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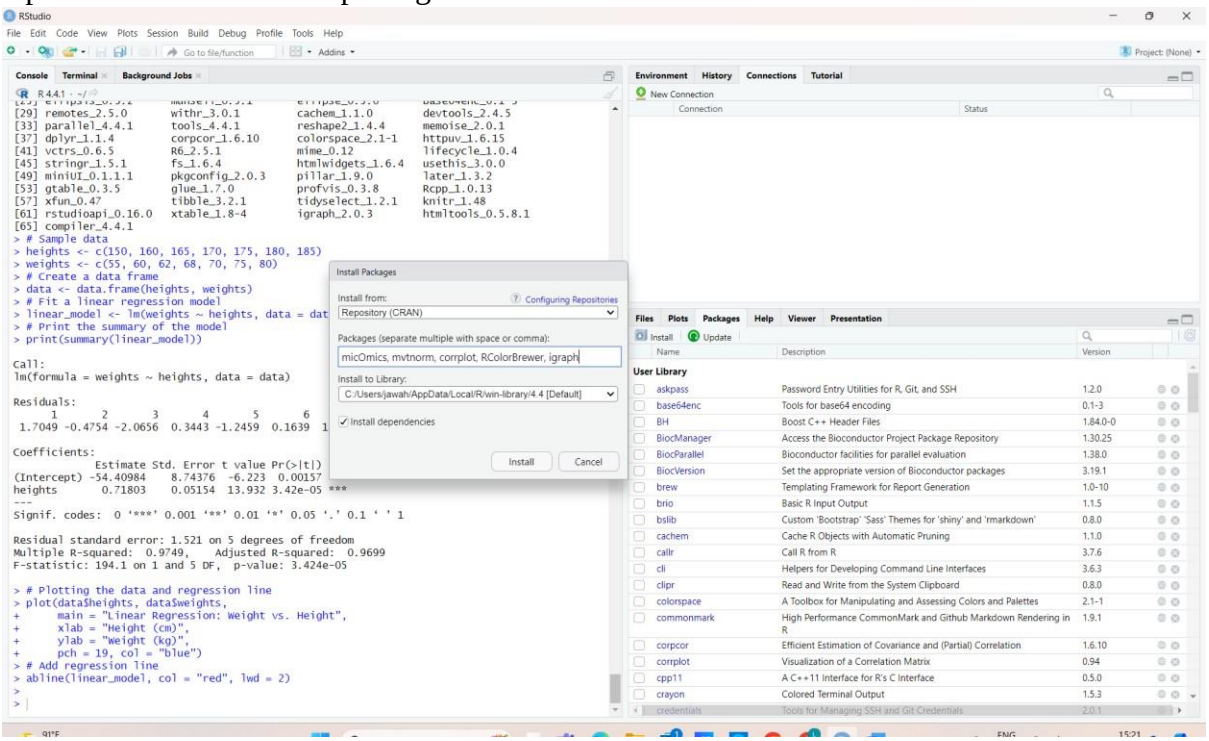
Ex 9 Implement clustering techniques – Hierarchical and K-Means

Aim:

To implement SVM/ Decision Tree classification technique in R Programming

PROCEDURE:

1. Install R for windows.
2. Install R Studio.
3. Open R Studio and install packages



Thus R studio is set up successfully.

a) HIERARCHIAL CLUSTERING

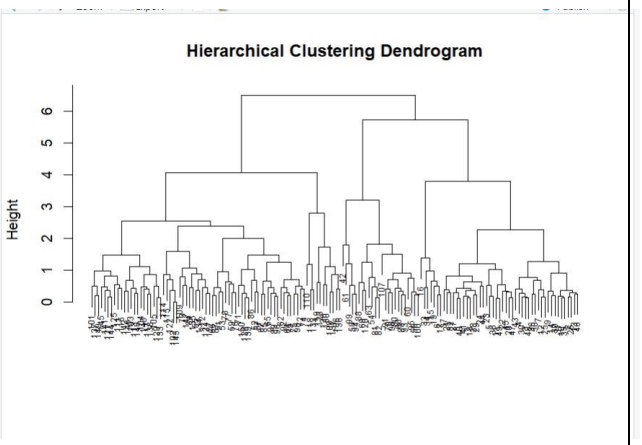
Program:

```
# 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:

```
> 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 1 1 1 1 1 1 2 1 1
 [45] 1 1 1 1 1 1 3 3 3 2 3 2 3 2 3 2 2 3 2 3 3 3 3 2 3 3 3 3 3 3 3 3 2 2 2 2 3 3 3 3 2
 [89] 3 2 2 3 2 2 2 3 3 3 2 2 3 3 3 3 3 3 2 3 3 3 3 3 3 3 3 3 3 3 2 3 3 3 3 3 3 3 3 3 3
[133] 3 3 3 3 3 3 3 3 3 3 3 3 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

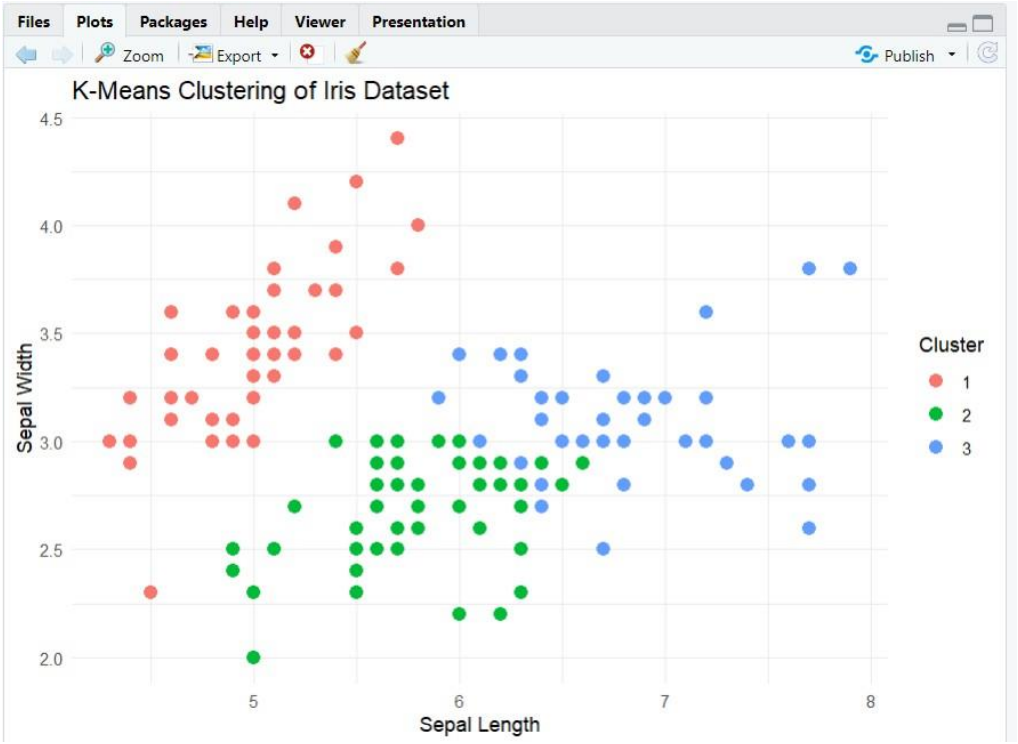
Program

```
# 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") +
  theme_minimal()  # Optional: makes the plot look cleaner
```

Output:

```
K-means clustering with 3 clusters of sizes 50, 53, 47

Cluster means:
  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

Clustering vector:
  [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 1 1 1 1 1 1 1 1 1
 [45] 1 1 1 1 1 1 3 3 3 2 2 2 3 2 2 2 2 2 2 2 3 2 2 2 2 3 2 2 2 3 3 3 2 2 2 2 2 2 2 3 3 2
 [89] 2 2 2 2 2 2 2 2 2 2 2 2 3 2 3 3 3 3 2 3 3 3 3 3 2 2 3 3 3 2 3 2 3 2 3 2 3 3 3 3 3 3
[133] 3 2 2 3 3 3 2 3 3 3 2 3 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" "betweenss"
[7] "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
>
```



Result:

Thus the k-means clustering and hierarchical clustering is implemented successfully using R Programming