**Exp. No : 9**

# Implement clustering techniques – Hierarchical and K-Means

**a) 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")

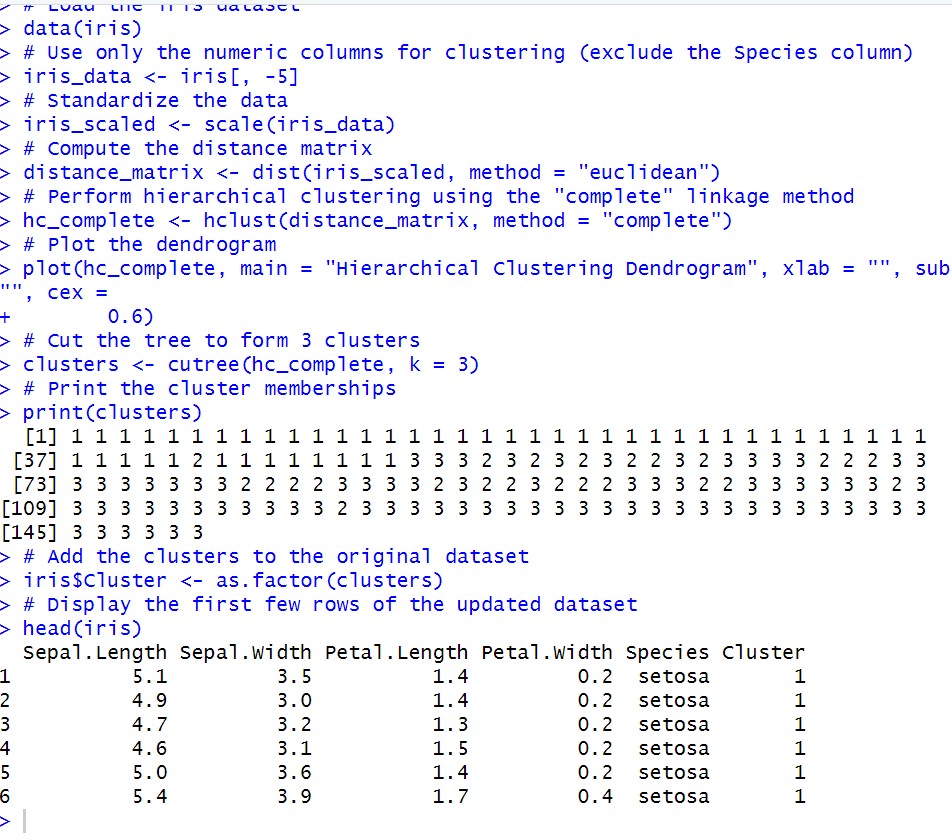
# Plot the dendrogram

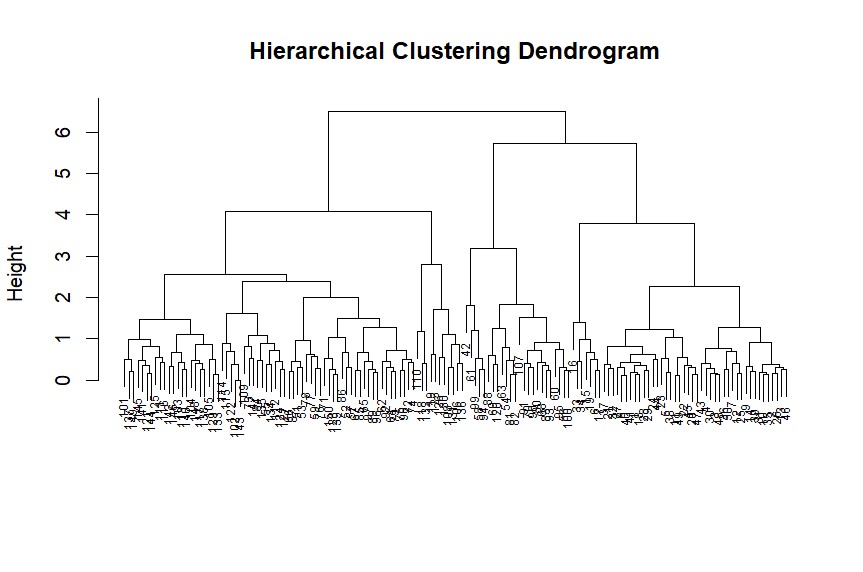
plot(hc\_complete, main = "Hierarchical Clustering Dendrogram", xlab = "", sub = "", cex = 0.6)

