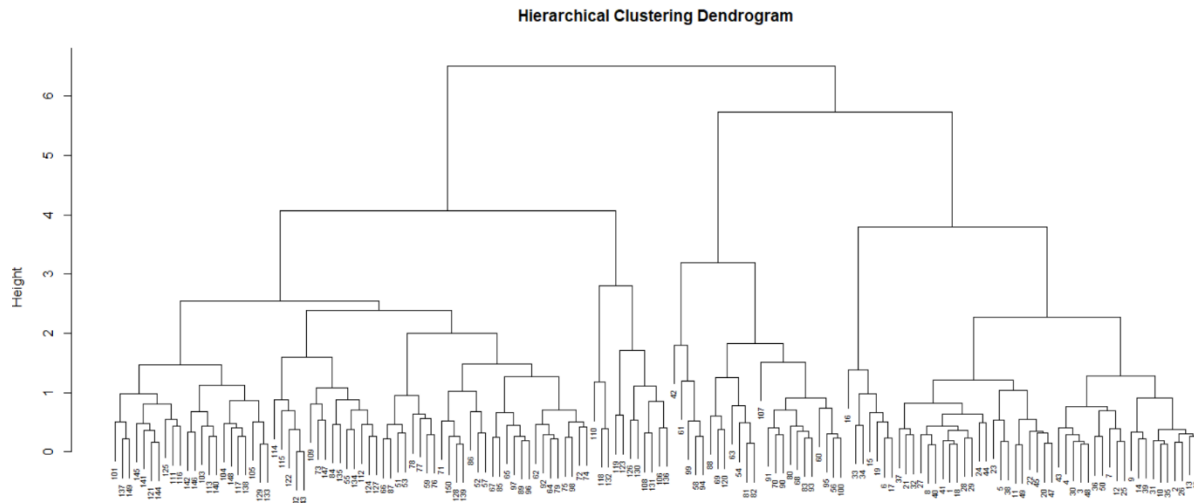


```
R GUI
File Edit Packages Windows Help

R Console
Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

[Previously saved workspace restored]

> # 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)
```



## 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:**