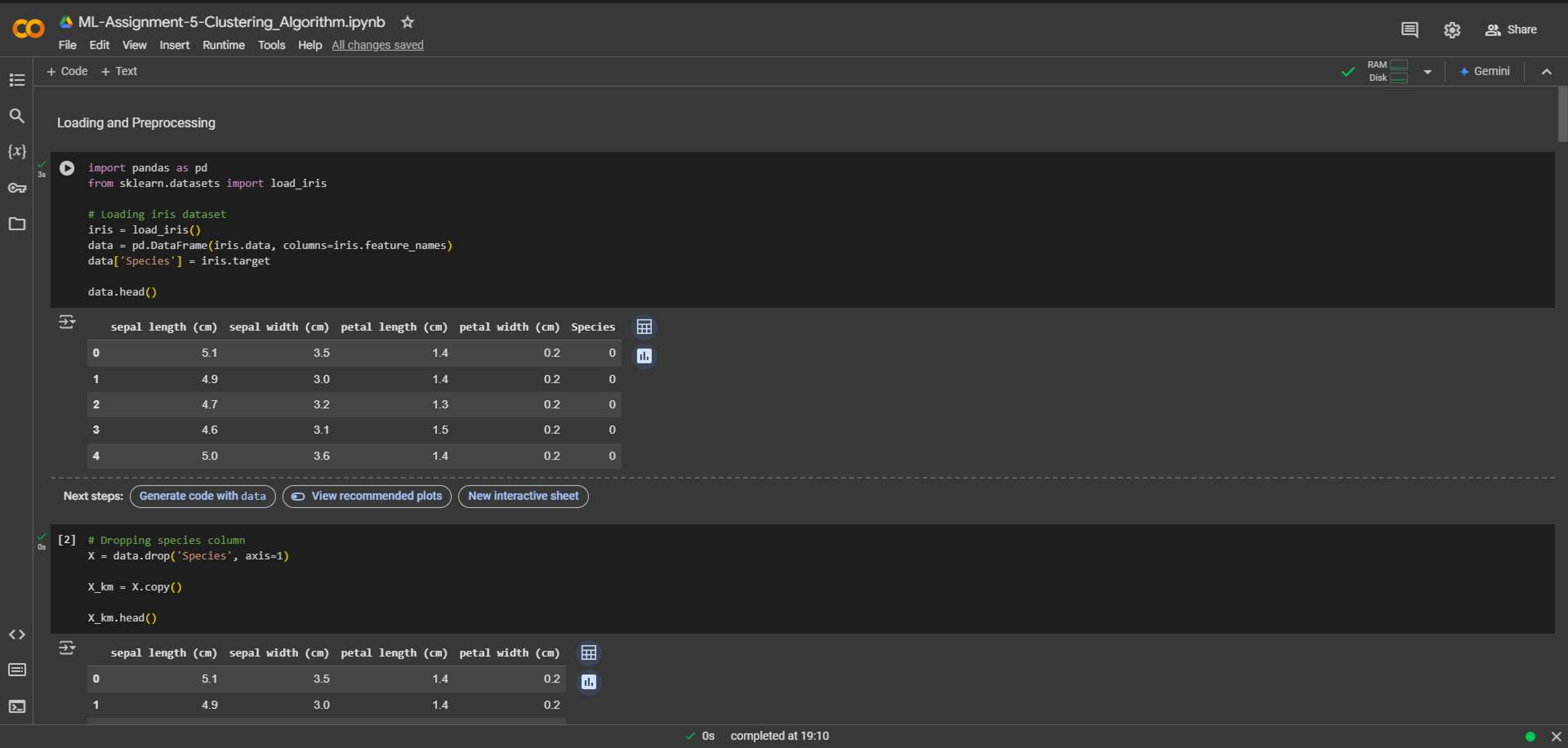
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Loading and Preprocessing

```
import pandas as pd
from sklearn.datasets import load_iris

# Loading iris dataset
iris = load_iris()
data = pd.DataFrame(iris.data, columns=iris.feature_names)
data['Species'] = iris.target

data.head()
```

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

Next steps: Generate code with data
View recommended plots
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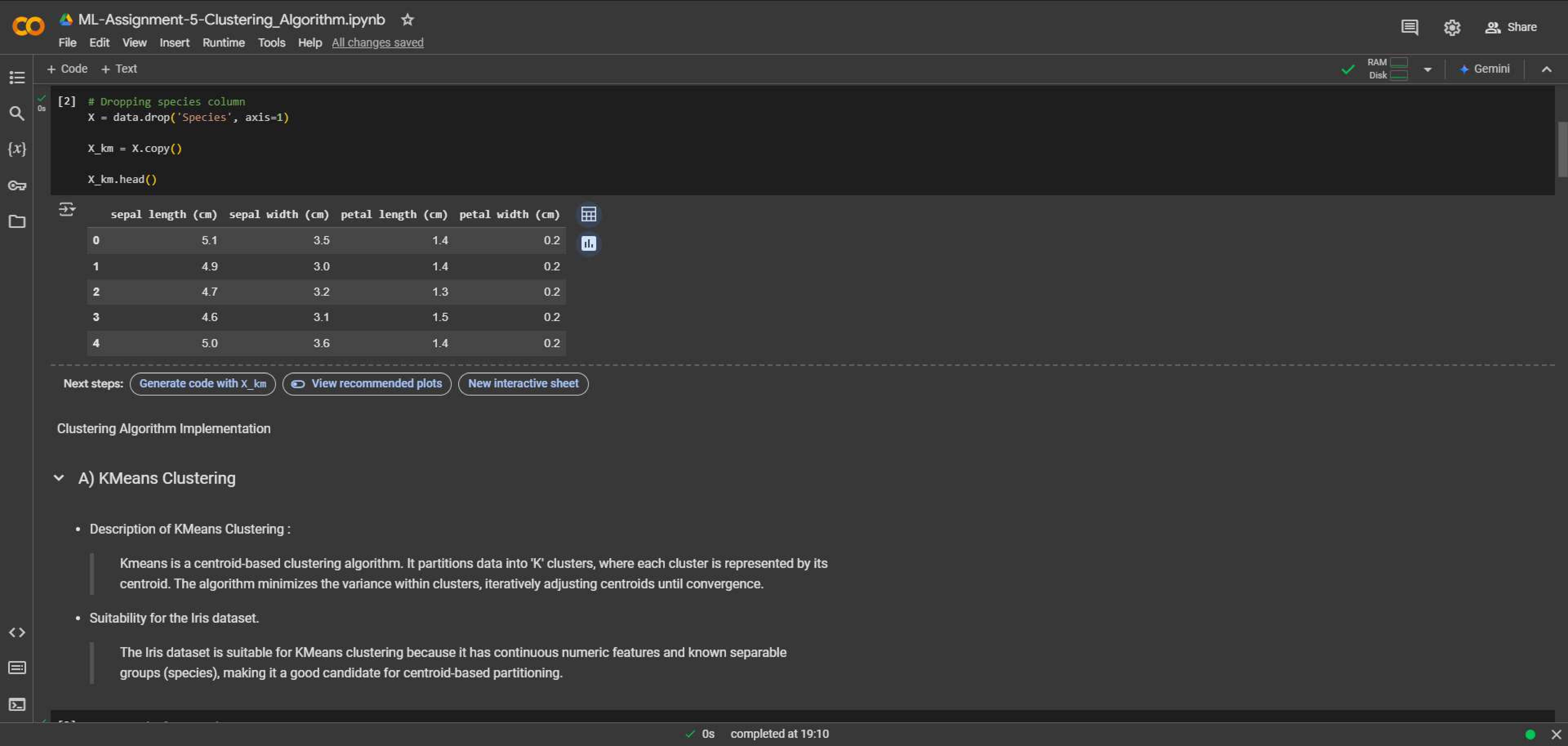
```
[2] # Dropping species column
X = data.drop('Species', axis=1)

X_km = X.copy()

X_km.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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```
[2] # Dropping species column
    X = data.drop('Species', axis=1)

    X_km = X.copy()

    X_km.head()
```

	sepal length (cm)	sepal width (cm)	petal length (cm)	petal width (cm)
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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

