

**EX.NO: 9**

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**DATE:**

**IMPLEMENT CLUSTERING TECHNIQUES – HIERARCHICAL AND K-MEANS AIM:**

To implement clustering techniques – Hierarchical and K-Means

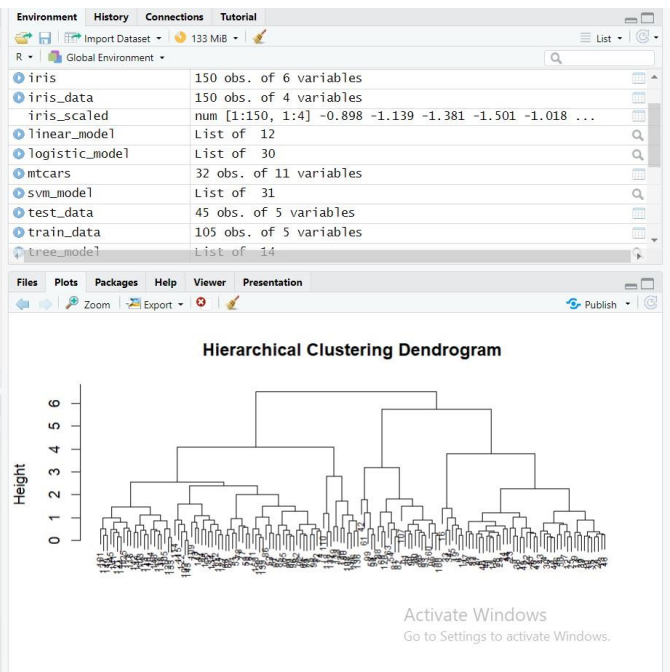
**PROGRAM CODE:**

**HIERARCHIAL CLUSTERING:**

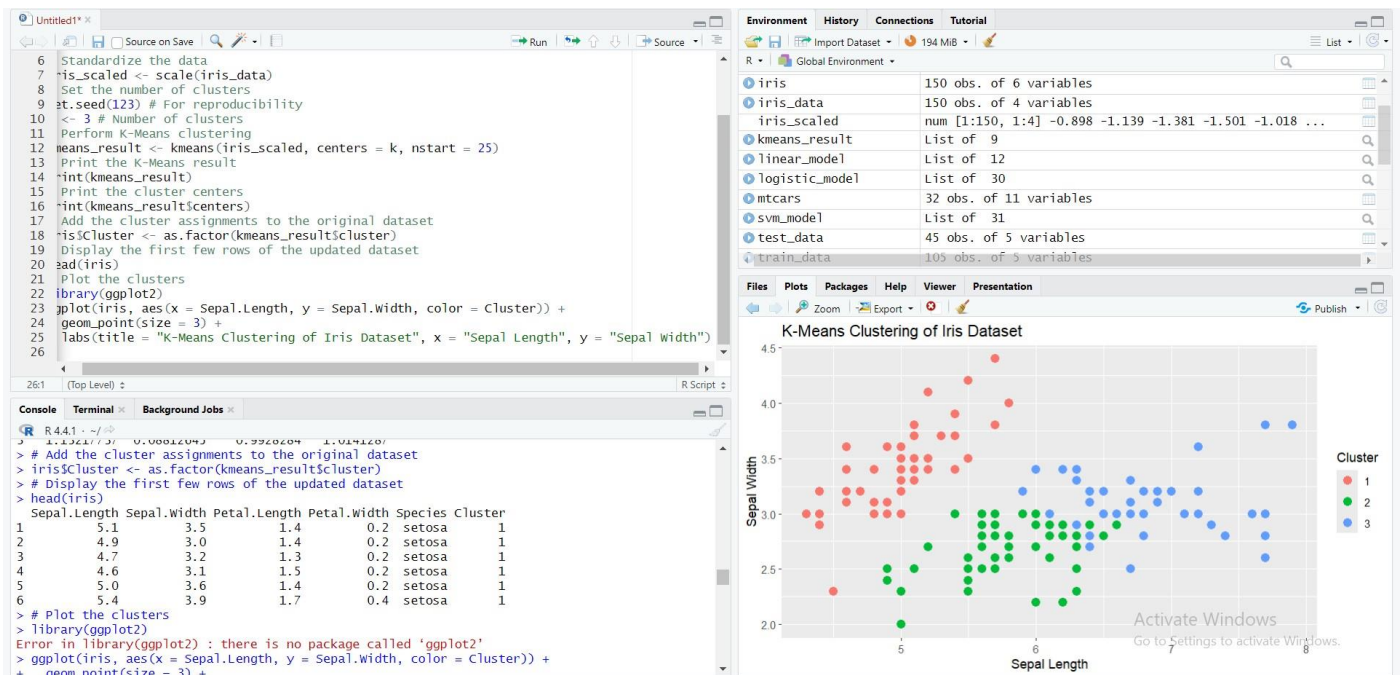
```
# Load the iris dataset data(iris)
# Use only the numeric columns for clustering (exclude the Species column)
iris_data <- iris[, -5] # Standardize the data iris_scaled <- scale(iris_data)
# Compute the distance matrix
distance_matrix <- dist(iris_scaled, method = "euclidean")
# Perform hierarchical 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)
```

**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$clus
ter) # 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) +
```



## Decision Tree in R:



## RESULT:

Thus the implementation of clustering techniques – Hierarchical and K-Means done successfully.