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Unit 4

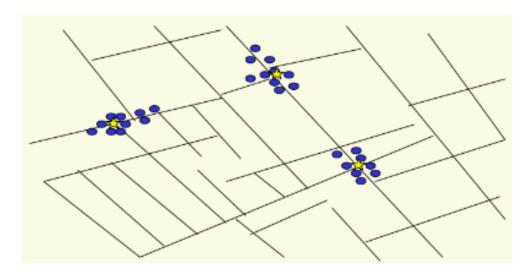
 Cost function optimization clustering algorithms: The hard clustering case

Clustering: A historic example(*)

Dr John Snow plotted the location of cholera deaths on a map during an outbreak at London in the 1850s

The locations were clustered around certain intersections where there were

polluted wells!!!



Questions:

- Which are the entities and how they are represented?
- Which dissimilarity measure could be used?
- What is the form of the resulted clusters?
- What kind of clusters should be able to reveal the adopted clustering criterion?

(*) Nina Mishra HP Labs

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Number of possible clusterings

Let $X = \{x_1, x_2, ..., x_N\}$ be a set of data points.

Question: In how many ways the N points of X can be assigned into m groups?

Answer:
$$S(N,m) = \frac{1}{m!} \sum_{i=0}^{m} (-1)^{m-1} {m \choose i} i^{N}$$

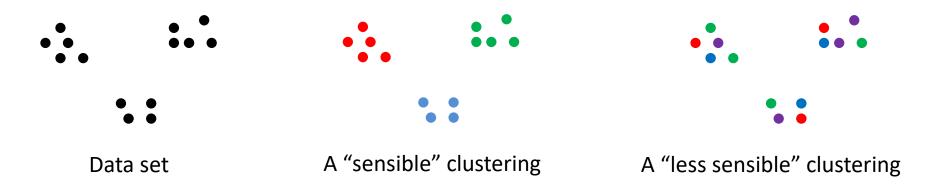
Examples:

- S(15,3) = 2,375,101
- S(20,4) = 45,232,115,901
- S(25,8) = 690,223,721,118,368,580
- $S(100,5) \approx 10^{68}!!$

NOTE: The above calculations are for $\underline{fixed} m$. If this varies, then we have to enumerate all clusterings, for all possible values of m!!



Evaluating all possible clusterings is impractical even for moderate values of N.



- Clustering algorithms may be **viewed** as schemes that <u>provide us with</u> <u>sensible clusterings by considering only a small fraction of all possible</u> <u>partitions of X</u>.
- This *fraction* depends on the adopted criteria.
- Thus a clustering algorithm is a learning procedure that tries to identify clusters formed by the data vectors, in accordance to the adopted criteria.

Major categories of clustering algorithms

A vast amount of algorithms exists based on very diverse criteria

⇒ Strict categorization is extremely difficult (rather impossible).

A rough categorization:

- Sequential: A single clustering is produced. One or few sequential passes on the data.
- Hierarchical: A sequence of (nested) clusterings is produced.

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Agglomerative
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Matrix theory

Graph theory

Divisive

Combinations of the above (e.g., the Chameleon algorithm.)

Major categories of clustering algorithms

A rough categorization:

Cost function optimization.

- For most of the cases a *single* clustering is obtained.
- They can be further **categorized** through the notion of "belongness". Hard clustering (each point belongs exclusively to a single cluster):
 - Basic hard clustering algorithms (e.g., k-means)
 - k-medoids algorithms
 - Mixture decomposition
 - Branch and bound
 - Simulated annealing

- Deterministic annealing
- Boundary detection
- Mode seeking
- Genetic clustering algorithms

Probabilistic clustering (a hard clustering case where probabilistic framework is utilized)

Fuzzy clustering (each point belongs to more than one clusters simultaneously).

Possibilistic clustering (it is based on the notion of the "degree of compatibility" of a point with a cluster).

Major categories of clustering algorithms A rough categorization:

Other.

- Algorithms based on graph theory (e.g., Spectral clustering, Minimum Spanning Tree, regions of influence, directed trees).
- Density-based algorithms.
- Competitive learning algorithms (basic competitive learning scheme, Kohonen self organizing maps).
- Subspace clustering algorithms.
- Ensemble of clusterings
- Kernel-based methods.

The common traits shared by the sequential clustering algorithms are:

- One or very few passes on the data are required.
- The number of clusters m is not known a-priori, except (possibly) an upper bound, q.
- The clusters are defined with the aid of
 - \checkmark An appropriately defined distance d(x, C) of a point from a cluster.
 - \checkmark A threshold Θ associated with the distance.

