

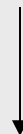
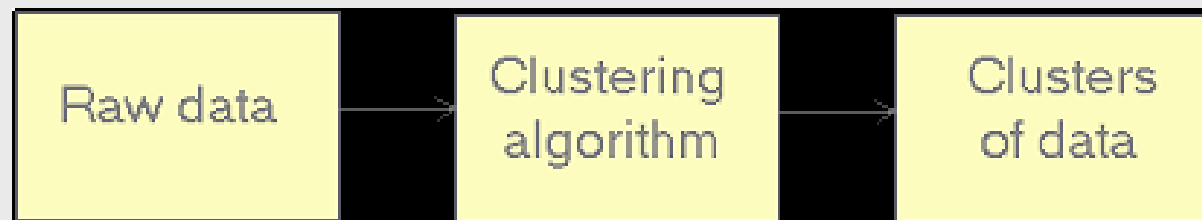
CLUSTERING

Overview

- Definition of Clustering
- Existing clustering methods
- Hierarchical clustering
- K-means
- K-means for large datasets.

Definition

- Clustering can be considered the most important *unsupervised learning* technique; so, as every other problem of this kind, it deals with finding a *structure* in a collection of unlabeled data.
- Clustering is “the process of organizing objects into groups whose members are similar in some way”.
- A *cluster* is therefore a collection of objects which are “similar” between them and are “dissimilar” to the objects belonging to other clusters.



Why clustering?

A few good reasons ...

- Simplifications
- Pattern detection
- Useful in data concept construction
- Unsupervised learning process

Where to use clustering?

- Data mining
 - intermediate step-classification or outlier analysis.
- Collaborative filtering
 - summarization of like minded users
- Customer Segmentation
 - recommendations for users.
- Data summarization
 - dimensionality reduction;easier to process and interpret
- Dynamic trend Detection
 - clustered into streams to identify pattern changes

Where to use clustering?

- Multimedia data analysis
 - music,documents,video or mix
 - Determine similar segments
- Biological data analysis
 - identify gene patterns
 - structured or sequenced
- Social network analysis
 - community network summarization

Constraints to consider

- Type of attributes in data
- Scalability to larger dataset
- Ability to work with irregular data
- Time cost
- complexity
- Data order dependency
- Result presentation

Measuring Similarity

- Dissimilarity/Similarity metric: Similarity is expressed in terms of a distance function, which is typically metric: $d(i, j)$
- Some distance calculation methods are The Euclidean distance, Jaccard distance and the Cosine distance.
- Distance metric constraints:
 - Triangle inequality: $d(x_i, x_k) \leq d(x_i, x_j) + d(x_j, x_k)$
 - $d(x_i, x_k) = 0 \Rightarrow x_i = x_k$.

Curse of Dimensionality

- Coined by Richard Bellman.
- Associated with the huge size of datasets.
- Data points become sparse-"lost in space"
- Clustering requires objects to be similar or close to each other. They are usually represented in the form of histograms where peaks represent the distance between the points-Dimensionality reduces that distance.

I.e

(max dist-min dist)

$$\lim_{d \rightarrow \infty} \frac{\text{max dist} - \text{min dist}}{\text{min dist}} = 0$$

Major Existing clustering methods

- Distance-based
- Hierarchical
- Partitioning
- Probabilistic

Hierarchical clustering

Agglomerative (bottom up)

1. start with 1 point (singleton)
2. recursively add two or more appropriate clusters
3. Stop when k number of clusters is achieved.

Divisive (top down)

1. Start with a big cluster
2. Recursively divide into smaller clusters
3. Stop when k number of clusters is achieved.

Hierarchical clustering types

- Single linkage clustering

Distance b/w clusters is the **shortest** distance b/w any one member of one cluster to any member of other cluster.

- Complete link clustering

Distance b/w clusters is the **longest** distance b/w any one member of one cluster to any member of other cluster.

