# Clustering algorithms Konstantinos Koutroumbas 

## Unit 11

- Density-based clust. Alg. (DENCLUE)
- Spectral clustering
- Clustering for high-dim. data (dim. reduction, subspace clust.)
- Combination of clusterings


## Density-based algorithms for large data sets

DENsity-based CLUstEring (DENCLUE) Algorithm
Definitions
The influence function $f^{y}(x)$ for a point $y \in X$ is a positive function that decays to zero as $\boldsymbol{x}$ "moves away" from $\boldsymbol{y}(d(\boldsymbol{x}, \boldsymbol{y}) \rightarrow \infty)$. Typical examples are:
$f^{y}(x)=\left\{\begin{array}{l}1, \\ \text { if } d(x, y)<\sigma \\ 0, \\ \text { otherwise }\end{array}, \quad f^{y}(x)=e^{-\frac{d(x, y)^{2}}{2 \sigma^{2}}}\right.$
where $\sigma$ is a user-defined function.

The density function based on $X$ is defined as (Remember the Parzen windows):

$$
f^{X}(\boldsymbol{x})=\sum_{i=1}^{N} f^{x_{i}}(\boldsymbol{x})
$$

## The Goal:

(a) Identify all "significant" local maxima, $\boldsymbol{x}_{j}^{*}, j=1, \ldots, m$, of $f^{X}(\boldsymbol{x})$
(b) Create a cluster $C_{j}$ for each $x_{j}^{*}$ and assign to $C_{j}$ all points $x$ of $X$ that lie within the "region of attraction" of $x_{j}^{*}$.

## Density-based algorithms for large data sets

The DENCLUE Algorithm (cont.)
Two clarifications

- The region of attraction of $x_{j}^{*}$ is defined as the set of points $x \in R^{l}$ such that if a "hill-climbing" (such as the steepest ascent) method is applied on $f^{X}(x)$, initialized by $x$, it will terminate arbitrarily close to $x_{j}^{*}$.
- A local maximum is considered as significant if $f^{X}\left(x_{j}^{*}\right) \geq \xi$ ( $\xi$ is a userdefined parameter).

Approximation of $f^{X}(\boldsymbol{x})$

$$
f^{X}(x)=\sum_{i=1}^{N} f^{x_{i}}(\boldsymbol{x}) \approx \sum_{x_{i} \in Y(x)} f^{x_{i}}(\boldsymbol{x})
$$

where $Y(\boldsymbol{x})$ is the set of points in $X$ that lie "close" to $\boldsymbol{x}$.

The above framework is used by the DENCLUE algorithm.

## Density-based algorithms for large data sets

The DENCLUE Algorithm (cont.)

## DENCLUE algorithm

- Preclustering stage (identification of regions dense in points of $X$ )
$>$ Apply an $l$-dimensional grid of edge-length $2 \sigma$ in the $R^{l}$ space.
$>$ Determine the set $D_{p}$ of the hypercubes that contain at least one point of $X$.
$>$ Determine the set $D_{S p}\left(\subset D_{p}\right)$ that contains the "highly populated" cubes of $D_{p}$ (that is, cubes that contain at least $\xi_{c}>1$ points of $X$ ).
$>$ For each $c \in D_{s p}$ define a connection with all neighboring cubes $c_{j}$ in $D_{p}$ for which $d\left(\boldsymbol{m}_{c}, \boldsymbol{m}_{c_{j}}\right) \leq 4 \sigma$, where $\boldsymbol{m}_{c}, \boldsymbol{m}_{c_{j}}$ are the means of $c$ and $c_{j}$, respectively.
- Main stage
$>$ Determine the set $D_{r}$ that contains:
-the highly populated cubes and
-the cubes that have at least one connection with a highly populated cube.



## Density-based algorithms for large data sets

DENCLUE algorithm (cont.)

- Main stage (cont.)
- For each point $x$ in a cube $c \in D_{r}$
$>$ Determine $Y(\boldsymbol{x})$ as the set of points that belong to cubes $c_{j}$ in $D_{r}$ such that the mean values of $c_{j}$ 's lie at distance less than $\lambda \cdot \sigma$ from $x$ (typically $\lambda=4)$.
$>$ Apply a hill climbing method on $f^{X}(x)=\sum_{x_{i} \in Y(x)} f^{x_{i}}(\boldsymbol{x})$ starting from $x$ and let $x^{*}$ be the local maximum to which the method converges.
$>$ If $x^{*}$ is a significant local maximum $\left(f^{X}\left(\boldsymbol{x}^{*}\right) \geq \xi\right)$ then -If a cluster $C$ associated with $x^{*}$ has already been created then $\mathrm{o}_{-} x$ is assigned to $C$
-Else
o Create a cluster $C$ associated with $x^{*}$
o Assign $x$ to $C$
-End if
$>$ End if
- End for



## Density-based algorithms for large data sets

The DENCLUE Algorithm (cont.)

## Remarks:

- Shortcuts allow the assignment of points to clusters, without having to apply the hill-climbing procedure.
- DENCLUE is able to detect arbitrarily shaped clusters.
- The algorithm deals with noise very satisfactory.
- The worst-case time complexity of DENCLUE is $O\left(N \log _{2} N\right)$.
- Experimental results indicate that the average time complexity is $O\left(\log _{2} N\right)$.
- It works efficiently with high-dimensional data.


## Spectral clustering

Spectral clustering is based on graph theory concepts.

Rationale: It actually maps the data from their original space, where they may form arbitrarily-shaped clusters, to a new space, where (their images) form compact clusters.

## Main stages:

$>$ Definition of a similarity graph $G$ based on the given data set $X$.
$>$ Utilization of the Laplacian matrix $L$ associated with $G$.
$>$ Mapping of the data set to a space spanned by some eigenvectors of $L$.
$>$ Performing clustering on the images of the data in the transformed space.

In principle, spectral clustering is able to recover arbitrarily shaped clusters (see discussion later).

## Spectral clustering

## Similarity graph

- Data set $X=\left\{\boldsymbol{x}_{1}, \boldsymbol{x}_{2}, \ldots, \boldsymbol{x}_{N}\right\}$ undirected graphs. $^{\text {- }}$
- Similarity graph $G=(V, E)$

Definition of a similarity graph About $V$

- The set $V$ consists of $N$ vertices/nodes, $v_{1}, v_{2}, \ldots, v_{N}$
- Each vertex $v_{i} \in V$ corresponds to a $\boldsymbol{x}_{i} \in X, i=1, \ldots, N$.


## About E

Various scenarios lead to various graphs:
(a) The $\varepsilon$-neighborhood graph:
$\begin{aligned} X & =\left\{x_{1}, x_{2}, \ldots, x_{N}\right\} \\ V & =\left\{v_{1}, v_{2}, \ldots, v_{N}\right\}\end{aligned}$
$>$ An edge $e_{i j}$ is added between vertices $v_{i}$ and $v_{j}$, if $d\left(\boldsymbol{x}_{i}, \boldsymbol{x}_{j}\right)<\varepsilon$.
$>$ Usually it is considered as an unweighted graph (it is $w_{i j}=1$, for all $e_{i j}{ }^{\prime} \mathrm{s}$ ).

