

Data Mining:

Concepts and Techniques


(3rd ed.)

— Chapter 10 —

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Chapter 10. Cluster Analysis: Basic Concepts and Methods

- Cluster Analysis: Basic Concepts 
- Partitioning Methods
- Hierarchical Methods
- Density-Based Methods
- Grid-Based Methods
- Evaluation of Clustering
- Summary

What is Cluster Analysis?

- Cluster: A collection of data objects
 - similar (or related) to one another within the same group
 - dissimilar (or unrelated) to the objects in other groups
- Cluster analysis (or *clustering*, *data segmentation*, ...)
 - Finding similarities between data according to the characteristics found in the data and grouping similar data objects into clusters
- **Unsupervised learning**: no predefined classes (i.e., *learning by observations* vs. learning by examples: supervised)
- Typical applications
 - As a **stand-alone tool** to get insight into data distribution
 - As a **preprocessing step** for other algorithms

Clustering for Data Understanding and Applications

- Biology: taxonomy of living things: kingdom, phylum, class, order, family, genus and species
- Information retrieval: document clustering
- Land use: Identification of areas of similar land use in an earth observation database
- Marketing: Help marketers discover distinct groups in their customer bases, and then use this knowledge to develop targeted marketing programs
- City-planning: Identifying groups of houses according to their house type, value, and geographical location
- Earth-quake studies: Observed earth quake epicenters should be clustered along continent faults
- Climate: understanding earth climate, find patterns of atmospheric and ocean
- Economic Science: market research

Clustering as a Preprocessing Tool (Utility)

- Summarization:
 - Preprocessing for regression, PCA, classification, and association analysis
- Compression:
 - Image processing: vector quantization
- Finding K-nearest Neighbors
 - Localizing search to one or a small number of clusters
- Outlier detection
 - Outliers are often viewed as those “far away” from any cluster

Quality: What Is Good Clustering?

- A good clustering method will produce high quality clusters
 - high intra-class similarity: **cohesive** within clusters
 - low inter-class similarity: **distinctive** between clusters
- The quality of a clustering method depends on
 - the similarity measure used by the method
 - its implementation, and
 - Its ability to discover some or all of the hidden patterns

Measure the Quality of Clustering

- Dissimilarity/Similarity metric
 - Similarity is expressed in terms of a distance function, typically metric: $d(i, j)$
 - The definitions of distance functions are usually rather different for interval-scaled, boolean, categorical, ordinal ratio, and vector variables
 - Weights should be associated with different variables based on applications and data semantics
- Quality of clustering:
 - There is usually a separate “quality” function that measures the “goodness” of a cluster.
 - It is hard to define “similar enough” or “good enough”
 - The answer is typically highly subjective

Considerations for Cluster Analysis

- Partitioning criteria
 - Single level vs. hierarchical partitioning (often, multi-level hierarchical partitioning is desirable)
- Separation of clusters
 - Exclusive (e.g., one customer belongs to only one region) vs. non-exclusive (e.g., one document may belong to more than one class)
- Similarity measure
 - Distance-based (e.g., Euclidian, road network, vector) vs. connectivity-based (e.g., density or contiguity)
- Clustering space
 - Full space (often when low dimensional) vs. subspaces (often in high-dimensional clustering)

Requirements and Challenges

- Scalability
 - Clustering all the data instead of only on samples
- Ability to deal with different types of attributes
 - Numerical, binary, categorical, ordinal, linked, and mixture of these
- Constraint-based clustering
 - User may give inputs on constraints
 - Use domain knowledge to determine input parameters
- Interpretability and usability
- Others
 - Discovery of clusters with arbitrary shape
 - Ability to deal with noisy data
 - Incremental clustering and insensitivity to input order
 - High dimensionality


Major Clustering Approaches (I)

- Partitioning approach:
 - Construct various partitions and then evaluate them by some criterion, e.g., minimizing the sum of square errors
 - Typical methods: k-means, k-medoids, CLARANS
- Hierarchical approach:
 - Create a hierarchical decomposition of the set of data (or objects) using some criterion
 - Typical methods: Diana, Agnes, BIRCH, CAMELEON
- Density-based approach:
 - Based on connectivity and density functions
 - Typical methods: DBSACN, OPTICS, DenClue
- Grid-based approach:
 - based on a multiple-level granularity structure
 - Typical methods: STING, WaveCluster, CLIQUE

Major Clustering Approaches (II)

- Model-based:
 - A model is hypothesized for each of the clusters and tries to find the best fit of that model to each other
 - Typical methods: EM, SOM, COBWEB
- Frequent pattern-based:
 - Based on the analysis of frequent patterns
 - Typical methods: p-Cluster
- User-guided or constraint-based:
 - Clustering by considering user-specified or application-specific constraints
 - Typical methods: COD (obstacles), constrained clustering
- Link-based clustering:
 - Objects are often linked together in various ways
 - Massive links can be used to cluster objects: SimRank, LinkClus

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Partitioning Algorithms: Basic Concept

- Partitioning method: Partitioning a database D of n objects into a set of k clusters, such that the sum of squared distances is minimized (where c_i is the centroid or medoid of cluster C_i)

$$E = \sum_{i=1}^k \sum_{p \in C_i} (p - c_i)^2$$

- Given k , find a partition of k clusters that optimizes the chosen partitioning criterion
 - Global optimal: exhaustively enumerate all partitions
 - Heuristic methods: *k-means* and *k-medoids* algorithms
 - *k-means* (MacQueen'67, Lloyd'57/'82): Each cluster is represented by the center of the cluster
 - *k-medoids* or PAM (Partition around medoids) (Kaufman & Rousseeuw'87): Each cluster is represented by one of the objects in the cluster

K means Clustering

Unsupervised Machine Learning is the process of teaching a computer to use unlabeled, unclassified data and enabling the algorithm to operate on that data without supervision. Without any previous data training, the machine's job in this case is to organize unsorted data according to parallels, patterns, and variations.

The goal of clustering is to divide the population or set of data points into a number of groups so that the data points within each group are more comparable to one another and different from the data points within the other groups. It is essentially a grouping of things based on how similar and different they are to one another.

We are given a data set of items, with certain features, and values for these features (like a vector). The task is to categorize those items into groups. To achieve this, we will use the K-means algorithm; an unsupervised learning algorithm. 'K' in the name of the algorithm represents the number of groups/clusters we want to classify our items into.

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 predefined 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.

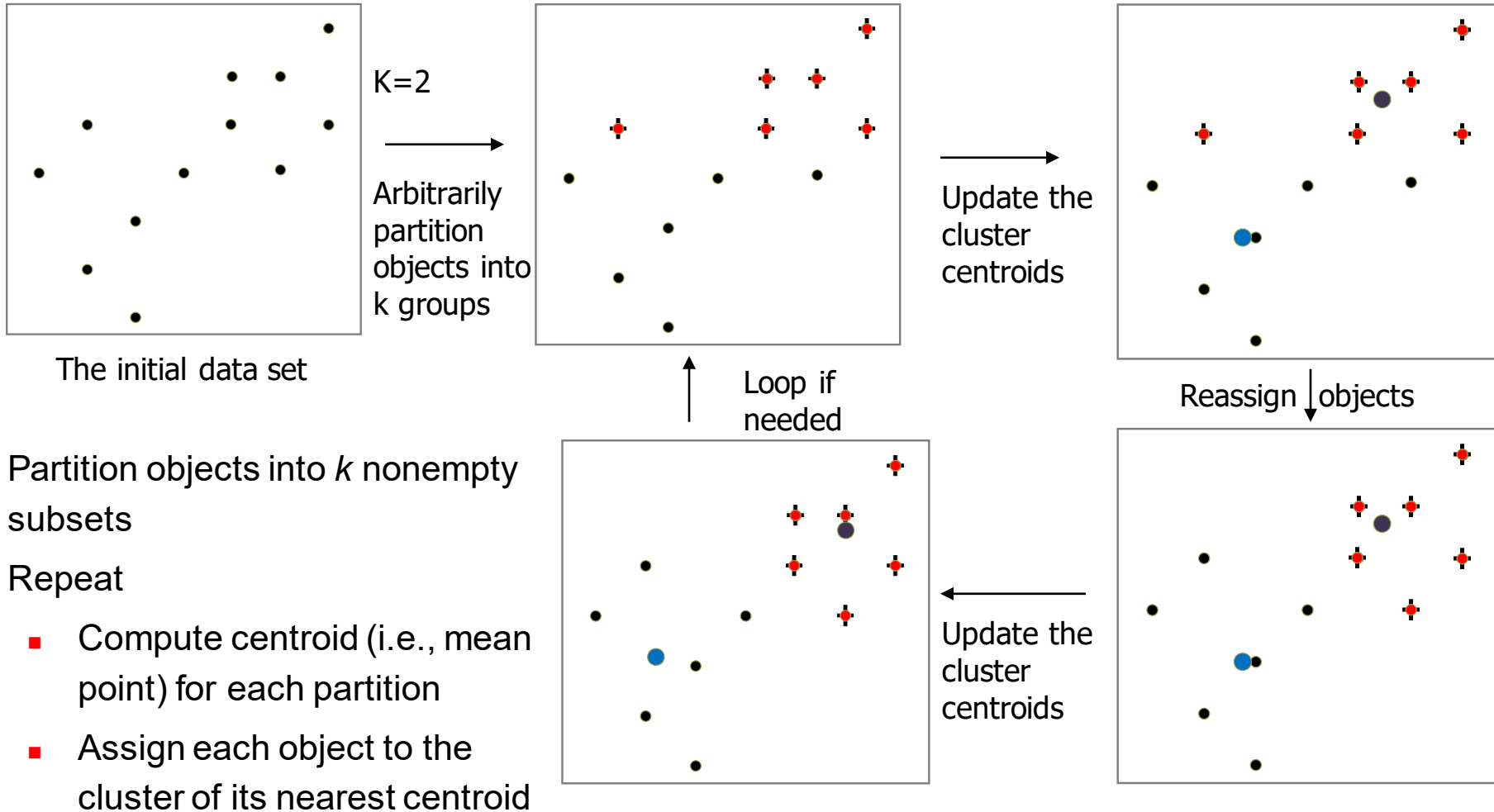
Step-6: If any reassignment occurs, then go to step-4 else go to FINISH.

Step-7: The model is ready.

The *K-Means* Clustering Method

- Given k , the *k-means* algorithm is implemented in four steps:
 - Partition objects into k nonempty subsets
 - Compute seed points as the centroids of the clusters of the current partitioning (the centroid is the center, i.e., *mean point*, of the cluster)
 - Assign each object to the cluster with the nearest seed point
 - Go back to Step 2, stop when the assignment does not change

An Example of *K-Means* Clustering



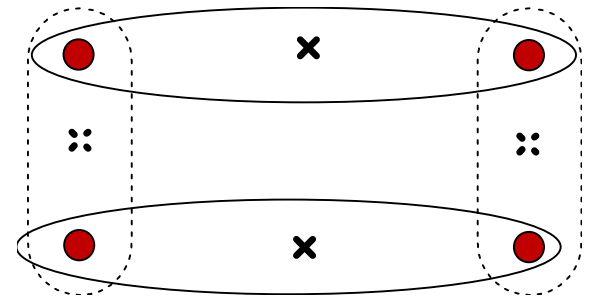
- Partition objects into k nonempty subsets
- Repeat
 - Compute centroid (i.e., mean point) for each partition
 - Assign each object to the cluster of its nearest centroid
- Until no change

Comments on the *K-Means* Method

- Strength: *Efficient*: $O(tkn)$, where n is # objects, k is # clusters, and t is # iterations. Normally, $k, t \ll n$.
 - Comparing: PAM: $O(k(n-k)^2)$, CLARA: $O(ks^2 + k(n-k))$
- Comment: Often terminates at a *local optimal*.
- Weakness
 - Applicable only to objects in a continuous n -dimensional space
 - Using the k -modes method for categorical data
 - In comparison, k -medoids can be applied to a wide range of data
 - Need to specify k , the *number* of clusters, in advance (there are ways to automatically determine the best k (see Hastie et al., 2009))
 - Sensitive to noisy data and *outliers*
 - Not suitable to discover clusters with *non-convex shapes*

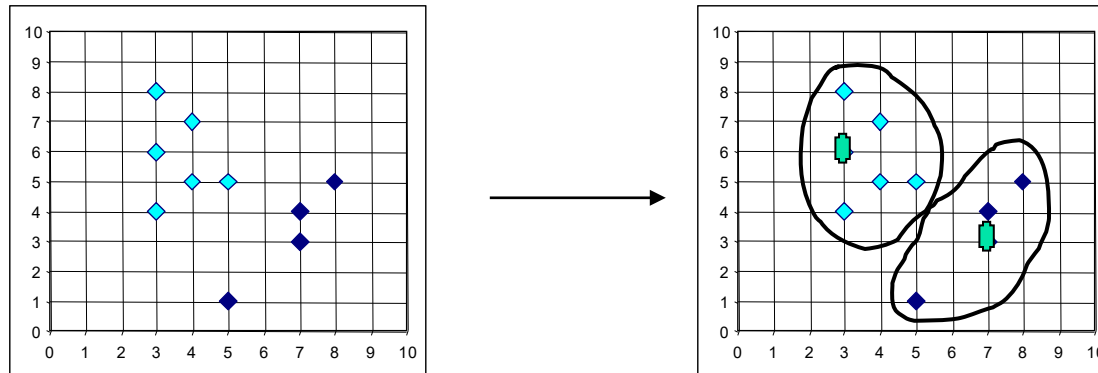
Variations of the *K-Means* Method

- Most of the variants of the *k-means* which differ in
 - Selection of the initial *k* means
 - Dissimilarity calculations
 - Strategies to calculate cluster means
- Handling categorical data: *k-modes*
 - Replacing means of clusters with modes
 - Using new dissimilarity measures to deal with categorical objects
 - Using a frequency-based method to update modes of clusters
 - A mixture of categorical and numerical data: *k-prototype* method



What Is the Problem of the K-Means Method?

- The k-means algorithm is sensitive to outliers !
 - Since an object with an extremely large value may substantially distort the distribution of the data
- K-Medoids: Instead of taking the **mean** value of the object in a cluster as a reference point, **medoids** can be used, which is the **most centrally located** object in a cluster



K-Medoids clustering-Theoretical Explanation

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K-Medoids and K-Means are two types of clustering mechanisms in Partition Clustering. First, Clustering is the process of breaking down an abstract group of data points/ objects into classes of similar objects such that all the objects in one cluster have similar traits. , a group of n objects is broken down into k number of clusters based on their similarities.

Two statisticians, Leonard Kaufman, and Peter J. Rousseeuw came up with this method. This tutorial explains what K-Medoids do, their applications, and the difference between K-Means and K-Medoids.

K-medoids is an unsupervised method with unlabelled data to be clustered. It is an **improved version of the K-Means algorithm** mainly designed to **deal with outlier data sensitivity**. Compared to other partitioning algorithms, the algorithm is **simple, fast, and easy to implement**.

K-Medoids:

Medoid: A Medoid is a point in the cluster from which the sum of distances to other data points is minimal.

(or)

A Medoid is a point in the cluster from which dissimilarities with all the other points in the clusters are minimal.

Instead of centroids as reference points in K-Means algorithms, the K-Medoids algorithm takes a Medoid as a reference point.

There are three types of algorithms for K-Medoids Clustering:

1. **PAM (Partitioning Around Clustering)**
2. **CLARA (Clustering Large Applications)**
3. **CLARANS (Randomized Clustering Large Applications)**

PAM is the most powerful algorithm of the three algorithms but has the disadvantage of time complexity. The following K-Medoids are performed using PAM. In the further parts, we'll see what CLARA and CLARANS are.

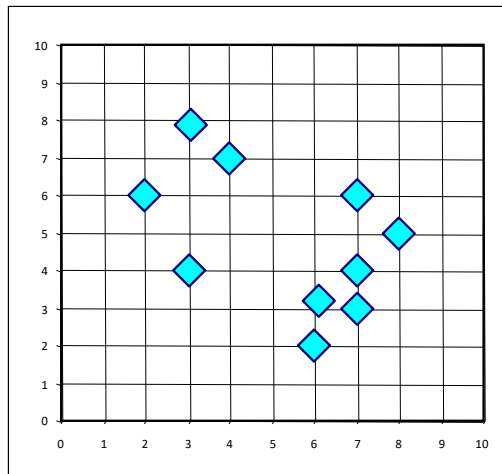
Algorithm:

Given the value of k and unlabelled data:

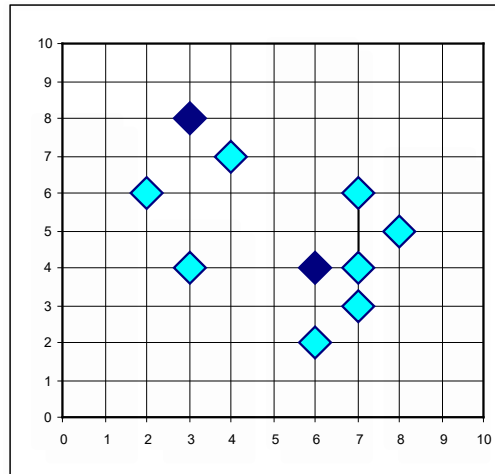
1. Choose k number of random points from the data and assign these k points to k number of clusters. These are the initial medoids.
2. For all the remaining data points, calculate the distance from each medoid and assign it to the cluster with the nearest medoid.
3. Calculate the total cost (Sum of all the distances from all the data points to the medoids)
4. Select a random point as the new medoid and swap it with the previous medoid. Repeat 2 and 3 steps.
5. If the total cost of the new medoid is less than that of the previous medoid, make the new medoid permanent and repeat step 4.
6. If the total cost of the new medoid is greater than the cost of the previous medoid, undo the swap and repeat step 4.
7. The Repetitions have to continue until no change is encountered with new medoids to classify data points.

