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1 Clustering Algorithm for Iris Dataset

1.1 Name: Ajo Babu A

1.2 Overview

The Iris dataset consists of 150 flower samples from three species, with four features: sepal length, sepal width, petal length, and petal width. In a clustering project, the goal is to apply unsupervised learning techniques like K-Means or DBSCAN to group the flowers based on these features and assess whether the algorithm can successfully identify the three species without using the target labels. The project involves data preprocessing, including visual exploration, feature scaling, and choosing an appropriate clustering algorithm to evaluate the results.

2 Objective

The objective of this project is to apply hierarchical clustering and K-Means clustering algorithms to the Iris dataset to identify groups of flowers based on their features (sepal length, sepal width, petal length, and petal width). The goal is to compare the effectiveness of both unsupervised learning methods in grouping the flowers into distinct clusters and evaluate how well these clusters align with the actual species in the dataset.

2.1 Dataset: Iris data from sklearn

2.2 Importing Libraries

[194]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns


from sklearn.cluster import KMeans

from sklearn.cluster import AgglomerativeClustering
import scipy.cluster.hierarchy as sch


from sklearn.metrics import silhouette_score
```

```
from sklearn.preprocessing import MinMaxScaler


import warnings
warnings.filterwarnings("ignore")
```

2.3 Loading data from sklearn

[84]:
```
from sklearn.datasets import load_iris
iris = load_iris()
```

[86]:
```
iris
```

[86]:
```
{'data': array([[5.1, 3.5, 1.4, 0.2],
        [4.9, 3. , 1.4, 0.2],
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```

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       2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2]),
 'frame': None,
 'target_names': array(['setosa', 'versicolor', 'virginica'], dtype='<U10'),
 'DESCR': '.. _iris_dataset:\n\nIris plants
dataset\n--------------------\n\n**Data Set Characteristics:**\n\n:Number of
Instances: 150 (50 in each of three classes)\n:Number of Attributes: 4 numeric,
predictive attributes and the class\n:Attribute Information:\n    - sepal length
in cm\n    - sepal width in cm\n    - petal length in cm\n    - petal width in
cm\n    - class:\n            - Iris-Setosa\n            - Iris-Versicolour\n
- Iris-Virginica\n\n:Summary Statistics:\n\n============== ==== ==== =======
===== ====================\n                Min  Max   Mean    SD   Class
Correlation\n============== ==== ==== ======= ===== ====================\nsepal
length:   4.3  7.9   5.84   0.83    0.7826\nsepal width:    2.0  4.4   3.05
0.43   -0.4194\npetal length:   1.0  6.9   3.76   1.76    0.9490  (high!)\npetal
width:    0.1  2.5   1.20   0.76    0.9565  (high!)\n============== ==== ====
======= ===== ====================\n\n:Missing Attribute Values: None\n:Class
Distribution: 33.3% for each of 3 classes.\n:Creator: R.A. Fisher\n:Donor:
Michael Marshall (MARSHALL%PLU@io.arc.nasa.gov)\n:Date: July, 1988\n\nThe famous
```