Next steps: Generate code with X_km View recommended plots New interactive sheet

Clustering Algorithm Implementation

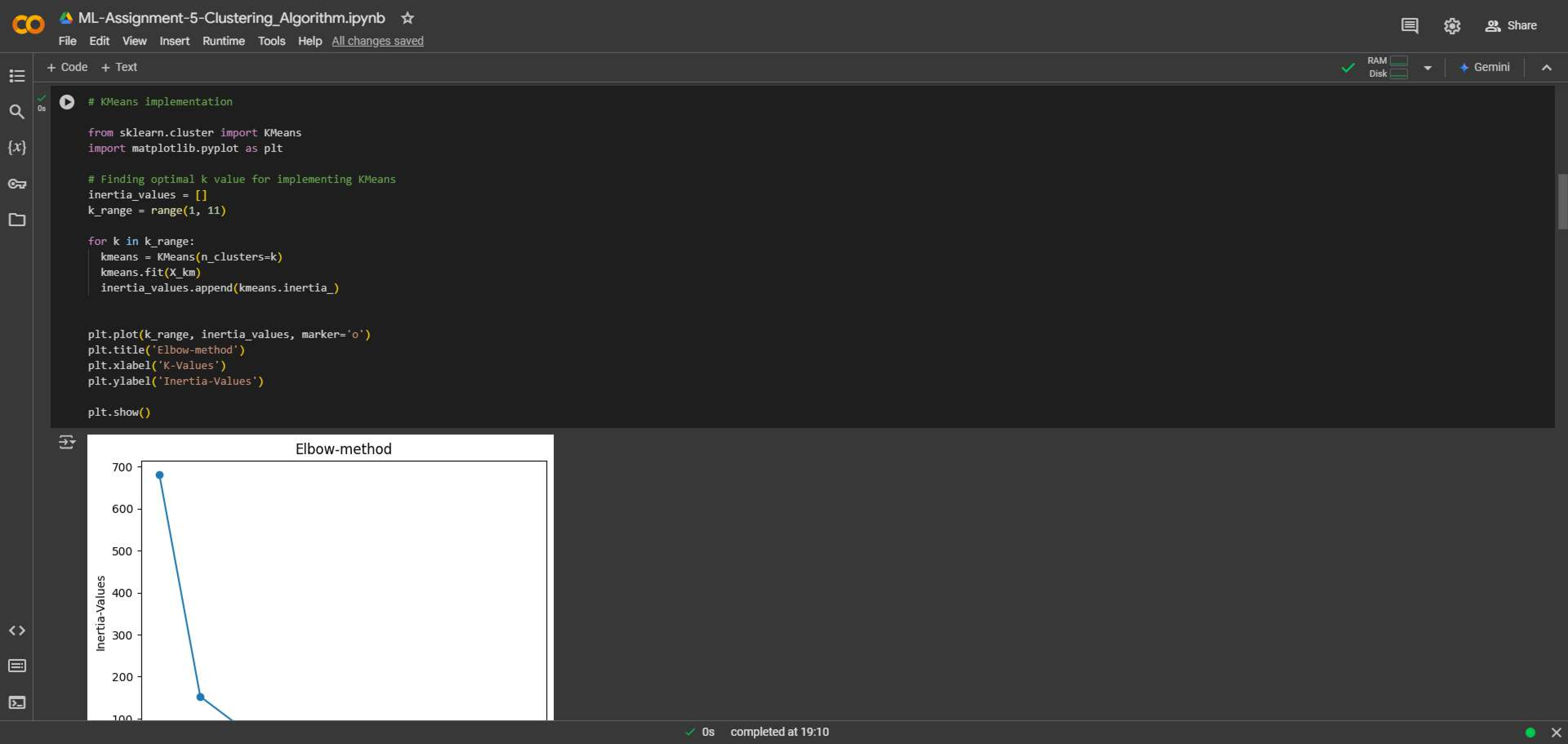
A) KMeans Clustering

- Description of KMeans Clustering :

> Kmeans is a centroid-based clustering algorithm. It partitions data into 'K' clusters, where each cluster is represented by its centroid. The algorithm minimizes the variance within clusters, iteratively adjusting centroids until convergence.

- Suitability for the Iris dataset.

> The Iris dataset is suitable for KMeans clustering because it has continuous numeric features and known separable groups (species), making it a good candidate for centroid-based partitioning.



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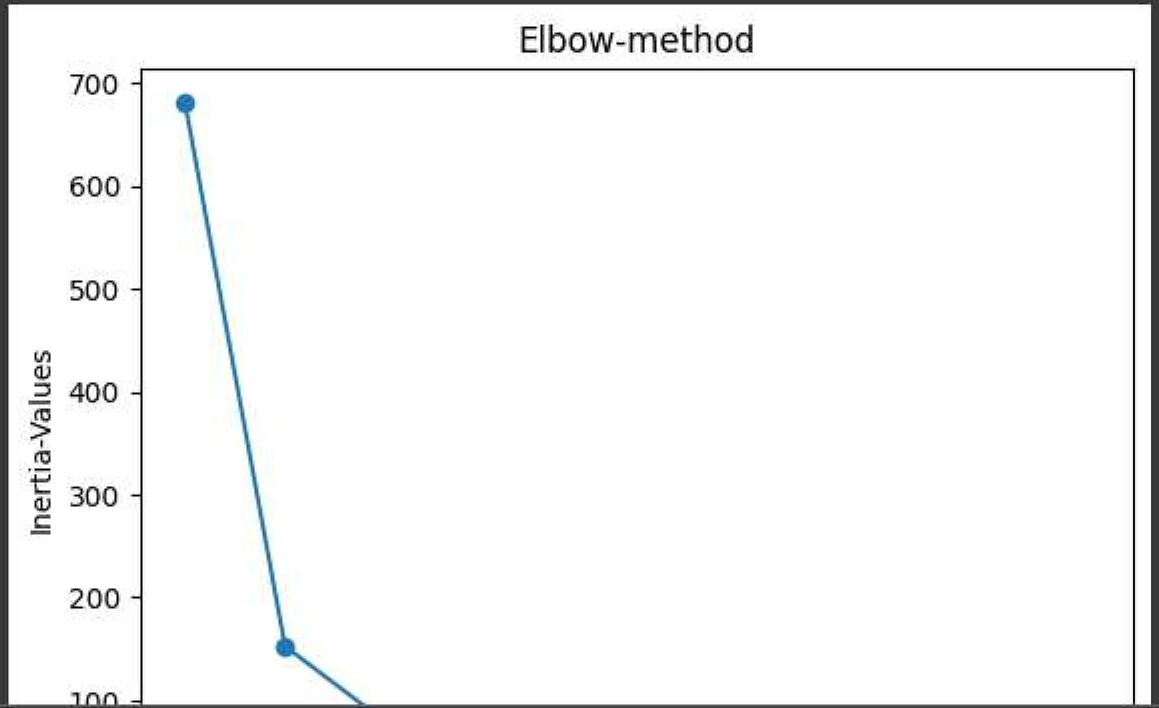
```python
# KMeans implementation

from sklearn.cluster import KMeans
import matplotlib.pyplot as plt

# Finding optimal k value for implementing KMeans
inertia_values = []
k_range = range(1, 11)

for k in k_range:
  kmeans = KMeans(n_clusters=k)
  kmeans.fit(X_km)
  inertia_values.append(kmeans.inertia_)


plt.plot(k_range, inertia_values, marker='o')
plt.title('Elbow-method')
plt.xlabel('K-Values')
plt.ylabel('Inertia-Values')

plt.show()
```