Basic Sequential Clustering Algorithm Scheme (BSAS)

- • $m = 1 \setminus \{number of clusters\} \setminus \{number of$ $X = \{x_1, \dots, x_N\}$ $\bullet C_m = \{x_1\}$ • For i=2 to N -Find C_k : $d(\mathbf{x}_i, C_k) = \min_{1 \le i \le m} d(\mathbf{x}_i, C_i)$ $-\text{If } (d(\mathbf{x}_i, C_k) > \Theta) \text{ AND } (m < q) \text{ then }$ > m = m + 1 $\succ C_m = \{x_i\}$ -Else $\triangleright C_k = C_k \cup \{x_i\}$ Where necessary, update representatives (*) —End {if} •End {for}
- (*) When the mean vector m_C is used as representative of the cluster C with n_C elements, the updating in the light of a new vector x becomes

$$\boldsymbol{m}_{C}^{new} = (n_{C} \, \boldsymbol{m}_{C}^{old} + \boldsymbol{x}) / (n_{C} + 1)$$

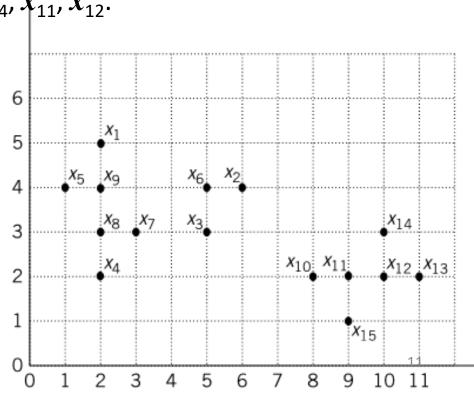
Basic Sequential Clustering Algorithm Scheme (BSAS)

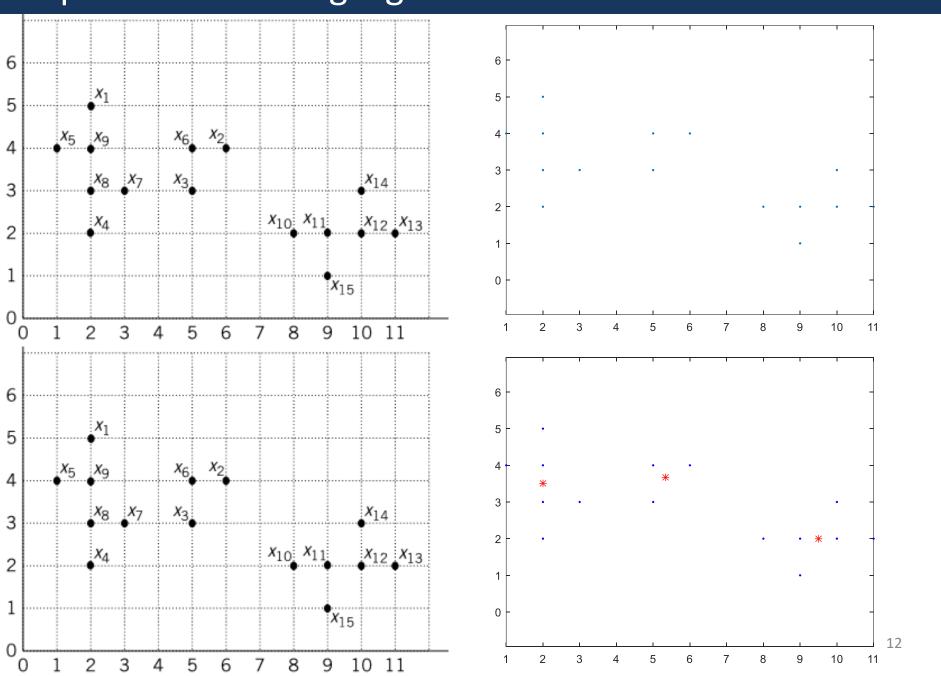
Remarks:

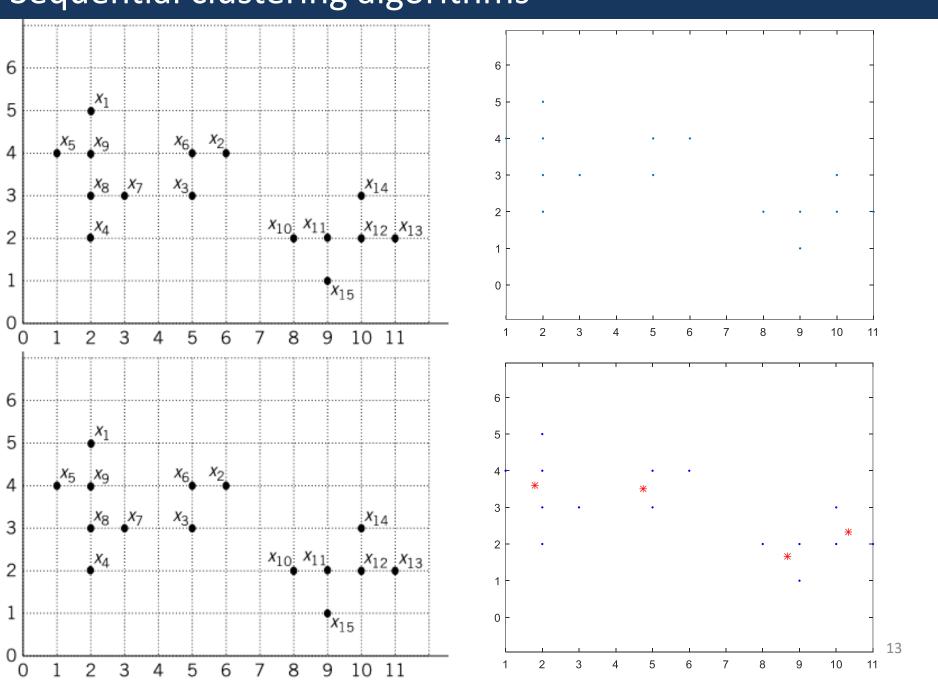
- The order of presentation of the data in the algorithm plays important role in the clustering results. Different order of presentation may lead to totally different clustering results, in terms of the number of clusters as well as the clusters themselves.
- The clustering results depend on the choice of the value of Θ .
- ullet In BSAS the decision for a vector $oldsymbol{x}$ is reached prior to the final cluster formation.
- BSAS perform a single pass on the data. Its complexity is O(N) (when point representatives are used).
- If clusters are represented by point representatives, compact clusters are favored.

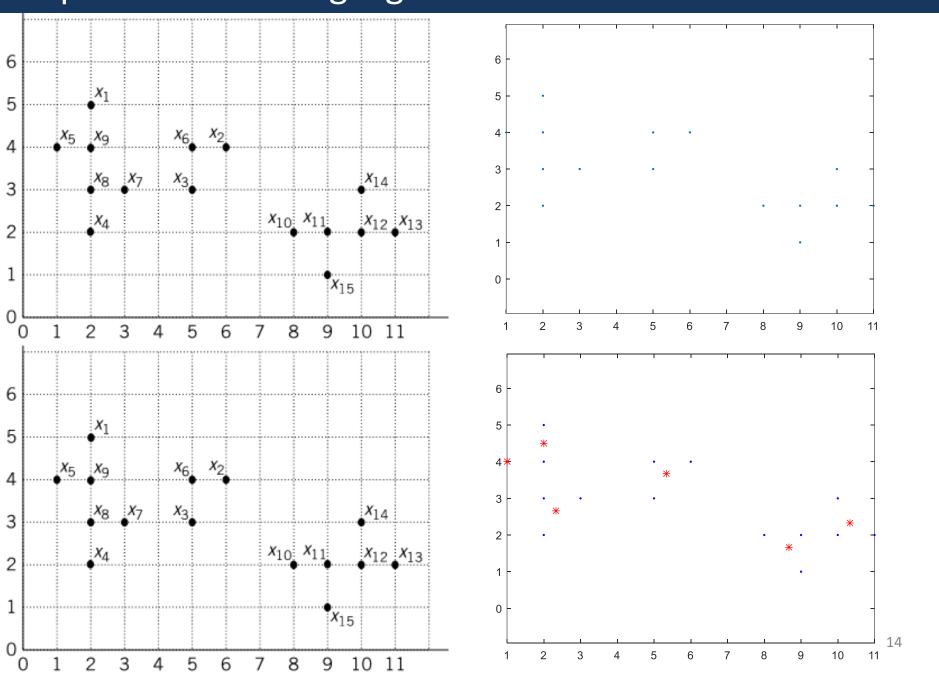
Example in MATLAB 1:

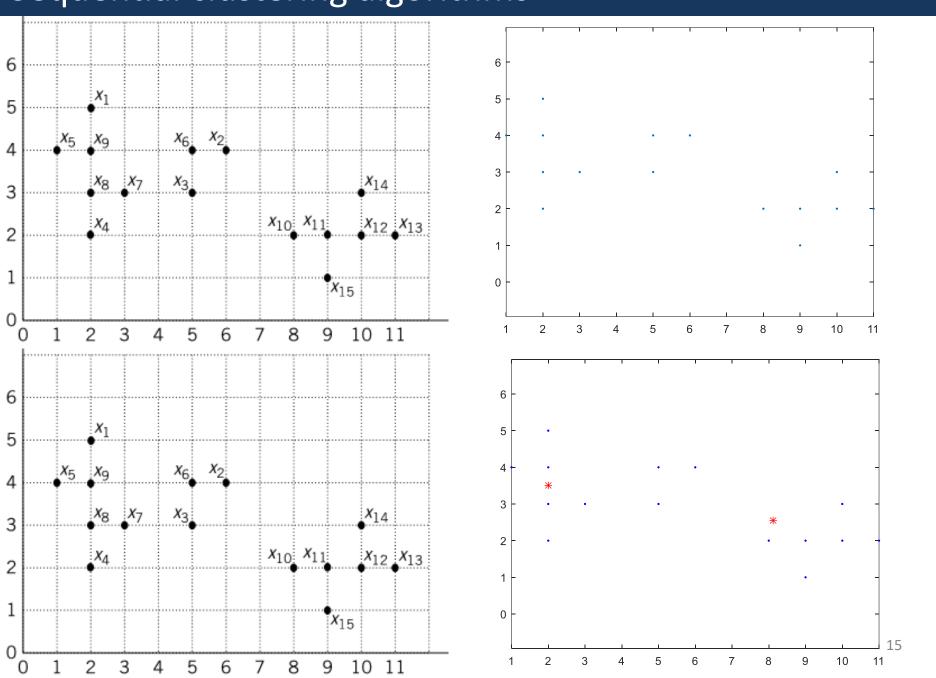
- Consider the data vectors depicted in the figure below and perform a "visual" clustering on it.
- 1. Apply the BSAS algorithm on X, presenting its elements in the order x_8 , x_6 , x_{11} , x_1 , x_5 , x_2 , x_3 , x_4 , x_7 , x_{10} , x_9 , x_{12} , x_{13} , x_{14} , x_{15} , for $\Theta = 2.5$ and q = 15.
- **2.** Repeat step 1, now with the order of presentation to the algorithm as $x_7, x_3, x_1, x_5, x_9, x_6, x_8, x_4, x_2, x_{10}, x_{15}, x_{13}, x_{14}, x_{11}, x_{12}$.
- **3.** Repeat step 1, now with $\Theta = 1.4$.
- **4.** Repeat step 1, now with q = 2.







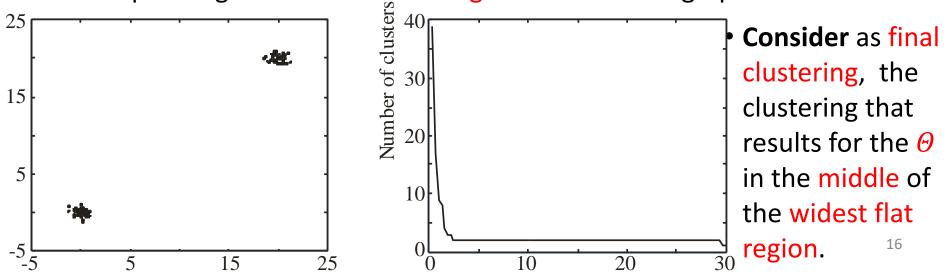




Basic Sequential Clustering Algorithm Scheme (BSAS) Estimating the number of clusters in the data set:

Let $BSAS(\Theta)$ denote the BSAS algorithm when the dissimilarity threshold is Θ .

- •For $\Theta = a$ to b step c
 - $-\mathbf{Run} \ \mathbf{S}$ times $BSAS(\Theta)$, each time presenting the data in a different order.
 - **–Estimate** the number of clusters m_{Θ} , as the most frequent number resulting from the s runs of $BSAS(\Theta)$.
- •Next Θ
- •Plot m_{Θ} versus Θ and identify the number of clusters m as the one corresponding to the widest flat region in the above graph.



MBSAS, a Modification of BSAS

- In BSAS a decision for a data vector \mathbf{x} is reached prior to the final cluster formation, which is determined after all vectors have been presented to the algorithm.
- MBSAS deals with this issue, at the cost of processing the data twice.

• MBSAS consists of:

- —A cluster determination phase (first pass on the data), which is the same as BSAS with the exception that no vector is assigned to an already formed cluster. At the end of this phase, each cluster consists of a single element.
- A pattern classification phase (second pass on the data),
 where each one of the unassigned vectors is assigned to its closest cluster.

