

# **Data Mining:**

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## **Concepts and Techniques**

**(3<sup>rd</sup> ed.)**

### **— Chapter 11 —**

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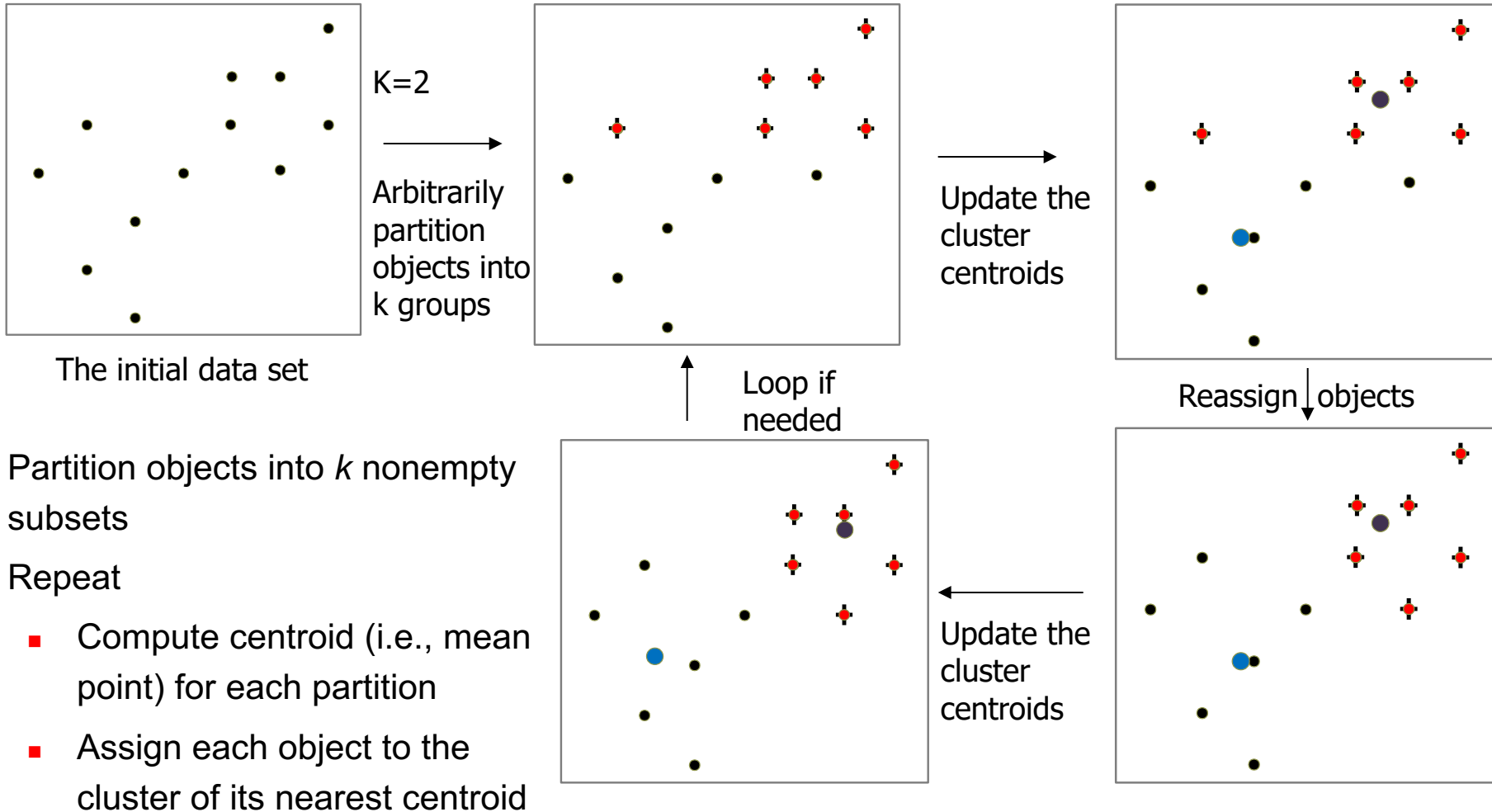
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# Review: Basic Cluster Analysis Methods (Chap. 10)

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- Cluster Analysis: Basic Concepts
  - Group data so that object similarity is high within clusters but low across clusters
- Partitioning Methods
  - K-means and k-medoids algorithms and their refinements
- Hierarchical Methods
  - Agglomerative and divisive method, Birch, Cameleon
- Density-Based Methods
  - DBScan, Optics and DenCLu
- Grid-Based Methods
  - STING and CLIQUE (subspace clustering)
- Evaluation of Clustering
  - Assess clustering tendency, determine # of clusters, and measure clustering quality

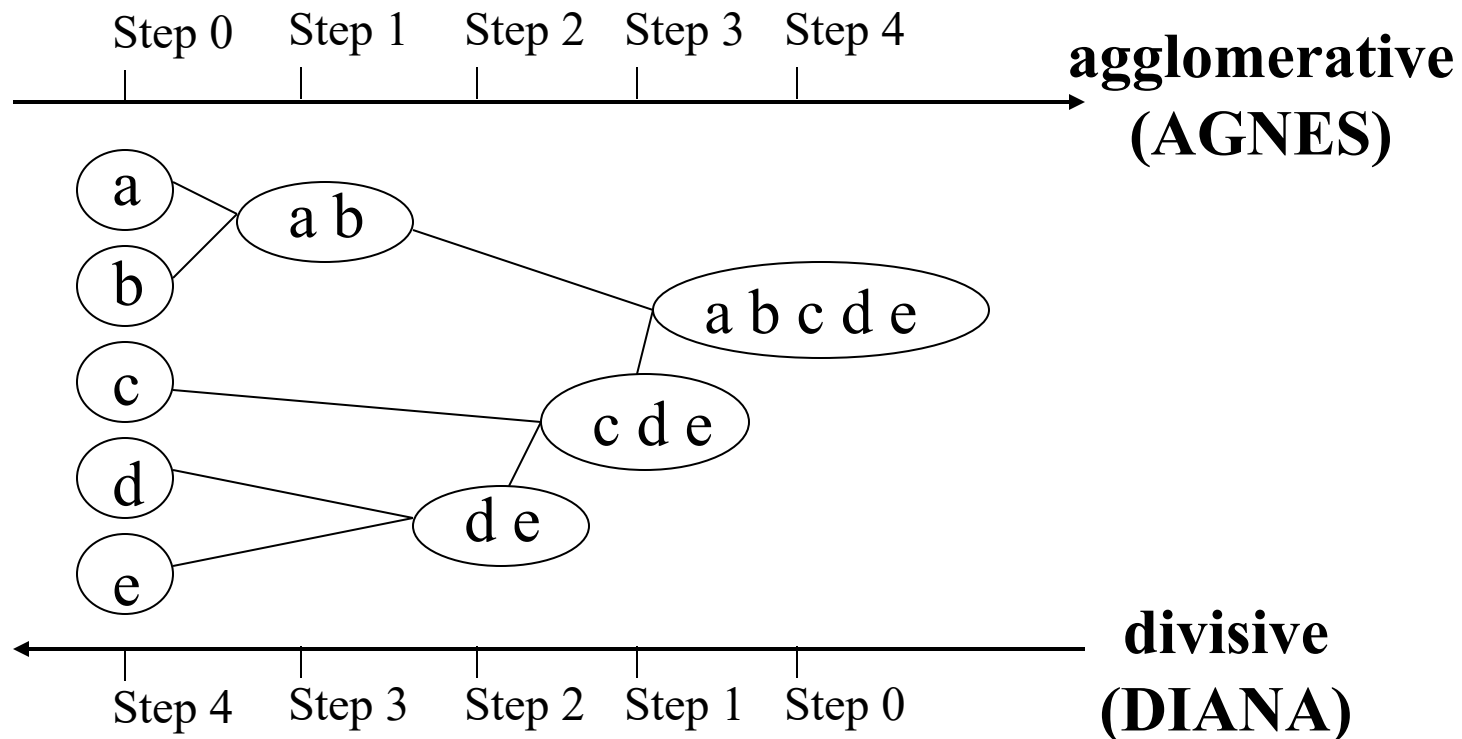
# *K*-Means Clustering



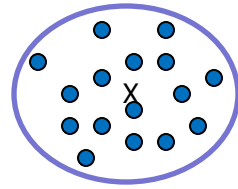
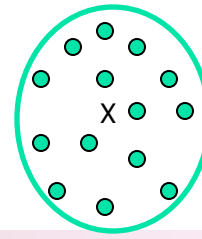
- Partition objects into  $k$  nonempty subsets
- Repeat
  - Compute centroid (i.e., mean point) for each partition
  - Assign each object to the cluster of its nearest centroid
- Until no change

# 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



# Distance between Clusters



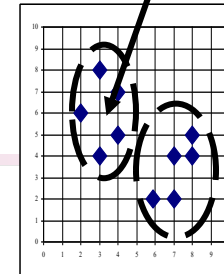
- **Single link:** smallest distance between an element in one cluster and an element in the other, i.e.,  $\text{dist}(K_i, K_j) = \min(t_{ip}, t_{jq})$
- **Complete link:** largest distance between an element in one cluster and an element in the other, i.e.,  $\text{dist}(K_i, K_j) = \max(t_{ip}, t_{jq})$
- **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

# BIRCH and the Clustering Feature (CF) Tree Structure

$B = 7$  Root

$L = 6$

CF <sub>1</sub>	CF <sub>2</sub>	CF <sub>3</sub>	.....	CF <sub>6</sub>
child <sub>1</sub>	child <sub>2</sub>	child <sub>3</sub>	.....	child <sub>6</sub>



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

(3,4)  
(2,6)  
(4,5)  
(4,7)  
(3,8)

Non-leaf node

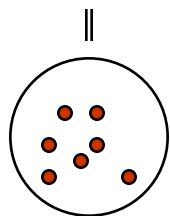
CF <sub>1</sub>	CF <sub>2</sub>	CF <sub>3</sub>	.....	CF <sub>5</sub>
child <sub>1</sub>	child <sub>2</sub>	child <sub>3</sub>	.....	child <sub>5</sub>

Leaf node

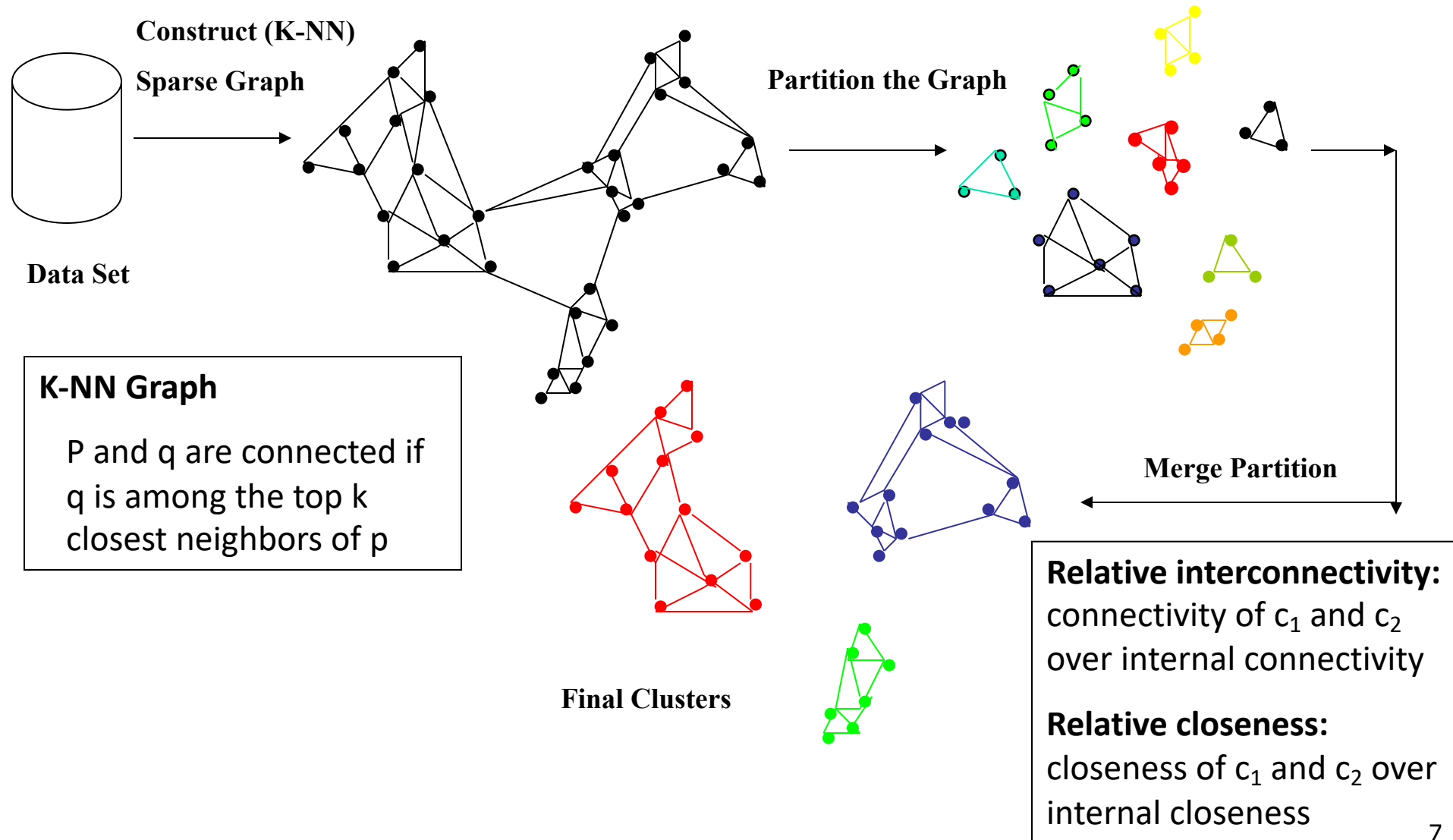
Leaf node

prev	CF <sub>1</sub>	CF <sub>2</sub>	.....	CF <sub>6</sub>	next
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prev	CF <sub>1</sub>	CF <sub>2</sub>	.....	CF <sub>4</sub>	next
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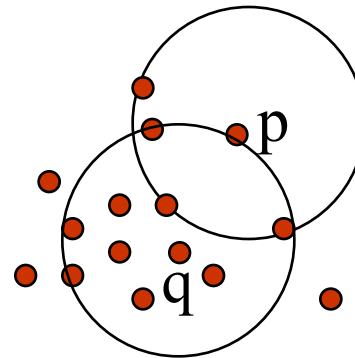
# Overall Framework of CHAMELEON



# Density-Based Clustering: DBSCAN

- 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:

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

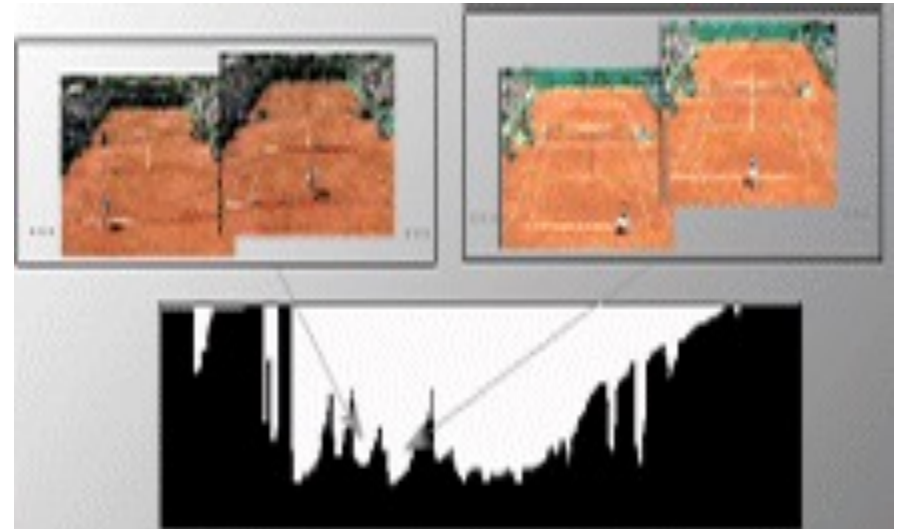
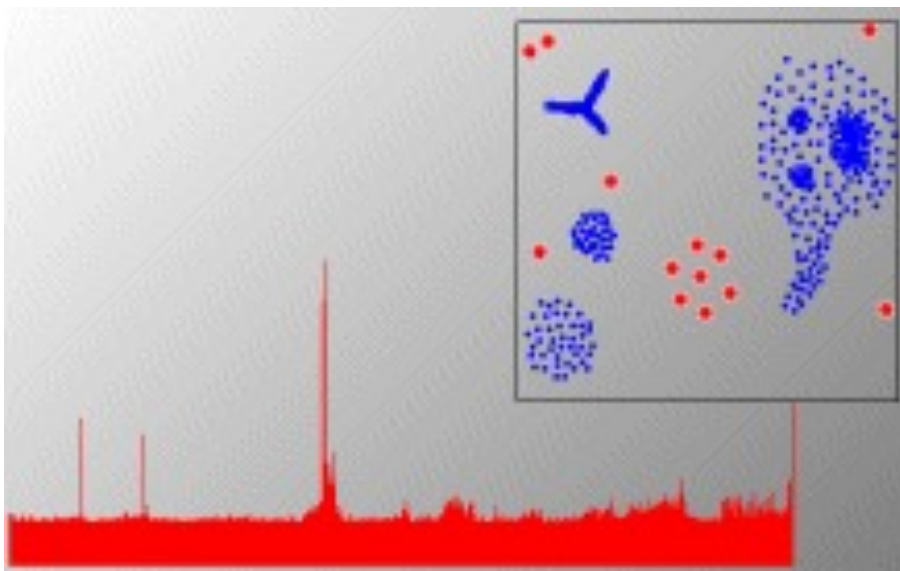
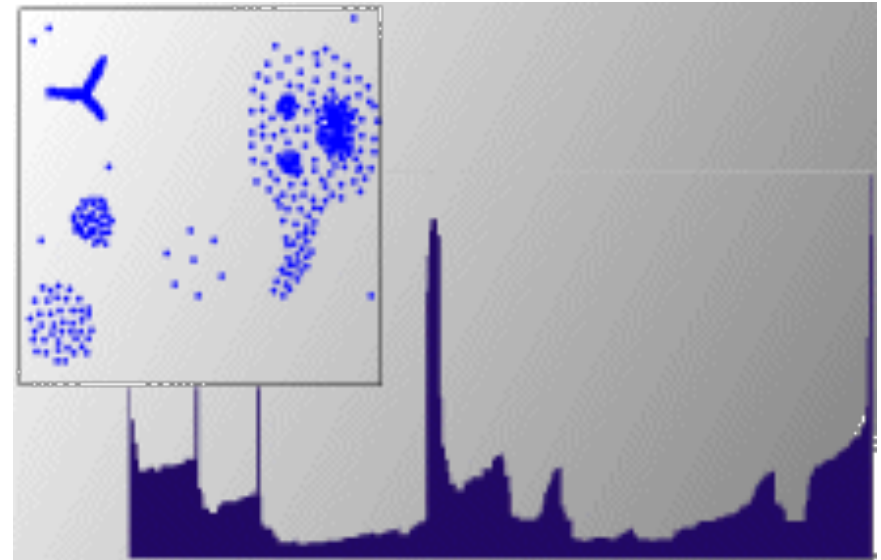
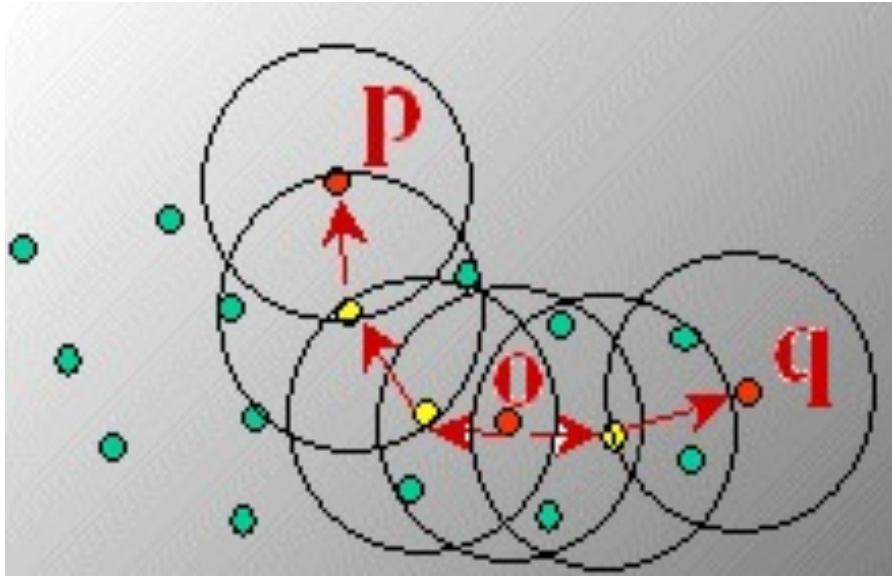


$MinPts = 5$

$Eps = 1 \text{ cm}$



# Density-Based Clustering: OPTICS & Its Applications



# DENCLU: Center-Defined and Arbitrary

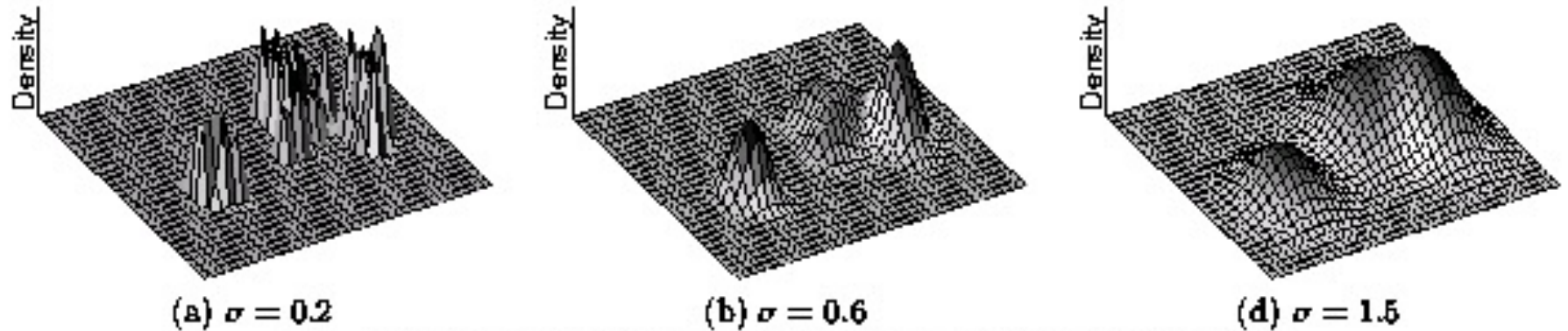


Figure 3: Example of Center-Defined Clusters for different  $\sigma$

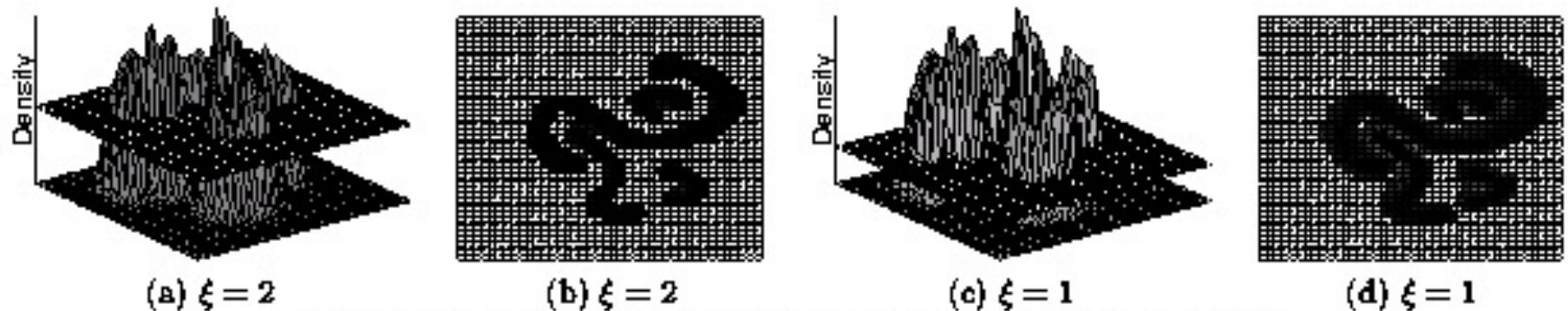
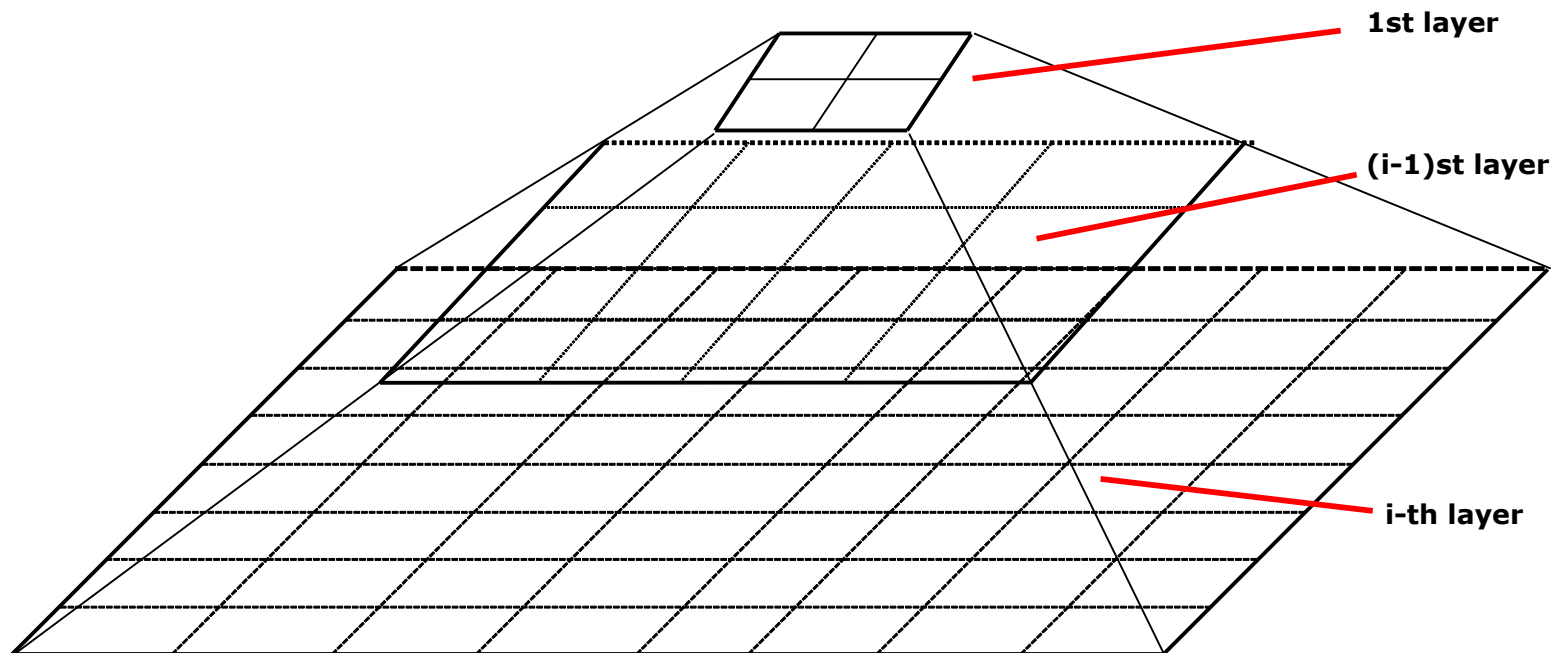