Hierarchical clustering types

- Average link clustering

Distance b/w clusters is the **average** of all distances between every pair of points from both clusters.

- Centroid link clustering

Distance b/w clusters is the distance between the two means of the data points of the clusters.

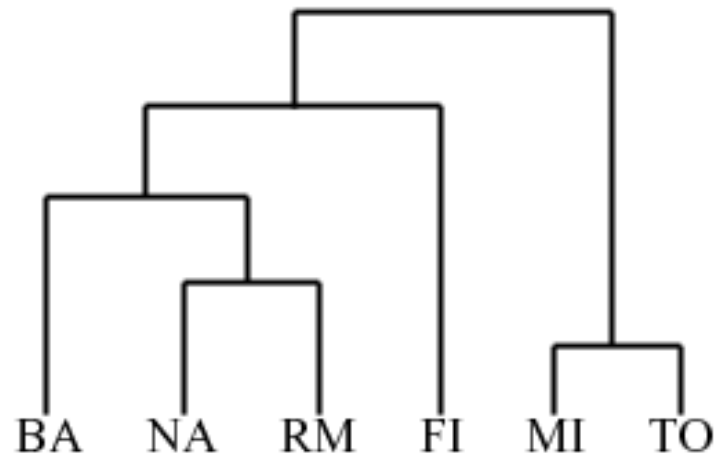
Stopping conditions: Hierarchical clustering

- Predetermined number of clusters is reached.
- Across splits or merges-little noticeable change.
- Max distance between any 2 points exceeds threshold.

Disadvantages:

- Inability to scale well.
- Undoing not possible

EXAMPLE OF A DENDROGRAM



K-mean algorithm

- It accepts the **number of clusters** to group data into, and the **dataset** to cluster as input values.
- It then creates the first **K initial clusters** (K = number of clusters needed) from the dataset by choosing K rows of data randomly from the dataset.
- ***For Example***, if there are 10,000 rows of data in the dataset and 3 clusters need to be formed, then the first **$K=3$ initial clusters** will be created by selecting 3 records randomly from the dataset as the initial clusters. Each of the 3 initial clusters formed will have just one row of data.

- The K-Means algorithm calculates the **Arithmetic Mean** of each cluster formed in the dataset. The Arithmetic Mean of a cluster is the mean of all the individual records in the cluster. In each of the first K initial clusters, there is only one record. The Arithmetic Mean of a cluster with one record is the set of values that make up that record.
- K-Means re-assigns each record in the dataset to the most similar cluster and re-calculates the arithmetic mean of all the clusters in the dataset. The arithmetic mean of a cluster is the arithmetic mean of all the records in that cluster.

- This new arithmetic mean becomes the center of this new cluster. Following the same procedure, new **cluster centers** are formed for all the existing clusters. K-Means re-assigns each record in the dataset to **only one** of the new clusters formed.
- A record or data point is assigned to the **nearest cluster** (the cluster which it is most similar to) using a measure of distance or similarity. The preceding steps are repeated until **stable clusters** are formed and the K-Means clustering procedure is completed.
- Stable clusters are formed when new iterations or repetitions of the K-Means clustering algorithm does not create new clusters as the cluster center or Arithmetic Mean of each cluster formed is the same as the old cluster center.

K-means for large datasets

- Designed for datasets that don't fit into the main memory. Output is just the cluster centroids and not the clusters per se.
- The BFR algorithm assumes data points from n -dimensional Euclidean space.
- Quality of cluster determined by the variance of the points within the cluster.
- Stores parameters such as N (number of points in cluster), i -Sum of the i^{th} coordinates of the points, SUM -sum of squares of i^{th} coordinates.

Reference

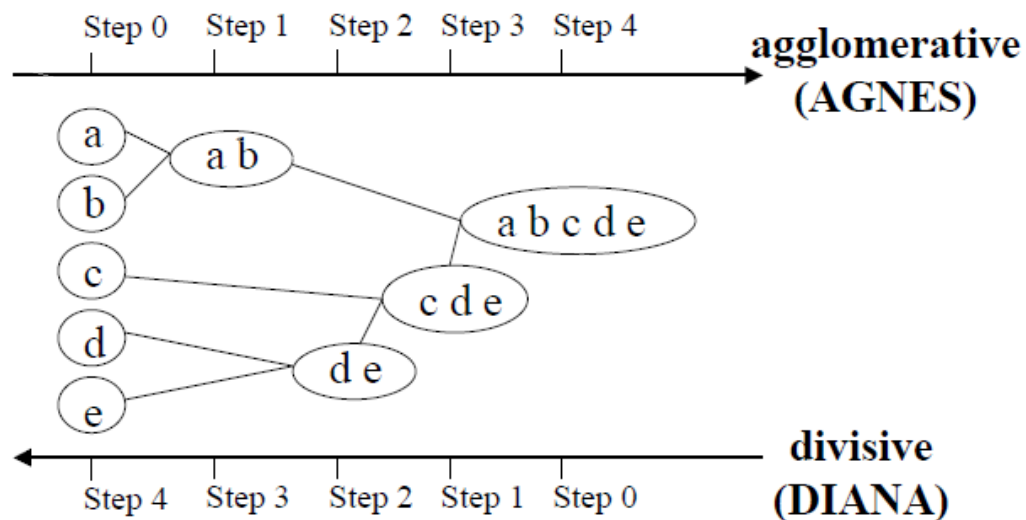
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Five Categories of Clustering Methods

- Partitioning algorithms: Construct various partitions and then evaluate them by some criterion
- Hierarchical algorithms: Create a hierarchical decomposition of the set of data (or objects) using some criterion
- Density-based algorithms: based on connectivity and density functions
- Grid-based algorithms: based on a multiple-level granularity structure
- Model-based: A model is hypothesized for each of the clusters and the idea is to find the best fit of that model to each other

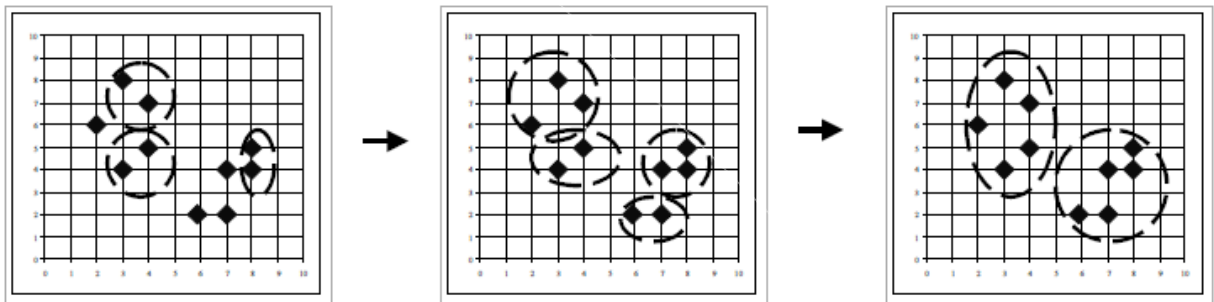
Hierarchical Clustering

- Use distance matrix as clustering criteria. This method does not require the number of clusters k as an input, but needs a termination condition



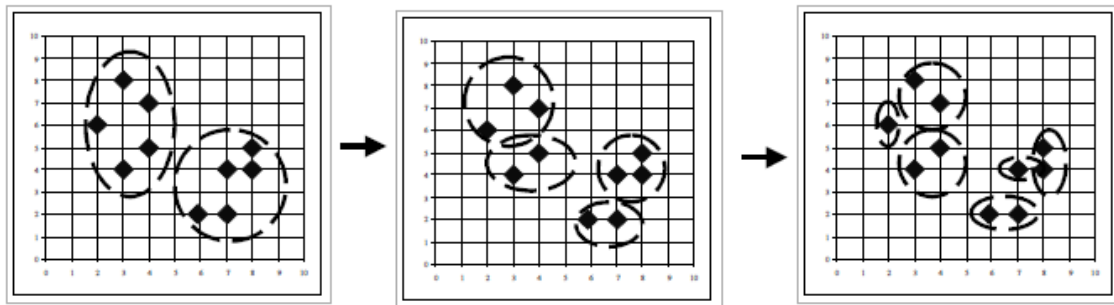
AGNES (Agglomerative Nesting)