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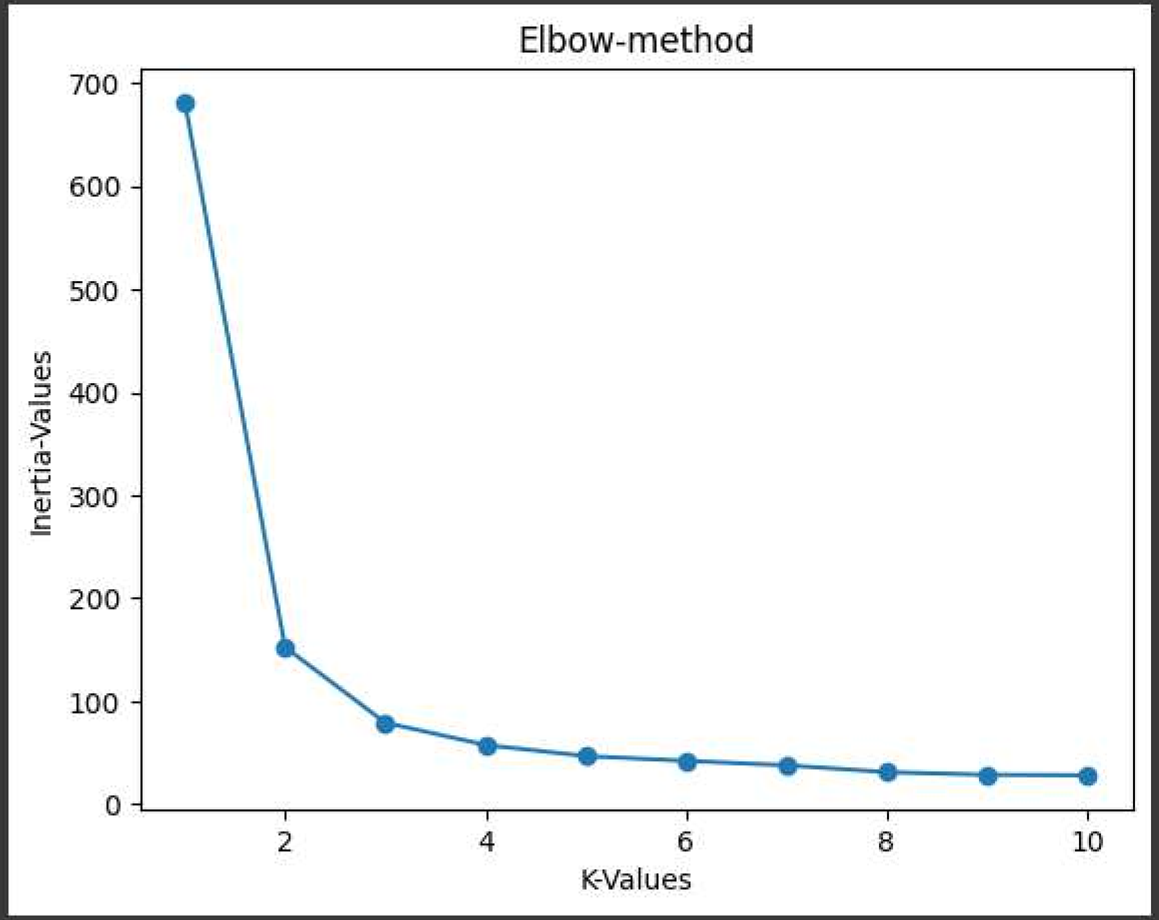
[3]



```
[4] from sklearn.metrics import silhouette_score, davies_bouldin_score

    # Range of k values to evaluate
    optimal_k_range = range(3, 6)

    for k in optimal_k_range:
      kmeans = KMeans(n_clusters=k, random_state=42, n_init=10)
      cluster_labels = kmeans.fit_predict(X_km)

      print(f'Optimal k values as {k}')
      print('-----------------------------')

      # Calculating Silhouette Score
      sil_score = silhouette_score(X_km, cluster_labels)
      print(f'Silhouette Score : {sil_score:.2f}')
```

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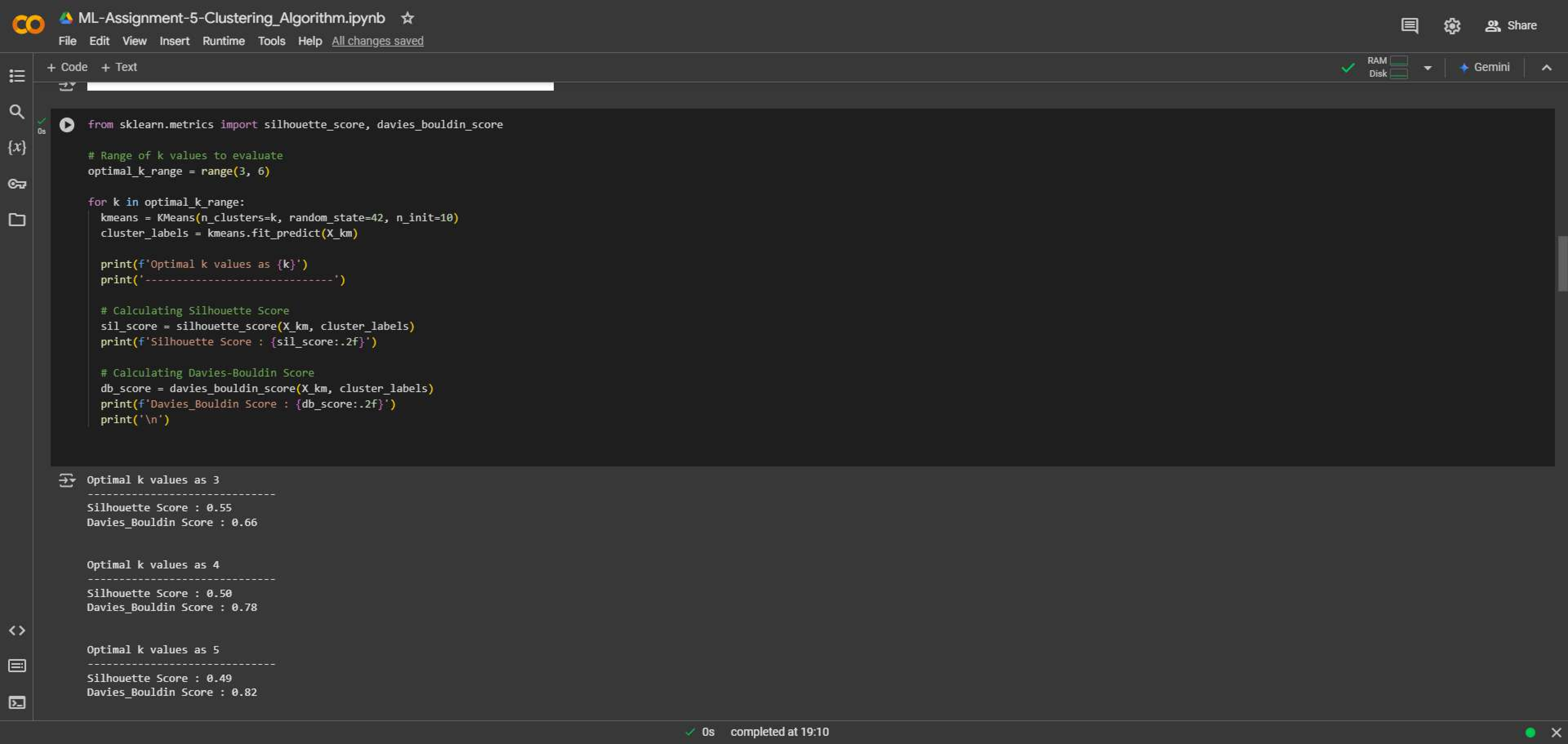
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```python
from sklearn.metrics import silhouette_score, davies_bouldin_score

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  cluster_labels = kmeans.fit_predict(X_km)

  print(f'Optimal k values as {k}')
  print('------------------------------')

  # Calculating Silhouette Score
  sil_score = silhouette_score(X_km, cluster_labels)
  print(f'Silhouette Score : {sil_score:.2f}')

