In [1]:
```
from sklearn.datasets import load_iris
import pandas as pd
```

In [4]:
```
iris = load_iris()
iris
```

Out[4]:
```
{'data': array([[5.1, 3.5, 1.4, 0.2],
        [4.9, 3. , 1.4, 0.2],
        [4.7, 3.2, 1.3, 0.2],
        [4.6, 3.1, 1.5, 0.2],
        [5. , 3.6, 1.4, 0.2],
        [5.4, 3.9, 1.7, 0.4],
        [4.6, 3.4, 1.4, 0.3],
        [5. , 3.4, 1.5, 0.2],
        [4.4, 2.9, 1.4, 0.2],
        [4.9, 3.1, 1.5, 0.1],
        [5.4, 3.7, 1.5, 0.2],
        [4.8, 3.4, 1.6, 0.2],
        [4.8, 3. , 1.4, 0.1],
        [4.3, 3. , 1.1, 0.1],
        [5.8, 4. , 1.2, 0.2],
        [5.7, 4.4, 1.5, 0.4],
        [5.4, 3.9, 1.3, 0.4],
        [5.1, 3.5, 1.4, 0.3],
        [5.7, 3.8, 1.7, 0.3],
```

In [5]:
```
iris_df = pd.DataFrame(iris.data,columns=iris.feature_names)
iris_df
```

Out[5]:

	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
...	...	...	...	...
145	6.7	3.0	5.2	2.3
146	6.3	2.5	5.0	1.9
147	6.5	3.0	5.2	2.0
148	6.2	3.4	5.4	2.3
149	5.9	3.0	5.1	1.8

150 rows × 4 columns

In [6]:
```
x= iris_df.copy()
```

In [8]:
```
from sklearn.cluster import KMeans
import matplotlib.pyplot as plt
```

In [9]:
```
kmeans = KMeans(n_clusters=3,random_state=42)
kmeans.fit(x)
```

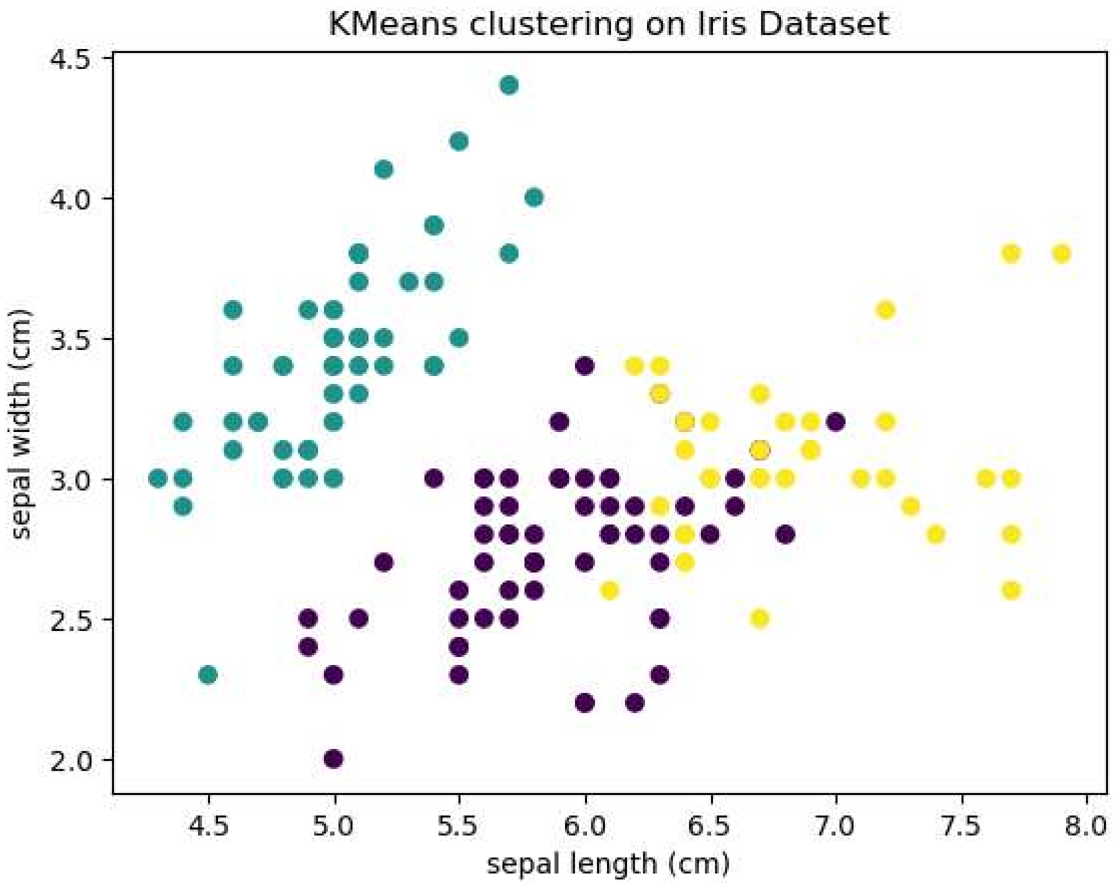
```
C:\Users\999ra\anaconda3\Lib\site-packages\sklearn\cluster\_kmeans.py:1412: FutureWarning: The default valu
e of `n_init` will change from 10 to 'auto' in 1.4. Set the value of `n_init` explicitly to suppress the wa
rning
  super()._check_params_vs_input(X, default_n_init=10)
C:\Users\999ra\anaconda3\Lib\site-packages\sklearn\cluster\_kmeans.py:1436: UserWarning: KMeans is known to
have a memory leak on Windows with MKL, when there are less chunks than available threads. You can avoid it
by setting the environment variable OMP_NUM_THREADS=1.
  warnings.warn(
```

Out[9]:
```
KMeans
KMeans(n_clusters=3, random_state=42)
```

In [11]:
```
x['cluster'] = kmeans.labels_
x['cluster']
```

Out[11]:
```
0      1
1      1
2      1
3      1
4      1
      ..
145    2
146    0
147    2
148    2
149    0
Name: cluster, Length: 150, dtype: int32
```

In [13]:
```
plt.scatter(x.iloc[:,0], x.iloc[:,1], c=x['cluster'], cmap='viridis')
plt.title('KMeans clustering on Iris Dataset')
plt.xlabel(iris.feature_names[0])
plt.ylabel(iris.feature_names[1])
plt.show()
```



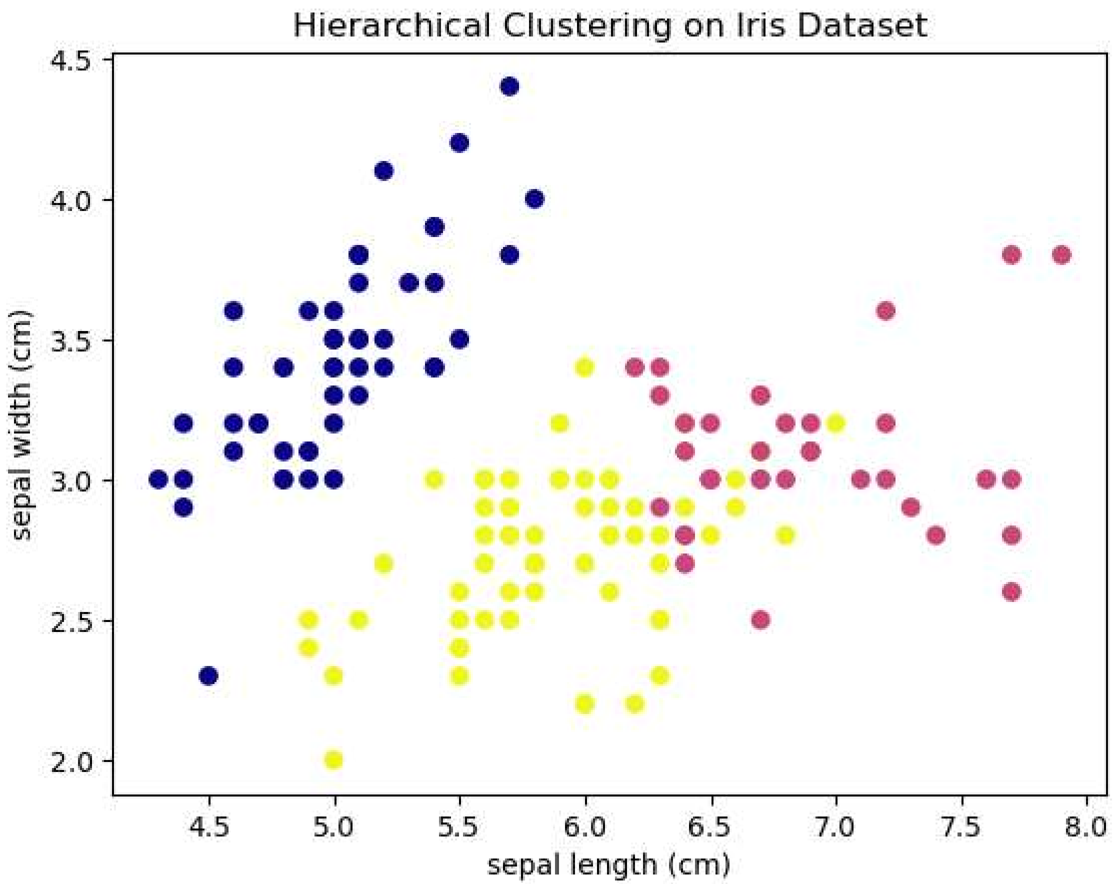
In [ ]:

```
#Description of KMeans Clustering
#KMeans is a centroid-based clustering algorithm that works by partitioning data into k distinct clusters.
#It tries to minimize the distance between the points and their assigned cluster centroids. The steps involve

#1. Randomly selecting k centroids.


#2. Assigning each data point to the nearest centroid.


#3. Updating the centroids based on the points assigned to each cluster.


#4. Repeating the process until the centroids do not change or a maximum number of iterations is reached.

#Why KMeans is suitable for Iris dataset
#KMeans is suitable for the Iris dataset because it's a simple, well-separated dataset.
#There are three known classes (species), and KMeans can cluster based on the inherent patterns in the featur
#without knowing the actual species labels. The continuous numeric features (sepal and petal lengths/widths)
#a good candidate for this dataset.
```

In [15]:

```
from scipy.cluster.hierarchy import dendrogram, linkage
import seaborn as sns