PAM: A Typical K-Medoids Algorithm

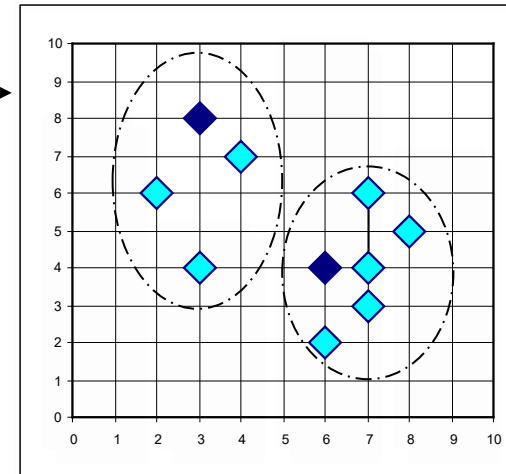
Total Cost = 20



Arbitrary
choose k
object as
initial
medoids



Assign
each remainin
g object to
nearest
medoids

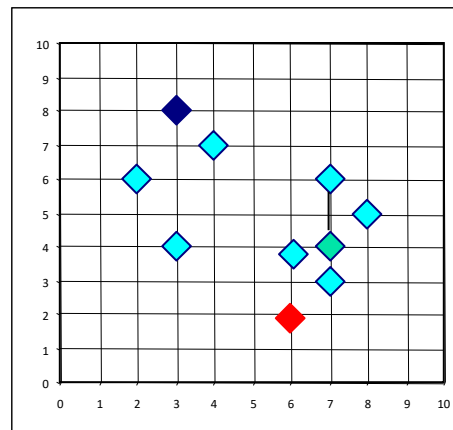


$K=2$

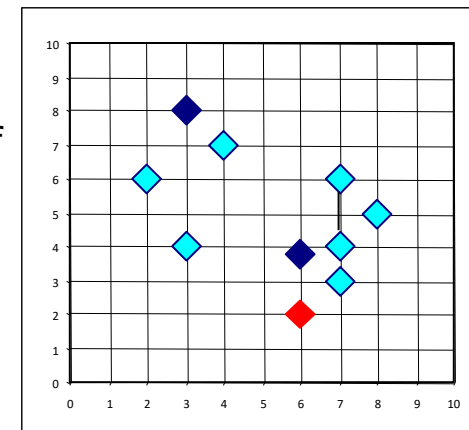
**Do loop
Until no
change**

Swapping O
and O_{random}
If quality is
improved.

Total Cost = 26



Compute
total cost of
swapping




Randomly select a
nonmedoid object, O_{random}

The K-Medoid Clustering Method

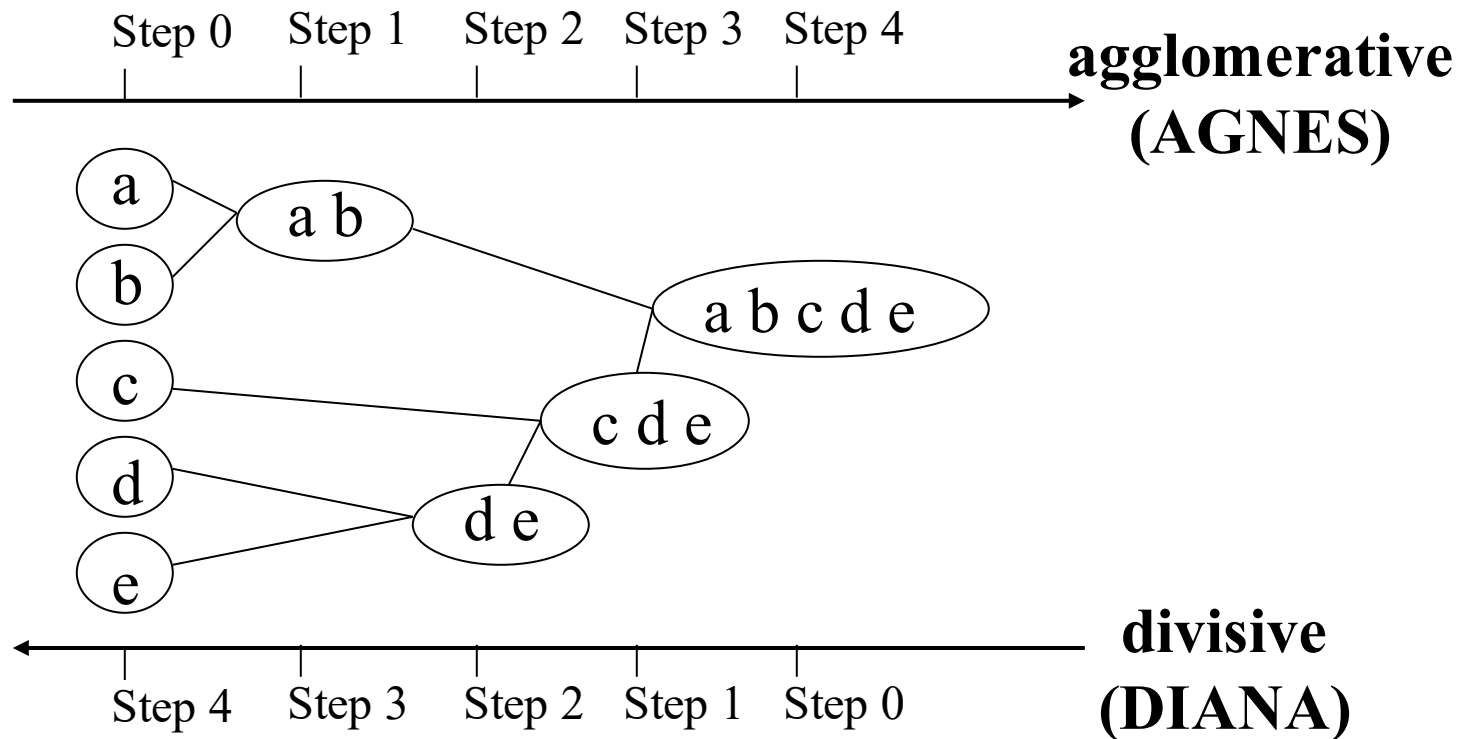
- *K-Medoids* Clustering: Find *representative* objects (medoids) in clusters
 - *PAM* (Partitioning Around Medoids, Kaufmann & Rousseeuw 1987)
 - Starts from an initial set of medoids and iteratively replaces one of the medoids by one of the non-medoids if it improves the total distance of the resulting clustering
 - *PAM* works effectively for small data sets, but does not scale well for large data sets (due to the computational complexity)
- Efficiency improvement on PAM
 - *CLARA* (Kaufmann & Rousseeuw, 1990): PAM on samples
 - *CLARANS* (Ng & Han, 1994): Randomized re-sampling

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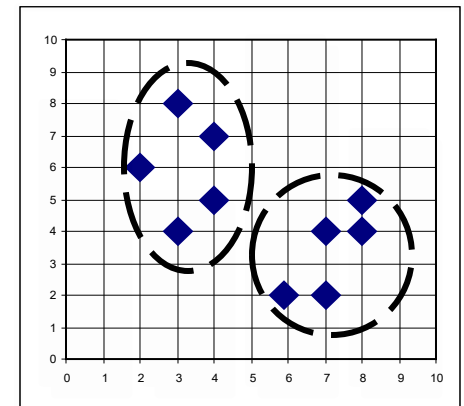
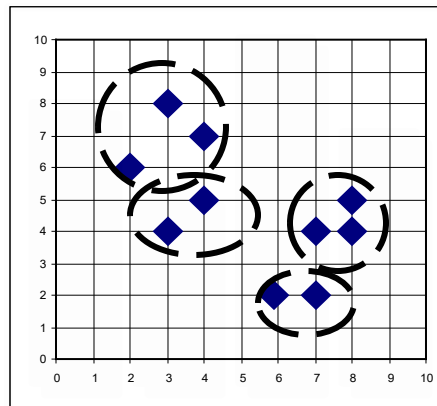
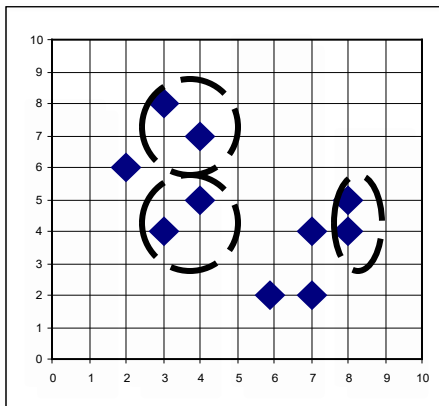
Hierarchical Clustering

- 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)

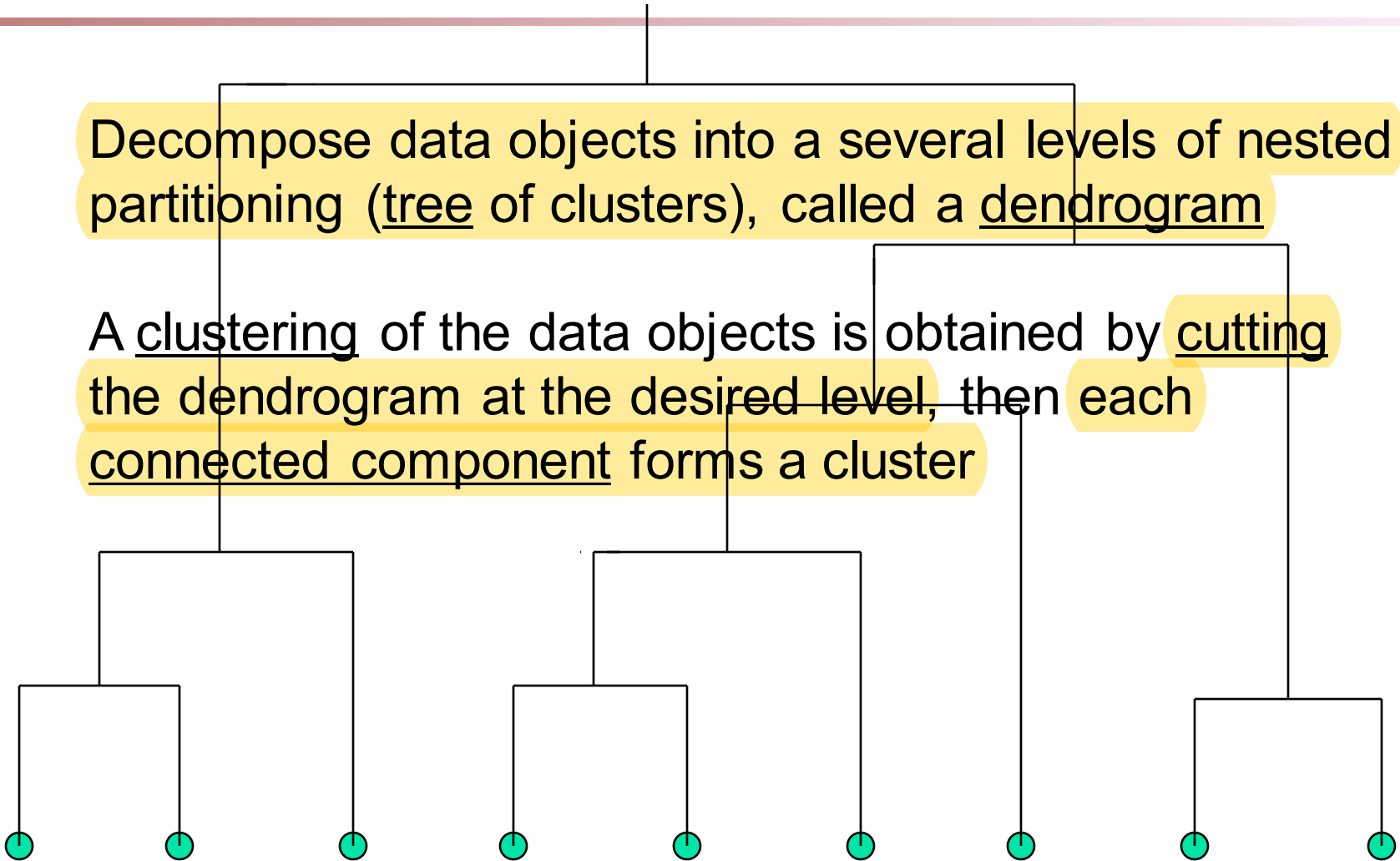
- Introduced in Kaufmann and Rousseeuw (1990)
- Implemented in statistical packages, e.g., Splus
- Use the **single-link** method and the dissimilarity matrix
- Merge nodes that have the least dissimilarity
- Go on in a non-descending fashion
- Eventually all nodes belong to the same cluster



Dendrogram: Shows How Clusters are Merged

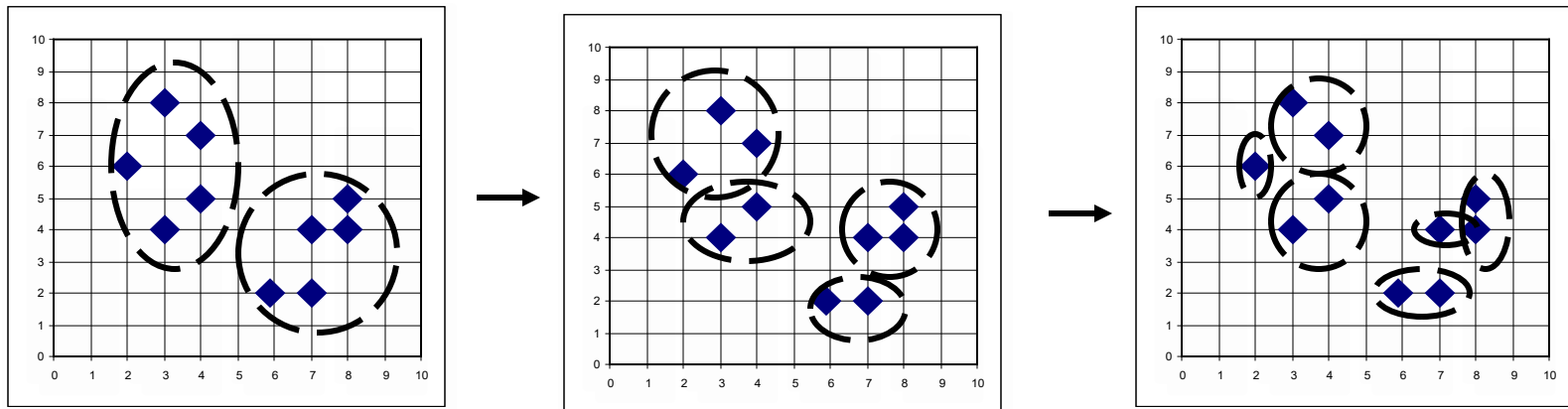
Decompose data objects into a several levels of nested partitioning (tree of clusters), called a dendrogram

A clustering of the data objects is obtained by cutting the dendrogram at the desired level, then each connected component forms a cluster

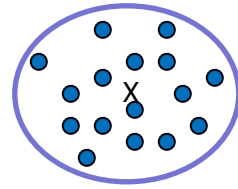
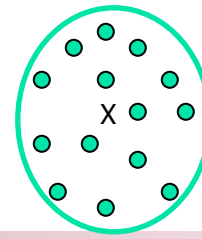


DIANA (Divisive Analysis)

- Introduced in Kaufmann and Rousseeuw (1990)
- Implemented in statistical analysis packages, e.g., Splus
- Inverse order of AGNES
- Eventually each node forms a cluster on its own



Distance between Clusters



- Single link: smallest distance between an element in one cluster and an element in the other, i.e., $\text{dist}(K_i, K_j) = \min(t_{ip}, t_{jq})$
- Complete link: largest distance between an element in one cluster and an element in the other, i.e., $\text{dist}(K_i, K_j) = \max(t_{ip}, t_{jq})$
- Average: avg distance between an element in one cluster and an element in the other, i.e., $\text{dist}(K_i, K_j) = \text{avg}(t_{ip}, t_{jq})$
- Centroid: distance between the centroids of two clusters, i.e., $\text{dist}(K_i, K_j) = \text{dist}(C_i, C_j)$
- Medoid: distance between the medoids of two clusters, i.e., $\text{dist}(K_i, K_j) = \text{dist}(M_i, M_j)$
 - Medoid: a chosen, centrally located object in the cluster

Centroid, Radius and Diameter of a Cluster (for numerical data sets)

- Centroid: the “middle” of a cluster

$$C_m = \frac{\sum_{i=1}^N (t_{ip})}{N}$$

- Radius: square root of average distance from any point of the cluster to its centroid

$$R_m = \sqrt{\frac{\sum_{i=1}^N (t_{ip} - c_m)^2}{N}}$$

- Diameter: square root of average mean squared distance between all pairs of points in the cluster

$$D_m = \sqrt{\frac{\sum_{i=1}^N \sum_{q=1}^N (t_{ip} - t_{iq})^2}{N(N-1)}}$$

Extensions to Hierarchical Clustering

- Major weakness of agglomerative clustering methods
 - Can never undo what was done previously
 - Do not scale well: time complexity of at least $O(n^2)$, where n is the number of total objects
- Integration of hierarchical & distance-based clustering
 - BIRCH (1996): uses CF-tree and incrementally adjusts the quality of sub-clusters
 - CHAMELEON (1999): hierarchical clustering using dynamic modeling

BIRCH (Balanced Iterative Reducing and Clustering Using Hierarchies)

- Zhang, Ramakrishnan & Livny, SIGMOD'96
- Incrementally construct a CF (Clustering Feature) tree, a hierarchical data structure for multiphase clustering
 - Phase 1: scan DB to build an initial in-memory CF tree (a multi-level compression of the data that tries to preserve the inherent clustering structure of the data)
 - Phase 2: use an arbitrary clustering algorithm to cluster the leaf nodes of the CF-tree
- *Scales linearly*: finds a good clustering with a single scan and improves the quality with a few additional scans
- *Weakness*: handles only numeric data, and sensitive to the order of the data record

Clustering Feature Vector in BIRCH

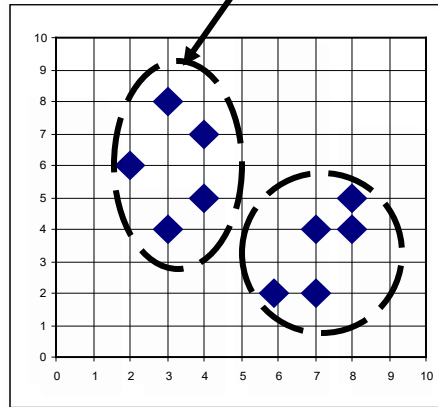
Clustering Feature (CF): $CF = (N, LS, SS)$

N : Number of data points

LS : linear sum of N points: $\sum_{i=1}^N X_i$

SS : square sum of N points

$$\sum_{i=1}^N X_i^2$$



$CF = (5, (16,30), (54,190))$

(3,4)

