ASSIGNMENT NO.3:

Aim – Implement K-means using R programming.

Theory:

K-Means Clustering is an unsupervised learning algorithm that is used to solve clustering problems in machine learning or data science. In this topic, we will learn what the K-means clustering algorithm, how is The algorithm works, along with the Python implementation of k-means clustering.

K-Means Algorithm: K-Means Clustering is an Unsupervised Learning algorithm, which groups the unlabeled dataset into different clusters. Here K defines the number of predefined clusters that need to be created in the process, as if K=2, there will be two clusters, and for K=3, there will be three clusters, and so on. It is an iterative algorithm that divides the unlabeled dataset into k different clusters in such a way that each dataset belongs to only one group that has similar properties. The k-means clustering algorithm mainly performs two tasks:

Determines the best value for K center points or centroids by an iterative process. Assigns each data point to its closest k-center. Those data points which are near the particular k-center, create a cluster. Hence each cluster has data points with some commonalities, and it is away from other clusters. K-Means algorithm:

Step-1: Select the number K to decide the number of clusters.

Step-2: Select random K points or centroids. (It can be other than the input dataset).

Step-3: Assign each data point to its closest centroid, which will form the predefined K clusters.

Step-4: Calculate the variance and place a new centroid of each cluster. Step-5: Repeat the third steps, which means reassigning each data point to the new closest centroid of each cluster.

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

Step-7: The model is ready.

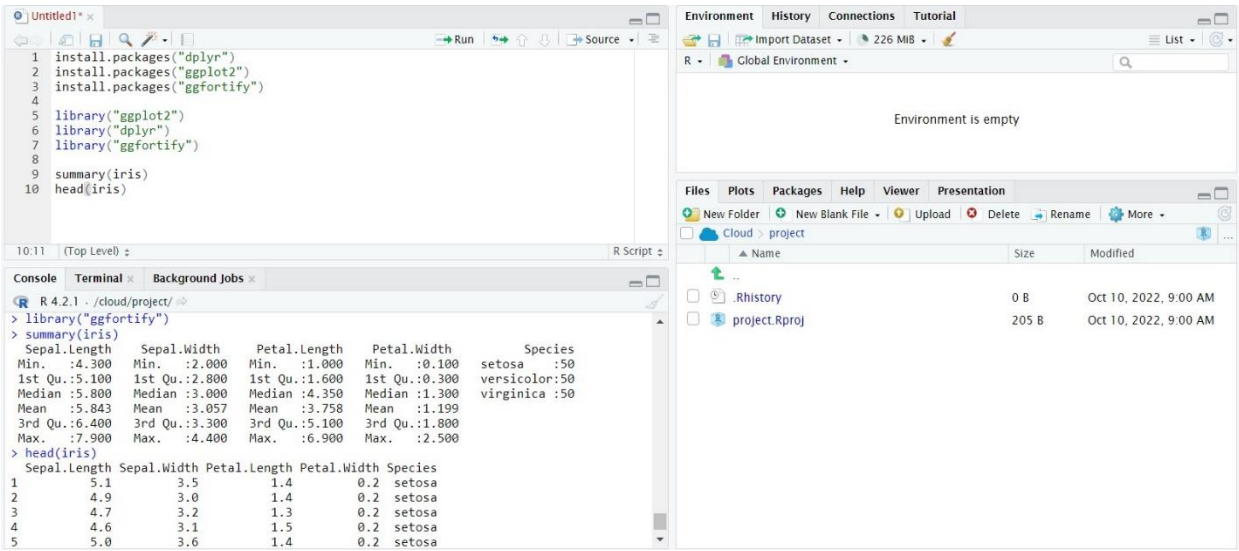
Elbow Method: In cluster analysis, the elbow method is a heuristic used in

determining the number of clusters in a data set. The method consists of plotting the explained variation as a function of the number of clusters and picking the elbow of the curve as the number of clusters to use. Using the "elbow" or "knee of a curve" as a cutoff point is a common heuristic in mathematical optimization to choose a point where diminishing returns are no longer worth the additional cost. In clustering, this means one should choose a number of clusters so that adding another cluster doesn't give a much better modeling of the data.

The Elbow method looks at the total WSS as a function of the number of clusters: One should choose a number of clusters so that adding another cluster doesn't improve much better the total WSS. The optimal number of clusters can be defined Calculate the Within-Cluster-Sum of Squared Errors (WSS) for different values of k, and choose the k for which WSS first starts to diminish. In the plot of WSS-versus-k, this is visible as an elbow. Within-Cluster-Sum of Squared Errors sounds a bit complex. Let’s break it down: The Squared Error for each point is the square of the distance of the point from its representation i.e. its predicted cluster center.

