

## Implement clustering techniques – Hierarchical and K-Means

### AIM:

To Implement clustering techniques Hierarchical and K-Means using R programming in R Studio.

#### 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:**

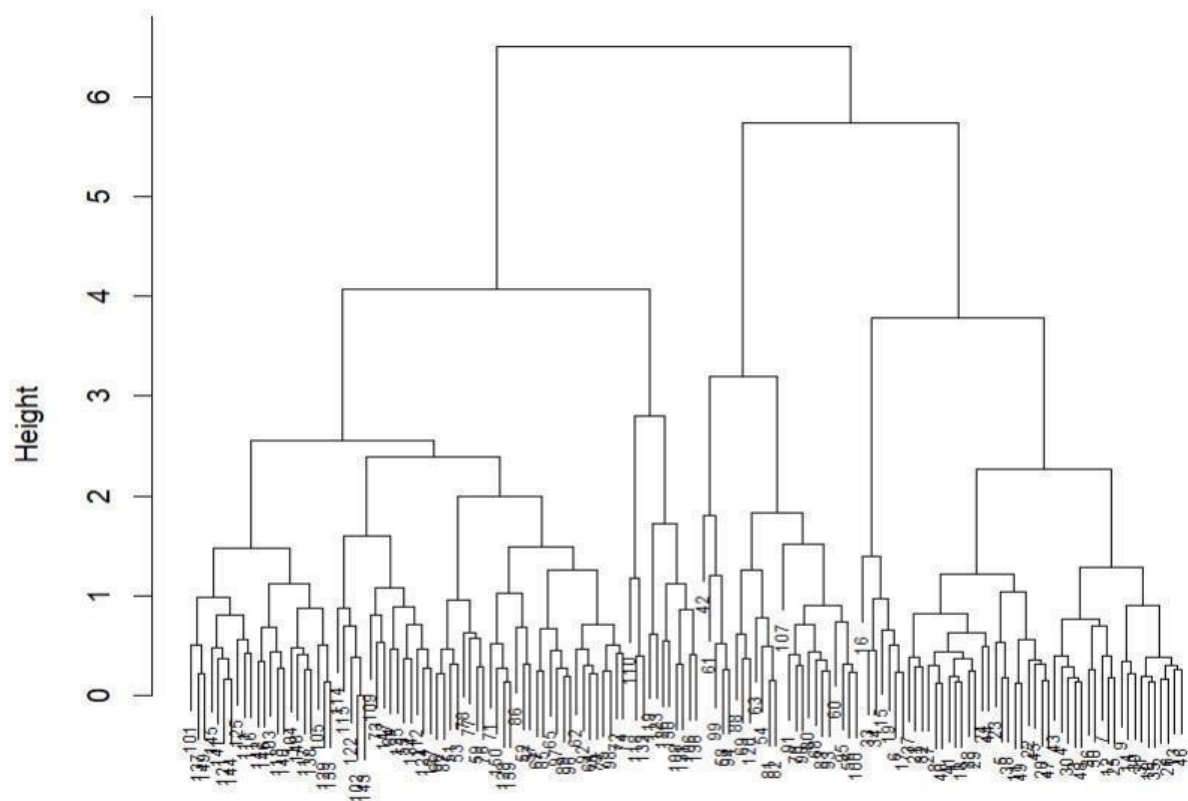
```

Hierarchial.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)