(2,6)

(4,5)

(4,7)

(3,8)

CF-Tree in BIRCH

- Clustering feature:
 - Summary of the statistics for a given subcluster: the 0-th, 1st, and 2nd moments of the subcluster from the statistical point of view
 - Registers crucial measurements for computing cluster and utilizes storage efficiently
- A CF tree is a height-balanced tree that stores the clustering features for a hierarchical clustering
 - A nonleaf node in a tree has descendants or “children”
 - The nonleaf nodes store sums of the CFs of their children
- A CF tree has two parameters
 - Branching factor: max # of children
 - Threshold: max diameter of sub-clusters stored at the leaf nodes

The CF Tree Structure

Root

$B = 7$

$L = 6$

CF_1	CF_2	CF_3	CF_6
child ₁	child ₂	child ₃		child ₆

Non-leaf node

CF_1	CF_2	CF_3	CF_5
child ₁	child ₂	child ₃		child ₅

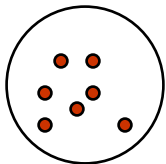
Leaf node

prev	CF_1	CF_2	CF_6	next
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Leaf node

prev	CF_1	CF_2	CF_4	next
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||



The Birch Algorithm

- Cluster Diameter

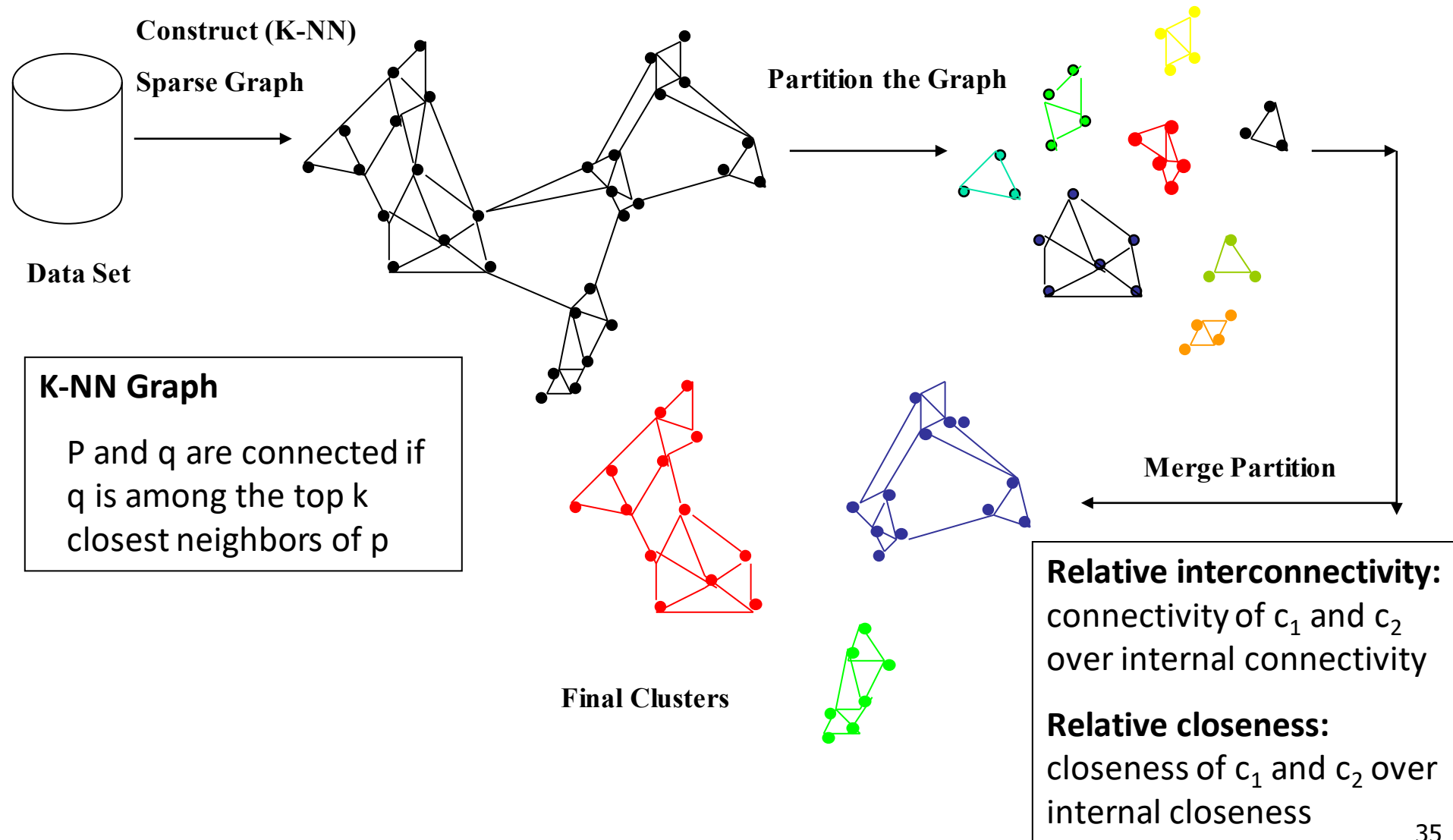
$$\sqrt{\frac{1}{n(n-1)} \sum (x_i - x_j)^2}$$

- For each point in the input
 - Find closest leaf entry
 - Add point to leaf entry and update CF
 - If entry diameter > max_diameter, then split leaf, and possibly parents
- Algorithm is $O(n)$
- Concerns
 - Sensitive to insertion order of data points
 - Since we fix the size of leaf nodes, so clusters may not be so natural
 - Clusters tend to be spherical given the radius and diameter measures

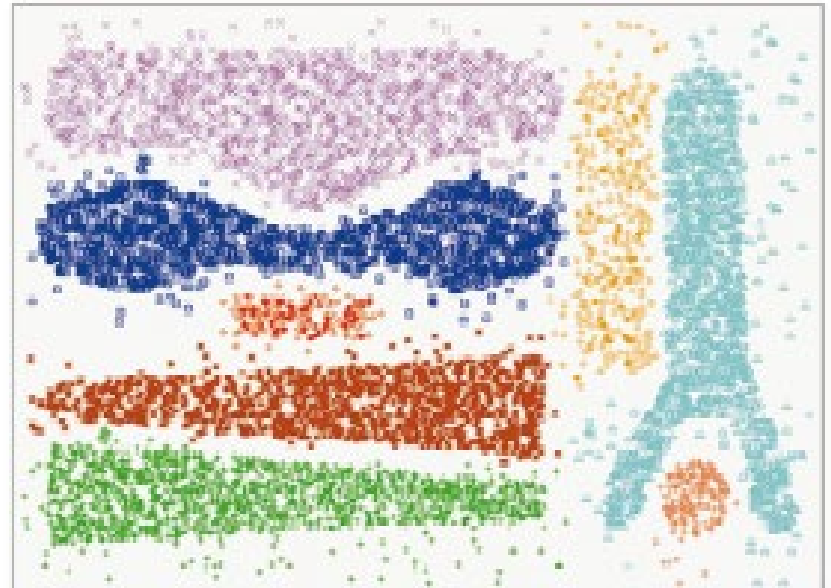
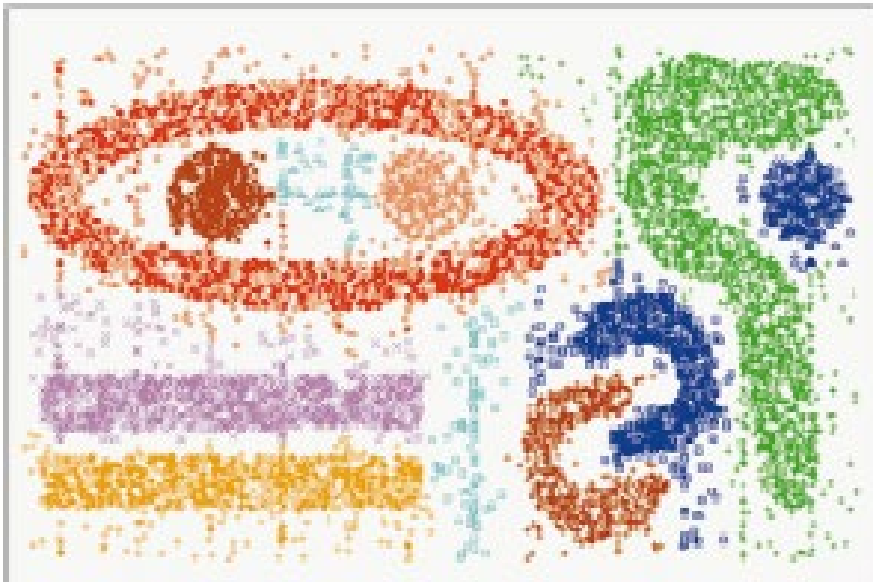
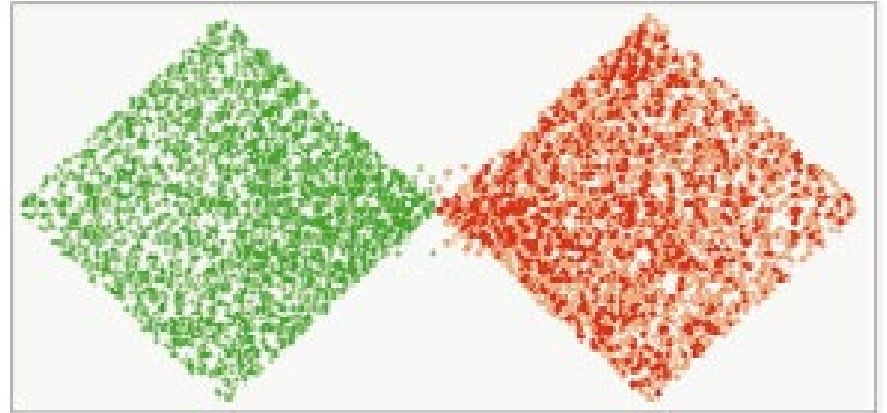
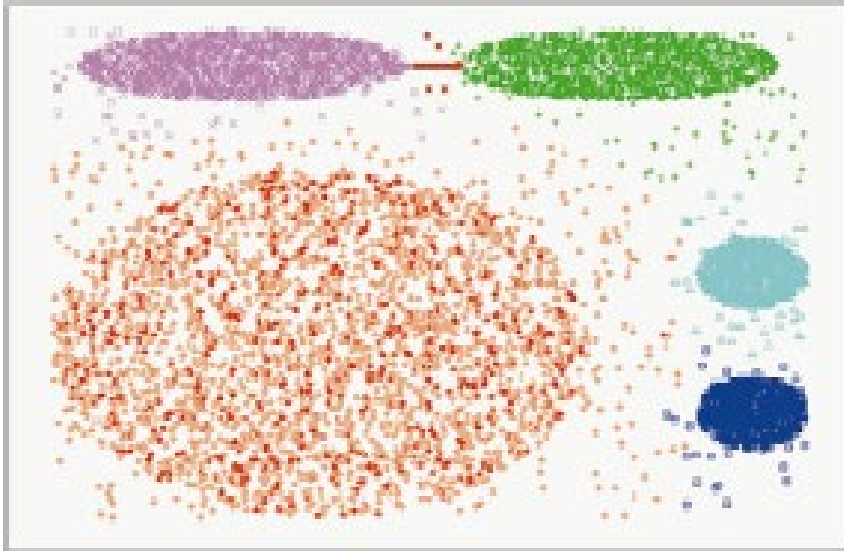
CHAMELEON: Hierarchical Clustering Using Dynamic Modeling (1999)

- CHAMELEON: G. Karypis, E. H. Han, and V. Kumar, 1999
- Measures the similarity based on a dynamic model
 - Two clusters are merged only if the *interconnectivity* and *closeness (proximity)* between two clusters are high *relative to* the internal interconnectivity of the clusters and closeness of items within the clusters
- Graph-based, and a two-phase algorithm
 1. Use a graph-partitioning algorithm: cluster objects into a large number of relatively small sub-clusters
 2. Use an agglomerative hierarchical clustering algorithm: find the genuine clusters by repeatedly combining these sub-clusters

Overall Framework of CHAMELEON



CHAMELEON (Clustering Complex Objects)



Probabilistic Hierarchical Clustering

- Algorithmic hierarchical clustering
 - Nontrivial to choose a good distance measure
 - Hard to handle missing attribute values
 - Optimization goal not clear: heuristic, local search
- Probabilistic hierarchical clustering
 - Use probabilistic models to measure distances between clusters
 - Generative model: Regard the set of data objects to be clustered as a sample of the underlying data generation mechanism to be analyzed
 - Easy to understand, same efficiency as algorithmic agglomerative clustering method, can handle partially observed data
- In practice, assume the generative models adopt common distributions functions, e.g., Gaussian distribution or Bernoulli distribution, governed by parameters

Generative Model

- Given a set of 1-D points $X = \{x_1, \dots, x_n\}$ for clustering analysis & assuming they are generated by a Gaussian distribution:

$$\mathcal{N}(\mu, \sigma^2) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{(x-\mu)^2}{2\sigma^2}}$$

- The probability that a point $x_i \in X$ is generated by the model

$$P(x_i|\mu, \sigma^2) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{(x_i-\mu)^2}{2\sigma^2}}$$

- The likelihood that X is generated by the model:

$$L(\mathcal{N}(\mu, \sigma^2) : X) = P(X|\mu, \sigma^2) = \prod_{i=1}^n \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{(x_i-\mu)^2}{2\sigma^2}}$$

- The task of learning the generative model: find the parameters μ and σ^2 such that

$$\mathcal{N}(\mu_0, \sigma_0^2) = \arg \max \{L(\mathcal{N}(\mu, \sigma^2) : X)\}$$

the maximum likelihood

A Probabilistic Hierarchical Clustering Algorithm

- For a set of objects partitioned into m clusters C_1, \dots, C_m , the quality can be measured by,

$$Q(\{C_1, \dots, C_m\}) = \prod_{i=1}^m P(C_i)$$

where $P()$ is the maximum likelihood

- Distance between clusters C_1 and C_2 : $dist(C_i, C_j) = -\log \frac{P(C_1 \cup C_2)}{P(C_1)P(C_2)}$
- Algorithm: Progressively merge points and clusters

Input: $D = \{o_1, \dots, o_n\}$: a data set containing n objects

Output: A hierarchy of clusters

Method

Create a cluster for each object $C_i = \{o_i\}$, $1 \leq i \leq n$;


For $i = 1$ to n {

Find pair of clusters C_i and C_j such that

$C_i, C_j = \operatorname{argmax}_{i \neq j} \{\log (P(C_i \cup C_j) / (P(C_i)P(C_j)))\}$;

If $\log (P(C_i \cup C_j) / (P(C_i)P(C_j))) > 0$ then merge C_i and C_j }

Chapter 10. Cluster Analysis: Basic Concepts and Methods

- Cluster Analysis: Basic Concepts
- Partitioning Methods
- Hierarchical Methods
- Density-Based Methods 
- Grid-Based Methods
- Evaluation of Clustering
- Summary

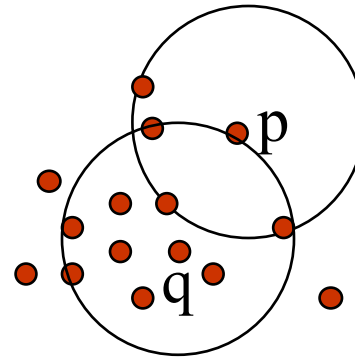
Density-Based Clustering Methods

- Clustering based on density (local cluster criterion), such as density-connected points
- Major features:
 - Discover clusters of arbitrary shape
 - Handle noise
 - One scan
 - Need density parameters as termination condition
- Several interesting studies:
 - DBSCAN: Ester, et al. (KDD'96)
 - OPTICS: Ankerst, et al (SIGMOD'99).
 - DENCLUE: Hinneburg & D. Keim (KDD'98)
 - CLIQUE: Agrawal, et al. (SIGMOD'98) (more grid-based)

Density-Based Clustering: Basic Concepts

- Two parameters:
 - **Eps**: Maximum radius of the neighbourhood
 - **MinPts**: Minimum number of points in an Eps-neighbourhood of that point
- $N_{Eps}(p)$: $\{q \text{ belongs to } D \mid \text{dist}(p,q) \leq Eps\}$
- **Directly density-reachable**: A point p is directly density-reachable from a point q w.r.t. Eps , $MinPts$ if
 - p belongs to $N_{Eps}(q)$
 - core point condition:

$$|N_{Eps}(q)| \geq MinPts$$



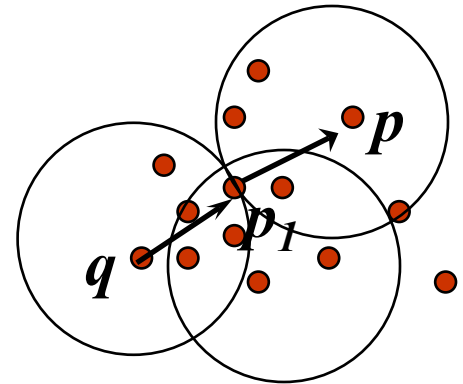
MinPts = 5

Eps = 1 cm

Density-Reachable and Density-Connected

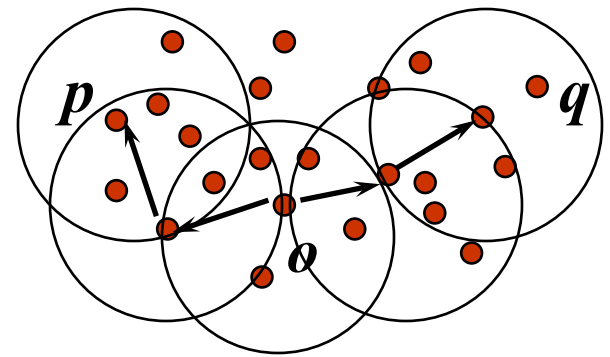
- Density-reachable:

- A point p is **density-reachable** from a point q w.r.t. Eps , $MinPts$ if there is a chain of points p_1, \dots, p_n , $p_1 = q$, $p_n = p$ such that p_{i+1} is directly density-reachable from p_i