  # Calculating Davies-Bouldin Score
  db_score = davies_bouldin_score(X_km, cluster_labels)
  print(f'Davies_Bouldin Score : {db_score:.2f}')
  print('\n')
```
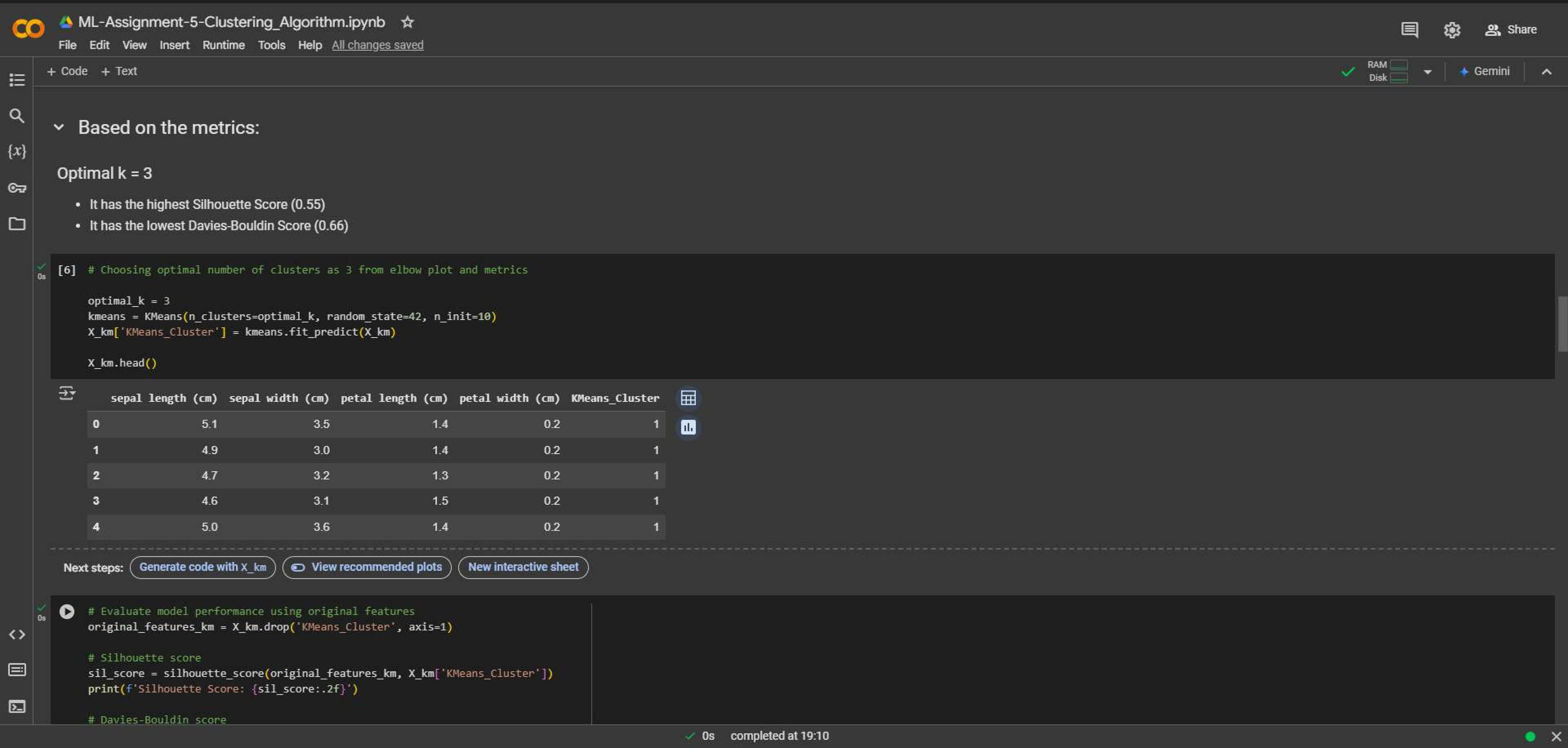

```
Optimal k values as 3
------------------------------
Silhouette Score : 0.55
Davies_Bouldin Score : 0.66


Optimal k values as 4
------------------------------
Silhouette Score : 0.50
Davies_Bouldin Score : 0.78


Optimal k values as 5
------------------------------
Silhouette Score : 0.49
Davies_Bouldin Score : 0.82
```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Based on the metrics:

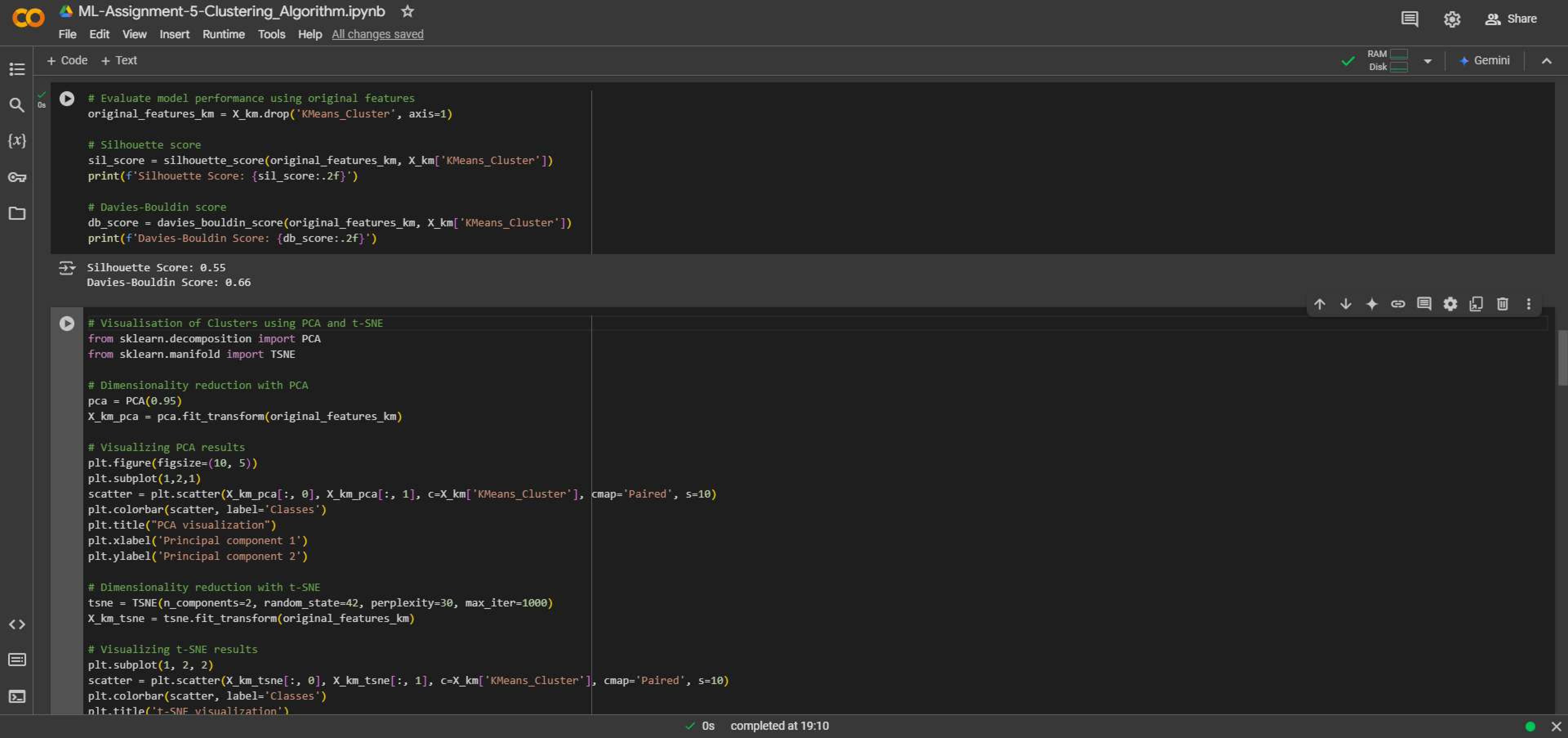
Optimal k = 3

- It has the highest Silhouette Score (0.55)
- It has the lowest Davies-Bouldin Score (0.66)

```
[6] # Choosing optimal number of clusters as 3 from elbow plot and metrics

    optimal_k = 3
    kmeans = KMeans(n_clusters=optimal_k, random_state=42, n_init=10)
    X_km['KMeans_Cluster'] = kmeans.fit_predict(X_km)

    X_km.head()
```

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

```
# Evaluate model performance using original features
original_features_km = X_km.drop('KMeans_Cluster', axis=1)

# Silhouette score
sil_score = silhouette_score(original_features_km, X_km['KMeans_Cluster'])
print(f'Silhouette Score: {sil_score:.2f}')