```

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**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))
```

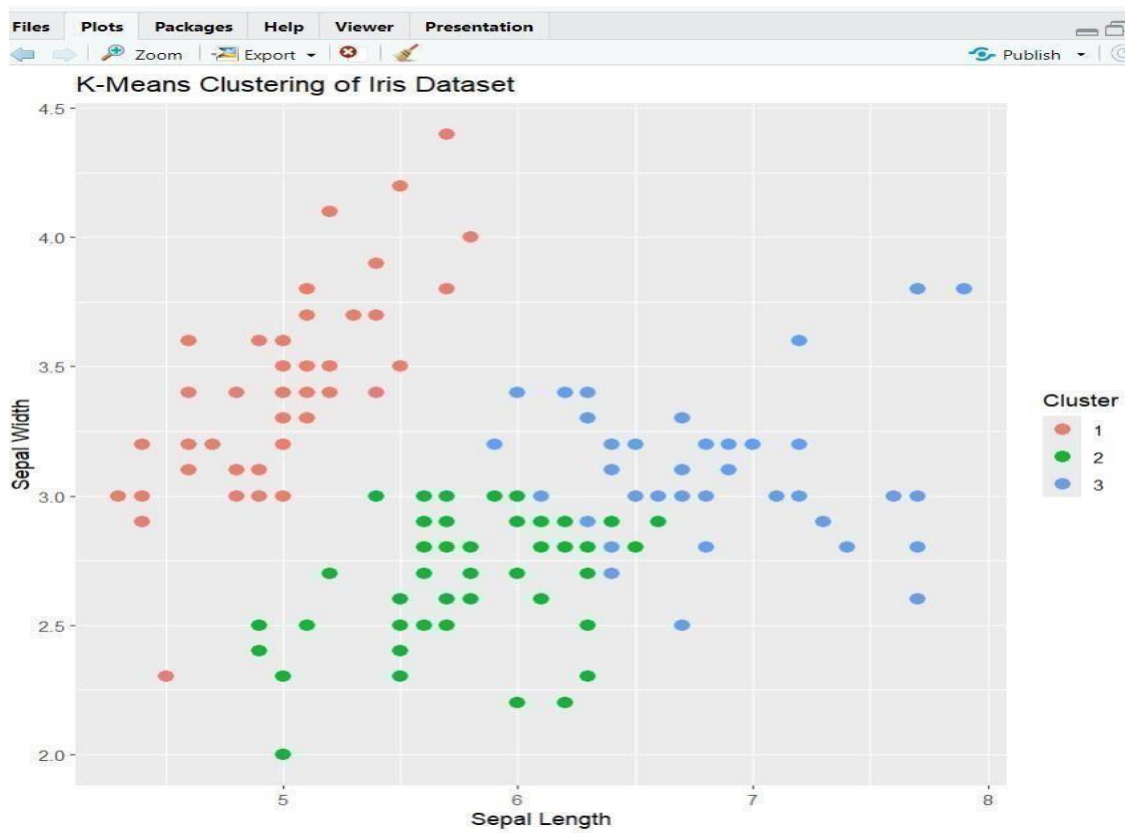
```
+ geom_point(size = 3) + labs(title = "K-Means Clustering of Iris Dataset", x = "Sepal
```

```
Length", y = "Sepal Width") OUTPUT:
```

```

1 # Load the iris dataset
2 data(iris)
3 # Load the iris dataset
4 data(iris)
5 # Use only the numeric columns for clustering (exclude the Species column)
6 iris_data <- iris[, -5]
7 # Standardize the data
8 iris_scaled <- scale(iris_data)
9 # Set the number of clusters
10 set.seed(123) # For reproducibility
11 k <- 3 # Number of clusters
12 # Perform K-Means clustering
13 kmeans_result <- kmeans(iris_scaled, centers = k, nstart = 25)
14 # Print the K-Means result
15 print(kmeans_result)
16 # Print the cluster centers
17 print(kmeans_result$centers)
18 # Add the cluster assignments to the original dataset
19 iris$Cluster <- as.factor(kmeans_result$cluster)
20 # Display the first few rows of the updated dataset
21 head(iris)
22 # Plot the clusters
23 library(ggplot2)
24 ggplot(iris, aes(x = Sepal.Length, y = Sepal.Width, color = Cluster)) +
25   geom_point(size = 3) +
26   labs(title = "K-Means Clustering of Iris Dataset", x = "Sepal Length", y = "Sepal width")
27

```



**RESULT:**

Thus, the Implement clustering techniques Hierarchical and K-Means using R programming in R Studio have been successfully executed.