Answer	Coding Efficiency	Viva	Timely Completion	Total	Dated Sign of Subject Teacher
5	5	5	5	20	

Expected Date of Completion:..... Actual Date of Completion:.....

Group B

Assignment No: 5

Title of the Assignment: Implement K-Means clustering/ hierarchical clustering on sales_data_sample.csv dataset. Determine the number of clusters using the elbow method.

Dataset Description: Sample Sales Data, Order Info, Sales, Customer, Shipping, etc., Used for Segmentation, Customer Analytics, Clustering and More. Inspired for retail analytics. This was originally used for Pentaho DI Kettle, But I found the set could be useful for Sales Simulation training.

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Link for Dataset: https://www.kaggle.com/datasets/kyanyoga/sample-sales-data

Objective of the Assignment:
Students should be able to learn the concept of K-Means clustering and Hierarchical clustering

Prerequisite:

1. Basic knowledge of Python
2. Concept of K-Means Clustering
3. Concept of Hierarchical Clustering

Contents of the Theory:

1. K-Means Clustering
2. Hierarchical Clustering
3. Principal Component Analysis(PCA)
4. Elbow Method

K-Means Clustering Algorithm

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

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 fi nd the best clusters. The value of k should be predetermined in this algorithm.

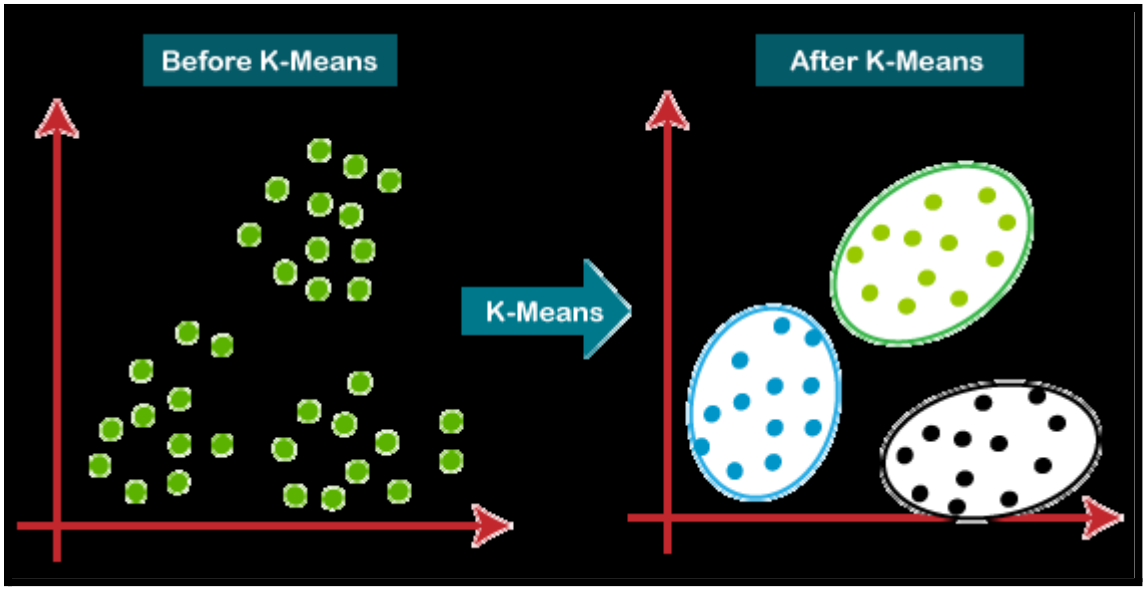
The k-means clustering

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 to the particular k-center, create a cluster.

Hence each cluster has datapoints with some commonalities, and it is away from other clusters.

The below diagram explains the working of the K-means Clustering Algorithm:



How does the K-Means Algorithm Work?

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

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

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

Step-3: Assign each data point to their closest centroid, which will form the predefi ned K clusters.

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

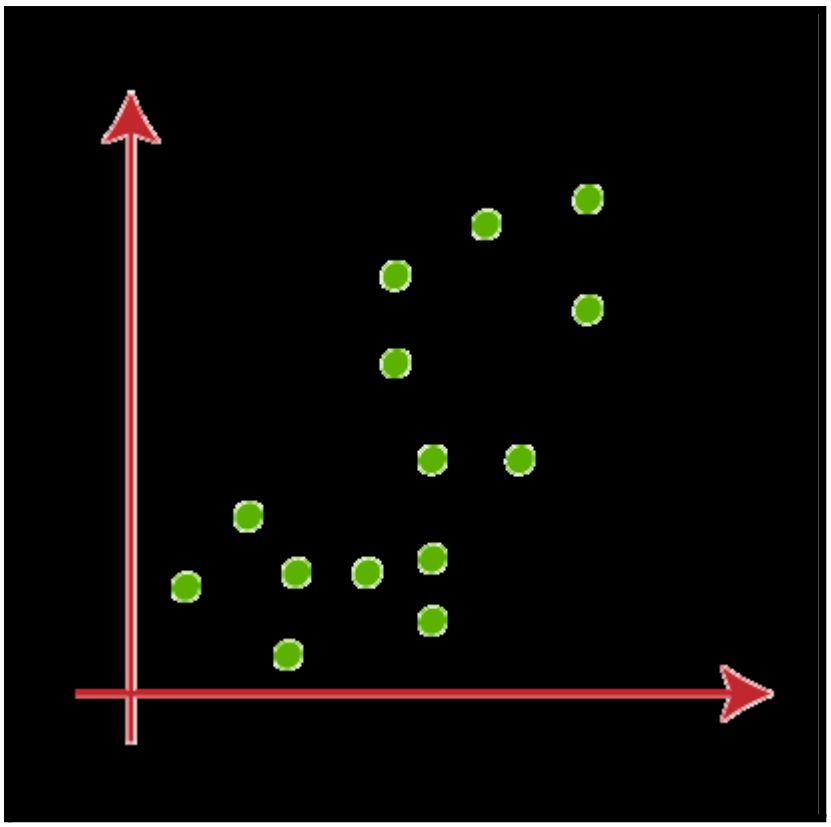
Step-5: Repeat the third steps, which means reassign each datapoint to the new closest centroid of each cluster.

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

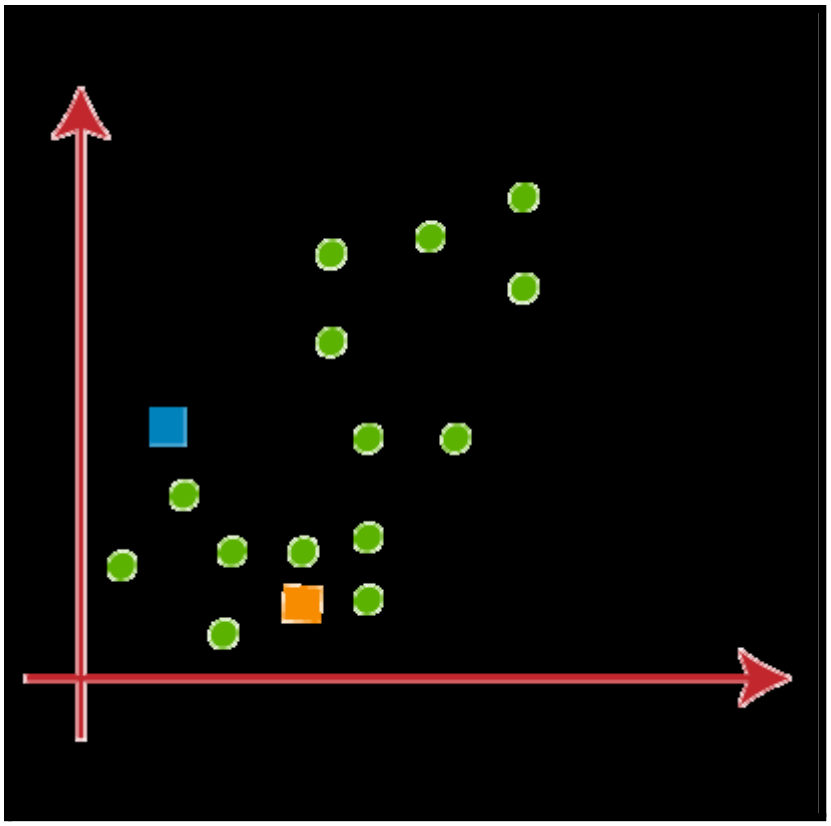
Step-7: The model is ready.