# Davies-Bouldin score
```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```
# Evaluate model performance using original features
original_features_km = X_km.drop('KMeans_Cluster', axis=1)

# Silhouette score
sil_score = silhouette_score(original_features_km, X_km['KMeans_Cluster'])
print(f'Silhouette Score: {sil_score:.2f}')

# Davies-Bouldin score
db_score = davies_bouldin_score(original_features_km, X_km['KMeans_Cluster'])
print(f'Davies-Bouldin Score: {db_score:.2f}')
```

```
Silhouette Score: 0.55
Davies-Bouldin Score: 0.66
```

```
# Visualisation of Clusters using PCA and t-SNE
from sklearn.decomposition import PCA
from sklearn.manifold import TSNE

# Dimensionality reduction with PCA
pca = PCA(0.95)
X_km_pca = pca.fit_transform(original_features_km)

# Visualizing PCA results
plt.figure(figsize=(10, 5))
plt.subplot(1,2,1)
scatter = plt.scatter(X_km_pca[:, 0], X_km_pca[:, 1], c=X_km['KMeans_Cluster'], cmap='Paired', s=10)
plt.colorbar(scatter, label='Classes')
plt.title("PCA visualization")
plt.xlabel('Principal component 1')
plt.ylabel('Principal component 2')

# Dimensionality reduction with t-SNE
tsne = TSNE(n_components=2, random_state=42, perplexity=30, max_iter=1000)
X_km_tsne = tsne.fit_transform(original_features_km)

# Visualizing t-SNE results
plt.subplot(1, 2, 2)
scatter = plt.scatter(X_km_tsne[:, 0], X_km_tsne[:, 1], c=X_km['KMeans_Cluster'], cmap='Paired', s=10)
plt.colorbar(scatter, label='Classes')
plt.title('t-SNE visualization')
```

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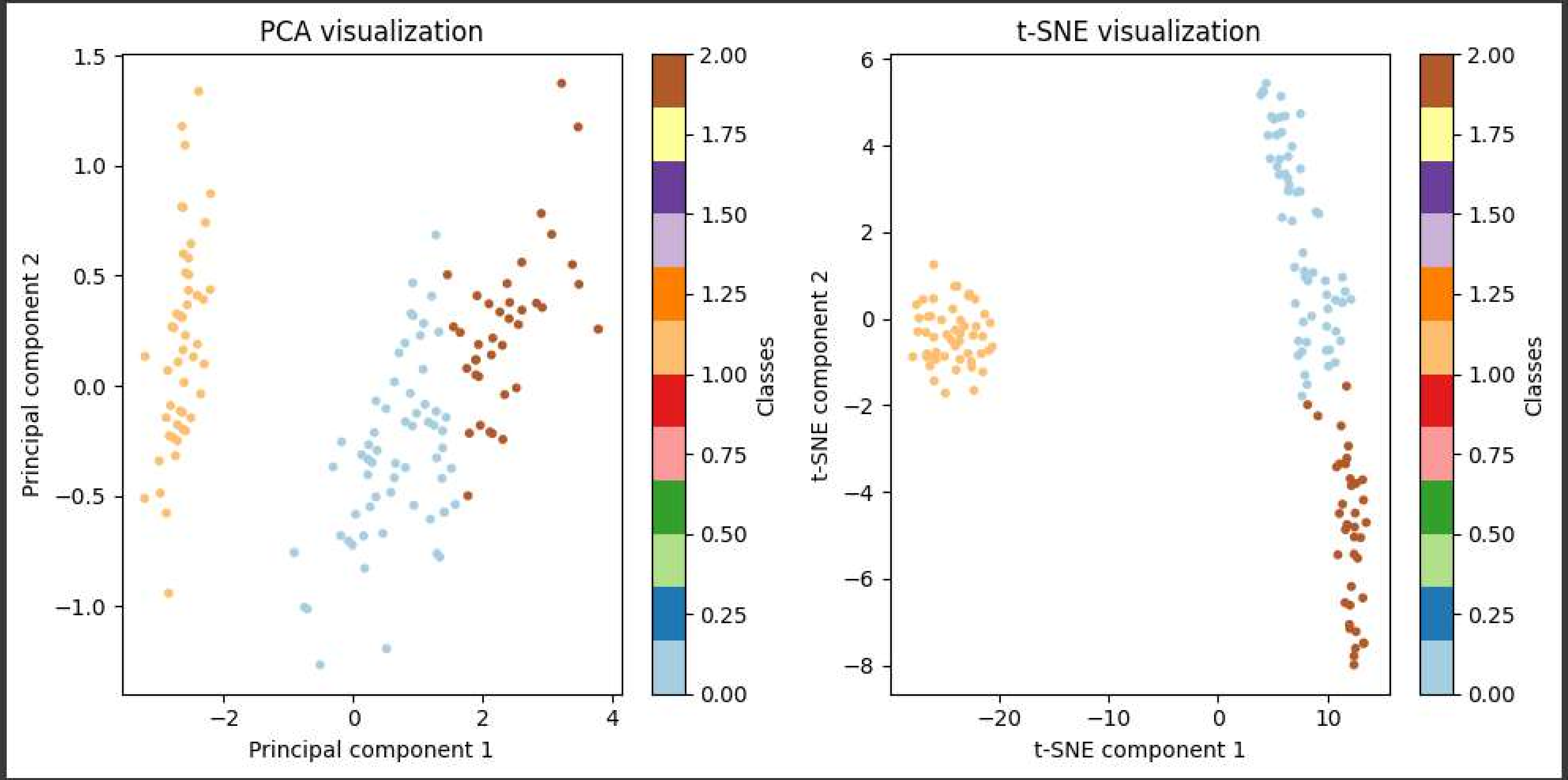


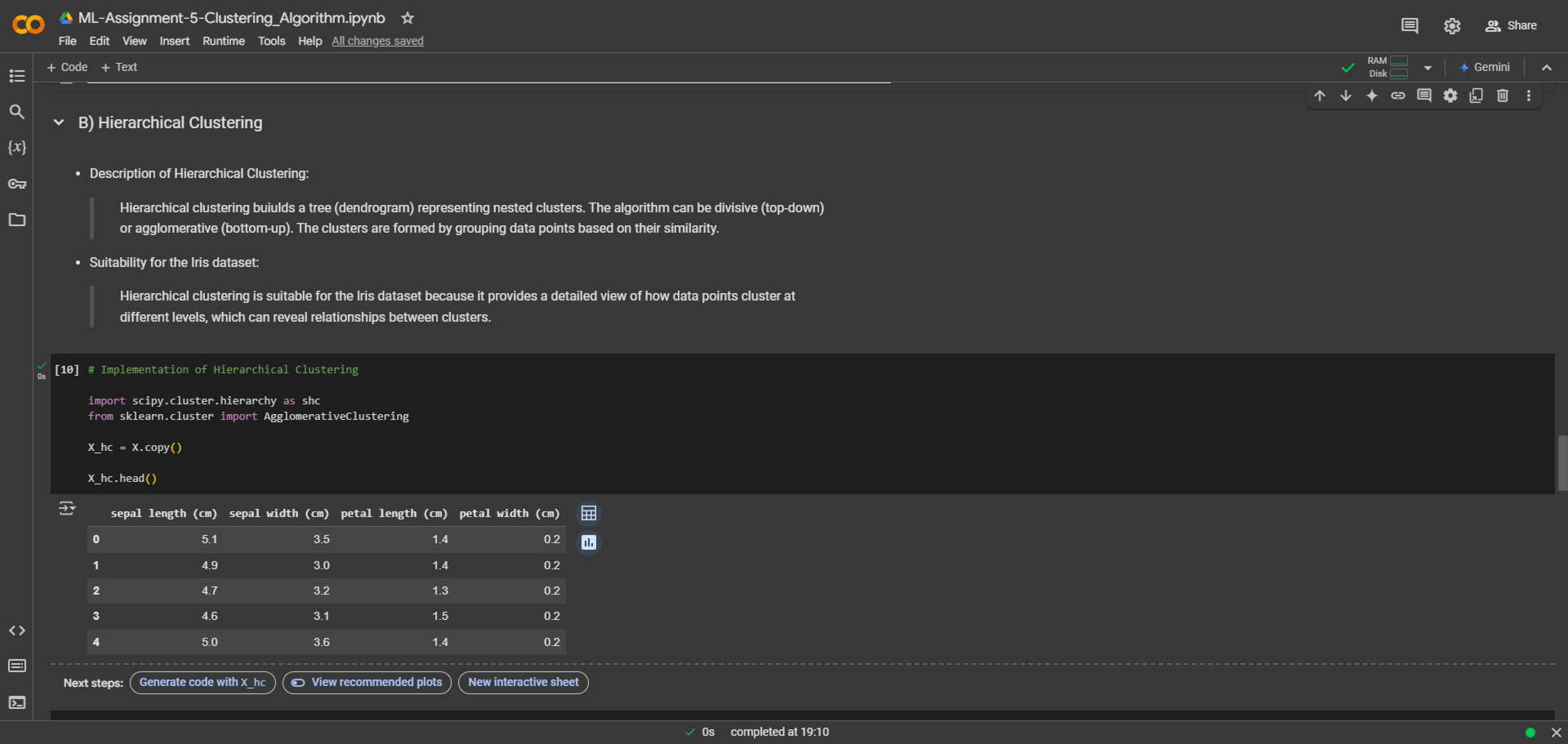
B) Hierarchical Clustering

- Description of Hierarchical Clustering:

  > Hierarchical clustering buiulds a tree (dendrogram) representing nested clusters. The algorithm can be divisive (top-down) or agglomerative (bottom-up). The clusters are formed by grouping data points based on their similarity.

