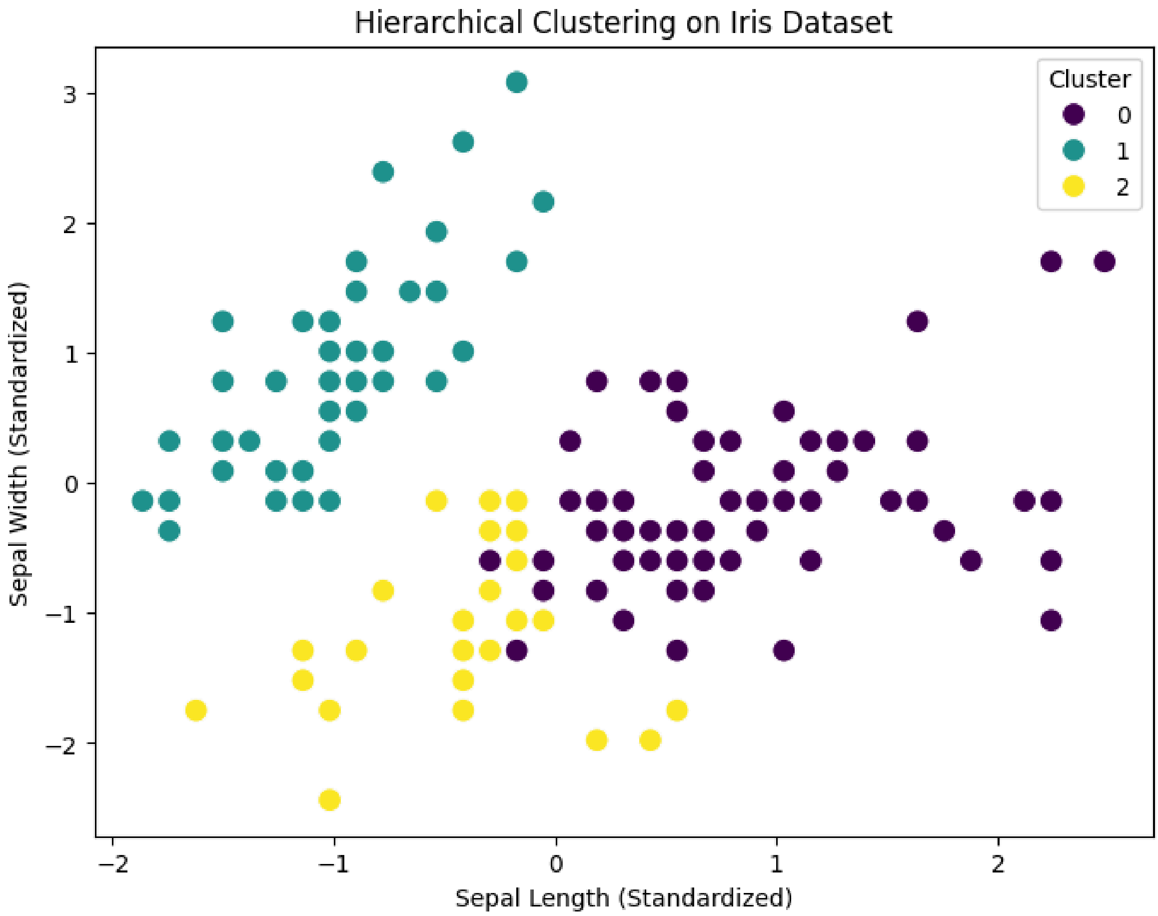
In [13]:
```
from scipy.cluster.hierarchy import dendrogram, linkage
from sklearn.cluster import AgglomerativeClustering
linkage_matrix = linkage(scaled_df.iloc[:, :-1], method='ward')

plt.figure(figsize=(10, 6))
dendrogram(linkage_matrix)
plt.title('Dendrogram for Hierarchical Clustering')
plt.xlabel('Data Points')
plt.ylabel('Distance')
plt.show()
hierarchical = AgglomerativeClustering(n_clusters=3, metric='euclidean', linkage
hierarchical_labels = hierarchical.fit_predict(scaled_df.iloc[:, :-1])
scaled_df['hierarchical_cluster'] = hierarchical_labels

plt.figure(figsize=(8, 6))
sns.scatterplot(
    x=scaled_df.iloc[:, 0],  # sepal length
    y=scaled_df.iloc[:, 1],  # sepal width
```

```
    hue=scaled_df['hierarchical_cluster'],  # color by cluster
    palette='viridis',
    s=100
)
plt.title('Hierarchical Clustering on Iris Dataset')
plt.xlabel('Sepal Length (Standardized)')
plt.ylabel('Sepal Width (Standardized)')
plt.legend(title='Cluster')
plt.show()
```



## Model Evaluation

In [14]:
```
from sklearn.metrics import silhouette_score
kmeans_silhouette = silhouette_score(scaled_df.iloc[:, :-2], cluster_labels)
print(f"Silhouette Score for KMeans Clustering: {kmeans_silhouette:.3f}")
hierarchical_silhouette = silhouette_score(scaled_df.iloc[:, :-2], hierarchical_
print(f"Silhouette Score for Hierarchical Clustering: {hierarchical_silhouette:.
```

```
Silhouette Score for KMeans Clustering: 0.494
Silhouette Score for Hierarchical Clustering: 0.450
```

*__KMeans Clustering Silhouette Score: 0.494__*

*__Hierarchical Clustering Silhouette Score: 0.450__*

## Interpretation

### Silhouette Score Comparison

The silhouette score for **KMeans clustering** is slightly higher than that for **Hierarchical clustering**. A higher silhouette score indicates that clusters are more compact and well-separated, signifying better clustering quality.

### Better Model

KMeans Clustering outperforms Hierarchical Clustering on the Iris dataset. Its clusters are better separated and internally consistent, leading to higher-quality results.

### Possible Reasons

1. **KMeans Clustering**:
    - Performs well on datasets with a clear, spherical cluster structure, such as the Iris dataset with its well-defined groupings of species.
2. **Hierarchical Clustering**:
    - May struggle due to sensitivity to noise or the choice of distance metric and linkage method, which can impact the quality of the resulting clusters.