Let's understand the above steps by considering the visual plots:

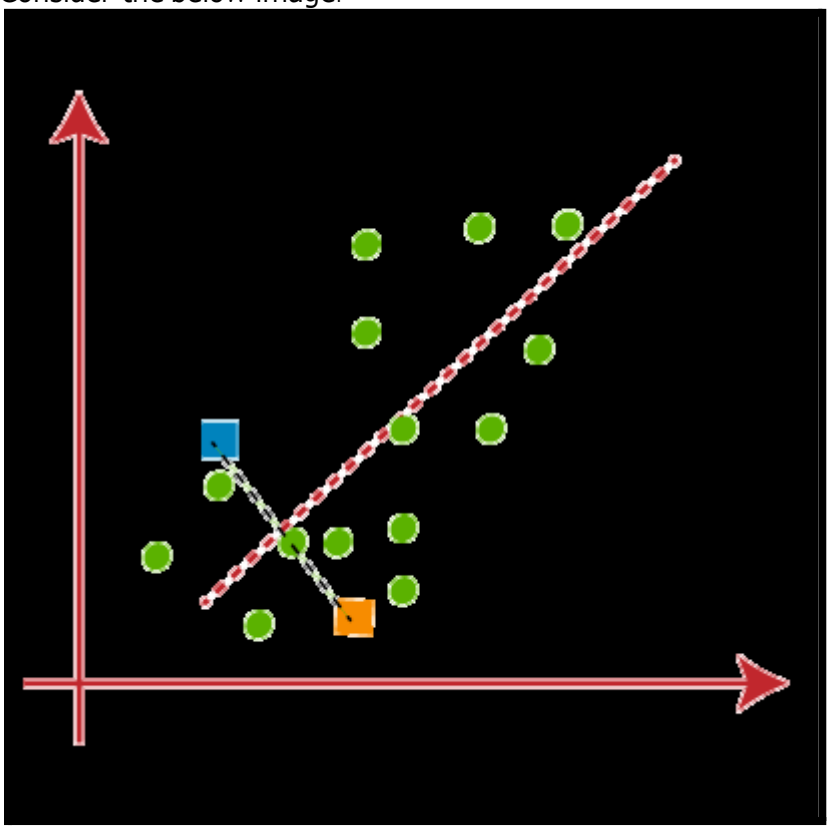
Suppose we have two variables M1 and M2. The x-y axis scatter plot of these two variables is given below:



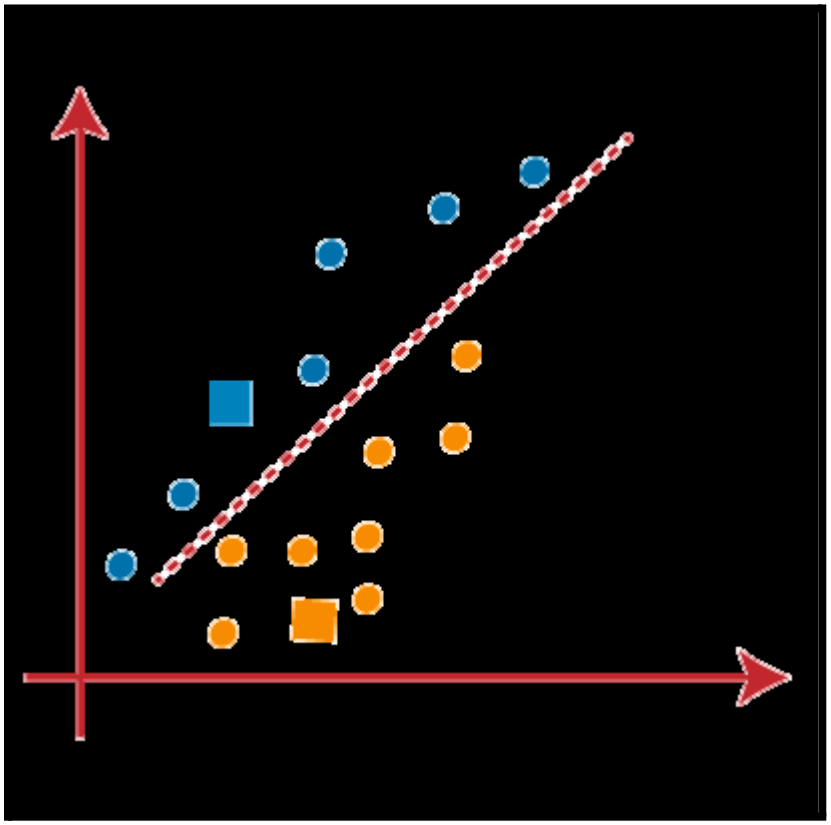
- Let's take number k of clusters, i.e., K=2, to identify the dataset and to put them into different clusters. It means here we will try to group these datasets into two different clusters.
- We need to choose some random k points or centroid to form the cluster. These points can be either the points from the dataset or any other point. So, here we are selecting the below two points as k points, which are not the part of our dataset. Consider the below image:



Now we will assign each data point of the scatter plot to its closest K-point or centroid. We will compute it by applying some mathematics that we have studied to calculate the distance between two points. So, we will draw a median between both the centroids. Consider the below image:

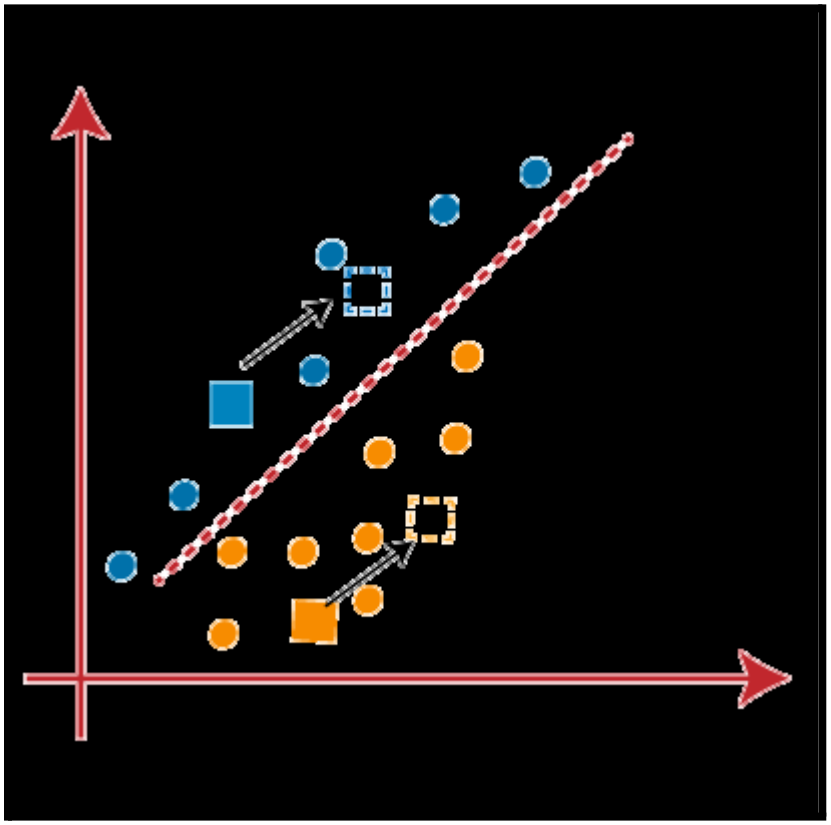


From the above image, it is clear that points left side of the line is near to the K1 or blue centroid, and points to the right of the line are close to the yellow centroid. Let's color them as blue and yellow for clear visualization.