- Suitability for the Iris dataset:

  > Hierarchical clustering is suitable for the Iris dataset because it provides a detailed view of how data points cluster at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Next steps: Generate code with X_hc View recommended plots New interactive sheet
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B) Hierarchical Clustering

- Description of Hierarchical Clustering:

> Hierarchical clustering buiulds a tree (dendrogram) representing nested clusters. The algorithm can be divisive (top-down) or agglomerative (bottom-up). The clusters are formed by grouping data points based on their similarity.

- Suitability for the Iris dataset:

> Hierarchical clustering is suitable for the Iris dataset because it provides a detailed view of how data points cluster at different levels, which can reveal relationships between clusters.

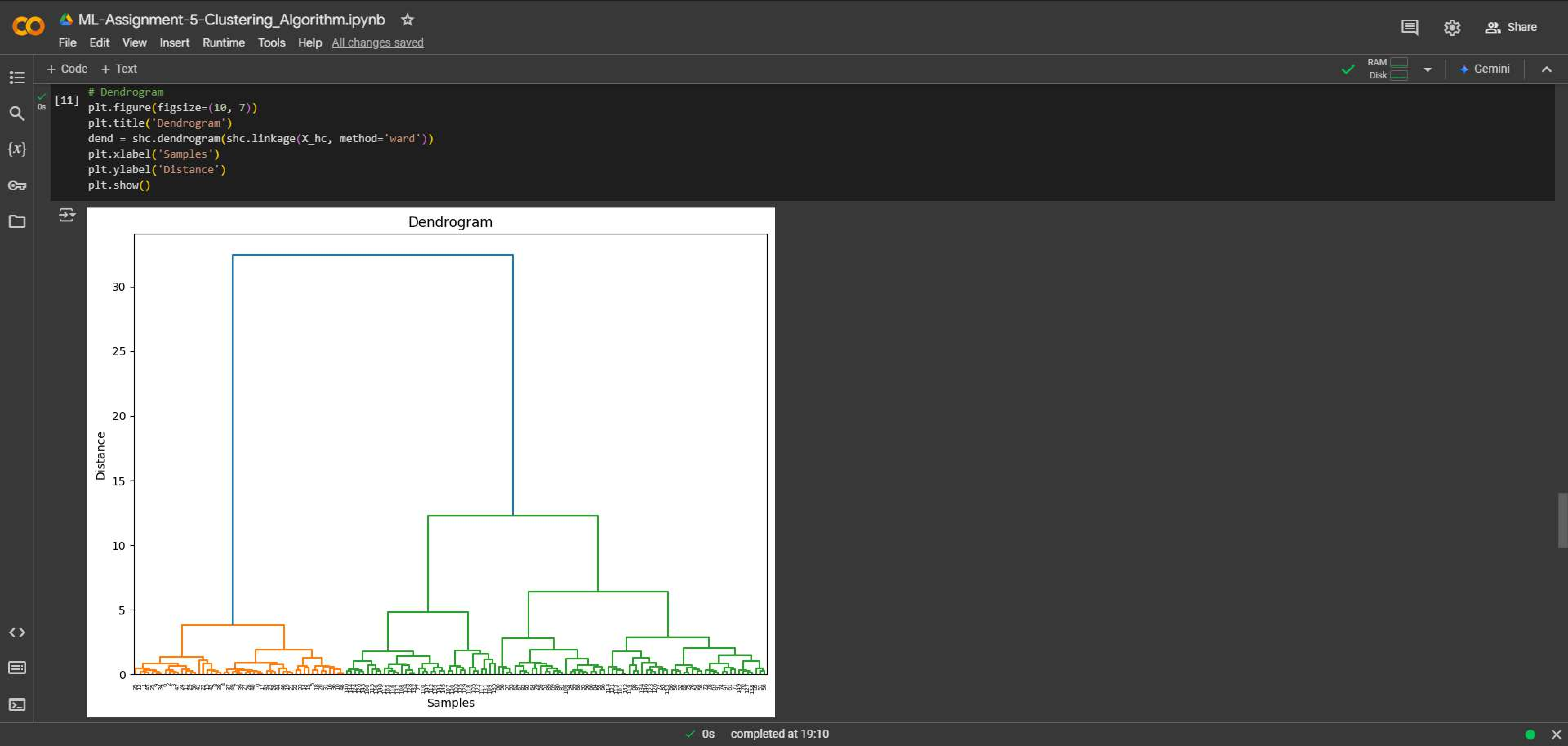
```
[10] # Implementation of Hierarchical Clustering

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

     X_hc = X.copy()

     X_hc.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
```



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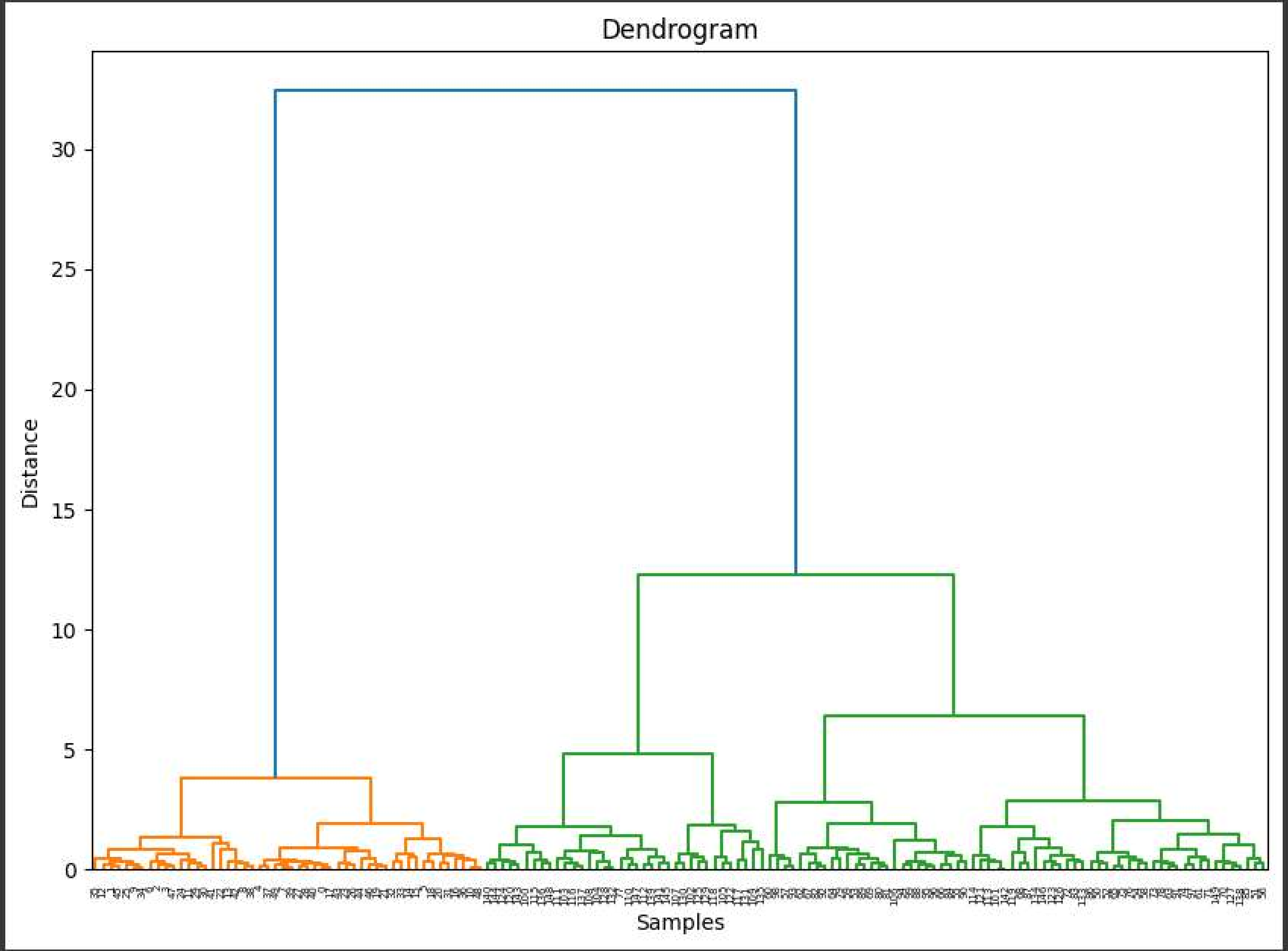
```
[11] # Dendrogram
     plt.figure(figsize=(10, 7))
     plt.title('Dendrogram')
     dend = shc.dendrogram(shc.linkage(X_hc, method='ward'))
     plt.xlabel('Samples')
     plt.ylabel('Distance')
     plt.show()
```



