Exp.No: 9

Implement clustering techniques – Hierarchical and K-Means

AIM:

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

PROCEDURE:

- Load the dataset from sources such as CSV files or databases using appropriate libraries.
- Perform data cleaning and preprocessing, including handling missing values and scaling features for consistency.
- Decide on the number of clusters (K) for K-Means or establish the stopping criterion for Hierarchical Clustering.
- Select the suitable clustering algorithm: utilize K-Means for partitioning or Hierarchical Clustering for creating nested groups.
- Implement the K-Means algorithm using fit_predict to categorize data points into clusters.
- Use Agglomerative Clustering for Hierarchical Clustering to create a hierarchy of clusters.
- Visualize the resulting clusters using scatter plots for K-Means and dendrograms for Hierarchical Clustering.
- Assess clustering performance through metrics such as silhouette score or inertia for K-Means.
- Tune the clustering process by modifying the number of clusters or adjusting linkage criteria.
- Analyze the results to gain insights into the data structure and the relationships among clusters.

PROGRAM:

Hierarchical Clustering.R:

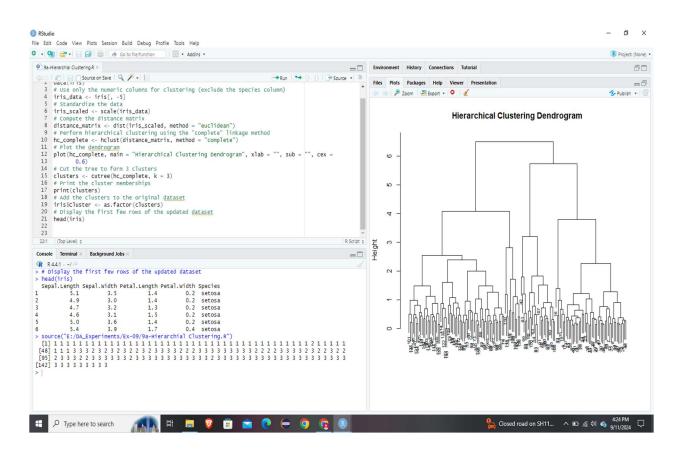
Load the iris dataset data(iris)

```
# Use only the numeric columns for clustering (exclude the Species column)
iris data <- iris[, -5]
# Standardize the data
iris scaled <- scale(iris data)</pre>
# 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")</pre>
# 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)</pre>
# Print the cluster memberships
print(clusters)
# Add the clusters to the original dataset
iris$Cluster <- as.factor(clusters)</pre>
# 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)</pre>
# 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
```

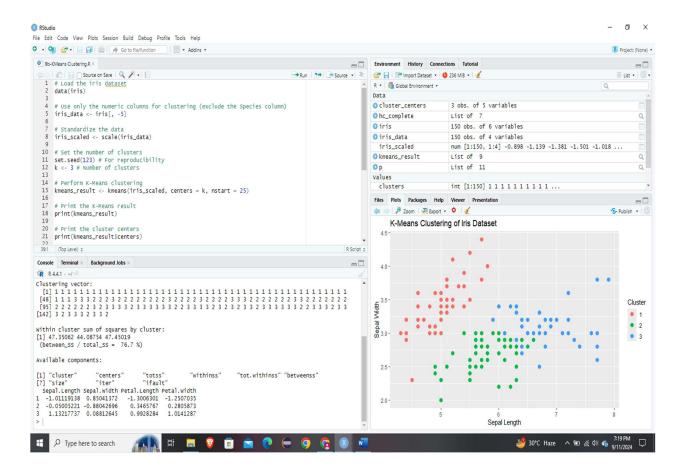
```
print(kmeans_result)
# Print the cluster centers
print(kmeans_result$centers)
# Add the cluster assignments to the original dataset
iris$Cluster <- as.factor(kmeans_result$cluster)
# Display the first few rows of the updated dataset
head(iris)
# Plot the clusters
library(ggplot2)
ggplot(iris, aes(x = 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")</pre>
```

OUTPUT:

Hierarchical Clustering:



K-Means Clustering:



RESULT:

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