Exp. No : 9

Implement clustering techniques – Hierarchical and K-Means

a) Hierarchical 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

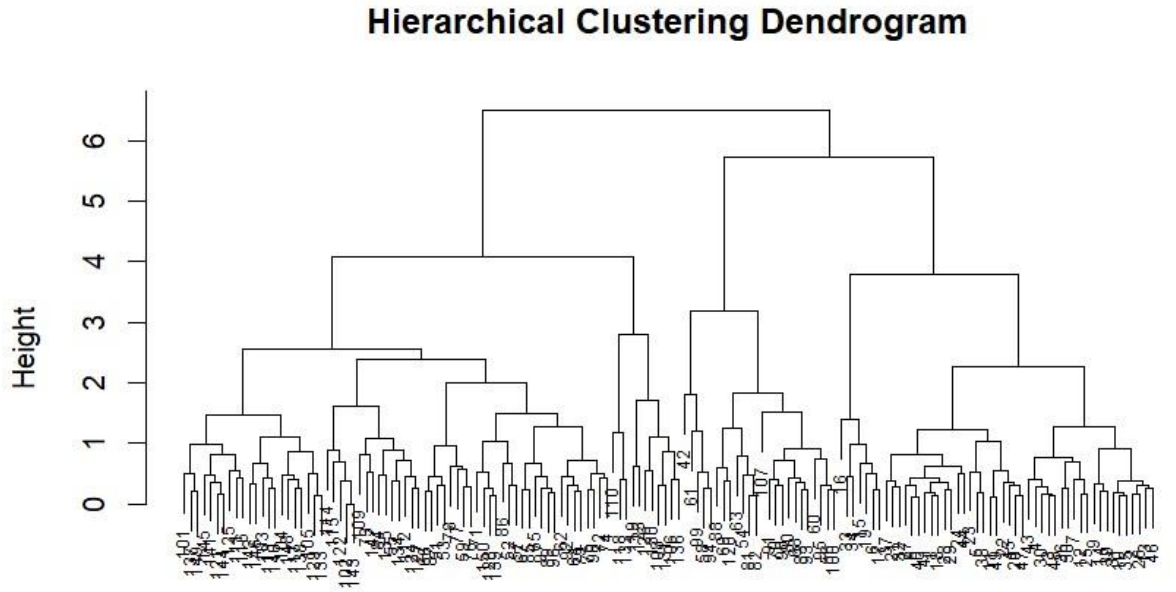
<- as.factor(clusters)

Display the first few rows of the updated dataset

head(iris)

Output :

```
> # 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)
  [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
 [37] 1 1 1 1 1 2 1 1 1 1 1 1 1 1 3 3 3 2 3 2 3 2 3 2 2 3 2 3 3 3 3 2 2 2 3 3
 [73] 3 3 3 3 3 3 3 2 2 2 2 3 3 3 3 2 3 2 2 3 2 2 2 3 3 3 2 2 3 3 3 3 3 3 2 3
[109] 3 3 3 3 3 3 3 3 3 3 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
[145] 3 3 3 3 3 3
> # Add the clusters to the original dataset
> iris$Cluster <- as.factor(clusters)
> # Display the first few rows of the updated dataset
> head(iris)
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species Cluster
1          5.1         3.5          1.4         0.2  setosa       1
2          4.9         3.0          1.4         0.2  setosa       1
3          4.7         3.2          1.3         0.2  setosa       1
4          4.6         3.1          1.5         0.2  setosa       1
5          5.0         3.6          1.4         0.2  setosa       1
6          5.4         3.9          1.7         0.4  setosa       1
>
```