## Spectral clustering

Similarity graph
Definition of a similarity graph
About E
(b) The $k$-nearest neighbor graph:
$>$ An edge $e_{i j}$ is added between vertices $v_{i}$ and $v_{j}$, if $v_{i}$ is among the $k-$ nearest neighbors of $v_{j} \mathbf{O R}$ vice versa.
$>$ Each $e_{i j}$ is weighted by the similarity between $x_{i}$ and $x_{j}$.
(c) The mutual $k$-nearest neighbor graph:
$>$ An edge $e_{i j}$ is added between vertices $v_{i}$ and $v_{j}$, if $v_{i}$ is among the $k$ nearest neighbors of $v_{j}$ AND vice versa.
$>$ Each $e_{i j}$ is weighted by the similarity between $\boldsymbol{x}_{i}$ and $\boldsymbol{x}_{j}$.
(d) The fully connected graph:
$>$ All possible edges $e_{i j}$ are added in the graph.
$>$ Each $e_{i j}$ is weighted by the similarity between $x_{i}$ and $x_{j}$, e.g.,

$$
s\left(x_{i}, x_{j}\right)=\exp \left(-\frac{| | x_{i}-x_{j} \|^{2}}{2 \sigma^{2}}\right)
$$

## Spectral clustering

Similarity graph

## Example:

The data set consists of
(i) two "half moon" clusters and
(ii) a compact cluster of different density from the previous ones.

The resulting graphs are shown in the figure.

Data points

kNN graph, k=5

epsilon-graph, epsilon $=0.3$


## Spectral clustering

## Graph Laplacians

- There are various definitions for graph Laplacian matrix.
- All such matrices share some properties that allow their exploitation in the frame of clustering.


## Some definitions:

- Weighted adjacency matrix:
$w_{i j}$ is the weight of the edge connecting $v_{i}$ and $v_{j}$.

$$
W=\left[w_{i j}\right]_{N \times N}
$$

- Degree of a vertex $v_{i}$ :

$$
d_{i}=\sum_{i=1}^{N} w_{i j}, i=1, \ldots, N
$$

- Degree matrix:

$$
D_{N \times N}=\operatorname{diag}\left(d_{1}, d_{2}, \ldots, d_{N}\right)=\left[\begin{array}{ccc}
d_{1} & \cdots & 0 \\
0 & \ddots & 0 \\
0 & \cdots & d_{N}
\end{array}\right]_{N \times N}
$$

- (Unnormalized) graph Laplacian matrix:

$$
L_{N \times N}=D-W
$$

## Spectral clustering

Graph Laplacians
Some results for the unnormalized graph Laplacian L:

1. $\forall \boldsymbol{x}=\left[x_{1}, \ldots, x_{N}\right]^{T} \in R^{N}$ it is

$$
\boldsymbol{x}^{T} L \boldsymbol{x}=\frac{1}{2} \sum_{i=1}^{N} \sum_{j=1}^{N} w_{i j}\left(x_{i}-x_{j}\right)^{2}
$$

2. $L$ is symmetric and positive semidefinite.
3. The smallest eigenvalue of $L$ is 0 .
4. $L$ has $N$ non-negative real-valued eigenvalues $0=\lambda_{1} \leq \lambda_{2} \leq \cdots \leq \lambda_{N}$.
5. Let $G$ be an undirected graph with nonnegative weights. Then the multiplicity $k$ of the zero eigenvalue equals to the number of the connected components $A_{1}, \ldots, A_{k}$, of the graph. In addition, the eigenspace of the zero eigenvalues is spanned by the ( $N$-dimensional) indicator vectors of those components, $\mathbf{1}_{A_{1}}, \ldots \mathbf{1}_{A_{k}}$.

The indicator vector $1_{A_{i}}$ has all of its components equal 0 except those corresponding to the points that belong to the $k$-th connected component., which are equal to 1.

## Spectral clustering

Graph Laplacians: Some results for the unnormalized graph Laplacian L:
5. Let $G$ be an undirected graph with nonnegative weights ( $w_{i j} \geq 0$ ). Then the multiplicity $k$ of the zero eigenvalue equals to the number of the connected components $A_{1}, \ldots, A_{k}$, of the graph. In addition, the eigenspace of the zero eigenvalue is spanned by the ( $N$-dimensional) indicator vectors of those components, $\mathbf{1}_{A_{1}}, \ldots, \mathbf{1}_{A_{k}}$.

- The $k=1$ case (connected graph): It is
$d_{i}=\sum_{j=1}^{N} w_{i j}, w_{i i}=0$

$$
=-\lambda\left|\begin{array}{ccc}
d_{2}+w_{12}-\lambda & \cdots & -w_{2 N}+w_{1 N} \\
\vdots & \ddots & \vdots \\
-w_{2 N}+w_{12} & \cdots & d_{N}+w_{1 N}-\lambda
\end{array}\right| \Leftrightarrow \lambda_{1}=0,\left(\lambda_{2}, \ldots \lambda_{N}>0\right)
$$

Thus, multiplicity of the zero eigenvalue is 1 . The associated eigenvector is the $\mathbf{1}$, since $\mathbf{0}=0 \cdot \mathbf{1}=L \cdot \mathbf{1}$ 。○ $d_{i}=\sum_{i=1}^{N} w_{i j}$

$$
\begin{aligned}
& 0=|L-\lambda \mathrm{I}|=\left|\begin{array}{cccc}
d_{1}-\lambda & -w_{12} & \cdots & -w_{1 N} \\
-w_{12} & d_{2}-\lambda & \cdots & -w_{2 N} \\
\vdots & \vdots & \ddots & \vdots \\
-w_{1 N} & -w_{2 N} & \cdots & d_{N}-\lambda
\end{array}\right|=\left|\begin{array}{cccc}
-\lambda & -w_{12} & \cdots & -w_{1 N} \\
-\lambda & d_{2}-\lambda & \cdots & -w_{2 N} \\
\vdots & \vdots & \ddots & \vdots \\
-\lambda & -w_{2 N} & \cdots & d_{N}-\lambda
\end{array}\right|= \\
& -\lambda\left|\begin{array}{cccc}
1 & -w_{12} & \cdots & -w_{1 N} \\
1 & d_{2}-\lambda & \cdots & -w_{2 N} \\
\vdots & \vdots & \ddots & \vdots \\
1 & -w_{2 N} & \cdots & d_{N}-\lambda
\end{array}\right|=-\lambda\left|\begin{array}{cccc}
1 & -w_{12} & \cdots & -w_{1 N} \\
0 & d_{2}+w_{12}-\lambda & \cdots & -w_{2 N}+w_{1 N} \\
\vdots & \vdots & \ddots & \vdots \\
0 & -w_{2 N}+w_{12} & \cdots & d_{N}+w_{1 N}-\lambda
\end{array}\right|
\end{aligned}
$$

## Spectral clustering

## Graph Laplacians: Some results for the unnormalized graph Laplacian L:

5. Let $G$ be an undirected graph with nonnegative weights ( $w_{i j} \geq 0$ ). Then the multiplicity $k$ of the zero eigenvalue equals to the number of the connected components $A_{1}, \ldots, A_{k}$, of the graph. In addition, the eigenspace of the zero eigenvalue is spanned by the ( $N$-dimensional) indicator vectors of those components, $\mathbf{1}_{A_{1}}, \ldots, \mathbf{1}_{A_{k}}$.

