Ex.No.6 Implementation of Clustering Techniques

Aim

To implement clustering techniques for iris data set.

Pre-lab Discussion

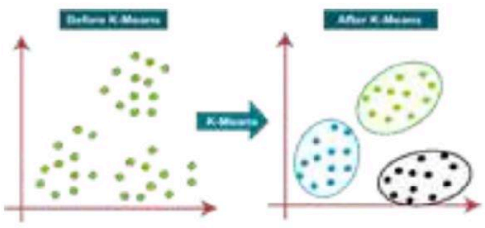
Theory

K-Means Clustering

K-Means Clustering is an unsupervised learning algorithm that is used to solve the clustering problems in machine learning or data science. It allows us to cluster the data into different groups and a convenient way to discover the categories of groups in the unlabeled dataset on its own without the need for any training. It is a centroid-based algorithm, where each cluster is associated with a centroid. The main aim of this algorithm is to minimize the sum of distances between the data point and their corresponding clusters.

The algorithm takes the unlabeled dataset as input, divides the dataset into k-number of clusters, and repeats the process until it does not find the best clusters. The value of k should be predetermined in this algorithm. The k-means clustering algorithm mainly performs two tasks:

1. Determines the best value for K center points or centroids by an iterative process.
2. Assigns each data point to its closest k-center. Those data points which are near to the particular k-center, create a cluster.



Working of K-Means Algorithm:

The working of the K-Means algorithm is explained in the below steps:

1. Select the number K to decide the number of clusters.

2. Select random K points or centroids. (It can be other from the input dataset).

3. Assign each data point to their closest centroid, which will form the predefined K clusters.

4. Calculate the variance and place a new centroid of each cluster.

5. Repeat the third steps, which means reassign each datapoint to the new closest centroid of each cluster.

6. If any reassignment occurs, then go to step-4 else go to FINISH.

PROGRAM:

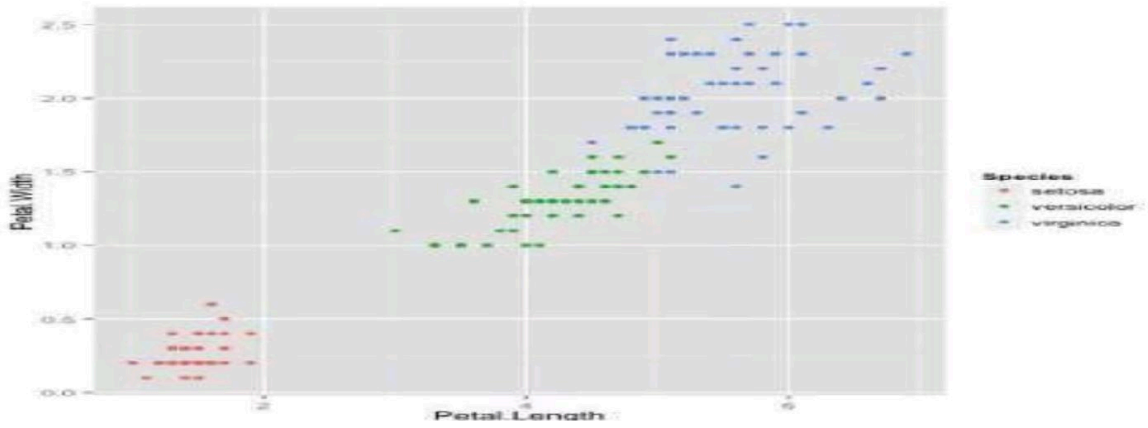
```
library(datasets)

head(iris)

library(ggplot2)

ggplot(iris, aes(Petal.Length, Petal.Width, color = Species)) + geom_point()

set.seed(20)

irisCluster <- kmeans(iris[, 3:4], 3, nstart = 20)

irisCluster

table(irisCluster$cluster, iris$Species)
```

OUTPUT:

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
1	5.1	3.5	1.4	0.2	setosa
2	4.9	3.0	1.4	0.2	setosa
3	4.7	3.2	1.3	0.2	setosa
4	4.6	3.1	1.5	0.2	setosa
5	5.0	3.6	1.4	0.2	setosa
6	5.4	3.9	1.7	0.4	setosa

```
ggplot(iris, aes(Petal.Length, Petal.Width, color =
Species)) + geom_point()
```

Here is the plot:



```
irisCluster
K-means clustering with 3 clusters of sizes 46, 54, 50

Cluster means:
  Petal.Length Petal.Width
1     5.626087    2.047826
2     4.292593    1.359259
3     1.462000    0.246000

Clustering vector:
  [1] 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 3 3 3 3 3 3 3 3 3 3 3 3
 [35] 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
 [69] 2 2 2 2 2 2 2 2 2 1 2 2 2 2 2 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 1 1
[103] 1 1 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 2 1 1 1 2 1 1 2 2 1 1 1 1 1 1 1 1 1 1 1
[137] 1 1 2 1 1 1 1 1 1 1 1 1 1 1

Within cluster sum of squares by cluster:
[1] 15.16348 14.22741  2.02200
 (between_SS / total_SS =  94.3 %)

Available components:

[1] "cluster"      "centers"      "totss"        "withinss"
[5] "tot.withinss" "betweenss"    "size"         "iter"
[9] "ifault"
```

Result

Thus, K-means clustering using iris dataset was executed.