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")
```

Output :

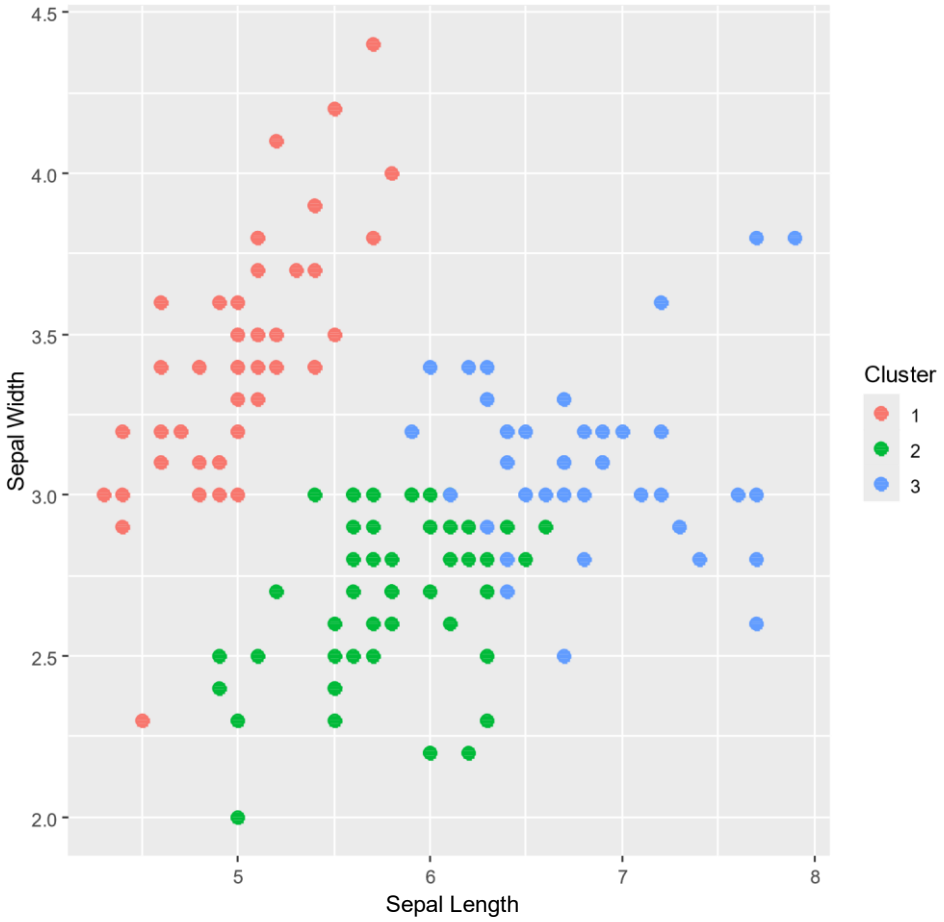
```
[145] 3 3 2 3 3 2

Within cluster sum of squares by cluster:
[1] 47.35062 44.08754 47.45019
 (between_SS / total_SS =  76.7 %)

Available components:

[1] "cluster"      "centers"      "totss"        "withinss"     "tot.withinss"
[6] "betweenss"    "size"         "iter"         "ifault"
> # Print the cluster centers
> print(kmeans_result$centers)
  Sepal.Length Sepal.Width Petal.Length Petal.Width
1  -1.01119138  0.85041372   -1.3006301  -1.2507035
2  -0.05005221 -0.88042696    0.3465767   0.2805873
3   1.13217737  0.08812645    0.9928284   1.0141287
> # Add the cluster assignments to the original dataset
> iris$Cluster <- as.factor(kmeans_result$cluster)
> # Display the first few rows of the updated dataset
> head(iris)
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species Cluster
1          5.1         3.5          1.4         0.2  setosa       1
2          4.9         3.0          1.4         0.2  setosa       1
3          4.7         3.2          1.3         0.2  setosa       1
4          4.6         3.1          1.5         0.2  setosa       1
5          5.0         3.6          1.4         0.2  setosa       1
6          5.4         3.9          1.7         0.4  setosa       1
> # 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 = "S
epal Width")
```

K-Means Clustering of Iris Dataset


4.5
4.0
3.5
3.0
2.5
2.0
Sepal Width
5
6
7
8
Sepal Length
Cluster
1
2
3