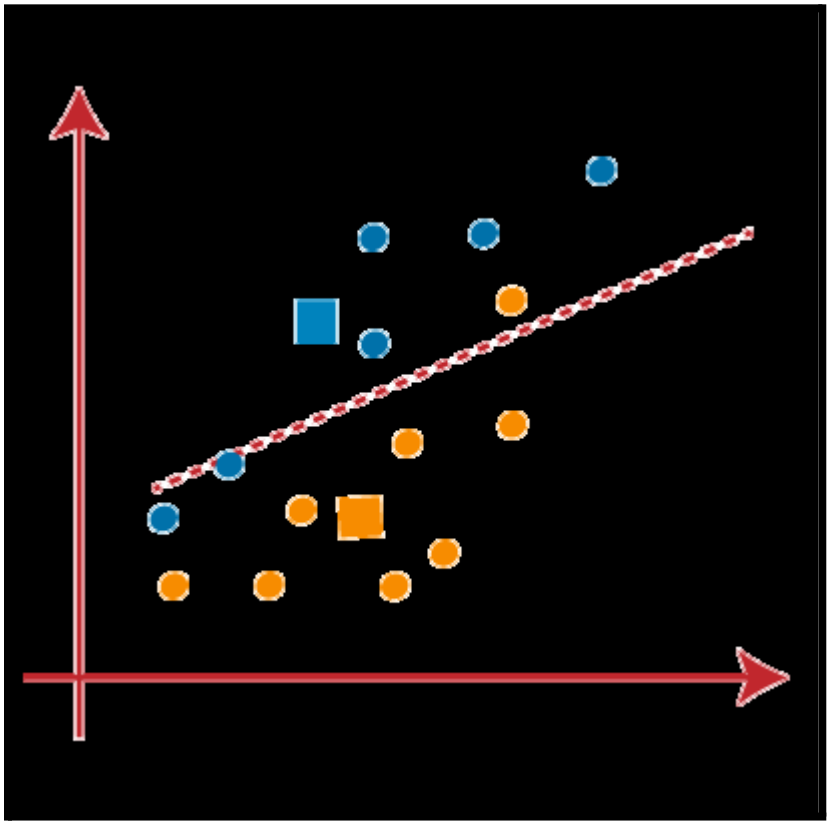


As we need to find the closest cluster, so we will repeat the process by choosing **a new centroid**. To choose the new centroids, we will compute the center of gravity of these

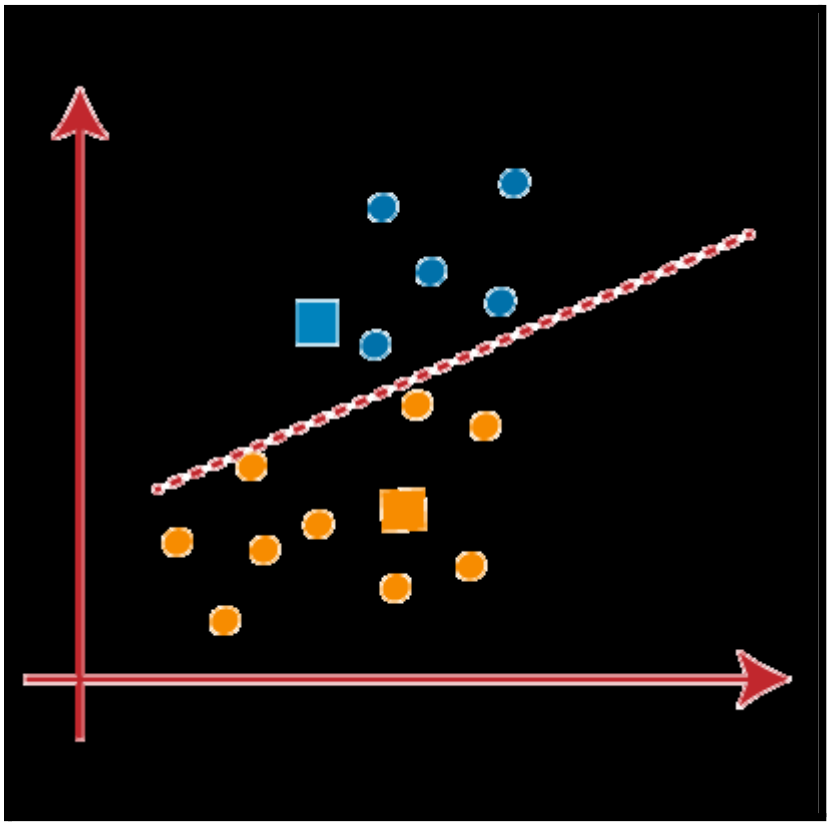
centroids, and will find new centroids as below:



Next, we will reassign each datapoint to the new centroid. For this, we will repeat the same process of finding a median line. The median will be like below image:

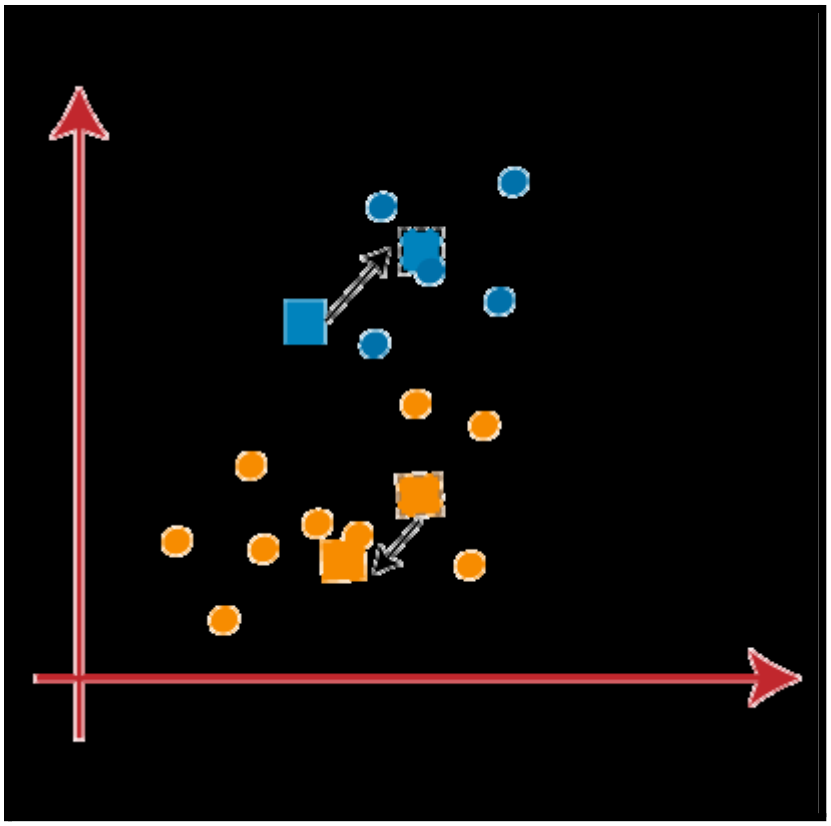


From the above image, we can see, one yellow point is on the left side of the line, and two blue points are right to the line. So, these three points will be assigned to new centroids.

