

**Implement clustering techniques – Hierarchical and K-Means****a) HIERARCHIAL CLUSTERING****CODE:**

```
# 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)

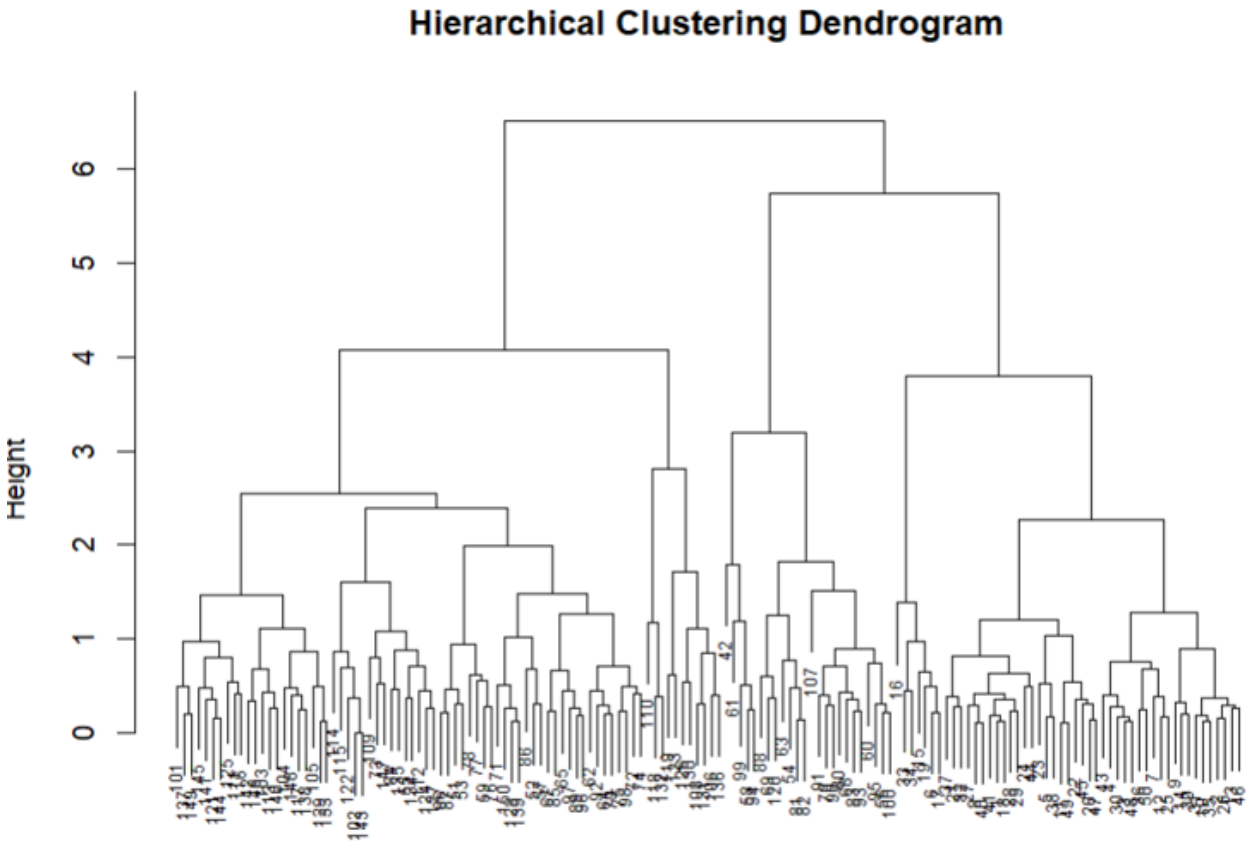
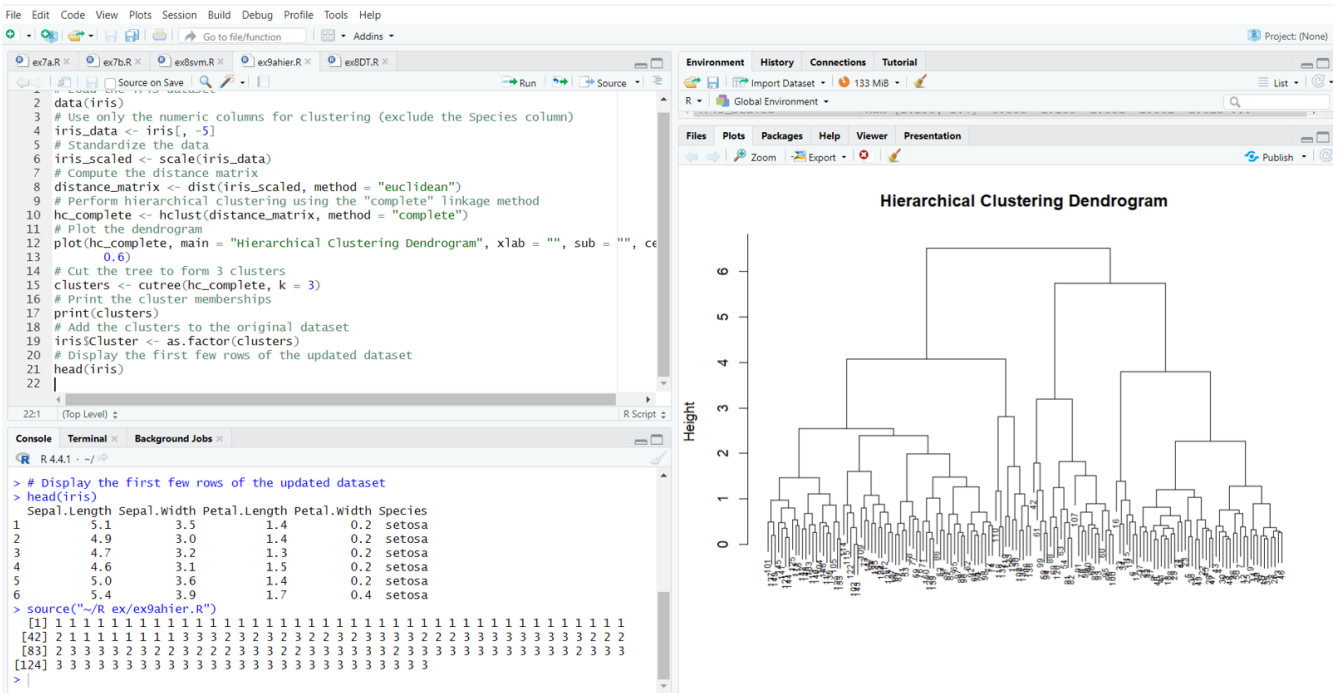
# Cut the tree to form 3 clusters
clusters <- cutree(hc_complete, k = 3)

# 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****CODE:**