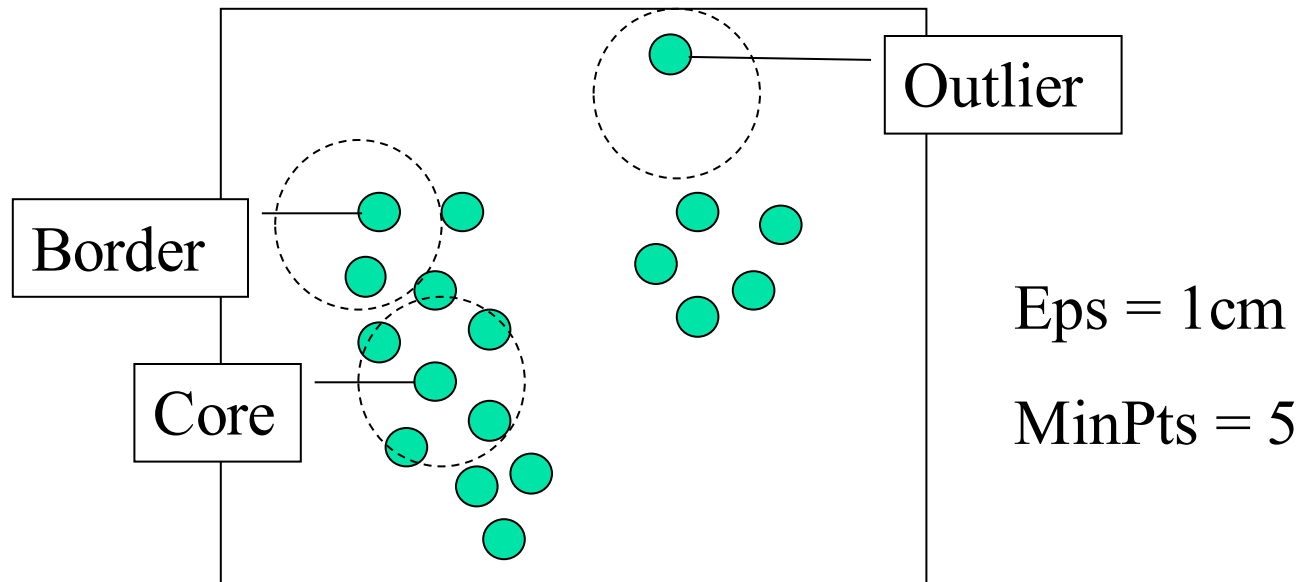
- Density-connected

- A point p is **density-connected** to a point q w.r.t. Eps , $MinPts$ if there is a point o such that both, p and q are density-reachable from o w.r.t. Eps and $MinPts$



DBSCAN: Density-Based Spatial Clustering of Applications with Noise

- Relies on a *density-based* notion of cluster: A *cluster* is defined as a maximal set of density-connected points
- Discovers clusters of arbitrary shape in spatial databases with noise



DBSCAN: The Algorithm

- Arbitrary select a point p
- Retrieve all points density-reachable from p w.r.t. Eps and $MinPts$
- If p is a core point, a cluster is formed
- If p is a border point, no points are density-reachable from p and DBSCAN visits the next point of the database
- Continue the process until all of the points have been processed

DBSCAN: Sensitive to Parameters

Figure 8. DBScan results for DS1 with MinPts at 4 and Eps at (a) 0.5 and (b) 0.4.

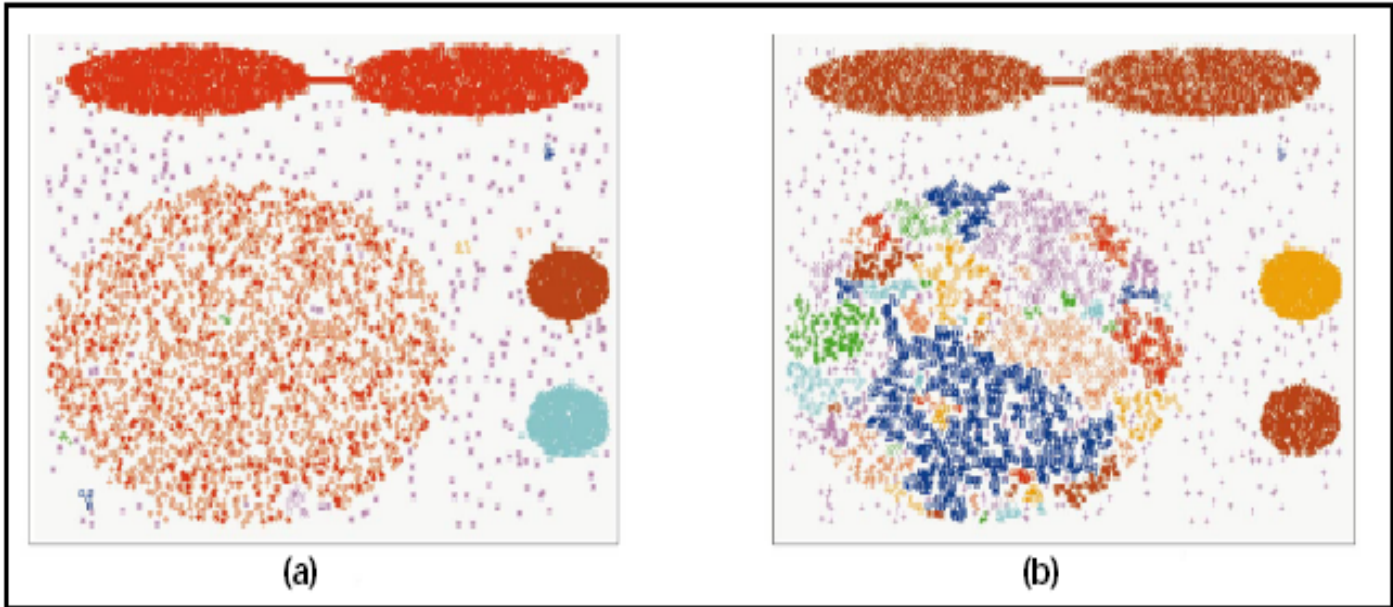
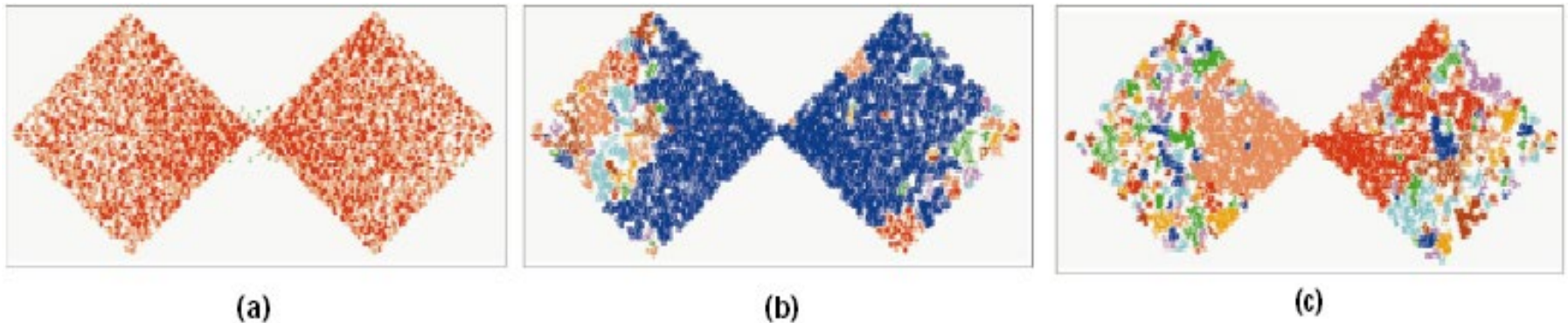


Figure 9. DBScan results for DS2 with MinPts at 4 and Eps at (a) 5.0, (b) 3.5, and (c) 3.0.



OPTICS: A Cluster-Ordering Method (1999)

- OPTICS: Ordering Points To Identify the Clustering Structure
 - Ankerst, Breunig, Kriegel, and Sander (SIGMOD'99)
 - Produces a special order of the database wrt its density-based clustering structure
 - This cluster-ordering contains info equiv to the density-based clusterings corresponding to a broad range of parameter settings
 - Good for both automatic and interactive cluster analysis, including finding intrinsic clustering structure
 - Can be represented graphically or using visualization techniques

OPTICS: Some Extension from DBSCAN

- Index-based:

- k = number of dimensions
- $N = 20$
- $p = 75\%$
- $M = N(1-p) = 5$

- Complexity: $O(N \log N)$

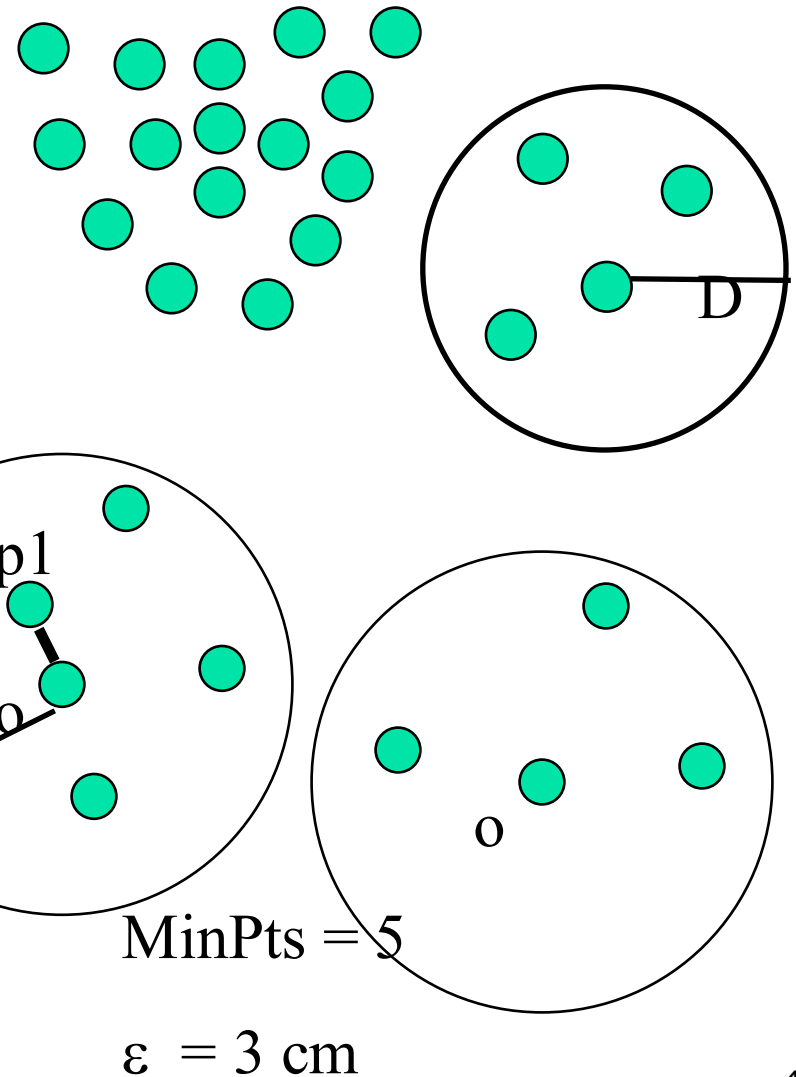
- Core Distance:

- min eps s.t. point is core

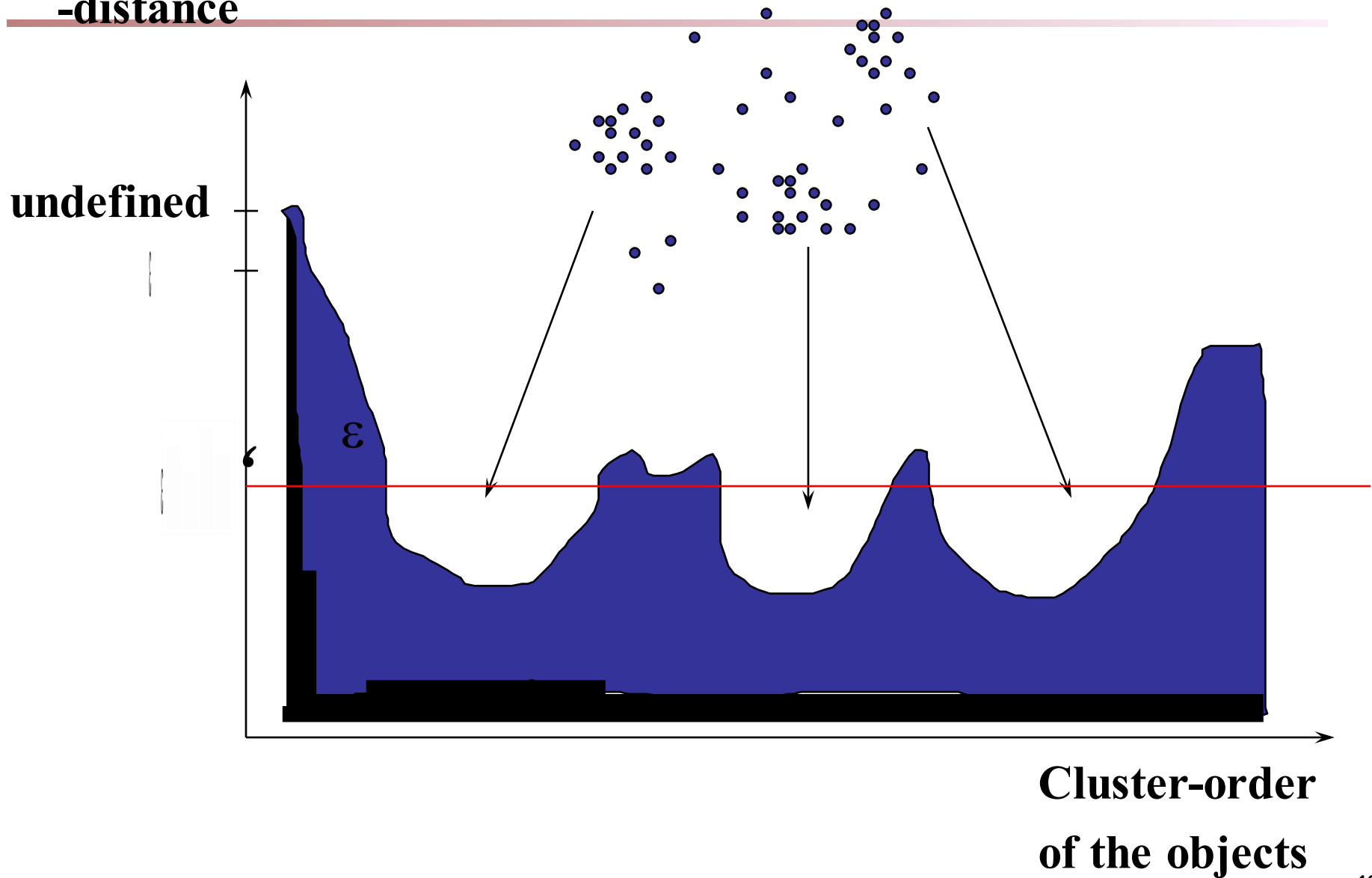
- Reachability Distance

$\text{Max}(\text{core-distance}(o), d(o, p))$

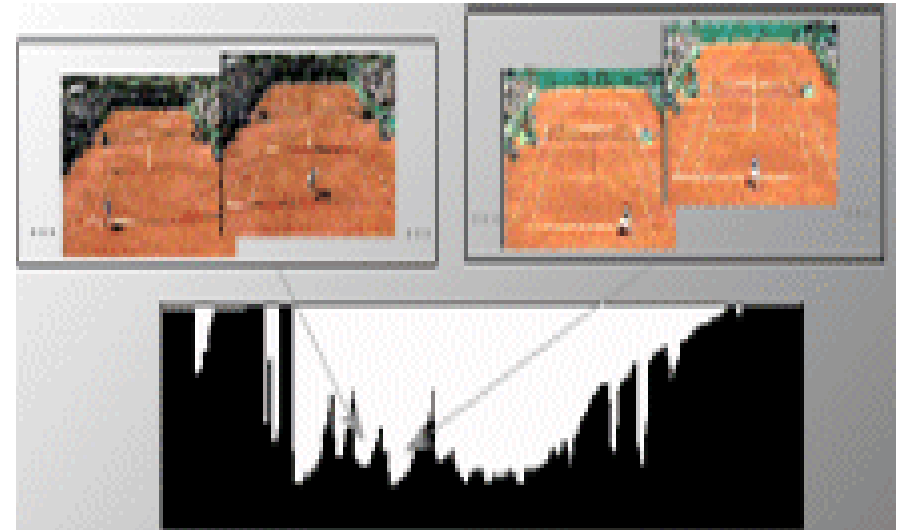
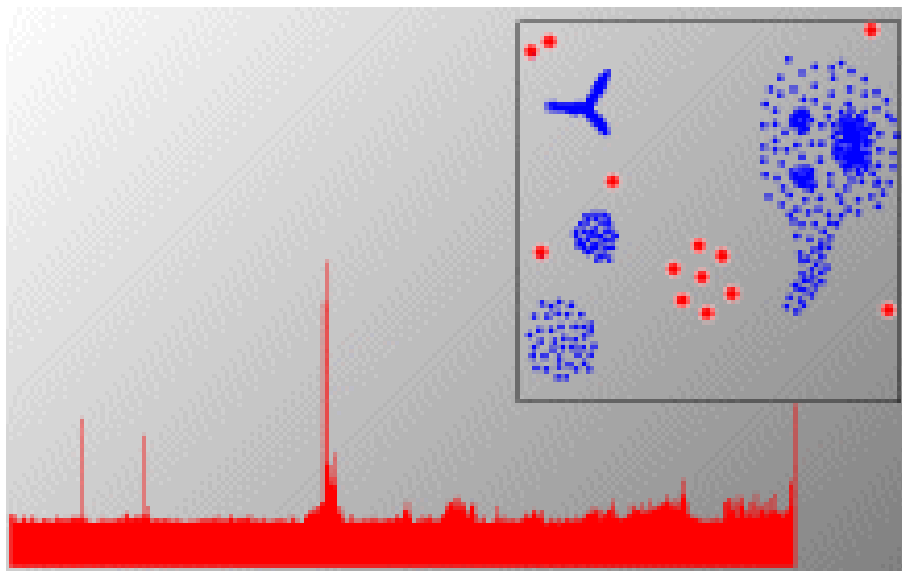
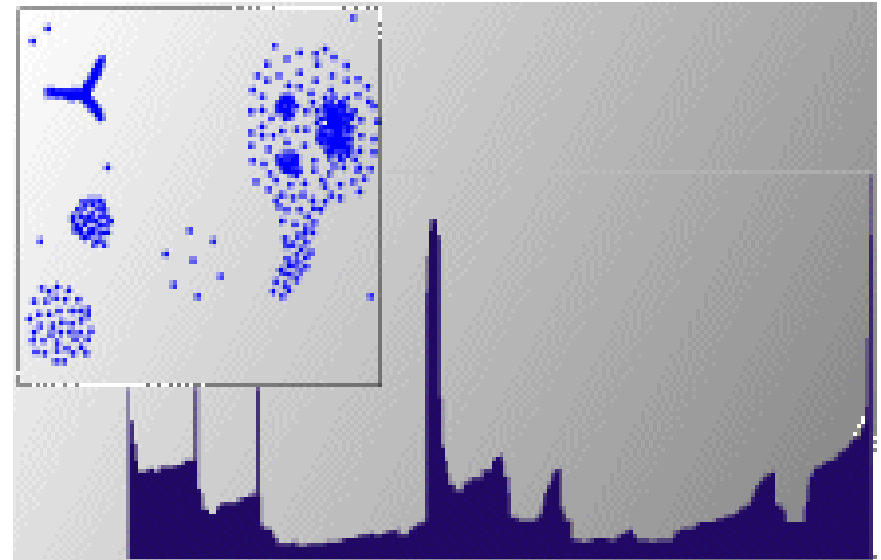
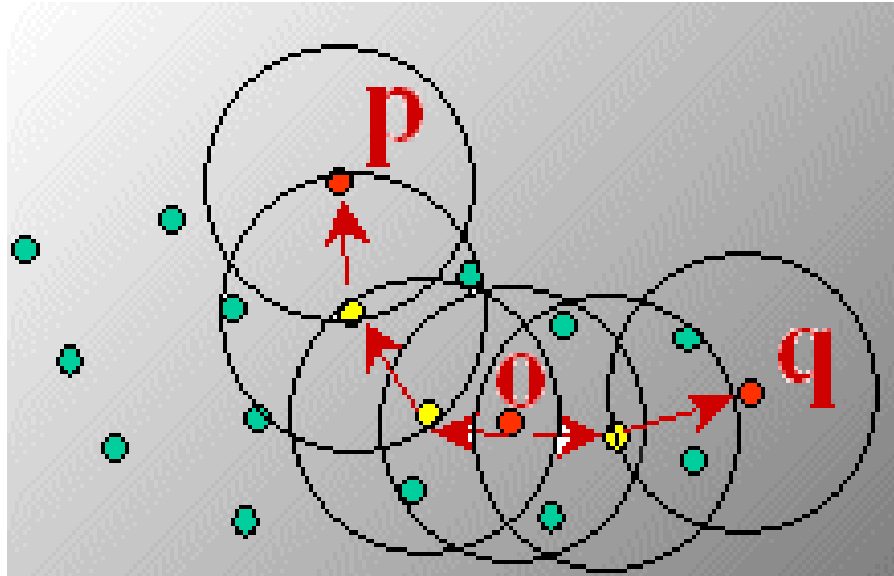
$r(p1, o) = 2.8\text{cm}$. $r(p2, o) = 4\text{cm}$



