**Hierarchical 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)

# 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

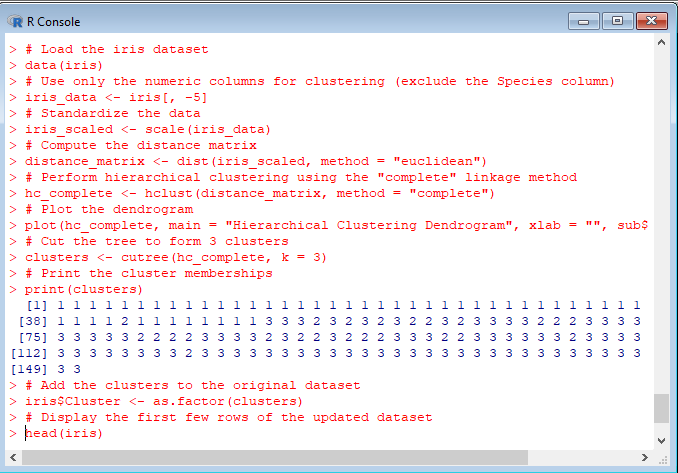
print(clusters)

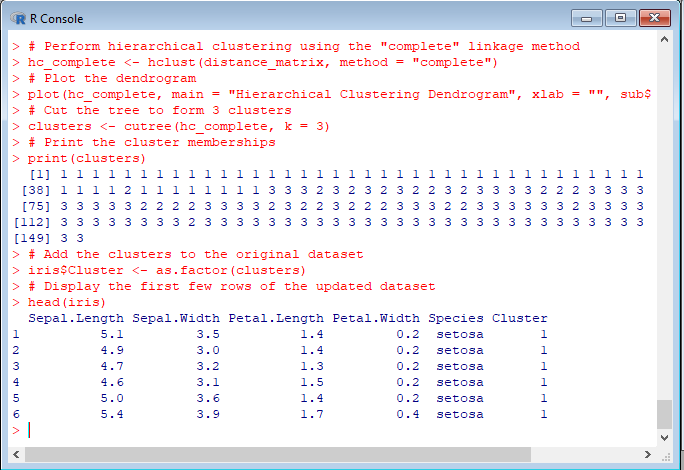
# Add the clusters to the original dataset

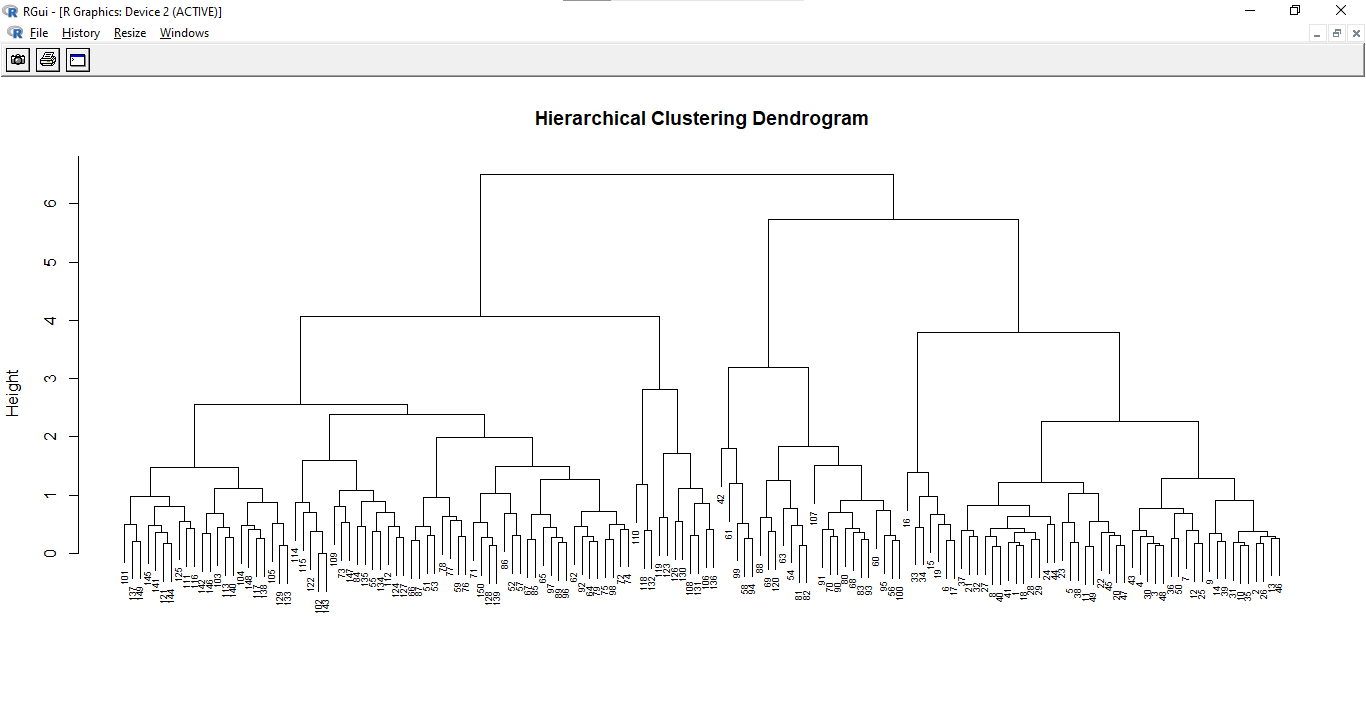
iris$Cluster <- as.factor(clusters)

# Display the first few rows of the updated dataset

head(iris)







**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")