Figure 4: Example of Arbitrary-Shape Clusters for different  $\xi$

# 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



# Evaluation of Clustering Quality

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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
- Determine the Number of Clusters
  - Empirical method: # of clusters  $\approx \sqrt{n/2}$
  - Elbow method: Use the turning point in the curve of sum of within cluster variance w.r.t # of clusters
  - Cross validation method
- Measuring Clustering Quality
  - Extrinsic: supervised
    - Compare a clustering against the ground truth using certain clustering quality measure
  - Intrinsic: unsupervised
    - Evaluate the goodness of a clustering by considering how well the clusters are separated, and how compact the clusters are

# Outline of Advanced Clustering Analysis

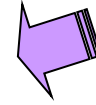
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- Probability Model-Based Clustering
  - Each object may take a probability to belong to a cluster
- Clustering High-Dimensional Data
  - Curse of dimensionality: Difficulty of distance measure in high-D space
- Clustering Graphs and Network Data
  - Similarity measurement and clustering methods for graph and networks
- Clustering with Constraints
  - Cluster analysis under different kinds of constraints, e.g., that raised from background knowledge or spatial distribution of the objects

# Chapter 11. Cluster Analysis: Advanced Methods

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- Probability Model-Based Clustering
- Clustering High-Dimensional Data
- Clustering Graphs and Network Data
- Clustering with Constraints
- Summary



# Fuzzy Set and Fuzzy Cluster

- Clustering methods discussed so far
  - Every data object is assigned to exactly one cluster
- Some applications may need for fuzzy or soft cluster assignment
  - Ex. An e-game could belong to both entertainment and software
- Methods: fuzzy clusters and probabilistic model-based clusters
- Fuzzy cluster: A fuzzy set  $S$ :  $F_S : X \rightarrow [0, 1]$  (value between 0 and 1)
- Example: Popularity of cameras is defined as a fuzzy mapping

Camera	Sales (units)
<i>A</i>	50
<i>B</i>	1320
<i>C</i>	860
<i>D</i>	270

$$\text{Pop}(o) = \begin{cases} 1 & \text{if 1,000 or more units of } o \text{ are sold} \\ \frac{i}{1000} & \text{if } i \text{ } (i < 1000) \text{ units of } o \text{ are sold} \end{cases}$$

- Then,  $A(0.05)$ ,  $B(1)$ ,  $C(0.86)$ ,  $D(0.27)$

# Fuzzy (Soft) Clustering

- Example: Let cluster features be
  - $C_1$  :“digital camera” and “lens”
  - $C_2$ : “computer”

Review-id	Keywords
$R_1$	digital camera, lens
$R_2$	digital camera
$R_3$	lens
$R_4$	digital camera, lens, computer
$R_5$	computer, CPU
$R_6$	computer, computer game

$$M = \begin{bmatrix} 1 & 0 \\ 1 & 0 \\ 1 & 0 \\ \frac{2}{3} & \frac{1}{3} \\ 0 & 1 \\ 0 & 1 \end{bmatrix}$$

- Fuzzy clustering
  - k fuzzy clusters  $C_1, \dots, C_k$ , represented as a partition matrix  $M = [w_{ij}]$
  - P1: for each object  $o_i$  and cluster  $C_j$ ,  $0 \leq w_{ij} \leq 1$  (fuzzy set)
  - P2: for each object  $o_i$ ,  $\sum_{j=1}^k w_{ij} = 1$ , equal participation in the clustering
  - P3: for each cluster  $C_j$ ,  $0 < \sum_{i=1}^n w_{ij} < n$  ensures there is no empty cluster

- Let  $c_1, \dots, c_k$  as the center of the k clusters

- For an object  $o_i$ , sum of the squared error (SSE), p is a parameter:

- For a cluster  $C_j$ , SSE: 
$$SSE(C_j) = \sum_{i=1}^n w_{ij}^p \text{dist}(o_i, c_j)^2 \quad SSE(o_i) = \sum_{j=1}^k w_{ij}^p \text{dist}(o_i, c_j)^2$$

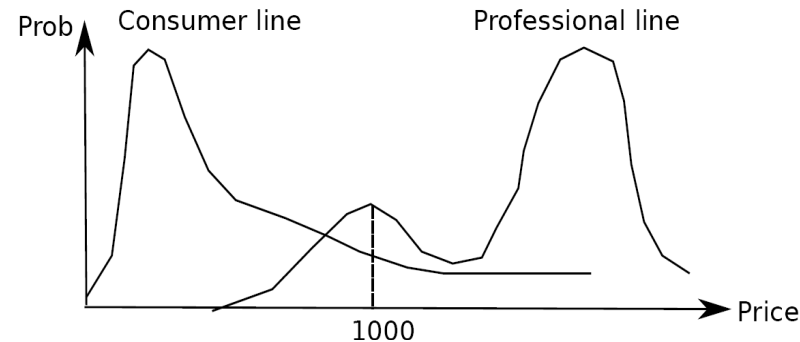
- Measure how well a clustering fits the data:

$$SSE(C) = \sum_{i=1}^n \sum_{j=1}^k w_{ij}^p \text{dist}(o_i, c_j)^2$$



# Probabilistic Model-Based Clustering

- Cluster analysis is to find hidden categories.
- A hidden category (i.e., *probabilistic cluster*) is a distribution over the data space, which can be mathematically represented using a probability density function (or distribution function).
- Ex. 2 categories for digital cameras sold
  - consumer line vs. professional line
  - density functions  $f_1, f_2$  for  $C_1, C_2$
  - obtained by probabilistic clustering
- A **mixture model** assumes that a set of observed objects is a mixture of instances from multiple probabilistic clusters, and conceptually each observed object is generated independently
- **Out task**: infer a set of  $k$  probabilistic clusters that is mostly likely to generate  $D$  using the above data generation process



# Model-Based Clustering

- A set  $C$  of  $k$  probabilistic clusters  $C_1, \dots, C_k$  with probability density functions  $f_1, \dots, f_k$ , respectively, and their probabilities  $\omega_1, \dots, \omega_k$ .
- Probability of an object  $o$  generated by cluster  $C_j$  is  $P(o|C_j) = \omega_j f_j(o)$
- Probability of  $o$  generated by the set of cluster  $\mathbf{C}$  is  $P(o|\mathbf{C}) = \sum_{j=1}^k \omega_j f_j(o)$
- Since objects are assumed to be generated independently, for a data set  $D = \{o_1, \dots, o_n\}$ , we have,

$$P(D|\mathbf{C}) = \prod_{i=1}^n P(o_i|\mathbf{C}) = \prod_{i=1}^n \sum_{j=1}^k \omega_j f_j(o_i)$$

- Task: Find a set  $C$  of  $k$  probabilistic clusters s.t.  $P(D|\mathbf{C})$  is maximized
- However, maximizing  $P(D|\mathbf{C})$  is often intractable since the probability density function of a cluster can take an arbitrarily complicated form
- To make it computationally feasible (as a compromise), assume the probability density functions being some parameterized distributions

# Univariate Gaussian Mixture Model

- $O = \{o_1, \dots, o_n\}$  ( $n$  observed objects),  $\Theta = \{\theta_1, \dots, \theta_k\}$  (parameters of the  $k$  distributions), and  $P_j(o_i | \theta_j)$  is the probability that  $o_i$  is generated from the  $j$ -th distribution using parameter  $\theta_j$ , we have

$$P(o_i | \Theta) = \sum_{j=1}^k \omega_j P_j(o_i | \theta_j) \quad P(O | \Theta) = \prod_{i=1}^n \sum_{j=1}^k \omega_j P_j(o_i | \theta_j)$$

- Univariate Gaussian mixture model
  - Assume the probability density function of each cluster follows a 1-d Gaussian distribution. Suppose that there are  $k$  clusters.
  - The probability density function of each cluster are centered at  $\mu_j$  with standard deviation  $\sigma_j$ ,  $\theta_j = (\mu_j, \sigma_j)$ , we have

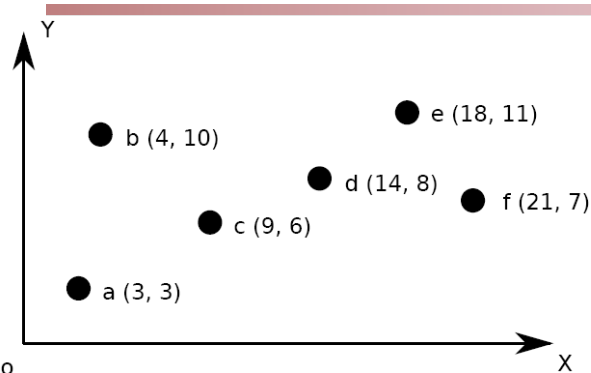
$$P(o_i | \theta_j) = \frac{1}{\sqrt{2\pi}\sigma_j} e^{-\frac{(o_i - \mu_j)^2}{2\sigma_j^2}} \quad P(o_i | \Theta) = \sum_{j=1}^k \frac{1}{\sqrt{2\pi}\sigma_j} e^{-\frac{(o_i - \mu_j)^2}{2\sigma_j^2}}$$
$$P(O | \Theta) = \prod_{i=1}^n \sum_{j=1}^k \frac{1}{\sqrt{2\pi}\sigma_j} e^{-\frac{(o_i - \mu_j)^2}{2\sigma_j^2}}$$

# The EM (Expectation Maximization) Algorithm

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- The k-means algorithm has two steps at each iteration:
  - **Expectation Step** (E-step): Given the current cluster centers, each object is assigned to the cluster whose center is closest to the object: An object is *expected to belong to the closest cluster*
  - **Maximization Step** (M-step): Given the cluster assignment, for each cluster, the algorithm *adjusts the center* so that *the sum of distance* from the objects assigned to this cluster and the new center is minimized
- **The (EM) algorithm:** A framework to approach maximum likelihood or maximum a posteriori estimates of parameters in statistical models.
  - **E-step** assigns objects to clusters according to the current fuzzy clustering or parameters of probabilistic clusters
  - **M-step** finds the new clustering or parameters that maximize the sum of squared error (SSE) or the expected likelihood

# Fuzzy Clustering Using the EM Algorithm



Iteration	E-step	M-step
1	$M^T = \begin{bmatrix} 1 & 0 & 0.48 & 0.42 & 0.41 & 0.47 \\ 0 & 1 & 0.52 & 0.58 & 0.59 & 0.53 \end{bmatrix}$	$c_1 = (8.47, 5.12),$ $c_2 = (10.42, 8.99)$
2	$M^T = \begin{bmatrix} 0.73 & 0.49 & 0.91 & 0.26 & 0.33 & 0.42 \\ 0.27 & 0.51 & 0.09 & 0.74 & 0.67 & 0.58 \end{bmatrix}$	$c_1 = (8.51, 6.11),$ $c_2 = (14.42, 8.69)$
3	$M^T = \begin{bmatrix} 0.80 & 0.76 & 0.99 & 0.02 & 0.14 & 0.23 \\ 0.20 & 0.24 & 0.01 & 0.98 & 0.86 & 0.77 \end{bmatrix}$	$c_1 = (6.40, 6.24),$ $c_2 = (16.55, 8.64)$

- Initially, let  $c_1 = a$  and  $c_2 = b$

- 1<sup>st</sup> E-step: assign  $o$  to  $c_1$ , w. wt =  $\frac{\frac{1}{\text{dist}(o, c_1)^2}}{\frac{1}{\text{dist}(o, c_1)^2} + \frac{1}{\text{dist}(o, c_2)^2}} = \frac{\text{dist}(o, c_2)^2}{\text{dist}(o, c_1)^2 + \text{dist}(o, c_2)^2}$ 
  - $w_{c, c_1} = \frac{41}{45+41} = 0.48$

- 1<sup>st</sup> M-step: recalculate the centroids according to the partition matrix, minimizing the sum of squared error (SSE)

$$c_j = \frac{\sum_{\text{each point } o} w_{o, c_j}^2 o}{\sum_{\text{each point } o} w_{o, c_j}^2} \quad c_1 = \left( \frac{1^2 \times 3 + 0^2 \times 4 + 0.48^2 \times 9 + 0.42^2 \times 14 + 0.41^2 \times 18 + 0.47^2 \times 21}{1^2 + 0^2 + 0.48^2 + 0.42^2 + 0.41^2 + 0.47^2}, \frac{1^2 \times 3 + 0^2 \times 10 + 0.48^2 \times 6 + 0.42^2 \times 8 + 0.41^2 \times 11 + 0.47^2 \times 7}{1^2 + 0^2 + 0.48^2 + 0.42^2 + 0.41^2 + 0.47^2} \right) = (8.47, 5.12)$$

- Iteratively calculate this until the cluster centers converge or the change is small enough

# Univariate Gaussian Mixture Model

- $O = \{o_1, \dots, o_n\}$  ( $n$  observed objects),  $\Theta = \{\theta_1, \dots, \theta_k\}$  (parameters of the  $k$  distributions), and  $P_j(o_i | \theta_j)$  is the probability that  $o_i$  is generated from the  $j$ -th distribution using parameter  $\theta_j$ , we have

$$P(o_i | \Theta) = \sum_{j=1}^k \omega_j P_j(o_i | \theta_j) \quad P(O | \Theta) = \prod_{i=1}^n \sum_{j=1}^k \omega_j P_j(o_i | \theta_j)$$

- Univariate Gaussian mixture model
  - Assume the probability density function of each cluster follows a 1-d Gaussian distribution. Suppose that there are  $k$  clusters.
  - The probability density function of each cluster are centered at  $\mu_j$  with standard deviation  $\sigma_j$ ,  $\theta_j = (\mu_j, \sigma_j)$ , we have

$$P(o_i | \theta_j) = \frac{1}{\sqrt{2\pi}\sigma_j} e^{-\frac{(o_i - \mu_j)^2}{2\sigma_j^2}} \quad P(o_i | \Theta) = \sum_{j=1}^k \frac{1}{\sqrt{2\pi}\sigma_j} e^{-\frac{(o_i - \mu_j)^2}{2\sigma_j^2}}$$
$$P(O | \Theta) = \prod_{i=1}^n \sum_{j=1}^k \frac{1}{\sqrt{2\pi}\sigma_j} e^{-\frac{(o_i - \mu_j)^2}{2\sigma_j^2}}$$

# Computing Mixture Models with EM

- Given  $n$  objects  $O = \{o_1, \dots, o_n\}$ , we want to mine a set of parameters  $\Theta = \{\theta_1, \dots, \theta_k\}$  s.t.,  $P(\mathbf{O}|\Theta)$  is maximized, where  $\theta_j = (\mu_j, \sigma_j)$  are the mean and standard deviation of the  $j$ -th univariate Gaussian distribution
- We initially assign random values to parameters  $\theta_j$ , then iteratively conduct the E- and M- steps until converge or sufficiently small change
- At the E-step, for each object  $o_i$ , calculate the probability that  $o_i$  belongs to each distribution,

$$P(\theta_j|o_i, \Theta) = \frac{P(o_i|\theta_j)}{\sum_{l=1}^k P(o_i|\theta_l)}$$

- At the M-step, adjust the parameters  $\theta_j = (\mu_j, \sigma_j)$  so that the expected likelihood  $P(\mathbf{O}|\Theta)$  is maximized

$$\mu_j = \sum_{i=1}^n o_i \frac{P(\theta_j|o_i, \Theta)}{\sum_{l=1}^k P(\theta_j|o_l, \Theta)} = \frac{\sum_{i=1}^n o_i P(\theta_j|o_i, \Theta)}{\sum_{i=1}^n P(\theta_j|o_i, \Theta)} \quad \sigma_j = \sqrt{\frac{\sum_{i=1}^n P(\theta_j|o_i, \Theta)(o_i - \mu_j)^2}{\sum_{i=1}^n P(\theta_j|o_i, \Theta)}}$$

# Advantages and Disadvantages of Mixture Models

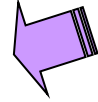
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- Strength
  - Mixture models are more general than partitioning and fuzzy clustering
  - Clusters can be characterized by a small number of parameters
  - The results may satisfy the statistical assumptions of the generative models
- Weakness
  - Converge to local optimal (overcome: run multi-times w. random initialization)
  - Computationally expensive if the number of distributions is large, or the data set contains very few observed data points
  - Need large data sets
  - Hard to estimate the number of clusters



# Chapter 11. Cluster Analysis: Advanced Methods

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- Probability Model-Based Clustering
- Clustering High-Dimensional Data 
- Clustering Graphs and Network Data
- Clustering with Constraints
- Summary

# Clustering High-Dimensional Data

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- Clustering high-dimensional data (How high is high-D in clustering?)
  - Many applications: text documents, DNA micro-array data
  - Major challenges:
    - Many irrelevant dimensions may mask clusters
    - Distance measure becomes meaningless—due to equi-distance
    - Clusters may exist only in some subspaces
- Methods
  - **Subspace-clustering:** Search for clusters existing in subspaces of the given high dimensional data space
    - CLIQUE, ProClus, and bi-clustering approaches
  - **Dimensionality reduction approaches:** Construct a much lower dimensional space and search for clusters there (may construct new dimensions by combining some dimensions in the original data)
    - Dimensionality reduction methods and spectral clustering

# Traditional Distance Measures May Not Be Effective on High-D Data

- Traditional distance measure could be dominated by noises in many dimensions
- Ex. Which pairs of customers are more similar?

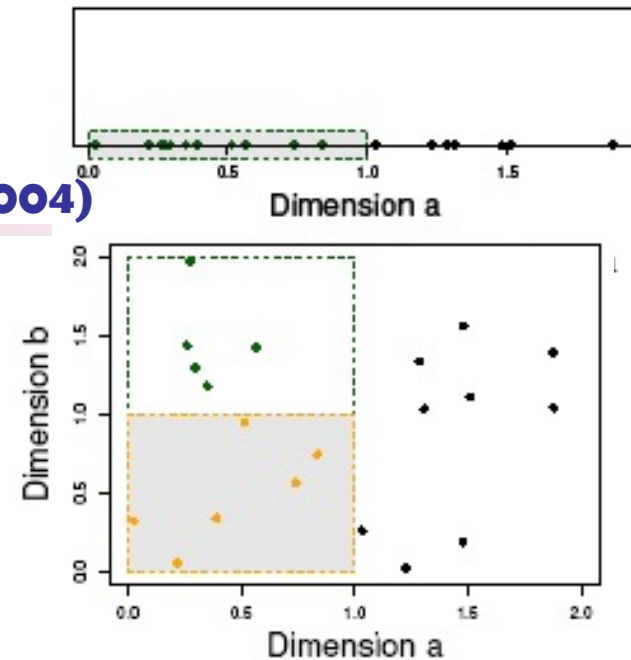
Customer	$P_1$	$P_2$	$P_3$	$P_4$	$P_5$	$P_6$	$P_7$	$P_8$	$P_9$	$P_{10}$
Ada	1	0	0	0	0	0	0	0	0	0
Bob	0	0	0	0	0	0	0	0	0	1
Cathy	1	0	0	0	1	0	0	0	0	1

- By Euclidean distance, we get,  
$$\text{dist}(\text{Ada}, \text{Bob}) = \text{dist}(\text{Bob}, \text{Cathy}) = \text{dist}(\text{Ada}, \text{Cathy}) = \sqrt{2}$$
  - despite Ada and Cathy look more similar
- Clustering should not only consider dimensions but also attributes (features)
  - Feature transformation: effective if most dimensions are relevant (PCA & SVD useful when features are highly correlated/redundant)
  - Feature selection: useful to find a subspace where the data have nice clusters

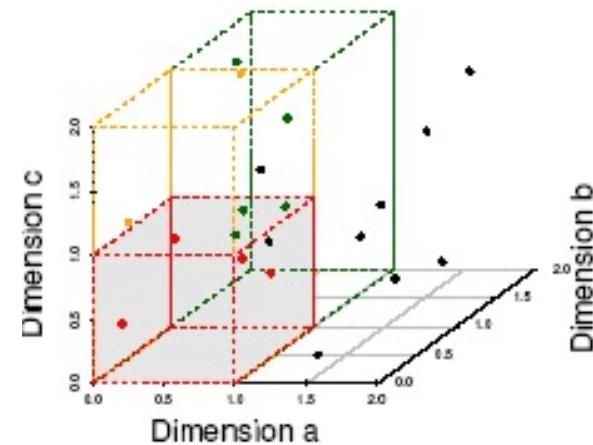
# The Curse of Dimensionality

(graphs adapted from Parsons et al. KDD Explorations 2004)

- Data in only one dimension is relatively packed
- Adding a dimension “stretch” the points across that dimension, making them further apart
- Adding more dimensions will make the points further apart—high dimensional data is extremely sparse
- Distance measure becomes meaningless—due to equi-distance



(b) 6 Objects in One Unit Bin

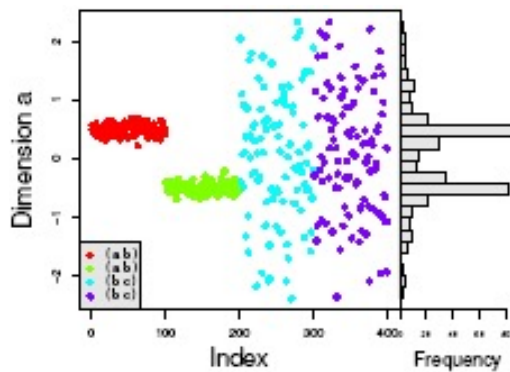
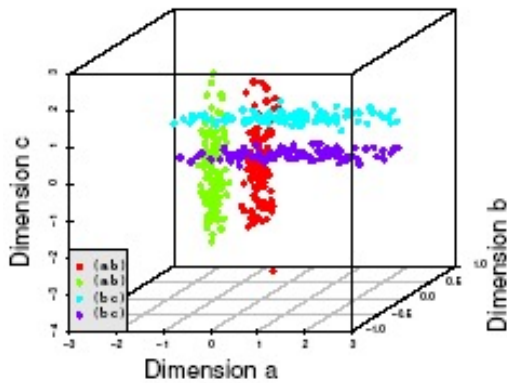


(c) 4 Objects in One Unit Bin

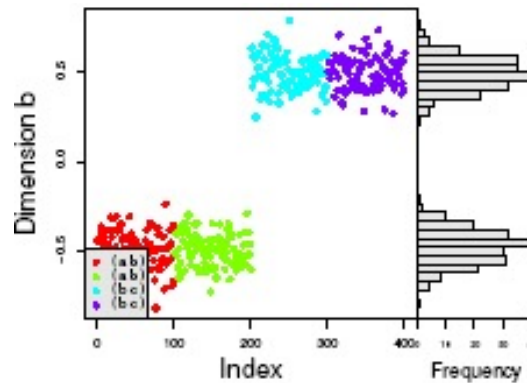
# Why Subspace Clustering?