Reachability -distance



Density-Based Clustering: OPTICS & Its Applications



DENCLUE: Using Statistical Density Functions

- DENsity-based CLUstEring by Hinneburg & Keim (KDD'98)

- Using statistical density functions:

$$f_{Gaussian}(x, y) = e^{-\frac{d(x, y)^2}{2\sigma^2}}$$

influence of y
on x

$$f_{Gaussian}^D(x) = \sum_{i=1}^N e^{-\frac{d(x, x_i)^2}{2\sigma^2}}$$

total influence
on x

- Major features

$$\nabla f_{Gaussian}^D(x, x_i) = \sum_{i=1}^N (x_i - x) \cdot e^{-\frac{d(x, x_i)^2}{2\sigma^2}}$$

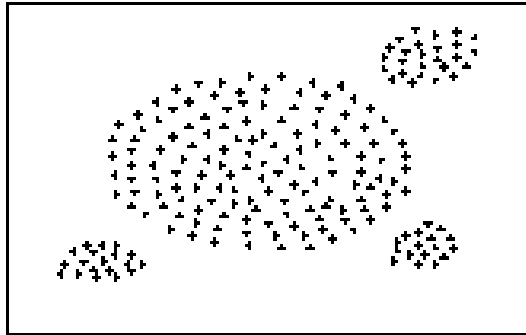
gradient of x in
the direction of
 x_i

- Solid mathematical foundation
- Good for data sets with large amounts of noise
- Allows a compact mathematical description of arbitrarily shaped clusters in high-dimensional data sets
- Significant faster than existing algorithm (e.g., DBSCAN)
- But needs a large number of parameters

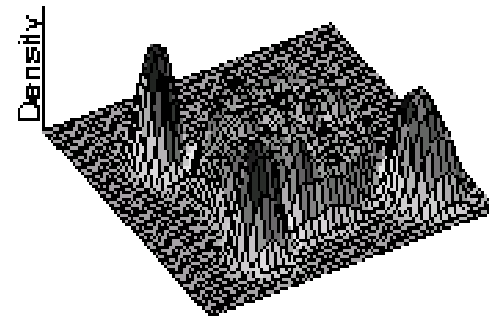
Denclue: Technical Essence

- Uses grid cells but only keeps information about grid cells that do actually contain data points and manages these cells in a tree-based access structure
- Influence function: describes the impact of a data point within its neighborhood
- Overall density of the data space can be calculated as the sum of the influence function of all data points
- Clusters can be determined mathematically by identifying density attractors
- Density attractors are local maximal of the overall density function
- Center defined clusters: assign to each density attractor the points density attracted to it
- Arbitrary shaped cluster: merge density attractors that are connected through paths of high density ($>$ threshold)

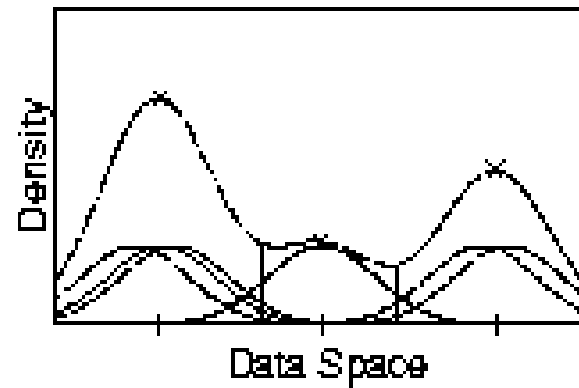
Density Attractor



(a) Data Set



(c) Gaussian



Center-Defined and Arbitrary

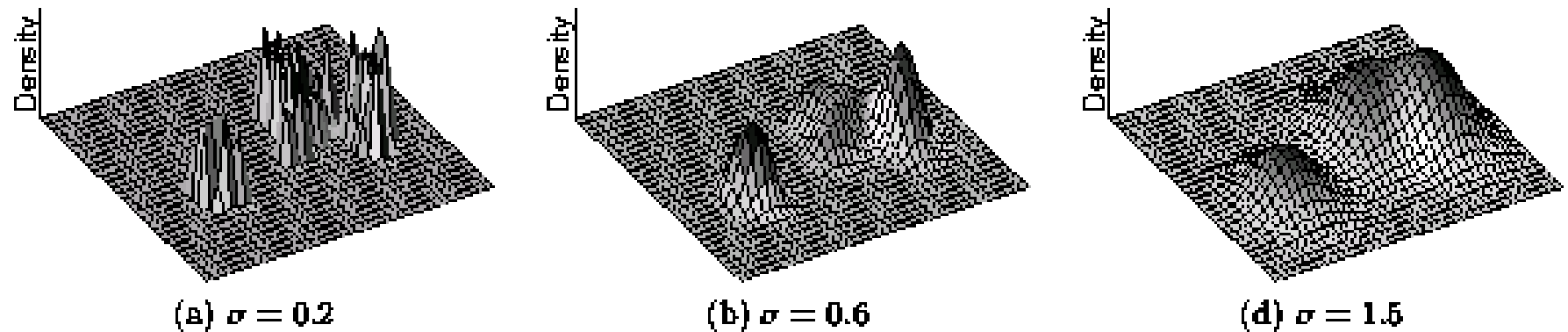


Figure 3: Example of Center-Defined Clusters for different σ

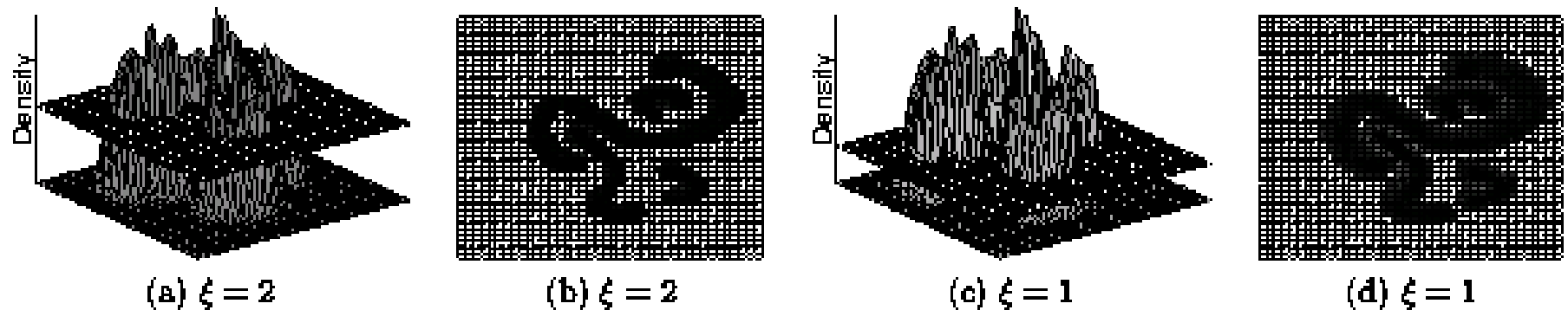



Figure 4: Example of Arbitrary-Shape Clusters for different ξ

Chapter 10. Cluster Analysis: Basic Concepts and Methods

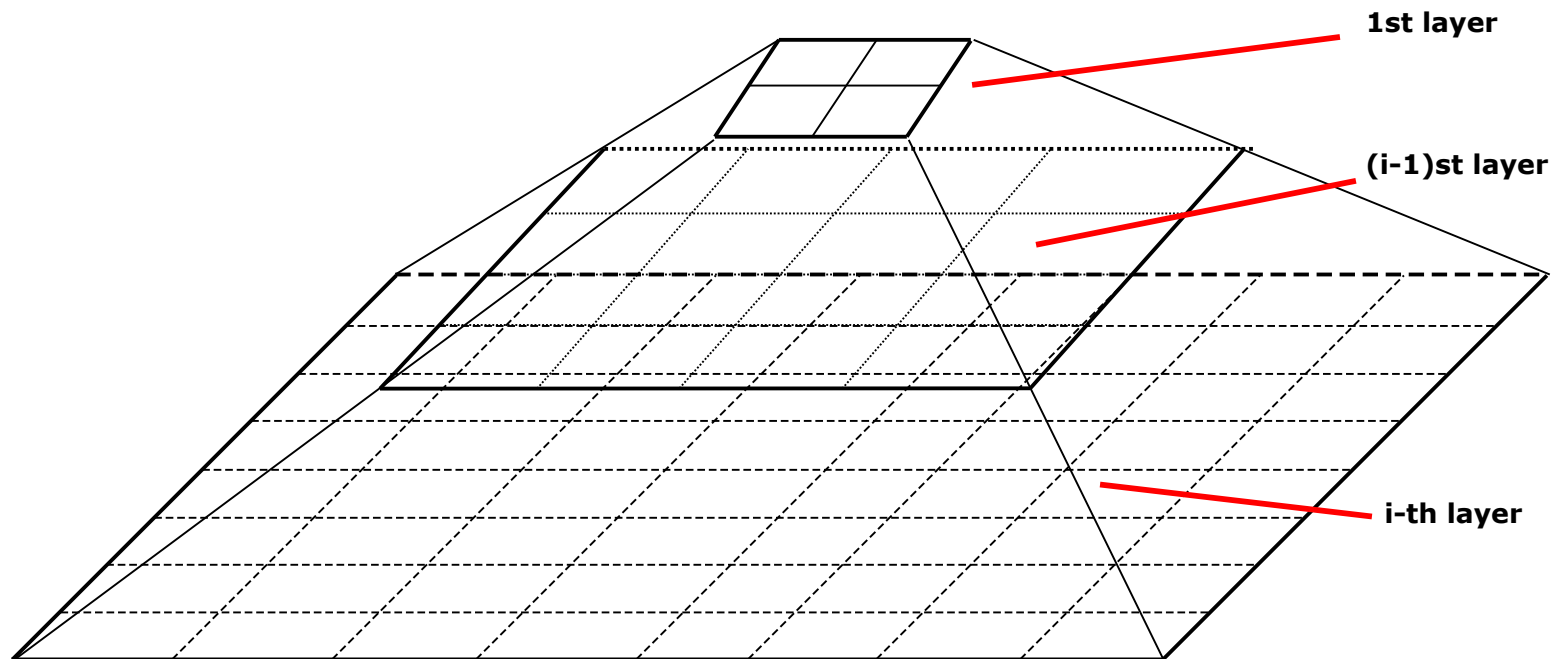
- Cluster Analysis: Basic Concepts
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Grid-Based Clustering Method

- Using multi-resolution grid data structure
- Several interesting methods
 - **STING** (a S**T**atistical **I**Nformation Grid approach) by Wang, Yang and Muntz (1997)
 - **WaveCluster** by Sheikholeslami, Chatterjee, and Zhang (VLDB'98)
 - A multi-resolution clustering approach using wavelet method
 - **CLIQUE**: Agrawal, et al. (SIGMOD'98)
 - Both grid-based and subspace clustering

STING: A Statistical Information Grid Approach

- Wang, Yang and Muntz (VLDB'97)
- The spatial area is divided into rectangular cells
- There are several levels of cells corresponding to different levels of resolution



The STING Clustering Method

- Each cell at a high level is partitioned into a number of smaller cells in the next lower level
- Statistical info of each cell is calculated and stored beforehand and is used to answer queries
- Parameters of higher level cells can be easily calculated from parameters of lower level cell
 - *count, mean, s, min, max*
 - type of distribution—*normal, uniform, etc.*
- Use a top-down approach to answer spatial data queries
- Start from a pre-selected layer—typically with a small number of cells
- For each cell in the current level compute the confidence interval

STING Algorithm and Its Analysis

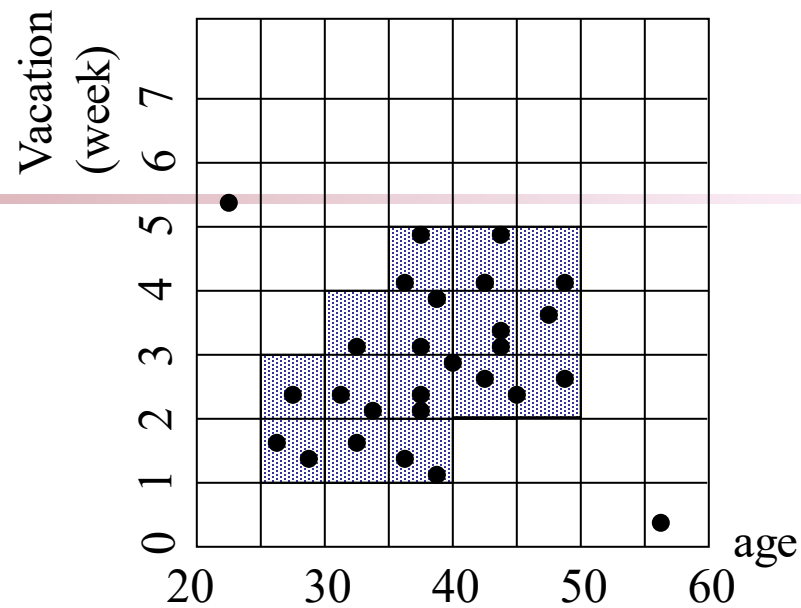
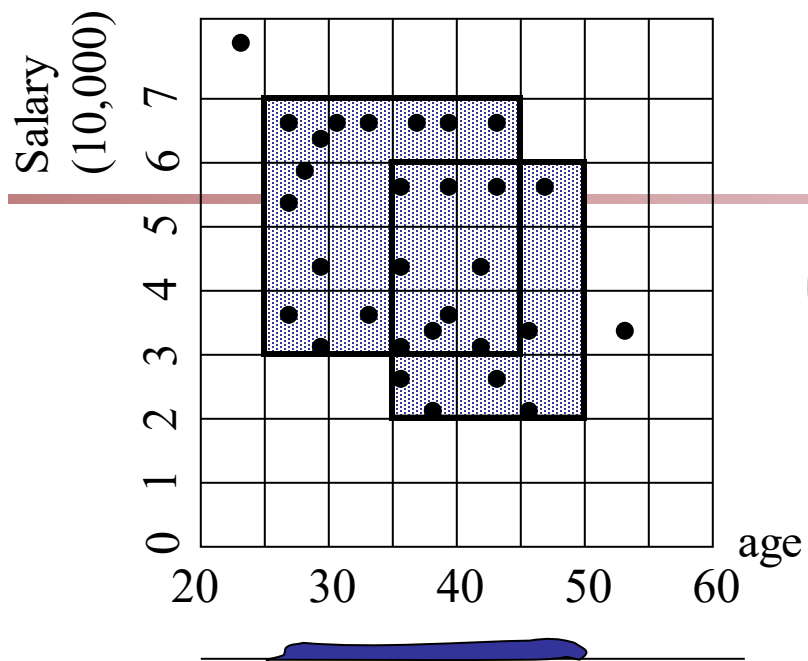
- Remove the irrelevant cells from further consideration
- When finish examining the current layer, proceed to the next lower level
- Repeat this process until the bottom layer is reached
- Advantages:
 - Query-independent, easy to parallelize, incremental update
 - $O(K)$, where K is the number of grid cells at the lowest level
- Disadvantages:
 - All the cluster boundaries are either horizontal or vertical, and no diagonal boundary is detected

CLIQUE (Clustering In QUEst)

