

```
# Load the iris dataset
data(iris)
# Use only the numeric columns for clustering (exclude the Species column)
iris_data <- iris[, -5]
# Standardize the data
iris_scaled <- scale(iris_data)
# Compute the distance matrix
distance_matrix <- dist(iris_scaled, method = "euclidean")
# Perform hierarchical clustering using the "complete" linkage method
hc_complete <- hclust(distance_matrix, method = "complete")
# Plot the dendrogram
plot(hc_complete, main = "Hierarchical Clustering Dendrogram", xlab = "", sub = "", cex =
0.6)
# Cut the tree to form 3 clusters
clusters <- cutree(hc_complete, k = 3)
# Print the cluster memberships
print(clusters)
# Add the clusters to the original dataset
iris$Cluster <- as.factor(clusters)
# Display the first few rows of the updated dataset
head(iris)
```

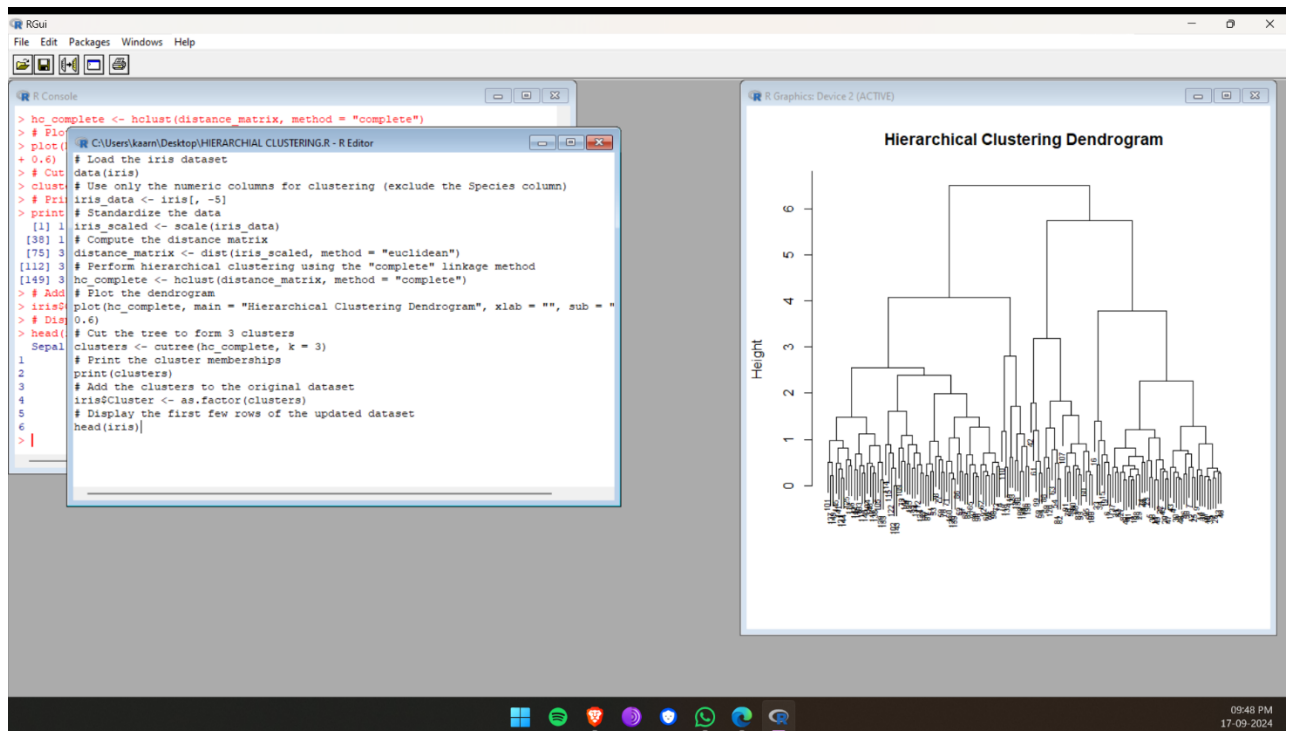
The screenshot shows the RGui interface with two windows. The 'R Console' window contains R commands for performing hierarchical clustering on the iris dataset using the 'complete' linkage method, plotting the dendrogram, cutting it into three clusters, and displaying the cluster membership. The output shows the first few rows of the updated dataset with their assigned clusters. The 'Untitled - R Editor' window contains the same R code as the console, serving as a script editor. The top menu bar includes File, Edit, Packages, Windows, and Help. The toolbar has icons for file operations like opening, saving, and printing.

```
> # Perform hierarchical clustering using the "complete" linkage method
> hc_complete <- hclust(distance_matrix, method = "complete")
> # Plot the dendrogram
> plot(hc_complete, main = "Hierarchical Clustering Dendrogram", xlab = "",
> # Cut the tree to form 3 clusters
> clusters <- cutree(hc_complete, k = 3)
> # Print the cluster memberships
> print(clusters)
[1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
[38] 1 1 1 1 2 1 1 1 1 1 1 1 3 3 3 2 3 2 3 2 3 2 3 2 3 3 3 3 2 2 3 3
[75] 3 3 3 3 3 2 2 2 3 3 3 3 2 3 2 2 3 2 2 3 3 3 2 2 3 3 3 3 3 3 2 3 3
[112] 3 3 3 3 3 3 3 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
[149] 3
> # Add the clusters to the original dataset
> iris$cluster <- as.factor(clusters)
> # Display the first few rows of the updated dataset
> head(iris)
```

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species	Cluster
1	5.1	3.5	1.4	0.2	setosa	1
2	4.9	3.0	1.4	0.2	setosa	1
3	4.7	3.2	1.3	0.2	setosa	1
4	4.6	3.1	1.5	0.2	setosa	1
5	5.0	3.6	1.4	0.2	setosa	1
6	5.4	3.9	1.7	0.4	setosa	1

```
> |
```

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iris_data <- iris[, -5]
# Standardize the data
iris_scaled <- scale(iris_data)
# Compute the distance matrix
distance_matrix <- dist(iris_scaled, method = "euclidean")
# Perform hierarchical clustering using the "complete" linkage method
hc_complete <- hclust(distance_matrix, method = "complete")
# Plot the dendrogram
plot(hc_complete, main = "Hierarchical Clustering Dendrogram", xlab = "", sub = "")
# Cut the tree to form 3 clusters
clusters <- cutree(hc_complete, k = 3)
# Print the cluster memberships
print(clusters)
# Add the clusters to the original dataset
iris$cluster <- as.factor(clusters)
# Display the first few rows of the updated dataset
head(iris)|
```



b) K-MEANS CLUSTERING

```
# Load the iris dataset
data(iris)
# Use only the numeric columns for clustering (exclude the Species column)
iris_data <- iris[, -5]
# Standardize the data
iris_scaled <- scale(iris_data)
# Set the number of clusters
set.seed(123) # For reproducibility
k <- 3 # Number of clusters
# Perform K-Means clustering
kmeans_result <- kmeans(iris_scaled, centers = k, nstart = 25)
# Print the K-Means result
print(kmeans_result)
# Print the cluster centers
print(kmeans_result$centers)
# Add the cluster assignments to the original dataset
iris$Cluster <- as.factor(kmeans_result$cluster)
# Display the first few rows of the updated dataset
head(iris)
# Plot the clusters
library(ggplot2)
ggplot(iris, aes(x = Sepal.Length, y = Sepal.Width, color = Cluster)) +
  geom_point(size = 3) +
  labs(title = "K-Means Clustering of Iris Dataset", x = "Sepal Length", y = "Sepal Width")
```

OUTPUT:

