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Implement clustering techniques – Hierarchical and K-Means

Aim:

To implement clustering techniques – Hierarchical and K-Means using RStudio.

Procedure:

a) HIERARCHICAL CLUSTERING

Load the iris dataset

data(iris)

Use only the numeric columns for clustering (exclude the Species column)

iris_data <- iris[, -5]</pre>

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

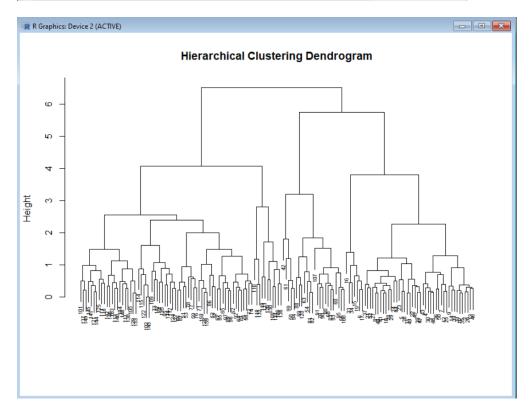
iris\$Cluster <- as.factor(clusters)</pre>

Display the first few rows of the updated dataset

head(iris)

Output:

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



b) K-MEANS CLUSTERING

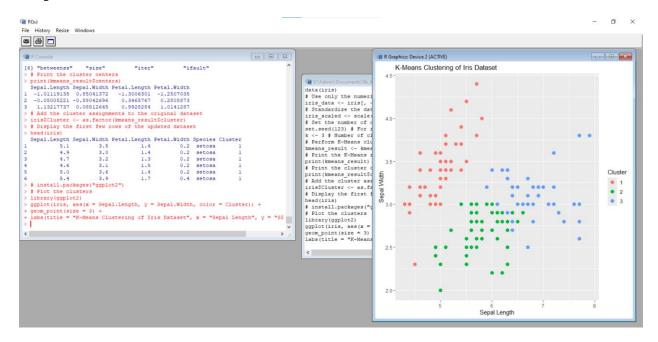
Load the iris dataset

data(iris)

Use only the numeric columns for clustering (exclude the Species column)

```
<u>iris_data <- iris[, -5]</u>
# 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)</pre>
# 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) +
<u>labs(title = "K-Means Clustering of Iris Dataset", x = "Sepal Length", y = "Sepal Width")</u>
```

Output:



Result:

 $Thus, \ clustering \ techniques-Hierarchical \ and \ K-Means \ using \ R \ and \ RStudio \ was implemented successfully.$