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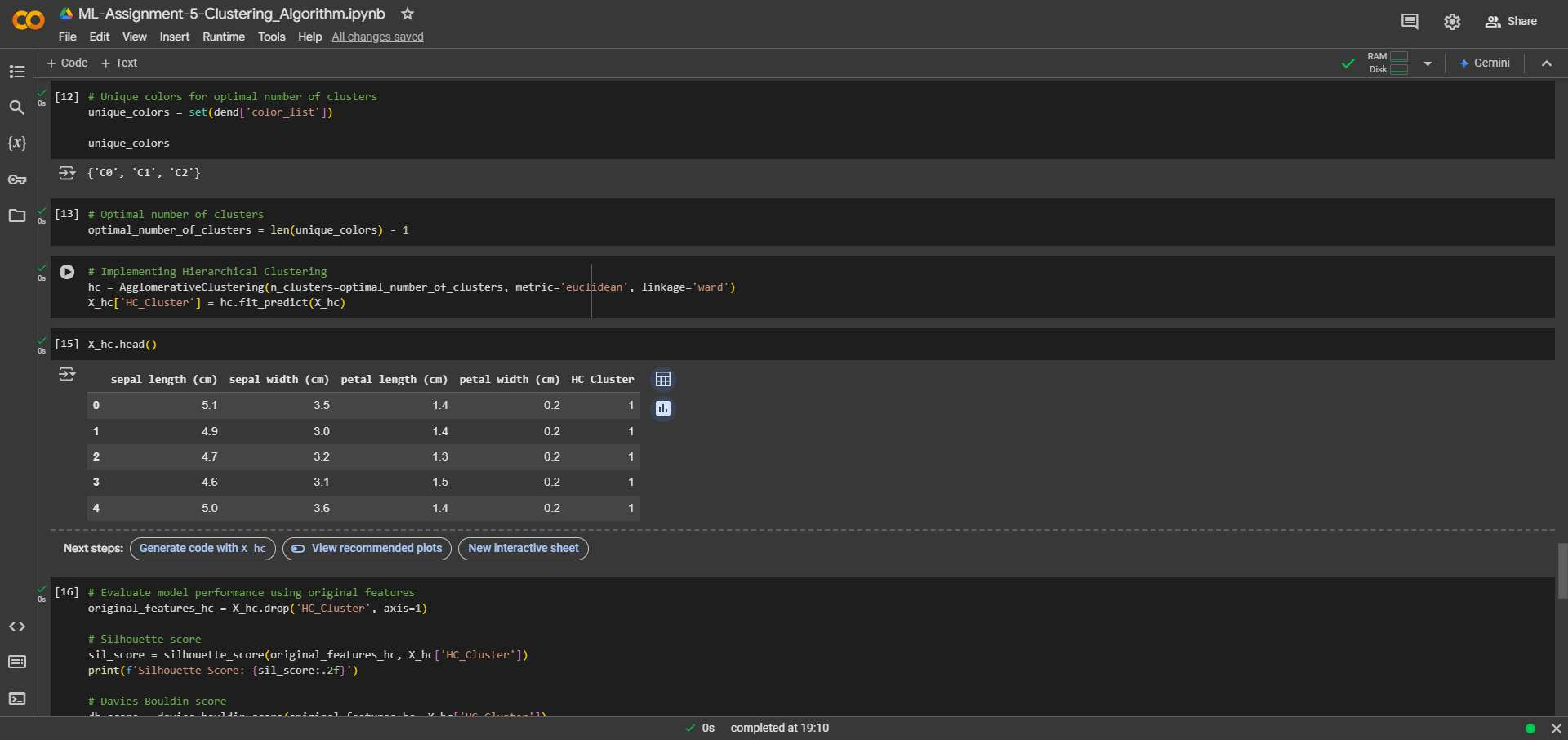
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[12]
```
# Unique colors for optimal number of clusters
unique_colors = set(dend['color_list'])

unique_colors
```

```
{'C0', 'C1', 'C2'}
```

[13]
```
# Optimal number of clusters
optimal_number_of_clusters = len(unique_colors) - 1
```

```
# Implementing Hierarchical Clustering
hc = AgglomerativeClustering(n_clusters=optimal_number_of_clusters, metric='euclidean', linkage='ward')
X_hc['HC_Cluster'] = hc.fit_predict(X_hc)
```

[15]
```
X_hc.head()
```

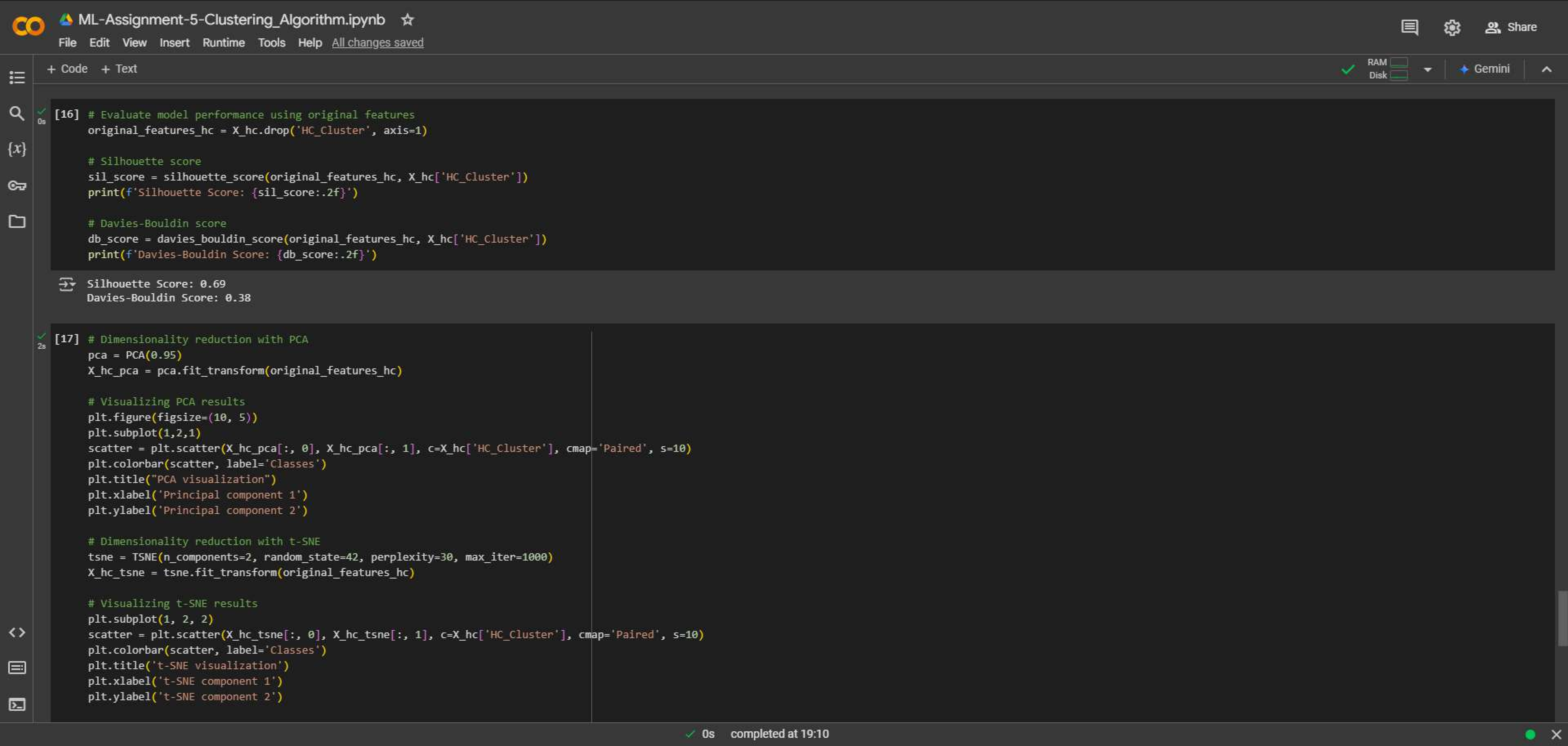
	sepal length (cm)	sepal width (cm)	petal length (cm)	petal width (cm)	HC_Cluster
0	5.1	3.5	1.4	0.2	1
1	4.9	3.0	1.4	0.2	1
2	4.7	3.2	1.3	0.2	1
3	4.6	3.1	1.5	0.2	1
4	5.0	3.6	1.4	0.2	1