(adapted from Parsons et al. SIGKDD Explorations 2004)

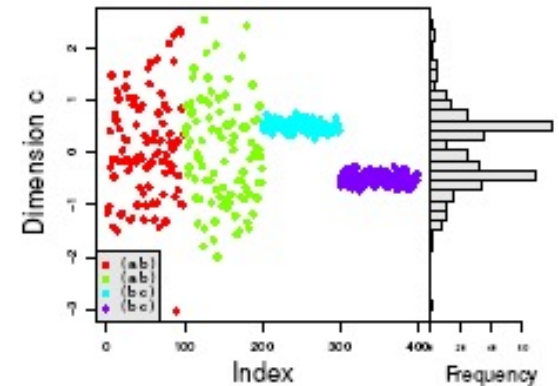
- Clusters may exist only in some subspaces
- Subspace-clustering: find clusters in all the subspaces



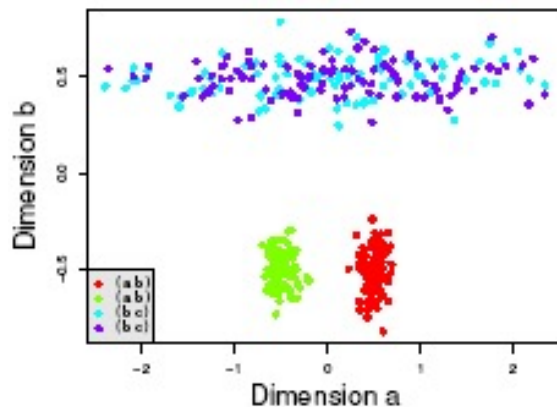
(a) Dimension *a*



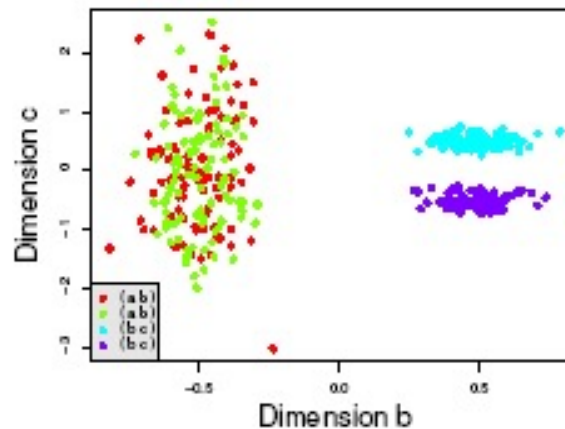
(b) Dimension *b*



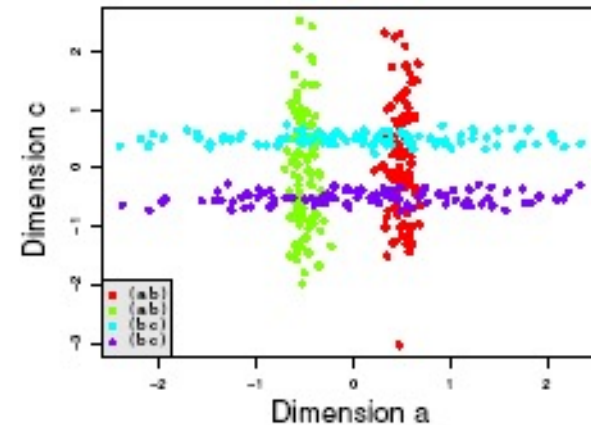
(c) Dimension *c*



(a) Dims *a* & *b*



(b) Dims *b* & *c*



(c) Dims *a* & *c*

# Subspace Clustering Methods

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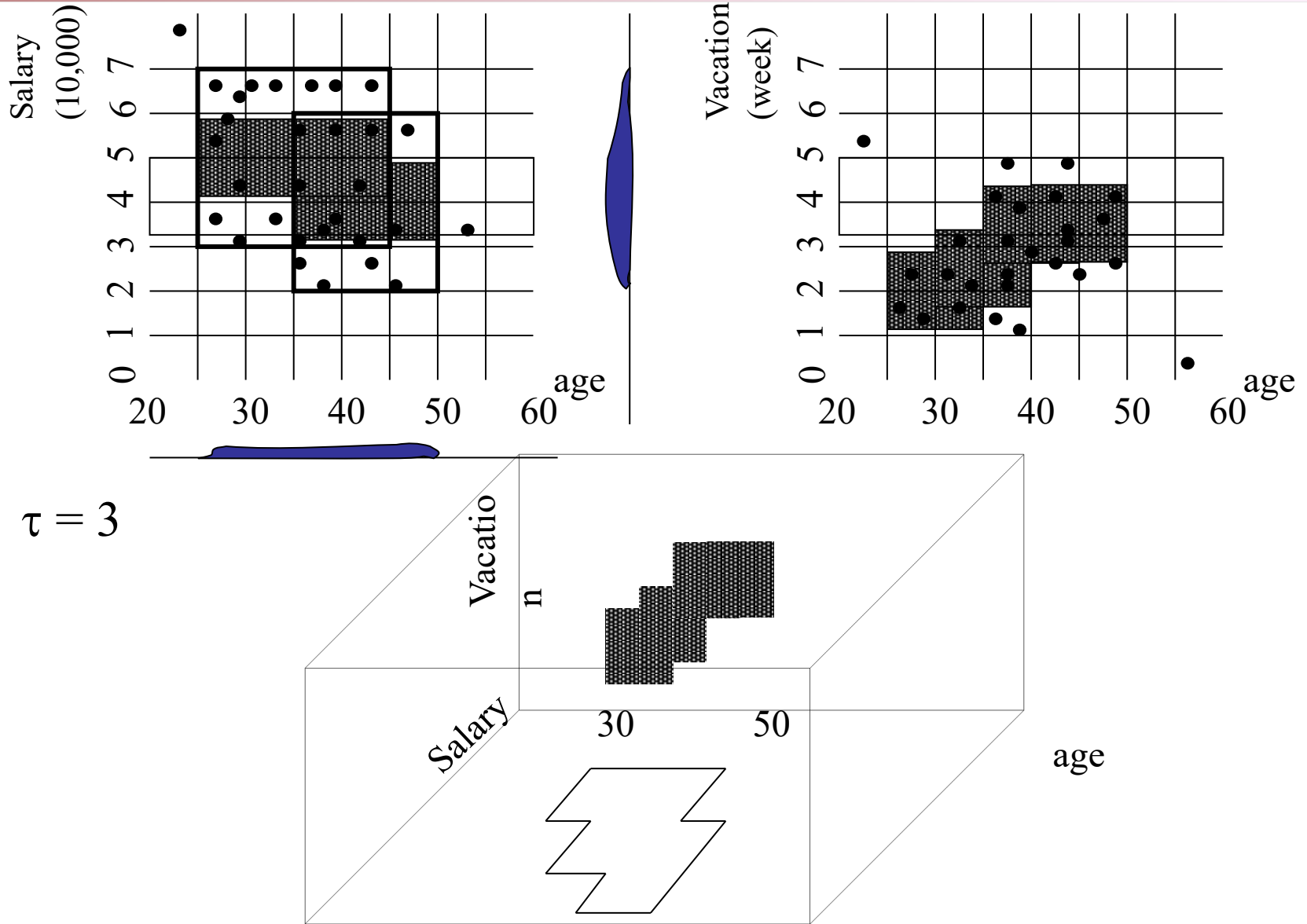
- Subspace search methods: Search various subspaces to find clusters
  - Bottom-up approaches
  - Top-down approaches
- Correlation-based clustering methods
  - E.g., PCA based approaches
- Bi-clustering methods
  - Optimization-based methods
  - Enumeration methods

# Subspace Clustering Method (I): Subspace Search Methods

---

- Search various subspaces to find clusters
- *Bottom-up approaches*
  - Start from low-D subspaces and search higher-D subspaces only when there may be clusters in such subspaces
  - Various pruning techniques to reduce the number of higher-D subspaces to be searched
  - Ex. CLIQUE (Agrawal et al. 1998)
- *Top-down approaches*
  - Start from full space and search smaller subspaces recursively
  - Effective only if the *locality assumption* holds: restricts that the subspace of a cluster can be determined by the local neighborhood
  - Ex. PROCLUS (Aggarwal et al. 1999): a  $k$ -medoid-like method

# CLIQUE: SubSpace Clustering with Aprori Pruning





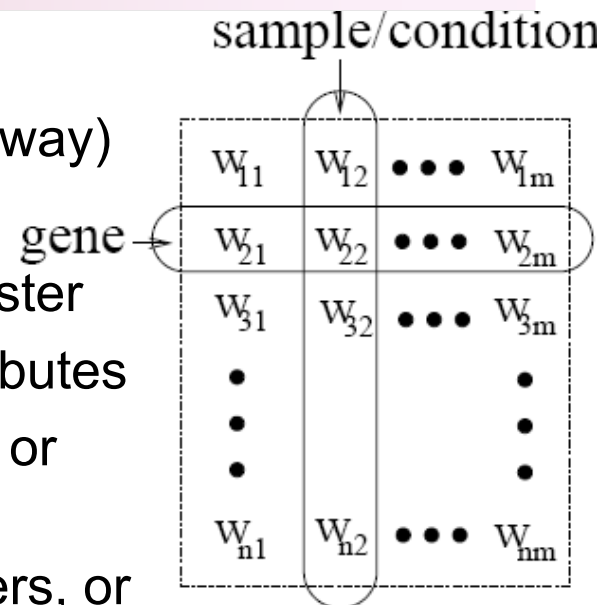
# Subspace Clustering Method (II): Correlation-Based Methods

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- Subspace search method: similarity based on distance or density
- Correlation-based method: based on advanced correlation models
- Ex. PCA-based approach:
  - Apply PCA (for Principal Component Analysis) to derive a set of new, uncorrelated dimensions,
  - then mine clusters in the new space or its subspaces
- Other space transformations:
  - Hough transform
  - Fractal dimensions

# Subspace Clustering Method (III): Bi-Clustering Methods

- Bi-clustering: Cluster both objects and attributes simultaneously (treat objs and attrs in symmetric way)
- Four requirements:
  - Only a small set of objects participate in a cluster
  - A cluster only involves a small number of attributes
  - An object may participate in multiple clusters, or does not participate in any cluster at all
  - An attribute may be involved in multiple clusters, or is not involved in any cluster at all



- Ex 1. *Gene expression or microarray data*: a gene sample/condition matrix.

- Each element in the matrix, a real number, records the expression level of a gene under a specific condition

customers

products

$w_{11}$	$w_{12}$	...	$w_{1m}$
$w_{21}$	$w_{22}$	...	$w_{2m}$
...	...	...	...
$w_{n1}$	$w_{n2}$	...	$w_{nm}$

- Ex. 2. Clustering customers and products

- Another bi-clustering problem

# Types of Bi-clusters

- Let  $A = \{a_1, \dots, a_n\}$  be a set of genes,  $B = \{b_1, \dots, b_n\}$  a set of conditions
- A bi-cluster: A submatrix where genes and conditions follow some consistent patterns

- 4 types of bi-clusters (ideal cases)

- Bi-clusters with constant values:

- for any  $i$  in  $I$  and  $j$  in  $J$ ,  $e_{ij} = c$

- Bi-clusters with constant values on rows:

- $e_{ij} = c + \alpha_i$

- Also, it can be constant values on columns

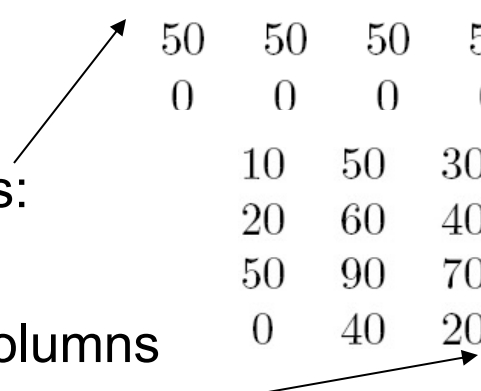
- Bi-clusters with *coherent values* (aka. *pattern-based clusters*)

- $e_{ij} = c + \alpha_i + \beta_j$

- Bi-clusters with *coherent* evolutions on rows

- $e_{ij}(e_{i1j1} - e_{i1j2})(e_{i2j1} - e_{i2j2}) \geq 0$

- i.e., only interested in the up- or down- regulated changes across genes or conditions without constraining on the exact values



10	10	10	10	10
20	20	20	20	20
50	50	50	50	50
0	0	0	0	0

10	50	30	70	20
20	60	40	80	30
50	90	70	110	60
0	40	20	60	10

10	50	30	70	20
20	100	50	1000	30
50	100	90	120	80
0	80	20	100	10

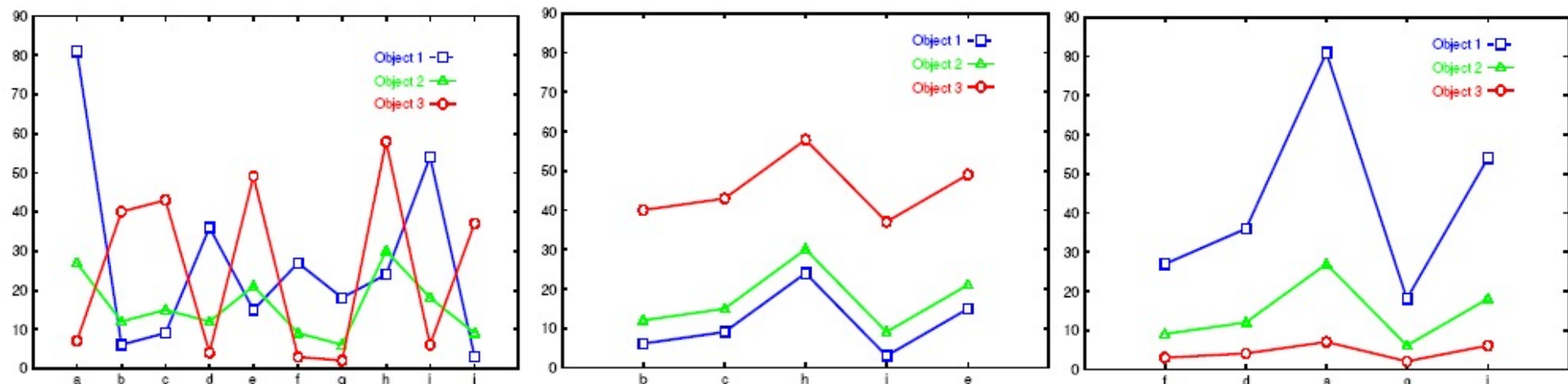
# Bi-Clustering Methods

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- Real-world data is noisy: Try to find approximate bi-clusters
- Methods: Optimization-based methods vs. enumeration methods
- Optimization-based methods
  - Try to find a submatrix at a time that achieves the best significance as a bi-cluster
  - Due to the cost in computation, greedy search is employed to find local optimal bi-clusters
  - Ex.  $\delta$ -Cluster Algorithm (Cheng and Church, ISMB'2000)
- Enumeration methods
  - Use a tolerance threshold to specify the degree of noise allowed in the bi-clusters to be mined
  - Then try to enumerate all submatrices as bi-clusters that satisfy the requirements
  - Ex.  $\delta$ -pCluster Algorithm (H. Wang et al.' SIGMOD'2002, MaPle: Pei et al., ICDM'2003)

# Bi-Clustering for Micro-Array Data Analysis

- Left figure: Micro-array “raw” data shows 3 genes and their values in a multi-D space: Difficult to find their patterns
- Right two: Some subsets of dimensions form nice **shift** and **scaling** patterns
- No globally defined similarity/distance measure
- Clusters may not be exclusive
  - An object can appear in multiple clusters



# Bi-Clustering (I): $\delta$ -Bi-Cluster

- For a submatrix  $I \times J$ , the mean of the  $i$ -th row:  $e_{iJ} = \frac{1}{|J|} \sum_{j \in J} e_{ij}$ 
  - The mean of the  $j$ -th column:  $e_{Ij} = \frac{1}{|I|} \sum_{i \in I} e_{ij}$
  - The mean of all elements in the submatrix is

$$e_{IJ} = \frac{1}{|I||J|} \sum_{i \in I, j \in J} e_{ij} = \frac{1}{|I|} \sum_{i \in I} e_{iJ} = \frac{1}{|J|} \sum_{j \in J} e_{Ij}$$

- The quality of the submatrix as a bi-cluster can be measured by the *mean squared residue* value

$$H(I \times J) = \frac{1}{|I||J|} \sum_{i \in I, j \in J} (e_{ij} - e_{iJ} - e_{Ij} + e_{IJ})^2$$

- A submatrix  $I \times J$  is  **$\delta$ -bi-cluster** if  $H(I \times J) \leq \delta$  where  $\delta \geq 0$  is a threshold. When  $\delta = 0$ ,  $I \times J$  is a perfect bi-cluster with coherent values. By setting  $\delta > 0$ , a user can specify the tolerance of average noise per element against a perfect bi-cluster
  - $\text{residue}(e_{ij}) = e_{ij} - e_{iJ} - e_{Ij} + e_{IJ}$

# Bi-Clustering (I): The $\delta$ -Cluster Algorithm

- **Maximal  $\delta$ -bi-cluster** is a  $\delta$ -bi-cluster  $I \times J$  such that there does not exist another  $\delta$ -bi-cluster  $I' \times J'$  which contains  $I \times J$
- Computing is costly: Use heuristic greedy search to obtain local optimal clusters
- Two phase computation: deletion phase and additional phase
- Deletion phase: Start from the whole matrix, iteratively remove rows and columns while the mean squared residue of the matrix is over  $\delta$ 
  - At each iteration, for each row/column, compute the *mean squared residue*:
$$d(i) = \frac{1}{|J|} \sum_{j \in J} (e_{ij} - e_{iJ} - e_{Ij} + e_{IJ})^2 \quad d(j) = \frac{1}{|I|} \sum_{i \in I} (e_{ij} - e_{iJ} - e_{Ij} + e_{IJ})^2$$
  - Remove the row or column of the largest mean squared residue
- Addition phase:
  - Expand iteratively the  $\delta$ -bi-cluster  $I \times J$  obtained in the deletion phase as long as the  $\delta$ -bi-cluster requirement is maintained
  - Consider all the rows/columns not involved in the current bi-cluster  $I \times J$  by calculating their mean squared residues
  - A row/column of the smallest mean squared residue is added into the current  $\delta$ -bi-cluster
- It finds only one  $\delta$ -bi-cluster, thus needs to run multiple times: replacing the elements in the output bi-cluster by random numbers

# Bi-Clustering (II): $\delta$ -pCluster

- Enumerating all bi-clusters ( $\delta$ -pClusters) [H. Wang, et al., Clustering by pattern similarity in large data sets. SIGMOD'02]
- Since a submatrix  $I \times J$  is a bi-cluster with (perfect) coherent values iff  $e_{i_1j_1} - e_{i_2j_1} = e_{i_1j_2} - e_{i_2j_2}$ . For any  $2 \times 2$  submatrix of  $I \times J$ , define  $p$ -score

$$p\text{-score} \begin{pmatrix} e_{i_1j_1} & e_{i_1j_2} \\ e_{i_2j_1} & e_{i_2j_2} \end{pmatrix} = |(e_{i_1j_1} - e_{i_2j_1}) - (e_{i_1j_2} - e_{i_2j_2})|$$

- A submatrix  $I \times J$  is a  **$\delta$ -pCluster** (pattern-based cluster) if the  $p$ -score of every  $2 \times 2$  submatrix of  $I \times J$  is at most  $\delta$ , where  $\delta \geq 0$  is a threshold specifying a user's tolerance of noise against a perfect bi-cluster
- The  $p$ -score controls the noise on every element in a bi-cluster, while the mean squared residue captures the average noise
- **Monotonicity:** If  $I \times J$  is a  $\delta$ -pClusters, every  $x \times y$  ( $x, y \geq 2$ ) submatrix of  $I \times J$  is also a  $\delta$ -pClusters.
- A  $\delta$ -pCluster is **maximal** if no more row or column can be added into the cluster and retain  $\delta$ -pCluster: We only need to compute all maximal  $\delta$ -pClusters.

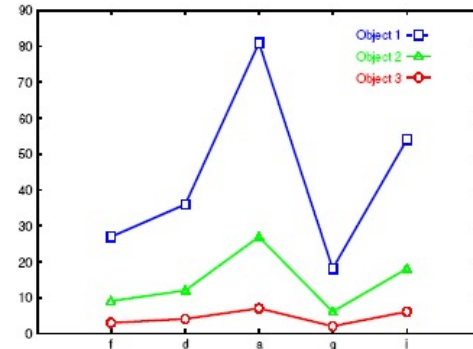
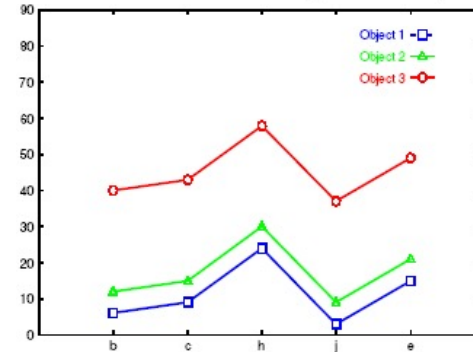
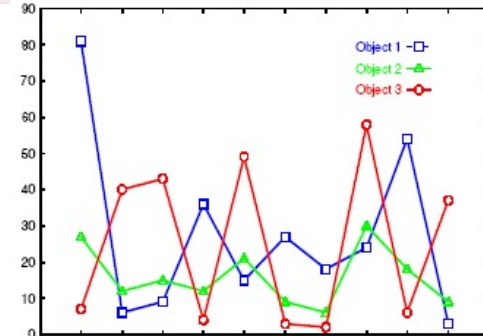


# MaPle: Efficient Enumeration of $\delta$ -pClusters

- Pei et al., MaPle: Efficient enumerating all maximal  $\delta$ -pClusters. ICDM'03
- Framework: Same as pattern-growth in frequent pattern mining (based on the downward closure property)
- For each condition combination J, find the maximal subsets of genes I such that I x J is a  $\delta$ -pClusters
  - If I x J is not a submatrix of another  $\delta$ -pClusters
  - then I x J is a maximal  $\delta$ -pCluster.
- Algorithm is very similar to mining frequent closed itemsets
- Additional advantages of  $\delta$ -pClusters:
  - Due to averaging of  $\delta$ -cluster, it may contain outliers but still within  $\delta$ -threshold
  - Computing bi-clusters for scaling patterns, take logarithmic on

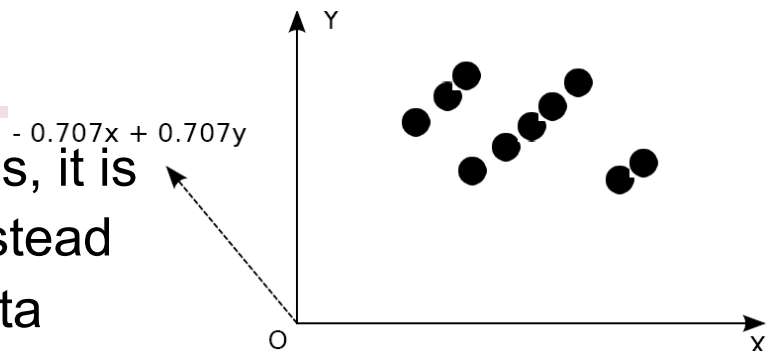
$$\frac{d_{xa} / d_{ya}}{d_{xb} / d_{yb}} < \delta$$

will lead to the p-score form



# Dimensionality-Reduction Methods

- Dimensionality reduction: In some situations, it is more effective to construct a new space instead of using some subspaces of the original data
- Ex. To cluster the points in the right figure, any subspace of the original one, X and Y, cannot help, since all the three clusters will be projected into the overlapping areas in X and Y axes.
  - Construct a new dimension as the dashed one, the three clusters become apparent when the points projected into the new dimension
- Dimensionality reduction methods
  - Feature selection and extraction: But may not focus on clustering structure finding
  - Spectral clustering: Combining feature extraction and clustering (i.e., use the *spectrum* of the similarity matrix of the data to perform dimensionality reduction for clustering in fewer dimensions)
    - Normalized Cuts (Shi and Malik, CVPR'97 or PAMI'2000)
    - The Ng-Jordan-Weiss algorithm (NIPS'01)

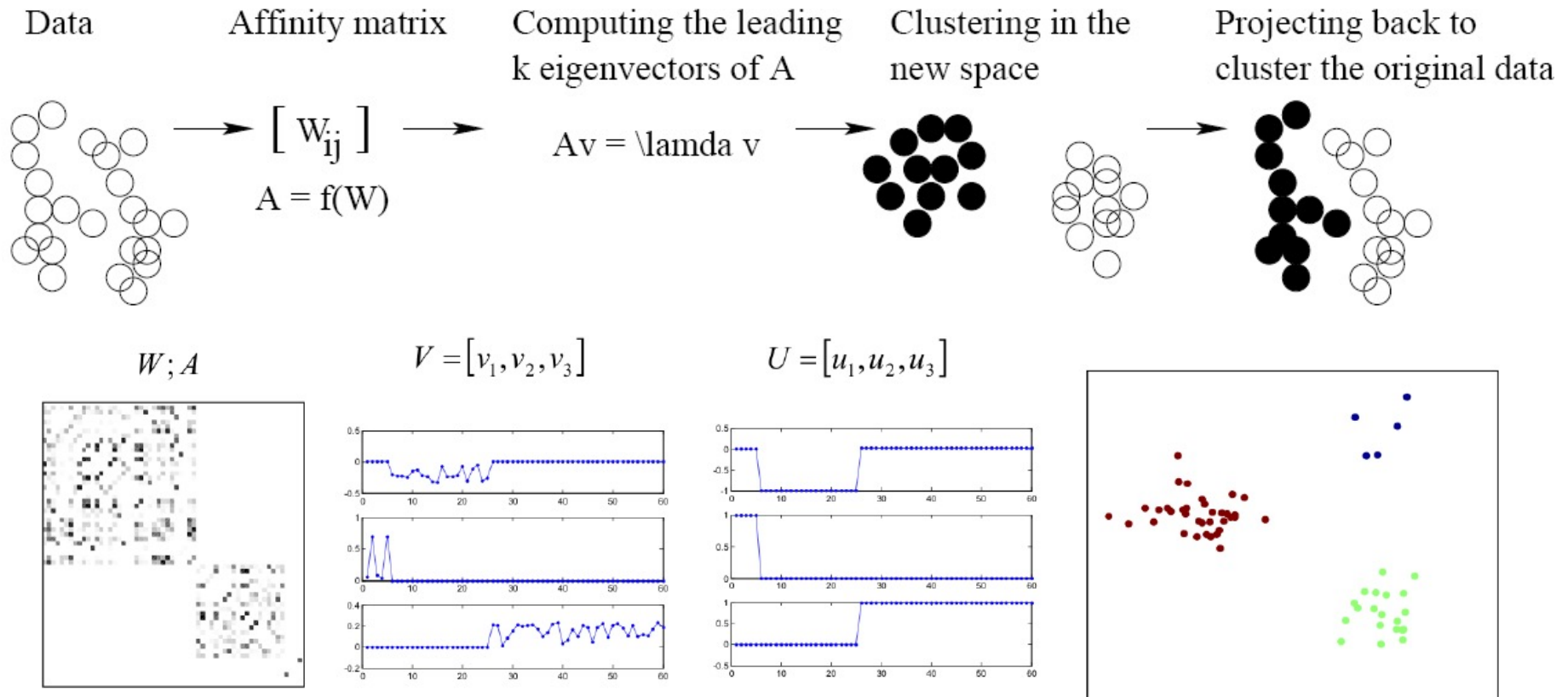


# Spectral Clustering:

## The Ng-Jordan-Weiss (NJW) Algorithm

- Given a set of objects  $o_1, \dots, o_n$ , and the distance between each pair of objects,  $\text{dist}(o_i, o_j)$ , find the desired number  $k$  of clusters
- Calculate an affinity matrix  $W$ , where  $\sigma$  is a scaling parameter that controls how fast the affinity  $W_{ij}$  decreases as  $\text{dist}(o_i, o_j)$  increases. In NJW, set  $W_{ij} = 0$ 
$$D_{ii} = \sum_{j=1}^n W_{ij}$$
- Derive a matrix  $A = f(W)$ . NJW defines a matrix  $D$  to be a diagonal matrix s.t.  $D_{ii}$  is the sum of the  $i$ -th row of  $W$ , i.e.,  $W_{ij} = e^{-\frac{\text{dist}(o_i, o_j)}{\sigma^2}}$   
Then,  $A$  is set to  $A = D^{-\frac{1}{2}} W D^{-\frac{1}{2}}$
- A spectral clustering method finds the  $k$  leading eigenvectors of  $A$ 
  - A vector  $v$  is an eigenvector of matrix  $A$  if  $Av = \lambda v$ , where  $\lambda$  is the corresponding eigen-value
- Using the  $k$  leading eigenvectors, project the original data into the new space defined by the  $k$  leading eigenvectors, and run a clustering algorithm, such as  $k$ -means, to find  $k$  clusters
- Assign the original data points to clusters according to how the transformed points are assigned in the clusters obtained