# Hierarchical Clustering
Z = linkage(x.iloc[:, :-1], method='ward')

# Plot the dendrogram
plt.figure(figsize=(10, 7))
dendrogram(Z)
plt.title('Hierarchical Clustering Dendrogram (Iris Dataset)')
plt.xlabel('Samples')
plt.ylabel('Distance')
plt.show()

# To create clusters from hierarchical clustering (choose 3 clusters)
from scipy.cluster.hierarchy import fcluster

# Cut the dendrogram to form 3 clusters
x['h_cluster'] = fcluster(Z, 3, criterion='maxclust')

# Visualize the clusters (using only the first two features for easy visualization)
plt.scatter(x.iloc[:, 0], x.iloc[:, 1], c=x['h_cluster'], cmap='plasma')
plt.title('Hierarchical Clustering on Iris Dataset')
plt.xlabel(iris.feature_names[0])
plt.ylabel(iris.feature_names[1])
plt.show()
```


Hierarchical Clustering Dendrogram (Iris Dataset)
Distance
Samples
0
5
10
15
20
25
30



In [ ]:

```
#Description of Hierarchical Clustering
#Hierarchical clustering builds a hierarchy of clusters by either a bottom-up approach (agglomerative) or
#a top-down approach (divisive). In agglomerative clustering, each point starts as its own cluster, and
#the algorithm recursively merges the closest clusters until only a single cluster or the desired number of c
#The clustering process can be visualized using a dendrogram.

#Why Hierarchical Clustering is suitable for Iris dataset
#Hierarchical clustering can reveal the nested structure of the data, which is useful when the number of clus
#not known a priori. It allows us to observe how the clusters merge at different levels, which could provide
#the relationships between different species in the Iris dataset.
```