- The $k=1$ case (connected graph):
- The associated eigenvector is the $\mathbf{1}$,since $\mathbf{0}=0 \cdot \mathbf{1}=L \cdot \mathbf{1}$

$$
\mathbf{0}=0 \cdot \mathbf{1}=0 \cdot\left[\begin{array}{c}
1 \\
1 \\
\vdots \\
1
\end{array}\right]=\left[\begin{array}{cccc}
d_{1} & -w_{12} & \cdots & -w_{1 N} \\
-w_{12} & d_{2} & \cdots & -w_{2 N} \\
\vdots & \vdots & \ddots & \vdots \\
-w_{1 N} & -w_{2 N} & \cdots & d_{N}
\end{array}\right]\left[\begin{array}{c}
1 \\
1 \\
\vdots \\
1
\end{array}\right]
$$

。


## Spectral clustering

Graph Laplacians: Some results for the unnormalized graph Laplacian L:
5. Let $G$ be an undirected graph with nonnegative weights ( $w_{i j} \geq 0$ ). Then the multiplicity $k$ of the zero eigenvalue equals to the number of the connected components $A_{1}, \ldots, A_{k}$, of the graph. In addition, the eigenspace of the zero eigenvalue is spanned by the ( $N$-dimensional) indicator vectors of those components, $\mathbf{1}_{A_{1}}, \ldots, \mathbf{1}_{A_{k}}$.

- The $k>1$ case ( $k$ connected components):
- Considering each connected component individually, the $i$-th component has its own associated Laplacian $L_{i}$
- Then the Laplacian for the whole graph can be written as

- Since, the multiplicity of the zero eigenvalue is 1 for each $L_{i} \Rightarrow$ the multiplicity of the zero eigenvalue is $k$ for $L$.
- Denoting $\left|A_{1}\right|=n_{1}, 1_{A_{1}}$ has its first $n_{1}$ (resp. remaining) components equal to 1 (resp. 0), $1_{A_{1}}=[1,1, \ldots, 1,0,0, \ldots, 0]^{T}$. Then,

$$
\mathbf{0}_{n_{1} \times 1}=0 \cdot \mathbf{1}_{n_{1} \times 1}=L_{1} \cdot \mathbf{1}_{n_{1} \times 1} \Rightarrow \mathbf{0}_{N \times 1}=0 \cdot \mathbf{1}_{A_{1}, N \times 1}=L \cdot \mathbf{1}_{N \times 1}
$$

## Spectral clustering

Unnormalized spectral clustering algorithm
Input: (a) Similarity matrix $S \in R^{N \times N}$, (b) the number of clusters $m$

- Construct a similarity graph with weighed adjacency matrix $W$.
- Compute the unnormalized Laplacian $L$.
- Compute the first $m$ (column) eigenvectors of $L, \boldsymbol{u}_{1}, \ldots, \boldsymbol{u}_{m}$.
- Stack $\boldsymbol{u}_{1}, \ldots, \boldsymbol{u}_{m}$ on an $N \times m$ matrix $U$.
- Represent each data vector $x_{i}$ by the $i$-th row $y_{i}$ of $U$.
- Cluster the points $y_{i} \in R^{m}, i=1, \ldots, N$, using e.g., the $k$-means algorithm, into clusters $C_{1}{ }^{\prime}, C_{2}{ }^{\prime}, \ldots, C_{m}{ }^{\prime}$.

Output: Clusters $C_{1}, C_{2}, \ldots, C_{m}$, with $C_{i}=\left\{\boldsymbol{x}_{\boldsymbol{j}}: \boldsymbol{y}_{j} \in C_{i}^{\prime}\right\}$

## Spectral clustering

Unnormalized spectral clustering algorithm

## Example:


Similarity graph:
$G=(V, E)=\left(\left\{v_{1}, v_{2}, v_{3}, v_{4}, v_{5}\right\},\left\{e_{13}, e_{24}, e_{25}, e_{45}\right\}\right)$
Nodes degree: $d_{1}=w_{13}, d_{2}=w_{24}+w_{25}, d_{3}=w_{13}$

$$
d_{4}=w_{24}+w_{45}, d_{5}=w_{25}+w_{45}
$$

Laplacian of the whole graph:

$$
\begin{aligned}
& L=D-W \\
& =\left[\begin{array}{ccccc}
w_{13} & 0 & -w_{13} & 0 & 0 \\
0 & w_{24}+w_{25} & 0 & -w_{24} & -w_{25} \\
-w_{13} & 0 & w_{13} & 0 & 0 \\
0 & -w_{24} & 0 & w_{24}+w_{45} & -w_{45} \\
0 & -w_{25} & 0 & -w_{45} & w_{25}+w_{45}
\end{array}\right] \\
& |L-\lambda I|=\cdots=\lambda^{2}\left|\begin{array}{ccc}
2 w_{13}-\lambda & 0 & 0 \\
0 & 2 w_{24}+w_{45}-\lambda & w_{25}-w_{45} \\
0 & w_{24}-w_{45} & 2 w_{25}+w_{45}-\lambda
\end{array}\right|=0 \Leftrightarrow
\end{aligned}
$$



## Spectral clustering

Unnormalized spectral clustering algorithm

## Example:

Data set $X=\left\{\boldsymbol{x}_{1}, \boldsymbol{x}_{2}, \boldsymbol{x}_{3}, \boldsymbol{x}_{4}, \boldsymbol{x}_{5}\right\}$
Corresponding eigenvectors $\boldsymbol{e}(L \cdot \boldsymbol{e}=0 \cdot \boldsymbol{e})$ :

$$
\boldsymbol{u}_{1}=[1,0,1,0,0]^{T} \text { and } \boldsymbol{u}_{2}=[0,1,0,1,1]^{T} \text { since }
$$

$\left[\begin{array}{ccccc}w_{13} & 0 & -w_{13} & 0 & 0 \\ 0 & w_{24}+w_{25} & 0 & -w_{24} & -w_{25} \\ -w_{13} & 0 & w_{13} & 0 & 0 \\ 0 & -w_{24} & 0 & w_{24}+w_{45} & -w_{45} \\ 0 & -w_{25} & 0 & -w_{45} & w_{25}+w_{45}\end{array}\right] \cdot\left[\begin{array}{c}1 \\ 0 \\ 1 \\ 0 \\ 0\end{array}\right]=0 \cdot-\left[\begin{array}{l}1 \\ 0 \\ 1 \\ 0 \\ 0\end{array}\right]$
$\left[\begin{array}{ccccc}w_{13} & 0 & -w_{13} & 0 & 0 \\ 0 & w_{24}+w_{25} & 0 & -w_{24} & -w_{25} \\ -w_{13} & 0 & w_{13} & 0 & 0 \\ 0 & -w_{24} & 0 & w_{24}+w_{45} & -w_{45} \\ 0 & -w_{25} & 0 & -w_{45} & w_{25}+w_{45}\end{array}\right] \cdot\left[\begin{array}{l}0 \\ 1 \\ 0 \\ 1 \\ 1\end{array}\right]=0 \cdot\left[\begin{array}{l}0 \\ 1 \\ 0 \\ 1 \\ 1\end{array}\right]$

## Spectral clustering

Unnormalized spectral clustering algorithm Example:



The eigenvectors corresponding to the zero eigenspace are $\boldsymbol{u}_{1}=[1,0,1,0,0]^{T}$ and $\boldsymbol{u}_{2}=[0,1,0,1,1]^{T}$

The matrix $U=\left[\begin{array}{ll}1 & 0 \\ 0 & 1 \\ 1 & 0 \\ 0 & 1 \\ 0 & 1\end{array}\right] \equiv \begin{array}{lll}\equiv & \boldsymbol{y}_{1} \rightarrow & \boldsymbol{x}_{1} \\ \equiv & \boldsymbol{y}_{2} \rightarrow & \boldsymbol{x}_{2} \\ \equiv & \boldsymbol{y}_{3} \rightarrow & \boldsymbol{x}_{3} \\ \equiv & \boldsymbol{y}_{4} \rightarrow & \boldsymbol{x}_{4} \\ \equiv & \boldsymbol{y}_{5} \rightarrow & \boldsymbol{x}_{5}\end{array}$
$(0,1) \square\left\{x_{2}, x_{4}, x_{5}\right\}$


## Spectral clustering

## Other Laplacian matrices

- Symmetric Laplacian matrix: $L_{\text {sym }}=D^{-1 / 2} \cdot L \cdot D^{-1 / 2}$
- Random walk Laplacian matrix: $L_{r w}=D^{-1} \cdot L$

All Laplacians share similar properties concerning the zero eigenvalue. In (von Luxburg, 2007), it is suggested to use $L_{r w}$.

## Spectral clustering

Choice of the number of clusters

## Example:

The ten smallest eigenvalues of $L_{r w}$ for a 1-dim. four-clusters problem.


In the case where $m$ is not apriori known, it can be estimated by sorting the Laplacian eigenvalues and determining the number of the first $m$ eigenvalues that (a) are sufficiently close to 0 and (b) the $m+1$ differs significantly from them.

## Clustering algorithms for high dimensional data sets

- What is a high-dimensionality space?

Dimensionality $l$ of the input space with

$$
20 \leq l \leq \text { few thousands }
$$

indicate high-dimensional data sets.

- Problems of considering simultaneously all dimensions in high-dimensional data sets:
$>$ "Curse of dimensionality". As a fixed number of points spread out in highdimensional spaces, they become almost equidistant (that is, the terms similarity and dissimilarity tend to become meaningless - alternatively, no clear structures are defined).
$>$ Several dimensions may be irrelevant to the identification of the clusters (that is, the clusters usually are identified in subspaces of the original feature space).
- A way out: Work on subspaces of dimension lower than l.
> Main approaches:
$\square$ Dimensionality reduction clustering approach.
$\square$ Subspace clustering approach.


## Clustering algorithms for high dimensional data sets

An example:

(a)

(b)

## Clustering algorithms for high dimensional data sets

Dimensionality Reduction Clustering Approach
Main idea

- Identify an appropriate $l^{\prime}$-dimensional space $H_{l^{\prime}}\left(l^{\prime}<l\right)$.
- Project the data points of $X$ into $H_{l^{\prime}}$.
- Apply a clustering algorithm on the projections of the points of $X$ into $H_{l^{\prime}}$.

Identification of $H_{l^{\prime}}$ may be carried out using either by:
> Feature generation methods,
$>$ Feature selection methods,
> Random projections.

## Clustering algorithms for high dimensional data sets

Dimensionality Reduction Clustering Approach (cont.)
Feature generation methods
> They produce new features via suitable transformations applied on the original ones.
> Typical Methods in this category are:
Principal component analysis (PCA). Singular value decomposition (SVD). Nonlinear PCA Robust PCA Independent comp. analysis (ICA).
$>$ In general, PCA and SVD methods

- preserve the distances between the points in the high-dimensional space, when these are mapped to the lower-dimensional space.
- produce compact representations (with reduced number of features) of the original high-dimensional feature space.
$>$ In some cases feature generation is applied iteratively in cooperation with a clustering algorithm ( $k$-means, EM).
$>$ They are useful in cases where a significant number of features contributes to the identification of all physical clusters.
> They are useful when all clusters are formed in the same subspace of the feature space.


## Principal Component Analysis (PCA)

## Principal component analysis (PCA):

It transforms the original space to a new orthogonal space (of the same dimensionality) where the features are uncorrelated. Specifically: along the, so called, $1^{\text {st }}$ principal axis the maximum possible variance of the data set is retained, along the $2^{\text {nd }}$ one the maximum possible remained variance is retained etc.

Projecting on the first few principal axes space we achieve dimensionality reduction.


## Principal Component Analysis - PCA

## Principal Component Analysis (PCA)




Projection along the $a_{1}\left(1^{\text {st }}\right)$ principal direction retains cluster separability.

CAUTION: Retaining the maximum possible variance of the data set DOES NOT imply that we necessarily retain the cluster separability.


Projection along the $a_{1}$ principal direction DOES NOT retain cluster separability.

## Subspace clustering

- Solution: Principal component analysis (PCA)
- Let $X_{l \times N}=\left[\begin{array}{llll}\boldsymbol{x}_{1} & \boldsymbol{x}_{2} & \cdots & \boldsymbol{x}_{N}\end{array}\right]$ and $Y_{l^{\prime} \times N}=\left[\begin{array}{llll}\boldsymbol{y}_{1} & \boldsymbol{y}_{2} & \because_{0} & \boldsymbol{y}_{N}\end{array}\right]$
- Compute $\boldsymbol{\mu}_{l \times 1}=\frac{1}{N} \sum_{i=1}^{N} \boldsymbol{x}_{i}$
- Consider $X^{\prime}{ }_{l \times N}=\left[\begin{array}{llll}\boldsymbol{x}_{1}-\boldsymbol{\mu} & \boldsymbol{x}_{2}-\boldsymbol{\mu} & \cdots & \boldsymbol{x}_{N}-\boldsymbol{\mu}\end{array}\right]$
- Perform singular value decomposition (SVD) on $X^{\prime}$ taking

$$
X_{l \times N}^{\prime}=U_{l \times l}^{\prime} \cdot \Sigma_{l \times N}^{\prime} \cdot V^{\prime T}{ }_{N \times N}
$$

- Keep the first $l^{\prime}$ singular values (as a consequence take also (a) the first $l^{\prime}$ columns of $U^{\prime}$ and (b) the first $l^{\prime}$ columns of $V^{\prime}\left(\Leftrightarrow\right.$ the first $l^{\prime}$ rows of $\left.V^{\prime T}\right)$ and approximate $X^{\prime}$ as

$$
X^{\prime a p p r}{ }_{l \times N}=U_{l \times l^{\prime}} \cdot \Sigma_{l^{\prime} \times l^{\prime}} \cdot V_{l^{\prime} \times N}^{T}
$$

- $B=U_{l \times l^{\prime}}$ is the subspace basis and
- $Y_{l^{\prime} \times N}=\Sigma_{l^{\prime} \times l^{\prime}} \cdot V^{T}{ }_{l^{\prime} \times N}$ contains (in columns) the representations/ projections of the (shifted by $\mu$ ) original data in the lower $l^{\prime}$-dim. space.

Theorem: $X^{\prime \text { appr }}$, as computed before, is the best approximation of $X^{\prime}$ wrt the Frobenius norm, subject to the constraint that the rank of $X^{\prime a p p r}$ is $l^{\prime}$.


## Subspace clustering

## More on SVD

Let $X^{\prime}{ }_{l \times N}=\left[\begin{array}{llll}\boldsymbol{x}_{1}-\boldsymbol{\mu} & \boldsymbol{x}_{2}-\boldsymbol{\mu} & \cdots & \boldsymbol{x}_{N}-\boldsymbol{\mu}\end{array}\right]$, with $\boldsymbol{\mu}_{l \times 1}=\frac{1}{N} \sum_{i=1}^{N} \boldsymbol{x}_{i}$
In the expression $X^{\prime}{ }_{l \times N}=U^{\prime}{ }_{l \times l} \cdot \Sigma^{\prime}{ }_{l \times N} \cdot V^{\prime T}{ }_{N \times N}$
$\Sigma^{\prime}{ }_{l \times N}$ (diagonal matrix) contains the singular values of $X^{\prime}{ }_{l \times N}$ in decreasing order in its main diagonal $(l<N)$
$U^{\prime}{ }_{l \times l}$ contains in its columns the eigenvectors of $X^{\prime} X^{\prime T}{ }_{l x l}$
$V^{\prime}{ }_{N \times N}$ contains in its columns the eigenvectors of $X^{T} X^{\prime}{ }_{N x N}$
Let

- $U^{\prime}=\left[\begin{array}{llll}\boldsymbol{u}_{1} & \boldsymbol{u}_{2} & \cdots & \boldsymbol{u}_{l}\end{array}\right]\left(\boldsymbol{u}_{i}{ }^{\prime}\right.$ s are $l$-dimensional column vectors)
$-V^{\prime}=\left[\begin{array}{llll}\boldsymbol{v}_{1} & \boldsymbol{v}_{2} & \cdots & \boldsymbol{v}_{N}\end{array}\right] \Rightarrow V^{\prime T}=\left[\begin{array}{c}\boldsymbol{v}_{1}{ }^{T} \\ \boldsymbol{v}_{2}{ }^{T} \\ \vdots \\ \boldsymbol{v}_{N}{ }^{T}\end{array}\right]\left(\boldsymbol{v}_{i}\right.$ 's are $N$-dimensional column
vectors and $v_{i}{ }^{T}$ 's are $N$-dimensional row vectors)
$-\Sigma_{l x N}^{\prime}=\left[\begin{array}{cccccc}\sigma_{1} & 0 & \cdots & 0 & \cdots & 0 \\ 0 & \sigma_{2} & \cdots & 0 & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots & \vdots & \vdots \\ 0 & 0 & \cdots & \sigma_{l} & \vdots & 0\end{array}\right]$


## Subspace clustering

## More on SVD

Then

$$
\begin{aligned}
& X_{l \times N}^{\prime}=U^{\prime}{ }_{l \times l} \cdot \Sigma^{\prime}{ }_{l \times N} \cdot V^{\prime T}{ }_{N \times N} \\
&=\left[\begin{array}{llll}
\boldsymbol{u}_{1} & \boldsymbol{u}_{2} & \cdots & \boldsymbol{u}_{l}
\end{array}\right]\left[\begin{array}{cccccc}
\sigma_{1} & 0 & \cdots & 0 & \cdots & 0 \\
0 & \sigma_{2} & \cdots & 0 & \cdots & 0 \\
\vdots & \vdots & \ddots & \vdots & \vdots & \vdots \\
0 & 0 & \cdots & \sigma_{l} & \vdots & 0
\end{array}\right]\left[\begin{array}{c}
\boldsymbol{v}_{1}{ }^{T} \\
\boldsymbol{v}_{2}{ }^{T} \\
\vdots \\
\boldsymbol{v}_{N}{ }^{T}
\end{array}\right] \\
&=\left[\begin{array}{llll}
\boldsymbol{u}_{1} & \boldsymbol{u}_{2} & \cdots & \boldsymbol{u}_{l}
\end{array}\right]\left[\begin{array}{c}
\sigma_{1} \boldsymbol{v}_{1}{ }^{T} \\
\sigma_{2} \boldsymbol{v}_{2}{ }^{T} \\
\vdots \\
\sigma_{l} \boldsymbol{v}_{l}{ }^{T}
\end{array}\right]= \\
& \sigma_{1} \boldsymbol{u}_{1} \boldsymbol{v}_{1}{ }^{T}+\sigma_{2} \boldsymbol{u}_{2} \boldsymbol{v}_{2}{ }^{T}+\cdots+\sigma_{l} \boldsymbol{u}_{l} \boldsymbol{v}_{l}{ }^{T}=\sum_{i=1}^{l} \sigma_{i} \boldsymbol{u}_{i} \boldsymbol{v}_{i}{ }^{T}
\end{aligned}
$$

Thus, $X^{\prime}$ is expressed as a sum of rank one matrices $\boldsymbol{u}_{i} \boldsymbol{v}_{i}{ }^{T}$ each one weighted by its corresponding $\sigma_{i}$.
By neglecting the terms with "small" $\sigma_{i}$ 's, we actually perform dimensionality reduction, or, in other words, we determine the subspace where the data "actually live".

## Clustering algorithms for high dimensional data sets

Dimensionality Reduction Clustering Approach (cont.)

Feature selection methods
$>$ They identify the original features that are the main contributors to the formation of the clusters.
$>$ The criteria used to evaluate the "goodness" of a specific subset of features follow either the

- Wrapper model (The clustering algorithm is first chosen and a set of features $F_{i}$ is evaluated through the results obtained from the application of the algorithm to $X$, where for each point only the features in $F_{i}$ are taken into account).
- Filter model (The evaluation of a subset of features is carried out using intrinsic properties of the data, prior to the application of the clustering algorithm).
$>$ They are useful when all clusters are formed in the same subspace of the feature space.


## Clustering algorithms for high dimensional data sets

Dimensionality Reduction Clustering Approach (cont.)
Clustering using Random Projections:
Here $H_{l^{\prime}}$ is identified in a random manner.
Note: The projection of an $l$-dimensional space to an $l^{\prime}$-dimensional space $\left(l^{\prime}<l\right)$ is uniquely defined via an $l^{\prime} \times l$ projection matrix $A$.

Issues to be addressed:
(a) Proper estimate of $l^{\prime}$. Estimates of $l^{\prime}$ guarantee (in probability) that the distances between the points of $X$, in the original data space will be preserved (with some distortion) after the projection to a randomly chosen $l^{\prime}$-dim. space, whose projection matrix is constructed via certain probabilistic rules
Note: Preservation of distances does not necessarily preserves clusters.
(b) Definition of the projection matrix $A$. Possible rules for constructing $A$ are:

1. Set each entry of $A$ equal to a value stemming from an i.i.d. zero mean, unit variance Gaussian distribution and then normalize each row to the unit length.
2. Set each entry of $A$ equal to -1 or +1 , with probability 0.5 .
3. Set each entry of $A$ equal to $+\sqrt{3},-\sqrt{3}$ or 0 , with probs $\frac{1}{6}, \frac{1}{6}$ and $\frac{2}{3}$, resp.

## Clustering algorithms for high dimensional data sets

Dimensionality Reduction Clustering Approach (cont.)

Having defined $A$ :

- Project the points of $X$ into $H_{l^{\prime}}$
- Perform a clustering algorithm on the projections of the points of $X$ into $H_{l^{\prime}}$.

Problem: Different random projections may lead to totally different results.

## Solution:

$>$ Perform several random projections $H_{l^{\prime}}$.
$>$ Apply a clustering algorithm on the projections of $X$ to each $H_{l^{\prime}}$.
$>$ Combine the clustering results and produce the final clustering.
A method in the above spirit is described next $\left(O\left(N^{2}\right)\right)$.

## Clustering algorithms for high dimensional data sets

## Clustering using Random Projections

- Select $l^{\prime}$.
- Generate $A_{1}, \ldots, A_{r}$ different projection matrices using the (b.1) rule given above.
- For $s=1$ to $r$
$>$ Run GPrAS with normal pdfs for the $s$-th random projection of $X$.
$>$ Compute the probability that $\boldsymbol{x}_{i}$ belongs to the $j$-th cluster in the $s$-th projection, $P\left(C_{j}^{S} \mid x_{i}\right), i=1, \ldots, N, j=1, \ldots, m_{s}$.
$\Rightarrow$ Create the similarity matrix $P^{s}=\left[P_{i j}^{S}\right]$, where $P_{i j}^{S}$ is the probability that $x_{i}$ and $x_{j}$ belong to the same cluster,

$$
P_{i j}^{s}=\sum_{q=1}^{m_{s}} P\left(C_{q}^{s} \mid \boldsymbol{x}_{i}\right) P\left(C_{q}^{s} \mid \boldsymbol{x}_{j}\right)
$$

$m_{s}$ : number of clusters in the $s$-th projection.

- End for
- Compute the average proximity matrix $P=\left[P_{i j}\right]$, so that $P_{i j}$ is the average of $P_{i j}^{S}$ 's, $s=1, \ldots, r$.
- Apply GAS (actually its complete link version) on $P$.
- Plot the similarity between the closest pair of clusters at each iteration versus the number of iterations.
- Select the clustering that corresponds to the most abrupt change in the plot.


## Clustering algorithms for high dimensional data sets

Subspace Clustering Approach

- This approach deals with the problem where clusters are formed in different subspaces of the feature space.
- The subspace clustering algorithms (SCA) reveal clusters as well as the subspaces where they reside.

An example:

(a)

(b)

## Subspace clustering

## Preliminaries:

- The data set $X=\left\{\boldsymbol{x}_{i} \in R^{l}, i=1, \ldots, N\right\}$
- (Affine linear) Subspace $S$ of $R^{l}$ : It is defined via
- a vector $\mu$ in $S$ and
- an $l x l^{\prime}$ (basis) matrix $B\left(l^{\prime}<l\right)$
as $S=\left\{\boldsymbol{x} \in R^{l}: \boldsymbol{x}=\mu+B \cdot \boldsymbol{y}\right\}$, where $\boldsymbol{y} \in R^{l^{\prime}}$
- Assuming that all the data points of $X$ lie in an $l^{\prime}$-dimensional (affine) subspace $S$, in order to determine it, we need to find:
- A vector $\mu \in S$
- The dimensionality $l^{\prime}$ of $S$
- The $l \times l^{\prime}$ matrix $B$.


Vidal R., "Subspace Clustering", IEEE Transactions on Signal Processing, 28(2), 2011.

## Subspace clustering

Basic assumption: In subspace clustering, the clusters formed by the data points "live" in subspaces of the original $l$-dimensional data space.

$$
S_{j}=\left\{\boldsymbol{x} \in R^{l}: \boldsymbol{x}=\mu_{j}+B_{j} \cdot \boldsymbol{y}\right\}
$$

- Aim of subspace clustering: Determine
- the number of subspaces $m$
- The dimensionalities $l_{1}, l_{2}, \ldots, l_{m}$, of the subspaces $S_{1}^{\circ}, S_{2}, \ldots, S_{m}$
- The basis matrices $B_{1}, B_{2}, \ldots, B_{m}$
- The points $\mu_{1}, \boldsymbol{\mu}_{2}, \ldots, \boldsymbol{\mu}_{m}$, of the subspaces $S_{1}, S_{2}, \ldots, S_{m} \bigcirc$
- The clusters $C_{1}, C_{2}, \ldots, C_{m}$.



## Subspace clustering

## Ways to tackle the problem

- Algebraic methods
- Spectral clustering methods
- Iterative cost function optimization methods (hard, probabilistic framework)

Iterative cost function optimization methods (hard framework) The $k$-subspace algorithm

Assumption: The number of clusters $m$ and the subspaces dimensionalities $l_{1}, l_{2}, \ldots, l_{m}$, are known.
Let:

- $U_{N \times m}=\left[u_{i j}\right]$, where $u_{i j}=\left\{\begin{array}{cc}1, & x_{i} \in C_{j} \\ 0, & \text { otherwise }\end{array}\right.$,
$-B=\left\{B_{1}, B_{2}, \ldots, B_{m}\right\}$
$-\boldsymbol{\mu}=\left\{\boldsymbol{\mu}_{1}, \boldsymbol{\mu}_{2}, \ldots, \boldsymbol{\mu}_{m}\right\}$
- $Y=\left\{Y_{1}, \ldots, Y_{m}\right\}$, with $Y_{j}=\left\{\boldsymbol{y}_{i}^{j}, i=1, \ldots, N\right\}$ be the set of projections of the data points to the $j$-th subspace.