# Spectral Clustering: Illustration and Comments

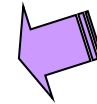


- Spectral clustering: Effective in tasks like image processing
- Scalability challenge: Computing eigenvectors on a large matrix is costly
- Can be combined with other clustering methods, such as bi-clustering

# Chapter 11. Cluster Analysis: Advanced Methods

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- Probability Model-Based Clustering
- Clustering High-Dimensional Data
- Clustering Graphs and Network Data
- Clustering with Constraints
- Summary

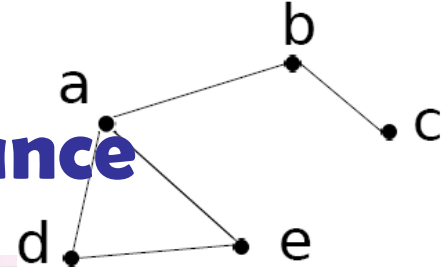


# Clustering Graphs and Network Data

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- Applications
  - Bi-partite graphs, e.g., customers and products, authors and conferences
  - Web search engines, e.g., click through graphs and Web graphs
  - Social networks, friendship/coauthor graphs
- Similarity measures
  - Geodesic distances
  - Distance based on random walk (SimRank)
- Graph clustering methods
  - Minimum cuts: FastModularity (Clauset, Newman & Moore, 2004)
  - Density-based clustering: SCAN (Xu et al., KDD'2007)

# Similarity Measure (I): Geodesic Distance



- Geodesic distance  $(A, B)$ : length (i.e., # of edges) of the shortest path between  $A$  and  $B$  (if not connected, defined as infinite)
- **Eccentricity** of  $v$ ,  $\text{eccen}(v)$ : The largest geodesic distance between  $v$  and any other vertex  $u \in V - \{v\}$ .
  - E.g.,  $\text{eccen}(a) = \text{eccen}(b) = 2$ ;  $\text{eccen}(c) = \text{eccen}(d) = \text{eccen}(e) = 3$
- **Radius** of graph  $G$ : The minimum eccentricity of all vertices, i.e., the distance between the “most central point” and the “farthest border”
  - $r = \min_{v \in V} \text{eccen}(v)$
  - E.g.,  $\text{radius}(g) = 2$
- **Diameter** of graph  $G$ : The maximum eccentricity of all vertices, i.e., the largest distance between any pair of vertices in  $G$ 
  - $d = \max_{v \in V} \text{eccen}(v)$
  - E.g.,  $\text{diameter}(g) = 3$
- A **peripheral vertex** is a vertex that achieves the diameter.
  - E.g., Vertices  $c$ ,  $d$ , and  $e$  are peripheral vertices

# SimRank: Similarity Based on Random Walk and Structural Context

- SimRank: structural-context similarity, i.e., based on the similarity of its neighbors
- In a directed graph  $G = (V, E)$ ,
  - *individual in-neighborhood* of  $v$ :  $I(v) = \{u \mid (u, v) \in E\}$
  - *individual out-neighborhood* of  $v$ :  $O(v) = \{w \mid (v, w) \in E\}$
- Similarity in SimRank: 
$$s(u, v) = \frac{C}{|I(u)||I(v)|} \sum_{x \in I(u)} \sum_{y \in I(v)} s(x, y)$$
  - Initialization:  $s_0(u, v) = \begin{cases} 0 & \text{if } u \neq v \\ 1 & \text{if } u = v \end{cases}$ 

$$P[t] = \begin{cases} \prod_{i=1}^{k-1} \frac{1}{|O(w_i)|} & \text{if } l(t) > 0 \\ 0 & \text{if } l(t) = 0. \end{cases}$$
  - Then we can compute  $s_{i+1}$  from  $s_i$  based on the definition
- Similarity based on random walk: in a strongly connected component
  - Expected distance:  $d(u, v) = \sum_{t: u \rightsquigarrow v} P[t]l(t)$   $P[t]$  is the probability of the tour
  - Expected meeting distance:  $m(u, v) = \sum_{t: (u,v) \rightsquigarrow (x,x)} P[t]l(t)$
  - Expected meeting probability:  $p(u, v) = \sum_{t: (u,v) \rightsquigarrow (x,x)} P[t]C^{l(t)}$



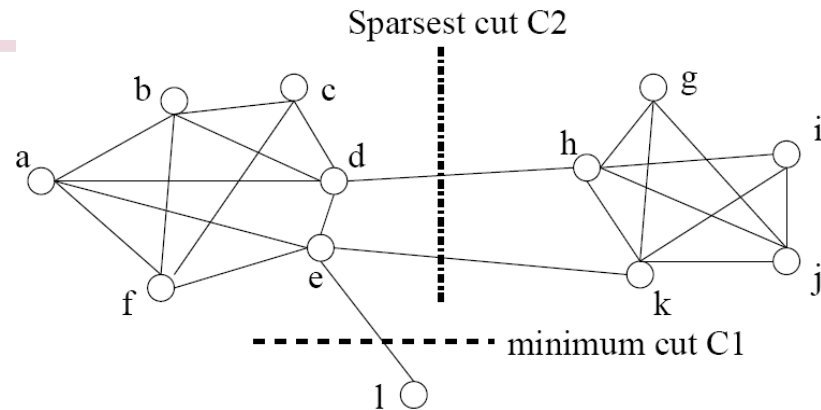
# Graph Clustering: Sparsest Cut

- $G = (V, E)$ . The *cut set* of a cut is the set of edges  $\{(u, v) \in E \mid u \in S, v \in T\}$  and  $S$  and  $T$  are in two partitions

- Size of the cut: # of edges in the cut set

- Min-cut (e.g.,  $C_1$ ) is not a good partition

- A better measure: **Sparsity**:  $\Phi = \frac{\text{the size of the cut}}{\min\{|S|, |T|\}}$



- A cut is **sparsest** if its sparsity is not greater than that of any other cut

- Ex. Cut  $C_2 = (\{a, b, c, d, e, f, l\}, \{g, h, i, j, k\})$  is the sparsest cut

- For  $k$  clusters, the **modularity** of a clustering assesses the quality of the clustering:

$$Q = \sum_{i=1}^k \left( \frac{l_i}{|E|} - \left( \frac{d_i}{2|E|} \right)^2 \right) \quad \begin{array}{l} l_i: \text{\# edges between vertices in the } i\text{-th cluster} \\ d_i: \text{the sum of the degrees of the vertices in the } i\text{-th cluster} \end{array}$$

- The *modularity* of a clustering of a graph is the difference between the fraction of all edges that fall into individual clusters and the fraction that would do so if the graph vertices were randomly connected

- The optimal clustering of graphs maximizes the modularity

# Graph Clustering: Challenges of Finding Good Cuts

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- High computational cost
  - Many graph cut problems are computationally expensive
  - The sparsest cut problem is NP-hard
  - Need to tradeoff between efficiency/scalability and quality
- Sophisticated graphs
  - May involve weights and/or cycles.
- High dimensionality
  - A graph can have many vertices. In a similarity matrix, a vertex is represented as a vector (a row in the matrix) whose dimensionality is the number of vertices in the graph
- Sparsity
  - A large graph is often sparse, meaning each vertex on average connects to only a small number of other vertices
  - A similarity matrix from a large sparse graph can also be sparse

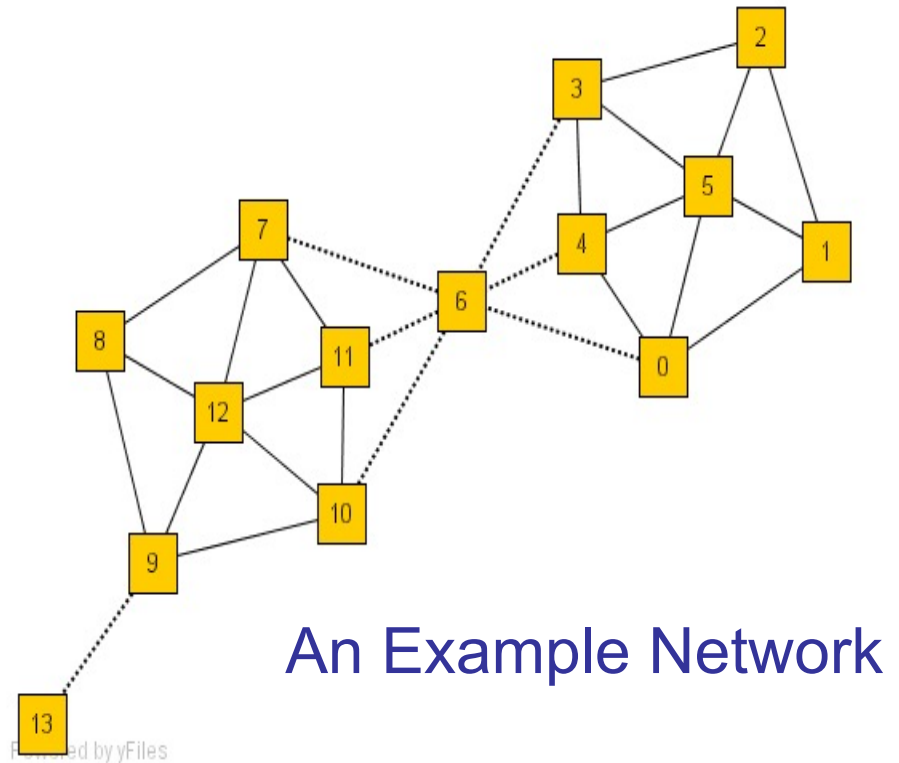
# Two Approaches for Graph Clustering

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- Two approaches for clustering graph data
  - Use *generic clustering methods* for high-dimensional data
  - *Designed specifically for clustering graphs*
- Using clustering methods for high-dimensional data
  - Extract a similarity matrix from a graph using a similarity measure
  - A generic clustering method can then be applied on the similarity matrix to discover clusters
  - Ex. Spectral clustering: approximate optimal graph cut solutions
- Methods specific to graphs
  - Search the graph to find well-connected components as clusters
  - Ex. SCAN (Structural Clustering Algorithm for Networks)
    - X. Xu, N. Yuruk, Z. Feng, and T. A. J. Schweiger, “SCAN: A Structural Clustering Algorithm for Networks”, KDD'07

# SCAN: Density-Based Clustering of Networks

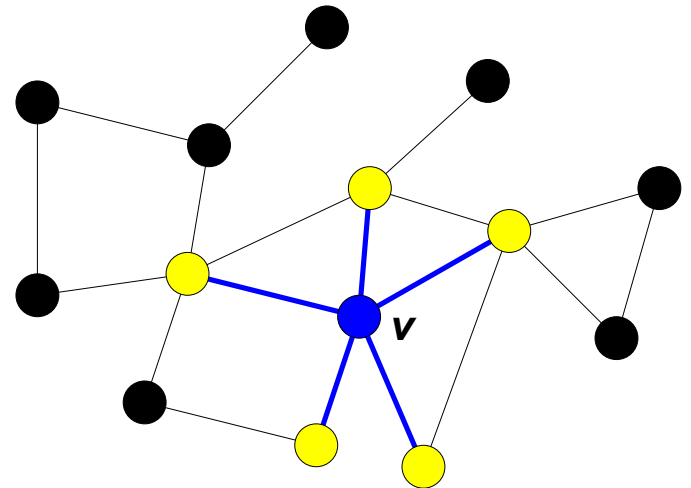
- How many clusters?
- What size should they be?
- What is the best partitioning?
- Should some points be segregated?



- Application: Given simply information of who associates with whom, could one identify clusters of individuals with common interests or special relationships (families, cliques, terrorist cells)?

# A Social Network Model

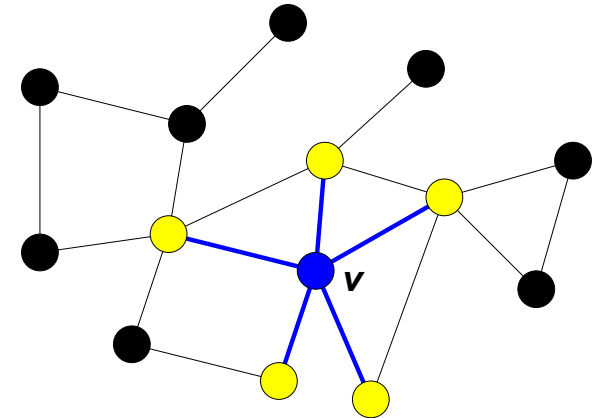
- Cliques, hubs and outliers
  - Individuals in a tight social group, or **clique**, know many of the same people, regardless of the size of the group
  - Individuals who are **hubs** know many people in different groups but belong to no single group. Politicians, for example bridge multiple groups
  - Individuals who are **outliers** reside at the margins of society. Hermits, for example, know few people and belong to no group
- The Neighborhood of a Vertex
  - Define  $\Gamma(v)$  as the immediate neighborhood of a vertex (i.e. the set of people that an individual knows )



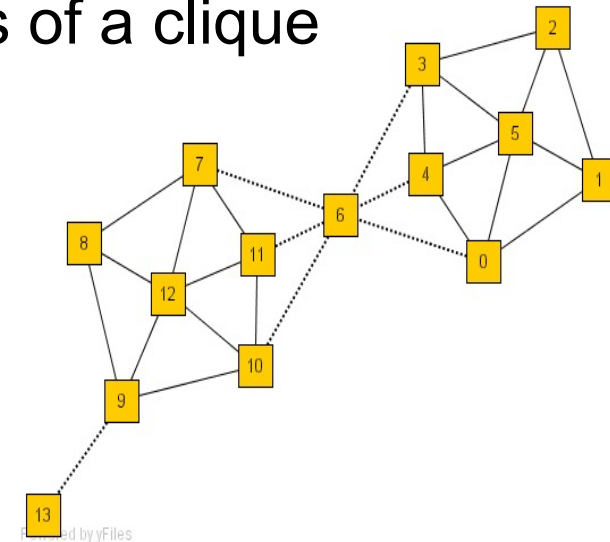
# Structure Similarity

- The desired features tend to be captured by a measure we call Structural Similarity

$$\sigma(v, w) = \frac{|\Gamma(v) \cap \Gamma(w)|}{\sqrt{|\Gamma(v)| |\Gamma(w)|}}$$



- Structural similarity is large for members of a clique and small for hubs and outliers



# Structural Connectivity [1]

---

- $\varepsilon$ -Neighborhood:  $N_\varepsilon(v) = \{w \in \Gamma(v) \mid \sigma(v, w) \geq \varepsilon\}$

- Core:  $CORE_{\varepsilon, \mu}(v) \Leftrightarrow |N_\varepsilon(v)| \geq \mu$

- Direct structure reachable:

$$DirRECH_{\varepsilon, \mu}(v, w) \Leftrightarrow CORE_{\varepsilon, \mu}(v) \wedge w \in N_\varepsilon(v)$$

- Structure reachable: transitive closure of direct structure reachability

- Structure connected:

$$CONNECT_{\varepsilon, \mu}(v, w) \Leftrightarrow \exists u \in V : RECH_{\varepsilon, \mu}(u, v) \wedge RECH_{\varepsilon, \mu}(u, w)$$

[1] M. Ester, H. P. Kriegel, J. Sander, & X. Xu (KDD'96) "A Density-Based Algorithm for Discovering Clusters in Large Spatial Databases"

# Structure-Connected Clusters

## ■ Structure-connected cluster C

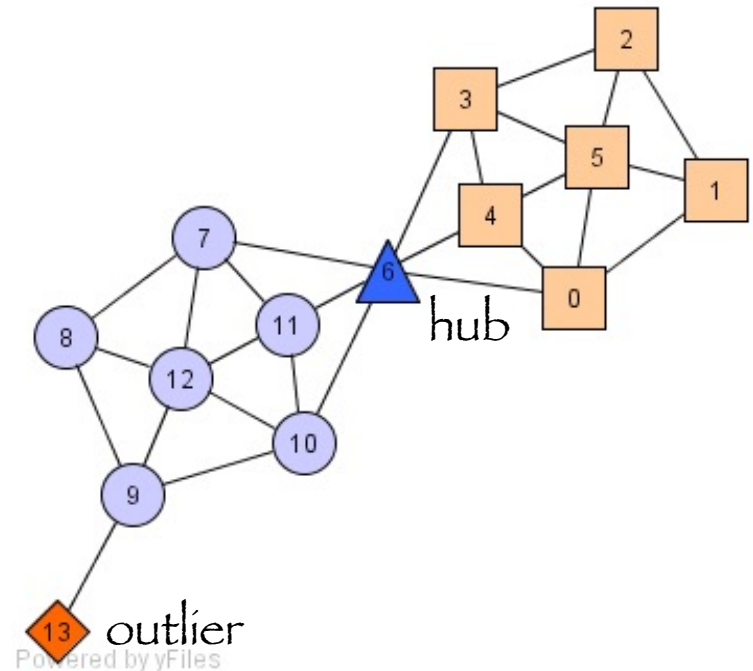
- Connectivity:  $\forall v, w \in C : CONNECT_{\varepsilon, \mu}(v, w)$
- Maximality:  $\forall v, w \in V : v \in C \wedge REACH_{\varepsilon, \mu}(v, w) \Rightarrow w \in C$

## ■ Hubs:

- Not belong to any cluster
- Bridge to many clusters

## ■ Outliers:

- Not belong to any cluster
- Connect to less clusters

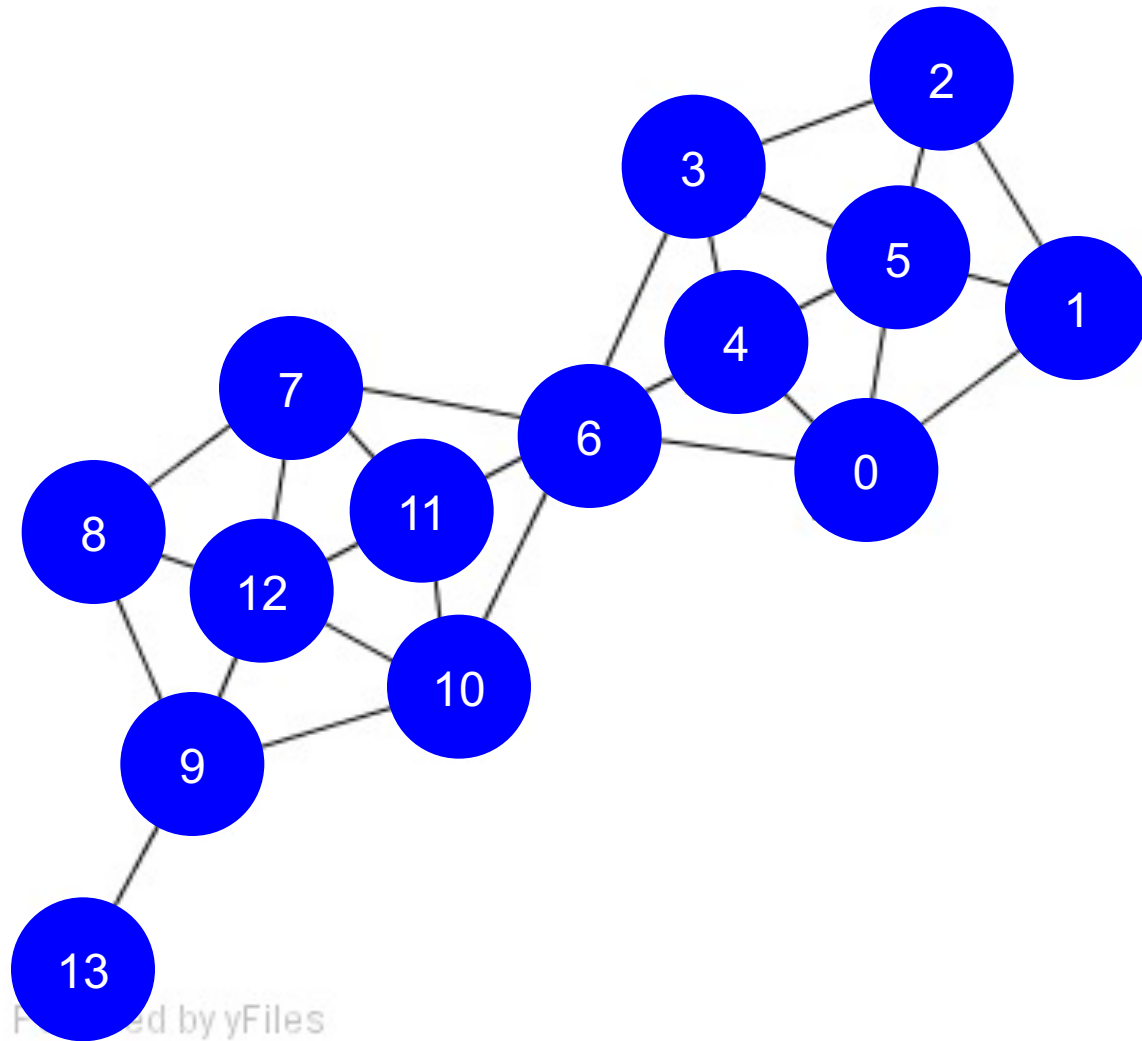




# Algorithm

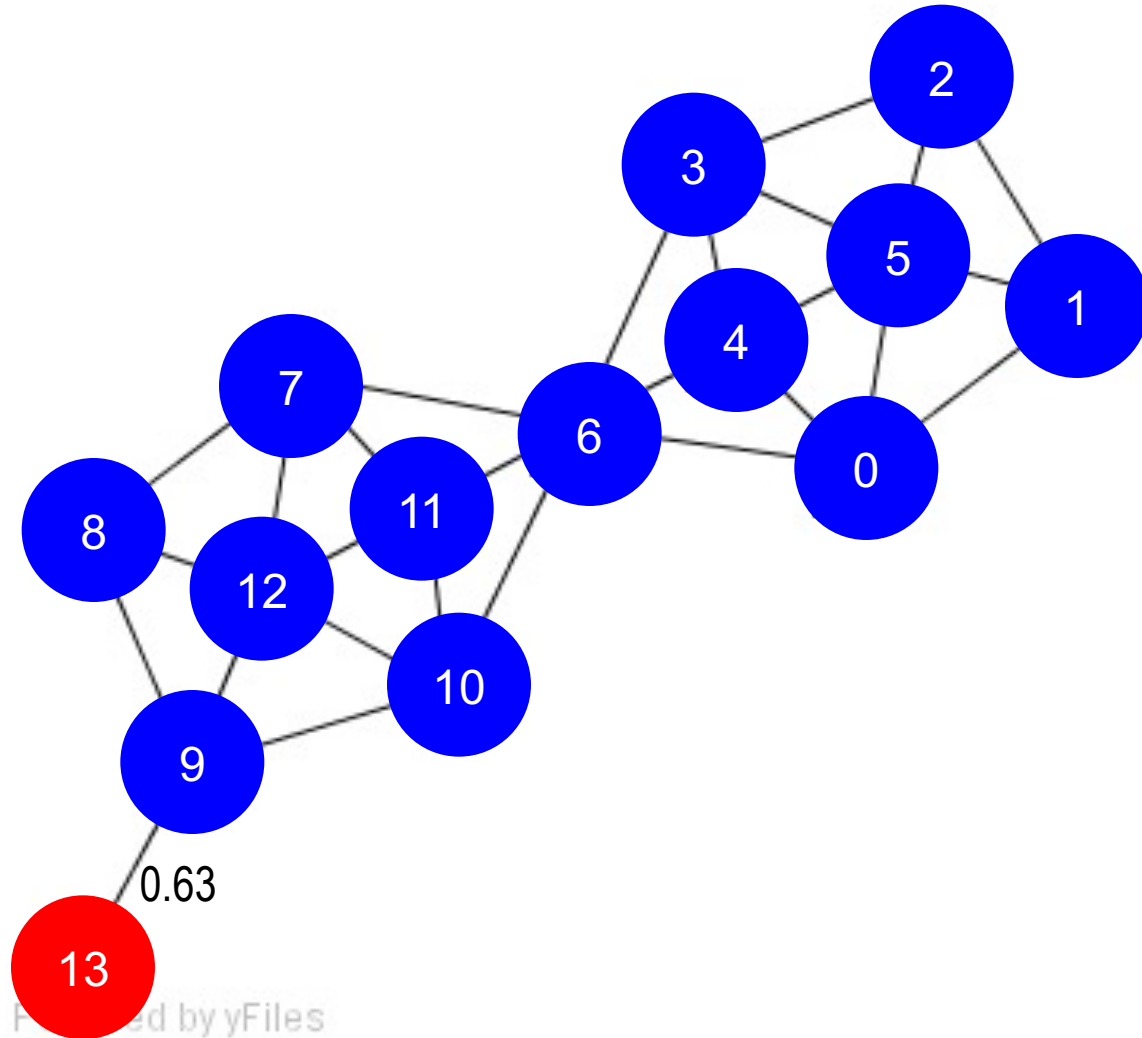
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$$\mu = 2$$
$$\varepsilon = 0.7$$



