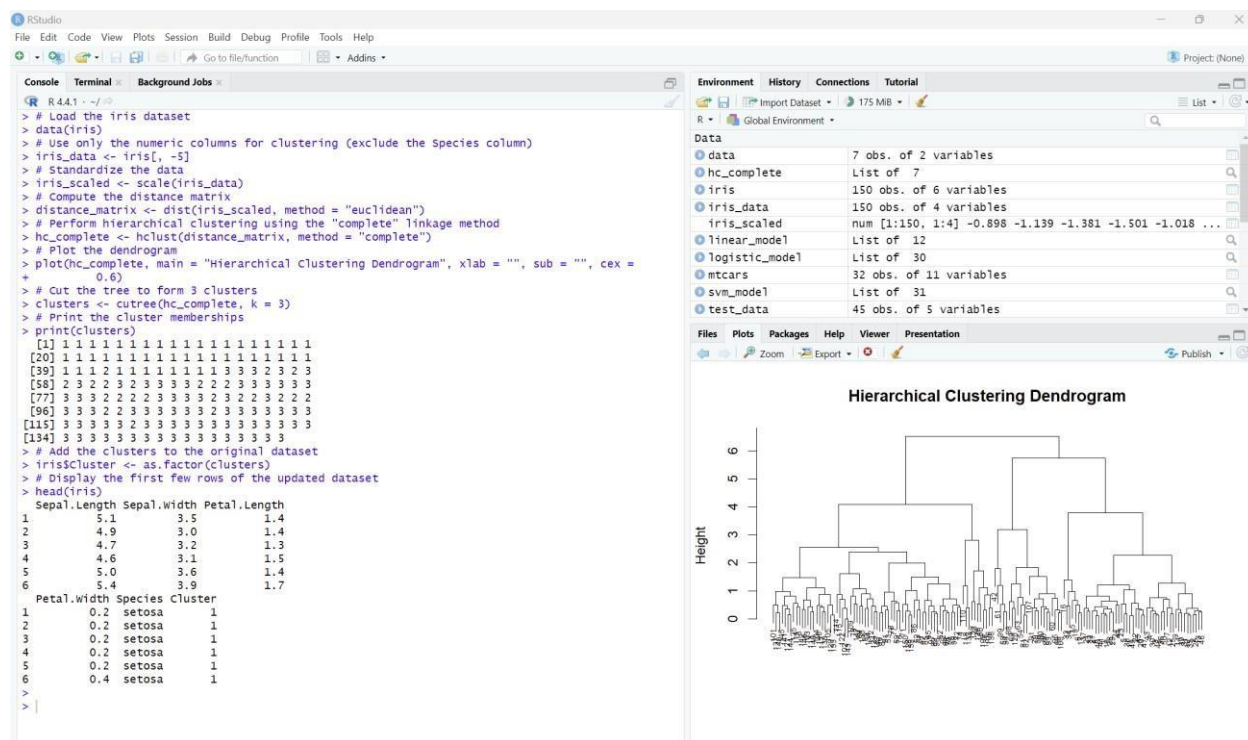




**Exp:9****Implement clustering techniques – Hierarchical and K-Means****a) HIERARCHIAL CLUSTERING**

```
# 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)
```



## **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")
```