```
Iris database, first used by Sir R.A. Fisher. The dataset is taken\nfrom
Fisher\'s paper. Note that it\'s the same as in R, but not as in the
UCI\nMachine Learning Repository, which has two wrong data points.\n\nThis is
perhaps the best known database to be found in the\npattern recognition
literature.  Fisher\'s paper is a classic in the field and\nis referenced
frequently to this day.  (See Duda & Hart, for example.)  The\ndata set contains
3 classes of 50 instances each, where each class refers to a\ntype of iris
plant.  One class is linearly separable from the other 2; the\nlatter are NOT
linearly separable from each other.\n\n|details-
start|\n**References**\n|details-split|\n\n- Fisher, R.A. "The use of multiple
measurements in taxonomic problems"\n  Annual Eugenics, 7, Part II, 179-188
(1936); also in "Contributions to\n  Mathematical Statistics" (John Wiley, NY,
1950).\n- Duda, R.O., & Hart, P.E. (1973) Pattern Classification and Scene
Analysis.\n  (Q327.D83) John Wiley & Sons.  ISBN 0-471-22361-1.  See page
218.\n- Dasarathy, B.V. (1980) "Nosing Around the Neighborhood: A New System\n
Structure and Classification Rule for Recognition in Partially Exposed\n
Environments".  IEEE Transactions on Pattern Analysis and Machine\n
Intelligence, Vol. PAMI-2, No. 1, 67-71.\n- Gates, G.W. (1972) "The Reduced
Nearest Neighbor Rule".  IEEE Transactions\n  on Information Theory, May 1972,
431-433.\n- See also: 1988 MLC Proceedings, 54-64.  Cheeseman et al"s AUTOCLASS
II\n  conceptual clustering system finds 3 classes in the data.\n- Many, many
more …\n\n|details-end|\n',
 'feature_names': ['sepal length (cm)',
  'sepal width (cm)',
  'petal length (cm)',
  'petal width (cm)'],
 'filename': 'iris.csv',
 'data_module': 'sklearn.datasets.data'}
```

[88]:
```
# Convert to DataFrame
df = pd.DataFrame(iris.data, columns=iris.feature_names)
df['species'] = iris.target
```

[90]:
```
# Drop the species column
features = df.drop(columns=['species'])
```

[92]:
```
df.columns
```

[92]:
```
Index(['sepal length (cm)', 'sepal width (cm)', 'petal length (cm)',
       'petal width (cm)', 'species'],
      dtype='object')
```

[94]:
```
# Dropping column
df = df.drop('species',axis=1)
```

[96]:
```
df.columns
```

[96]:
```
Index(['sepal length (cm)', 'sepal width (cm)', 'petal length (cm)',
       'petal width (cm)'],
      dtype='object')
```

[98]:
```
len(df.columns)
```

[98]:
```
4
```

[100]:
```
df.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
```

[102]:
```
df.describe()
```

[102]:
```
       sepal length (cm)  sepal width (cm)  petal length (cm)  \
count         150.000000        150.000000         150.000000
mean            5.843333          3.057333           3.758000
std             0.828066          0.435866           1.765298
min             4.300000          2.000000           1.000000
25%             5.100000          2.800000           1.600000
50%             5.800000          3.000000           4.350000
75%             6.400000          3.300000           5.100000
max             7.900000          4.400000           6.900000

