

EXP NO: 9 IMPLEMENT CLUSTERING TECHNIQUES – HIERARCHICAL AND K- MEANS

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:

```
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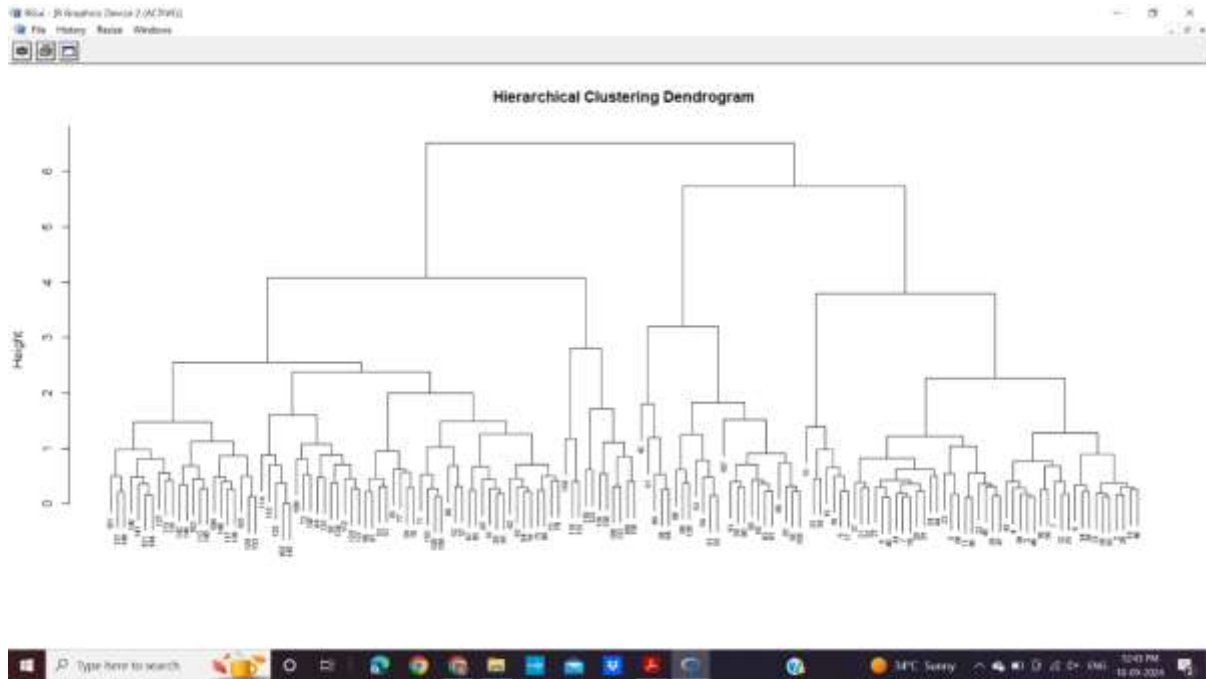
```

> print(confusion_matrix)
      Actual
Predicted setosa versicolour virginica
setosa      46      0      0
versicolour 0     48      0
virginica   0      0     52
Accuracy: 91.33333 %

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# 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  5.4         4.4         1.5         0.4 setosa      1
4  5.4         3.7         1.5         0.2 setosa      1
5  6.7         3.0         5.2         2.3 versicolour 2
6  6.0         2.6         4.8         1.9 versicolour 2
7  5.4         3.9         1.7         0.4 versicolour 2
8  5.1         3.5         1.4         0.2 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")
```

OUTPUT: