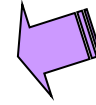

Data Mining:

Cluster Analysis: Advanced Methods

- 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)
A	50
B	1320
C	860
D	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”

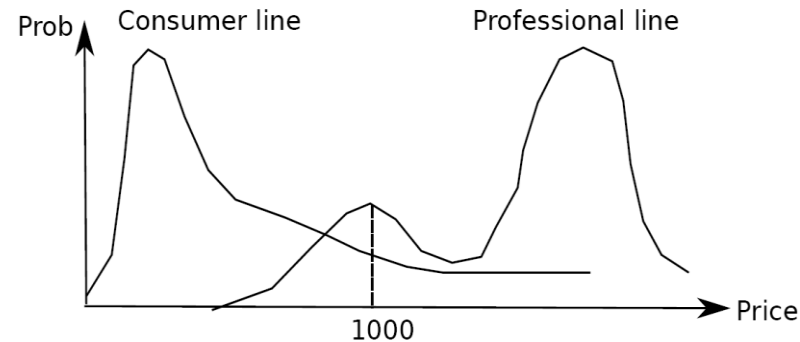
Review-id	Keywords
R_1	digital camera, lens
R_2	digital camera
R_3	lens
R_4	digital camera, lens, computer
R_5	computer, CPU
R_6	computer, computer game

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

- 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 C is $P(o|C) = \sum_{j=1}^k \omega_j f_j(o)$
- Since objects are assumed to be generated independently, for a data set $D = \{o_1, \dots, o_n\}$, we have,

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

- Task: Find a set C of k probabilistic clusters s.t. $P(D|C)$ is maximized
- However, maximizing $P(D|C)$ 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 θ_j , we have

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

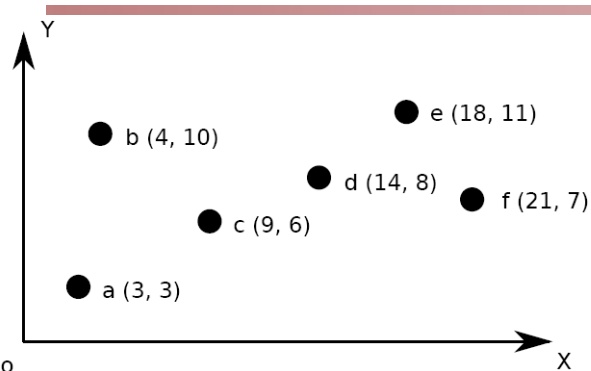
- Univariate Gaussian mixture model
 - Assume the probability density function of each cluster follows a 1-d Gaussian distribution. Suppose that there are k clusters.
 - The probability density function of each cluster are centered at μ_j with standard deviation σ_j , $\theta_j = (\mu_j, \sigma_j)$,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

- 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 $c_2 = b$

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

- 1st 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 θ_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 μ_j with standard deviation σ_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 $\mathbf{O} = \{o_1, \dots, o_n\}$, 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 θ_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,

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

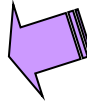
- At the M-step, adjust the parameters $\theta_j = (\mu_j, \sigma_j)$ so that the expected likelihood $P(\mathbf{O}|\Theta)$ is maximized

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

Advantages and Disadvantages of Mixture Models

- 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

Cluster Analysis: Advanced Methods

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

Clustering High-Dimensional Data

- 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,

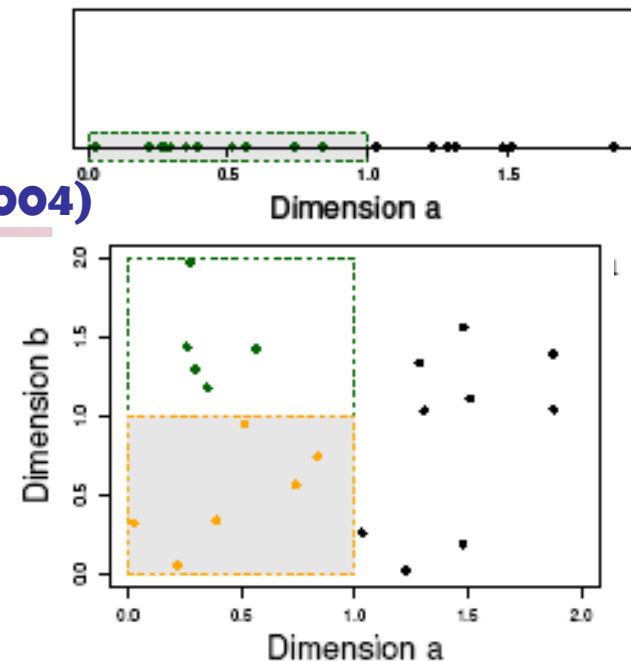
$$\text{dist}(\text{Ada}, \text{Bob}) = \text{dist}(\text{Bob}, \text{Cathy}) = \text{dist}(\text{Ada}, \text{Cathy}) = \sqrt{2}$$

- 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

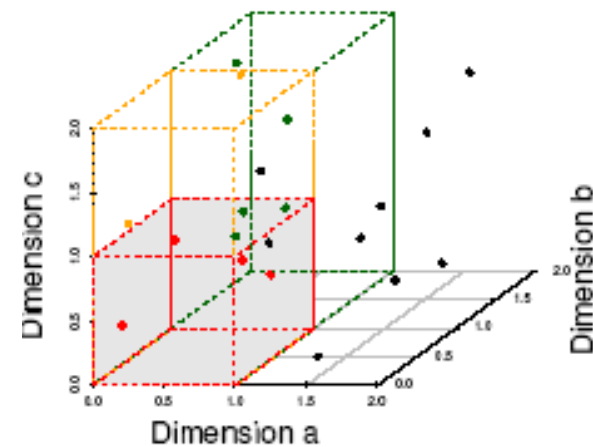
The Curse of Dimensionality

(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

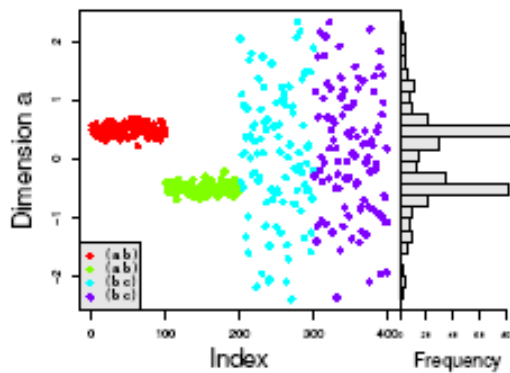
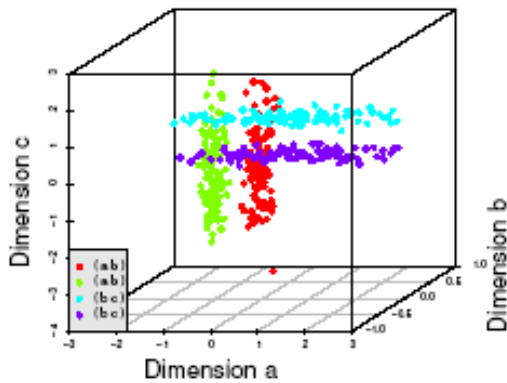


(c) 4 Objects in One Unit Bin

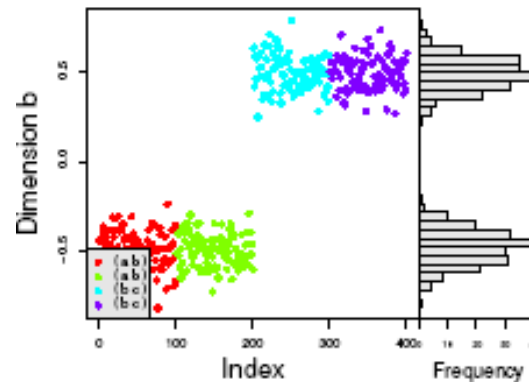
Why Subspace Clustering?

(adapted from Parsons et al. SIGKDD Explorations 2004)

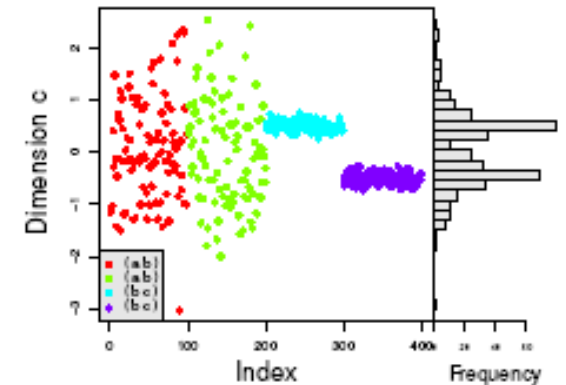
- Clusters may exist only in some subspaces
- Subspace-clustering: find clusters in all the subspaces



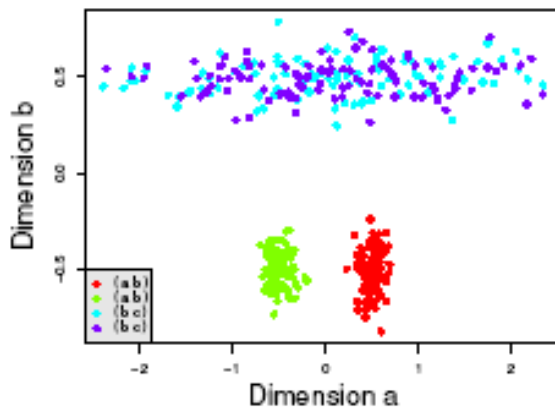
(a) Dimension *a*



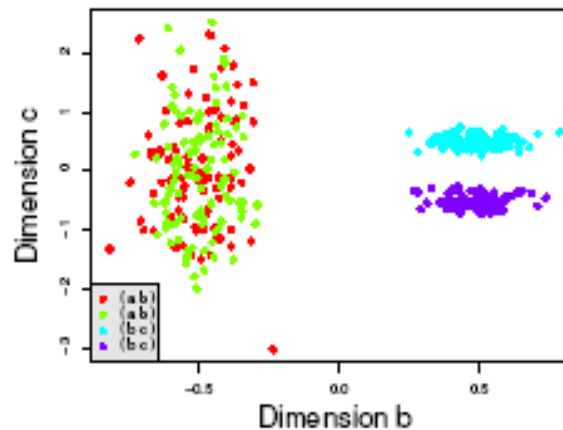
(b) Dimension *b*



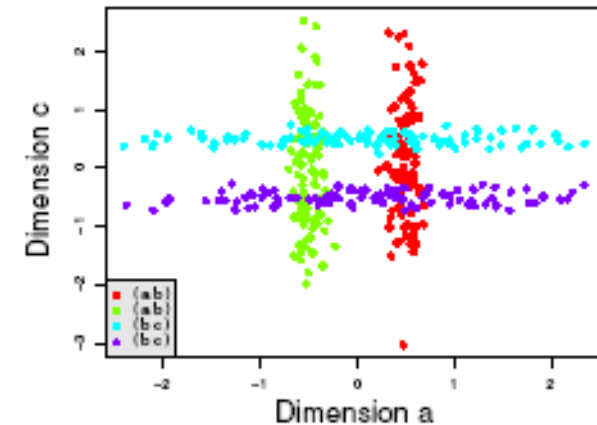
(c) Dimension *c*



(a) Dims *a* & *b*



(b) Dims *b* & *c*



(c) Dims *a* & *c*

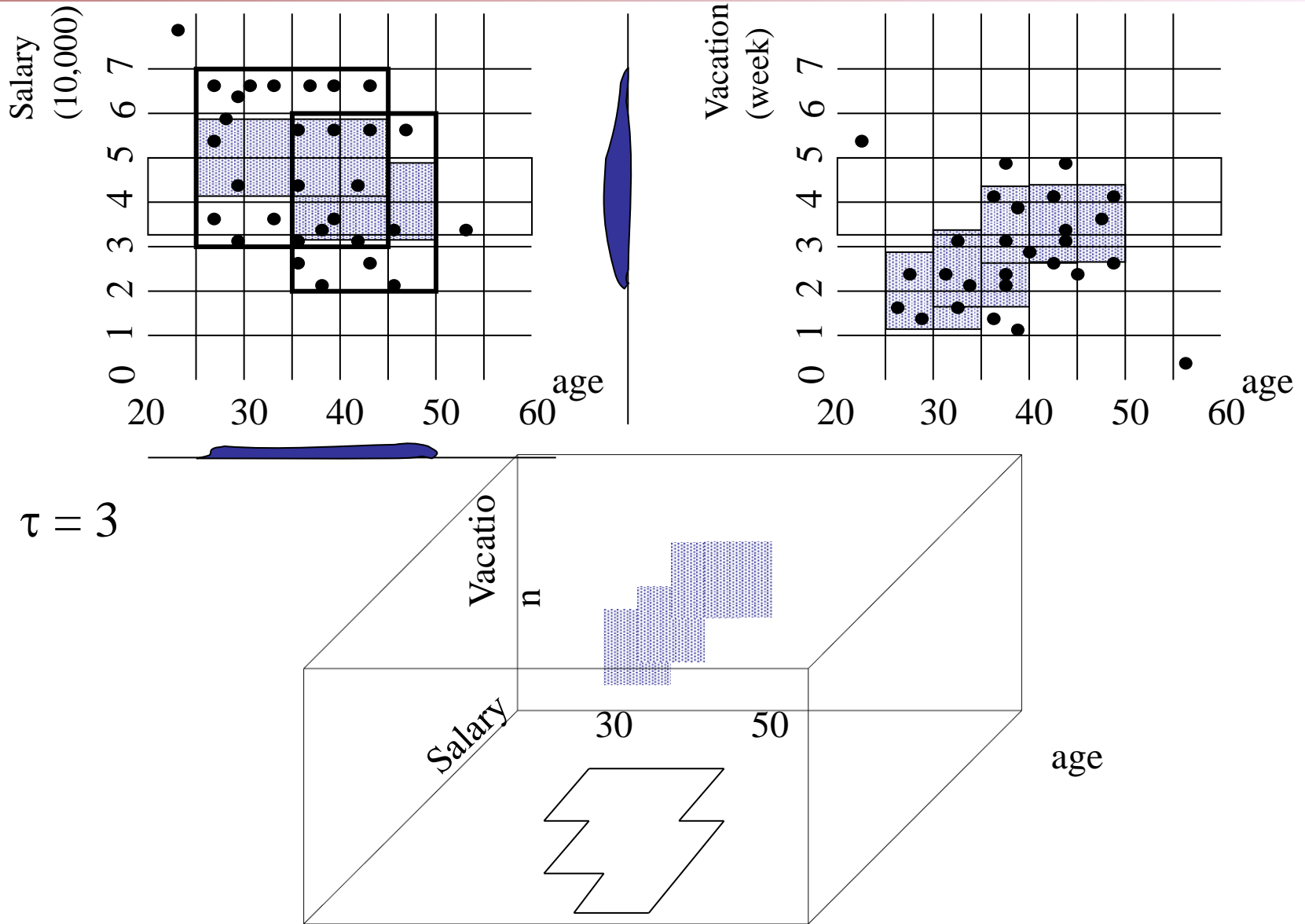
Subspace Clustering Methods

- 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

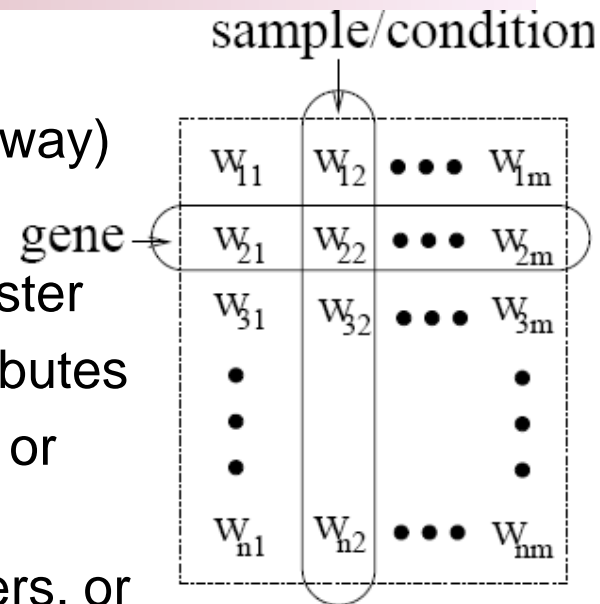


Subspace Clustering Method (II): Correlation-Based Methods

- 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

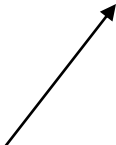
- Bi-clusters with *coherent values* (aka. *pattern-based clusters*)

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

- 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



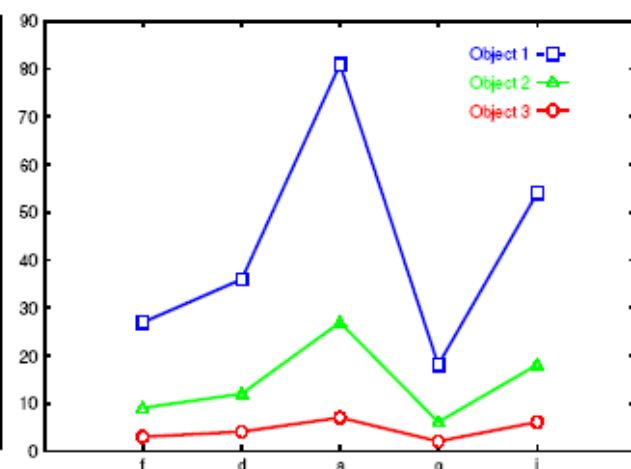
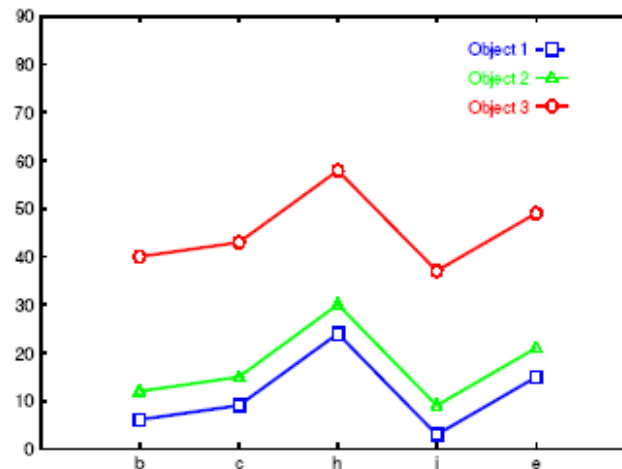
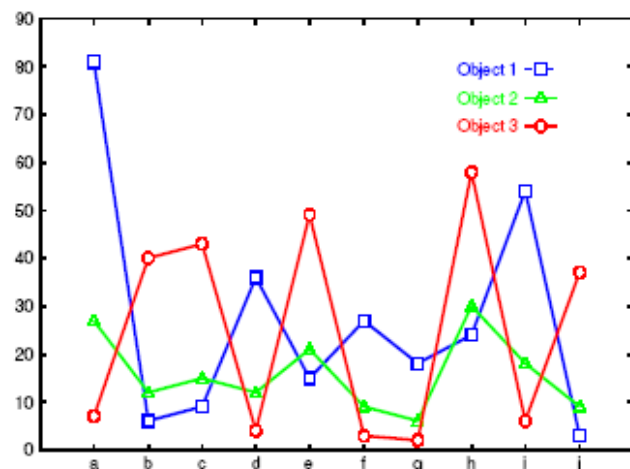
10	50	30	70	20
20	100	50	1000	30
50	100	90	120	80
0	80	20	100	10

Bi-Clustering Methods

- 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. δ -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. δ -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): δ -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 **δ -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 δ -Cluster Algorithm

- **Maximal δ -bi-cluster** is a δ -bi-cluster $I \times J$ such that there does not exist another δ -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 δ
 - 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 δ -bi-cluster $I \times J$ obtained in the deletion phase as long as the δ -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 δ -bi-cluster
- It finds only one δ -bi-cluster, thus needs to run multiple times: replacing the elements in the output bi-cluster by random numbers

Bi-Clustering (II): δ -pCluster

- Enumerating all bi-clusters (δ -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 2×2 submatrix of $I \times J$, define p -score

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

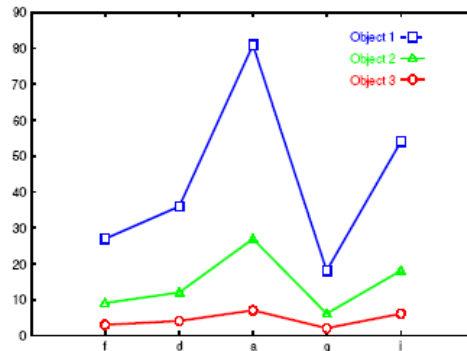
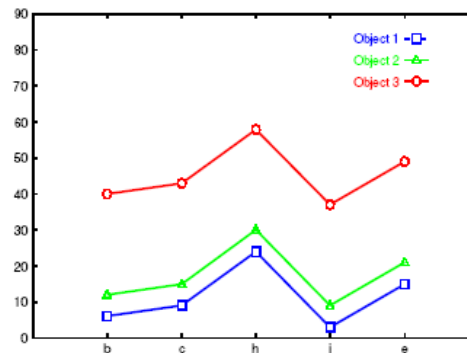
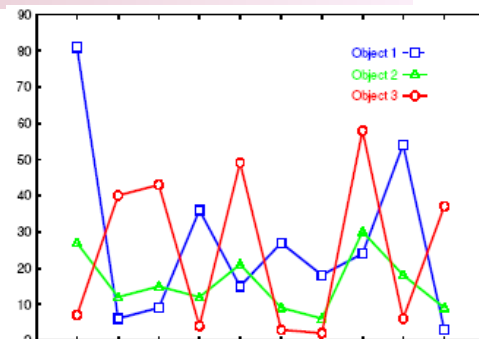
- A submatrix $I \times J$ is a **δ -pCluster** (pattern-based cluster) if the p -score of every 2×2 submatrix of $I \times J$ is at most δ , where $\delta \geq 0$ is a threshold specifying a user's tolerance of noise against a perfect bi-cluster
- The p -score controls the noise on every element in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

MaPle: Efficient Enumeration of δ -pClusters

- Pei et al., MaPle: Efficient enumerating all maximal δ -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 δ -pClusters
 - If I x J is not a submatrix of another δ -pClusters
 - then I x J is a maximal δ -pCluster.
- Algorithm is very similar to mining frequent closed itemsets
- Additional advantages of δ -pClusters:
 - Due to averaging of δ -cluster, it may contain outliers but still within δ -threshold
 - Computing bi-clusters for scaling patterns, take logarithmic on

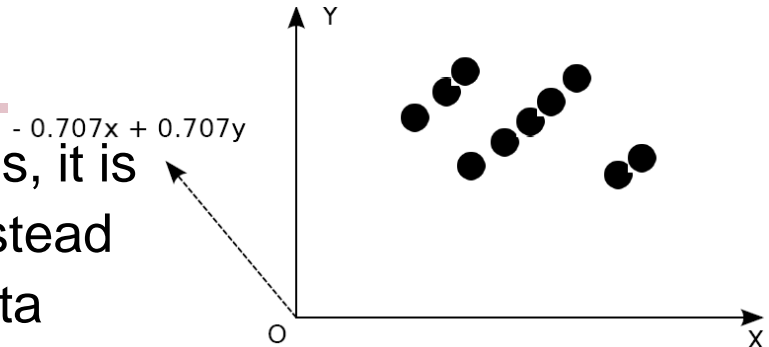
$$\frac{d_{xa} / d_{ya}}{d_{xb} / d_{yb}} < \delta$$

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)

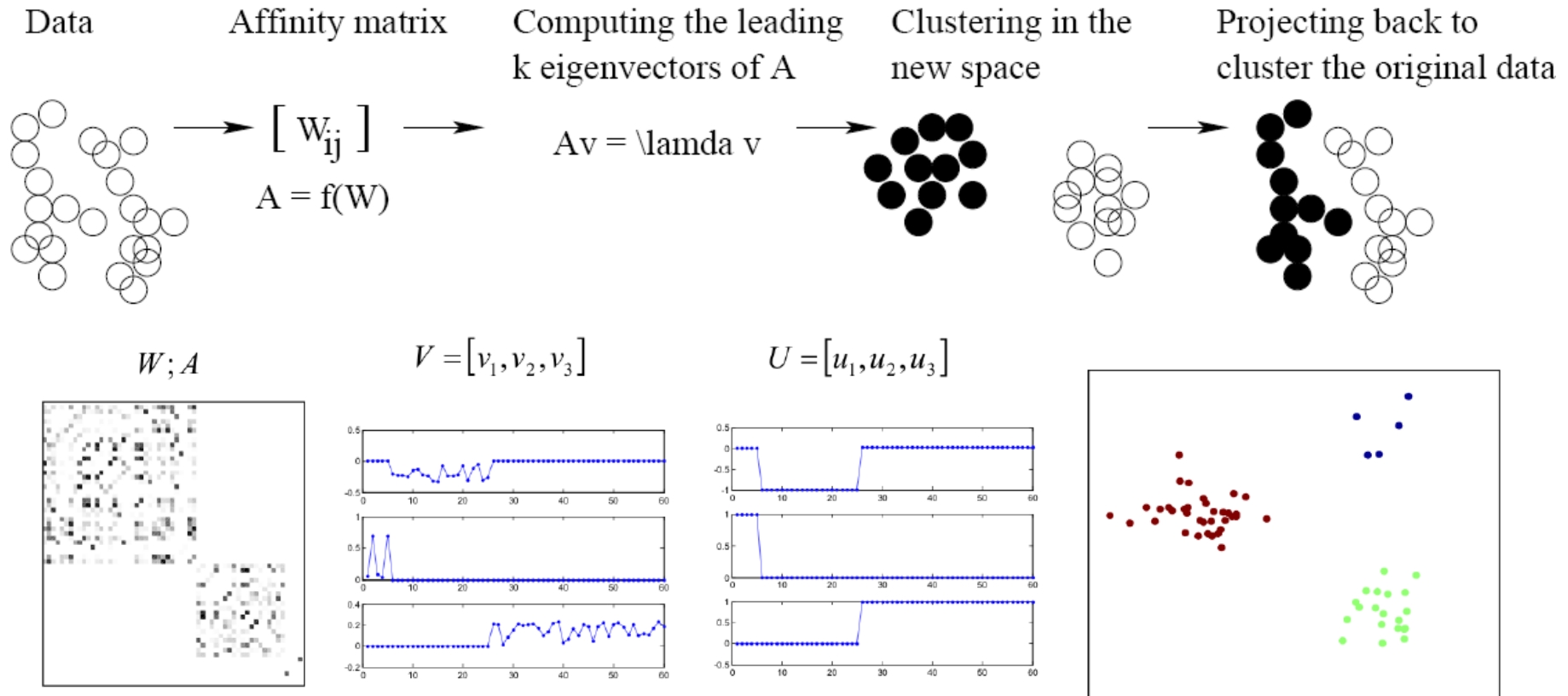


Spectral Clustering:

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 σ 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 λ 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

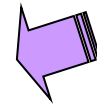
Spectral Clustering: Illustration and Comments



- 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

Cluster Analysis: Advanced Methods

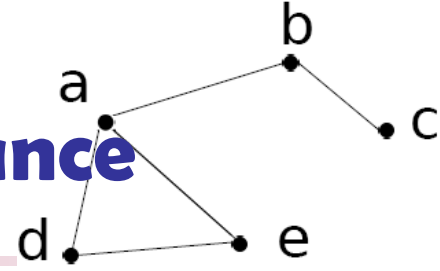
- Probability Model-Based Clustering
- Clustering High-Dimensional Data
- Clustering Graphs and Network Data
- Clustering with Constraints
- Summary



Clustering Graphs and Network Data

- 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: $p(u, v) = \sum_{t: (u, v) \rightsquigarrow (x, x)} P[t]C^{l(t)}$

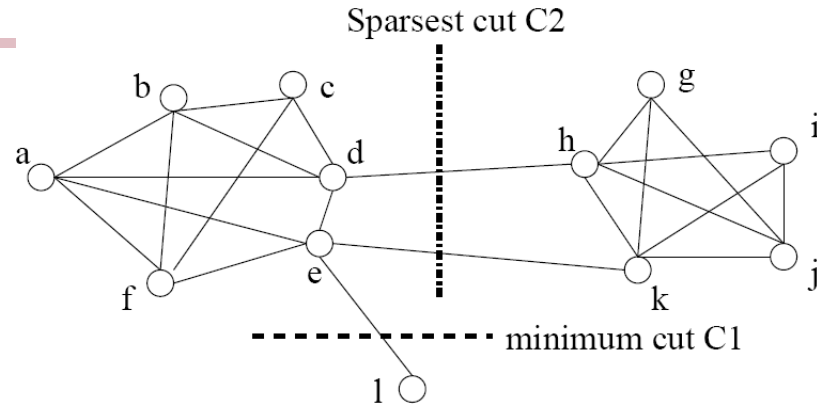
Graph Clustering: Sparsest Cut

- $G = (V, E)$. 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

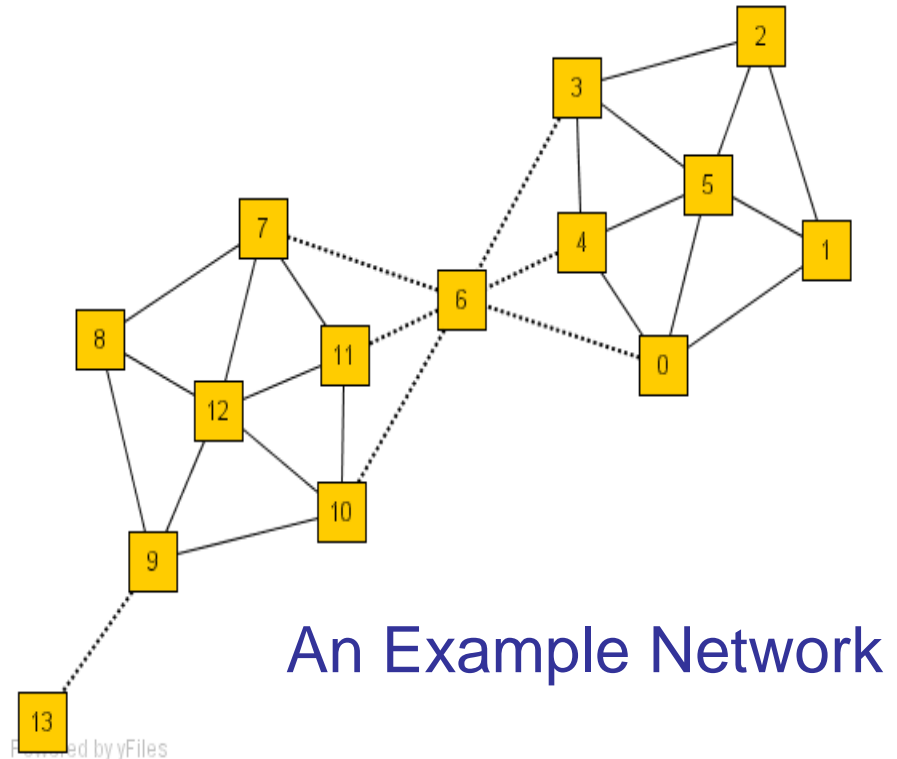
- High computational cost
 - Many graph cut problems are computationally expensive
 - The sparsest cut problem is NP-hard
 - Need to tradeoff between efficiency/scalability and quality
- Sophisticated graphs
 - May involve weights and/or cycles.
- High dimensionality
 - A graph can have many vertices. 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

- 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

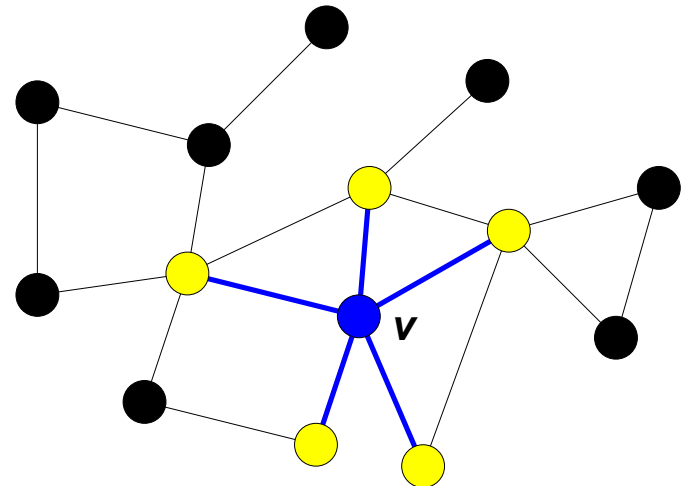
- How many clusters?
- What size should they be?
- What is the best partitioning?
- Should some points be segregated?



- 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

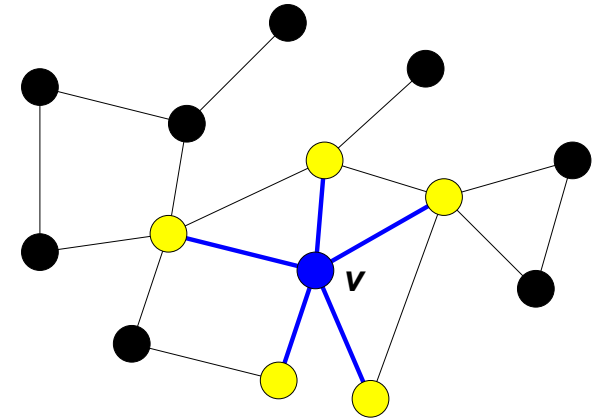
- Cliques, hubs and outliers
 - Individuals in a tight social group, or **clique**, know many of the same people, regardless of the size of the group
 - Individuals who are **hubs** know many people in different groups but belong to no single group. Politicians, for example bridge multiple groups
 - 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)



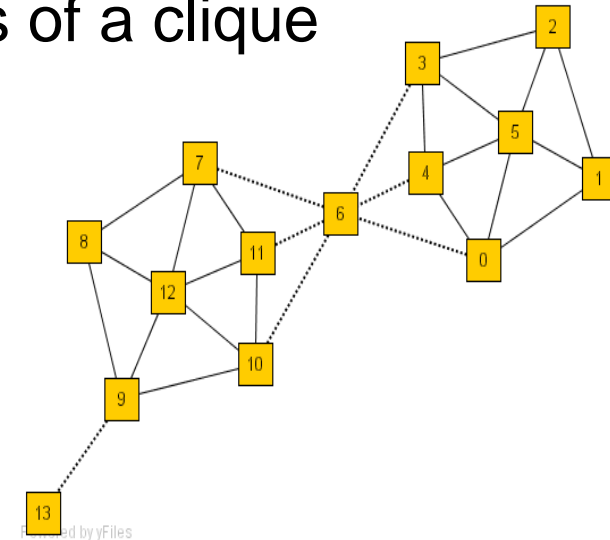
Structure Similarity

- 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]

- ε -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

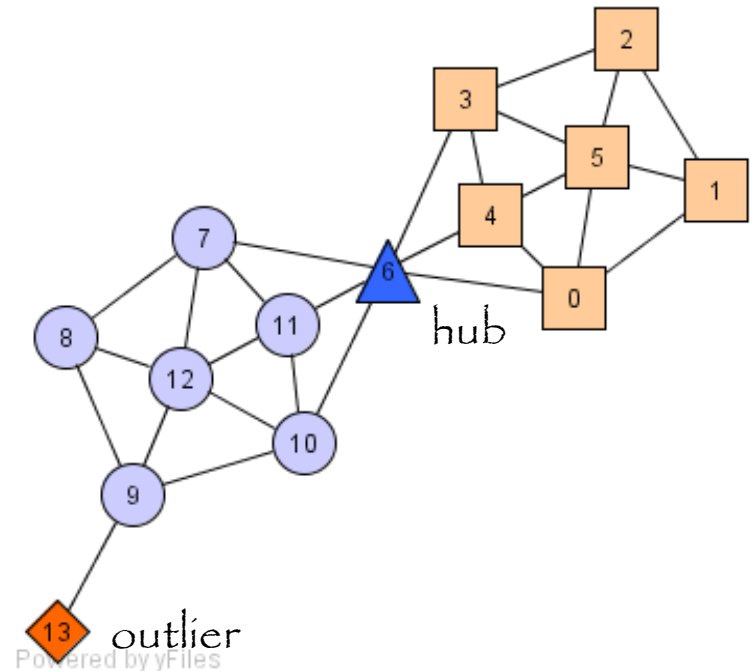
- Connectivity: $\forall v, w \in C : CONNECT_{\varepsilon, \mu}(v, w)$
- Maximality: $\forall v, w \in V : v \in C \wedge REACH_{\varepsilon, \mu}(v, w) \Rightarrow w \in C$

- Hubs:

- Not belong to any cluster
- Bridge to many clusters

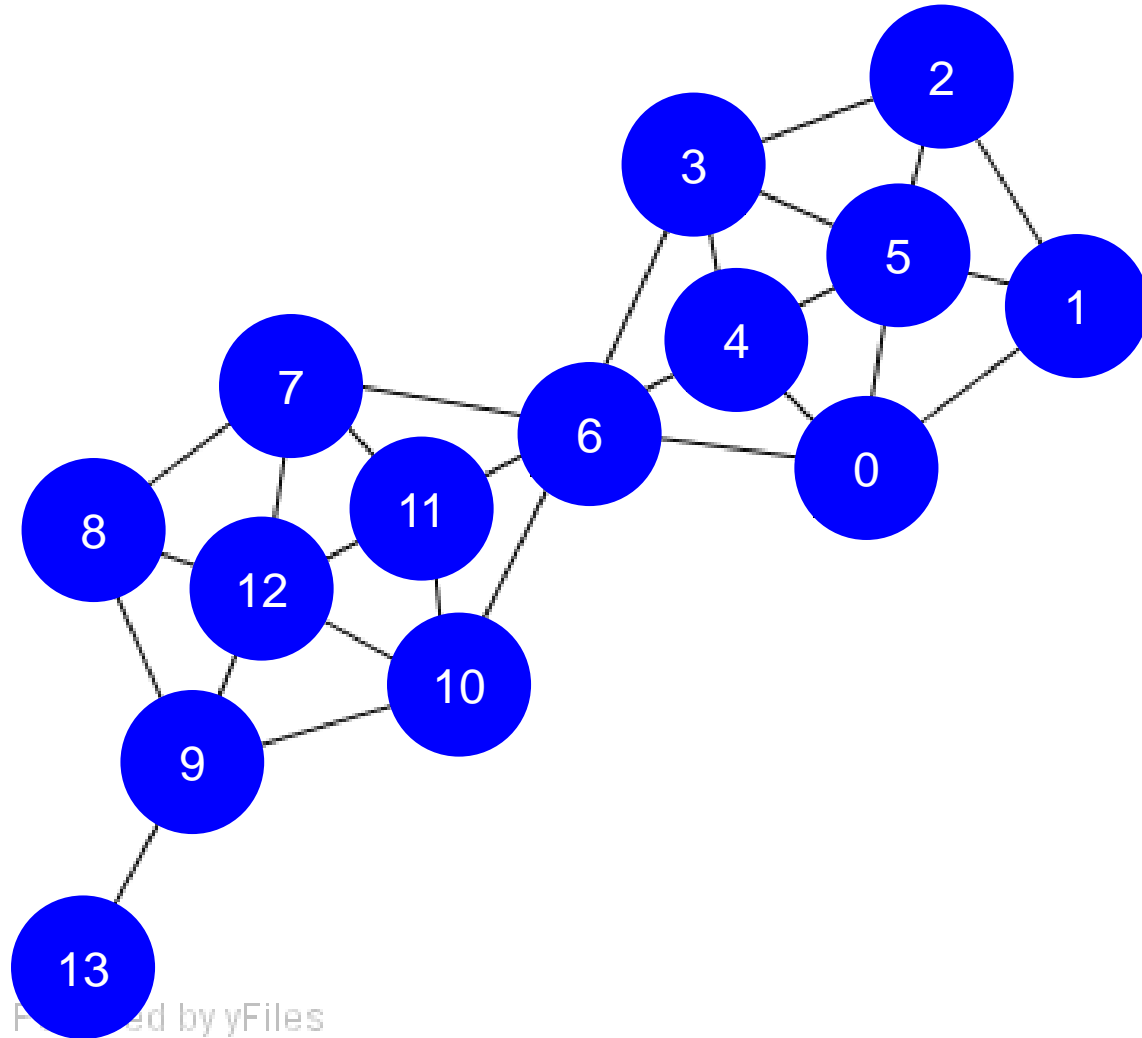
- Outliers:

- Not belong to any cluster
- Connect to less clusters



Algorithm

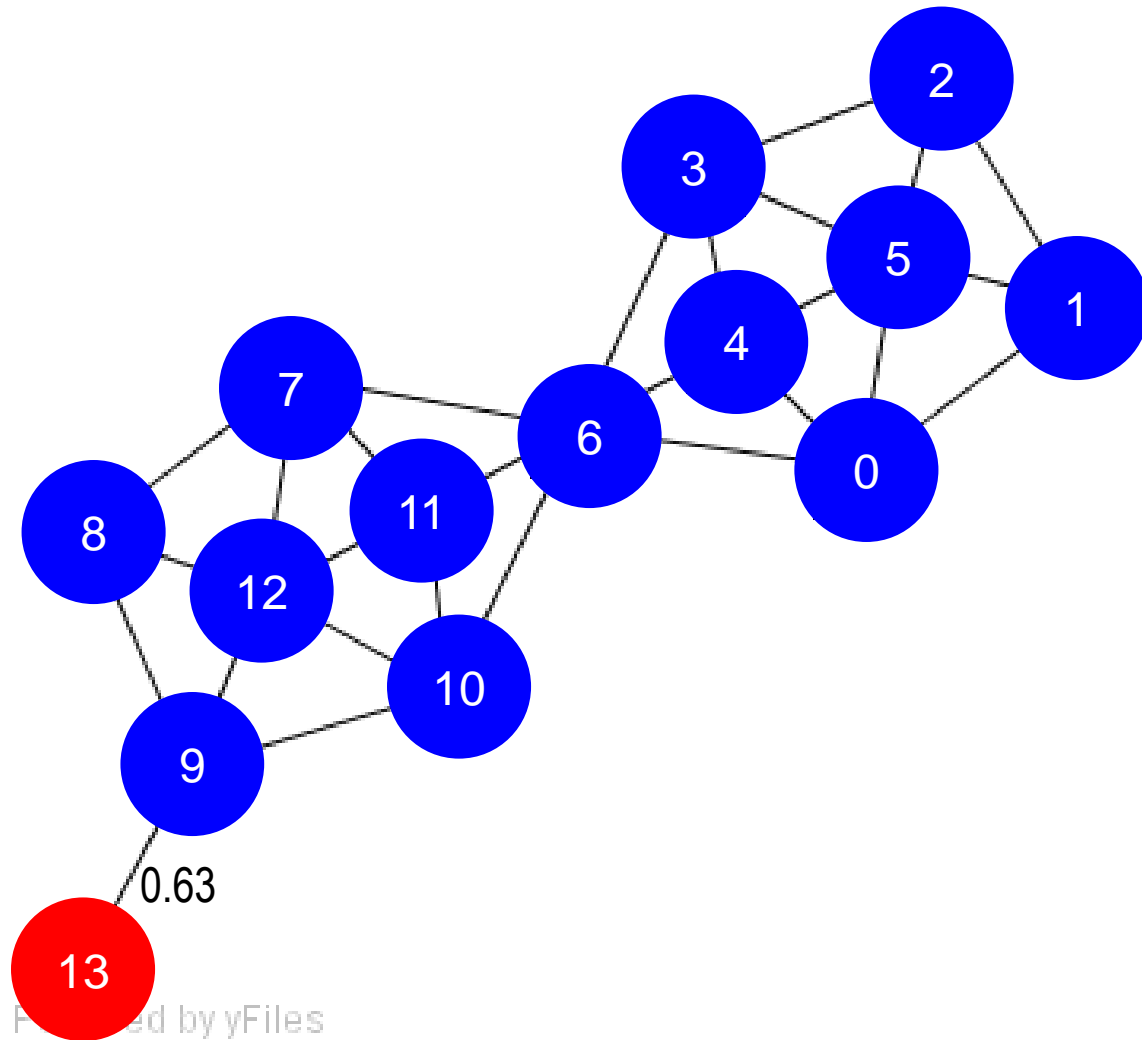
$$\mu = 2$$
$$\varepsilon = 0.7$$



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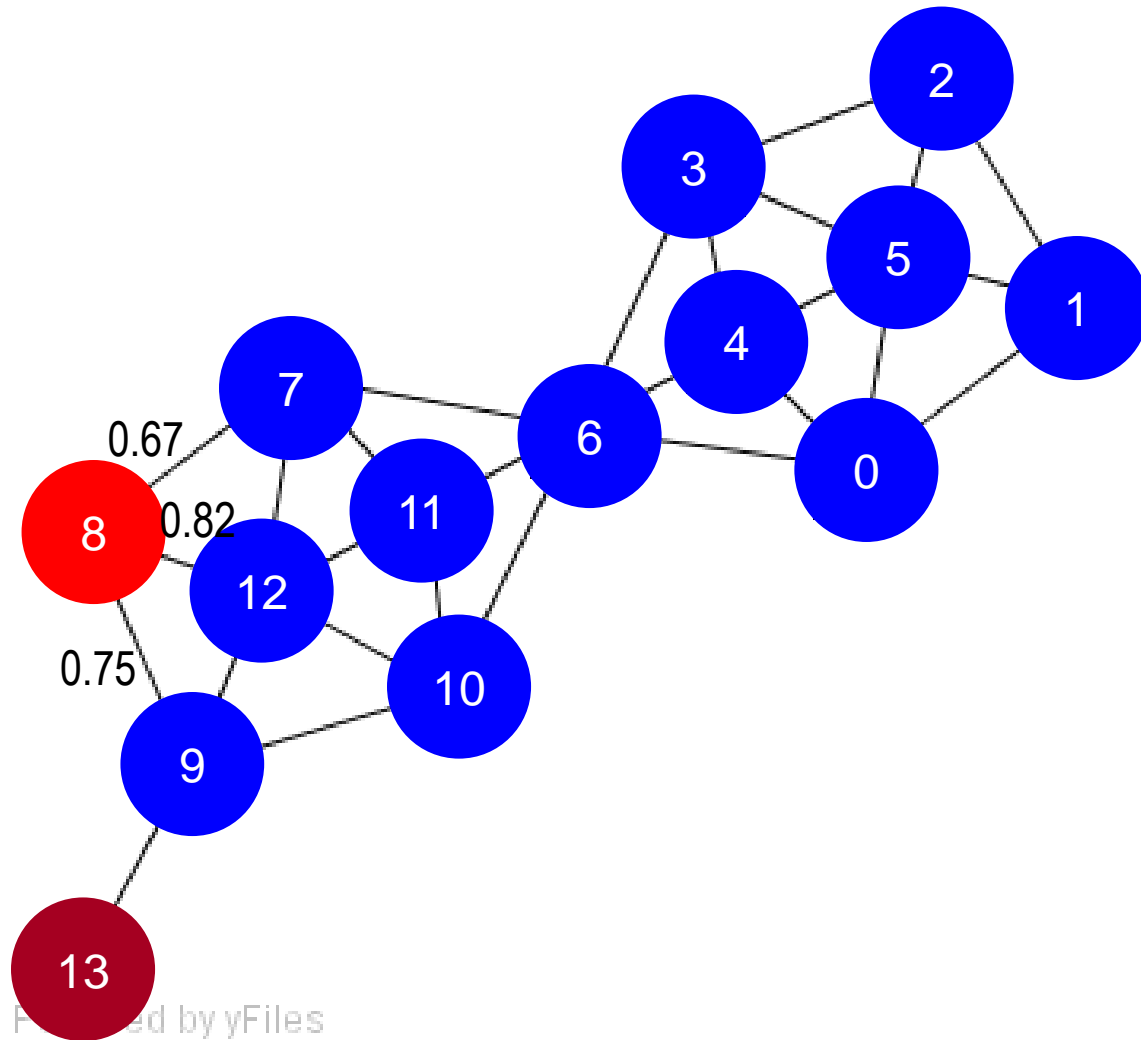
Algorithm

$$\mu = 2$$
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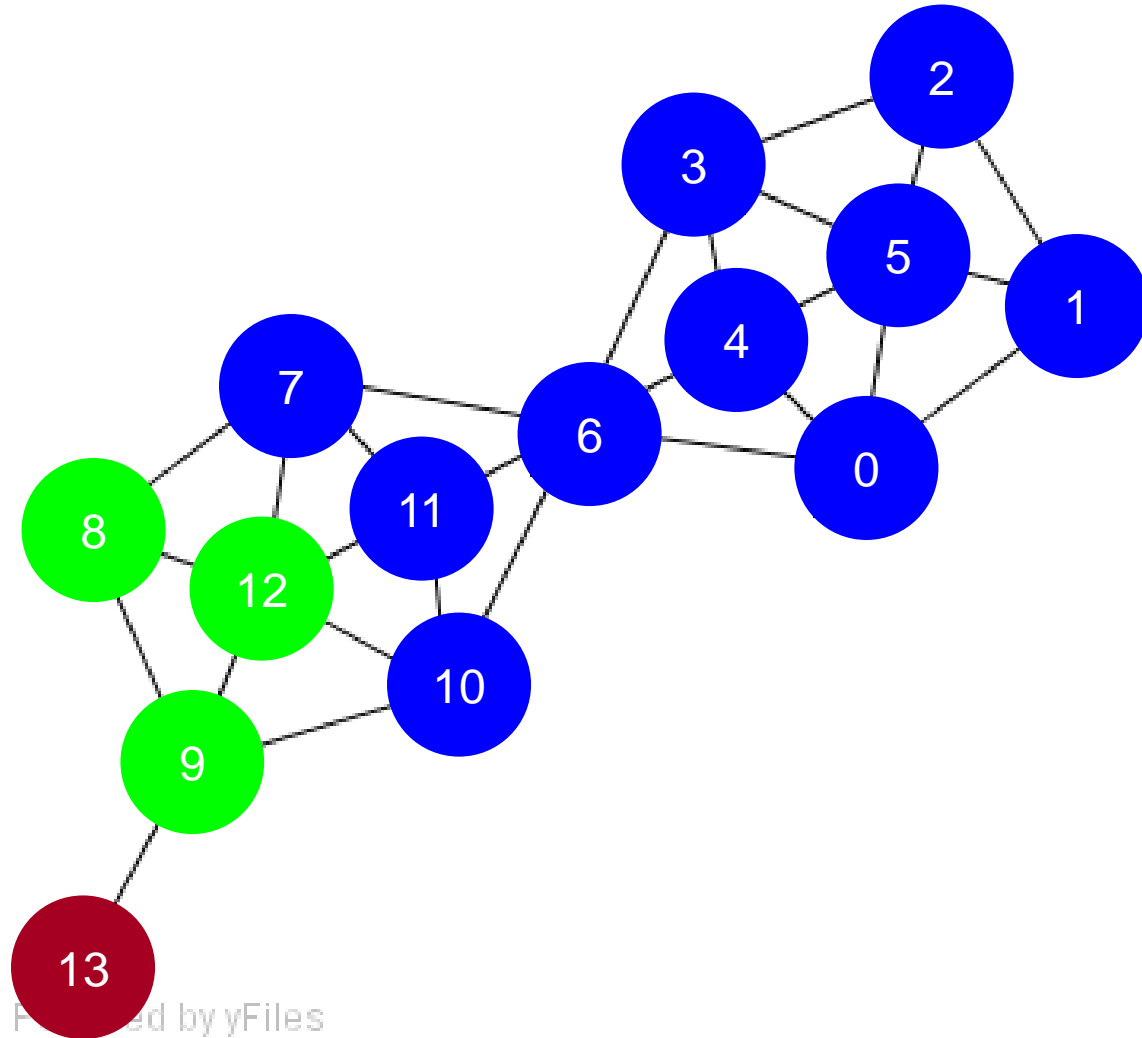
Algorithm

$$\mu = 2$$
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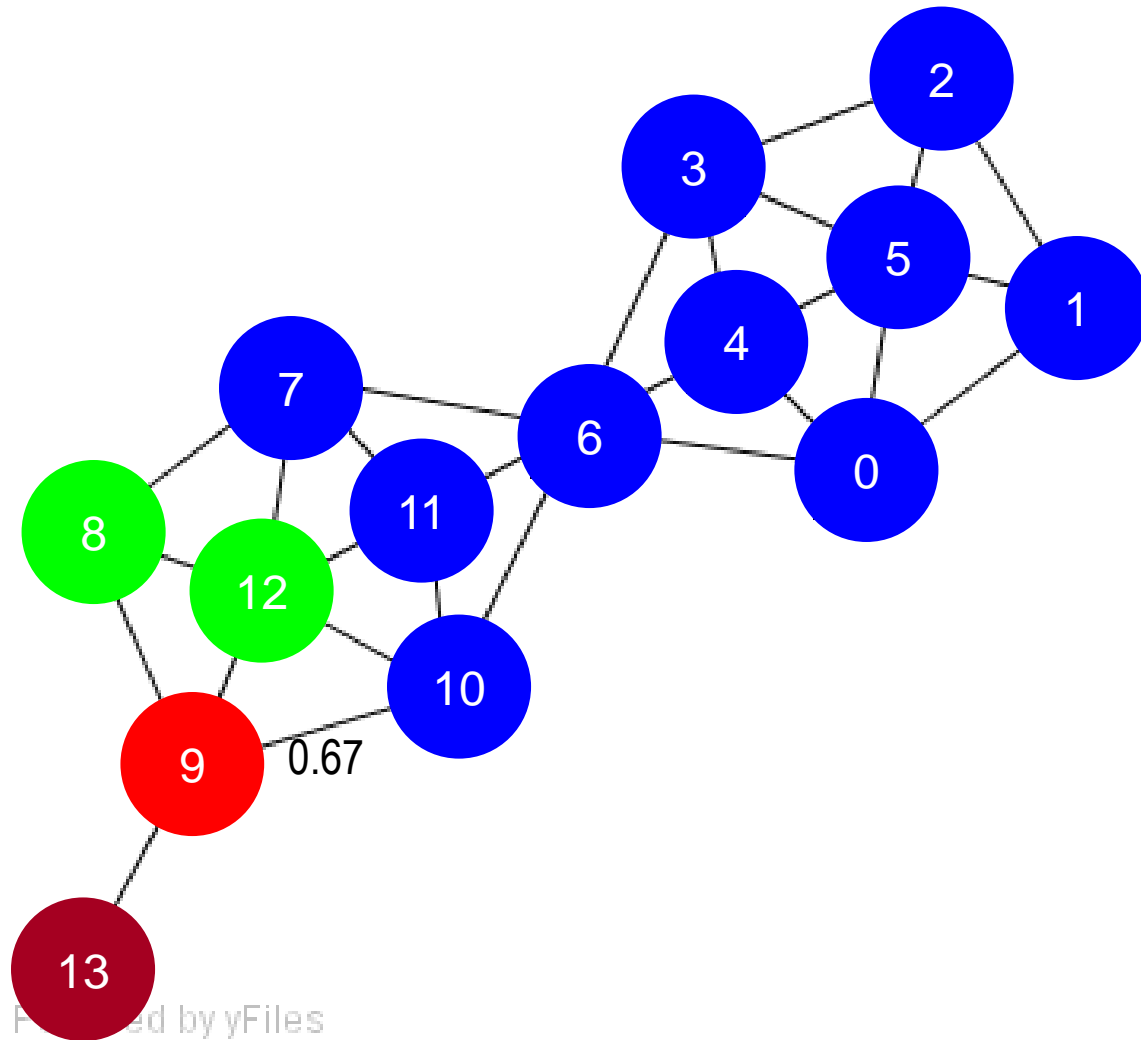
Algorithm

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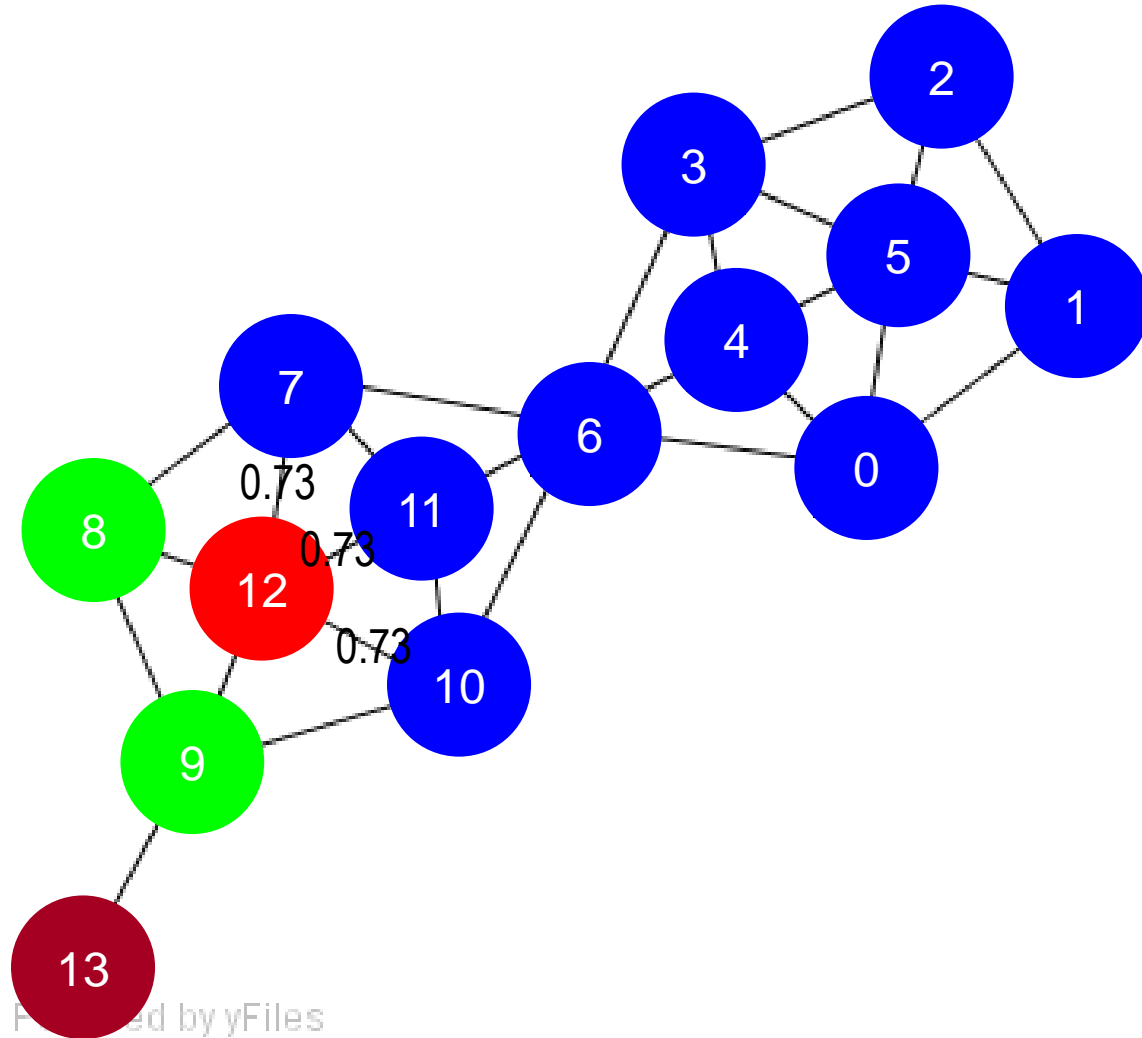
Algorithm

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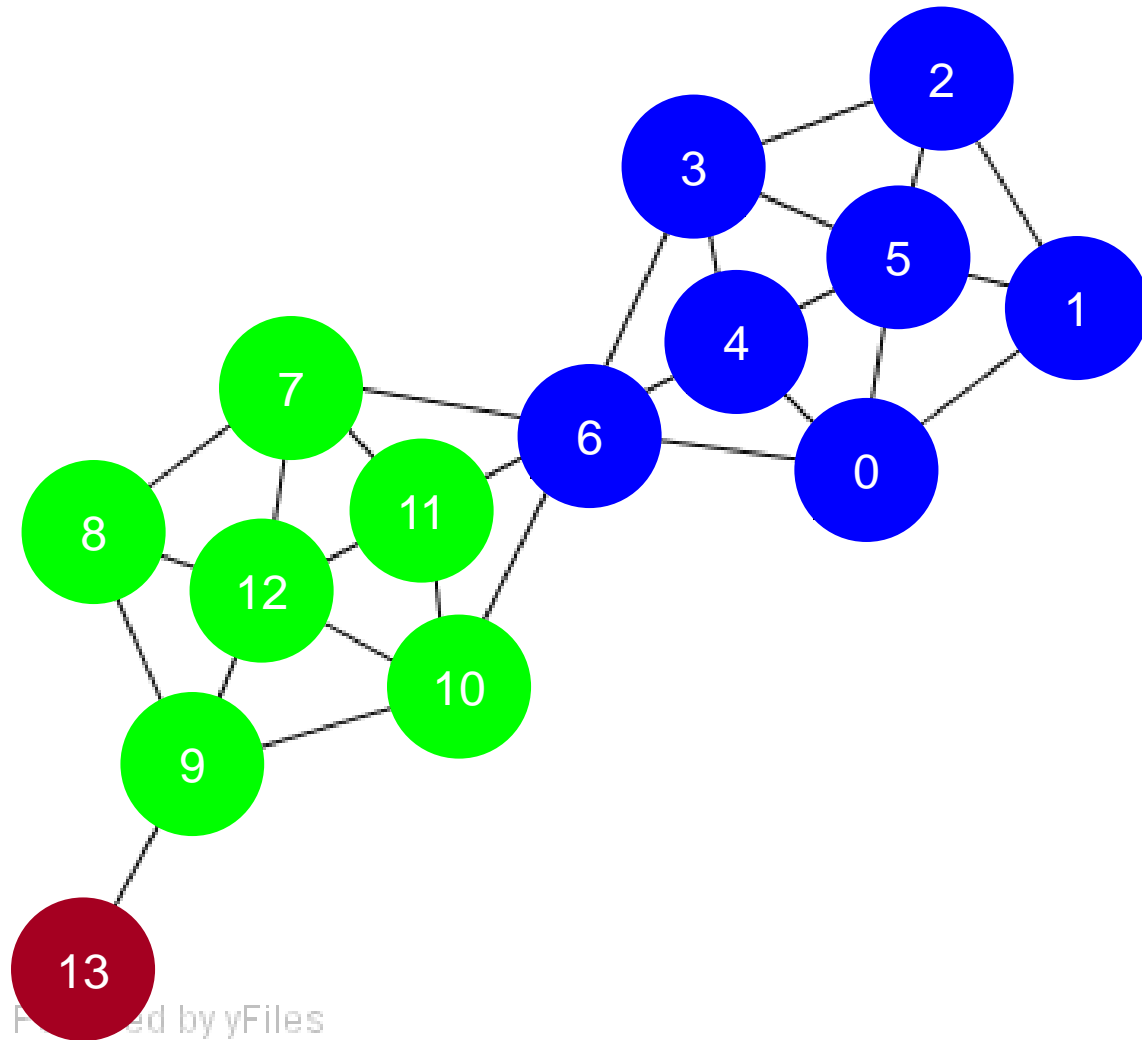
Algorithm

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Algorithm

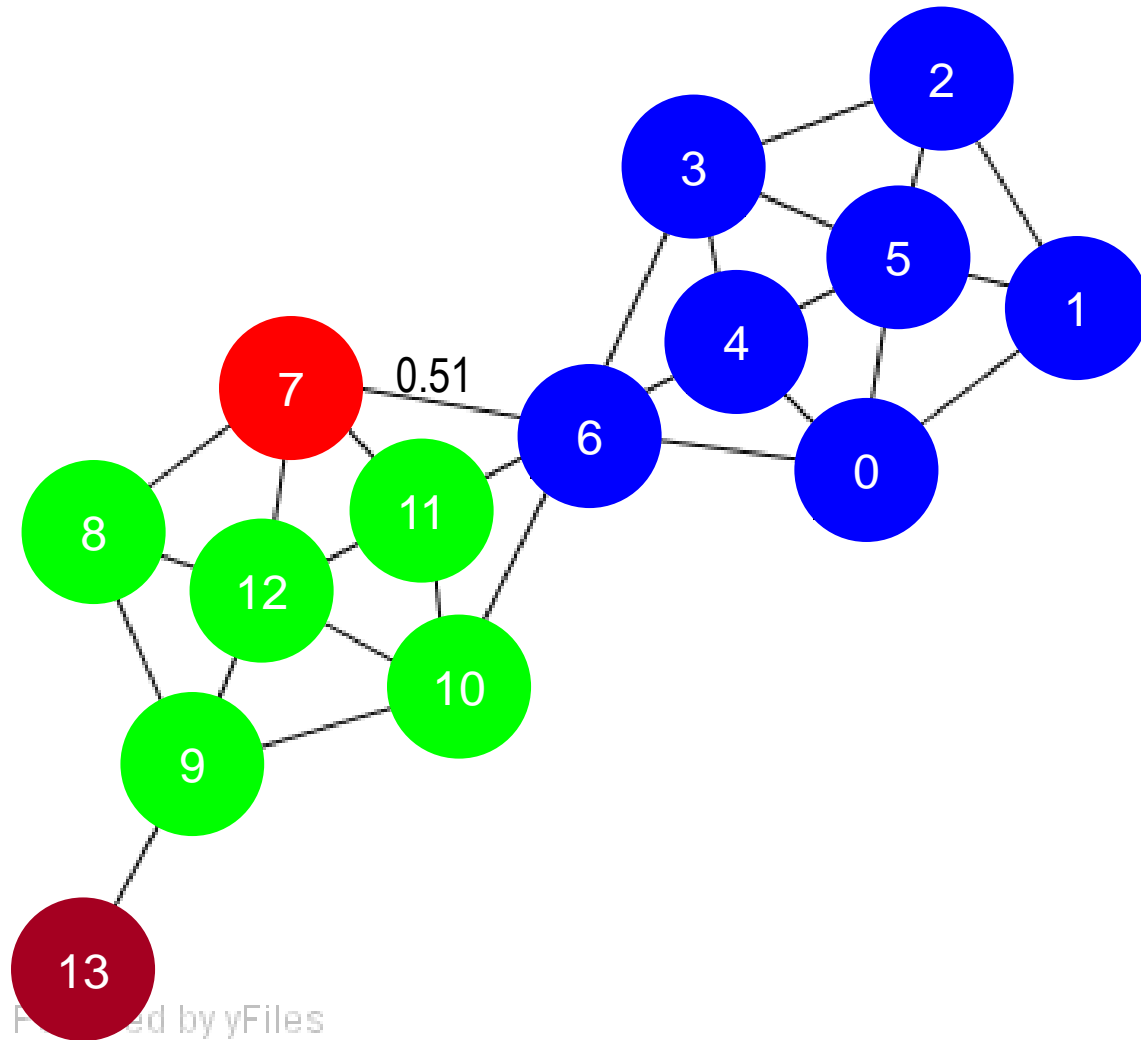
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Algorithm

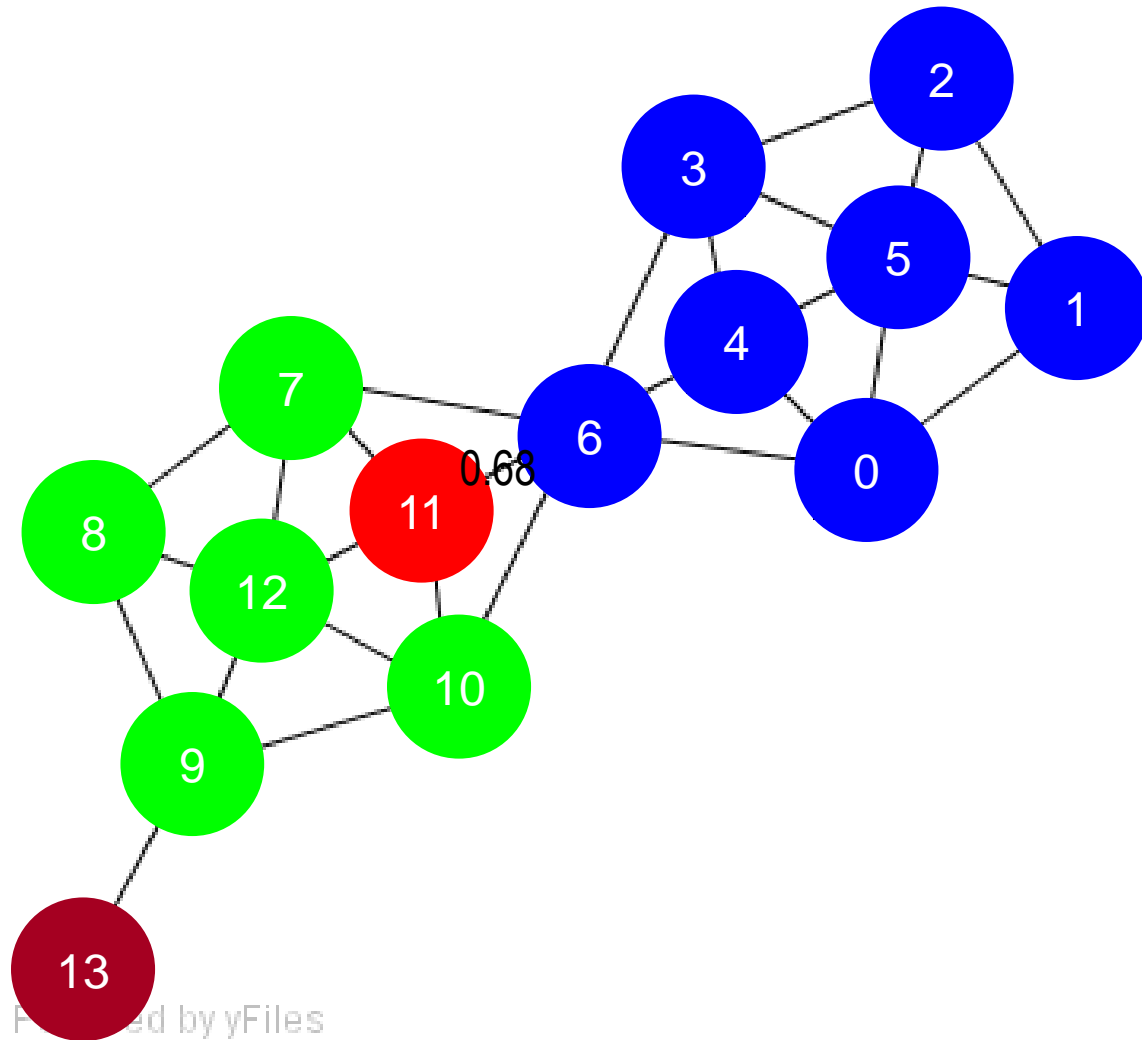
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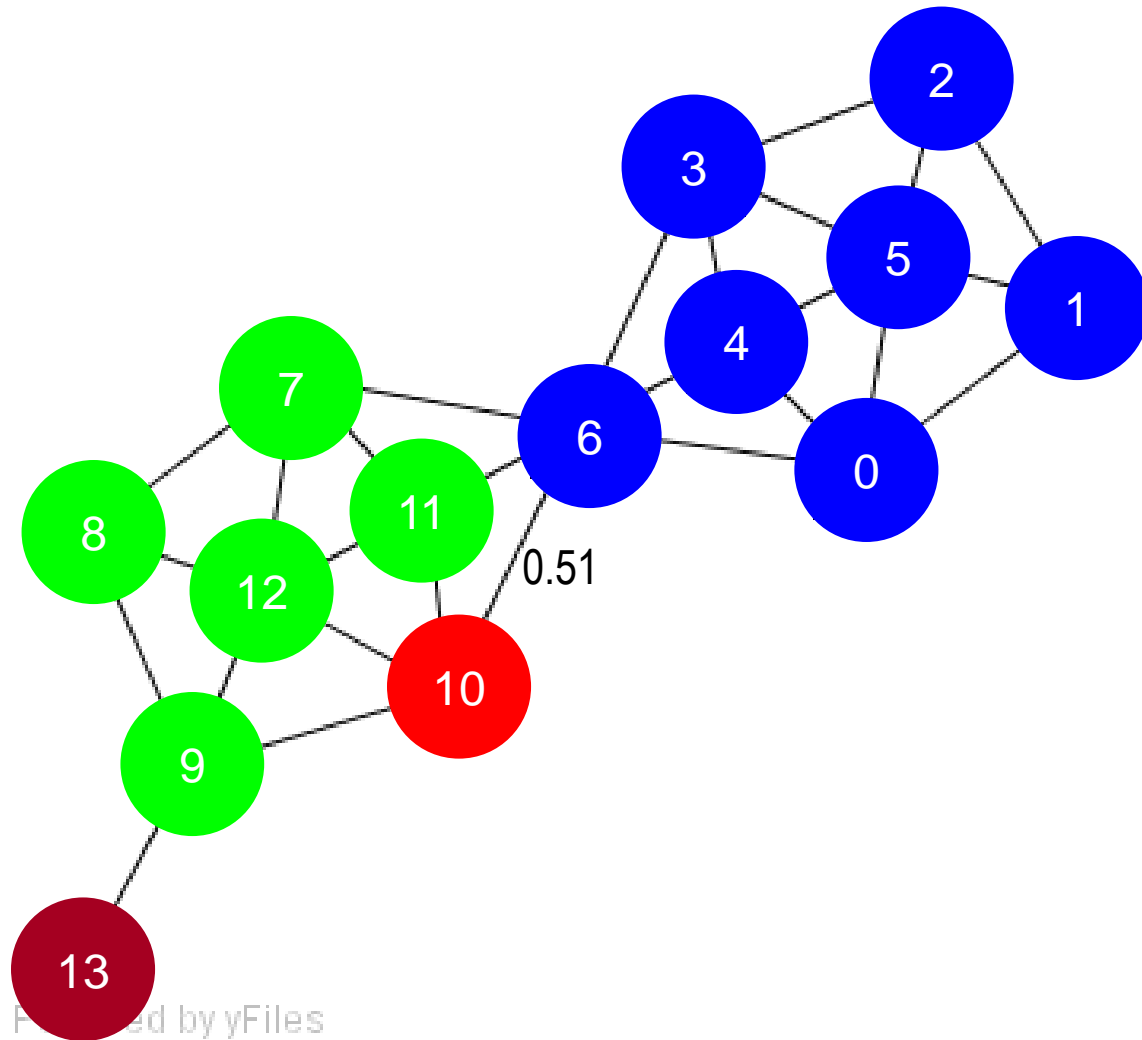
Algorithm

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Algorithm

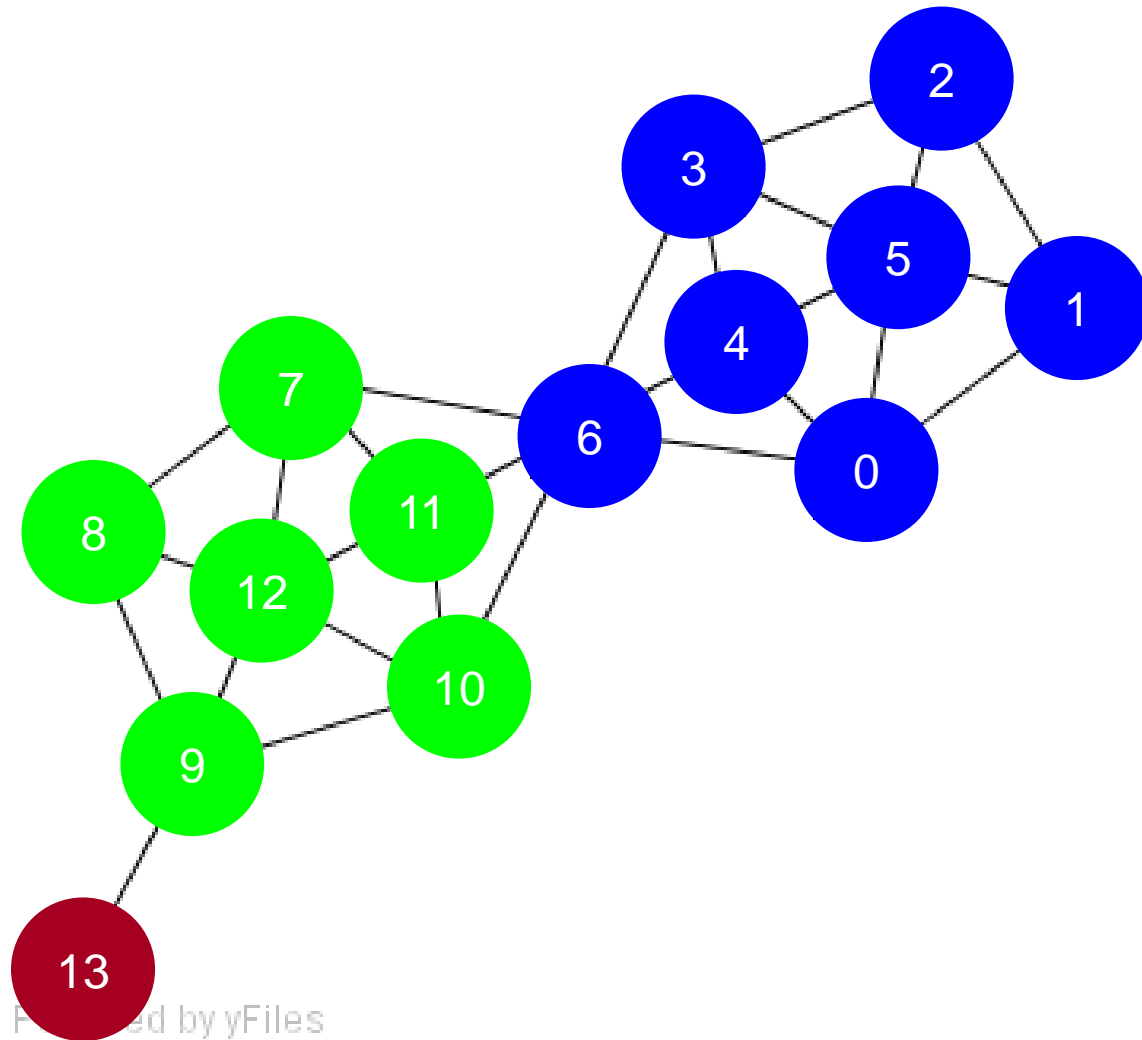
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Algorithm

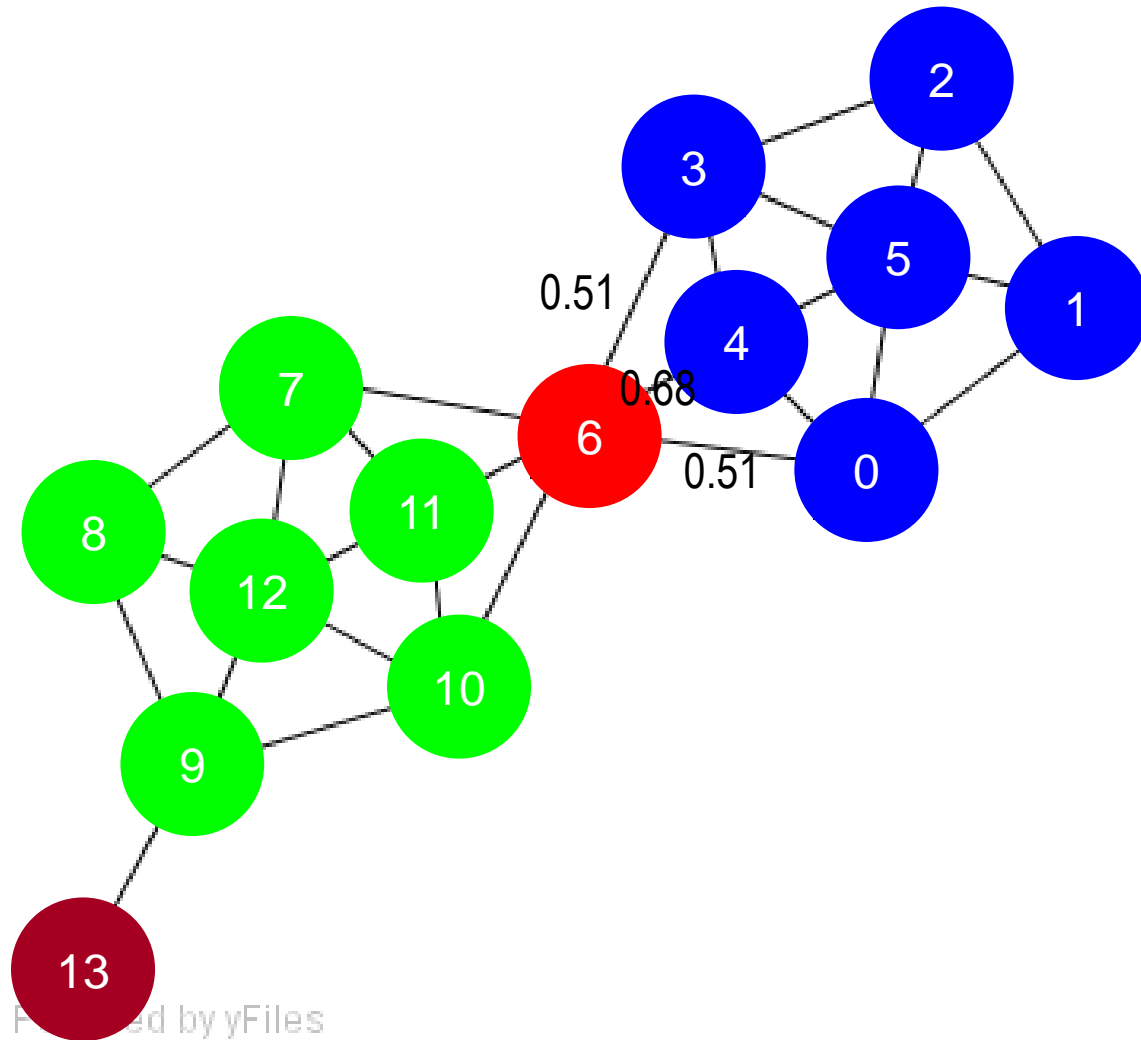
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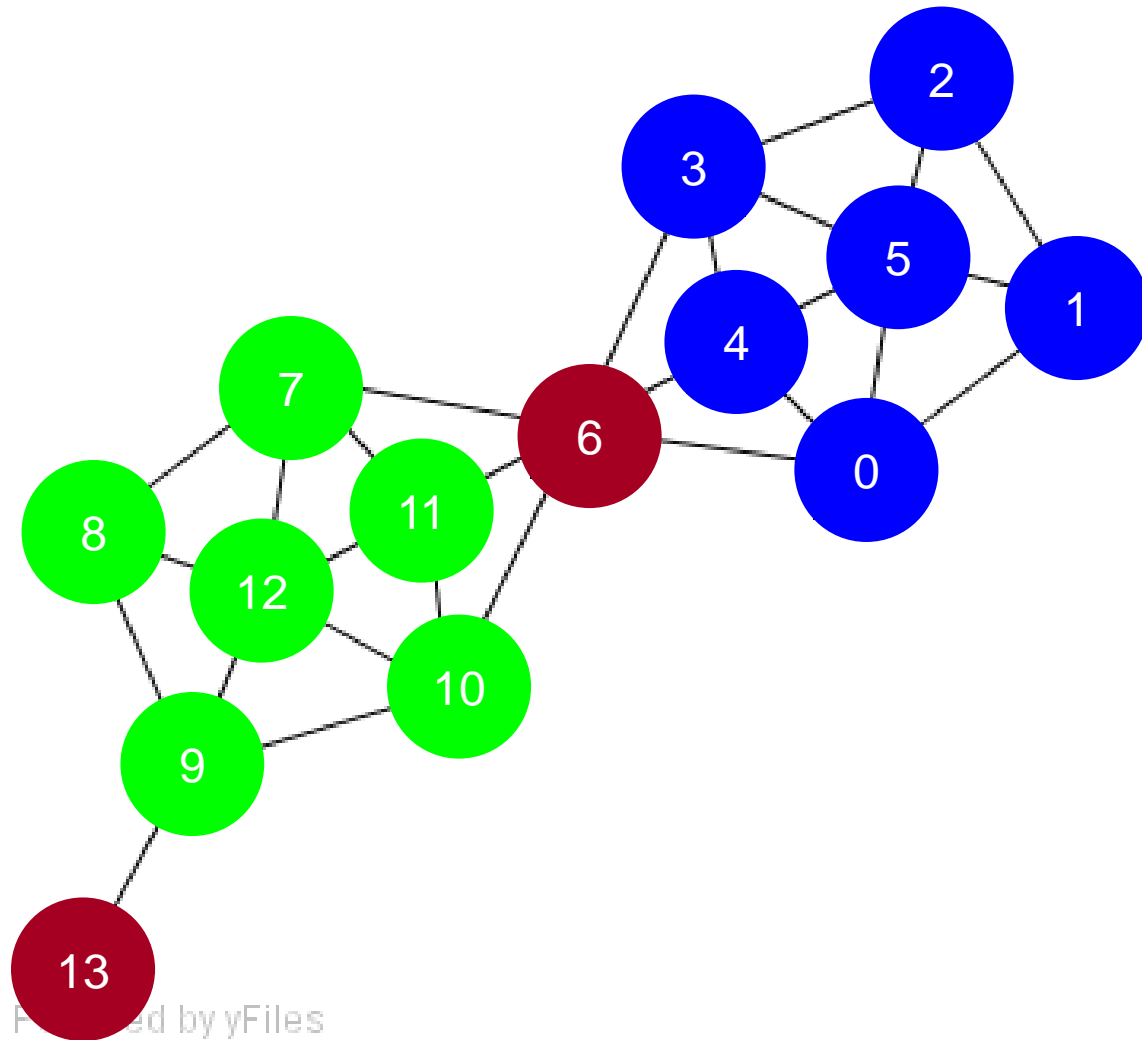
Algorithm

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Algorithm

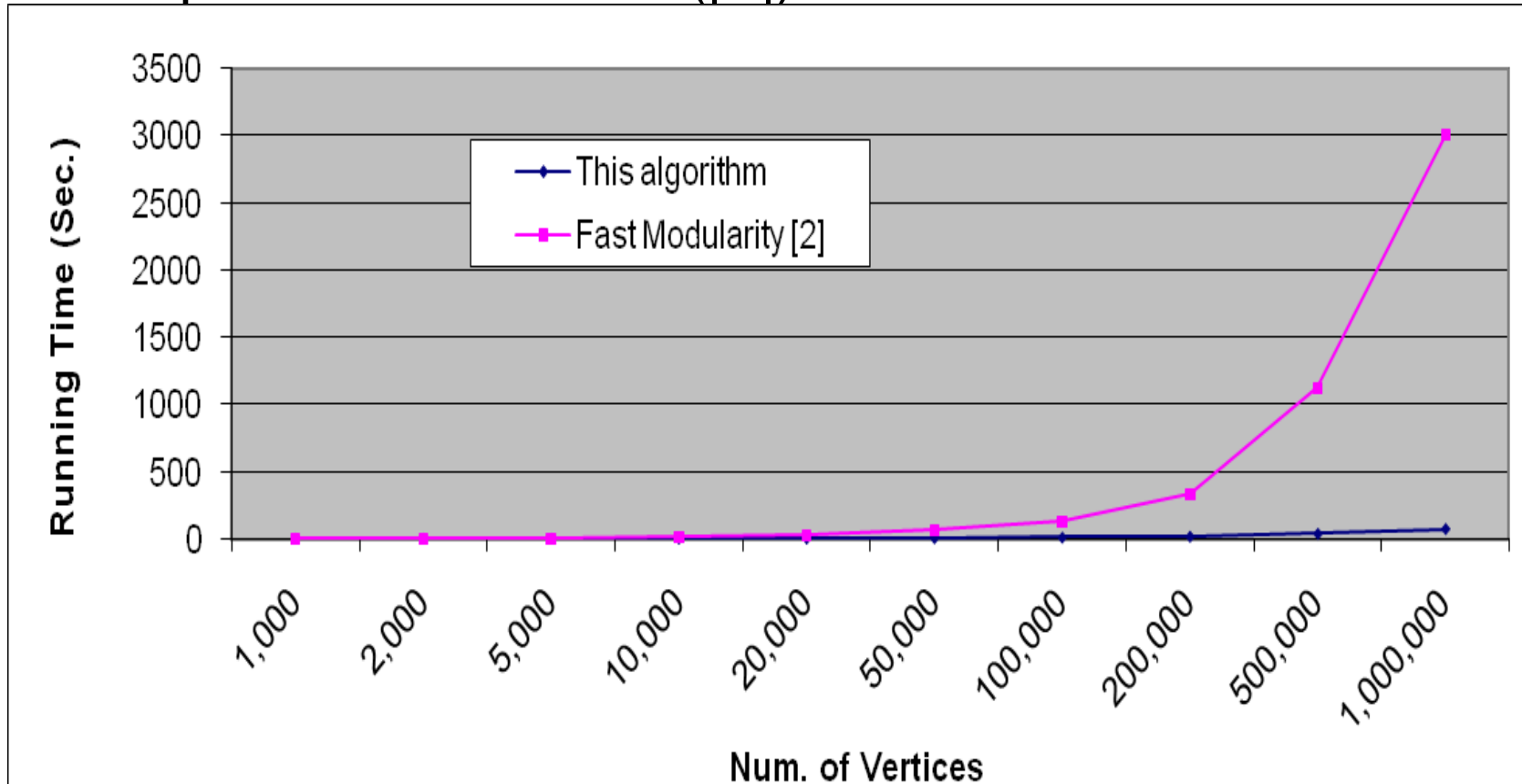
$$\mu = 2$$
$$\varepsilon = 0.7$$



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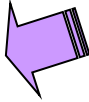
Running Time

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



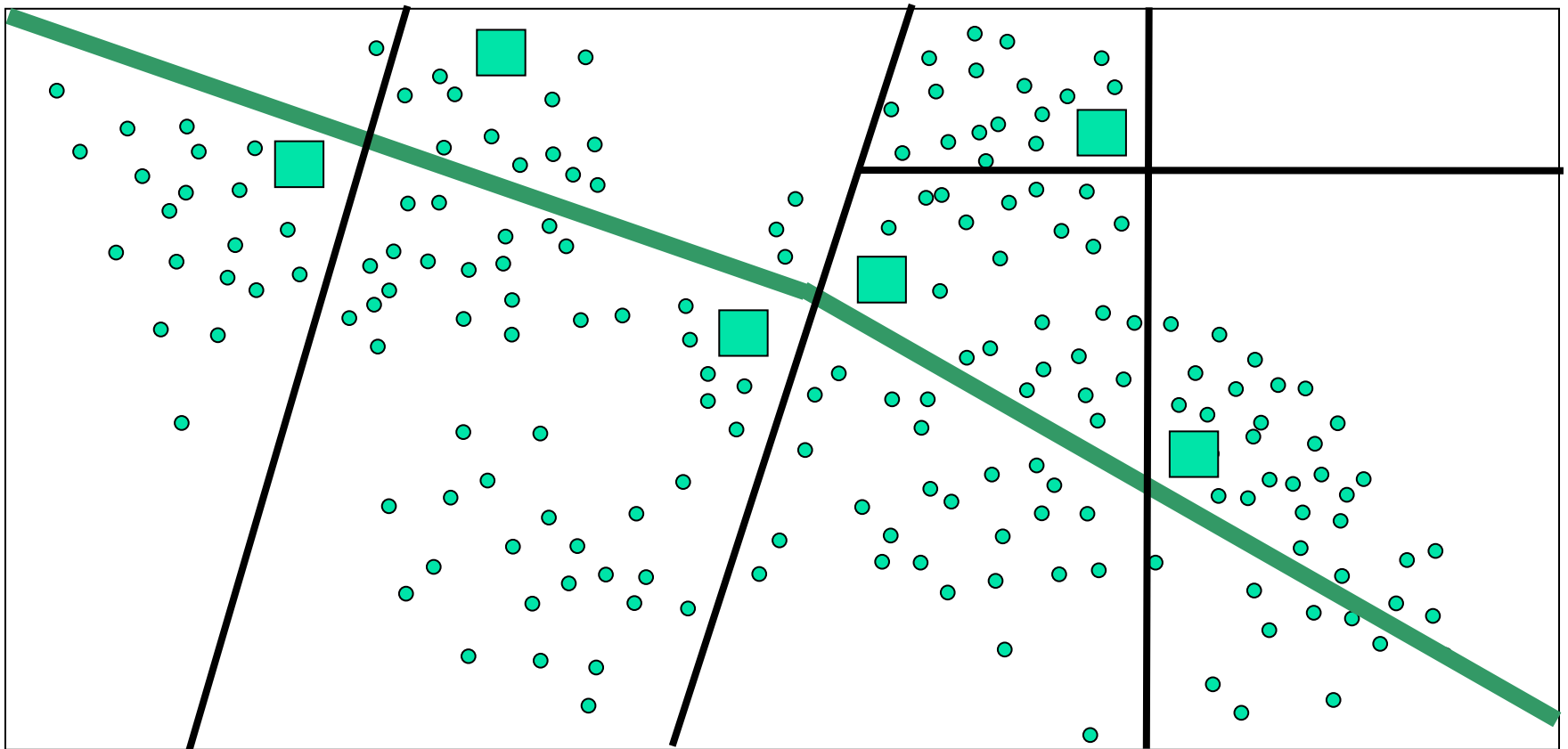
[2] A. Clauset, M. E. J. Newman, & C. Moore, *Phys. Rev. E* **70**, 066111 (2004).

Cluster Analysis: Advanced Methods

- 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

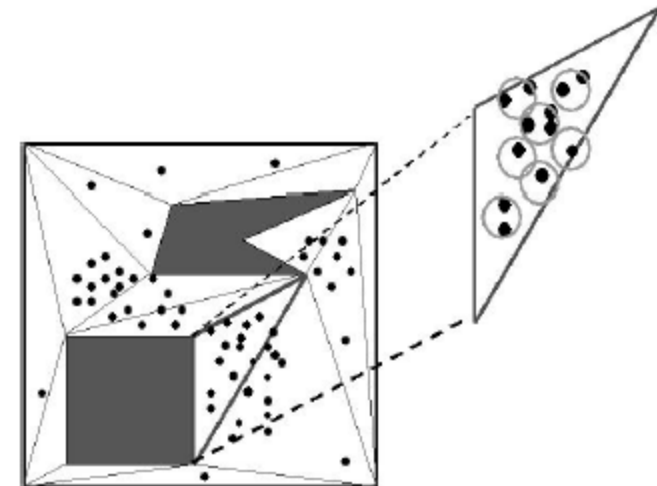
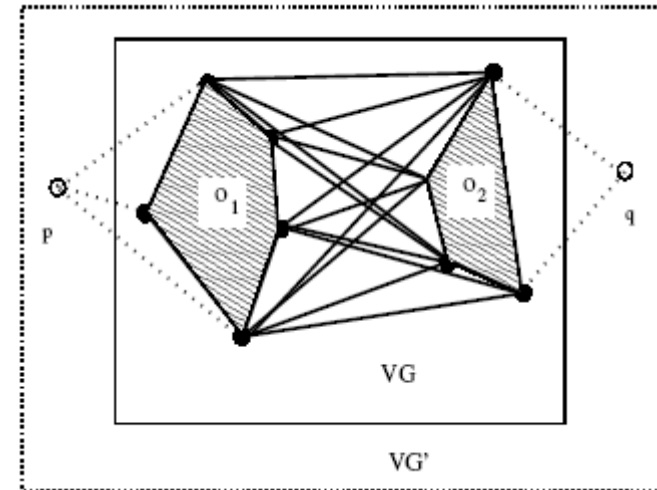
- Handling hard constraints: Strictly respect the constraints in cluster assignments
- Example: The COP-k-means algorithm
 - Generate super-instances for must-link constraints
 - Compute the transitive closure of the must-link constraints
 - To represent such a subset, replace all those objects in the 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

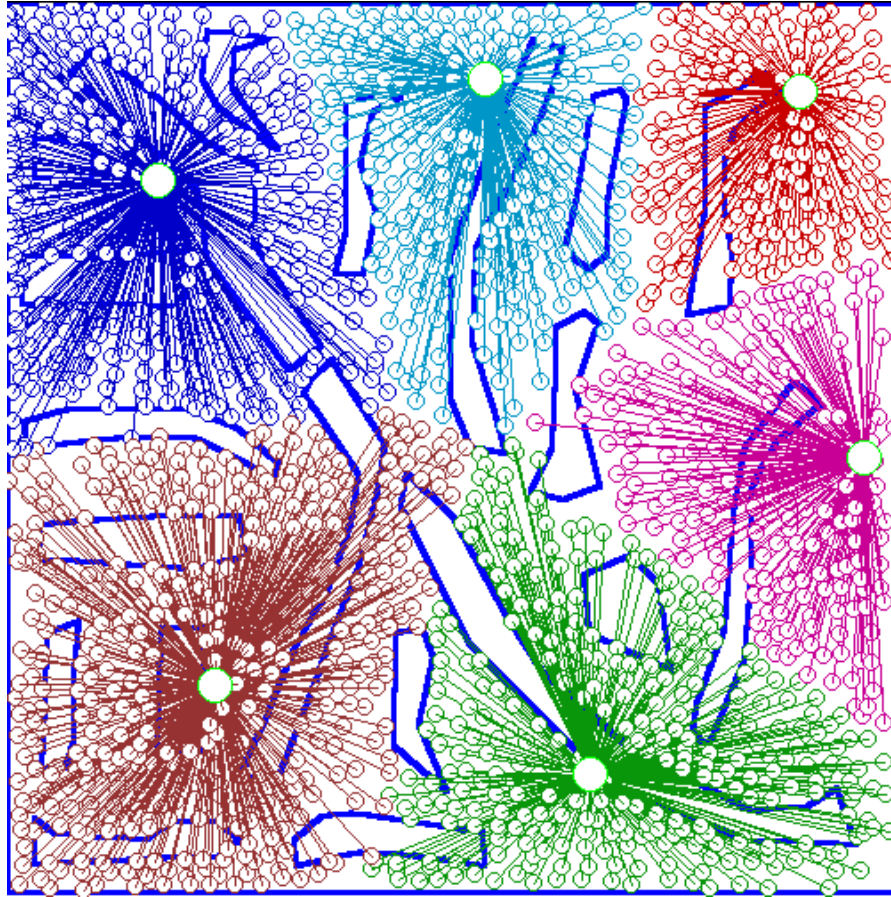
- Treated as an optimization problem: When a clustering violates a soft constraint, a penalty is imposed on the clustering
- Overall objective: Optimizing the clustering quality, and minimizing the constraint violation penalty
- Ex. CVQE (Constrained Vector Quantization Error) algorithm: Conduct k-means 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

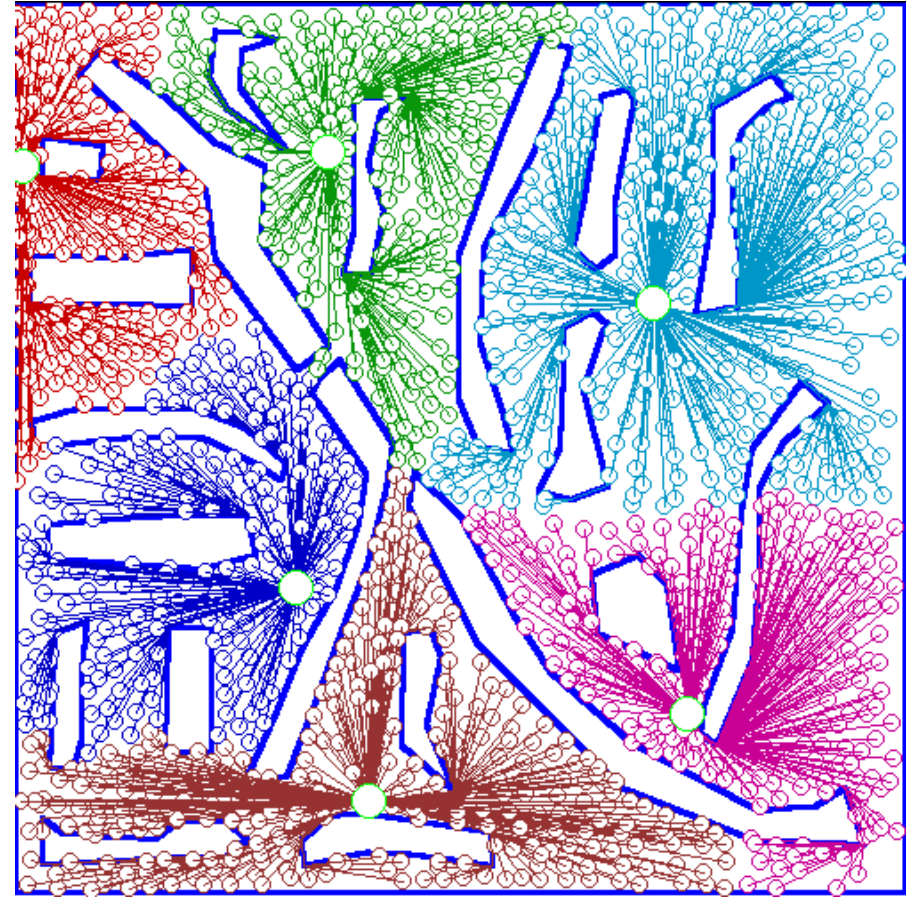
- It is costly to compute some constrained clustering
- Ex. Clustering with obstacle objects: Tung, Hou, and Han. Spatial clustering in the presence of obstacles, ICDE'01
- K-medoids is more preferable since k-means may locate the ATM center in the middle of a lake
- Visibility graph and shortest path
- 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

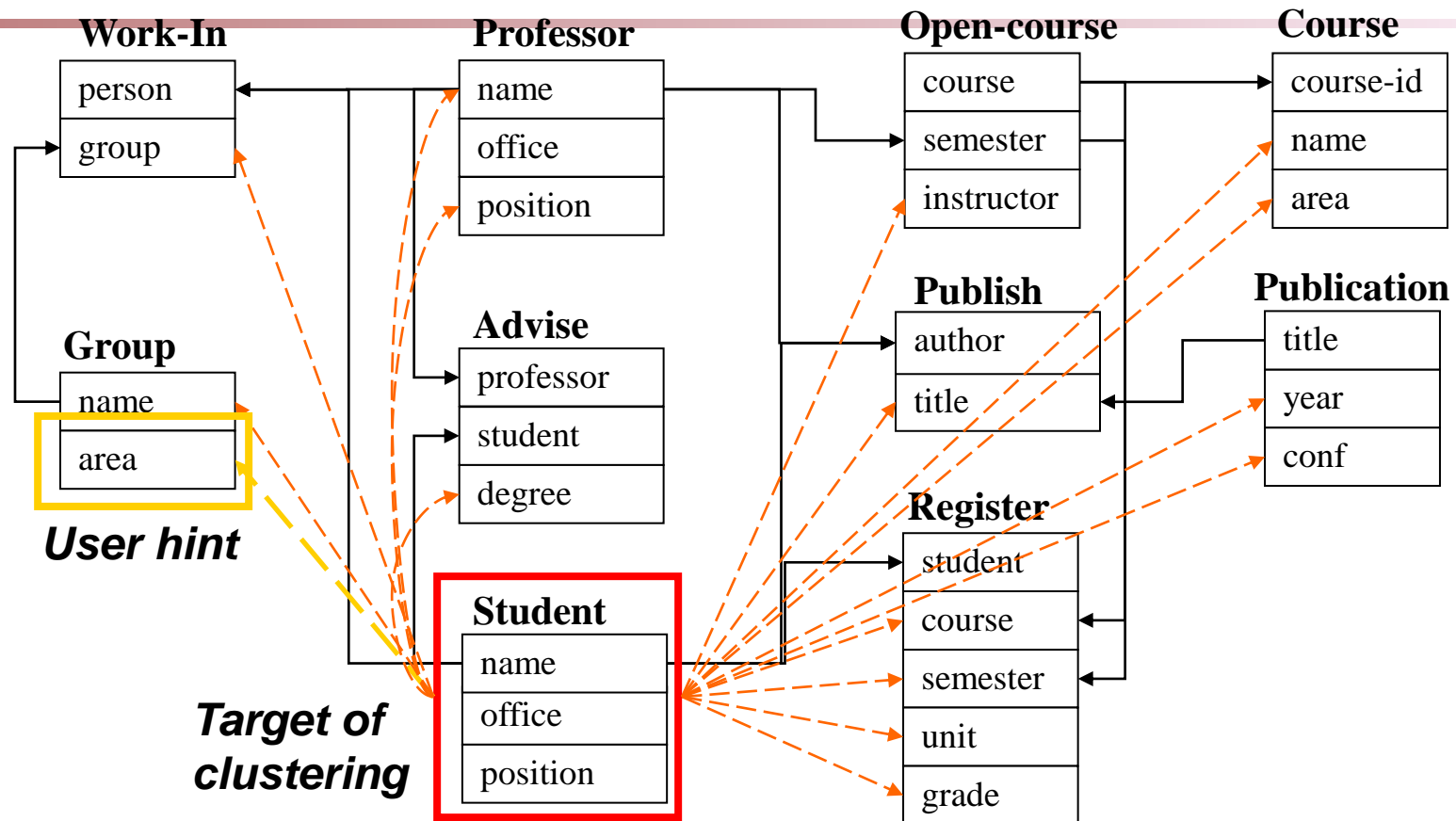


Not Taking obstacles into account



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

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

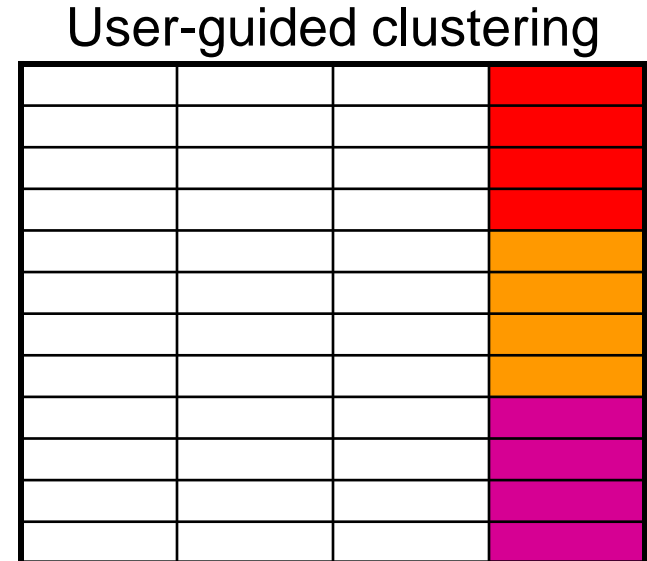
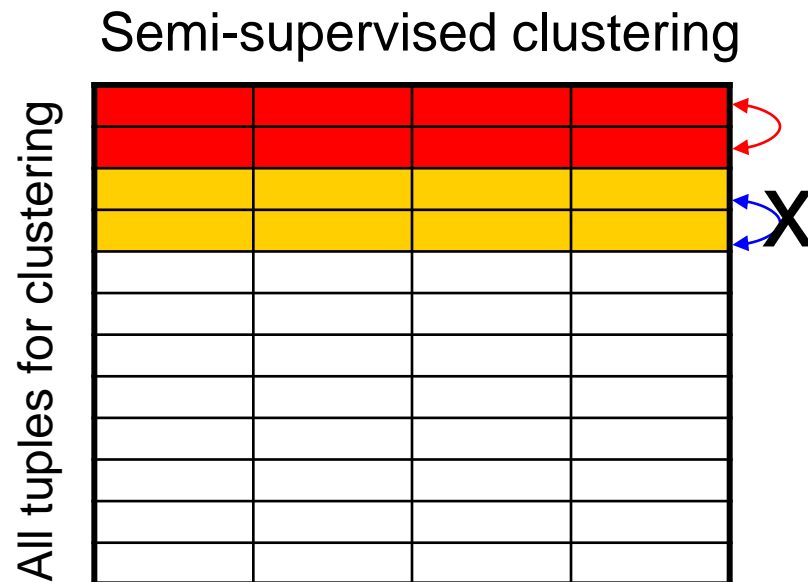
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			Red
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			Orange
			Orange
			Magenta
			Magenta
			Magenta
			Magenta
			Magenta

All tuples for clustering

- 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

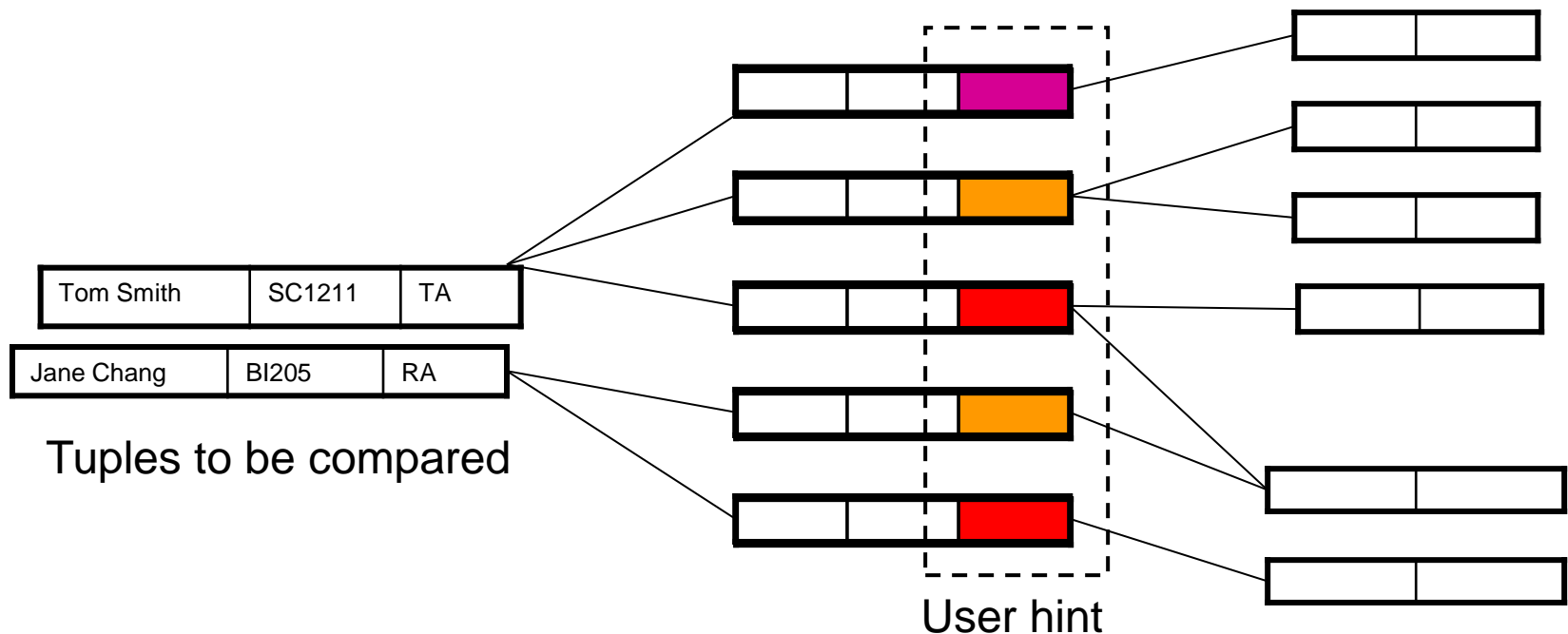
- Semi-supervised clustering: User provides a training set consisting of “similar” (“must-link”) and “dissimilar” (“cannot link”) pairs of objects
- User-guided clustering: User specifies an attribute as a hint, and more relevant features are found for clustering



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 $f = [Student \rightarrow Register \rightarrow OpenCourse \rightarrow Course, Course.area, null]$

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

$f(t_1)$



$f(t_2)$



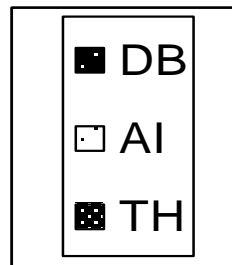
$f(t_3)$



$f(t_4)$



$f(t_5)$

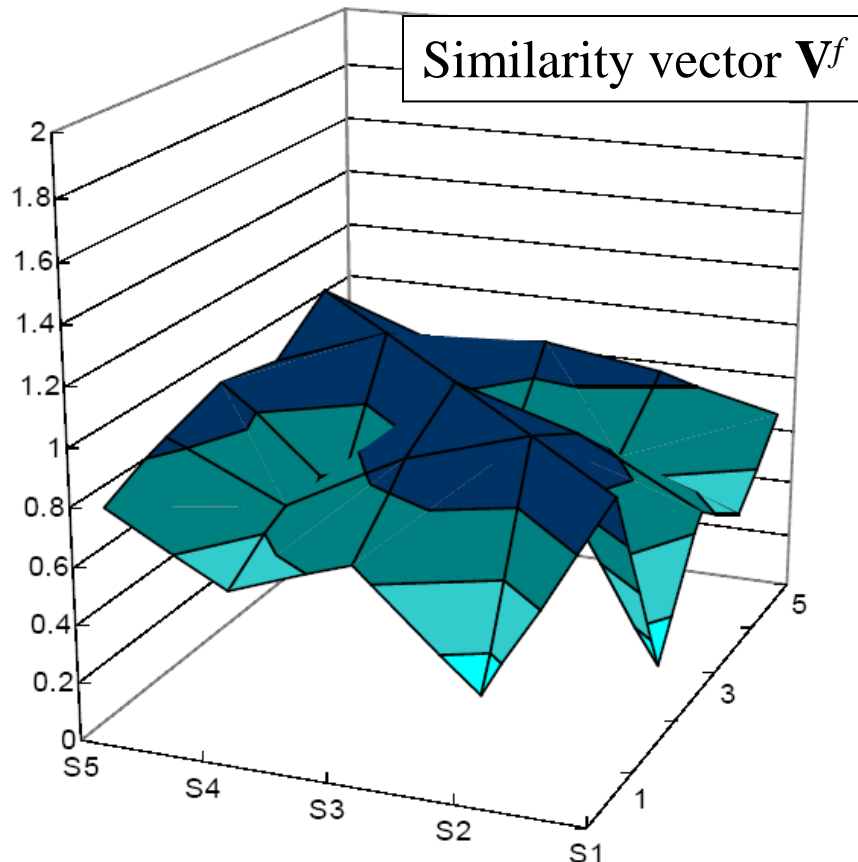


Representing Features

- 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

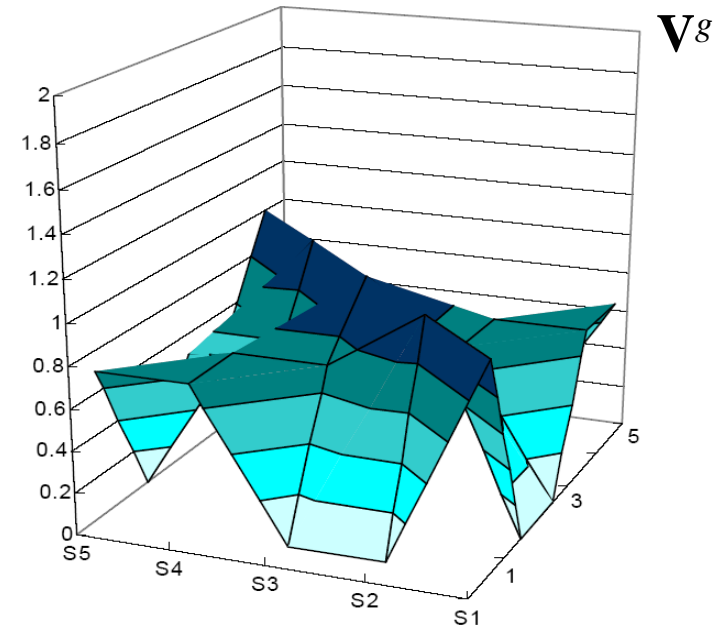
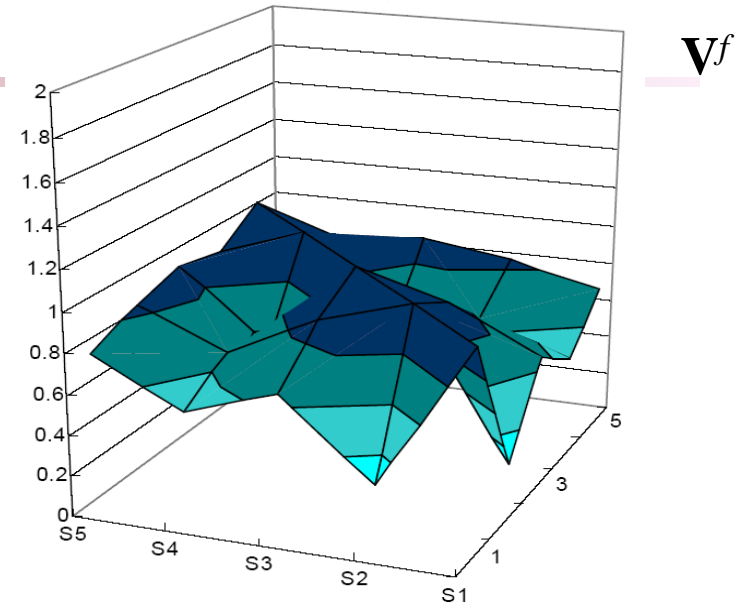
Similarity Between Features

Values of Feature f and g

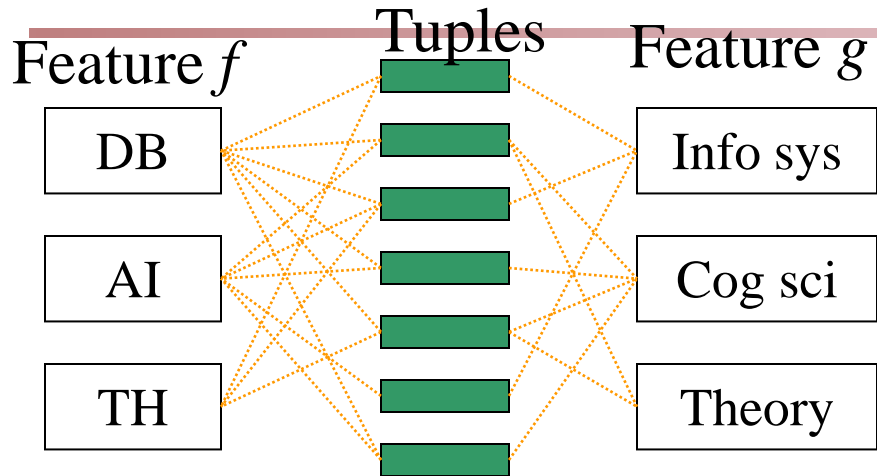
	Feature f (course)				Feature g (group)		
	DB	AI	TH		Info sys	Cog sci	Theory
t_1	0.5	0.5	0		1	0	0
t_2	0	0.3	0.7		0	0	1
t_3	0.1	0.5	0.4		0	0.5	0.5
t_4	0.5	0	0.5		0.5	0	0.5
t_5	0.3	0.3	0.4		0.5	0.5	0

Similarity between two features –
cosine similarity of two vectors

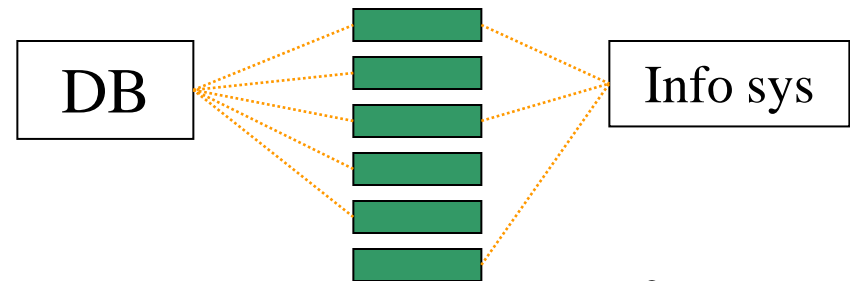
$$\text{sim}(f, g) = \frac{V^f \cdot V^g}{|V^f| |V^g|}$$



Computing Feature Similarity



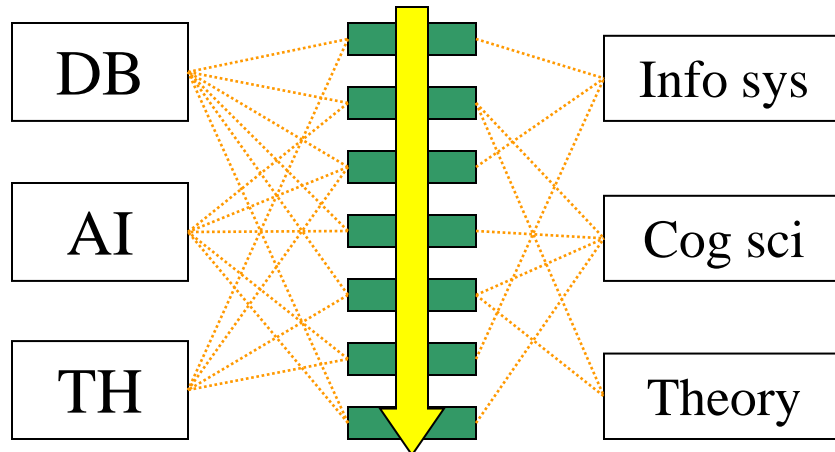
Similarity between feature values w.r.t. the tuples

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


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

sim(t_i, t_j): tuple similarities, hard to compute

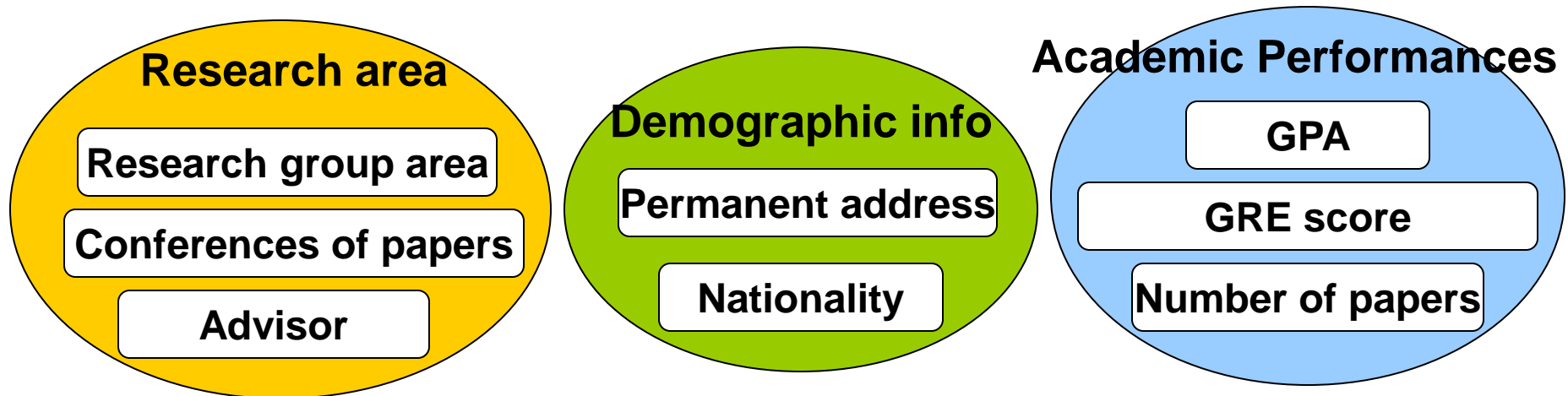
sim(f_k, g_q): feature value similarities, easy to compute



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

Searching for Pertinent Features

- Different features convey different aspects of information

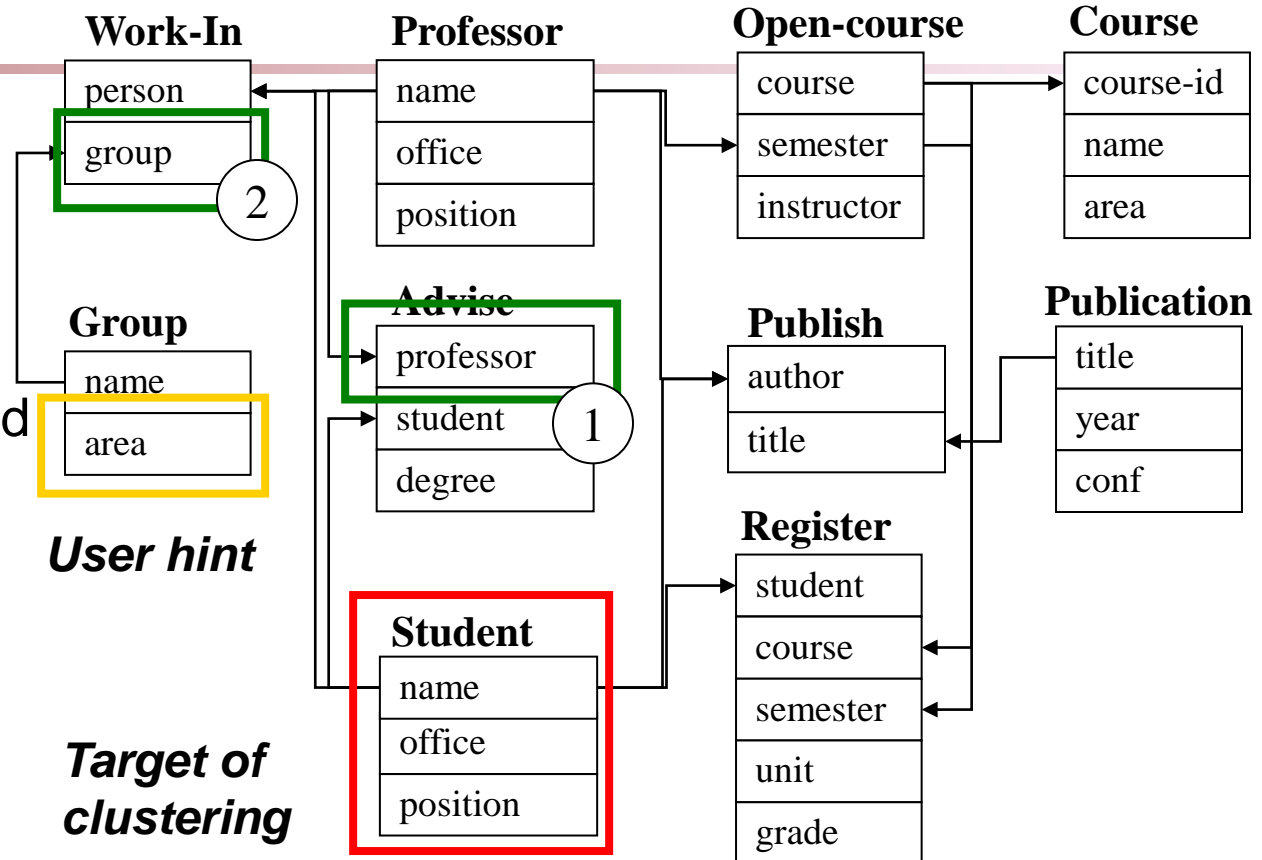


- Features conveying same aspect of information usually cluster tuples in more similar ways
 - Research group areas vs. conferences of publications
- Given user specified feature
 - Find pertinent features by computing feature similarity

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

- 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

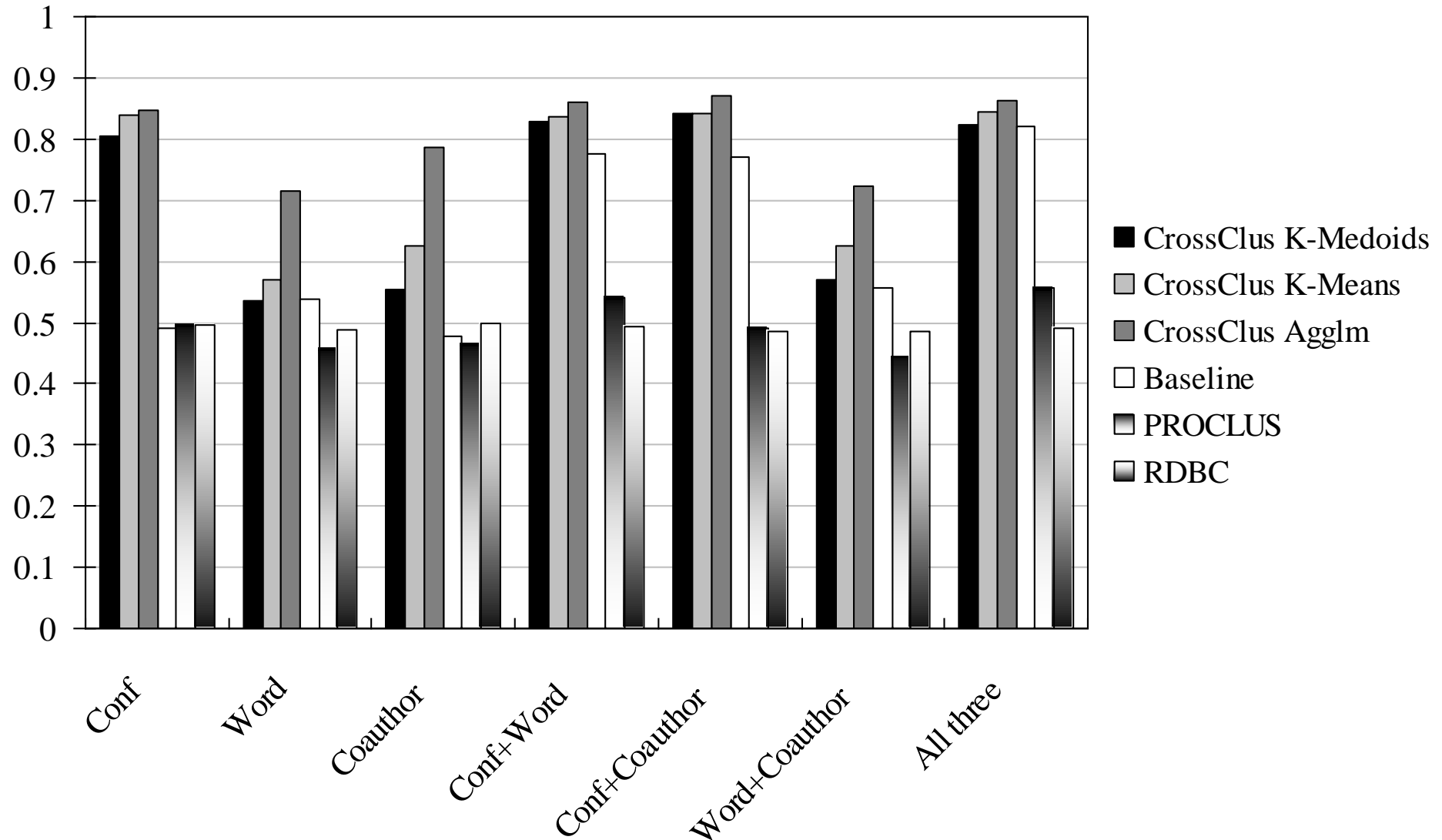
- Baseline: Only use the user specified feature
- PROCLUS [Aggarwal, et al. 99]: a state-of-the-art subspace clustering algorithm
 - Use a subset of features for each cluster
 - We convert relational database to a table by propositionalization
 - User-specified feature is forced to be used in every cluster
- 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


- 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



Cluster Analysis: Advanced Methods

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

Summary

- 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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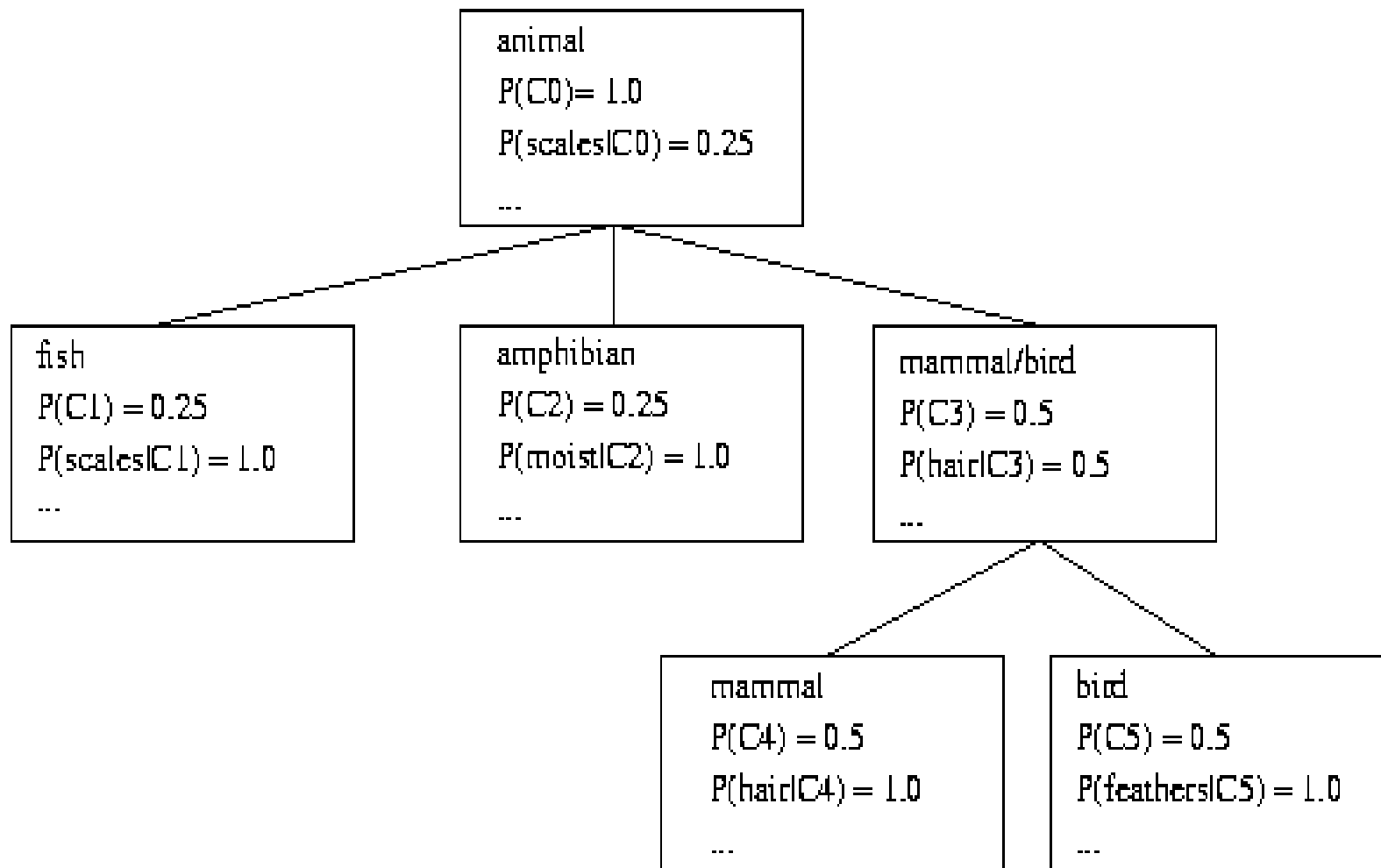
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Conceptual Clustering

- 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

- 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

- 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)

- 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

