Ex No 9

Implement clustering techniques – Hierarchical and K-Means

AIM:

To Implement clustering techniques – Hierarchical and K-Means using R.

PROCEDURE:

- Collect and load the dataset from sources like CSV files or databases.
- Clean and preprocess the data, including handling missing values and scaling features.
- Determine the number of clusters (K) for K-Means, or decide on the stopping criterion for Hierarchical Clustering.
- Choose the appropriate clustering algorithm: K-Means for partitioning, Hierarchical for nested clustering.
- Apply the K-Means algorithm using fit_predict to assign data points to clusters.
- Apply the Hierarchical Clustering algorithm using Agglomerative Clustering for hierarchical clusters.
- Visualize the clusters with scatter plots for K-Means, and dendrograms for Hierarchical Clustering.
- Evaluate clustering performance using metrics like silhouette score or inertia (for K-Means).
- Fine-tune the clustering by adjusting the number of clusters or linkage criteria.
- Interpret the results to understand the structure and relationships within the data.

CODE:

Hierarchical Clustering.R:

```
# 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)
```

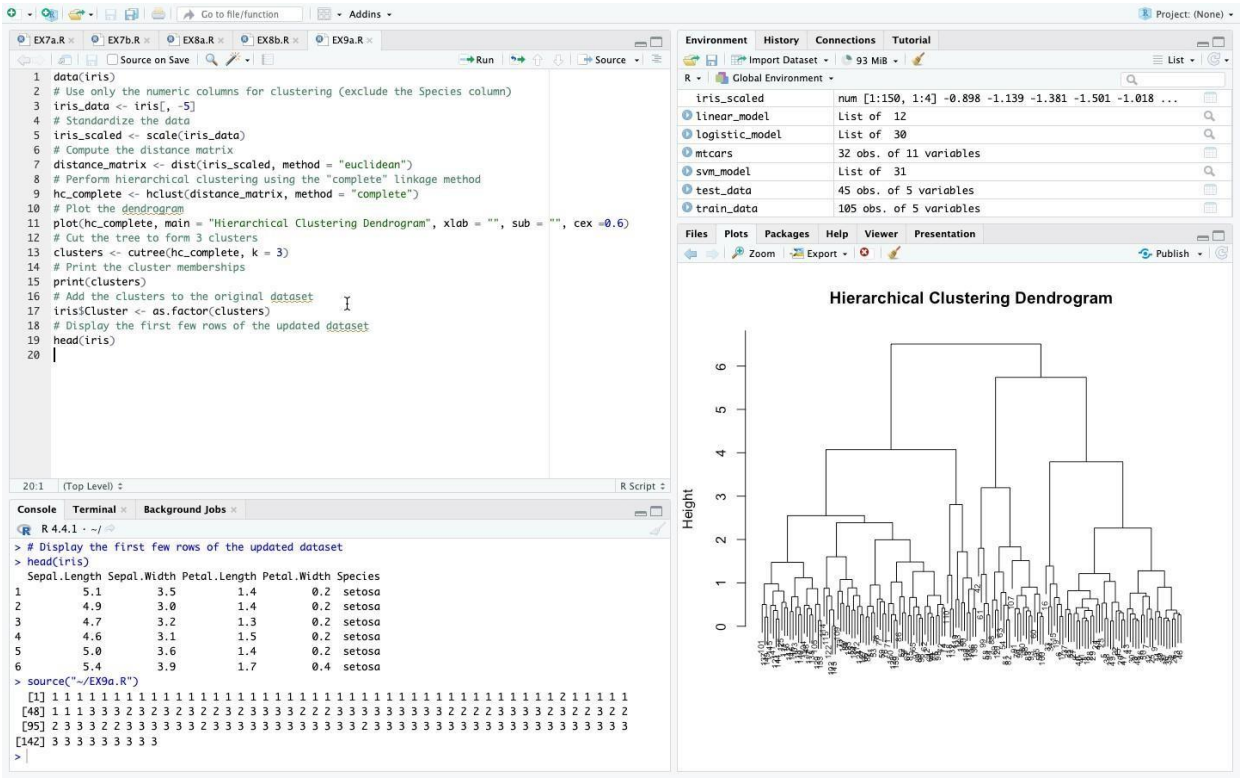
K-Means Clustering.R:

```
# 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)
```