- Agglomerative, Bottom-up approach
- Merge nodes that have the least dissimilarity
- Go on in a non-descending fashion
- Eventually all nodes belong to the same cluster

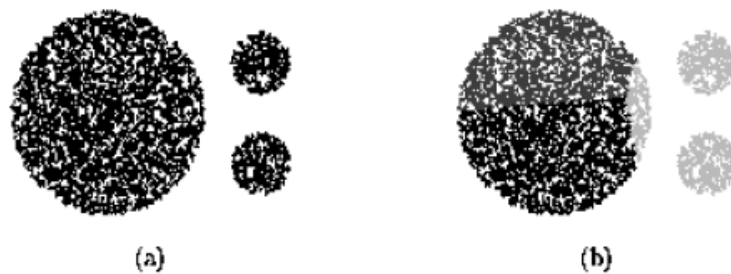


DIANA (Divisive Analysis)

- Top-down approach
- Inverse order of AGNES
- Eventually each node forms a cluster on its own



CURE (Clustering Using REpresentatives)

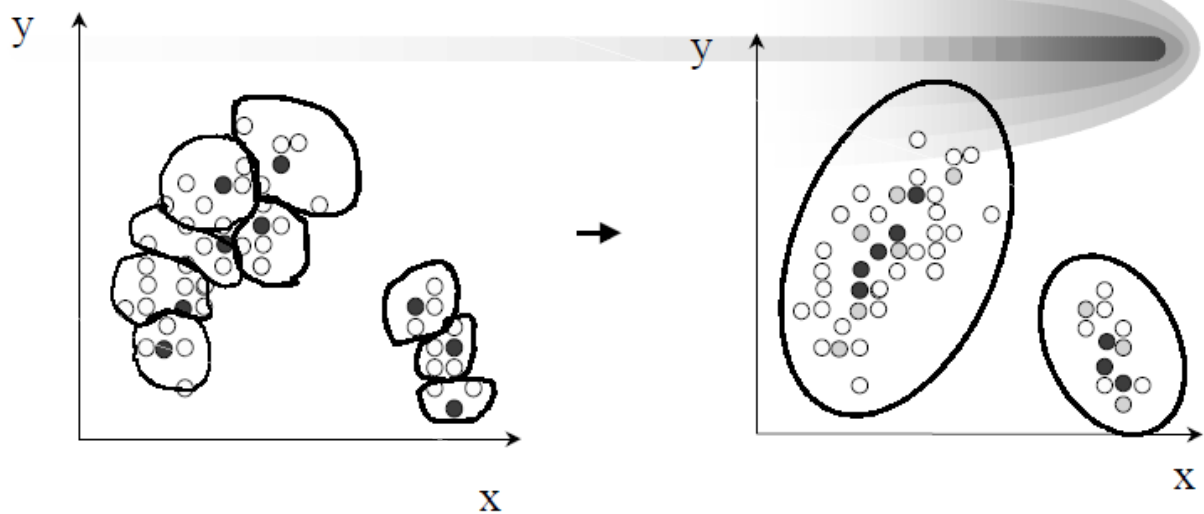


- CURE: proposed by Guha, Rastogi & Shim, 1998
 - Stops the creation of a cluster hierarchy if a level consists of k clusters
 - Uses multiple representative points to evaluate the distance between clusters, adjusts well to arbitrary shaped clusters and avoids single-link effect