# Algorithm

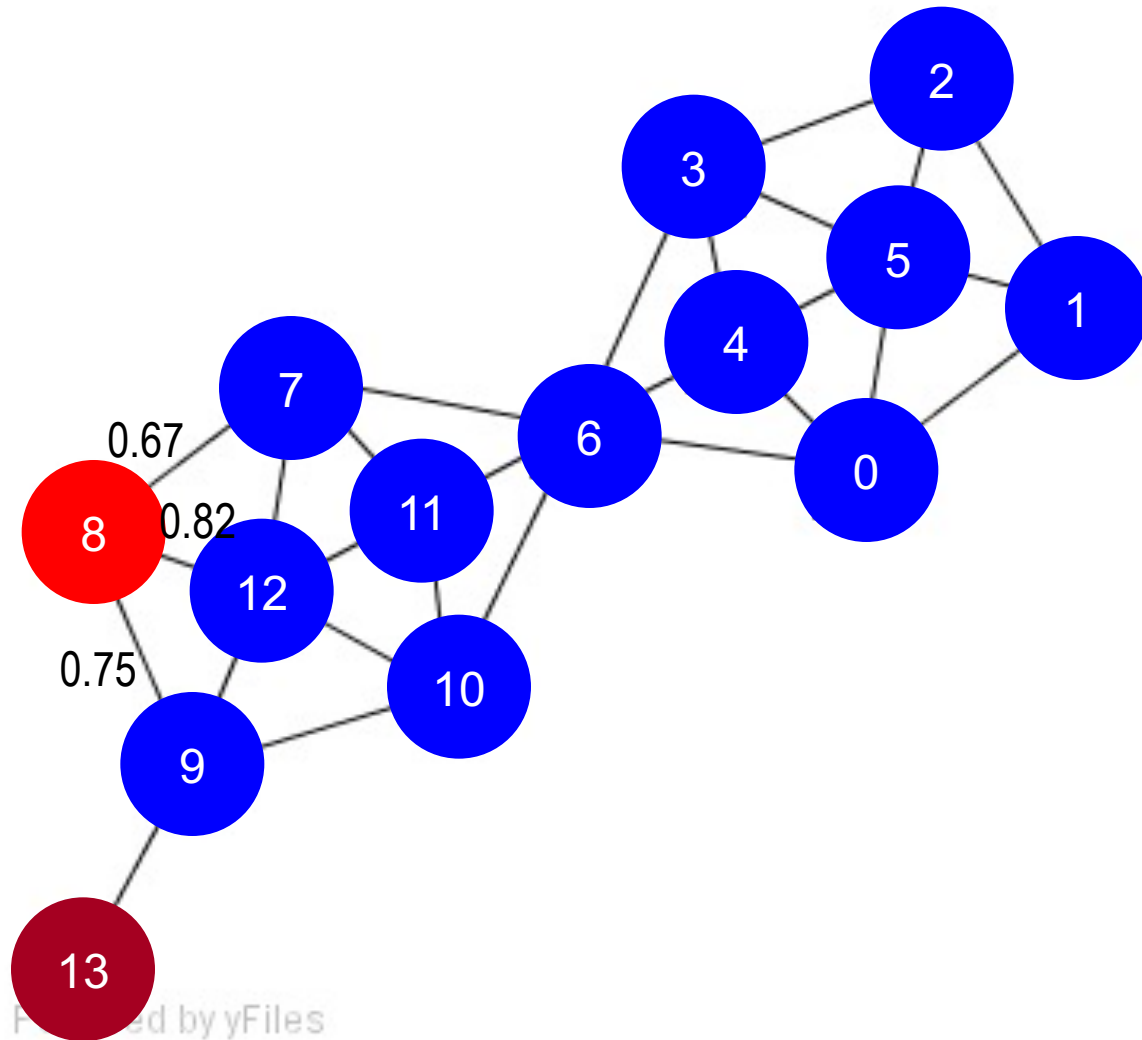
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# Algorithm

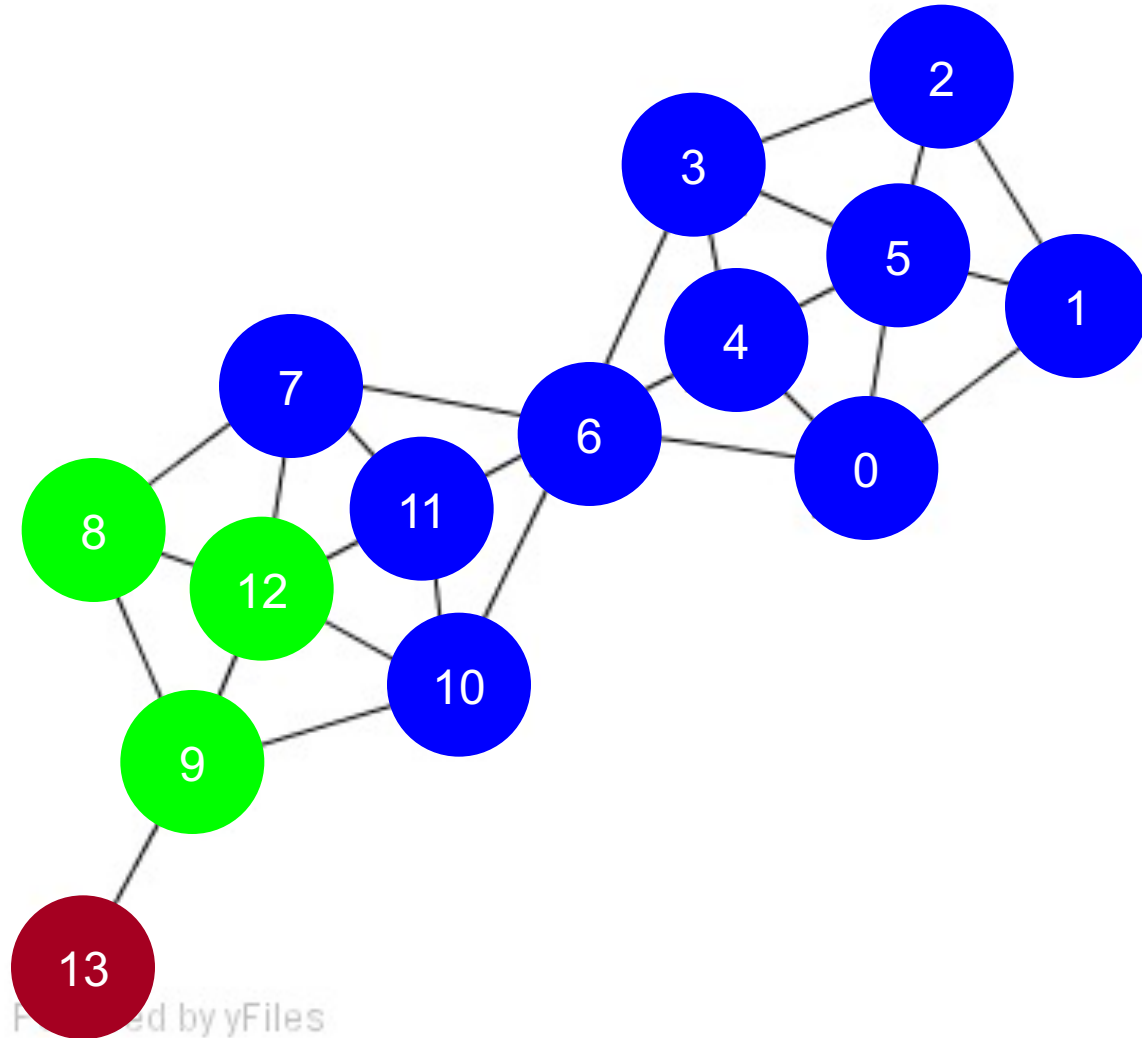
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# Algorithm

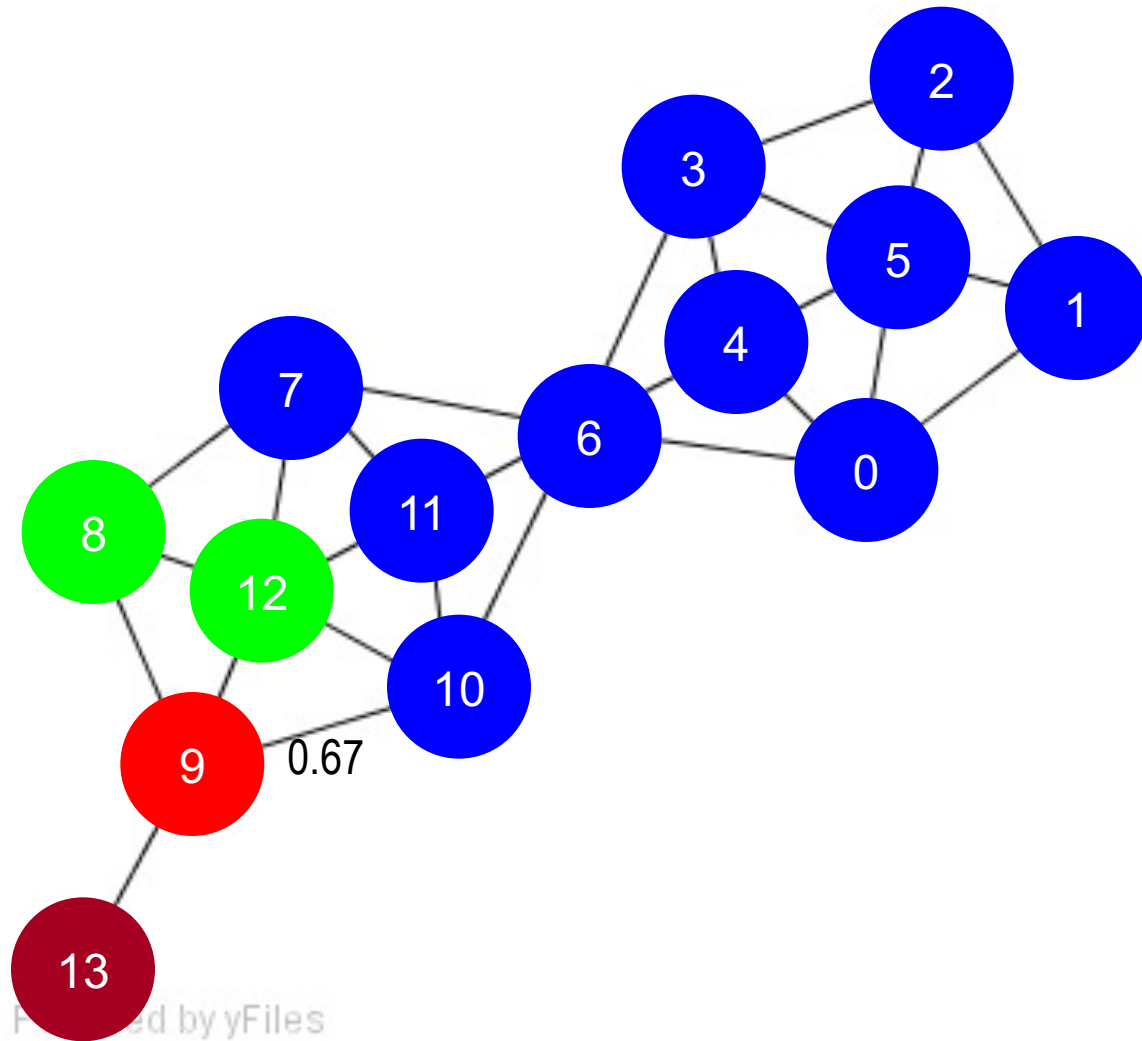
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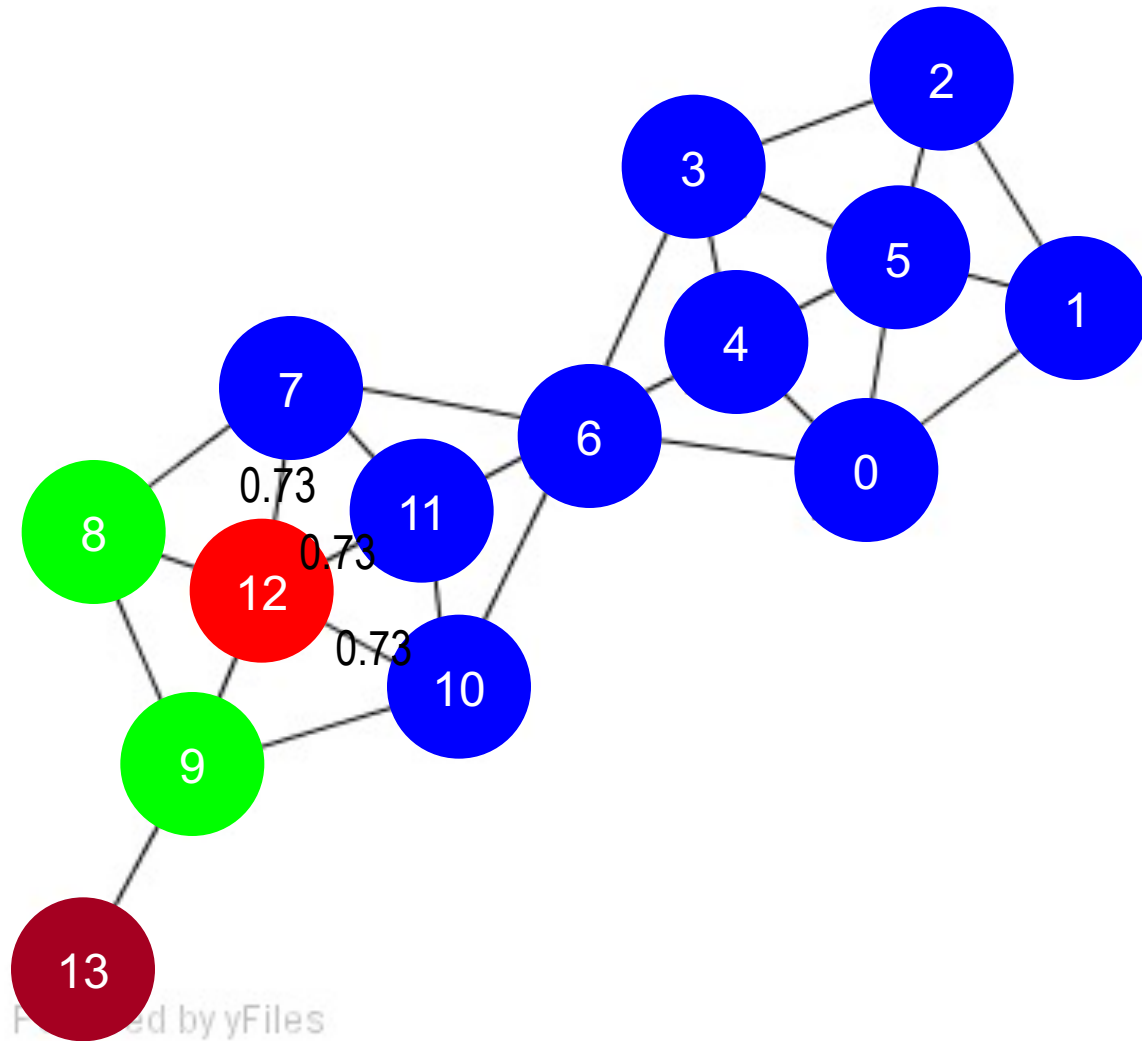
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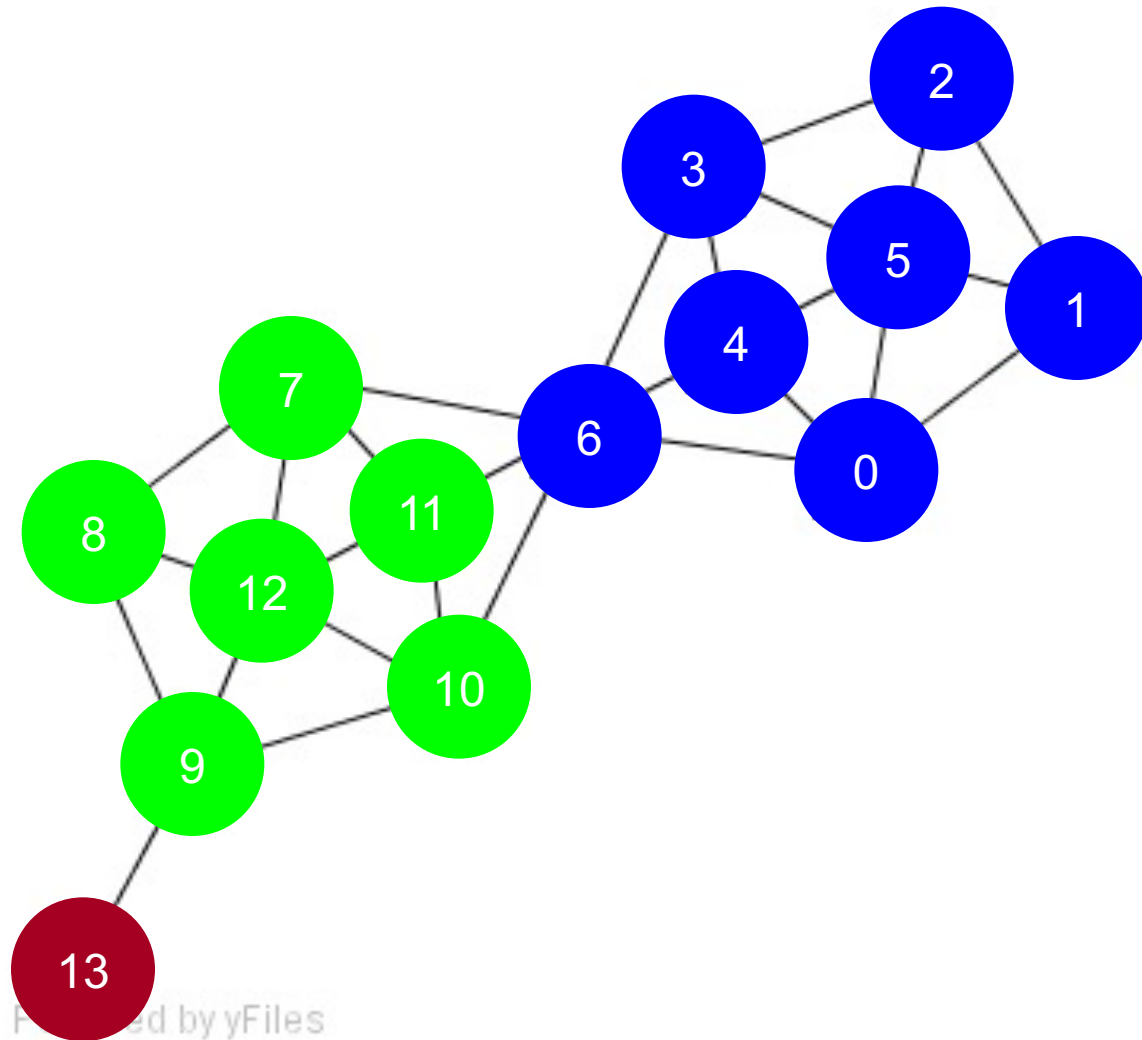
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# Algorithm

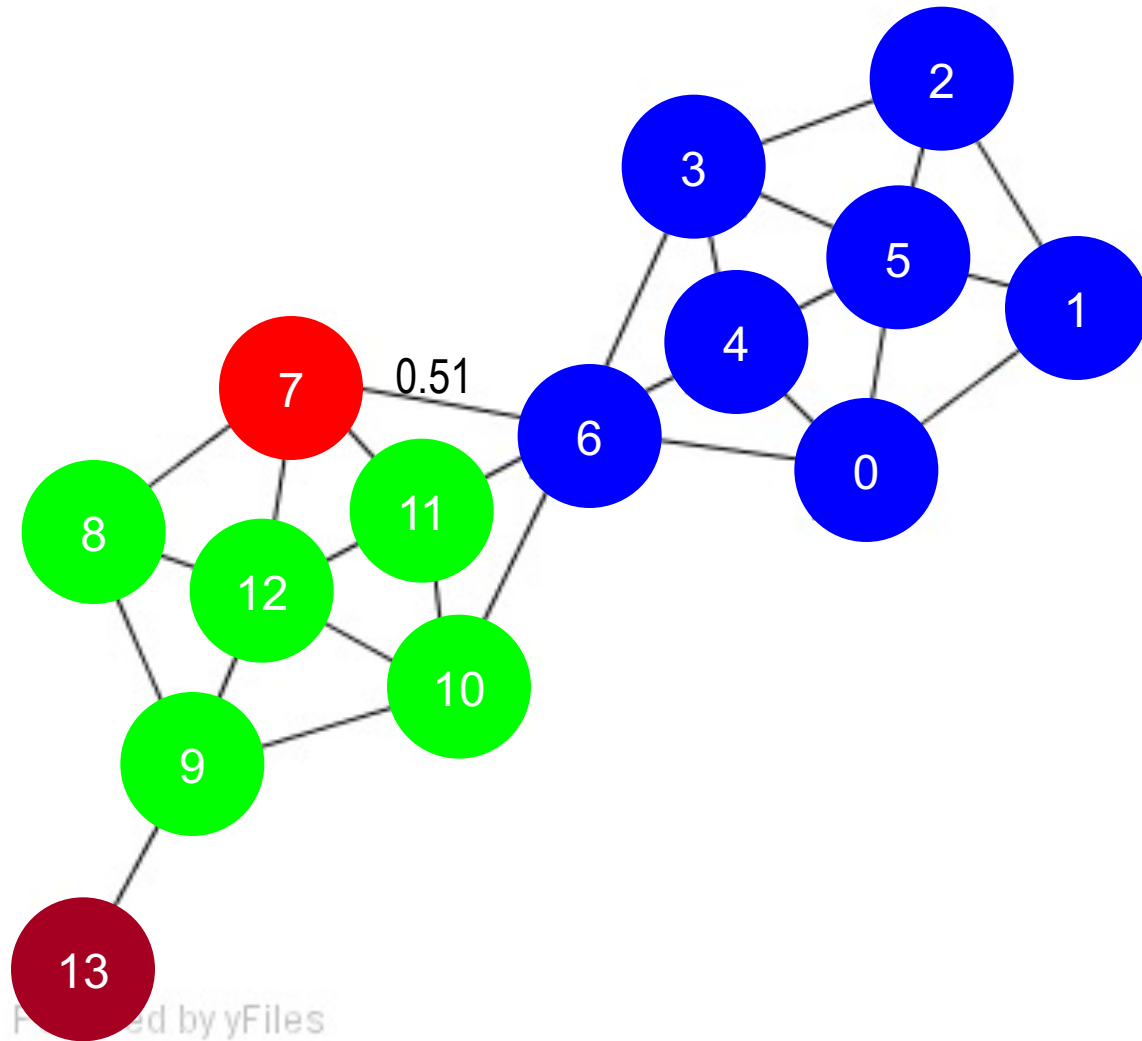
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# Algorithm