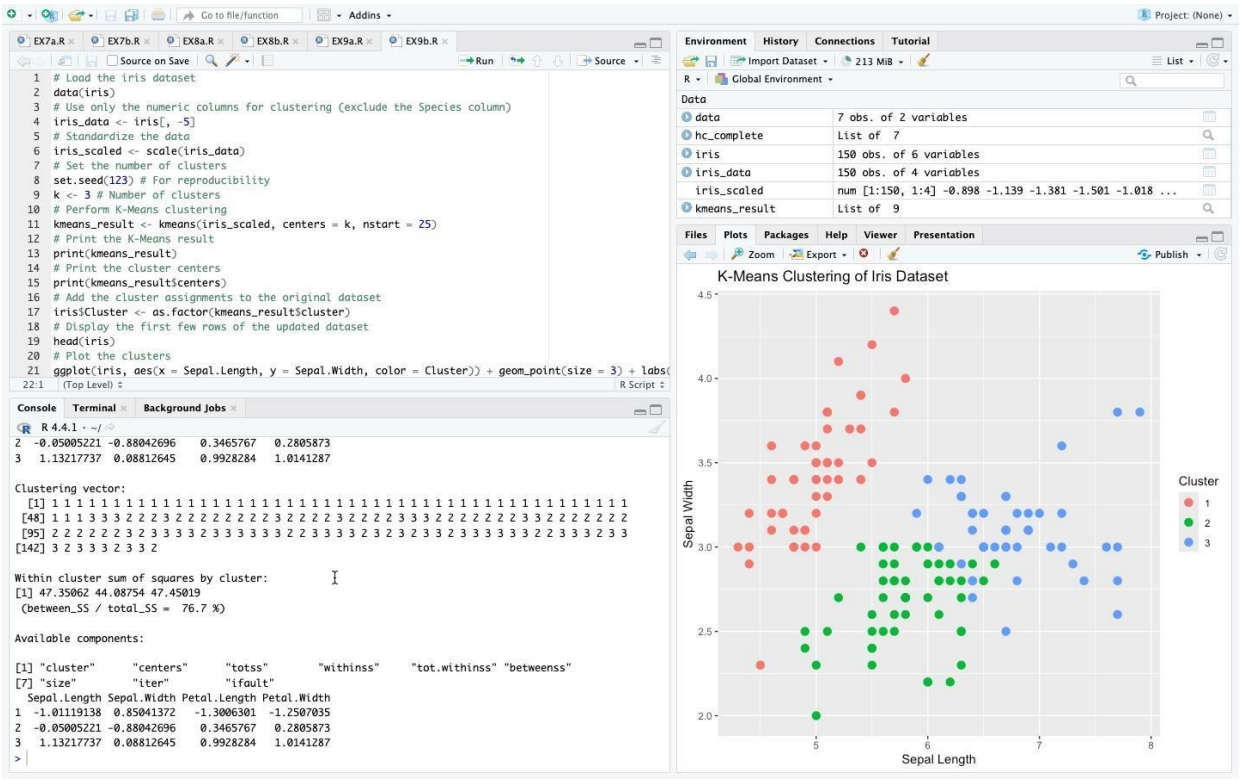
```
# Add the cluster assignments to the original dataset
iris$Cluster <- as.factor(kmeans_result$cluster) #
Display the first few rows of the updated dataset
head(iris) # Plot the clusters library(ggplot2)

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:

Hierarchical Clustering:



K-Means Clustering:



RESULT:

Thus, to implement clustering techniques – Hierarchical and K-Means using R has been successfully executed.