Next steps: Generate code with X_hc View recommended plots New interactive sheet

[16]
```
# Evaluate model performance using original features
original_features_hc = X_hc.drop('HC_Cluster', axis=1)

# Silhouette score
sil_score = silhouette_score(original_features_hc, X_hc['HC_Cluster'])
print(f'Silhouette Score: {sil_score:.2f}')

# Davies-Bouldin score
db_score = davies_bouldin_score(original_features_hc, X_hc['HC_Cluster'])
```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[16]
```
# Evaluate model performance using original features
original_features_hc = X_hc.drop('HC_Cluster', axis=1)

# Silhouette score
sil_score = silhouette_score(original_features_hc, X_hc['HC_Cluster'])
print(f'Silhouette Score: {sil_score:.2f}')

# Davies-Bouldin score
db_score = davies_bouldin_score(original_features_hc, X_hc['HC_Cluster'])
print(f'Davies-Bouldin Score: {db_score:.2f}')
```

```
Silhouette Score: 0.69
Davies-Bouldin Score: 0.38
```

[17]
```
# Dimensionality reduction with PCA
pca = PCA(0.95)
X_hc_pca = pca.fit_transform(original_features_hc)

# Visualizing PCA results
plt.figure(figsize=(10, 5))
plt.subplot(1,2,1)
scatter = plt.scatter(X_hc_pca[:, 0], X_hc_pca[:, 1], c=X_hc['HC_Cluster'], cmap='Paired', s=10)
plt.colorbar(scatter, label='Classes')
plt.title("PCA visualization")
plt.xlabel('Principal component 1')
plt.ylabel('Principal component 2')

# Dimensionality reduction with t-SNE
tsne = TSNE(n_components=2, random_state=42, perplexity=30, max_iter=1000)
X_hc_tsne = tsne.fit_transform(original_features_hc)

# Visualizing t-SNE results
plt.subplot(1, 2, 2)
scatter = plt.scatter(X_hc_tsne[:, 0], X_hc_tsne[:, 1], c=X_hc['HC_Cluster'], cmap='Paired', s=10)
plt.colorbar(scatter, label='Classes')
plt.title('t-SNE visualization')
plt.xlabel('t-SNE component 1')
plt.ylabel('t-SNE component 2')
```

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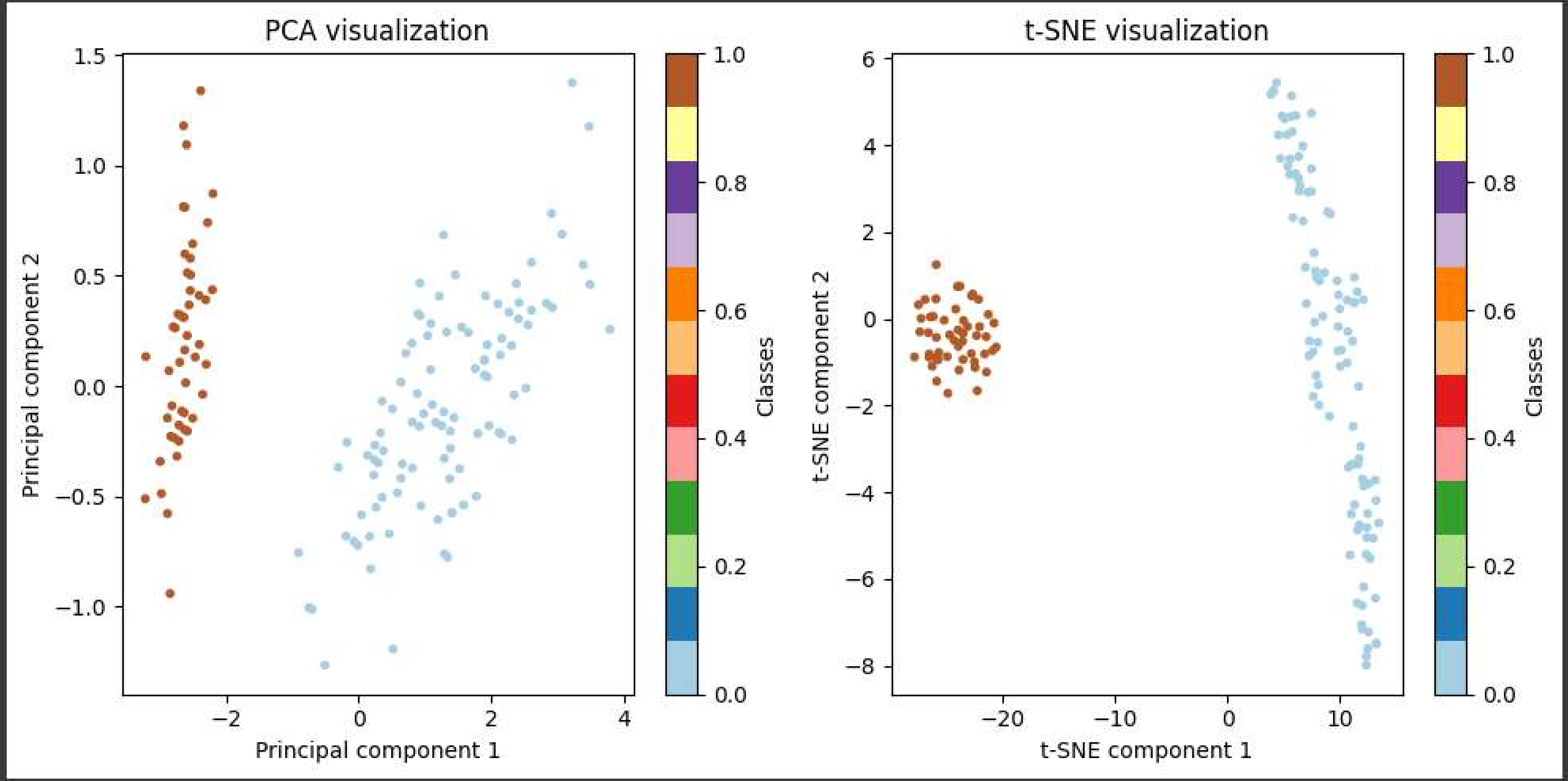
```
tsne = TSNE(n_components=2, random_state=42, perplexity=30, max_iter=1000)
X_hc_tsne = tsne.fit_transform(original_features_hc)

# Visualizing t-SNE results
plt.subplot(1, 2, 2)
scatter = plt.scatter(X_hc_tsne[:, 0], X_hc_tsne[:, 1], c=X_hc['HC_Cluster'], cmap='Paired', s=10)
plt.colorbar(scatter, label='Classes')
plt.title('t-SNE visualization')
plt.xlabel('t-SNE component 1')
plt.ylabel('t-SNE component 2')

plt.tight_layout()
plt.show()
```



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