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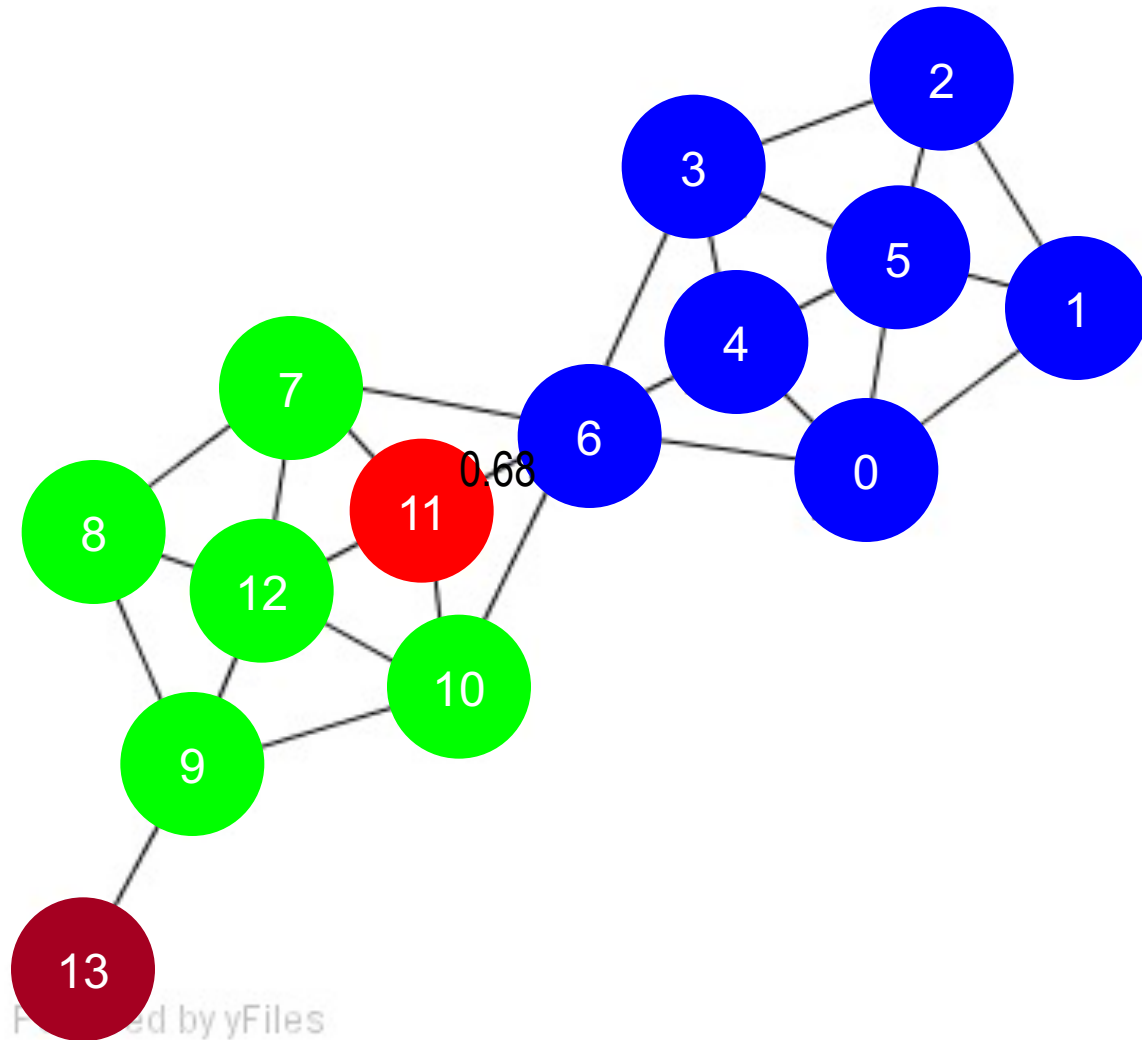


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# Algorithm

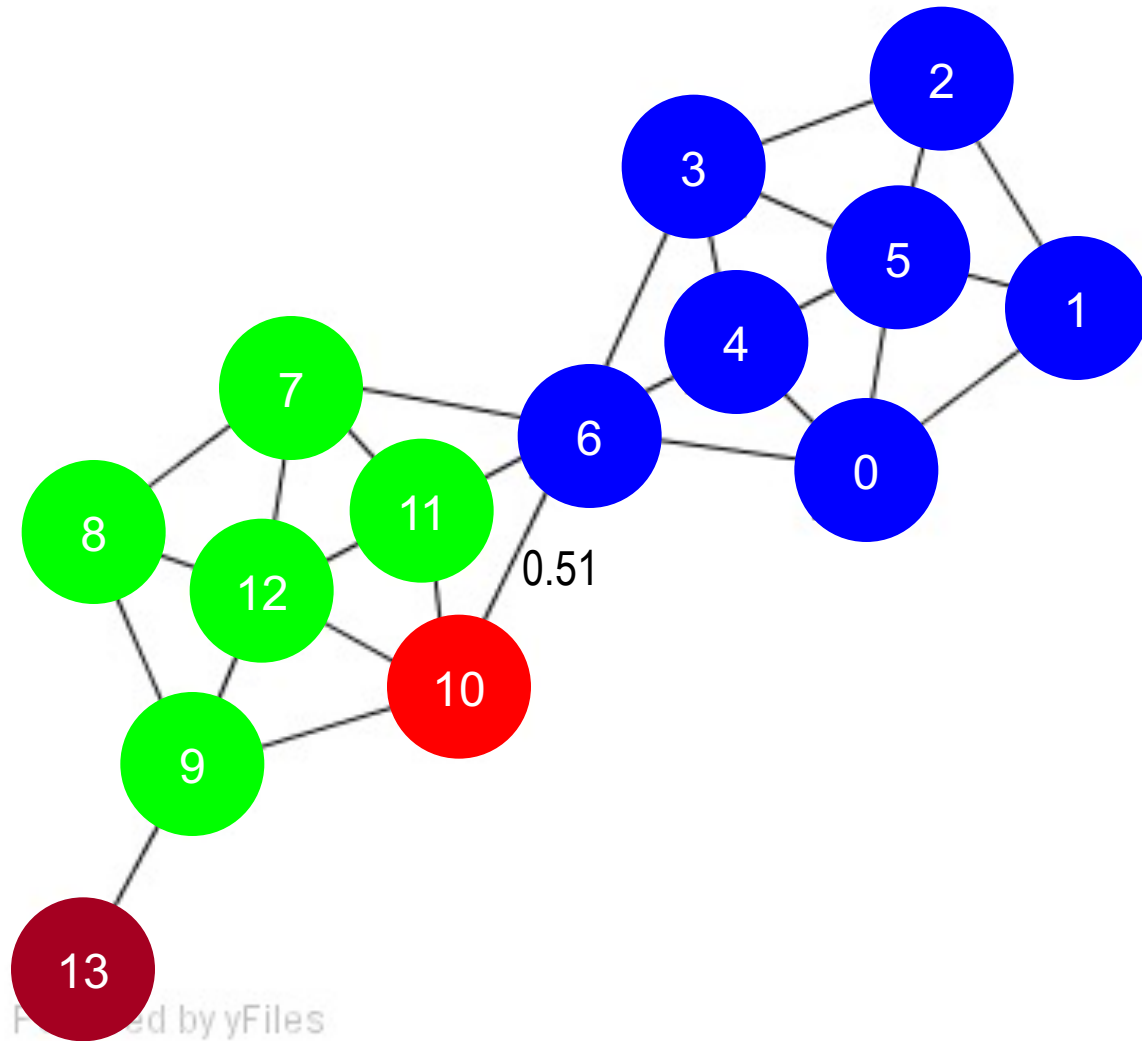
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# Algorithm

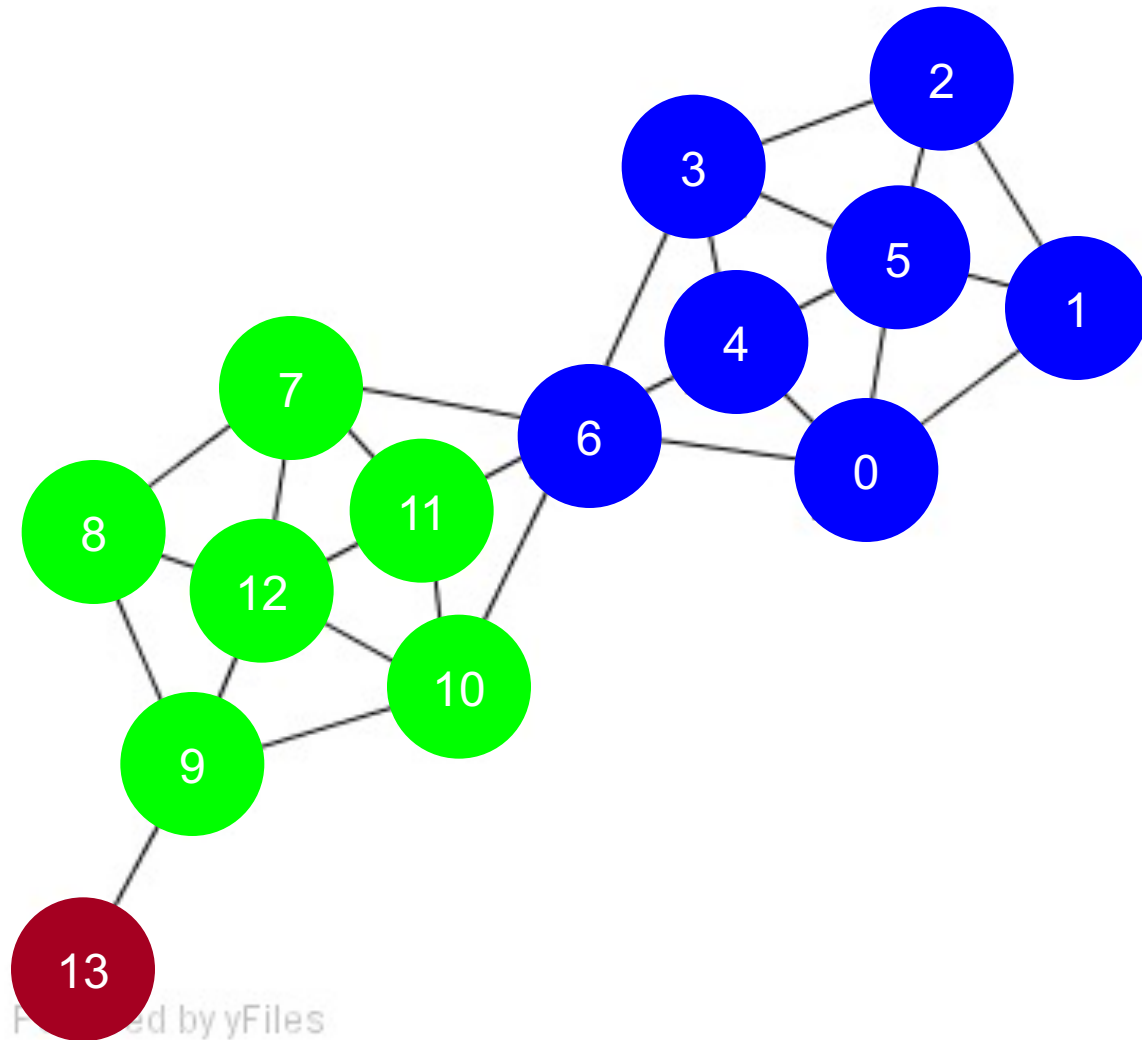
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# Algorithm

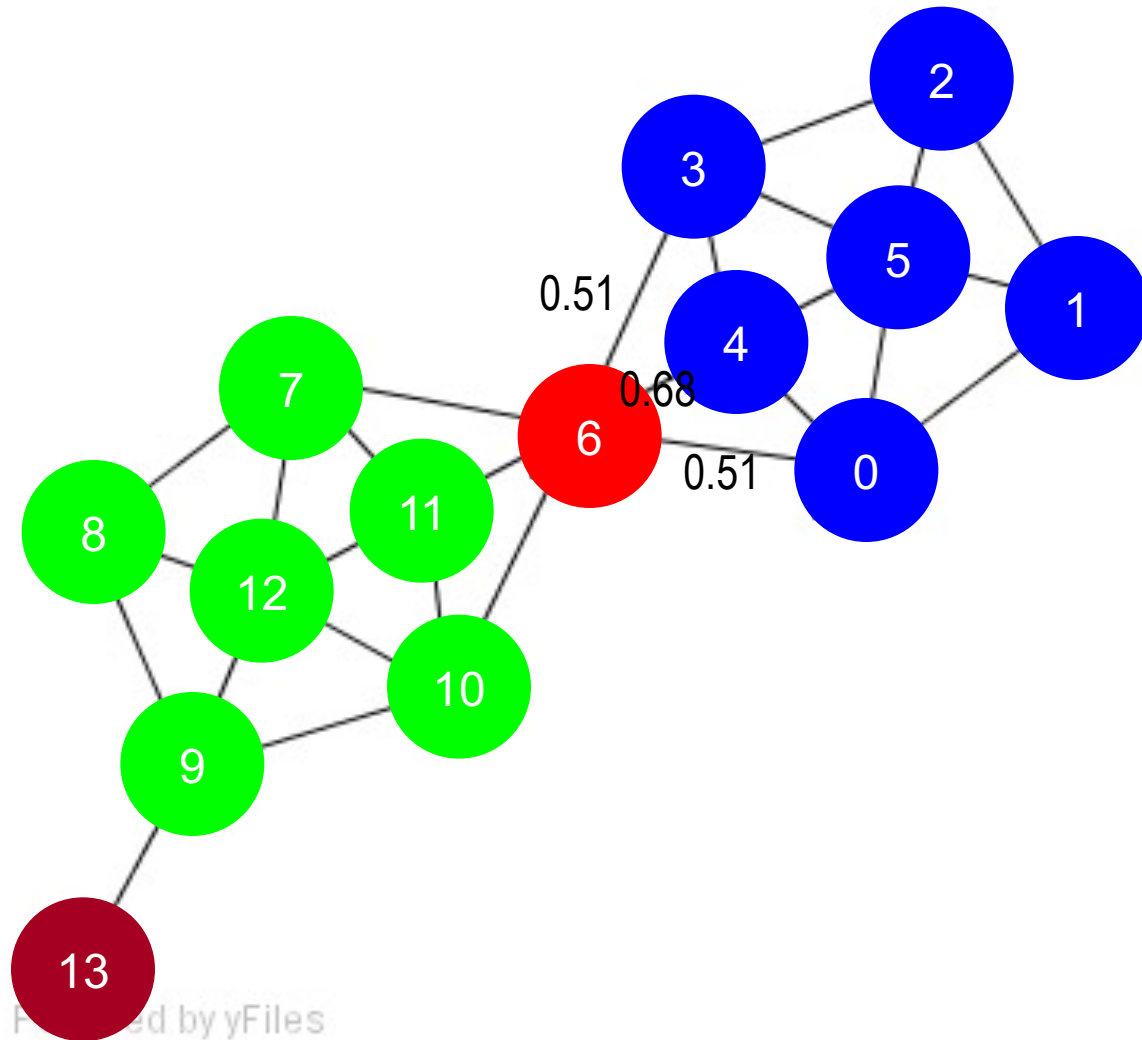
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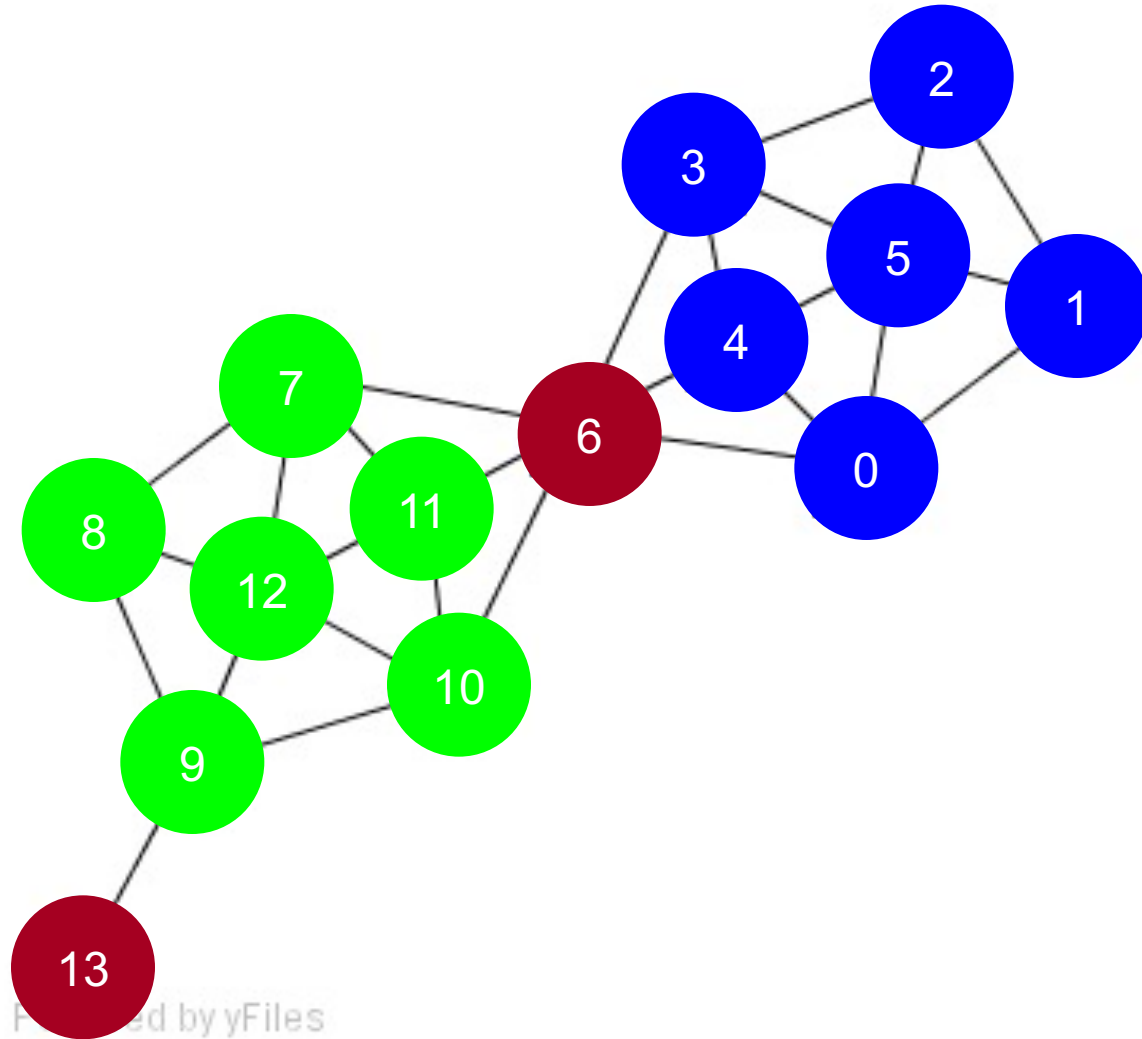
# Algorithm

$$\mu = 2$$
$$\varepsilon = 0.7$$



# Algorithm

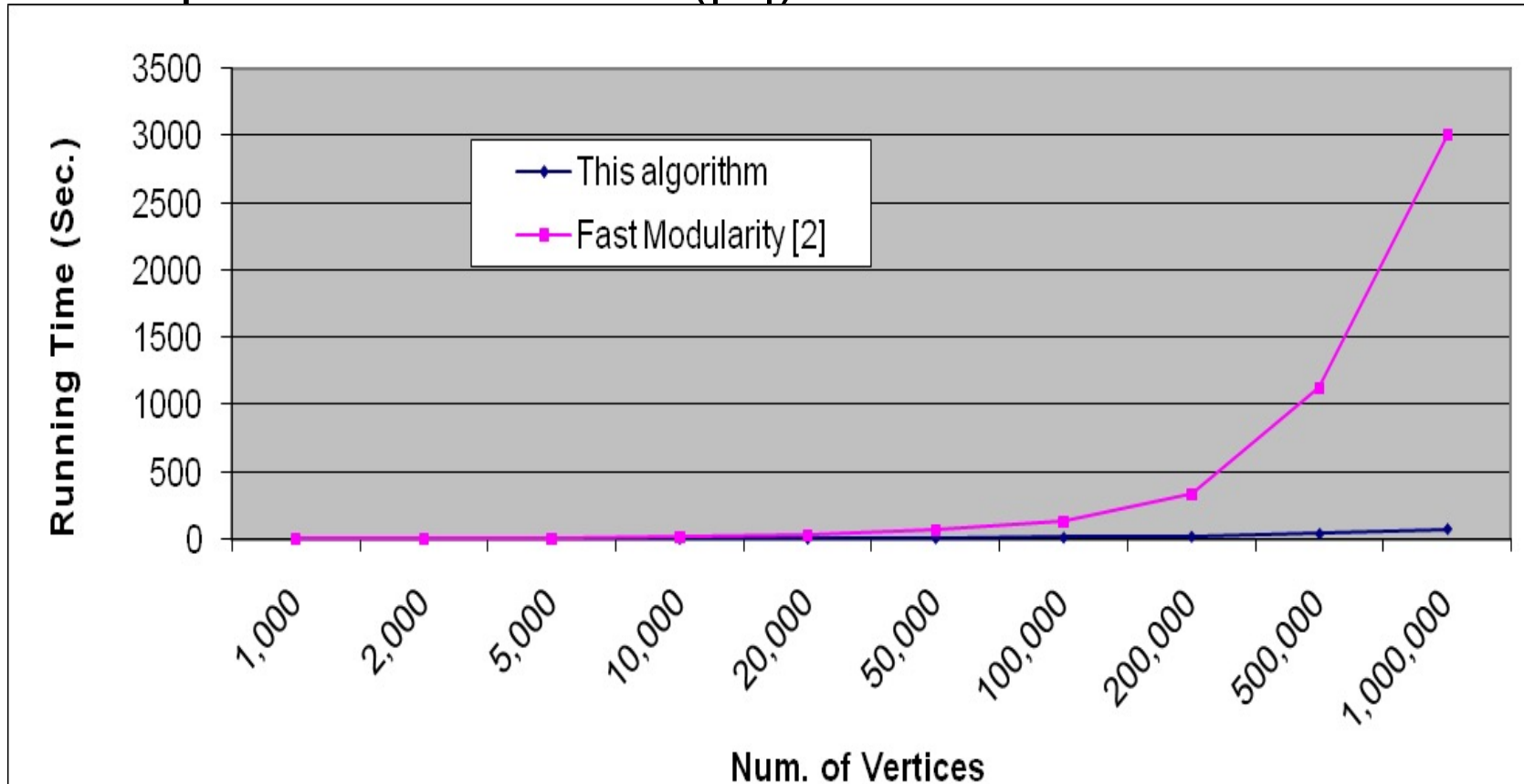
$$\mu = 2$$
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# Running Time

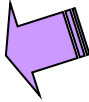
- Running time =  $O(|E|)$
- For sparse networks =  $O(|V|)$



[2] A. Clauset, M. E. J. Newman, & C. Moore, *Phys. Rev. E* **70**, 066111 (2004).

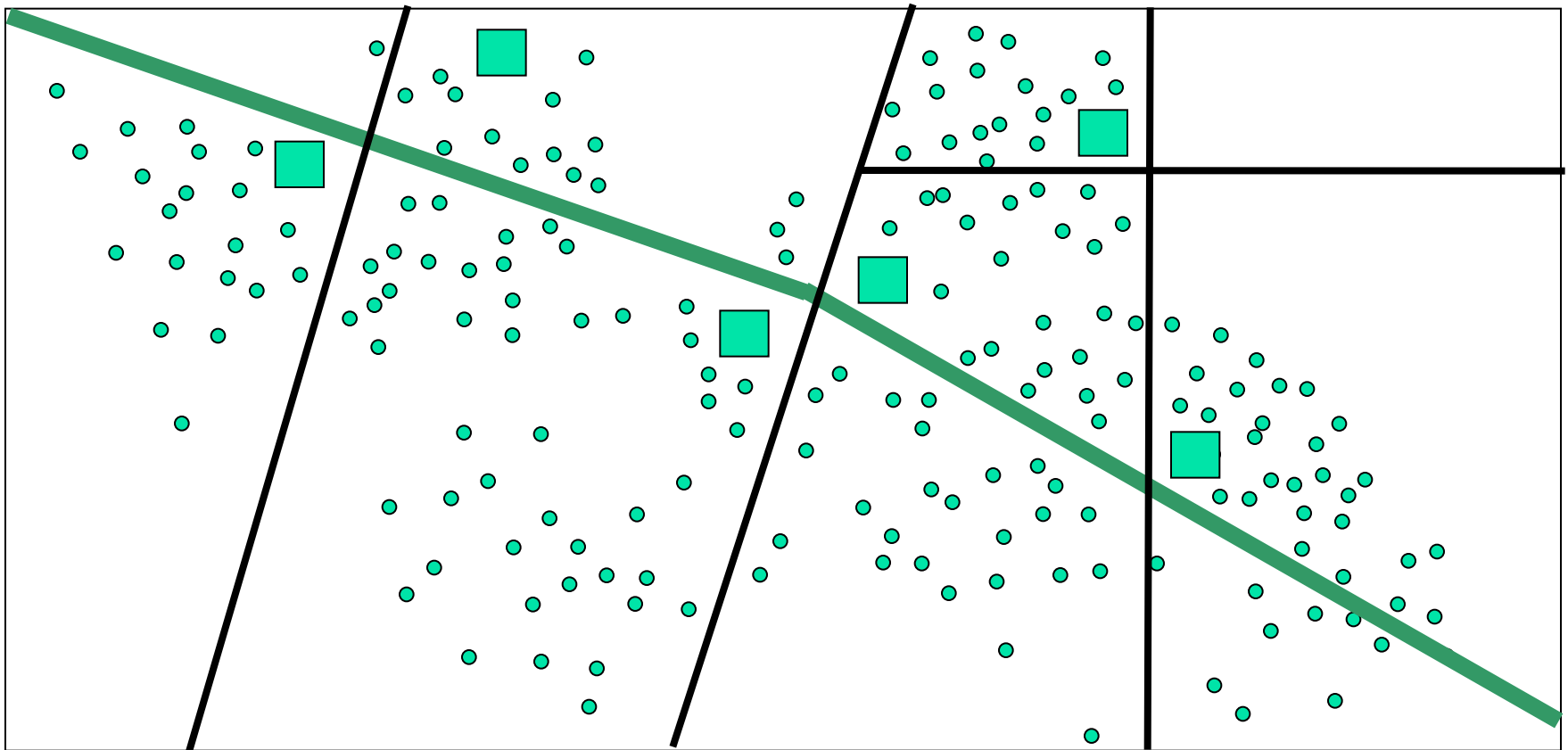
# Chapter 11. Cluster Analysis: Advanced Methods

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- Probability Model-Based Clustering
- Clustering High-Dimensional Data
- Clustering Graphs and Network Data
- Clustering with Constraints 
- Summary

# Why Constraint-Based Cluster Analysis?

- Need user feedback: Users know their applications the best
- Less parameters but more user-desired constraints, e.g., an ATM allocation problem: obstacle & desired clusters





# Categorization of Constraints

---

- Constraints on instances: specifies how a pair or a set of instances should be grouped in the cluster analysis
  - Must-link vs. cannot link constraints
    - $\text{must-link}(x, y)$ :  $x$  and  $y$  should be grouped into one cluster
  - Constraints can be defined using variables, e.g.,
    - $\text{cannot-link}(x, y)$  if  $\text{dist}(x, y) > d$
- Constraints on clusters: specifies a requirement on the clusters
  - E.g., specify the min # of objects in a cluster, the max diameter of a cluster, the shape of a cluster (e.g., a convex), # of clusters (e.g.,  $k$ )
- Constraints on similarity measurements: specifies a requirement that the similarity calculation must respect
  - E.g., driving on roads, obstacles (e.g., rivers, lakes)
- Issues: Hard vs. soft constraints; conflicting or redundant constraints

