Ex.No:9

Implement clustering techniques – Hierarchical and K-Means

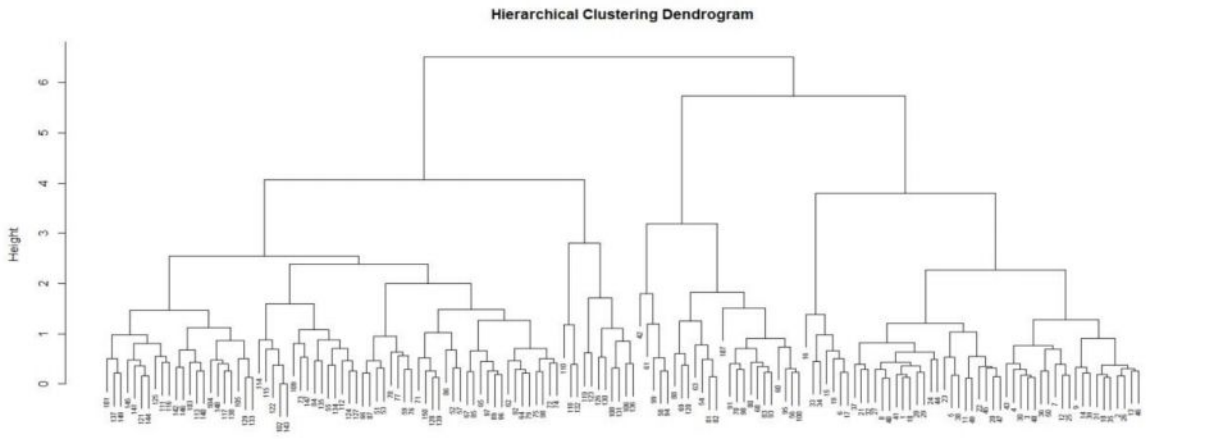
AIM:

To implement clustering techniques (hierarchical and K Means) using R language.

a) HIERARCHIAL CLUSTERING

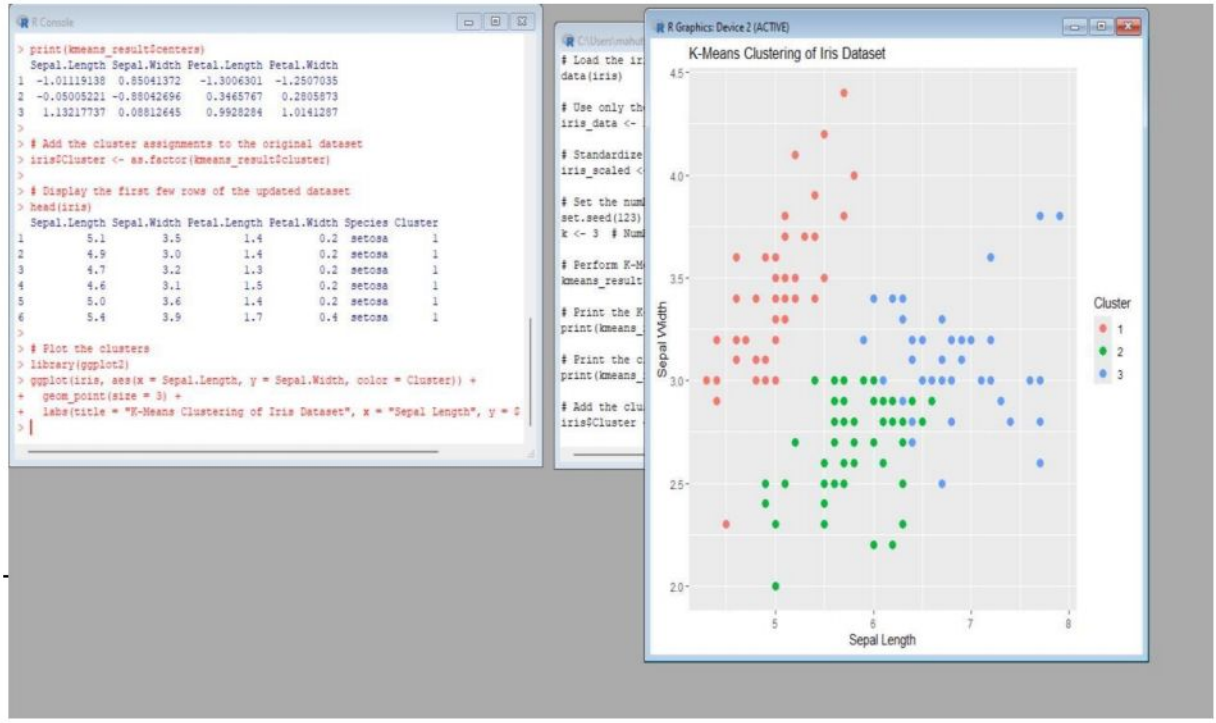
```
# Load the iris dataset data(iris)

# 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)
```

```
R Console

>
> # Cut the tree to form 3 clusters
> clusters <- cutree(hc_complete, k = 3)
>
> # Print the cluster memberships
> print(clusters)
  [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
 [38] 1 1 1 1 2 1 1 1 1 1 1 1 1 3 3 3 2 3 2 3 2 3 2 2 3 2 3 3 3 3 2 2 2 3 3 3 3
 [75] 3 3 3 3 3 2 2 2 2 3 3 3 3 2 3 2 2 3 2 2 2 3 3 3 2 2 3 3 3 3 3 3 2 3 3 3 3
[112] 3 3 3 3 3 3 3 3 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
[149] 3 3
>
> # Add the clusters to the original dataset
> iris$Cluster <- as.factor(clusters)
>
> # Display the first few rows of the updated dataset
> head(iris)
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species Cluster
1          5.1         3.5          1.4         0.2  setosa       1
2          4.9         3.0          1.4         0.2  setosa       1
3          4.7         3.2          1.3         0.2  setosa       1
4          4.6         3.1          1.5         0.2  setosa       1
5          5.0         3.6          1.4         0.2  setosa       1
6          5.4         3.9          1.7         0.4  setosa       1
>
```



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")
```



RESULT:

Thus to implement clustering techniques (hierarchical and K Means) using R language is successfully completed.