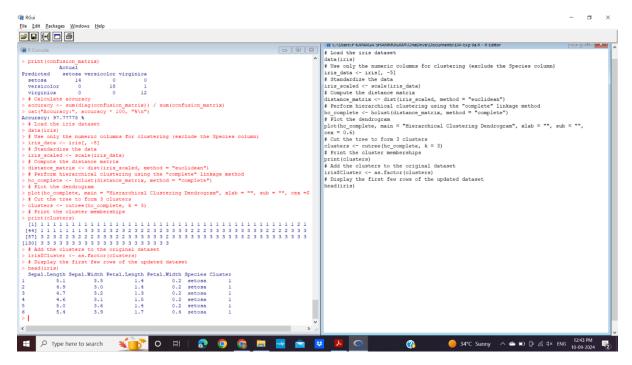
ROLL NUMBER: 210701096

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

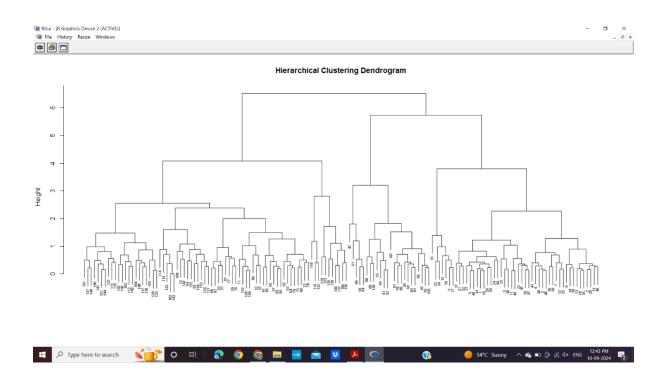
a) HIERARCHIAL CLUSTERING

```
# 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)</pre>
# Display the first few rows of the updated dataset
head(iris)
```

OUTPUT:



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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)</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) +
labs(title = "K-Means Clustering of Iris Dataset", x = "Sepal Length", y = "Sepal Width")
```

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OUTPUT:

