

Experiment No 8

Aim: Implementation of any one Hierarchical Clustering method

Theory:

A Hierarchical clustering method works via grouping data into a tree of clusters. Hierarchical clustering begins by treating every data point as a separate cluster. Then, it repeatedly executes the subsequent steps:

Identify the 2 clusters which can be closest together, and
Merge the 2 maximum comparable clusters. We need to continue these steps until all the clusters are merged together.

In Hierarchical Clustering, the aim is to produce a hierarchical series of nested clusters. A diagram called a Dendrogram (A Dendrogram is a tree-like diagram that statistics the sequences of merges or splits) graphically represents this hierarchy and is an inverted tree that describes the order in which factors are merged (bottom-up view) or clusters are broken up (top-down view).

Hierarchical clustering is a method of cluster analysis in data mining that creates a hierarchical representation of the clusters in a dataset. The method starts by treating each data point as a separate cluster and then iteratively combines the closest clusters until a stopping criterion is reached. The result of hierarchical clustering is a tree-like structure, called a dendrogram, which illustrates the hierarchical relationships among the clusters.

Hierarchical clustering has a number of advantages over other clustering methods, including:

1. The ability to handle non-convex clusters and clusters of different sizes and densities.
2. The ability to handle missing data and noisy data.
3. The ability to reveal the hierarchical structure of the data, can be useful for understanding the relationships among the clusters. However, it also has some drawbacks, such as:
4. The a need for a criterion to stop the clustering process and determine the final number of clusters.
5. The computational cost and memory requirements of the method can be high, especially for large datasets.
6. The results can be sensitive to the initial conditions, linkage criterion, and distance metric used.

In summary, Hierarchical clustering is a method of data mining that groups similar data points into clusters by creating a hierarchical structure of the clusters.

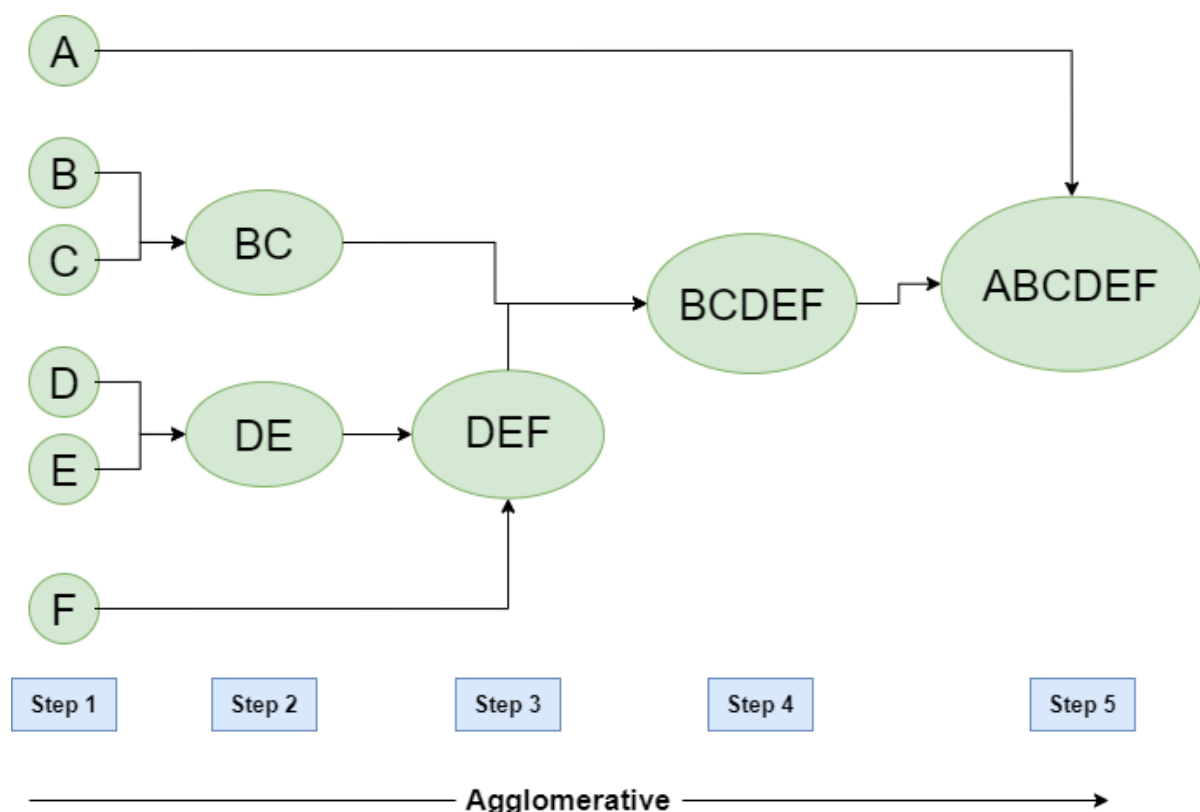
7. This method can handle different types of data and reveal the relationships among the clusters. However, it can have high computational cost and results can be sensitive to some conditions.

Agglomerative: Initially consider every data point as an individual Cluster and at every step, merge the nearest pairs of the cluster. (It is a bottom-up method). At first, every dataset is considered an individual entity or cluster. At every iteration, the clusters merge with different clusters until one cluster is formed.

The algorithm for Agglomerative Hierarchical Clustering is:

- Calculate the similarity of one cluster with all the other clusters (calculate proximity matrix)
- Consider every data point as an individual cluster
- Merge the clusters which are highly similar or close to each other.
- Recalculate the proximity matrix for each cluster
- Repeat Steps 3 and 4 until only a single cluster remains.

Let's say we have six data points A, B, C, D, E, and F.



Step 1: Consider each alphabet as a single cluster and calculate the distance of one cluster from all the other clusters.

Step 2: In the second step comparable clusters are merged together to form a single cluster. Let's say cluster (B) and cluster (C) are very similar to each other therefore we merge them in the second step similarly to cluster (D) and (E) and at last, we get the clusters [(A), (BC), (DE), (F)]

Step 3: We recalculate the proximity according to the algorithm and merge the two nearest clusters([(DE), (F)]) together to form new clusters as [(A), (BC), (DEF)]

Step 4: Repeating the same process; The clusters DEF and BC are comparable and merged together to form a new cluster. We're now left with clusters [(A), (BCDEF)].

Step 5: At last the two remaining clusters are merged together to form a single cluster [(ABCDEF)].

Output:

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```

import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
# For better readability,
import matplotlib
matplotlib.rcParams['font.size'] = 16
matplotlib.rcParams['figure.figsize'] = (12, 6)
matplotlib.rcParams['figure.facecolor'] = '#00000000'
df = pd.read_csv('/content/inventory.csv')
df

```

	transaction_id	product_id	product_name	product_category	product_brand	warehouse_id	warehouse_name	warehouse_location	city_id	supplier_id	supplier_name	contact_id
0	1	P2859	Titan T27	watches	Titan	W7276	BombayX	Mumbai	C7597	S3535	Stewart, Clayton and Martinez	C2483
1	2	P5937	Samsung QLED 21	tv	Samsung	W7001	DelhiCaps	Delhi	C7099	S7973	Carroll, Brady and Hancock	C8454
2	3	P1553	Philips Iron I4	Electrical App	Philips	W1296	BombayZ	Mumbai	C7597	S2142	Singh-Johnson	C8265
3	4	P7296	Nike Nex	Wear	Nike	W8451	BangaloreIS	Bangalore	C9293	S3115	Boyer Ltd	C3118
4	5	P9813	US Polo Black Denim	Wear	US Polo	W8571	KeralaSweep	Kerala	C6336	S8922	Davis Ltd	C7283
...
195	196	P5145	LG hair dryer	Electrical App	LG	W9621	GurgaonHDES	Gurgaon	C5676	S5845	Dixon and Sons	C9036
196	197	P7799	Apple watch series 8	watches	Apple	W4993	HyderabadHub	Hyderabad	C5055	S7793	Booth LLC	C7568

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[ ] dataset = df[['product_id', 'number_of_boxes']]
dataset

```

	product_id	number_of_boxes
0	P2859	16
1	P5937	77
2	P1553	62
3	P7296	71
4	P9813	37
...
195	P5145	45
196	P7799	80
197	P3507	38
198	P3238	54
199	P4930	75

200 rows x 2 columns

```

X = np.array(dataset)

class Distance_computation_grid(object):
    def __init__(self):
        pass

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```

X = np.array(dataset)

class Distance_computation_grid(object):
    def __init__(self):
        pass

    def compute_distance(self, samples):
        Distance_mat = np.zeros((len(samples), len(samples)))

        for i in range(Distance_mat.shape[0]):
            for j in range(Distance_mat.shape[0]):
                if i != j:
                    Distance_mat[i, j] = float(self.distance_calculate(samples[i], samples[j]))
                else:
                    Distance_mat[i, j] = 10**4
        return Distance_mat

    # For two samples
    def distance_calculate(self, sample1, sample2):
        dist = []

        for i in range(len(sample1)):
            for j in range(len(sample2)):
                try:
                    # Try to convert elements to float and calculate distance
                    dist.append(np.linalg.norm(np.array(float(sample1[i])) - np.array(float(sample2[j]))))
                except (ValueError, TypeError):
                    # Handle non-numeric or missing values (e.g., NaN) here
                    pass

        if not dist:
            return float('inf') # Return a large value for cases with no valid numeric values
        return min(dist)

```

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1
if not dist:
    return float('inf') # Return a large value for cases with no valid numeric values
return min(dist)