# Constraint-Based Clustering Methods (I): Handling Hard Constraints

---

- Handling hard constraints: Strictly respect the constraints in cluster assignments
- Example: The COP-k-means algorithm
  - Generate super-instances for must-link constraints
    - Compute the transitive closure of the must-link constraints
    - To represent such a subset, replace all those objects in the subset by the mean.
    - The super-instance also carries a weight, which is the number of objects it represents
  - Conduct modified k-means clustering to respect cannot-link constraints
    - Modify the center-assignment process in k-means to a *nearest feasible center assignment*
    - An object is assigned to the nearest center so that the assignment respects all cannot-link constraints

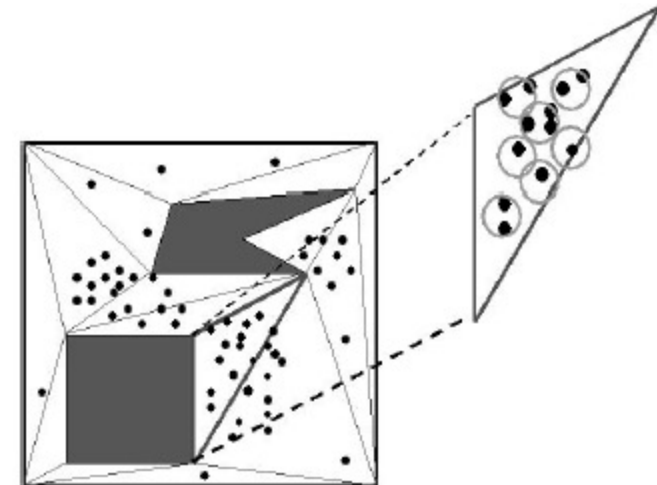
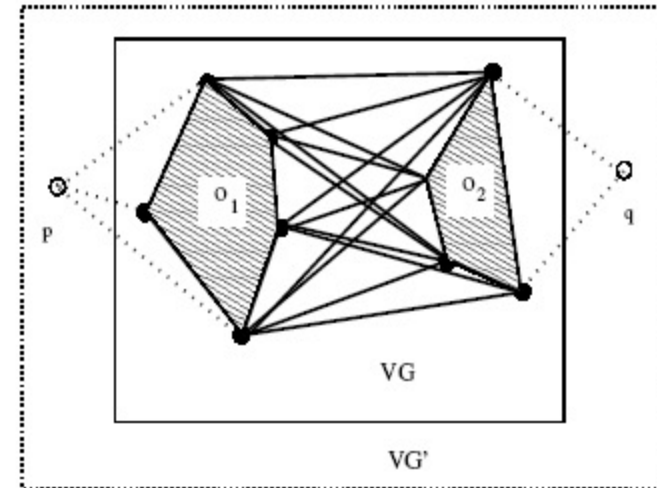
# Constraint-Based Clustering Methods (II): Handling Soft Constraints

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- Treated as an optimization problem: When a clustering violates a soft constraint, a penalty is imposed on the clustering
- Overall objective: Optimizing the clustering quality, and minimizing the constraint violation penalty
- Ex. CVQE (Constrained Vector Quantization Error) algorithm: Conduct k-means clustering while enforcing constraint violation penalties
- Objective function: Sum of distance used in k-means, adjusted by the constraint violation penalties
  - Penalty of a *must-link* violation
    - If objects  $x$  and  $y$  must-be-linked but they are assigned to two different centers,  $c_1$  and  $c_2$ ,  $\text{dist}(c_1, c_2)$  is added to the objective function as the penalty
  - Penalty of a cannot-link violation
    - If objects  $x$  and  $y$  cannot-be-linked but they are assigned to a common center  $c$ ,  $\text{dist}(c, c')$ , between  $c$  and  $c'$  is added to the objective function as the penalty, where  $c'$  is the closest cluster to  $c$  that can accommodate  $x$  or  $y$

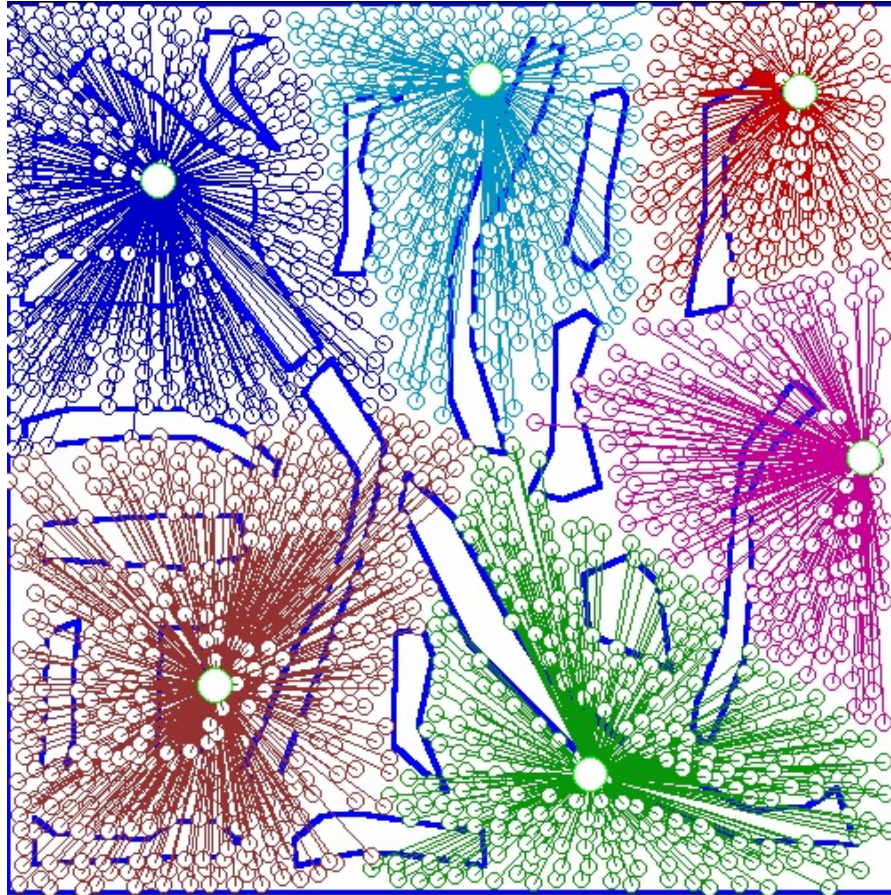
# Speeding Up Constrained Clustering

- It is costly to compute some constrained clustering
- Ex. Clustering with obstacle objects: Tung, Hou, and Han. Spatial clustering in the presence of obstacles, ICDE'01
- K-medoids is more preferable since k-means may locate the ATM center in the middle of a lake
- Visibility graph and shortest path
- Triangulation and micro-clustering
- Two kinds of join indices (shortest-paths) worth pre-computation
  - VV index: indices for any pair of obstacle vertices
  - MV index: indices for any pair of micro-cluster and obstacle indices

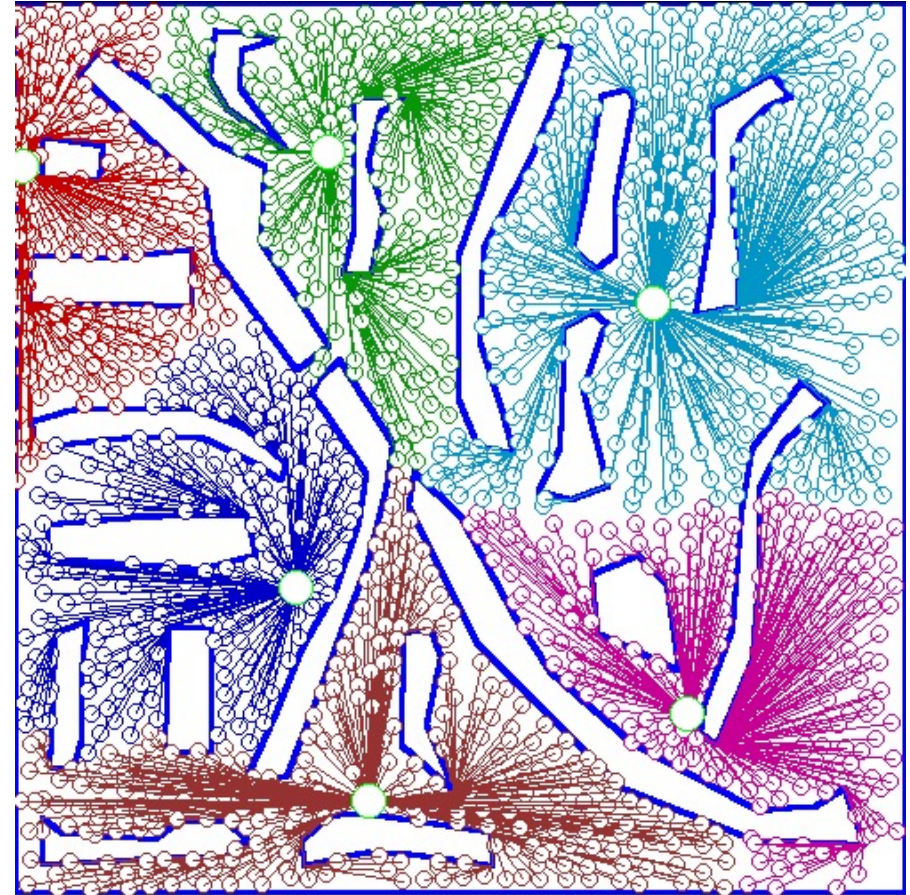




# An Example: Clustering With Obstacle Objects

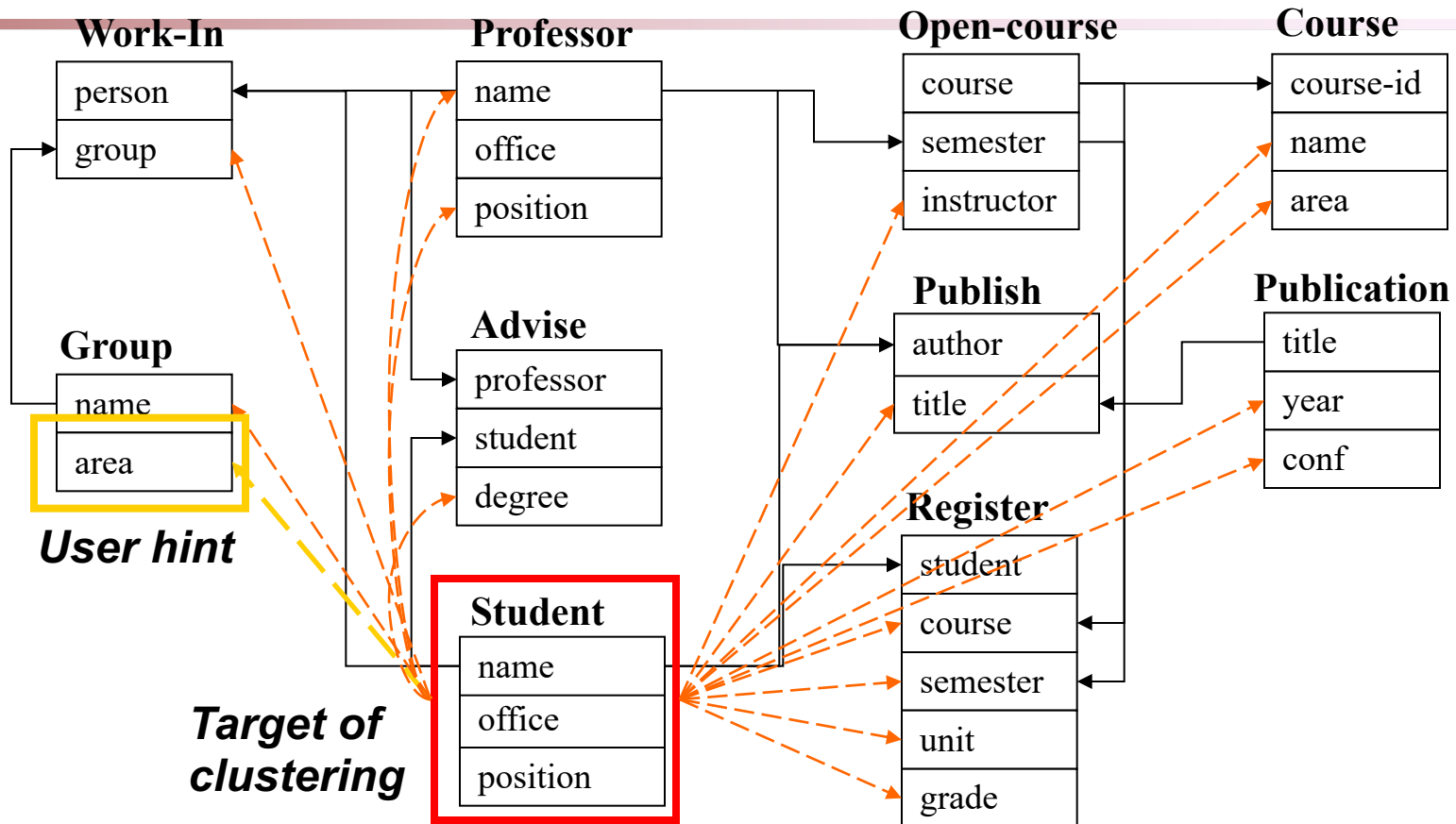


**Not** Taking obstacles into account



Taking obstacles into account

# User-Guided Clustering: A Special Kind of Constraints



- X. Yin, J. Han, P. S. Yu, "Cross-Relational Clustering with User's Guidance", KDD'05
- User usually has a goal of clustering, e.g., clustering students by research area
- User specifies his clustering goal to CrossClus

## Comparing with Classification

			Red
			Orange
			Purple

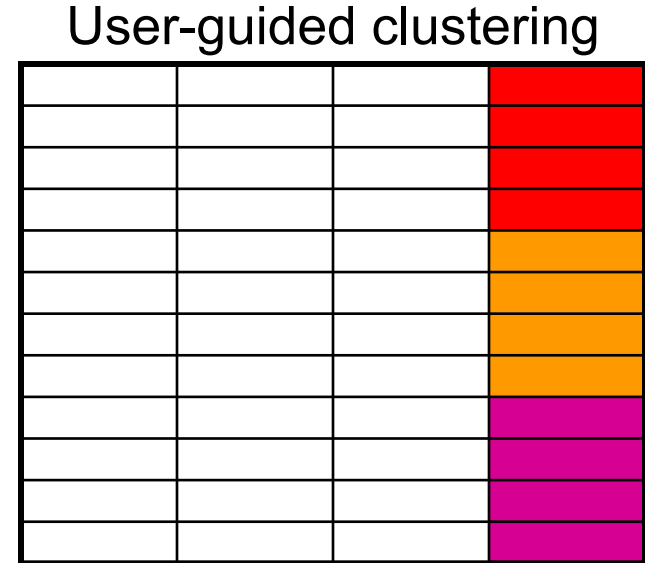
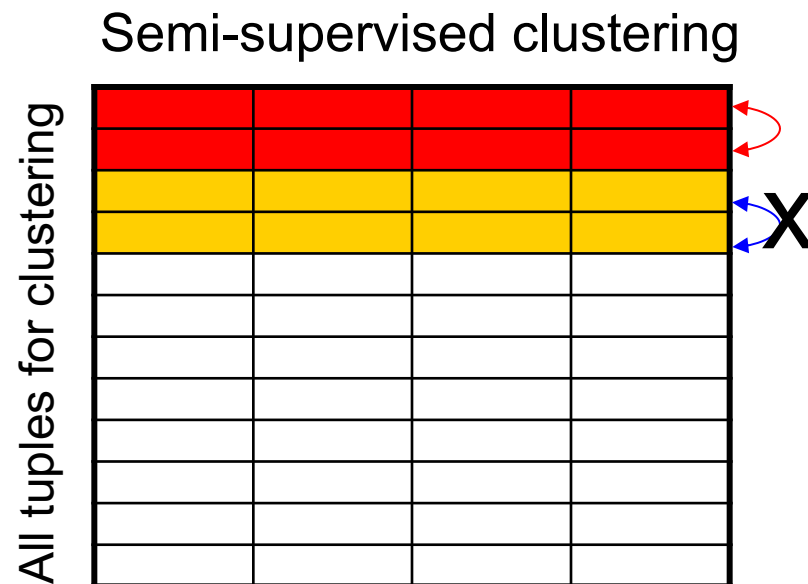
## All tuples for clustering

- User-specified *feature* (in the form of *attribute*) is used as a hint, not class labels

  - The attribute may contain too many or too few distinct values, e.g., a user may want to cluster students into 20 clusters instead of 3
  - Additional features need to be included in cluster analysis

# Comparing with Semi-Supervised Clustering

- Semi-supervised clustering: User provides a training set consisting of “similar” (“must-link”) and “dissimilar” (“cannot link”) pairs of objects
- User-guided clustering: User specifies an attribute as a hint, and more relevant features are found for clustering

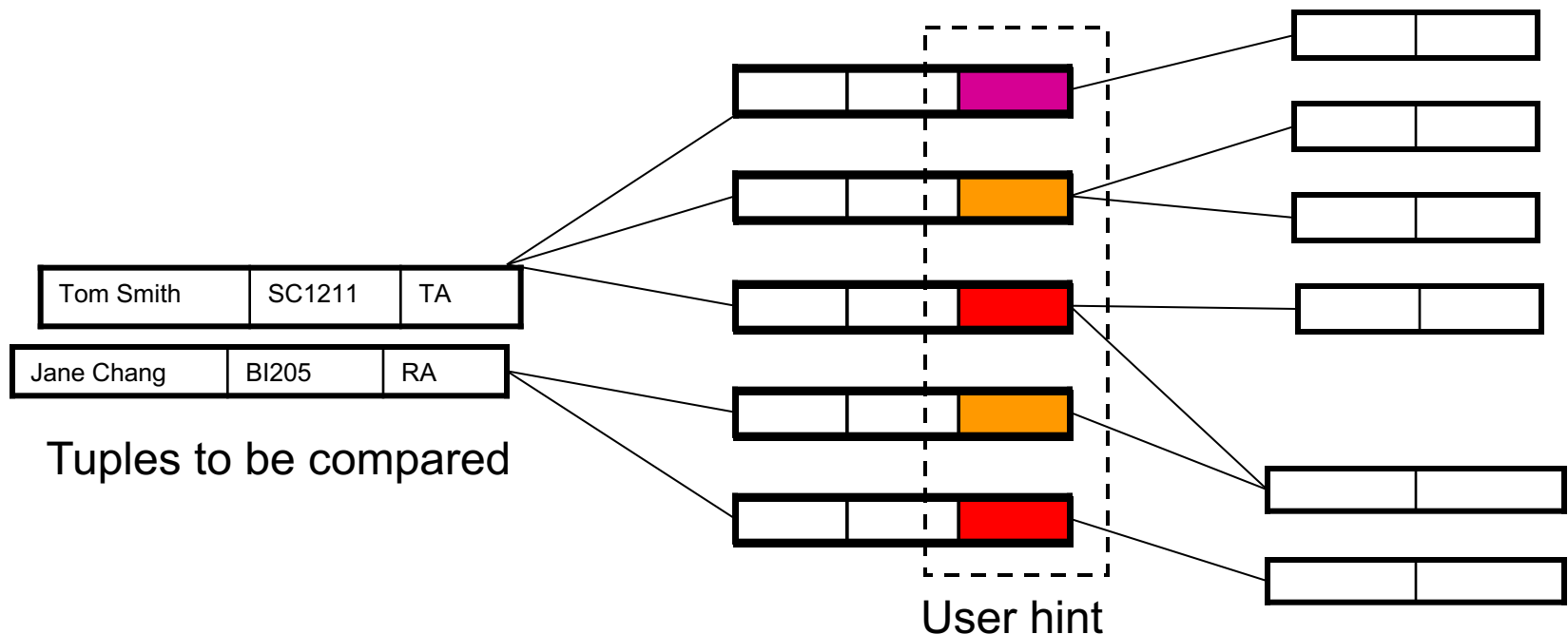


All tuples for clustering



# Why Not Semi-Supervised Clustering?

- Much information (in multiple relations) is needed to judge whether two tuples are similar
- A user may not be able to provide a good training set
- It is much easier for a user to specify an attribute as a hint, such as a student's *research area*



# CrossClus: An Overview

---

- Measure *similarity between features* by how they group objects into clusters
- Use a heuristic method to search for pertinent features
  - *Start from user-specified feature and gradually expand search range*
- Use *tuple ID propagation* to create feature values
  - Features can be easily created during the expansion of search range, by propagating IDs
- Explore three clustering algorithms: *k*-means, *k*-medoids, and hierarchical clustering

# Multi-Relational Features

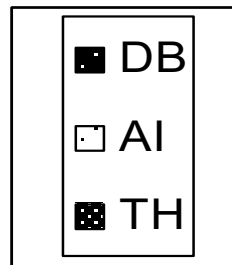
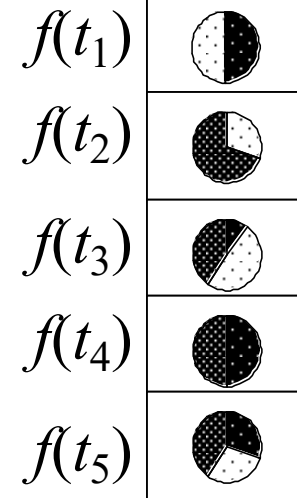
- A multi-relational feature is defined by:
  - A join path, e.g.,  $Student \rightarrow Register \rightarrow OpenCourse \rightarrow Course$
  - An attribute, e.g.,  $Course.area$
  - (For numerical feature) an aggregation operator, e.g., sum or average
- Categorical feature  $f = [Student \rightarrow Register \rightarrow OpenCourse \rightarrow Course, Course.area, \text{null}]$

areas of courses of each student

Tuple	Areas of courses		
	<i>DB</i>	<i>AI</i>	<i>TH</i>
$t_1$	5	5	0
$t_2$	0	3	7
$t_3$	1	5	4
$t_4$	5	0	5
$t_5$	3	3	4

Values of feature  $f$

Tuple	Feature $f$		
	<i>DB</i>	<i>AI</i>	<i>TH</i>
$t_1$	0.5	0.5	0
$t_2$	0	0.3	0.7
$t_3$	0.1	0.5	0.4
$t_4$	0.5	0	0.5
$t_5$	0.3	0.3	0.4

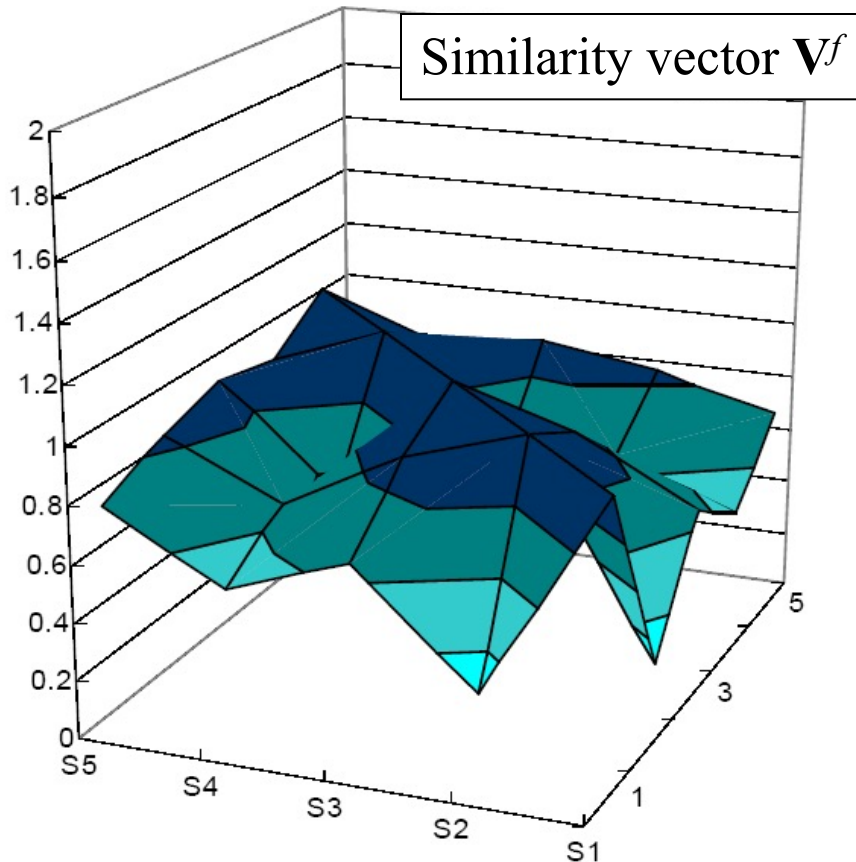


# Representing Features

- Similarity between tuples  $t_1$  and  $t_2$  w.r.t. categorical feature  $f$

- Cosine similarity between vectors  $f(t_1)$  and  $f(t_2)$

$$\text{sim}_f(t_1, t_2) = \frac{\sum_{k=1}^L f(t_1).p_k \cdot f(t_2).p_k}{\sqrt{\sum_{k=1}^L f(t_1).p_k^2} \cdot \sqrt{\sum_{k=1}^L f(t_2).p_k^2}}$$



- Most important information of a feature  $f$  is how  $f$  groups tuples into clusters
- $f$  is represented by similarities between every pair of tuples indicated by  $f$
- The horizontal axes are the tuple indices, and the vertical axis is the similarity
- This can be considered as a vector of  $N \times N$  dimensions