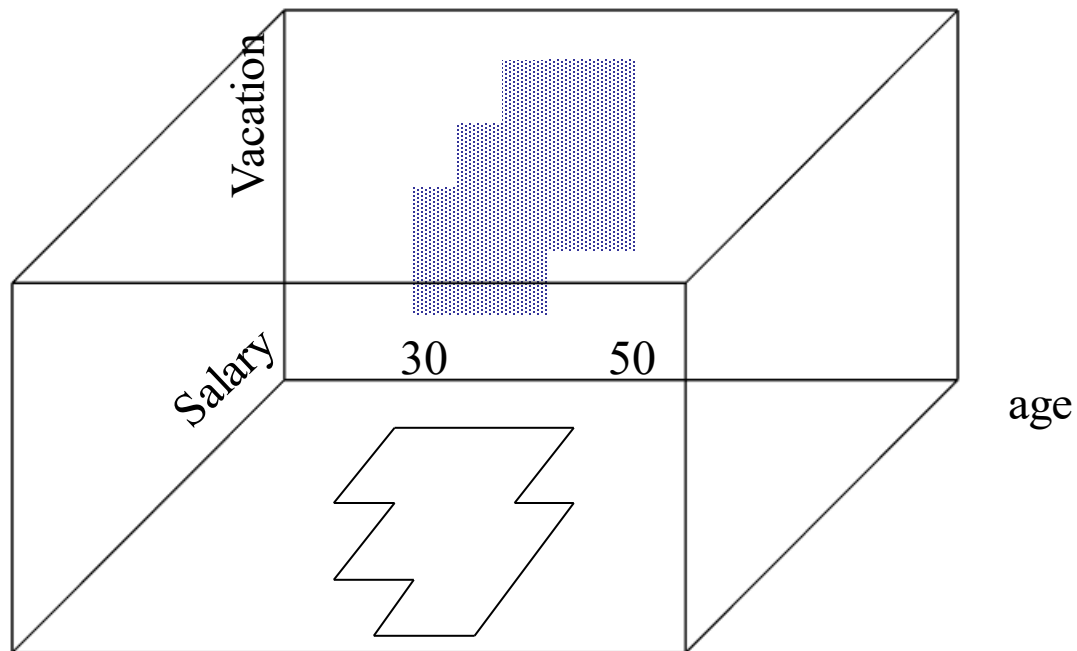
- Agrawal, Gehrke, Gunopulos, Raghavan (SIGMOD'98)
- Automatically identifying subspaces of a high dimensional data space that allow better clustering than original space
- CLIQUE can be considered as both density-based and grid-based
 - It partitions each dimension into the same number of equal length 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



$\tau = 3$



Strength and Weakness of *CLIQUE*


■ Strength

- *automatically* finds subspaces of the highest dimensionality such that high density clusters exist in those subspaces
- *insensitive* to the order of records in input and does not presume some canonical data distribution
- 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

Chapter 10. Cluster Analysis: Basic Concepts and Methods

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Assessing Clustering Tendency

- Assess if non-random structure exists in the data by measuring the probability that the data is generated by a uniform data distribution
- Test spatial randomness by statistic test: Hopkins Static
 - Given a dataset D regarded as a sample of a random variable o , determine how far away o is from being uniformly distributed in the data space
 - Sample n points, p_1, \dots, p_n , uniformly from D . For each p_i , find its nearest neighbor in D : $x_i = \min\{\text{dist}(p_i, v)\}$ where v in D
 - Sample n points, q_1, \dots, q_n , uniformly from D . For each q_i , find its nearest neighbor in $D - \{q_i\}$: $y_i = \min\{\text{dist}(q_i, v)\}$ where v in D and $v \neq q_i$
 - Calculate the Hopkins Statistic:
$$H = \frac{\sum_{i=1}^n y_i}{\sum_{i=1}^n x_i + \sum_{i=1}^n y_i}$$
 - If D is uniformly distributed, $\sum x_i$ and $\sum y_i$ will be close to each other and H is close to 0.5. If D is highly skewed, H is close to 0

Determine the Number of Clusters

- Empirical method
 - # of clusters $\approx \sqrt{n/2}$ for a dataset of n points
- Elbow method
 - Use the turning point in the curve of sum of within cluster variance w.r.t the # of clusters
- Cross validation method
 - Divide a given data set into m parts
 - Use $m - 1$ parts to obtain a clustering model
 - Use the remaining part to test the quality of the clustering
 - E.g., For each point in the test set, find the closest centroid, and use the sum of squared distance between all points in the test set and the closest centroids to measure how well the model fits the test set
 - For any $k > 0$, repeat it m times, compare the overall quality measure w.r.t. different k 's, and find # of clusters that fits the data the best


Measuring Clustering Quality

- Two methods: extrinsic vs. intrinsic
- Extrinsic: supervised, i.e., the ground truth is available
 - Compare a clustering against the ground truth using certain clustering quality measure
 - Ex. BCubed precision and recall metrics
- Intrinsic: unsupervised, i.e., the ground truth is unavailable
 - Evaluate the goodness of a clustering by considering how well the clusters are separated, and how compact the clusters are
 - Ex. Silhouette coefficient

Measuring Clustering Quality: Extrinsic Methods

- Clustering quality measure: $Q(C, C_g)$, for a clustering C given the ground truth C_g .
- Q is good if it satisfies the following 4 essential criteria
 - Cluster homogeneity: the purer, the better
 - Cluster completeness: should assign objects belong to the same category in the ground truth to the same cluster
 - Rag bag: putting a heterogeneous object into a pure cluster should be penalized more than putting it into a *rag bag* (i.e., “miscellaneous” or “other” category)
 - Small cluster preservation: splitting a small category into pieces is more harmful than splitting a large category into pieces

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Summary

- **Cluster analysis** groups objects based on their **similarity** and has wide applications
- Measure of similarity can be computed for **various types of data**
- Clustering algorithms can be **categorized** into partitioning methods, hierarchical methods, density-based methods, grid-based methods, and model-based methods
- **K-means** and **K-medoids** algorithms are popular partitioning-based clustering algorithms
- **Birch** and **Chameleon** are interesting hierarchical clustering algorithms, and there are also probabilistic hierarchical clustering algorithms
- **DBSCAN**, **OPTICS**, and **DENCLU** are interesting density-based algorithms
- **STING** and **CLIQUE** are grid-based methods, where **CLIQUE** is also a subspace clustering algorithm
- Quality of clustering results can be evaluated in various ways

CS512-Spring 2011: An Introduction

- Coverage
 - Cluster Analysis: Chapter 11
 - Outlier Detection: Chapter 12
 - Mining Sequence Data: BK2: Chapter 8
 - Mining Graphs Data: BK2: Chapter 9
 - Social and Information Network Analysis
 - BK2: Chapter 9
 - Partial coverage: Mark Newman: “Networks: An Introduction”, Oxford U., 2010
 - Scattered coverage: Easley and Kleinberg, “Networks, Crowds, and Markets: Reasoning About a Highly Connected World”, Cambridge U., 2010
 - Recent research papers
 - Mining Data Streams: BK2: Chapter 8
- Requirements
 - One research project
 - One class presentation (15 minutes)
 - Two homeworks (no programming assignment)
 - Two midterm exams (no final exam)

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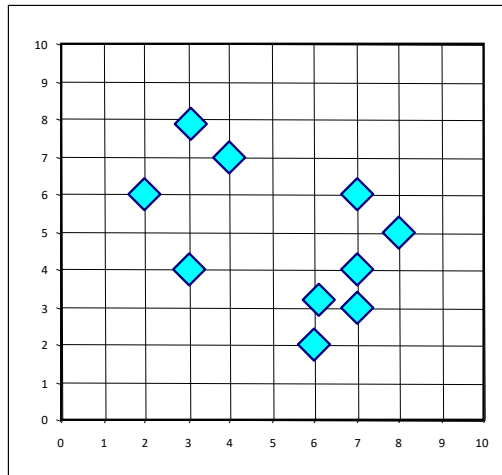
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- G. J. McLachlan and K.E. Bkasford. Mixture Models: Inference and Applications to Clustering. John Wiley and Sons, 1988.
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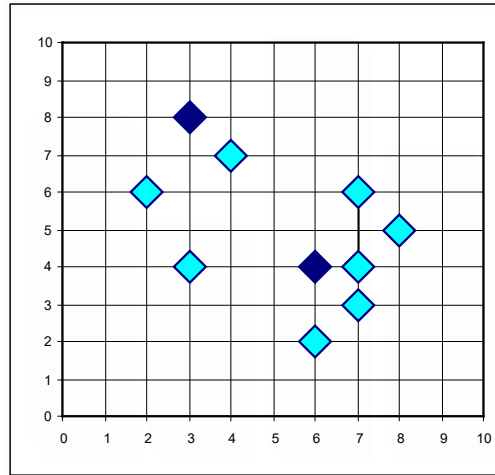
Slides unused in class

A Typical K-Medoids Algorithm (PAM)

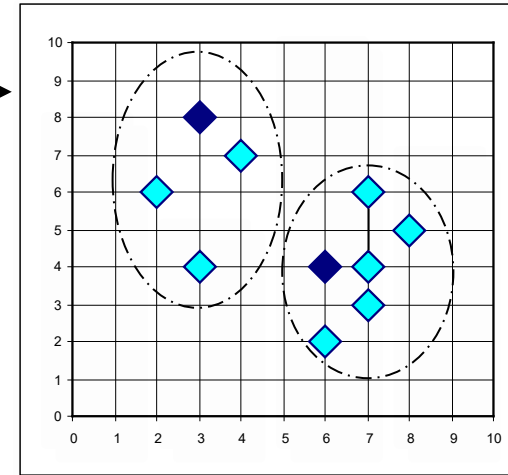
Total Cost = 20



Arbitrary
choose k
object as
initial
medoids



Assign
each remainin
g object to
nearest
medoids

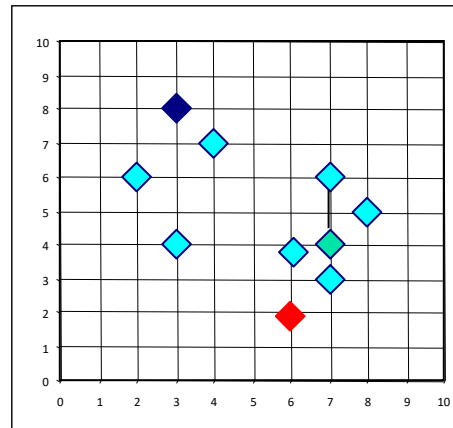


$K=2$

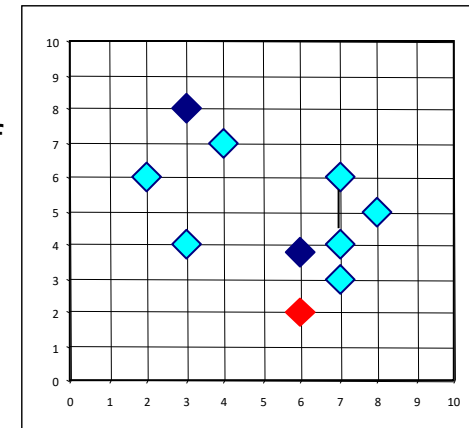
**Do loop
Until no
change**

Swapping O
and O_{random}
If quality is
improved.

Total Cost = 26



Compute
total cost of
swapping

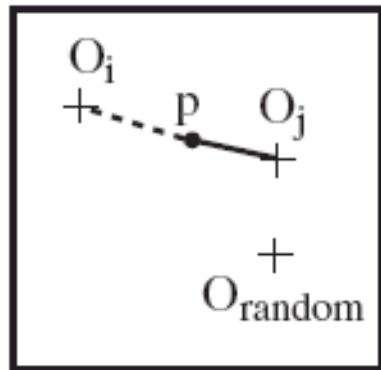


PAM (Partitioning Around Medoids) (1987)

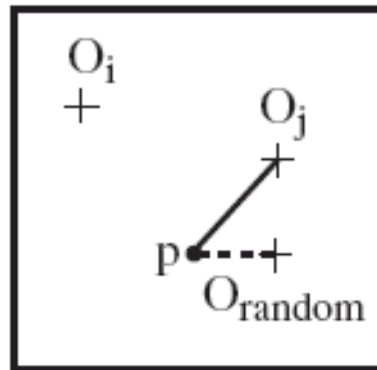
- PAM (Kaufman and Rousseeuw, 1987), built in Splus
- Use real object to represent the cluster
 - Select k representative objects arbitrarily
 - For each pair of non-selected object h and selected object i , calculate the total swapping cost TC_{ih}
 - For each pair of i and h ,
 - If $TC_{ih} < 0$, i is replaced by h
 - Then assign each non-selected object to the most similar representative object
 - repeat steps 2-3 until there is no change

PAM Clustering: Finding the Best Cluster Center

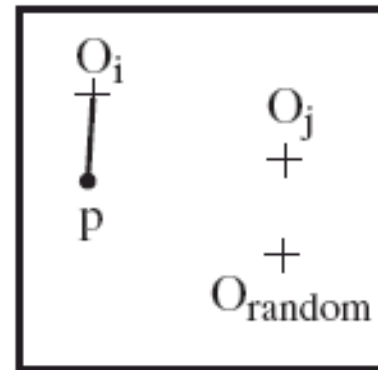
- Case 1: p currently belongs to o_j . If o_j is replaced by o_{random} as a representative object and p is the closest to one of the other representative object o_i , then p is reassigned to o_i



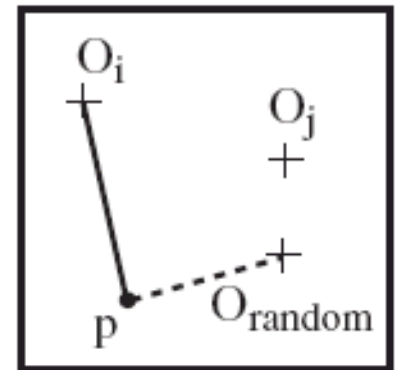
1. Reassigned to O_i



2. Reassigned to O_{random}



3. No change



4. Reassigned to O_{random}

- data object
- + cluster center
- before swapping
- after swapping

What Is the Problem with PAM?

- Pam is more robust than k-means in the presence of noise and outliers because a medoid is less influenced by outliers or other extreme values than a mean
- Pam works efficiently for small data sets but does not **scale well** for large data sets.
 - $O(k(n-k)^2)$ for each iteration

where n is # of data, k is # of clusters

➔ Sampling-based method

CLARA(Clustering LARge Applications)

CLARA (Clustering Large Applications) (1990)

- CLARA (Kaufmann and Rousseeuw in 1990)
 - Built in statistical analysis packages, such as SPlus
 - It draws *multiple samples* of the data set, applies *PAM* on each sample, and gives the best clustering as the output
- Strength: deals with larger data sets than *PAM*
- Weakness:
 - Efficiency depends on the sample size
 - A good clustering based on samples will not necessarily represent a good clustering of the whole data set if the sample is biased

***CLARANS* (“Randomized” CLARA) (1994)**

- **CLARANS** (A Clustering Algorithm based on Randomized Search) (Ng and Han'94)
 - Draws sample of neighbors dynamically
 - The clustering process can be presented as searching a graph where every node is a potential solution, that is, a set of k medoids
 - If the local optimum is found, *it* starts with new randomly selected node in search for a new local optimum
- Advantages: More efficient and scalable than both *PAM* and *CLARA*
- Further improvement: Focusing techniques and spatial access structures (Ester et al.'95)

ROCK: Clustering Categorical Data

- ROCK: RObust Clustering using linkS
 - S. Guha, R. Rastogi & K. Shim, ICDE'99
- Major ideas
 - Use links to measure similarity/proximity
 - Not distance-based
- Algorithm: sampling-based clustering
 - Draw random sample
 - Cluster with links
 - Label data in disk
- Experiments
 - Congressional voting, mushroom data

Similarity Measure in ROCK

- Traditional measures for categorical data may not work well, e.g., Jaccard coefficient
- Example: Two groups (clusters) of transactions
 - C_1 . $\langle a, b, c, d, e \rangle$: $\{a, b, c\}, \{a, b, d\}, \{a, b, e\}, \{a, c, d\}, \{a, c, e\}, \{a, d, e\}, \{b, c, d\}, \{b, c, e\}, \{b, d, e\}, \{c, d, e\}$
 - C_2 . $\langle a, b, f, g \rangle$: $\{a, b, f\}, \{a, b, g\}, \{a, f, g\}, \{b, f, g\}$
- Jaccard co-efficient may lead to wrong clustering result
 - C_1 : 0.2 ($\{a, b, c\}, \{b, d, e\}$) to 0.5 ($\{a, b, c\}, \{a, b, d\}$)
 - C_1 & C_2 : could be as high as 0.5 ($\{a, b, c\}, \{a, b, f\}$)
- Jaccard co-efficient-based similarity function:

$$Sim(T_1, T_2) = \frac{|T_1 \cap T_2|}{|T_1 \cup T_2|}$$

- Ex. Let $T_1 = \{a, b, c\}$, $T_2 = \{c, d, e\}$

$$Sim(T_1, T_2) = \frac{|\{c\}|}{|\{a, b, c, d, e\}|} = \frac{1}{5} = 0.2$$

Link Measure in ROCK

■ Clusters

- $C_1: \langle a, b, c, d, e \rangle: \{a, b, c\}, \{a, b, d\}, \{a, b, e\}, \{a, c, d\}, \{a, c, e\}, \{a, d, e\}, \{b, c, d\}, \{b, c, e\}, \{b, d, e\}, \{c, d, e\}$
- $C_2: \langle a, b, f, g \rangle: \{a, b, f\}, \{a, b, g\}, \{a, f, g\}, \{b, f, g\}$

■ Neighbors

- Two transactions are neighbors if $\text{sim}(T_1, T_2) > \text{threshold}$
- Let $T_1 = \{a, b, c\}$, $T_2 = \{c, d, e\}$, $T_3 = \{a, b, f\}$
 - T_1 connected to: $\{a, b, d\}, \{a, b, e\}, \{a, c, d\}, \{a, c, e\}, \{b, c, d\}, \{b, c, e\}, \{a, b, f\}, \{a, b, g\}$
 - T_2 connected to: $\{a, c, d\}, \{a, c, e\}, \{a, d, e\}, \{b, c, e\}, \{b, d, e\}, \{b, c, d\}$
 - T_3 connected to: $\{a, b, c\}, \{a, b, d\}, \{a, b, e\}, \{a, b, g\}, \{a, f, g\}, \{b, f, g\}$

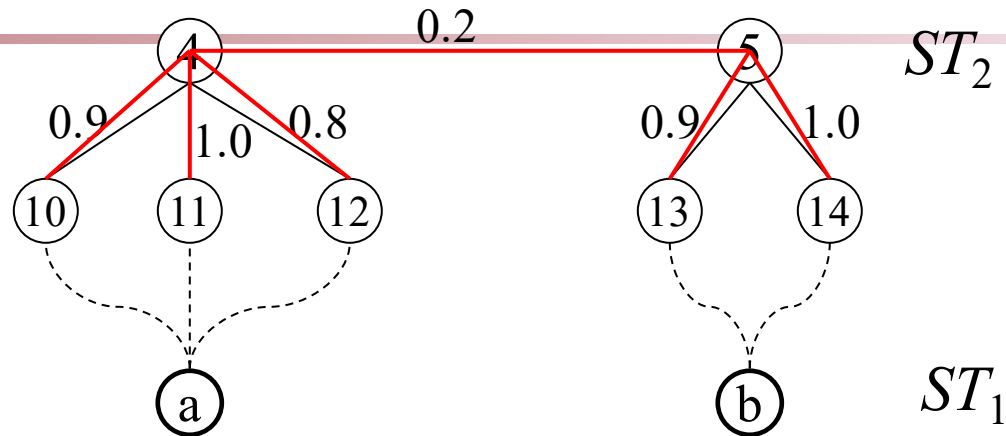
■ Link Similarity

- Link similarity between two transactions is the # of common neighbors
- $\text{link}(T_1, T_2) = 4$, *since they have 4 common neighbors*
 - $\{a, c, d\}, \{a, c, e\}, \{b, c, d\}, \{b, c, e\}$
- $\text{link}(T_1, T_3) = 3$, *since they have 3 common neighbors*
 - $\{a, b, d\}, \{a, b, e\}, \{a, b, g\}$

Rock Algorithm

- Method
 - Compute similarity matrix
 - Use link similarity
 - Run agglomerative hierarchical clustering
 - When the data set is big
 - Get sample of transactions
 - Cluster sample
- Problems:
 - Guarantee cluster interconnectivity
 - any two transactions in a cluster are very well connected
 - Ignores information about closeness of two clusters
 - two separate clusters may still be quite connected

Aggregation-Based Similarity Computation



For each node $n_k \in \{n_{10}, n_{11}, n_{12}\}$ and $n_l \in \{n_{13}, n_{14}\}$, their path-based similarity $sim_p(n_k, n_l) = s(n_k, n_4) \cdot s(n_4, n_5) \cdot s(n_5, n_l)$.