R Program CODE:

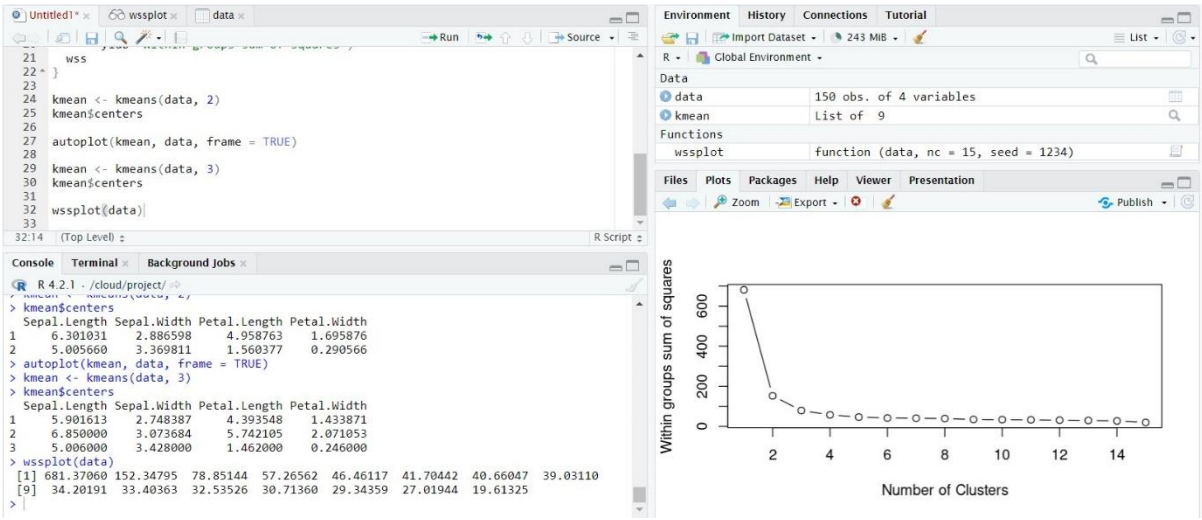
Reading & Summary of data



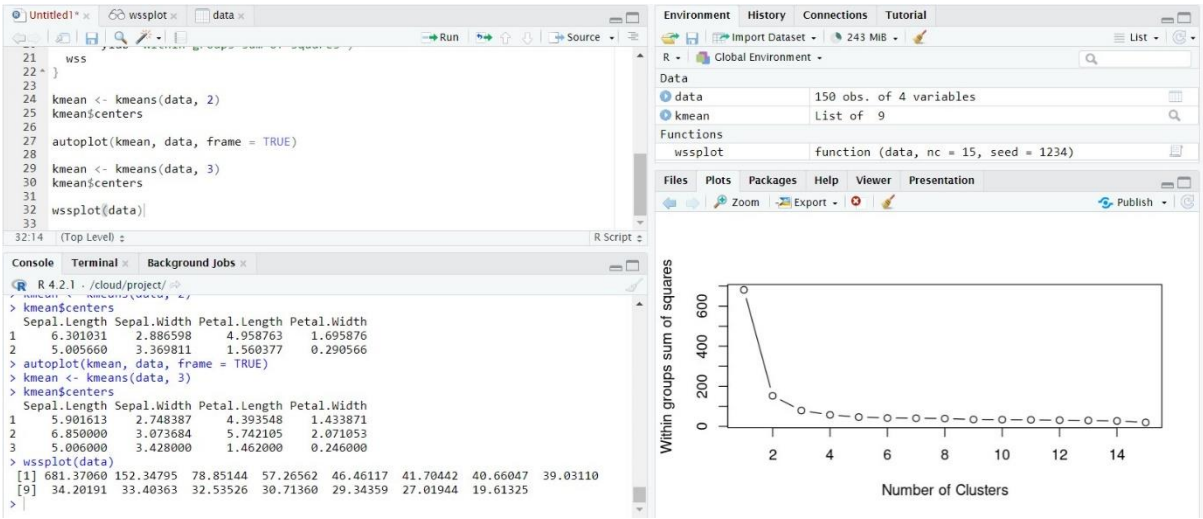
```
> summary(iris)
       Id          SepalLengthCm    SepalWidthCm    PetalLengthCm    PetalWidthCm       Species
 Min.   :  1.00   Min.   :4.300   Min.   :2.000   Min.   :1.000   Min.   :0.100   Length:150
 1st Qu.: 38.25   1st Qu.:5.100   1st Qu.:2.800   1st Qu.:1.600   1st Qu.:0.300   Class :character
 Median : 75.50   Median :5.800   Median :3.000   Median :4.350   Median :1.300   Mode  :character
 Mean   : 75.50   Mean   :5.843   Mean   :3.054   Mean   :3.759   Mean   :1.199
 3rd Qu.:112.75   3rd Qu.:6.400   3rd Qu.:3.300   3rd Qu.:5.100   3rd Qu.:1.800
 Max.   :150.00   Max.   :7.900   Max.   :4.400   Max.   :6.900   Max.   :2.500
```

Selecting the columns for clustering excluding the classes of dataset

data <- select(iris, c(1:4))