## Subspace clustering

Iterative CFO methods (hard framework) - The $k$-subspace algorithm
Consider the cost function
$y_{i}^{j}:$ Projection of $x_{i}$ to the $j$-th subspace

$$
J(B, \mu, Y, U)=\sum_{i=1}^{N} \sum_{j=1}^{m} u_{i j}\left\|\boldsymbol{x}_{i}-\boldsymbol{\mu}_{j}-B_{j} \boldsymbol{y}_{i}^{j}\right\|^{2}
$$

This is minimized in a two-stage iterative fashion (recall $k$-means)
For fixed $\boldsymbol{\mu}_{j}^{\prime} s, B_{j}^{\prime} s, y_{i}^{j \prime} s$ :
Define $u_{i j}=\left\{\begin{array}{lc}1, & \text { if }\left\|\boldsymbol{x}_{i}-\boldsymbol{\mu}_{j}-B_{j} \boldsymbol{y}_{i}^{j}\right\|^{2}=\min _{q=1, \ldots, m}\left\|\boldsymbol{x}_{i}-\boldsymbol{\mu}_{q}-B_{q} \boldsymbol{y}_{i}^{q}\right\|^{2} \\ 0, & \text { otherwise }\end{array}\right.$
For fixed $u_{i j}$ 's: Solve the following $\underline{m}$ independent problems

$$
\min _{\left\{\boldsymbol{\mu}_{j},\left(B_{j}, y_{i}^{j}\right)\right\}} \sum_{x_{i}: u_{i j}=1}\left\|\boldsymbol{x}_{i}-\boldsymbol{\mu}_{j}-B_{j} \boldsymbol{y}_{i}^{j}\right\|^{2} \equiv \min _{\left\{\mu_{j},\left(B_{j}, y_{i}^{j}\right)\right\}} \sum_{i=1}^{N} u_{i j}\left\|x_{i}-\boldsymbol{\mu}_{j}-B_{j} y_{i}^{j}\right\|^{2}
$$

For each such problem
(a) Fix $\boldsymbol{\mu}_{j}^{\prime} s$ and apply PCA, to estimate $B_{j}^{\prime} s, y_{i}^{j \prime} s$.
(b) Fix $B_{j}^{\prime} s, \boldsymbol{y}_{i}^{j \prime} s$ and apply the $k$-means rationale, to estimate $\boldsymbol{\mu}_{j}^{\prime} s$.

## Subspace clustering

## Remark:

There are also subspace clustering methods (e.g., CLIQUE, ENCLUS) that "quantize" the region where the data belongs through the use of a grid. Then, clusters (at different subspaces) are defined through boxes that contain a significant number of data points.

## Combinations of clusterings

- The data set $X=\left\{\boldsymbol{x}_{i} \in R^{l}, i=1, \ldots, N\right\}$
- Ensemble of clusterings of $X: \quad \mathcal{E}=\left\{\mathcal{R}_{1}, \mathcal{R}_{2}, \ldots, \mathcal{R}_{n}\right\}$ where $\mathcal{R}_{i}=\left\{C_{i}{ }^{1}, C_{i}{ }^{2}, \ldots, C_{i}{ }^{m_{i}}\right\}$
$C_{i}^{j}$ : the $j$-th cluster of the $i$-th clustering
$m_{i}$ : the number of clusters in the $i$-th clustering.


In general, $\mathcal{R}_{i}$ 's are not constraint to have the same number of clusters

- Alternative representation of a clustering:

$$
\mathcal{R}_{i} \leftrightarrow \boldsymbol{y}_{i}=\left[y_{i}(1), y_{i}(2), \ldots, y_{i}(k), \ldots, y_{i}(N)\right]
$$

where $y_{i}(k)$ the cluster label of the $k$-th data point.
Example: Let $\mathcal{R}_{i}=\left\{C_{i}^{1}, C_{i}^{2}, C_{i}^{3}\right\}=\left\{\left\{\boldsymbol{x}_{1}, \boldsymbol{x}_{2}, \boldsymbol{x}_{6}, \boldsymbol{x}_{10}\right\},\left\{\boldsymbol{x}_{3}, \boldsymbol{x}_{4}, \boldsymbol{x}_{7}\right\},\left\{\boldsymbol{x}_{5}, \boldsymbol{x}_{8}, \boldsymbol{x}_{9}\right\}\right\}$ Then $y_{i}=[1,1,2,2,3,1,2,3,3,1]$.
The two main issues in this framework are:
(A) The generation of the ensemble of clusterings
(B) The combination of the clusterings.

## Combinations of clusterings

A. Generation of ensemble of clusterings

It involves two steps:
(a) The choice of the subspace to project the data points of $X$.
(b) The application of a clustering algorithm on the resulting projections.

General directions:

- All data, all features:
- All $l$ features and all $N$ data points are used.
- Either different algorithms are applied
- or the same algorithm with different parameter values (e.g., in $k$-means, different number of cluster, or different initial conditions).
- All data, some features:
- All $N$ data points are used.
- $n$ data sets $X_{i}$ are formed from $X$
- Either by selecting a number of features (feature distributed clustering)
- or by projecting onto a randomly chosen lower dimensional space.
- The same or different algorithms can be applied on the $X_{i}$ 's.


## Combinations of clusterings

A. Generation of ensemble of clusterings

General directions:

- Some data, all features:
- All $l$ features are used.
- $n$ data sets $X_{i}$ are formed from $X$ using techniques like bootstrapping and sampling.
- (Usually) the same algorithm is applied on the $X_{i}$ 's.
- The points that have not been selected to participate in $X_{i}$ are assigned to their nearest cluster in $\mathcal{R}_{i}$.
B. Combination of clusterings

Problem: Given $\mathcal{E}=\left\{\mathcal{R}_{1}, \mathcal{R}_{2}, \ldots, \mathcal{R}_{n}\right\}$, determine the consensus clustering $\mathcal{F}=\left\{F_{1}, F_{2}, \ldots, F_{m}\right\}$.

A useful tool in this direction is the co-association matrix $C$.
It is an $N \times N$ matrix $C=\left[c_{i j}\right]$ with $c_{i j}=\frac{n_{i j}}{n}$
where $n_{i j}$ is the number of times where the $i$-th and the $j$-th points of $X$ are assigned to the same cluster, among the $n$ clusterings of $\mathcal{E}$.

## Combinations of clusterings

B. Combination of clusterings

Three main directions are used:

- Co-association matrix based methods
- Graph-based methods
- Function optimization methods.

Co-association matrix based methods

- Compute the co-association matrix.
- Use it as a similarity matrix and run a hierarchical algorithm (single-link, complete-link etc)
- From the produced dendrogram determine the final clustering as the one having the larger lifetime.

Note: A large number of clusterings is required, in order to estimate more accurately the elements of $C$.

## Combinations of clusterings

B. Combination of clusterings

## Graph-based methods

- Instance-based graph formulation (IBGF)
- Cluster-based graph formulation (CBGF)
- Hybric bipartite graph formulation (HBGF)


## Combinations of clusterings

B. Combination of clusterings

Graph-based methods

- Instance-based graph formulation (IBGF)
- Cluster-based graph formulation (CBGF)
- Hybric bipartite graph formulation (HBGF)
> Construct a fully connected graph $G=(V, E)$ where
$>$ Each vertex of $V$ corresponds to a data point and
$>$ Each edge $e_{i j}$ of $E$ is weighted by $c_{i j}$ (the $(i, j)$ element of $C$ ).
$>$ Partition the graph into $m$ disjoint subsets of vertices $V_{1}, V_{2}, \ldots, V_{m}$ such that
- The sum of weights of the edges that connect vertices between any pair of two different subsets is minimized and
- All $V_{j}$ 's have approximately the same size.

Note: The normalized-cut and the Ratio-cut criteria can be used for partitioning the graph.

## Combinations of clusterings

## B. Combination of clusterings

## Graph-based methods

- Instance-based graph formulation (IBGF)

Example: Consider a data set $X=\left\{\boldsymbol{x}_{1}, \boldsymbol{x}_{2}, \boldsymbol{x}_{3}, \boldsymbol{x}_{4}\right\}$ and assume that the co-
association matrix is $C=\left[c_{i j}\right]=\left[\begin{array}{cccc}1 & 0.9 & 0.07 & 0.05 \\ 0.9 & 1 & 0.03 & 0.02 \\ 0.07 & 0.03 & 1 & 0.9 \\ 0.05 & 0.02 & 0.9 & 1\end{array}\right]\left[\begin{array}{l}C \text { indicates that the } \\ \text { physical clusters are } \\ C_{1}=\left\{\boldsymbol{x}_{1}, \boldsymbol{x}_{2}\right\}, \\ C_{2}=\left\{\boldsymbol{x}_{3}, \boldsymbol{x}_{4}\right\} .\end{array}\right.$

Consider the fully connected graph with four vertices $v_{1}\left(\boldsymbol{x}_{1}\right), v_{2}\left(\boldsymbol{x}_{2}\right)$, $v_{3}\left(\boldsymbol{x}_{3}\right), v_{4}\left(\boldsymbol{x}_{4}\right)$, with the weight of each edge $w_{i j}$ being equal to $c_{i j}$.
For the possible (equally-sized clusters) two-clusters graph partitions it is:

| Partition | Edges connecting diff. clusters (weights) | Total weight of <br> connecting edges |
| :--- | :--- | :---: |
| $\left\{\left\{v_{1}, v_{2}\right\},\left\{v_{3}, v_{4}\right\}\right\}$ | $e_{13}(0.07), e_{14}(0.05), e_{23}(0.03), e_{24}(0.02)$ | $0.17\left(^{*}\right)$ |
| $\left\{\left\{v_{1}, v_{3}\right\},\left\{v_{2}, v_{4}\right\}\right\}$ | $e_{12}(0.9), e_{14}(0.05), e_{32}(0.02), e_{34}(0.9)$ | 1.87 |
| $\left\{\left\{v_{1}, v_{4}\right\},\left\{v_{2}, v_{3}\right\}\right\}$ | $e_{12}(0.9), e_{13}(0.07), e_{42}(0.02), e_{43}(0.9)$ | 1.87 |

The partition with the smallest total weight of connecting edges corresponds to the physical clustering of the data set.

## Combinations of clusterings

B. Combination of clusterings

Function optimization methods

- Utility function optimization
- Normalized mutual information
- Mixture model formulation

Here, the final clustering (also called median clustering) $\mathcal{F}=\left\{F_{1}, F_{2}, \ldots, F_{m}\right\}$, results from the optimization of an appropriate cost function.

## Combinations of clusterings

## B. Combination of clusterings

## Function optimization methods

- Utility function optimization (probabilistic arguments)
- Normalized mutual information function optimization (information theory ingredients)
- Mixture model formulation

A function $U\left(\mathcal{F}^{\prime}, \mathcal{R}_{i}\right)$ is adopted, measuring the quality of a candidate median $\mathcal{F}^{\prime}$ against some other clustering $\mathcal{R}_{i}$.

The overall utility of $\mathcal{F}^{\prime}$ on $\varepsilon=\left\{\mathcal{R}_{1}, \mathcal{R}_{2}, \ldots, \mathcal{R}_{n}\right\}$ is defined as

$$
U\left(\mathcal{F}^{\prime}, \varepsilon\right)=\sum_{i=1}^{n} U\left(\mathcal{F}^{\prime}, \mathcal{R}_{i}\right)
$$

The final (median) clustering $\mathcal{F}$ results as

$$
\mathcal{F}=\operatorname{argmax}_{\mathcal{F}^{\prime}} U\left(\mathcal{F}^{\prime}, \varepsilon\right)
$$

## Combinations of clusterings

## B. Combination of clusterings

## Function optimization methods

Mixture model formulation

- Represent the data points as follows

| $y_{1}$ | $\cdots$ | $y_{n}$ |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: |
| $y_{1}(1)$ | $\cdots$ | $y_{n}(1)$ | $]$ | $\equiv$ | $x_{1}{ }^{\prime}$ |
| $y_{1}(2)$ | $\cdots$ | $y_{n}(2)$ | $]$ | $\equiv$ | $x_{2}{ }^{\prime}$ |
|  | $\vdots$ |  |  |  | $\vdots$ |
| $y_{1}(N)$ | $\cdots$ | $y_{n}(N)$ | $]$ | $\equiv$ | $x_{N}{ }^{\prime}$ |

Note: The representations $x_{i}{ }^{\prime}$ are discrete-valued.

- Define the probability function $P\left(x^{\prime} ; \Theta\right)$ as the (weighted) summation of $m$ ( $n$-dimensional) probability functions, each one corresponding to a cluster.
- Assuming independence among the components of $x^{\prime}$, each $n$-dimensional probability function is written as the product of $n$ one-dimensional prob. functions, each one modeled by a multinomial distribution.
- The estimation of the respective parameters is carried out via the utilization of the EM algorithm.


## Multinomial distribution

- Multinomial distribution $\operatorname{Mult}(\boldsymbol{x} \mid n, \mathbf{P})$

Discrete RV distribution

$$
\begin{aligned}
& \mathbf{x}=\left[\mathrm{x}_{1}, \mathrm{x}_{2}, \ldots, \mathrm{x}_{K}\right]^{T^{\prime}} \boldsymbol{P}=\left[p_{1}, \ldots, p_{K}\right]^{T}: \\
& \sum_{i=1}^{K} p_{i}=1
\end{aligned}
$$

$-0<p_{i}<1, i=1, \ldots, K$,
-Sample space: $X=\{0,1, \ldots, K\}$
-Outcome of the experiment: non-binary. No. of repetitions: $\boldsymbol{n}$ - $x_{i}$ : number of times the $i$-th outcome occurs in the $n$ repetitions - It is

$$
>P(\boldsymbol{x})=\binom{n}{x_{1}, x_{2}, \ldots, x_{K}} \prod_{i=1}^{K} P_{i}^{x_{i}}
$$

$$
\begin{aligned}
& \text { s.t. } x_{1}+x_{2}+\ldots+x_{K}=n \\
& >E[x]=n \boldsymbol{P} \\
& \partial \sigma_{i}^{2}=n P_{i}\left(1-P_{i}\right), i=1, \ldots, K . \\
& >\operatorname{cov}\left(x_{i}, x_{j}\right)=-n P_{i} P_{j}, i \neq j .
\end{aligned}
$$