Cure: The Algorithm

- Draw random sample s .
- Partition sample to p partitions with size s/p
- Partially cluster partitions into s/pq clusters
- Eliminate outliers
 - By random sampling
 - If a cluster grows too slow, eliminate it.
- Cluster partial clusters.
- Label data in disk

Cure: Shrinking Representative Points



- Shrink the multiple representative points towards the gravity center by a fraction of α .
- Multiple representatives capture the shape of the cluster

CLIQUE (Clustering In QUEst)

- Agrawal, Gehrke, Gunopulos, Raghavan (SIGMOD'98).
- Automatically identifying subspaces of a high dimensional data space that allow better clustering than original space
- CLIQUE can be considered as both density-based and grid-based
 - It partitions each dimension into the same number of equal length interval
 - It partitions an m-dimensional data space into non-overlapping rectangular units
 - A unit is dense if the fraction of total data points contained in the unit exceeds the input model parameter
 - A cluster is a maximal set of connected dense units within a subspace

CLIQUE: The Major Steps

- Partition the data space and find the number of points that lie inside each cell of the partition.
- Identify the subspaces that contain clusters using the Apriori principle
- Identify clusters:
 - Determine dense units in all subspaces of interests
 - Determine connected dense units in all subspaces of interests.
- Generate minimal description for the clusters
 - Determine maximal regions that cover a cluster of connected dense units for each cluster
 - Determination of minimal cover for each cluster

Strength and Weakness of CLIQUE

- Strength
 - It *automatically finds* subspaces of the highest dimensionality such that high density clusters exist in those subspaces
 - It is *insensitive* to the order of records in input and does not presume some canonical data distribution
 - It scales *linearly* with the size of input and has good scalability as the number of dimensions in the data increases
- Weakness
 - The accuracy of the clustering result may be degraded at the expense of simplicity of the method

PROCLUS

- PROCLUS is a top-down approach
- Samples the data and selects a set of k medoids and iteratively improves the subspace clusters.
- 3 phase implementation of algorithm.
- INITIALISATION PHASE:
Choose sample set of points.
Choose a set of data point which is probably the medoid.
(Uses greedy algorithm to do so).

PROCLUS

- ITERATION PHASE:
looks to find the best medoids from previous phase..
Replace bad ones with the good medoids.
For each data point ,assign it to the medoid m_i if its manhattan distance is minimum.
- REFINEMENT PHASE:
Computes new dimensions for each medoid based on clusters and reassigns points to medoids,removing outliers.
- PROCLUS is baiased to spherical data.
- Faster than CLIQUE.

FREQUENT PATTERN BASED CLUSTERING METHODS

- Definition of pattern matrix:
Submatrix that follows a particular pattern-rows change in a synchronised way w.r.t the columns and vice versa.
- Δ -pcluster-pscore > 0
- POPULAR ALGO-**MAPLE**
Enumerates all maximal pclusters.
Using Depth first search.
Apriori pruning of data sets(Monotonicity and apriori)

CLUSTERING STREAMS

- Challenges with streams:

Massive in size.

Patterns are continuously changing and evolving.

Domain based challenges arise-difficult to generalise.

Offline processing not possible.

CLUSTERING STREAMS

- A simple streaming model:

Based on k-medians methodology.

Divide into chunks based on the size of main memory. each chunk is represented as one point in space.

Sliding window consists of most recent N points.

BDMO ALGORITHM:

1. Summarised by buckets whose size is a power of 2.
2. Only one or two buckets of same size.
3. Bucket size has to be non-decreasing.
4. Contents of bucket-size, timestamp, collection of records(cluster points)

CLUSTERING STREAMS

INITIALIZING BUCKETS:

Smallest bucket of size $2(p)$.

Timestamp is the most recent point's timestamp in the bucket.

The centroid for the cluster which is added to the record.

MERGING BUCKETS:

Drop if timestamp greater than N time units prior to current time.

If three buckets of same size, merge oldest 2-recursive merging.