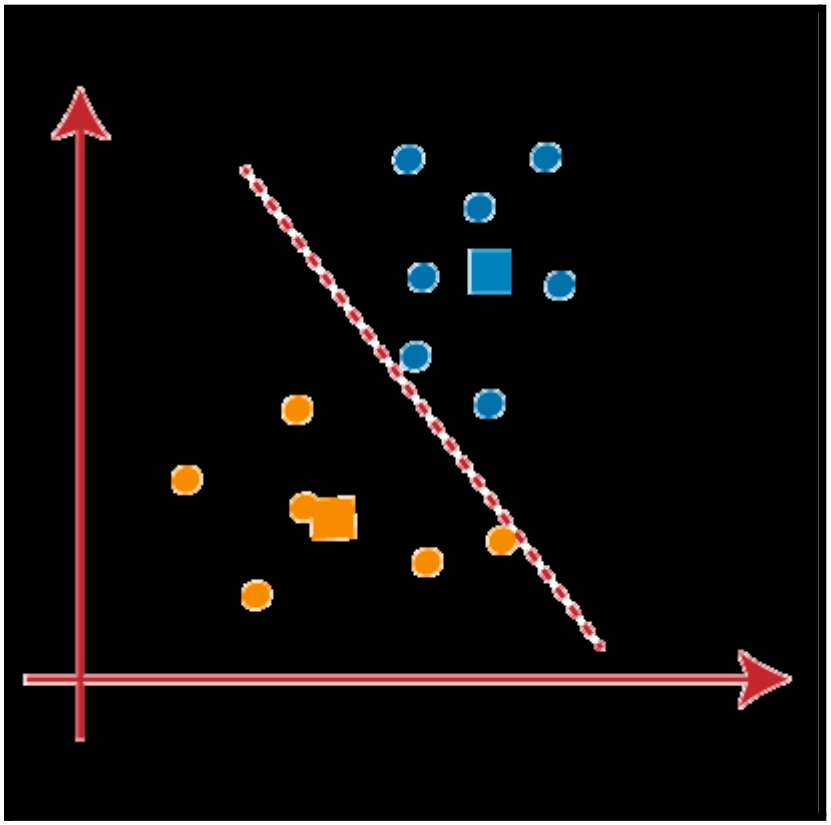


As reassignment has taken place, so we will again go to the step-4, which is fi nding new centroids or K-points.

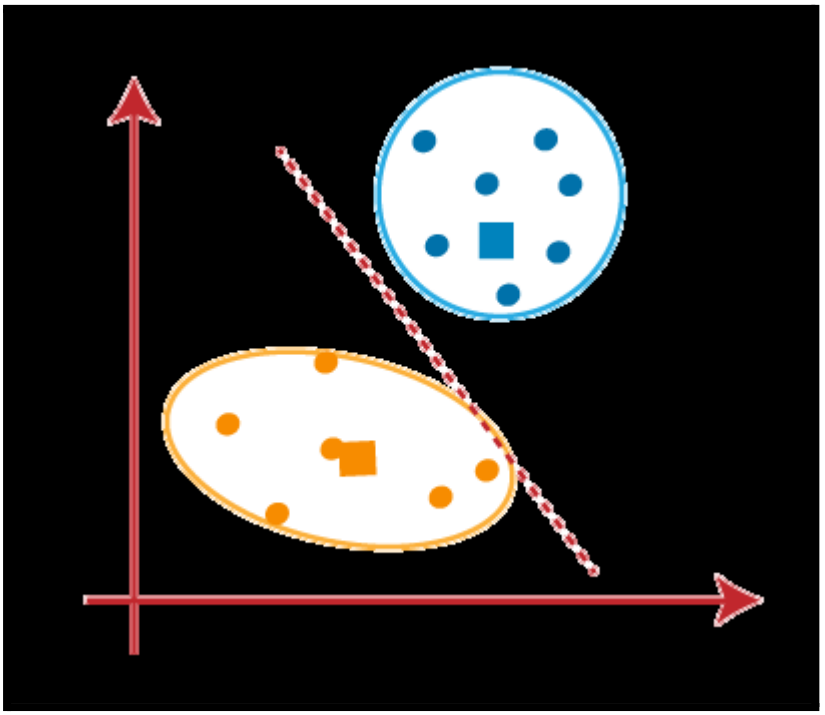
- We will repeat the process by fi nding the center of gravity of centroids, so the new centroids will be as shown in the below image:



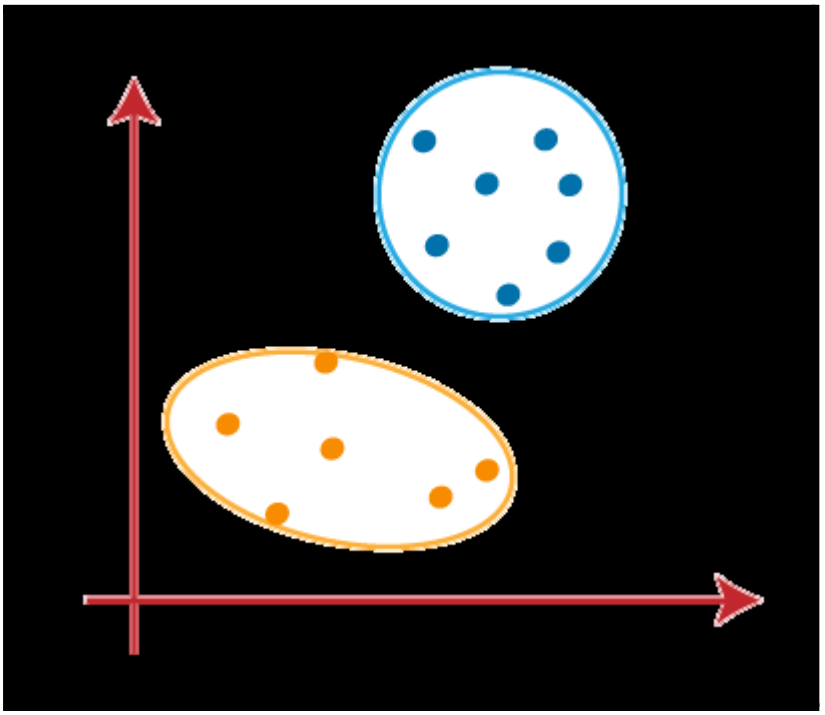
As we got the new centroids so again will draw the median line and reassign the data points. So, the image will be:



We can see in the above image; there are no dissimilar data points on either side of the line, which means our model is formed. Consider the below image:



As our model is ready, so we can now remove the assumed centroids, and the two final clusters will be as shown in the below image:



Hierarchical Clustering:

Hierarchical clustering is another unsupervised machine learning algorithm, which is used to group the unlabeled datasets into a cluster and also known as **hierarchical cluster analysis** or HCA.

