

## Implement Clustering Techniques – Hierarchical and K Means

### Hierarchial Clustering:

#### Code:

```
# 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)

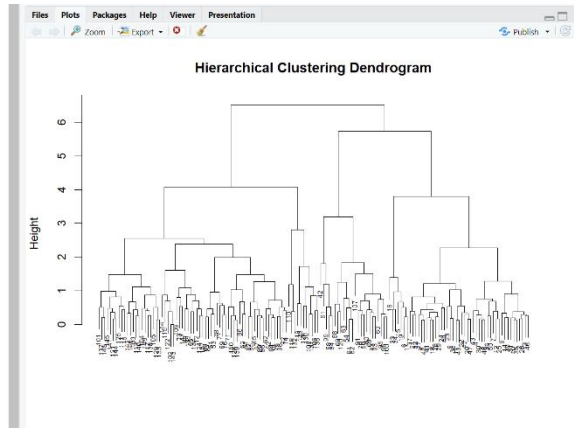
# Print the cluster memberships
print(clusters)

# Add the clusters to the original dataset
iris$Cluster <- as.factor(clusters)

# Display the first few rows of the updated dataset
head(iris)
```

#### Output:

210701120

[illegible]

### K-Means Clustering:

**Code:**

```
# 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)
```