       petal width (cm)
count        150.000000
mean           1.199333
std            0.762238
min            0.100000
25%            0.300000
50%            1.300000
75%            1.800000
max            2.500000
```

[104]:
```
df.dtypes
```

[104]:
```
sepal length (cm)    float64
sepal width (cm)     float64
petal length (cm)    float64
petal width (cm)     float64
dtype: object
```

[106]:
```
df.shape
```

[106]:
```
(150, 4)
```

[108]:
```
df.head()
```

[108]:

	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

[110]:
```
df.duplicated()
```

[110]:
```
0      False
1      False
2      False
3      False
4      False
       …
145    False
146    False
147    False
148    False
149    False
Length: 150, dtype: bool
```

[112]:
```
df.duplicated().sum()
```

[112]:
```
1
```

[114]:
```
df = df.drop_duplicates()
```

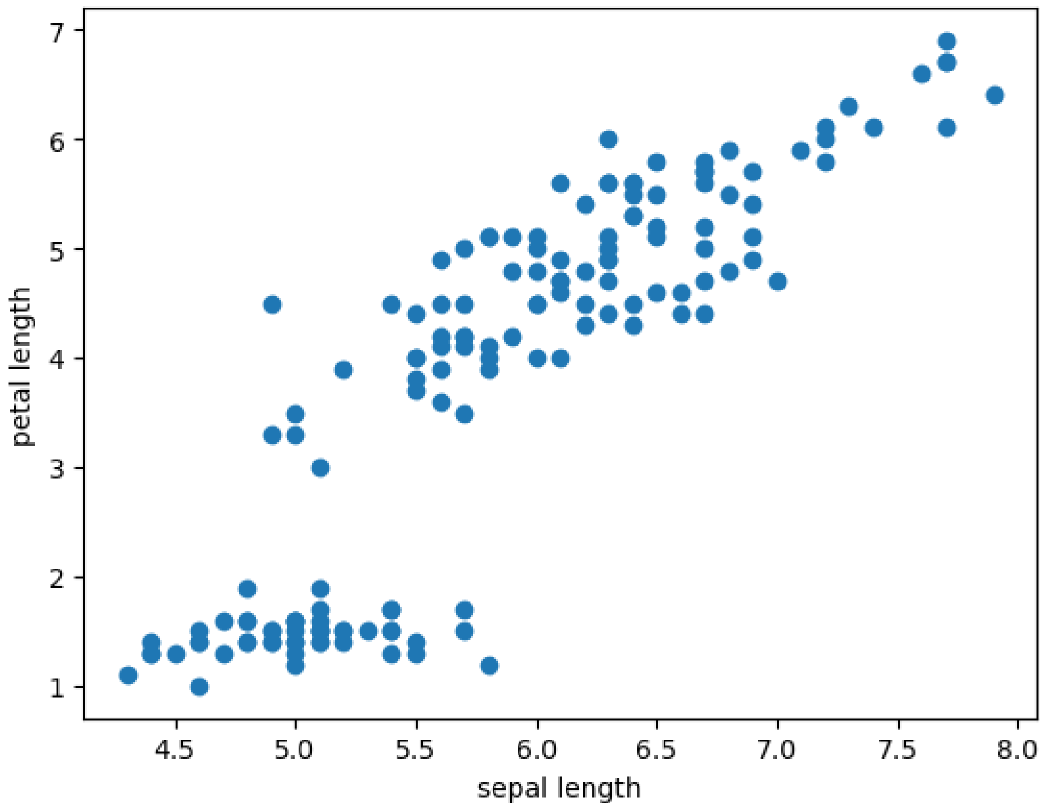
[116]:
```
df.duplicated().sum()
```

[116]:
```
0
```

2.4 Finding number of clusters

[124]:
```
## Drawing scatterplot to find the number of clusters
plt.scatter(df['sepal length (cm)'],df['petal length (cm)'])
plt.xlabel('sepal length')
plt.ylabel('petal length')
```

[124]: Text(0, 0.5, 'petal length')



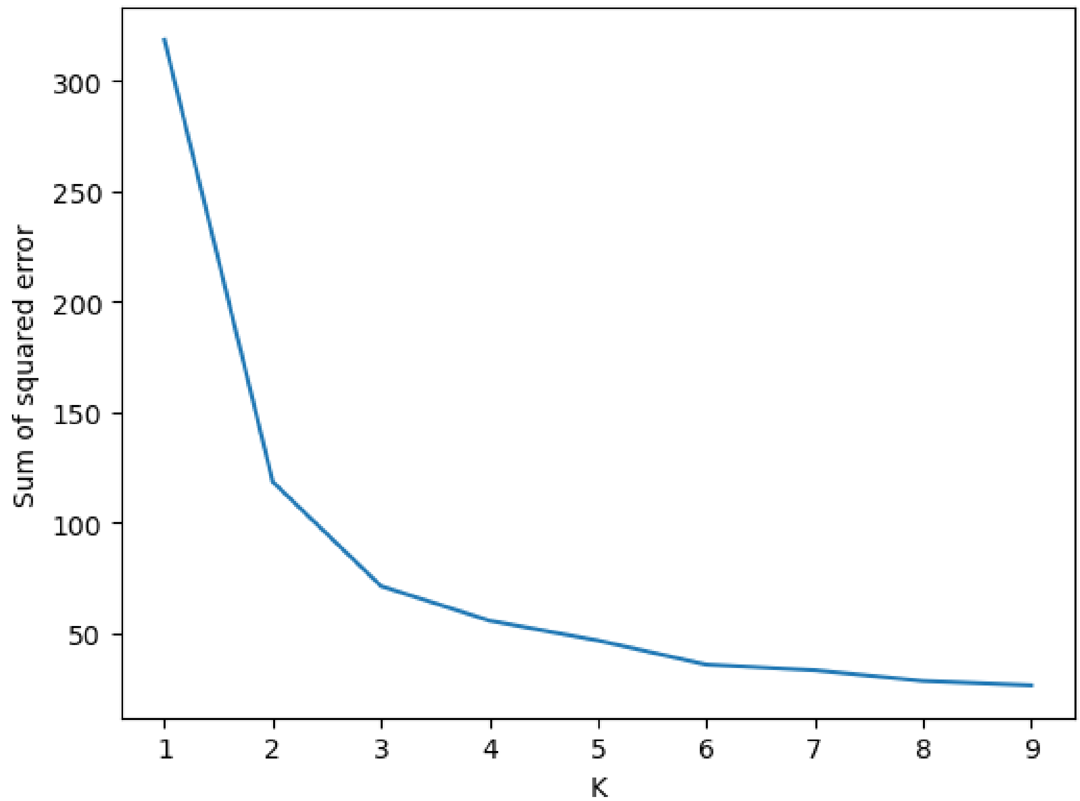
2.5 Elbow method

[133]:
```
sse = []  #WCSS
k_rng = range(1,10)
for k in k_rng:
    km = KMeans(n_clusters=k)
    km.fit(df[['sepal length (cm)','sepal length (cm)','sepal width␣
 ↪(cm)','petal width (cm)']])
    sse.append(km.inertia_)
```

[139]:
```
plt.xlabel('K')
plt.ylabel('Sum of squared error')
```