In this algorithm, we develop the hierarchy of clusters in the form of a tree, and this tree-shaped structure is known as the **dendrogram**.

Sometimes the results of K-means clustering and hierarchical clustering may look similar, but they both differ depending on how they work. As there is no requirement to predetermine the number of clusters as we did in the K-Means algorithm.

The hierarchical clustering technique has two approaches:

Agglomerative Hierarchical clustering:

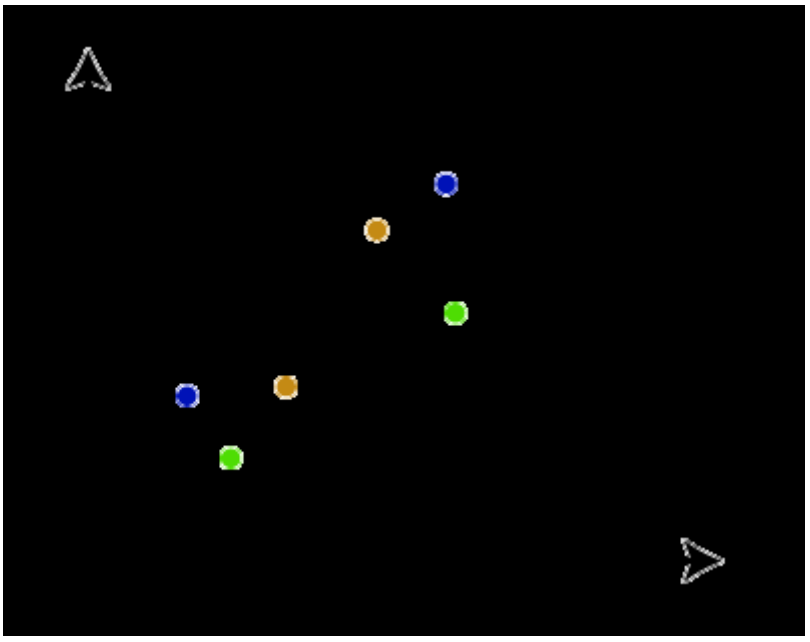
The agglomerative hierarchical clustering algorithm is a popular example of HCA. To group the datasets into clusters, it follows the **bottom-up approach**. It means, this algorithm considers each dataset as a single cluster at the beginning, and then start combining the closest pair of clusters together. It does this until all the clusters are merged into a single cluster that contains all the datasets.

This hierarchy of clusters is represented in the form of the dendrogram.

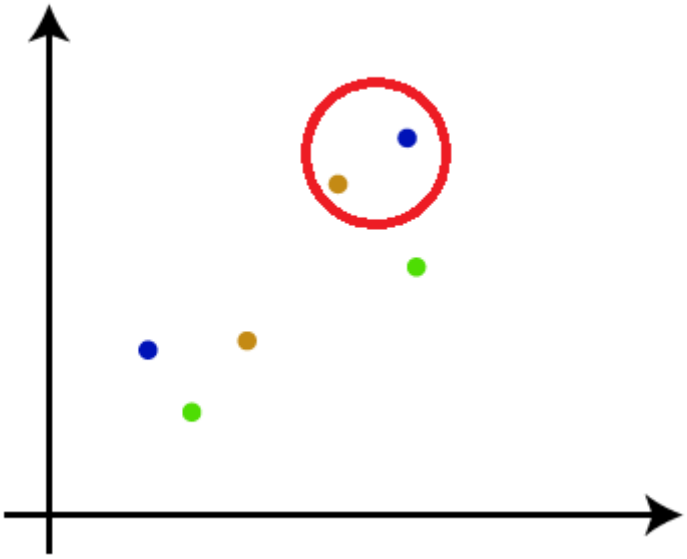
How the Agglomerative Hierarchical clustering Work?

The working of the AHC algorithm can be explained using the below steps:

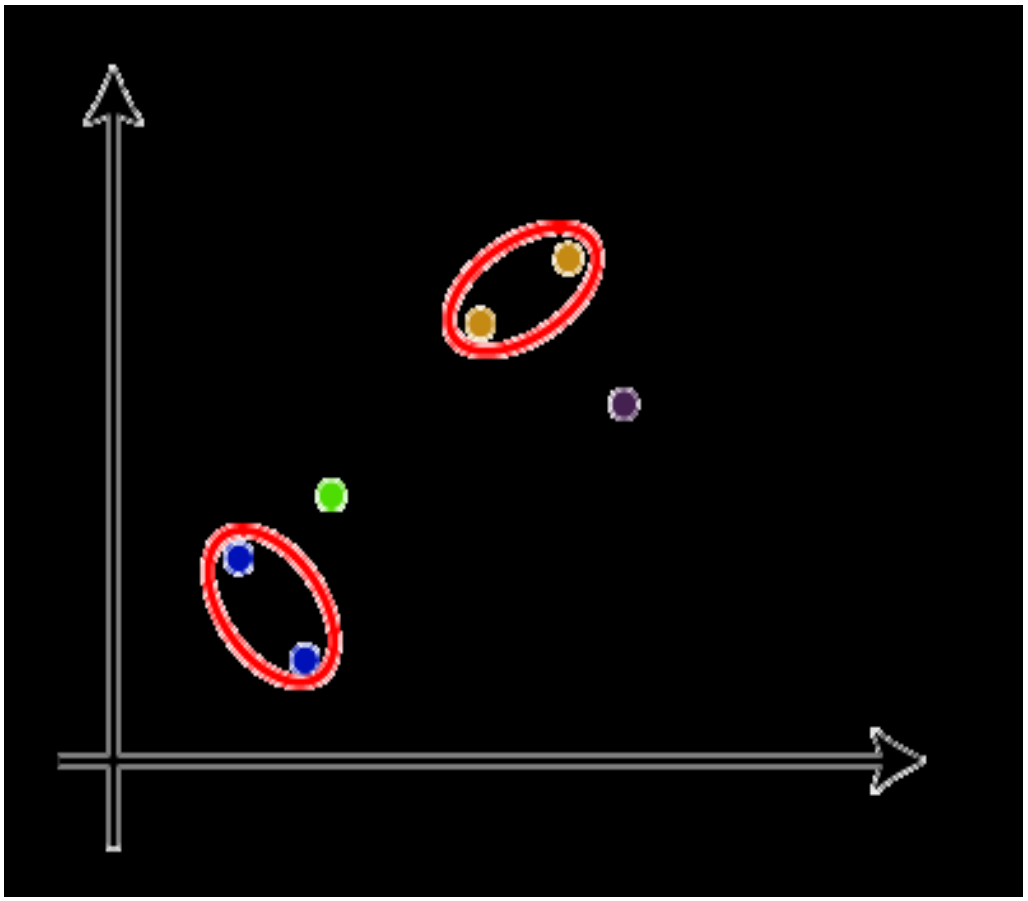
Step-1: Create each data point as a single cluster. Let's say there are N data points, so the number of clusters will also be N.



- **Step-2:** Take two closest data points or clusters and merge them to form one cluster. So, there will now be N-1 clusters.