# For one sample and one cluster
def intersampledlist(self, s1, s2):
    if str(type(s2[0])) != '<class \'list\'>':
        s2 = [s2]
    if str(type(s1[0])) != '<class \'list\'>':
        s1 = [s1]
    m = len(s1)
    n = len(s2)
    dist = []

    if n >= m:
        for i in range(m):
            for j in range(n):
                if (len(s2[i]) >= len(s1[j])) and str(type(s2[i][0])) != '<class \'list\'>':
                    dist.append(self.interclusterdist(s2[i], s1[j]))
                else:
                    dist.append(np.linalg.norm(np.array(s2[i]) - np.array(s1[j])))
            else:
                for i in range(m):
                    for j in range(n):
                        if (len(s1[i]) >= len(s2[j])) and str(type(s1[i][0])) != '<class \'list\'>':
                            dist.append(self.interclusterdist(s1[i], s2[j]))
                        else:
                            dist.append(np.linalg.norm(np.array(s1[i]) - np.array(s2[j])))
    return min(dist)

```

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# For two clusters
def interclusterdist(self, cl, sample):
    dist = []

    for i in range(len(cl)):
        for j in range(len(sample)):
            try:
                cl_value = float(cl[i])
                sample_value = float(sample[j])
                dist.append(np.linalg.norm(cl_value - sample_value))
            except (ValueError, TypeError):
                # Handle non-numeric or missing values (e.g., NaN) here
                pass

    if not dist:
        return float('inf') # Return a large value for non-numeric cases
    return min(dist)

progression = [[i] for i in range(X.shape[0])]
samples = [[list(X[i])] for i in range(X.shape[0])]
m = len(samples)
distcal = Distance_computation_grid()

while m > 1:
    print('Sample size before clustering:', m)
    Distance_mat = distcal.compute_distance(samples)
    sample_ind_needed = np.where(Distance_mat == Distance_mat.min())[0]
    value_to_add = samples.pop(sample_ind_needed[1])
    samples[sample_ind_needed[0]].append(value_to_add)
    print('Cluster Node 1:', progression[sample_ind_needed[0]])
    print('Cluster Node 2:', progression[sample_ind_needed[1]])

```

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1
while m > 1:
    print('Sample size before clustering:', m)
    Distance_mat = distcal.compute_distance(samples)
    sample_ind_needed = np.where(Distance_mat == Distance_mat.min())[0]
    value_to_add = samples.pop(sample_ind_needed[1])
    samples[sample_ind_needed[0]].append(value_to_add)
    print('Cluster Node 1:', progression[sample_ind_needed[0]])
    print('Cluster Node 2:', progression[sample_ind_needed[1]])
    progression[sample_ind_needed[0]].append(progression[sample_ind_needed[1]])
    progression[sample_ind_needed[0]] = progression[sample_ind_needed[0]]
    v = progression.pop(sample_ind_needed[1])
    m = len(samples)
    print('Progression (Current Sample):', progression)
    print('Cluster attained:', progression[sample_ind_needed[0]])
    print('Sample size after clustering:', m)
    print('\n')

Sample size before clustering: 200
Cluster Node 1: [0]
Cluster Node 2: [1]
Progression (Current Sample): [[[0, [1]], [2], [3], [4], [5], [6], [7], [8], [9], [10], [11], [12], [13], [14], [15], [16], [17], [18], [19], [20], [21], [22], [23], [24], [25], [26], [27], [28], [29], [30], [31], [32], [33], [34], [35], [36], [37], [38], [39], [40], [41], [42], [43], [44], [45], [46], [47], [48], [49], [50], [51], [52], [53], [54], [55], [56], [57], [58], [59], [60], [61], [62], [63], [64], [65], [66], [67], [68], [69], [70], [71], [72], [73], [74], [75], [76], [77], [78], [79], [80], [81], [82], [83], [84], [85], [86], [87], [88], [89], [90], [91], [92], [93], [94], [95], [96], [97], [98], [99]]]
Cluster attained: [[0, [1]]]
Sample size after clustering: 199

Sample size before clustering: 199
Cluster Node 1: [[0, [1]]]
Cluster Node 2: [2]
Progression (Current Sample): [[[[0, [1]], [2]], [3], [4], [5], [6], [7], [8], [9], [10], [11], [12], [13], [14], [15], [16], [17], [18], [19], [20], [21], [22], [23], [24], [25], [26], [27], [28], [29], [30], [31], [32], [33], [34], [35], [36], [37], [38], [39], [40], [41], [42], [43], [44], [45], [46], [47], [48], [49], [50], [51], [52], [53], [54], [55], [56], [57], [58], [59], [60], [61], [62], [63], [64], [65], [66], [67], [68], [69], [70], [71], [72], [73], [74], [75], [76], [77], [78], [79], [80], [81], [82], [83], [84], [85], [86], [87], [88], [89], [90], [91], [92], [93], [94], [95], [96], [97], [98], [99]]]
Cluster attained: [[[[0, [1]], [2]]]
Sample size after clustering: 198

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