Ex No: 9 **Roll No: 210701123**

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)
```

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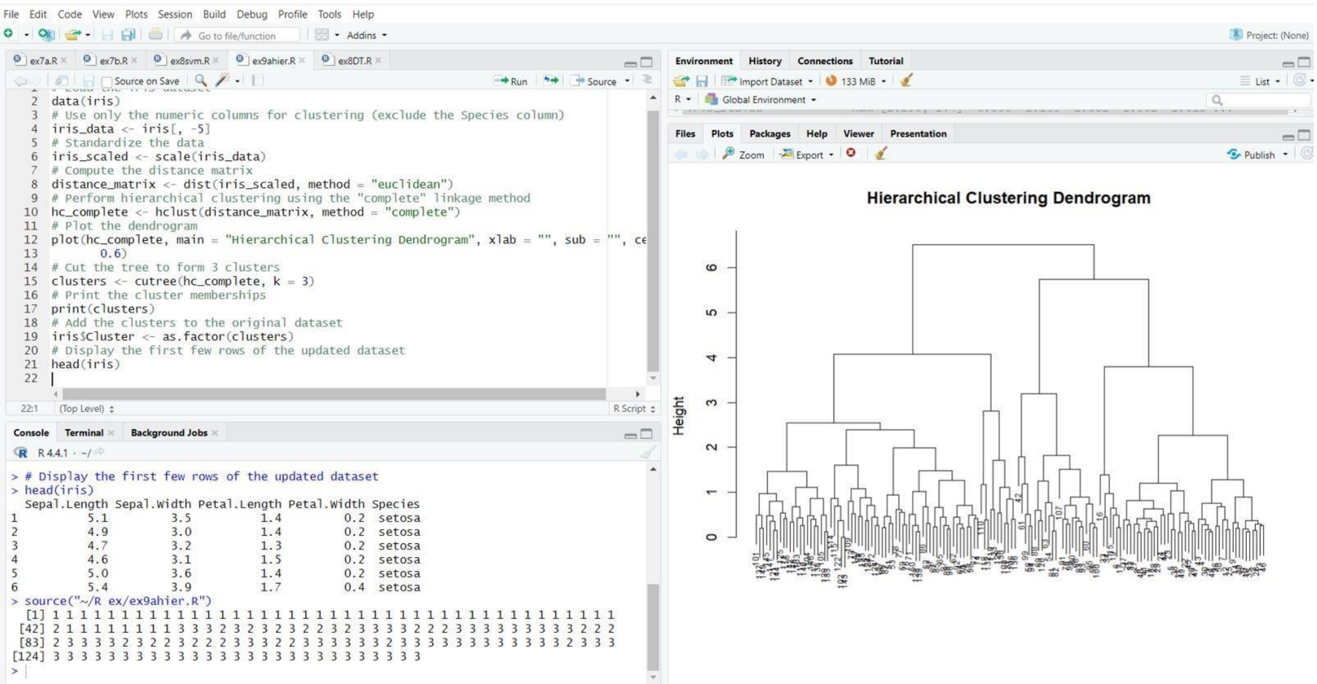
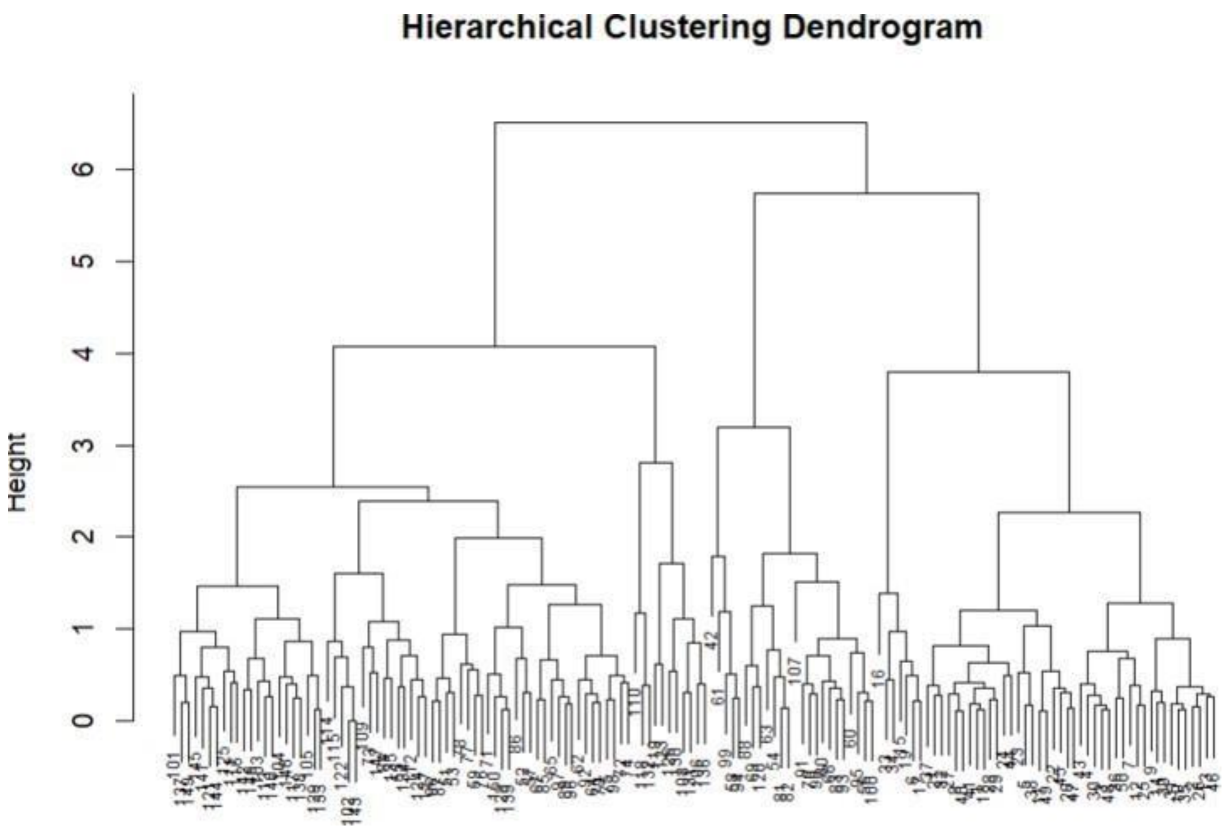
OUTPUT:





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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")
```

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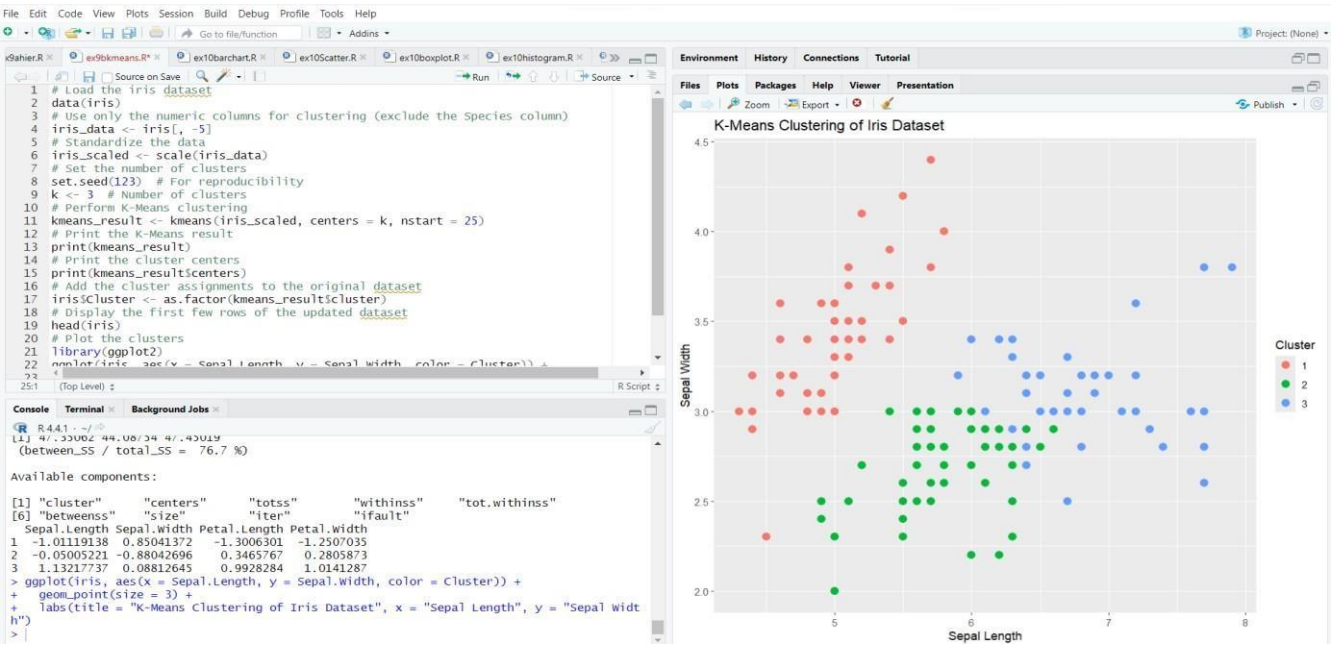