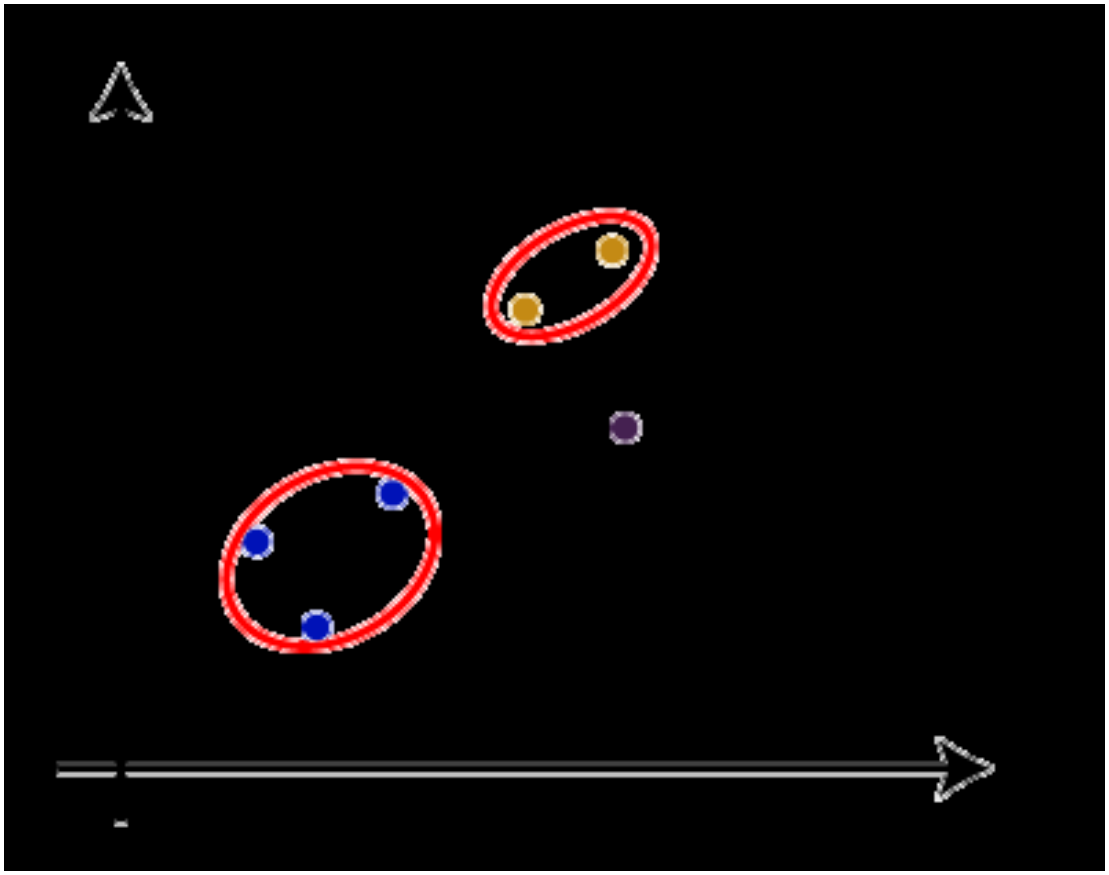


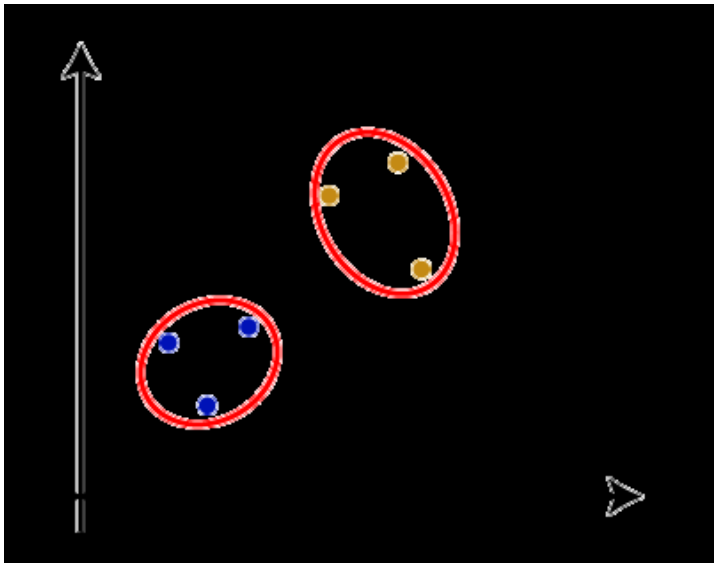
- **Step-3**: Again, take the two closest clusters and merge them together to form one cluster. There will be N-2 clusters.

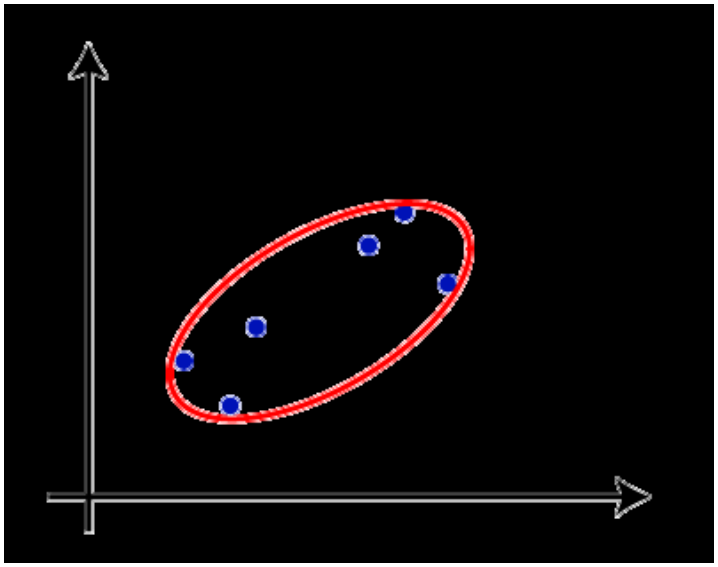


Step-4: Repeat Step 3 until only one cluster left. So, we will get the following clusters.

Consider the below images:





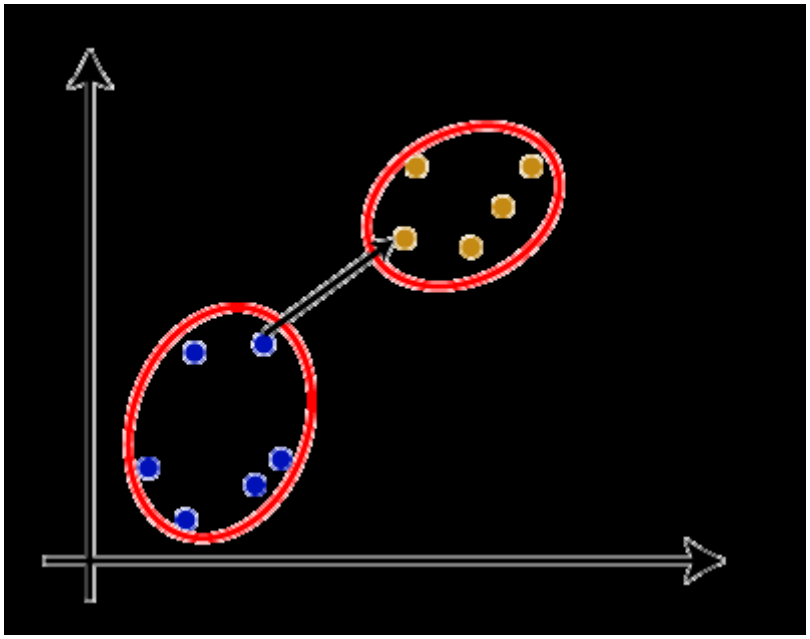


- **Step-5:** Once all the clusters are combined into one big cluster, develop the dendrogram to divide the clusters as per the problem.