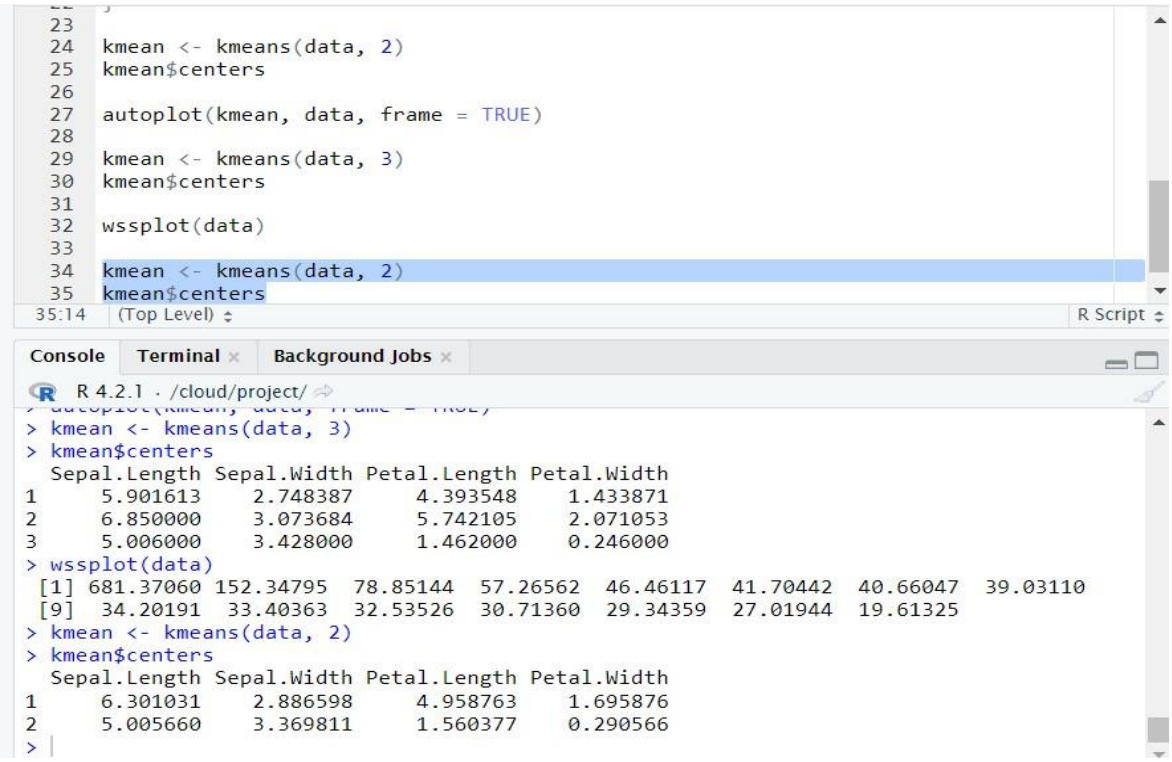
lets find the WCSS score to find the no of clusters



In the above plot WCSS can observe that if we use 2 cluster then it is best choice for us because after k=2 the WCSS is gradual.

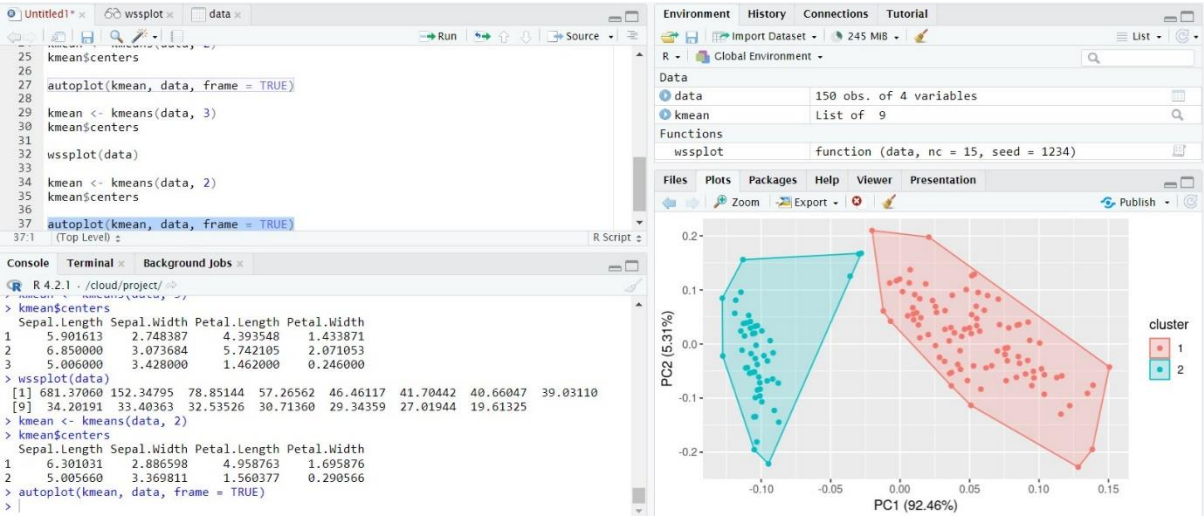
Implementing K-means

```
kmean <- kmeans(data, 2)
kmean$centers
```



Plotting our data-points in clusters

```
autoplot(kmean, data, frame = TRUE)
```



Conclusion:

WSS helps to identify the K value