Remarks:

Exercise: Write the pseudocode for MBSAS (in the spirit of the BSAS pseudocode).

- \bullet In MBSAS, a decision for a vector x during the pattern classification phase is reached taking into account all clusters.
- MBSAS is sensitive to the order of presentation of the vectors.
- •MBSAS requires two passes on the data. Its complexity is O(N).

Refinement stages

End {if}

The problem of closeness of clusters: "<u>In all the above algorithms it may</u> <u>happen that two formed clusters lie very close to each other</u>". (they may be parts of the same **physical** cluster)

A simple merging procedure

```
(A) Find C_i, C_j (i < j) such that d(C_i, C_j) = \min_{k,r=1,\cdots,m,k\neq r} d(C_k, C_r) If d(C_i, C_j) \leq M_1 then \{M_1 \text{ is a user-defined threshold } \}

-Merge C_i, C_j to C_i and eliminate C_j.

-If necessary, update the cluster representative of C_i.

-Rename the clusters C_{j+1}, ..., C_m to C_j, ..., C_{m-1}, respectively.

-m = m - 1

-Go to (A)

Else

-Stop
```

Refinement stages

The problem of sensitivity to the order of data presentation:

"A vector \underline{x} may have been assigned to a cluster C_i at the current stage but another cluster C_i may be formed at a later stage that lies closer to \underline{x} "

A simple reassignment procedure

- For i=1 to N-Find C_j such that $d(x_i, C_j) = \min_{k=1,\cdots,m} d(x_i, C_k)$ -Set $b(i) = j \setminus \{b(i) \text{ is the index of the cluster that lies closest to } \underline{x}_i \setminus \}$
- End {for}
- For j=1 to m-Set $C_j=\{\pmb{x}_i{\in}X\colon b(i)=j\}$ -If necessary, update representatives
- End {for}

Example in MATLAB 2:

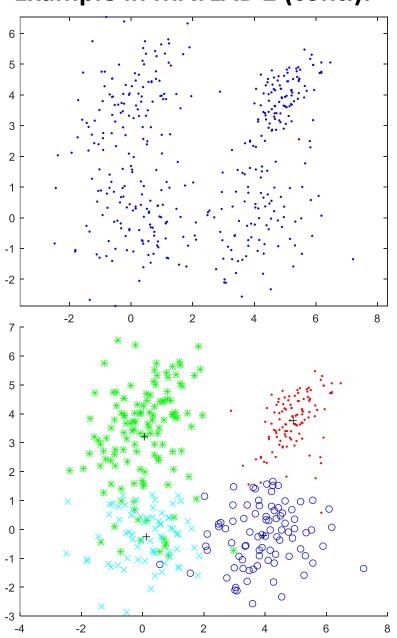
Generate and plot a data set X_1 , that consists of N=400 2-dim. data vectors. These vectors form **four groups**, each one of which contains vectors that stem from Gaussian distributions with means $\mathbf{m}_1 = [0,0]^T$, $\mathbf{m}_2 = [4,0]^T$, $\mathbf{m}_3 = [0,4]^T$, $\mathbf{m}_4 = [5,4]^T$, respectively, and respective covariance matrices $S_1 = I$, $S_2 = \begin{bmatrix} 1 & 0.2 \\ 0.2 & 1.5 \end{bmatrix}$, $S_3 = \begin{bmatrix} 1 & 0.4 \\ 0.4 & 1.1 \end{bmatrix}$, $S_2 = \begin{bmatrix} 0.3 & 0.2 \\ 0.2 & 0.5 \end{bmatrix}$. Then do the following:

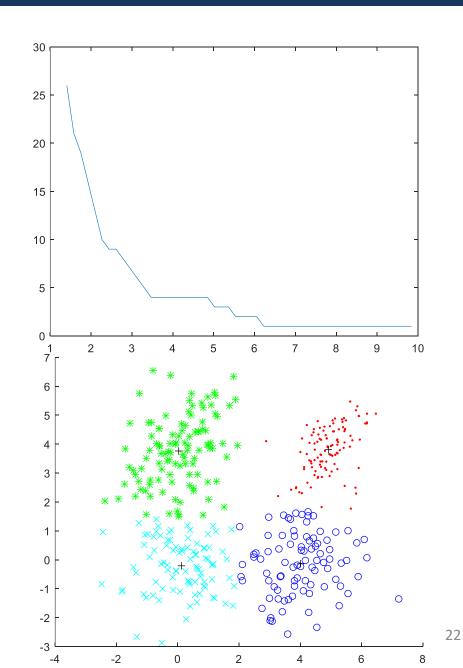
- 1. Determine the number of clusters formed in X_1 by doing the following:
 - a. Determine the maximum, d_{max} , and the minimum, d_{min} , distances between any two points in the data set.
 - b. Determine the values of Θ for which the BSAS will run. These may be defined as Θ_{min} , $\Theta_{min} + s$, $\Theta_{min} + 2s$,..., Θ_{max} , where $\Theta_{min} = 0.25 \frac{d_{min} + d_{max}}{2}$, $\Theta_{max} = 1.75 \frac{d_{min} + d_{max}}{2}$ and $s = \frac{\Theta_{min} + \Theta_{max}}{n_{\Theta}}$, n_{Θ} is the number of successive values of Θ that will be considered. Use $n_{\Theta} = 50$.