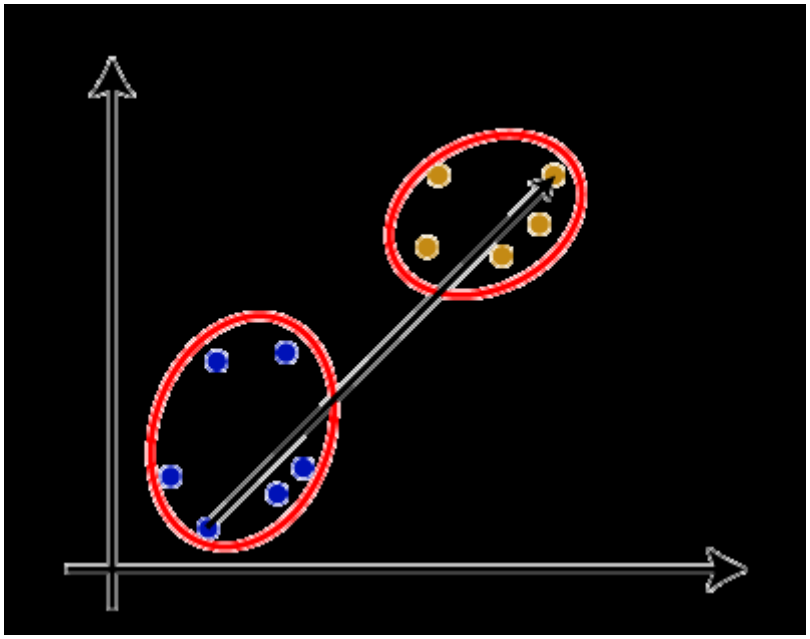
Measure for the distance between two clusters

As we have seen, the **closest distance** between the two clusters is crucial for the hierarchical clustering. There are various ways to calculate the distance between two clusters, and these ways decide the rule for clustering. These measures are called **Linkage methods**. Some of the popular linkage methods are given below:

1. **Single Linkage:** It is the Shortest Distance between the closest points of the clusters. Consider the below image:

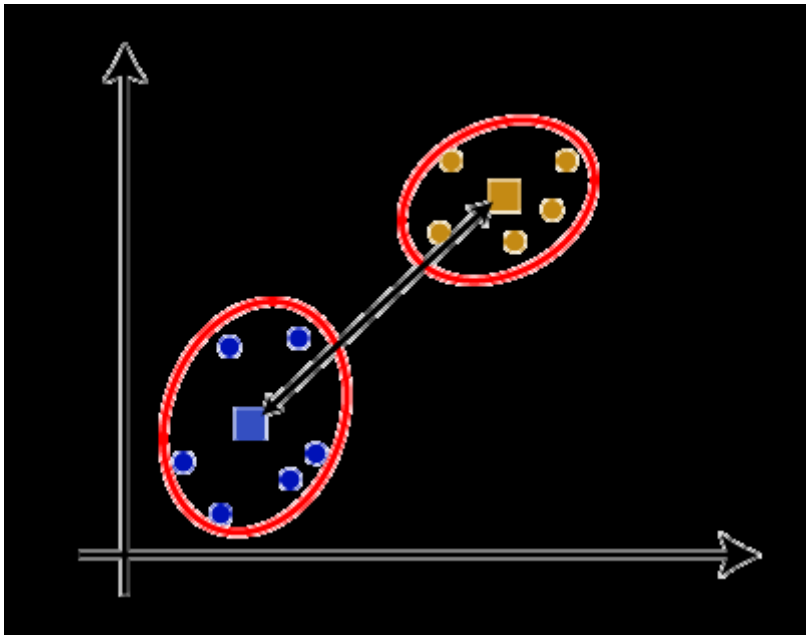


2. **Complete Linkage:** It is the farthest distance between the two points of two different clusters. It is one of the popular linkage methods as it forms tighter clusters than single-linkage.



3. **Average Linkage:** It is the linkage method in which the distance between each pair of datasets is added up and then divided by the total number of datasets to calculate the average distance between two clusters. It is also one of the most popular linkage methods.

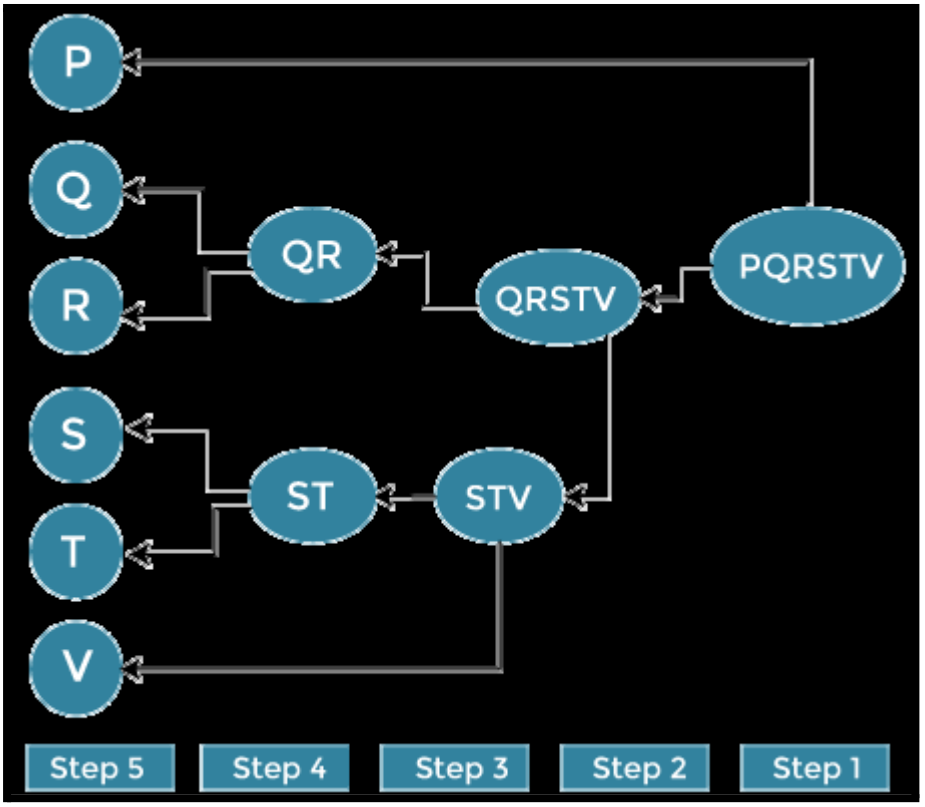
4. **Centroid Linkage:** It is the linkage method in which the distance between the centroid of the clusters is calculated. Consider the below image:



From the above-given approaches, we can apply any of them according to the type of problem or business requirement.

Divise Hierarchical Clustering:

Divisive hierarchical clustering is exactly the opposite of Agglomerative Hierarchical clustering. In Divisive Hierarchical clustering, all the data points are considered an individual cluster, and in every iteration, the data points that are not similar are separated from the cluster. The separated data points are treated as an individual cluster. Finally, we are left with N clusters.



Principal Component Analysis:

Principal Component Analysis is an unsupervised learning algorithm that is used for the dimensionality reduction in machine learning

. It is a statistical process that converts the observations of correlated features into a set of linearly uncorrelated features with the help of orthogonal transformation. These new transformed features are called the **Principal Components**. It is one of the popular tools that is used for exploratory data analysis and predictive modeling. It is a technique to draw strong patterns from the given dataset by reducing the variances.

