EXPERIMENT NO:9

AIM: To Perform K-Means Clustering on NC160 Dataset.

DESCRIPTION: K-means clustering is a technique in which we place each observation in a dataset into one of K clusters. The end goal is to have K clusters in which the observations within each cluster are quite similar to each other while the observations in different clusters are quite different from each other.

In practice, we use the following steps to perform K-means clustering:

1.Choose a value for K.

• First, we must decide how many clusters we'd like to identify in the data. Often we have to simply test several different values for K and analyze the results to see which number of clusters seems to make the most sense for a given problem.

2. Randomly assign each observation to an initial cluster, from 1 to K.

3. Perform the following procedure until the cluster assignments stop changing.

• For each of the K clusters, compute the cluster centroid. This is simply the vector of the p feature means for the observations in the kth cluster.

• Assign each observation to the cluster whose centroid is closest. Here, closest is defined using Euclidean distance.

K-Means Clustering in R.

The following tutorial provides a step-by-step example of how to perform k-means clustering in R.

Step 1: Load the Necessary Packages

First, we'll load two packages that contain several useful functions for k-means clustering in R

Step 2: Load and Prep the Data

For this example we'll use the USArrests dataset built into R, which contains the number of arrests per 100,000 residents in each U.S. state in 1973 for Murder, Assault, and Rape along with the percentage of the population in each state living in urban areas, UrbanPop.

The following code shows how to do the following:

• Load the USArrests dataset

• Remove any rows with missing values

• Scale each variable in the dataset to have a mean of 0 and a standard deviation of 1

Step 3: Find the Optimal Number of Clusters

To perform k-means clustering in R we can use the built-in kmeans() function, which uses the following syntax:

kmeans(data, centers, nstart)

where:

• data: Name of the dataset.

• centers: The number of clusters, denoted k.

• nstart: The number of initial configurations. Because it's possible that different initial starting clusters can lead to different results, it's recommended to use several different initial configurations. The k-means algorithm will find the initial configurations that lead to the smallest within-cluster variation.

Since we don't know beforehand how many clusters is optimal, we'll create two different plots that can help us decide:

1.Number of Clusters vs. the Total Within Sum of Squares

First, we'll use the fviz_nbclust() function to create a plot of the number of clusters vs. the total within sum of squares.

Typically when we create this type of plot we look for an "elbow" where the sum of squares begins to "bend" or level off. This is typically the optimal number of clusters.

For this plot it appears that there is a bit of an elbow or "bend" at k = 4 clusters.

2. Number of Clusters vs. Gap Statistic

Another way to determine the optimal number of clusters is to use a metric known as the gap statistic, which compares the total intra-cluster variation for different values of k with their expected values for a distribution with no clustering.

We can calculate the gap statistic for each number of clusters using the clusGap() function from the cluster package along with a plot of clusters vs. gap statistic using the fviz_gap_stat() function

From the plot we can see that gap statistic is highest at k = 4 clusters, which matches the elbow method we used earlier.

Step 4: Perform K-Means Clustering with Optimal K

Lastly, we can perform k-means clustering on the dataset using the optimal value for k of 4.

From the results we can see that:

- 16 states were assigned to the first cluster
- 13 states were assigned to the second cluster
- 13 states were assigned to the third cluster
- 8 states were assigned to the fourth cluster.

We can visualize the clusters on a scatterplot that displays the first two principal components on the axes using the fivz_cluster() function

We can also use the aggregate() function to find the mean of the variables in each cluster.

We interpret this output is as follows:

- The mean number of murders per 100,000 citizens among the states in cluster 1 is 3.6.
- The mean number of assaults per 100,000 citizens among the states in cluster 1 is 78.5.
- The mean percentage of residents living in an urban area among the states in cluster 1 is 52.1%.
- The mean number of rapes per 100,000 citizens among the states in cluster 1 is 12.2.

And so on.

We can also append the cluster assignments of each state back to the original dataset.

CODE:

```
#Load necessary packages
library(factoextra)
library(cluster)

#load data
df <- USArrests

#remove rows with missing values
df <- na.omit(df)

#scale each variable to have a mean of 0 and sd of 1
df <- scale(df)

#view first six rows of dataset
head(df)

#Number of Clusters vs. the Total Within Sum of Squares
fviz_nbclust(df, kmeans, method = "wss")

#calculate gap statistic based on number of clusters
gap_stat <- clusGap(df,FUN = kmeans,
                nstart = 25,
                K.max = 10,
                B = 50)
```

OUTPUT:

```
> head(df)
              Murder   Assault    UrbanPop         Rape
Alabama    1.24256408 0.7828393 -0.5209066 -0.003416473
Alaska     0.50786248 1.1068225 -1.2117642  2.484202941
Arizona    0.07163341 1.4788032  0.9989801  1.042878388
Arkansas   0.23234938 0.2308680 -1.0735927 -0.184916602
California 0.27826823 1.2628144  1.7589234  2.067820292
Colorado   0.02571456 0.3988593  0.8608085  1.864967207
```

```
Clustering k = 1,2,..., K.max (= 10): .. done
Bootstrapping, b = 1,2,..., B (= 50)  [one "." per sample]:
.................................................. 50
```

CODE:

#plot number of clusters vs. gap statistic

fviz_gap_stat(gap_stat)

#make this example reproducible

set.seed(1**)**

#perform k-means clustering with k = 4 clusters

km <- kmeans(df, centers = 4, nstart = 25)

CODE:

#view results

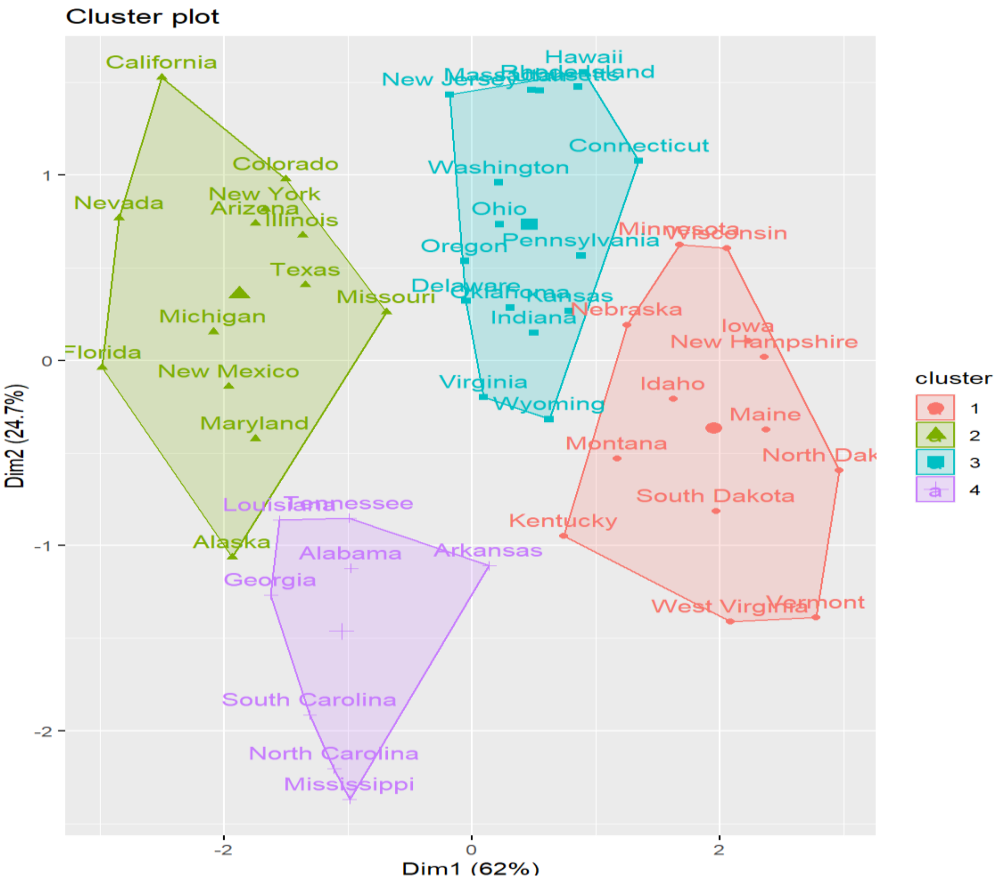
Km

#plot results of final k-means model

fviz_cluster(km, data = df)

OUTPUT:

```
> km
K-means clustering with 4 clusters of sizes 13, 13, 16, 8

Cluster means:
      Murder    Assault   UrbanPop        Rape
1 -0.9615407 -1.1066010 -0.9301069 -0.96676331
2  0.6950701  1.0394414  0.7226370  1.27693964
3 -0.4894375 -0.3826001  0.5758298 -0.26165379
4  1.4118898  0.8743346 -0.8145211  0.01927104

Clustering vector:
       Alabama         Alaska        Arizona       Arkansas     California       Colorado    Connecticut 
             4              2              2              4              2              2              3 
      Delaware        Florida        Georgia         Hawaii          Idaho       Illinois        Indiana 
             3              2              4              3              1              2              3 
          Iowa         Kansas       Kentucky      Louisiana          Maine       Maryland  Massachusetts 
             1              3              1              4              1              2              3 
      Michigan      Minnesota    Mississippi       Missouri        Montana       Nebraska         Nevada 
             2              1              4              2              1              1              2 
 New Hampshire     New Jersey     New Mexico       New York North Carolina   North Dakota           Ohio 
             1              3              2              2              4              1              3 
      Oklahoma         Oregon   Pennsylvania   Rhode Island South Carolina   South Dakota      Tennessee 
             3              3              3              3              4              1              4 
         Texas           Utah        Vermont       Virginia     Washington  West Virginia      Wisconsin 
             2              3              1              3              3              1              1 
       Wyoming 
             3 

Within cluster sum of squares by cluster:
[1] 11.952463 19.922437 16.212213  8.316061
 (between_SS / total_SS =  71.2 %)

Available components:

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



CODE:

#find means of each cluster

aggregate(USArrests, by=list(cluster=km$cluster),mean)

#add cluster assigment to original data

final_data <- cbind(USArrests, cluster = km$cluster)

#view final data

head(final_data)

OUTPUT:

```
> aggregate(USArrests, by=list(cluster=km$cluster),
+           mean)
  cluster   Murder   Assault UrbanPop     Rape
1       1  3.60000  78.53846 52.07692 12.17692
2       2 10.81538 257.38462 76.00000 33.19231
3       3  5.65625 138.87500 73.87500 18.78125
4       4 13.93750 243.62500 53.75000 21.41250
> head(final_data)
           Murder Assault UrbanPop Rape cluster
Alabama      13.2     236       58 21.2       4
Alaska       10.0     263       48 44.5       2
Arizona       8.1     294       80 31.0       2
Arkansas      8.8     190       50 19.5       4
California    9.0     276       91 40.6       2
Colorado      7.9     204       78 38.7       2
```

Pros & Cons of K-Means Clustering:

K-means clustering offers the following benefits:

- It is a fast algorithm.
- It can handle large datasets well.

However, it comes with the following potential drawbacks:

- It requires us to specify the number of clusters before performing the algorithm.
- It's sensitive to outliers.

Two alternatives to k-means clustering are k-means clustering and hierarchical clustering.