```
plt.plot(k_rng,sse)
```

[139]: [<matplotlib.lines.Line2D at 0x21012d0bda0>]



Number of clusters can be said as 3

2.6 Scaling

[213]:
```
# Applying MinMax scaler

scaler = MinMaxScaler()
scaled_data = scaler.fit_transform(df)
```

2.7 Implementing clustering methods

2.8 Kmeans clustering

KMeans clustering is an unsupervised machine learning algorithm that partitions the data into k clusters based on feature similarity. It assigns each data point to the nearest cluster centroid and iterates to minimize the sum of squared distances between data points and their assigned cluster centers. The steps of the KMeans algorithm are:

Choose k initial centroids randomly. Assign each data point to the nearest centroid. Recompute the centroids based on the assigned data points. Repeat steps 2 and 3 until convergence (centroids don't change significantly).

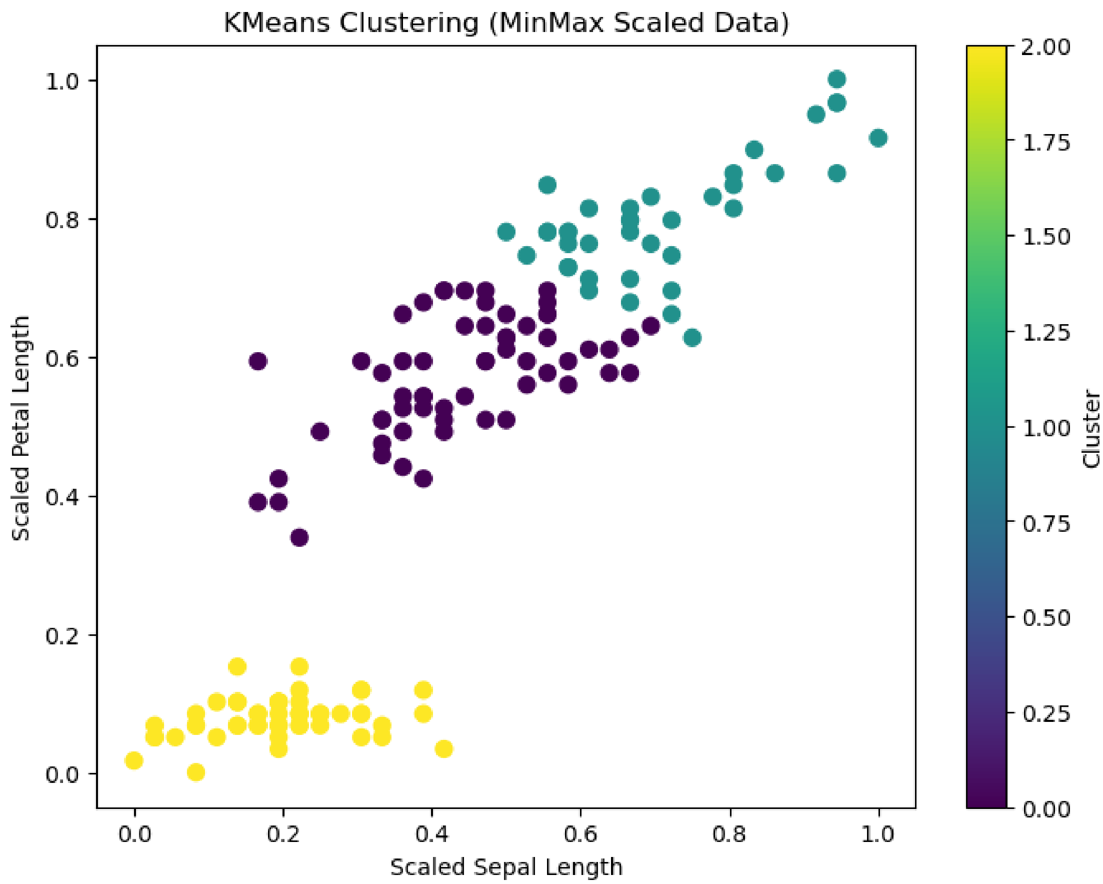
2.9 Why suitable for iris Dataset

The Iris dataset has well-separated flower species based on features like sepal length, sepal width, petal length, and petal width. Since the dataset has inherent groupings (species of flowers), KMeans can effectively group similar data points together.The Iris dataset has well-separated flower species based on features like sepal length, sepal width, petal length, and petal width. Since the dataset has inherent groupings (species of flowers), KMeans can effectively group similar data points together.

[215]:
```
# KMeans Clustering
# Apply KMeans Clustering
kmeans = KMeans(n_clusters=3, random_state=42)  # Assuming 3 clusters
kmeans_labels = kmeans.fit_predict(scaled_data)