PCA generally tries to fi nd the lower-dimensional surface to project the high-dimensional data.

PCA works by considering the variance of each attribute because the high attribute shows the good split between the classes, and hence it reduces the dimensionality. Some real-world applications of PCA are ***image processing, movie recommendation system, optimizing the power allocation in various communication channels.*** It is a feature extraction technique, so it contains the important variables and drops the least important variable.

The PCA algorithm is based on some mathematical concepts such as:

- Variance and Covariance

- Eigenvalues and Eigen factors

Some common terms used in PCA algorithm:

- **Dimensionality:** It is the number of features or variables present in the given dataset. More easily, it is the number of columns present in the dataset.
- **Correlation:** It signifies that how strongly two variables are related to each other. Such as if one changes, the other variable also gets changed. The correlation value ranges from -1 to +1. Here, -1 occurs if variables are inversely proportional to each other, and +1 indicates that variables are directly proportional to each other.
- **Orthogonal:** It defines that variables are not correlated to each other, and hence the correlation between the pair of variables is zero.
- **Eigenvectors:** If there is a square matrix M, and a non-zero vector v is given. Then v will be eigenvector if Av is the scalar multiple of v.
- **Covariance Matrix:** A matrix containing the covariance between the pair of variables is called the Covariance Matrix.

Steps for PCA Algorithm

1. **Getting the dataset**

   Firstly, we need to take the input dataset and divide it into two subparts X and Y, where X is the training set, and Y is the validation set.

2. **Representing data into a structure**

   Now we will represent our dataset into a structure. Such as we will represent the two-dimensional matrix of independent variable X. Here each row corresponds to the data items, and the column corresponds to the Features. The number of columns is the dimensions of the dataset.

3. **Standardizing the data**

   In this step, we will standardize our dataset. Such as in a particular column, the features with high variance are more important compared to the features with lower variance.

   If the importance of features is independent of the variance of the feature, then we

will divide each data item in a column with the standard deviation of the column. Here we will name the matrix as Z.

4. **Calculating the Covariance of Z**

   To calculate the covariance of Z, we will take the matrix Z, and will transpose it. After transpose, we will multiply it by Z. The output matrix will be the Covariance matrix of Z.

5. **Calculating the Eigen Values and Eigen Vectors**

   Now we need to calculate the eigenvalues and eigenvectors for the resultant covariance matrix Z. Eigenvectors or the covariance matrix are the directions of the axes with high information. And the coefficients of these eigenvectors are defi ned as the eigenvalues.

6. **Sorting the Eigen Vectors**

   In this step, we will take all the eigenvalues and will sort them in decreasing order, which means from largest to smallest. And simultaneously sort the eigenvectors accordingly in matrix P of eigenvalues. The resultant matrix will be named as P*.

7. **Calculating the new features Or Principal Components**

   Here we will calculate the new features. To do this, we will multiply the P* matrix to the Z. In the resultant matrix Z*, each observation is the linear combination of original features. Each column of the Z* matrix is independent of each other.

8. **Remove less or unimportant features from the new dataset.**

   The new feature set has occurred, so we will decide here what to keep and what to remove. It means, we will only keep the relevant or important features in the new dataset, and unimportant features will be removed out

Elbow Method

The Elbow method is one of the most popular ways to fi nd the optimal number of clusters. This method uses the concept of WCSS value. **WCSS** stands for **Within Cluster Sum of Squares**, which defi nes the total variations within a cluster. The formula to calculate the value of WCSS (for 3 clusters) is given below:

$$WCSS= \sum_{Pi \text{ in Cluster1}} \text{distance}(P_i\ C_1)^2 + \sum_{Pi \text{ in Cluster2}} \text{distance}(P_i\ C_2)^2 + \sum_{Pi \text{ in CLuster3}} \text{distance}(P_i\ C_3)^2$$

In the above formula of WCSS,

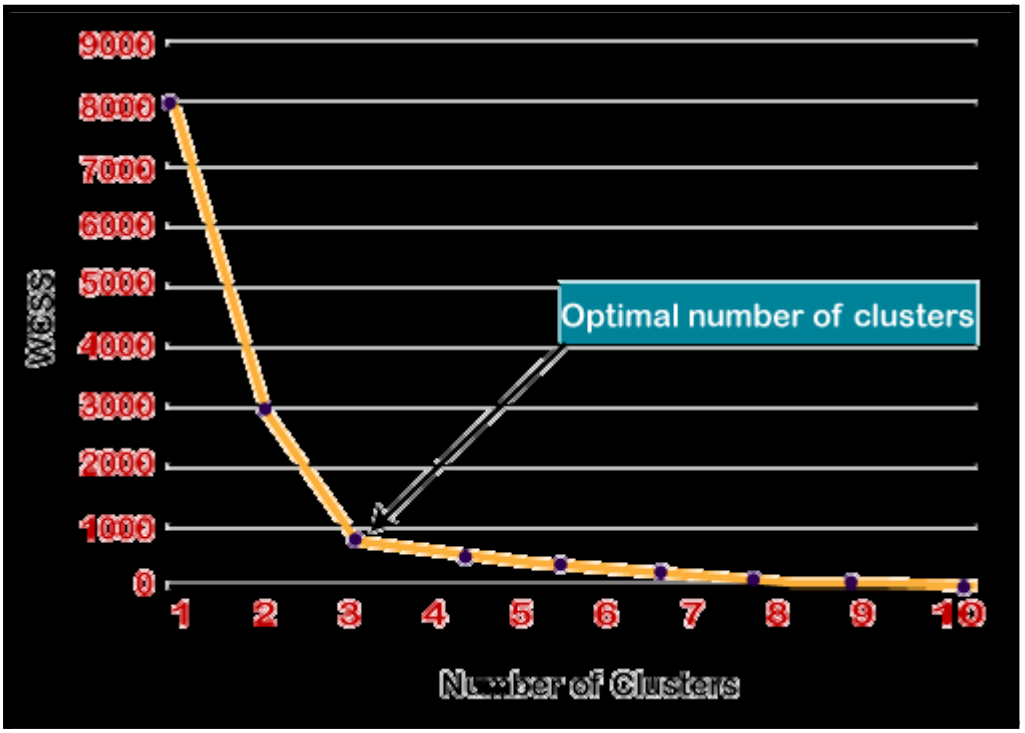
$\sum_{Pi \text{ in Cluster1}}$ distance$(P_i\ C_1)^2$: It is the sum of the square of the distances between each data point and its centroid within a cluster1 and the same for the other two terms.

To measure the distance between data points and centroid, we can use any method such as Euclidean distance or Manhattan distance.

To find the optimal value of clusters, the elbow method follows the below steps:

- It executes the K-means clustering on a given dataset for different K values (ranges from 1-10).
- For each value of K, calculates the WCSS value.
- Plots a curve between calculated WCSS values and the number of clusters K.
- The sharp point of bend or a point of the plot looks like an arm, then that point is considered as the best value of K.

Since the graph shows the sharp bend, which looks like an elbow, hence it is known as the elbow method. The graph for the elbow method looks like the below image:



Conclusion:

In this we have successfully implemented the above assignment.

Assignment Questions:

1) Explain K-Means Clustering?
2) Explain Hierarchical Clustering?
3) Explain Principal Component Analysis?
4) Explain Elbow Method?
5) Defi ne Eigenvectors?