```
# 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)

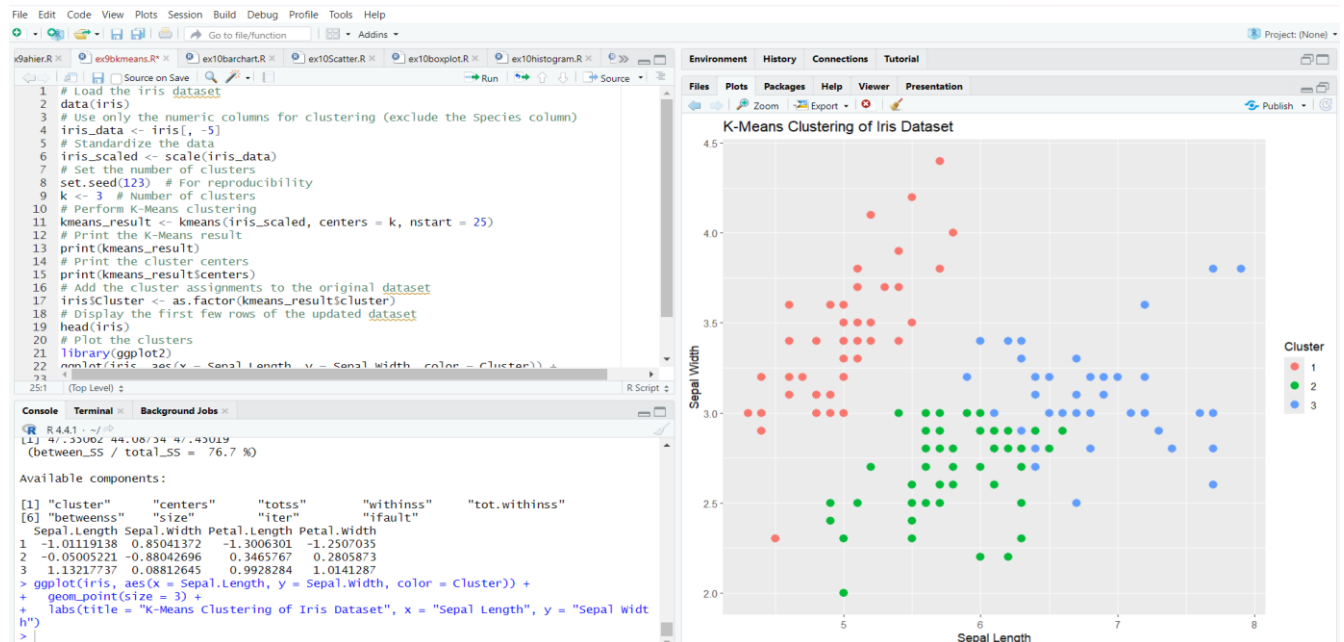
# Print the cluster centers
print(kmeans_result$centers)

# 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")
```

**RESULT:**

Thus clustering techniques such as Hierarchical and K-Means clustering implemented successfully.