# 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) **Output :**





**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)

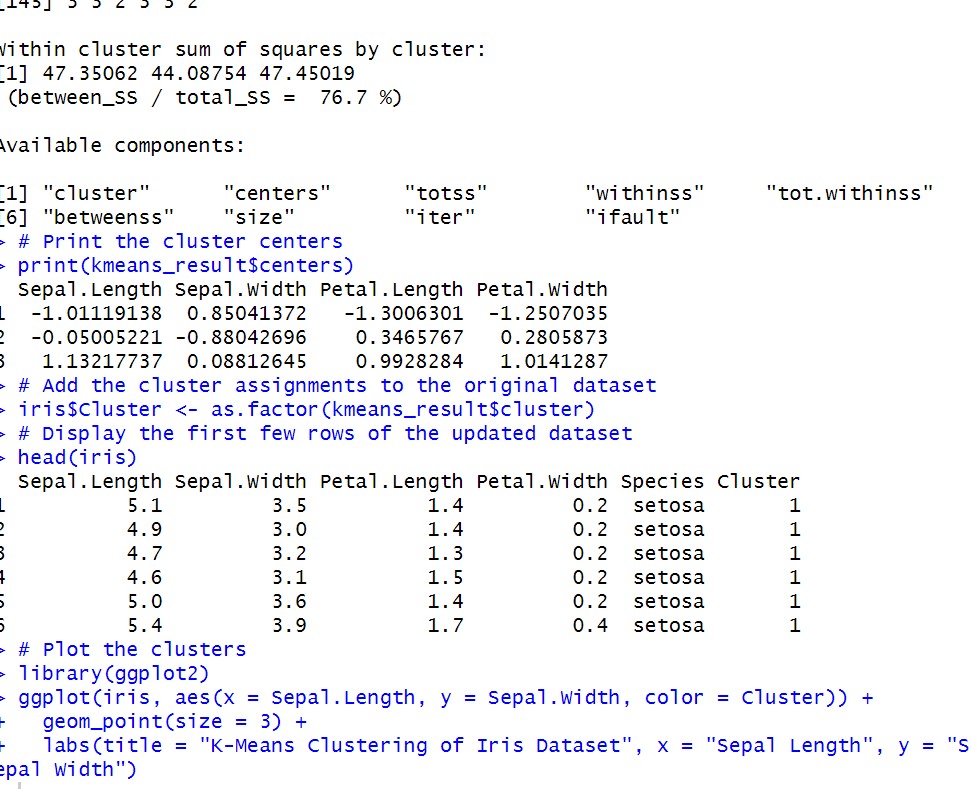
# Print the K-Means result print(kmeans\_result)

# Print the cluster centers

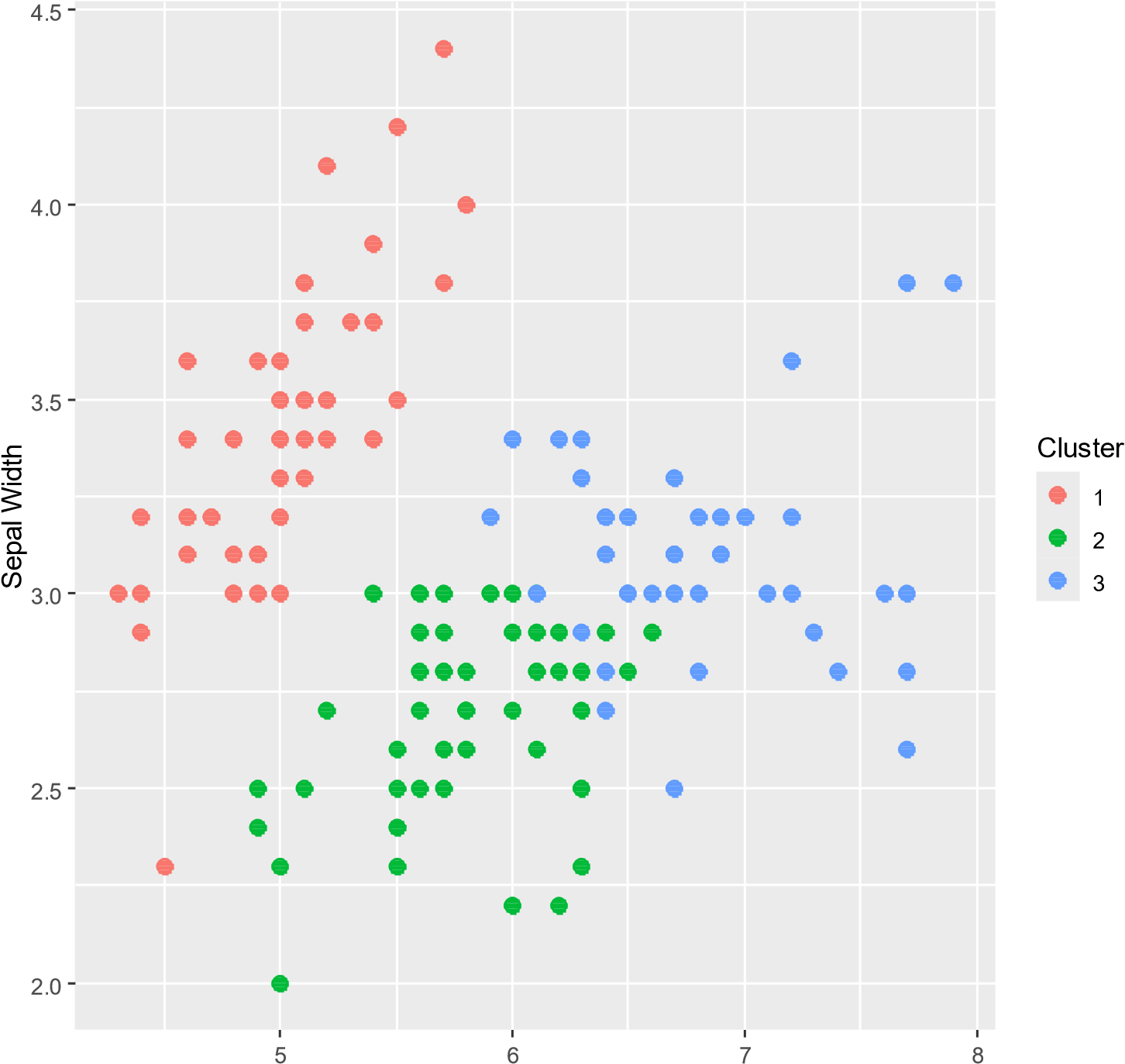
print(kmeans\_result$centers)

# 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 :**



K-Means Clustering of Iris Dataset



Sepal Length