

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) #
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)
```

```
# Load the iris dataset
```

```
# Use only the numeric columns for clustering (exclude the Species column)
```

```
# Standardize the data
```

```
# Set the number of clusters
```

```
k <- 3 # Number of clusters
```

```
kmeans result <- kmeans(iris_scaled, centers = k, nstart = 25)
```

```
# Print the K-Means result
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```
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")

```