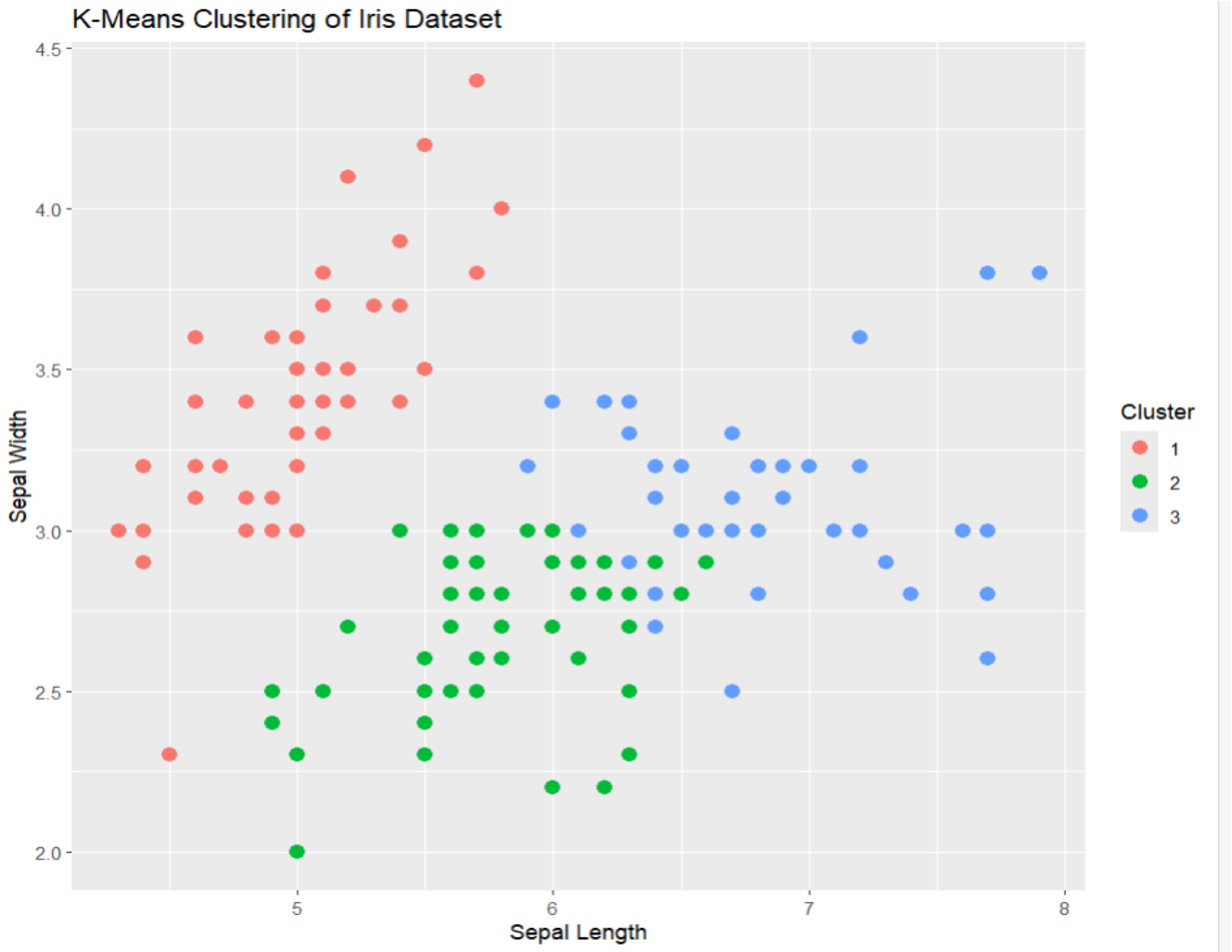
```
# Load the iris dataset
data(iris)
# Use only the numeric columns for clustering (exclude the Species column)
iris_data <- iris[, -5]
# Standardize the data
iris_scaled <- scale(iris_data)
# Set the number of clusters
set.seed(123)  # For reproducibility
k <- 3  # Number of clusters
# Perform K-Means 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)
```

```
 (between_SS / total_SS =  76.7 %)

Available components:

[1] "cluster"      "centers"      "totss"        "withinss"     "tot.withinss"
[6] "betweenss"    "size"         "iter"         "ifault"
  Sepal.Length Sepal.Width Petal.Length Petal.Width
1  -1.01119138  0.85041372   -1.3006301  -1.2507035
2  -0.05005221 -0.88042696    0.3465767   0.2805873
3   1.13217737  0.08812645    0.9928284   1.0141287
> 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 Widt
h")
```





RESULT:

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