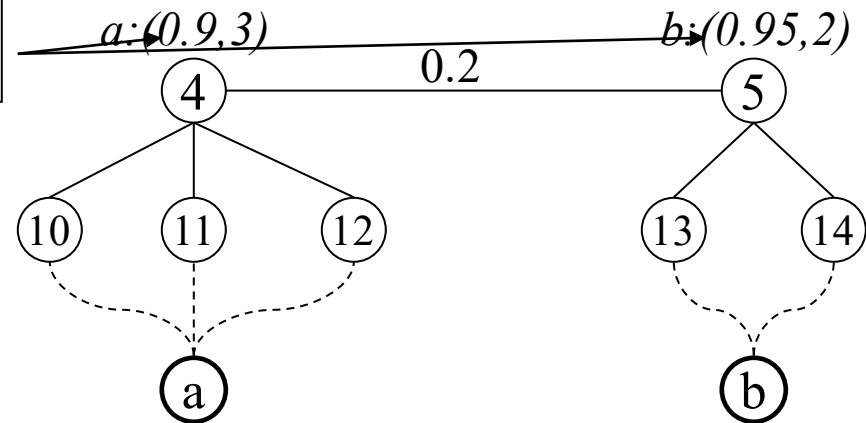
$$sim(n_a, n_b) = \frac{\sum_{k=10}^{12} s(n_k, n_4)}{3} \cdot s(n_4, n_5) \cdot \frac{\sum_{l=13}^{14} s(n_l, n_5)}{2} = 0.171$$

takes $O(3+2)$ time

After aggregation, we reduce quadratic time computation to linear time computation.

Computing Similarity with Aggregation

Average similarity
and total weight




$sim(n_a, n_b)$ can be computed
from aggregated similarities

$$sim(n_a, n_b) = avg_sim(n_a, n_4) \times s(n_4, n_5) \times avg_sim(n_b, n_5) \\ = 0.9 \times 0.2 \times 0.95 = 0.171$$

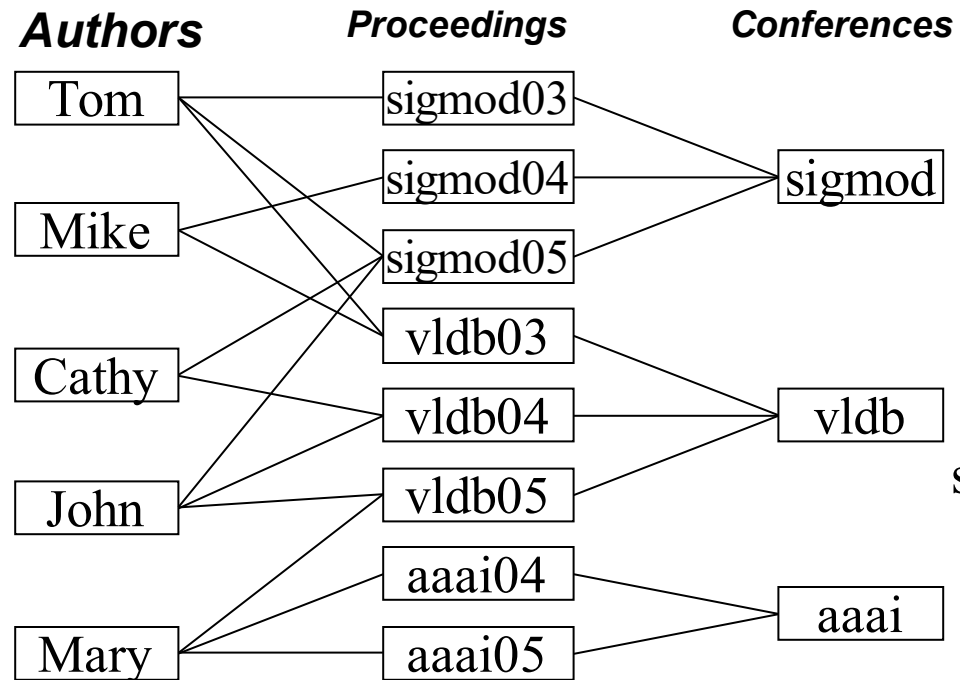
To compute $sim(n_a, n_b)$:

- Find all pairs of sibling nodes n_i and n_j , so that n_a linked with n_i and n_b with n_j .
- Calculate similarity (and weight) between n_a and n_b w.r.t. n_i and n_j .
- Calculate weighted average similarity between n_a and n_b w.r.t. all such pairs.

Chapter 10. Cluster Analysis: Basic Concepts and Methods

- Cluster Analysis: Basic Concepts
- Overview of Clustering Methods
- Partitioning Methods
- Hierarchical Methods
- Density-Based Methods 
- Grid-Based Methods
- Summary

Link-Based Clustering: Calculate Similarities Based On Links



- The similarity between two objects x and y is defined as the average similarity between objects linked with x and those with y :

$$\text{sim}(a, b) = \frac{C}{|I(a)||I(b)|} \sum_{i=1}^{|I(a)|} \sum_{j=1}^{|I(b)|} \text{sim}(I_i(a), I_j(b))$$

- Issue: Expensive to compute:
 - For a dataset of N objects and M links, it takes $O(N^2)$ space and $O(M^2)$ time to compute all similarities.

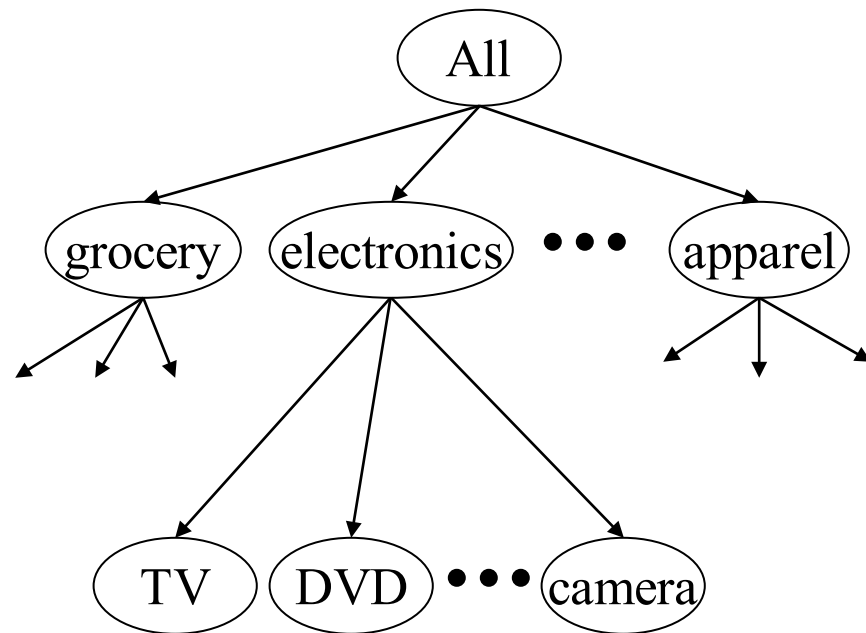
Jeh & Widom, KDD'2002: *SimRank*

Two objects are similar if they are linked with the same or similar objects

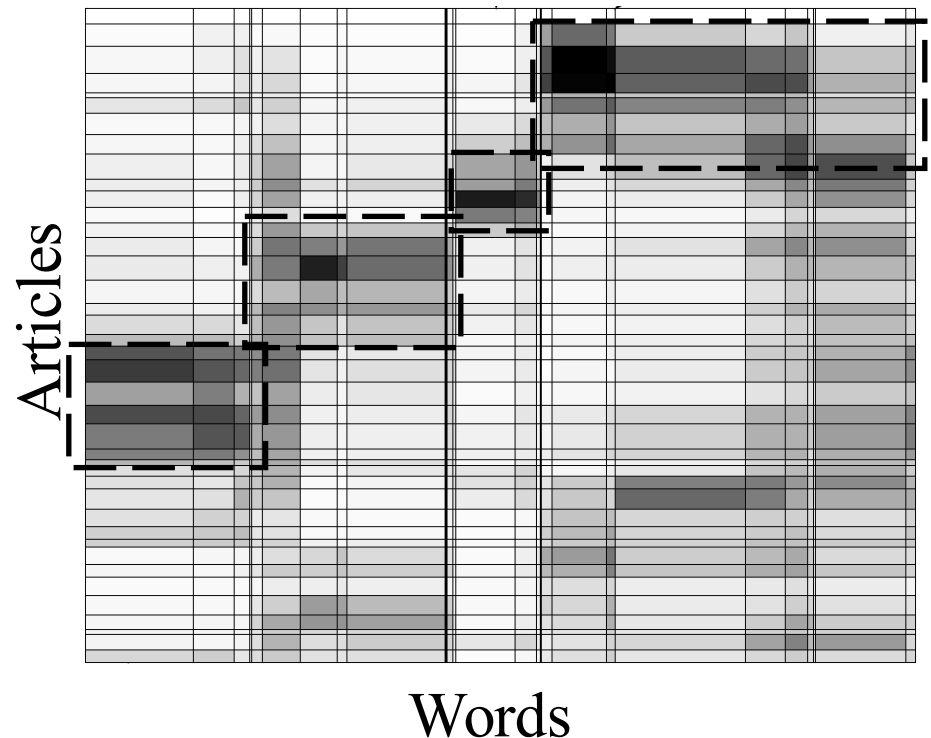
Observation 1: Hierarchical Structures

- Hierarchical structures often exist naturally among objects (e.g., taxonomy of animals)

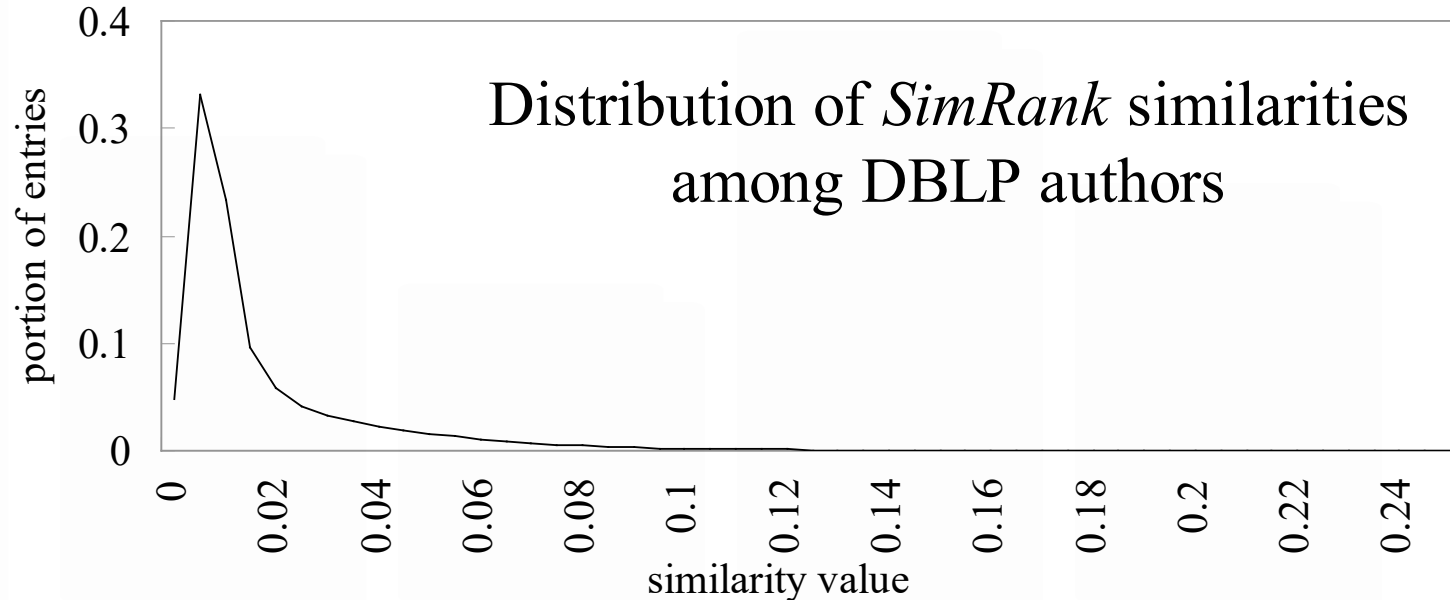
A hierarchical structure of products in Walmart



Relationships between articles and words (Chakrabarti, Papadimitriou, Modha, Faloutsos, 2004)