# Add cluster labels to the DataFrame
df['kmeans_labels'] = kmeans_labels


# Scatter plot to visualize clusters
plt.figure(figsize=(8, 6))
plt.scatter(scaled_data[:, 0], scaled_data[:, 2], c=kmeans_labels,
 ↪cmap='viridis', s=50)
plt.title('KMeans Clustering (MinMax Scaled Data)')
plt.xlabel('Scaled Sepal Length')
plt.ylabel('Scaled Petal Length')
plt.colorbar(label='Cluster')
plt.show()
```



3 Hierarchical Clustering

Hierarchical clustering is an unsupervised machine learning algorithm that builds a hierarchy of clusters either by:

Agglomerative (Bottom-Up): Starts with each data point as its own cluster and iteratively merges the closest clustersved.

Divisive (Top-Down): Starts with all data points in one cluster and recursively splits them.

Agglomerative clustering is more commonly used. The process continues until all points are grouped into a single cluster or until the desired number of clusters is achieved.

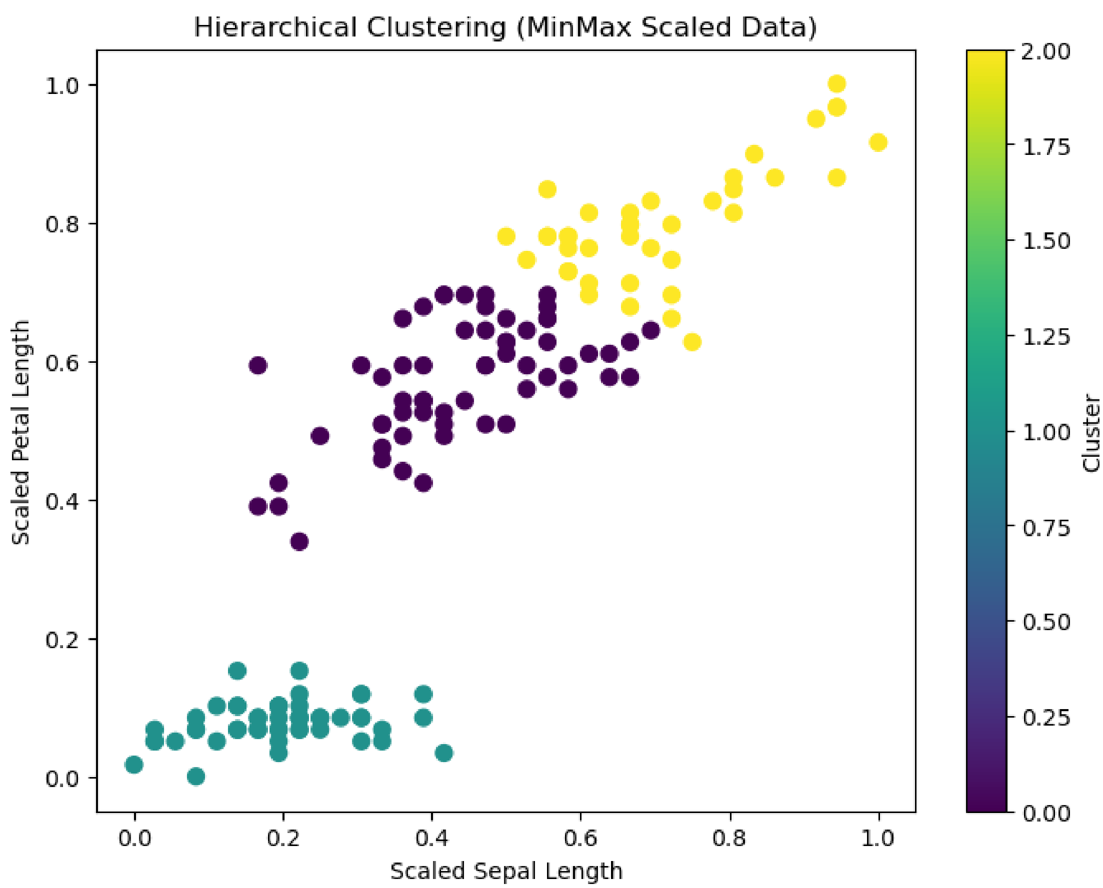
Why Hierarchical Clustering Might Be Suitable for the Iris Dataset:

Hierarchical clustering doesn't require the number of clusters to be pre-defined. It is useful for understanding the data structure and dendrograms can help visualize how clusters are formed. The Iris dataset, with its relatively small size and clear separation between classes, works well with hierarchical clustering.

[217]:
```
# Apply Hierarchical Clustering
hc = AgglomerativeClustering(n_clusters=3, linkage='ward', metric='euclidean')
hc_labels = hc.fit_predict(scaled_data)  # Fit and predict cluster labels

# Add cluster labels to the DataFrame
df['hc_labels'] = hc_labels
```

[219]:
```
# Scatter plot to visualize clusters
plt.figure(figsize=(8, 6))
plt.scatter(scaled_data[:, 0], scaled_data[:, 2], c=hc_labels, cmap='viridis',␣
  ↪s=50)
plt.title('Hierarchical Clustering (MinMax Scaled Data)')
plt.xlabel('Scaled Sepal Length')
plt.ylabel('Scaled Petal Length')
plt.colorbar(label='Cluster')
plt.show()
```



3.1 Valuation

[223]:
```
# Calculate Silhouette Score
silhouette = silhouette_score(scaled_data, kmeans_labels)
print(f"Silhouette Score (KMeans with MinMax Scaling): {silhouette:.4f}")
```

```
Silhouette Score (KMeans with MinMax Scaling): 0.7814
```

[225]:
```
# Calculate Silhouette Score
silhouette = silhouette_score(scaled_data, hc_labels)
print(f"Silhouette Score (Hierarchical Clustering with MinMax Scaling):␣
↪{silhouette:.4f}")
```

```
Silhouette Score (Hierarchical Clustering with MinMax Scaling): 0.7814
```

[ ]:
```

```