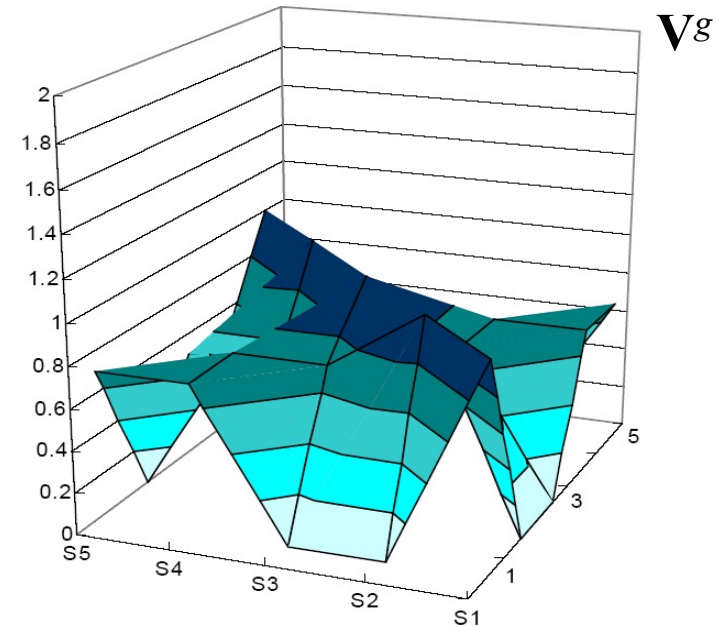
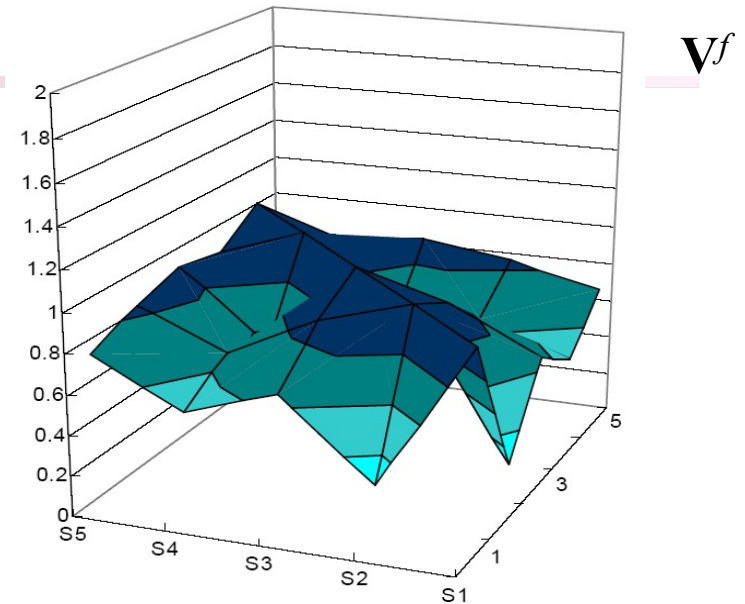
# Similarity Between Features

Values of Feature  $f$  and  $g$

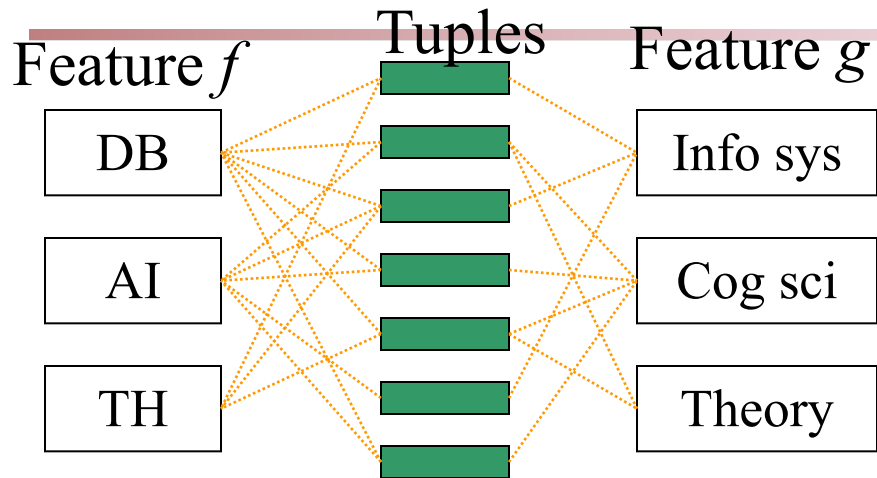
	Feature $f$ (course)				Feature $g$ (group)		
	DB	AI	TH		Info sys	Cog sci	Theory
$t_1$	0.5	0.5	0		1	0	0
$t_2$	0	0.3	0.7		0	0	1
$t_3$	0.1	0.5	0.4		0	0.5	0.5
$t_4$	0.5	0	0.5		0.5	0	0.5
$t_5$	0.3	0.3	0.4		0.5	0.5	0

Similarity between two features –  
cosine similarity of two vectors

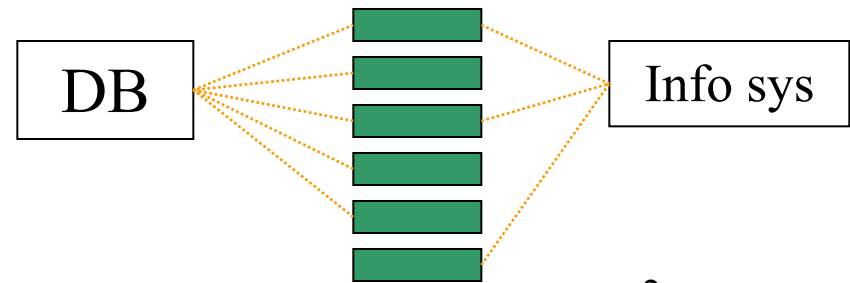
$$\text{sim}(f, g) = \frac{V^f \cdot V^g}{|V^f| |V^g|}$$



# Computing Feature Similarity



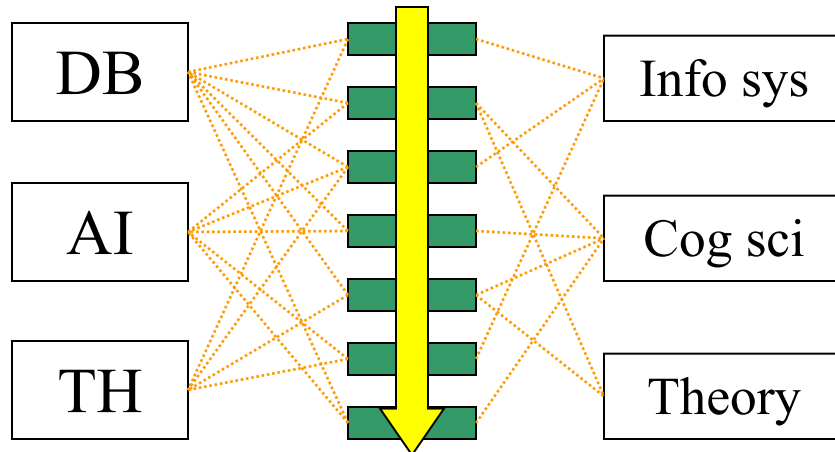
Similarity between feature values w.r.t. the tuples

$$\text{sim}(f_k, g_q) = \sum_{i=1 \text{ to } N} f(t_i) \cdot p_k \cdot g(t_i) \cdot p_q$$


$$V^f \cdot V^g = \sum_{i=1}^N \sum_{j=1}^N \text{sim}(t_i, t_j) \cdot \text{sim}_g(t_i, t_j) = \sum_{k=1}^l \sum_{q=1}^m \text{sim}(f_k, g_q)^2$$

*Tuple similarities, hard to compute*

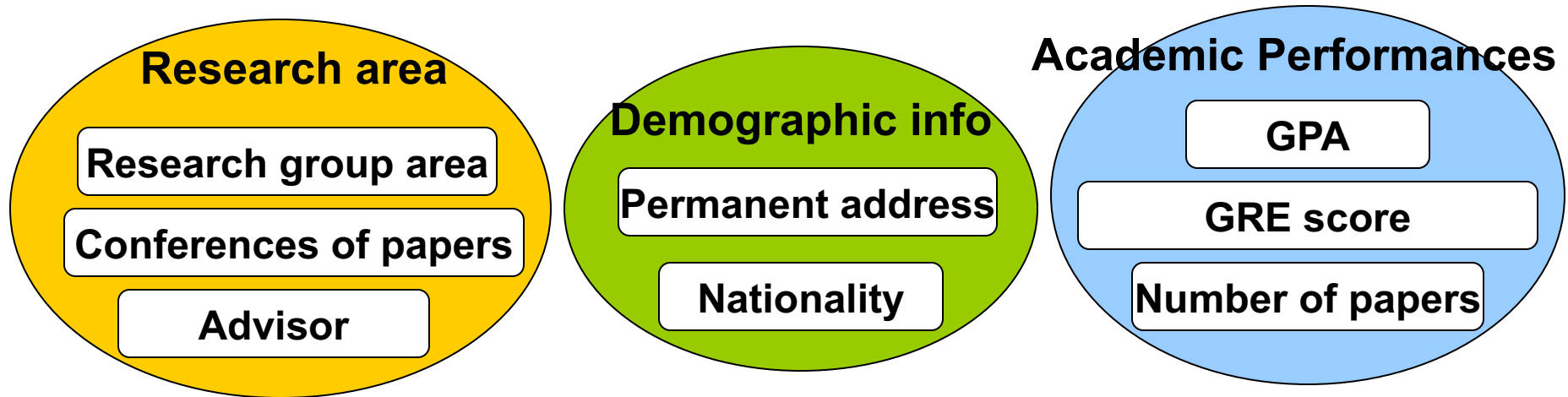
*Feature value similarities, easy to compute*



Compute similarity between each pair of feature values by one scan on data

# Searching for Pertinent Features

- Different features convey different aspects of information

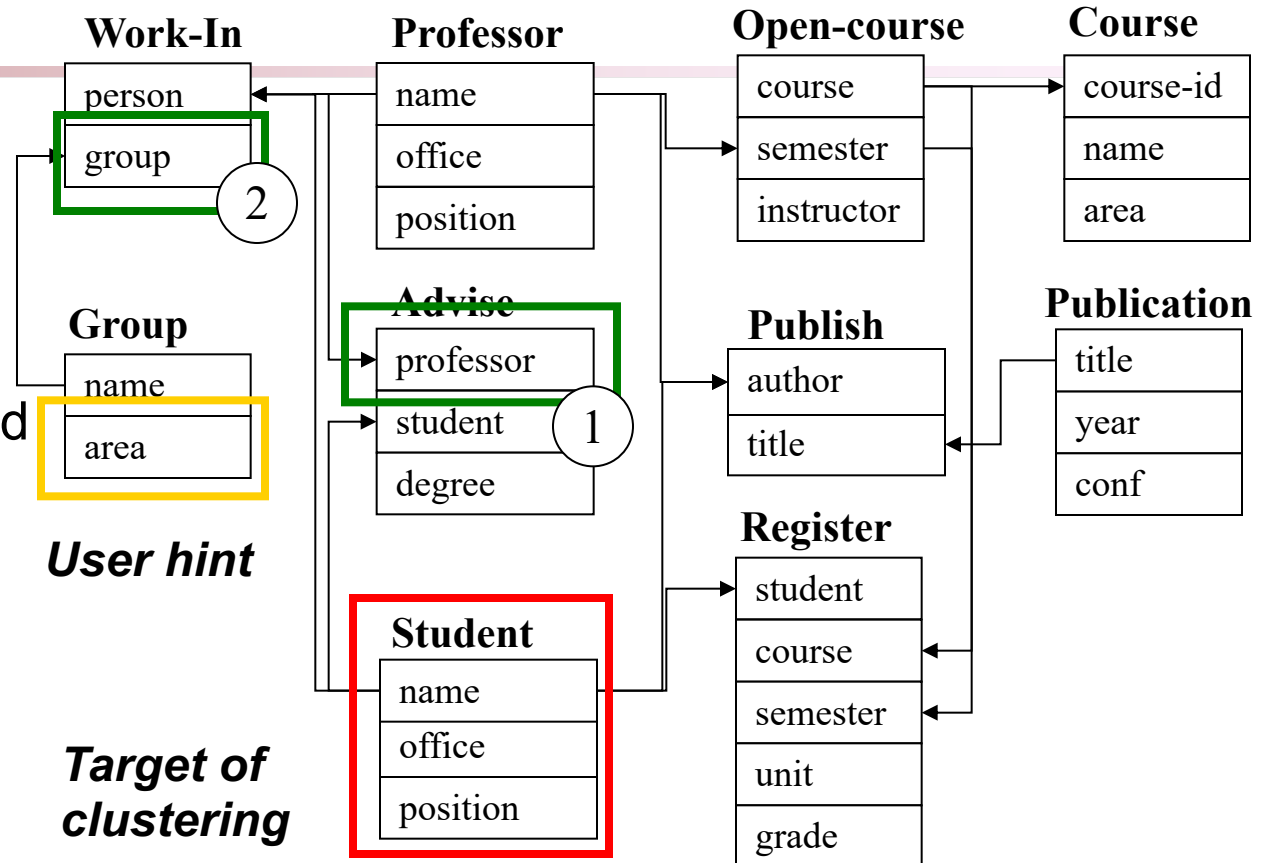


- Features conveying same aspect of information usually cluster tuples in more similar ways
  - Research group areas vs. conferences of publications
- Given user specified feature
  - Find pertinent features by computing feature similarity

# Heuristic Search for Pertinent Features

## Overall procedure

1. Start from the user-specified feature
2. Search in neighborhood of existing pertinent features
3. Expand search range gradually



- Tuple ID propagation is used to create multi-relational features
  - IDs of target tuples can be propagated along any join path, from which we can find tuples joinable with each target tuple



# Clustering with Multi-Relational Features

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- Given a set of  $L$  pertinent features  $f_1, \dots, f_L$ , similarity between two tuples

$$\text{sim}(t_1, t_2) = \sum_{i=1}^L \text{sim}_{f_i}(t_1, t_2) \cdot f_i.\text{weight}$$

- Weight of a feature is determined in feature search by its similarity with other pertinent features
- Clustering methods
  - CLARANS [Ng & Han 94], a scalable clustering algorithm for non-Euclidean space
  - K-means
  - Agglomerative hierarchical clustering

# Experiments: Compare CrossClus with

---

- Baseline: Only use the user specified feature
- PROCLUS [Aggarwal, et al. 99]: a state-of-the-art subspace clustering algorithm
  - Use a subset of features for each cluster
  - We convert relational database to a table by propositionalization
  - User-specified feature is forced to be used in every cluster
- RDBC [Kirsten and Wrobel'00]
  - A representative ILP clustering algorithm
  - Use neighbor information of objects for clustering
  - User-specified feature is forced to be used

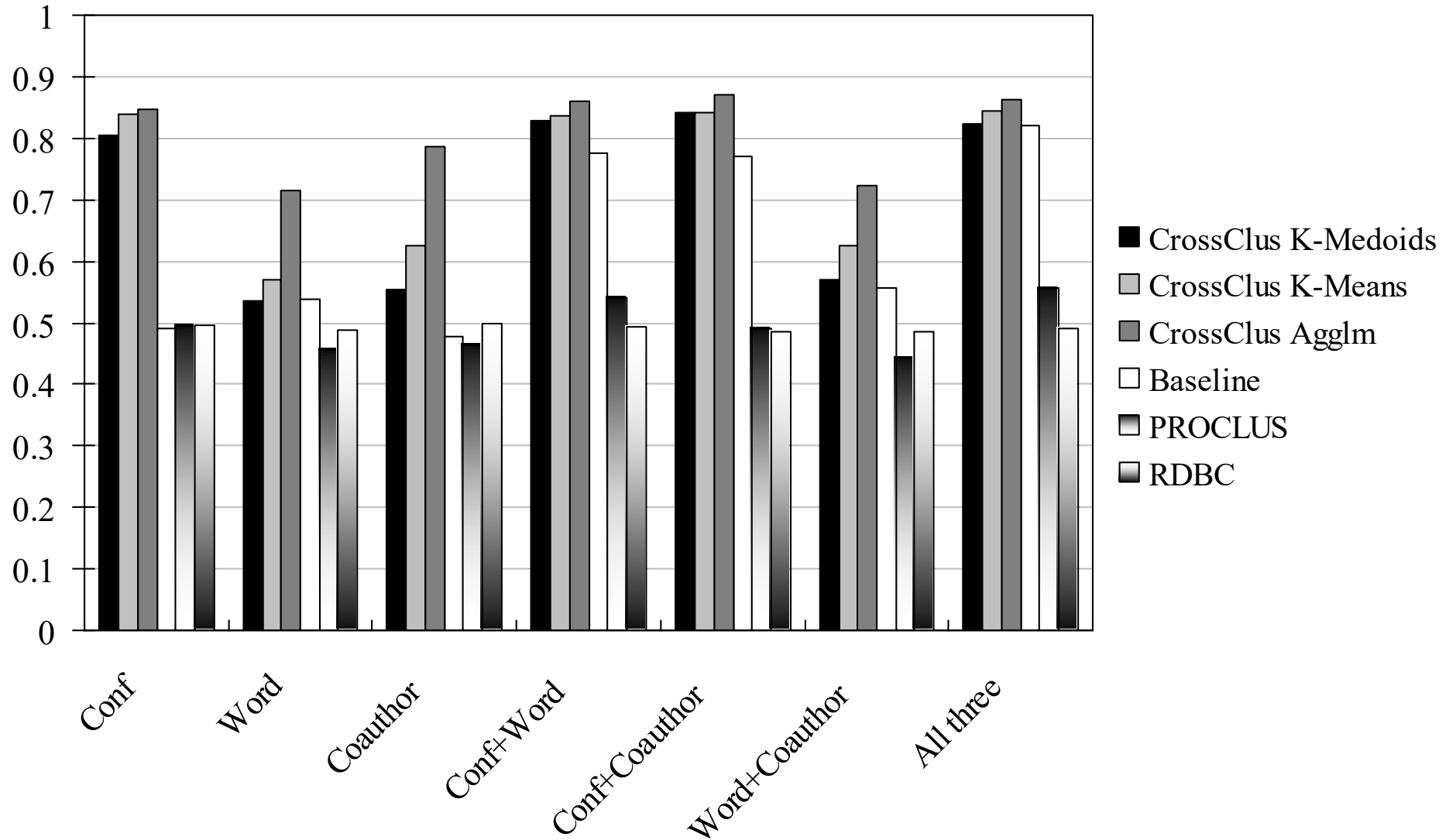
# Measure of Clustering Accuracy

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- Accuracy
  - Measured by manually labeled data
    - We manually assign tuples into clusters according to their properties (e.g., professors in different research areas)
  - Accuracy of clustering: Percentage of pairs of tuples in the same cluster that share common label
    - This measure favors many small clusters
    - We let each approach generate the same number of clusters


# DBLP Dataset

Clustering Accuracy - DBLP



# Chapter 11. Cluster Analysis: Advanced Methods

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- Probability Model-Based Clustering
- Clustering High-Dimensional Data
- Clustering Graphs and Network Data
- Clustering with Constraints
- Summary 

# Summary

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- Probability Model-Based Clustering
  - Fuzzy clustering
  - Probability-model-based clustering
  - The EM algorithm
- Clustering High-Dimensional Data
  - Subspace clustering: bi-clustering methods
  - Dimensionality reduction: Spectral clustering
- Clustering Graphs and Network Data
  - Graph clustering: min-cut vs. sparsest cut
  - High-dimensional clustering methods
  - Graph-specific clustering methods, e.g., SCAN
- Clustering with Constraints
  - Constraints on instance objects, e.g., Must link vs. Cannot Link
  - Constraint-based clustering algorithms

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- X. Yin, J. Han, and P.S. Yu, “Cross-Relational Clustering with User's Guidance”, KDD'05



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**Slides Not to Be Used in Class**

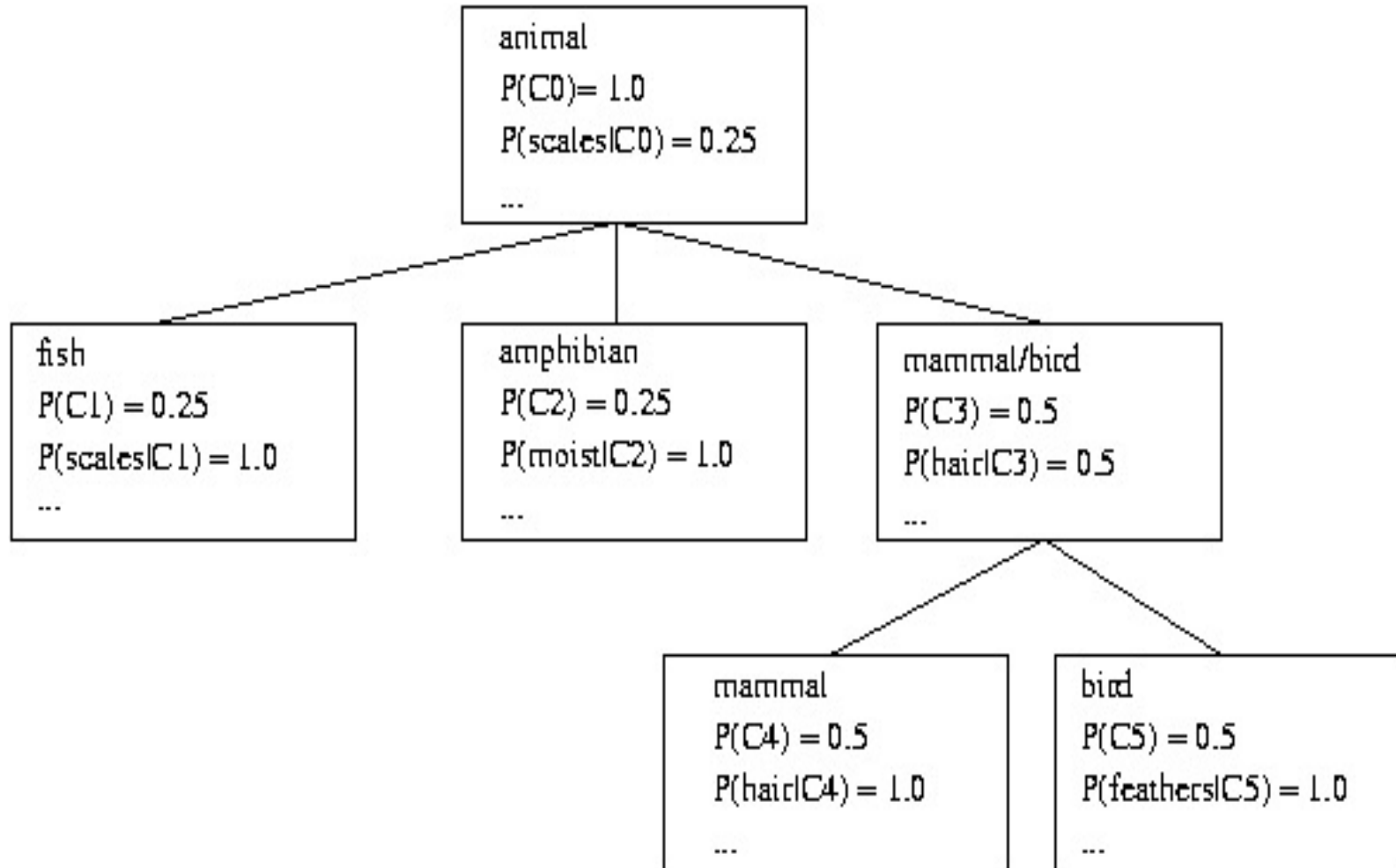
# Conceptual Clustering

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- Conceptual clustering
  - A form of clustering in machine learning
  - Produces a classification scheme for a set of unlabeled objects
  - Finds characteristic description for each concept (class)
- COBWEB (Fisher'87)
  - A popular a simple method of incremental conceptual learning
  - Creates a hierarchical clustering in the form of a **classification tree**
  - Each node refers to a concept and contains a probabilistic description of that concept

# COBWEB Clustering Method

## A classification tree



# More on Conceptual Clustering

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- Limitations of COBWEB
  - The assumption that the attributes are independent of each other is often too strong because correlation may exist
  - Not suitable for clustering large database data – skewed tree and expensive probability distributions
- CLASSIT
  - an extension of COBWEB for incremental clustering of continuous data
  - suffers similar problems as COBWEB
- AutoClass (Cheeseman and Stutz, 1996)
  - Uses Bayesian statistical analysis to estimate the number of clusters
  - Popular in industry

# Neural Network Approaches

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- Neural network approaches
  - Represent each cluster as an exemplar, acting as a “prototype” of the cluster
  - New objects are distributed to the cluster whose exemplar is the most similar according to some distance measure
- Typical methods
  - SOM (Soft-Organizing feature Map)
  - Competitive learning
    - Involves a hierarchical architecture of several units (neurons)
    - Neurons compete in a “winner-takes-all” fashion for the object currently being presented

# Self-Organizing Feature Map (SOM)

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- SOMs, also called topological ordered maps, or Kohonen Self-Organizing Feature Map (KSOMs)
- It maps all the points in a high-dimensional source space into a 2 to 3-d target space, s.t., the distance and proximity relationship (i.e., topology) are preserved as much as possible
- Similar to k-means: cluster centers tend to lie in a low-dimensional manifold in the feature space
- Clustering is performed by having several units competing for the current object
  - The unit whose weight vector is closest to the current object wins
  - The winner and its neighbors learn by having their weights adjusted
- SOMs are believed to resemble processing that can occur in the brain
- Useful for visualizing high-dimensional data in 2- or 3-D space

# Web Document Clustering Using SOM

- The result of SOM clustering of 12088 Web articles
- The picture on the right: drilling down on the keyword “mining”
- Based on websom.hut.fi Web page