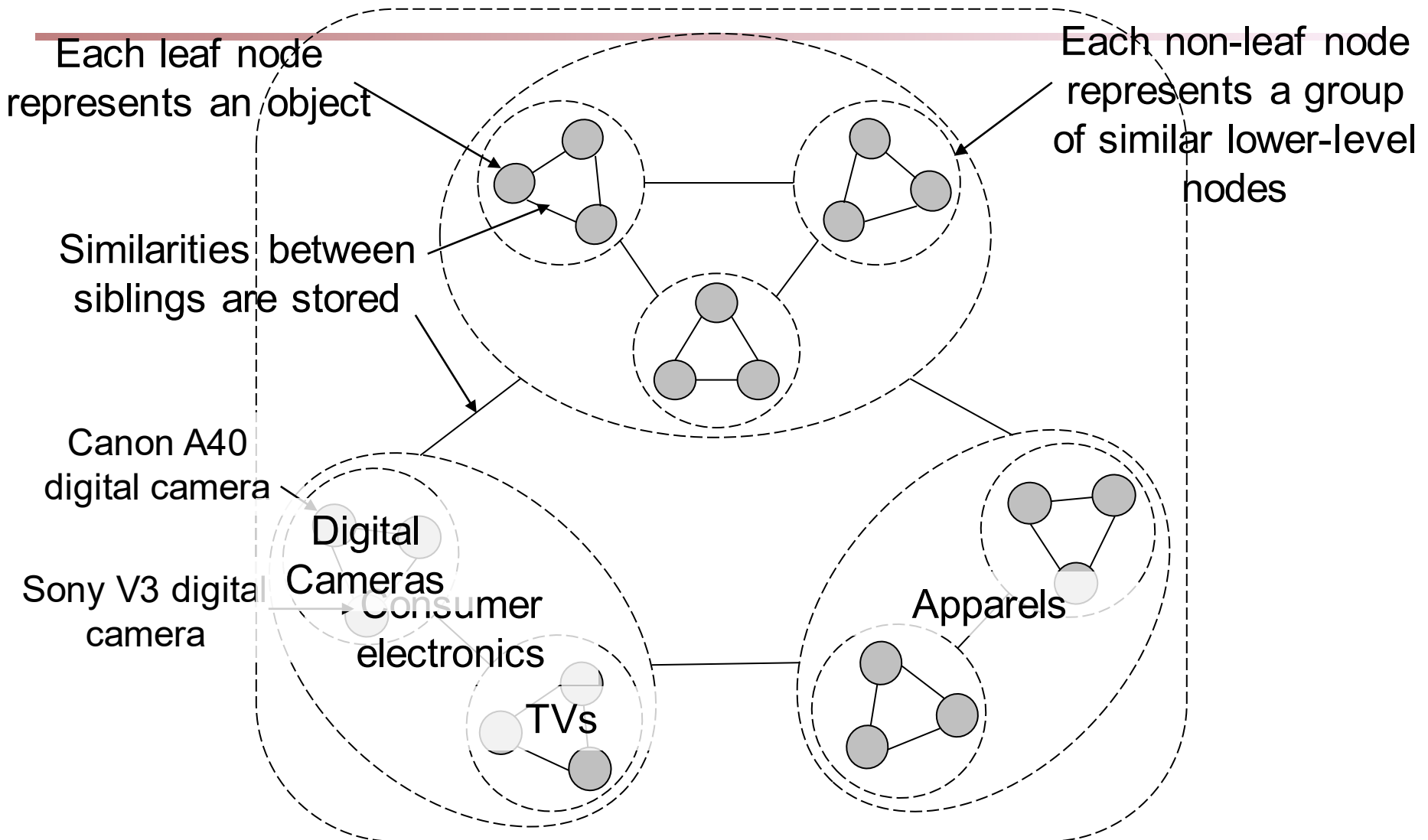


Observation 2: Distribution of Similarity

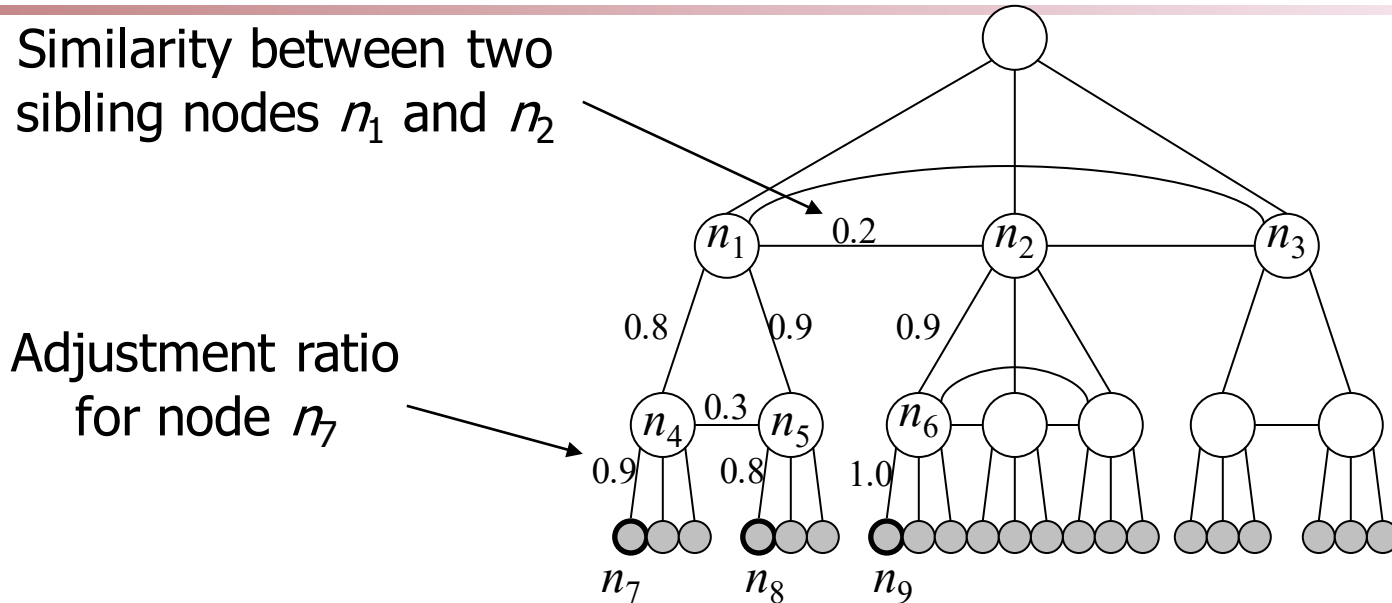


- Power law distribution exists in similarities
 - 56% of similarity entries are in $[0.005, 0.015]$
 - 1.4% of similarity entries are larger than 0.1
 - Can we design a data structure that stores the significant similarities and compresses insignificant ones?

A Novel Data Structure: SimTree



Similarity Defined by SimTree



- Path-based node similarity

- $sim_p(n_7, n_8) = s(n_7, n_4) \times s(n_4, n_5) \times s(n_5, n_8)$

- Similarity between two nodes is the average similarity between objects linked with them in other SimTrees

- Adjust/ ratio for $x = \frac{\text{Average similarity between } x \text{ and all other nodes}}{\text{Average similarity between } x\text{'s parent and all other nodes}}$

LinkClus: Efficient Clustering via Heterogeneous Semantic Links

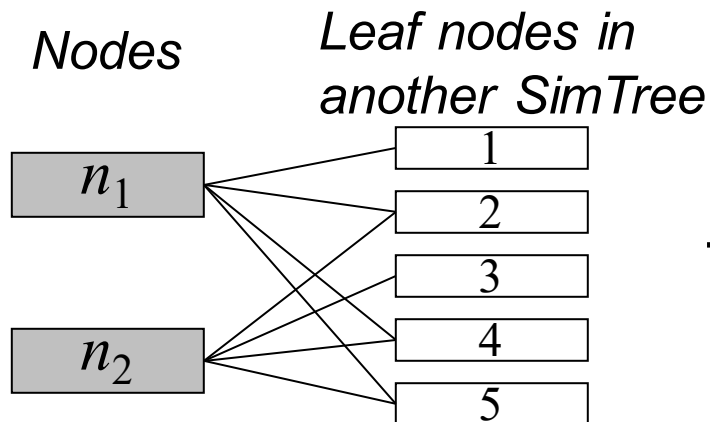
Method

- Initialize a SimTree for objects of each type
- Repeat until stable
 - For each SimTree, update the similarities between its nodes using similarities in other SimTrees
 - Similarity between two nodes x and y is the average similarity between objects linked with them
 - Adjust the structure of each SimTree
 - Assign each node to the parent node that it is most similar to

For details: X. Yin, J. Han, and P. S. Yu, “LinkClus: Efficient Clustering via Heterogeneous Semantic Links”, VLDB'06

Initialization of SimTrees

- Initializing a SimTree
 - Repeatedly find groups of tightly related nodes, which are merged into a higher-level node
- Tightness of a group of nodes
 - For a group of nodes $\{n_1, \dots, n_k\}$, its tightness is defined as the number of leaf nodes in other SimTrees that are connected to all of $\{n_1, \dots, n_k\}$

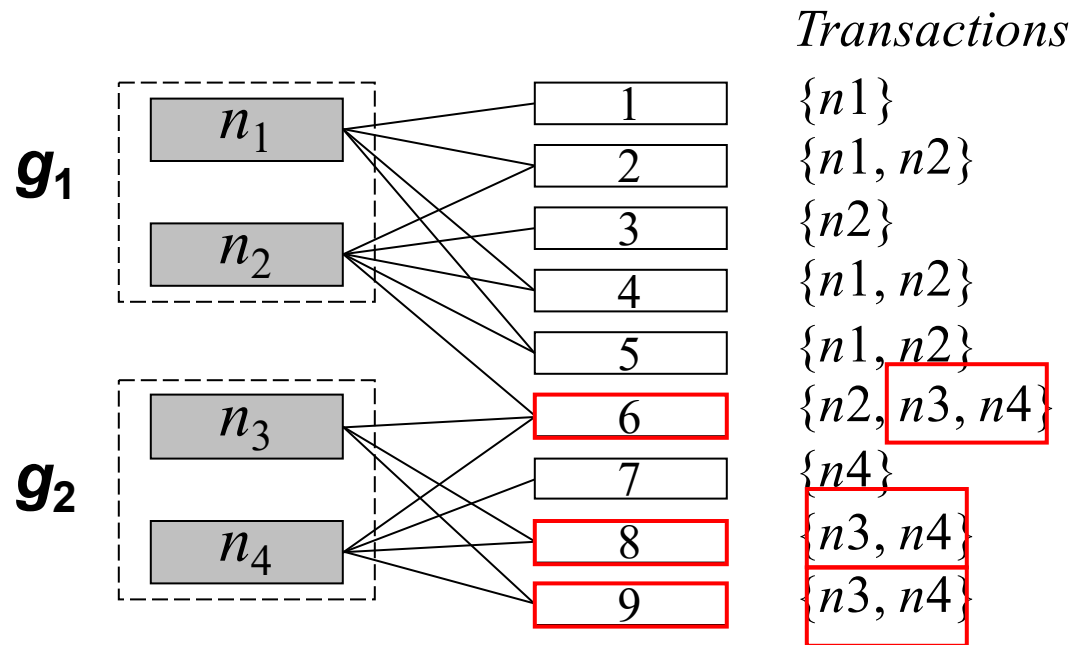


The tightness of $\{n_1, n_2\}$ is 3

Finding Tight Groups by Freq. Pattern Mining

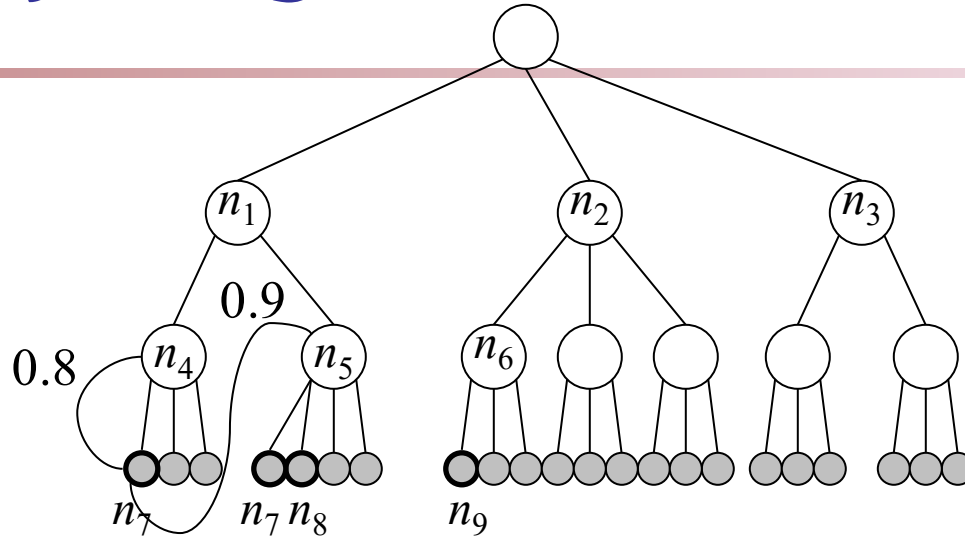
- Finding tight groups \longrightarrow Frequent pattern mining
Reduced to

The tightness of a group of nodes is the support of a frequent pattern



- Procedure of initializing a tree
 - Start from leaf nodes (level-0)
 - At each level l , find non-overlapping groups of similar nodes with frequent pattern mining

Adjusting SimTree Structures



- After similarity changes, the tree structure also needs to be changed
 - If a node is more similar to its parent's sibling, then move it to be a child of that sibling
 - Try to move each node to its parent's sibling that it is most similar to, under the constraint that each parent node can have at most c children

Complexity

For two types of objects, N in each, and M linkages between them.

	Time	Space
Updating similarities	$O(M(\log N)^2)$	$O(M+N)$
Adjusting tree structures	$O(N)$	$O(N)$
<i>LinkClus</i>	$O(M(\log N)^2)$	$O(M+N)$
<i>SimRank</i>	$O(M^2)$	$O(N^2)$

Experiment: Email Dataset

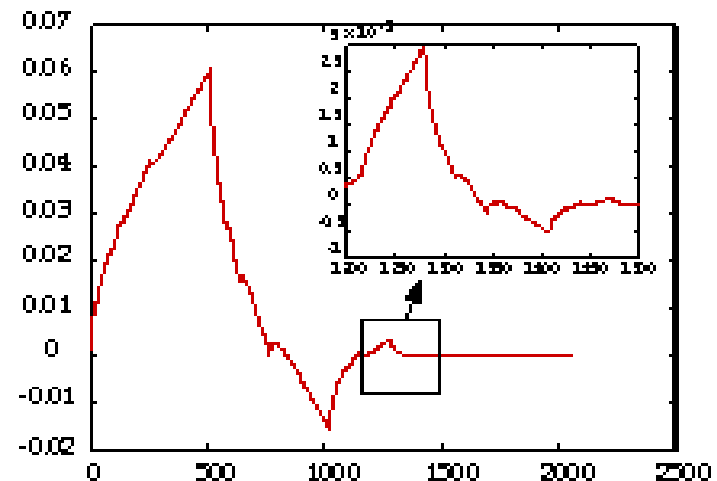
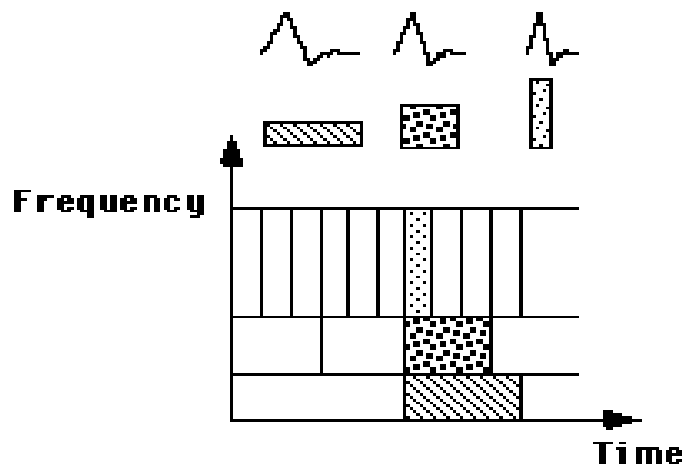
- F. Nielsen. Email dataset.
www.imm.dtu.dk/~rem/data/Email-1431.zip
- 370 emails on conferences, 272 on jobs, and 789 spam emails
- Accuracy: measured by manually labeled data
- Accuracy of clustering: % of pairs of objects in the same cluster that share common label

<i>Approach</i>	<i>Accuracy</i>	<i>time (s)</i>
LinkClus	0.8026	1579.6
SimRank	0.7965	39160
ReCom	0.5711	74.6
F-SimRank	0.3688	479.7
CLARANS	0.4768	8.55

- Approaches compared:
 - SimRank (Jeh & Widom, KDD 2002): Computing pair-wise similarities
 - SimRank with FingerPrints (F-SimRank): Fogaras & R'acz, WWW 2005
 - pre-computes a large sample of random paths from each object and uses samples of two objects to estimate SimRank similarity
 - ReCom (Wang et al. SIGIR 2003)
 - Iteratively clustering objects using cluster labels of linked objects

WaveCluster: Clustering by Wavelet Analysis (1998)

- Sheikholeslami, Chatterjee, and Zhang (VLDB'98)
- A multi-resolution clustering approach which applies wavelet transform to the feature space; both grid-based and density-based
- Wavelet transform: A signal processing technique that decomposes a signal into different frequency sub-band
 - Data are transformed to preserve relative distance between objects at different levels of resolution
 - Allows natural clusters to become more distinguishable



The WaveCluster Algorithm

- How to apply wavelet transform to find clusters
 - Summarizes the data by imposing a multidimensional grid structure onto data space
 - These multidimensional spatial data objects are represented in a n-dimensional feature space
 - Apply wavelet transform on feature space to find the dense regions in the feature space
 - Apply wavelet transform multiple times which result in clusters at different scales from fine to coarse
- Major features:
 - Complexity $O(N)$
 - Detect arbitrary shaped clusters at different scales
 - Not sensitive to noise, not sensitive to input order
 - Only applicable to low dimensional data

Quantization & Transformation

- Quantize data into m-D grid struc then wavelet transform
 - a) scale 1: high resolution
 - b) scale 2: medium resolution
 - c) scale 3: low resolution

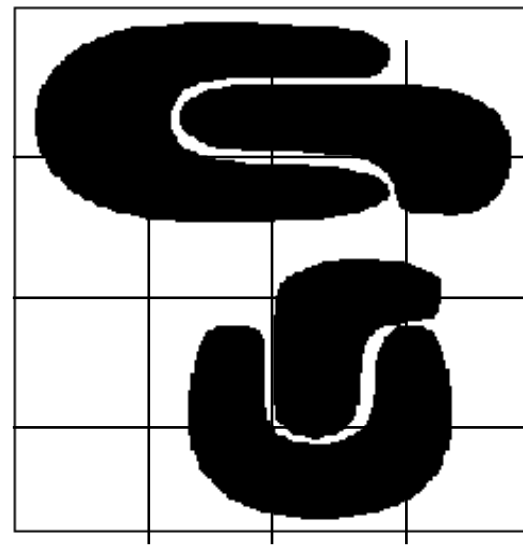
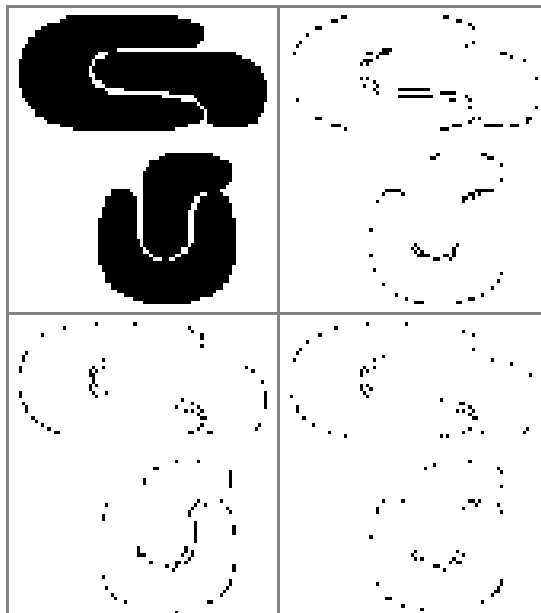


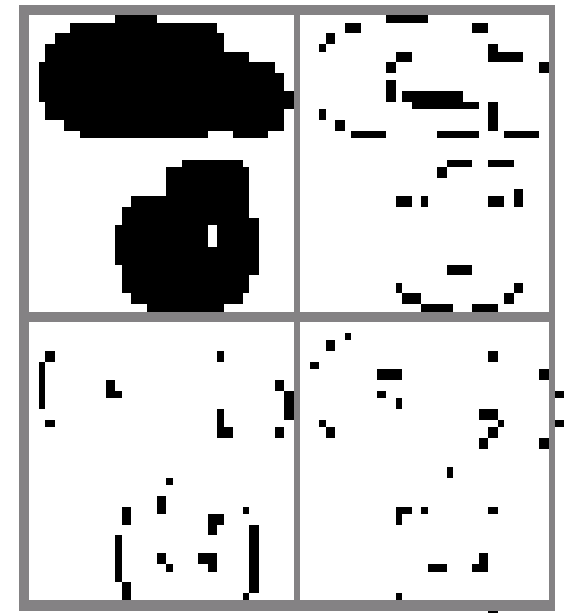
Figure 1: A sample 2-dimensional feature space.



a)



b)



c)