Exp.No: 9

IMPLEMENTCLUSTERINGTECHNIQUES–HIERARCHICALANDKMEANS

AIM:

To write an R code to implement hierarchical and k-means clustering techniques.

PROCEDURE:

1. Load the iris dataset and use only the numeric columns for clustering by excluding the Species column.

2. Standardize the data to ensure all variables have equal weight in the clustering process.

3. Compute the distance matrix using the Euclidean method and perform hierarchical clustering using the "complete" linkage method, plot the dendrogram, and cut the tree to form 3 clusters.

4. Perform K-means clustering by setting the number of clusters, run the clustering algorithm, and add cluster assignments to the original dataset.

5. Display the first few rows of the updated dataset and plot the clusters using ggplot2 for visualization.

PROGRAM CODE:

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 =
```
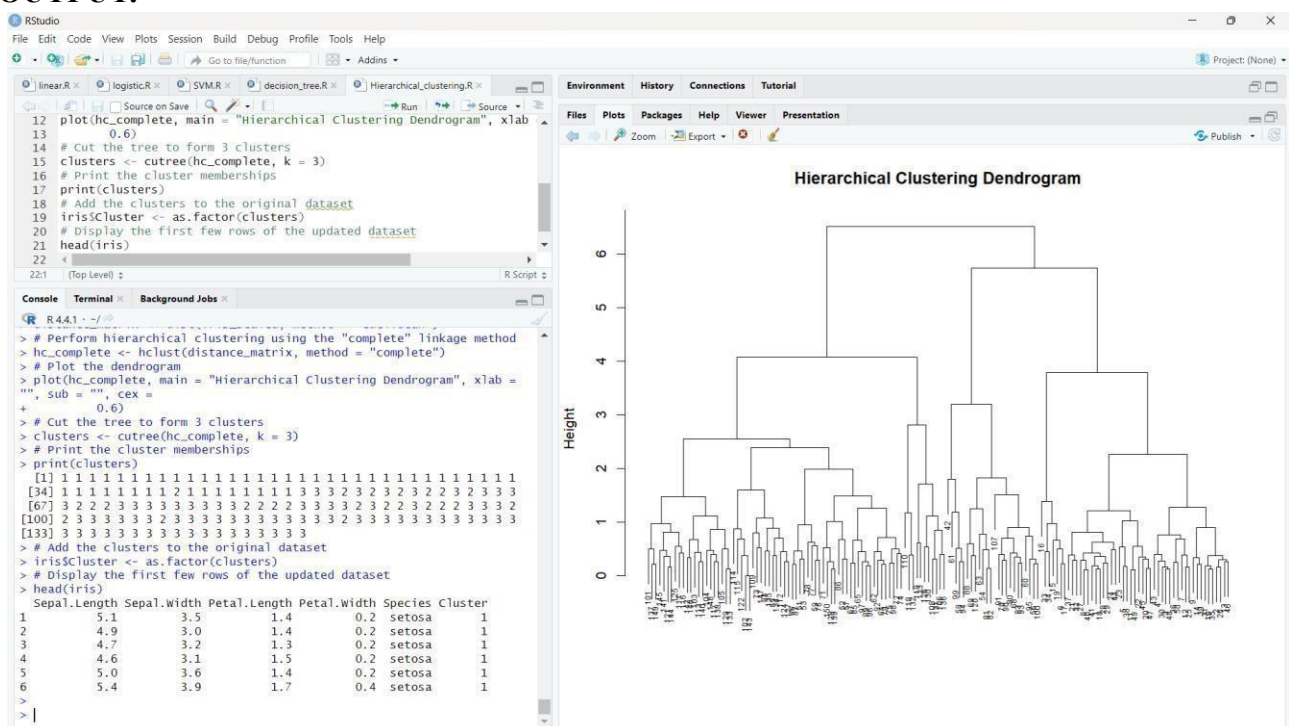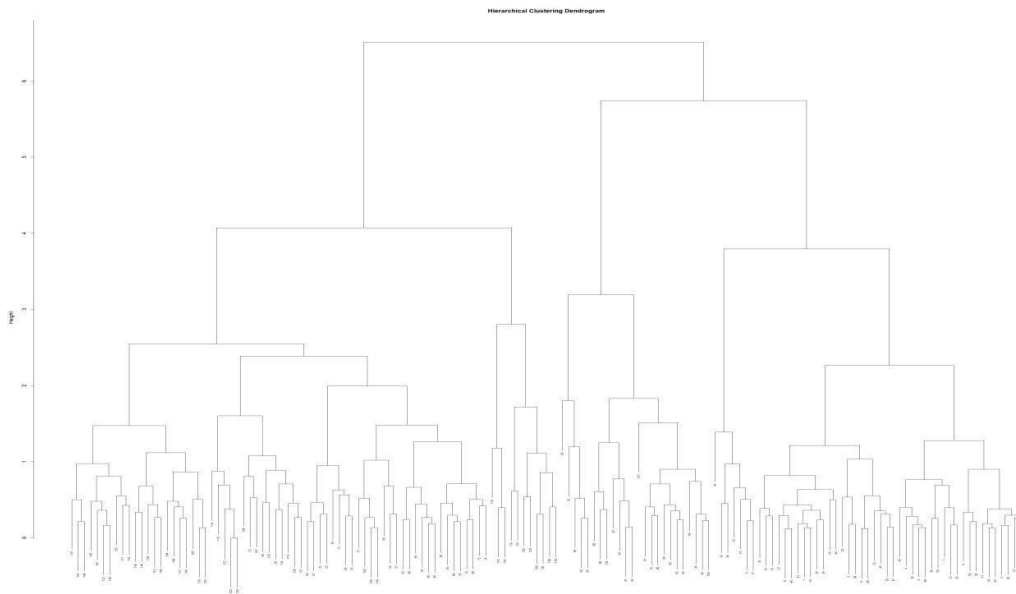
0.6)

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)

OUTPUT:

Hierarchical Clustering Dendrogram

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)
```
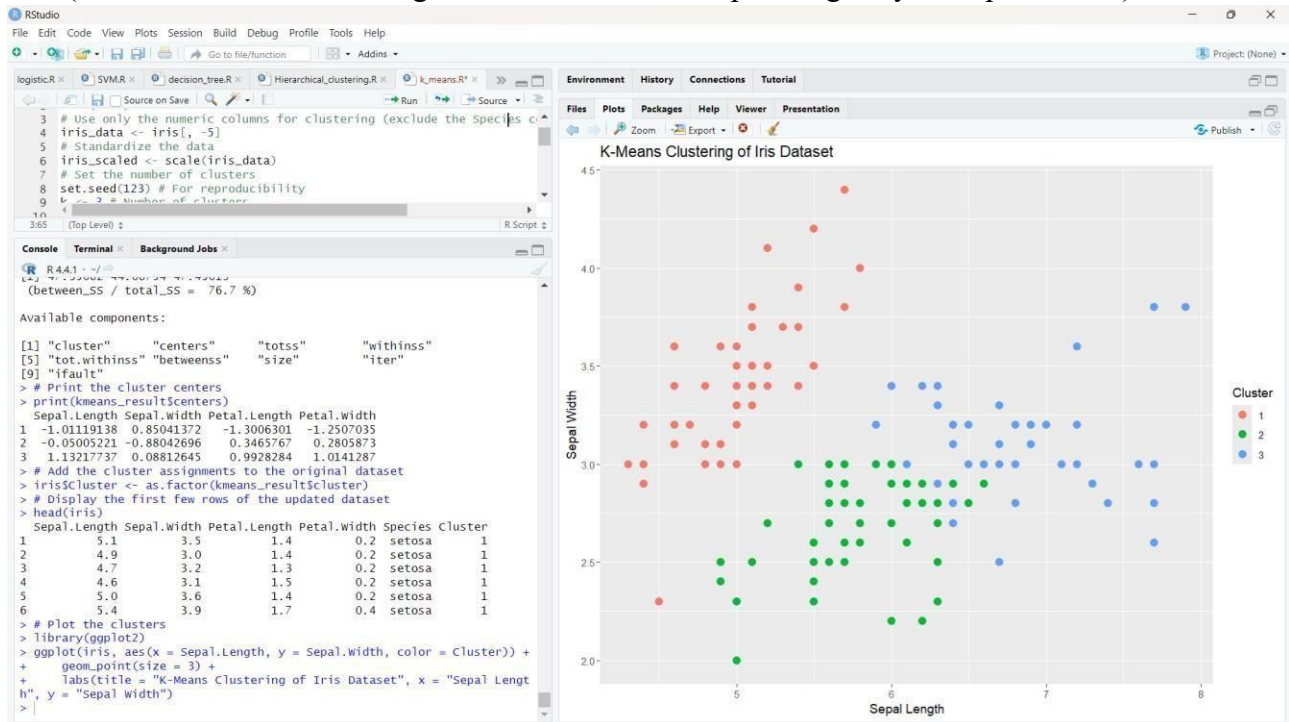
Display the first few rows of the updated dataset head(iris)

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:**

RESULT:

   Thus the R program to implement hierarchical and k-means clustering techniques has been executed and verified successfully.