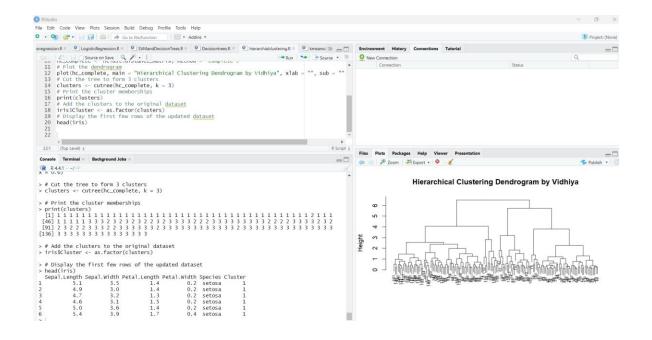
### **Exp:9**

# 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)</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")
# 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)
```



## 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")