Example in MATLAB 2 (cont.):

- c. For each of the previously defined values of Θ , run the BSAS algorithm $n_{times}=10$, so that the data vectors are presented with different ordering to BSAS in each run. From the n_{times} estimates of the number of clusters, select the most frequently met value, m_{Θ} , as the most accurate. Let \boldsymbol{m}_{tot} be the n_{Θ} -dimensional vector, which contains the m_{Θ} values. d. Plot m_{Θ} versus Θ . Determine the widest flat region, r, of Θ 's (excluding
- the one that corresponds to the single-cluster case) and let n_r be the number of Θ 's in $\{\Theta_{min}, \Theta_{min} + s, \dots, \Theta_{max}\}$ that also lie in r. If n_r is "significant" (e.g., greater than 10% of n_{Θ}), the corresponding number of clusters, m_{best} , is selected as the best estimate and the mean of the values of Θ in r is chosen as the corresponding best value for Θ (Θ_{best}). Otherwise, the single-cluster clustering is adopted.
- 2. Run the BSAS algorithm for $\Theta=\Theta_{best}$ and plot the data set using different colors and symbols for points from different clusters.
- 3. Apply the reassignment procedure on the clustering results obtained in the previous step and plot the new clustering.

Example in MATLAB 2 (cont.):





A two-threshold sequential scheme (TTSAS)

- The formation of the clusters, as well as the assignment of vectors to clusters, is carried out concurrently (like BSAS and unlike MBSAS)
- Two thresholds Θ_1 and Θ_2 ($\Theta_1 < \Theta_2$) are **employed**.
- The general idea is the following:

If the distance d(x, C) of x from its closest cluster, C, is greater than Θ_2 then:

–A new cluster represented by $oldsymbol{x}$ is created.

Else if $d(x, C) < \Theta_1$ then -x is assigned to C.

Else

—The decision is postponed to a later stage.
End {if}

• <u>The unassigned vectors are presented iteratively to the algorithm until all of</u> them are classified.

Remarks:

- •In practice, a few passes (≥ 2) of the data set are required.
- •TTSAS is less sensitive to the order of data presentation, compared to BSAS.

The maxmin algorithm

W may be initialized by (a) the two most distant points or(b) the mean of the data set.

Let W be the set of all points that have been chosen to define clusters up to the current iteration step. The <u>definition of clusters</u> is carried out as follows:

- For each $x \in X W$ determine $d_x = \min_{z \in W} d(x, z)$
- Determine y: $d_v = max_{x \in X W} d_x$
- If d_y is greater than a prespecified threshold (Θ) then
 - y defines a new cluster
- else
 - -the cluster determination phase of the algorithm terminates.
- End {if}

After the definition of the clusters, each unassigned vector is assigned to its closest cluster.

Remarks:

- •The maxmin algorithm is more computationally demanding than MBSAS.
- •Its result is independent of the order of data presentation to the algorithm.
- •It is expected to produce better clustering results than MBSAS.
- Its performance may be degraded in the presence of noise.

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Cost Function Optimization clustering algorithms: A unified view

Data

$$X = \{ \boldsymbol{x}_j \in R^l, j = 1, \dots, N \}$$

Basic parameters - notation

- $\checkmark \quad \Theta = \{\theta_j, j = 1, ..., m\}$ (θ_j is the representative of cluster C_j).
 - Proximity between x_i and C_i : $d(x_i, \theta_i)$

$$V \qquad U = \begin{bmatrix} u_{11} & u_{12} & \cdots & u_{1m} \\ u_{21} & u_{22} & \cdots & u_{2m} \\ \vdots & \vdots & \ddots & \vdots \\ u_{N1} & u_{N2} & \cdots & u_{Nm} \end{bmatrix} \equiv \begin{bmatrix} \boldsymbol{u}_1^T \\ \boldsymbol{u}_2^T \\ \vdots \\ \boldsymbol{u}_N^T \end{bmatrix}$$

In the probabilistic case u_{ij} stands for $P(j|x_i)$

- $u_{ij} \in [0,1]$ quantifies the "relation" between x_i and C_j .
- "Large" ("small") u_{ij} values indicate close (loose) relation between x_i and C_j .

 $\Rightarrow u_{ij}$ varies inversely proportional wrt $d(x_i, \theta_j)$.

• u_i : vector containing the u_{ii} 's of x_i with all clusters.

^(*) Unless otherwise stated, the case where **cluster representatives** are used is considered.

Aim:

✓ To place the representatives into dense in data regions (physical clusters).

How this is achieved:

 \checkmark Via the minimization of the following type of cost function (wrt Θ , U)

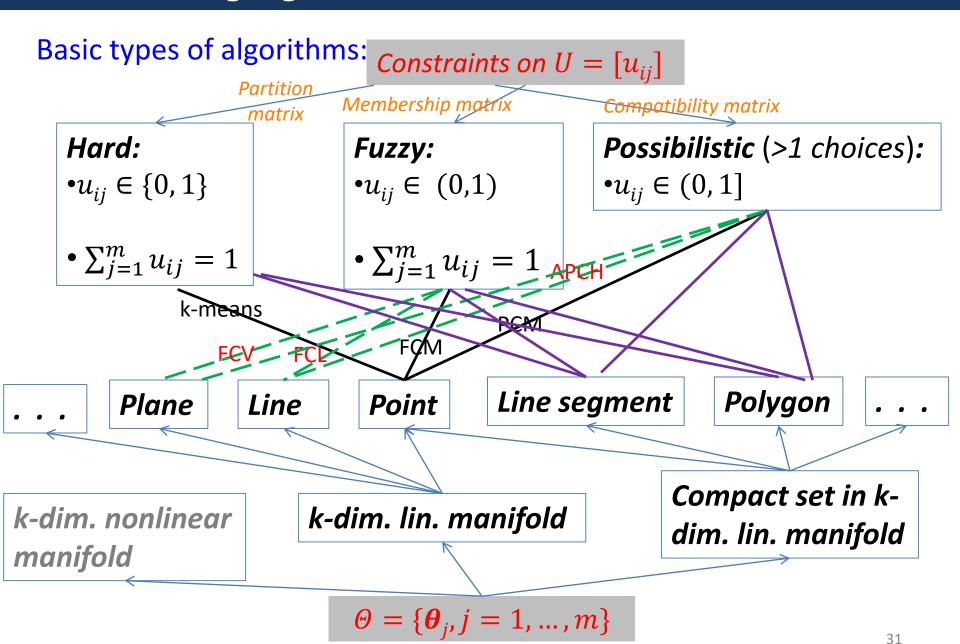
$$J(\Theta, U) = \sum_{i=1}^{N} \sum_{j=1}^{m} u_{ij}^{q} d(\mathbf{x}_{i}, \boldsymbol{\theta}_{j}) (q \ge 1)$$

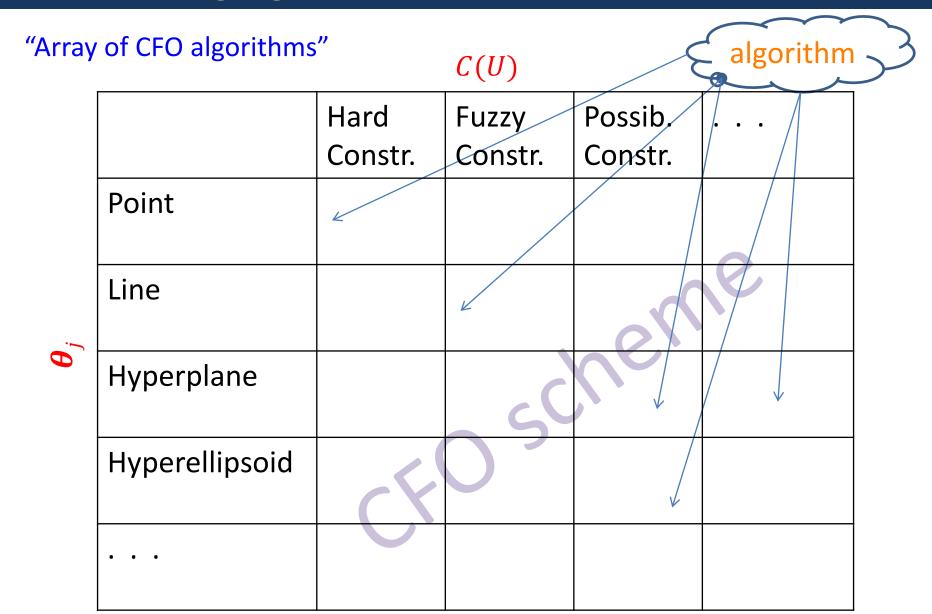
s.t. some **constraints** on U, C(U).

For the probabilistic case $d(x_i, \theta_j)$ is embedded in the log-likelihood of suitably defined exponential distributions

Intuition:

- \checkmark For **fixed** θ_i 's, $J(\theta, U)$ is a weighted sum of **fixed** distances $d(x_i, \theta_i)$.
- \Rightarrow Minimization of $J(\Theta, U)$ wrt u_{ij} instructs for large weights (u_{ij}) for small distances $d(x_i, \theta_i)$.
- For **fixed** u_{ij} 's, **minimization** of $J(\Theta, U)$ wrt θ_j 's leads θ_j 's closer to their most relative data points.





There are **several** unexplored areas (groups of algorithms) in this array.

"Array of CFO algorithms"

C(U)

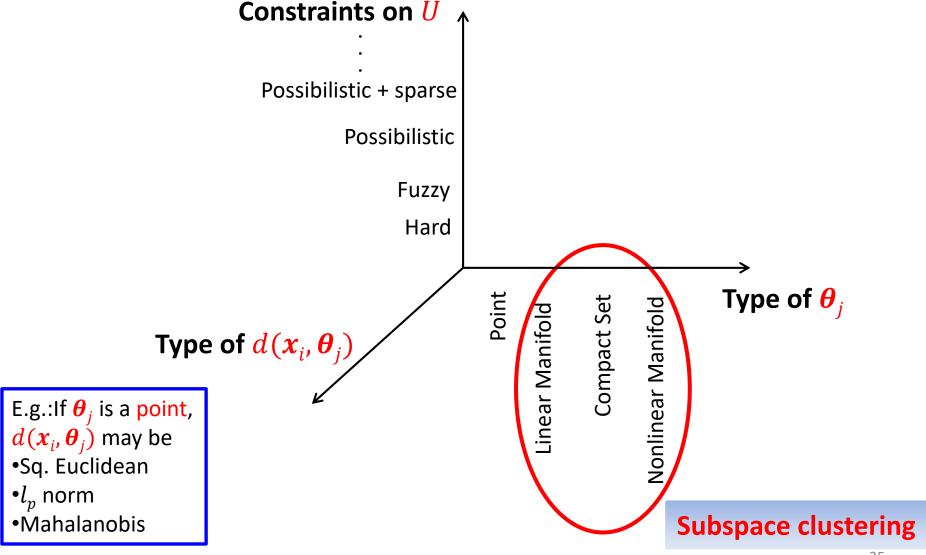
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"Array of CFO algorithms"

C(U)

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CFO clustering algorithms: A loose presentation



General cost function opt. (CFO) scheme:

- ✓ Initialize $\Theta = \Theta(0)$
- $\checkmark t = 0$
- ✓ Repeat
 - $U(t) = argmin_U J(\Theta(t), U)$, s.t. C(U(t))
 - t = t + 1

fixed

- $\Theta(t) = argmin_{\Theta} J(\Theta, U(t-1))$
- ✓ Until convergence

"Array of CFO algorithms"

C(U)

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Cost function optimization (CFO) algorithms

Hard clustering algorithms:

Let $X = \{x_1, x_2, ..., x_N\}$ be a set of data points.

Each vector belongs exclusively to a single cluster.

Each cluster is **represented** by a representative θ_j (point repr., hyperplane...). Let $\Theta = \{\theta_1, \theta_2, ..., \theta_m\}$

Define
$$u_{ij} = \begin{cases} 1, & if \ x_i \in C_j \\ 0, & otherwise \end{cases}$$
 and $U = [u_{ij}]_{Nxm}$

It is
$$\sum_{j=1}^m u_{ij} = 1$$
 , $i = 1, ...$, N

Define the cost function

$$J(U,\Theta) = \sum_{i=1}^{N} \sum_{j=1}^{m} u_{ij} d(\mathbf{x}_i, \boldsymbol{\theta}_j) = \sum_{j=1}^{m} \sum_{\mathbf{x}_i \in C_i} d(\mathbf{x}_i, \boldsymbol{\theta}_j)$$

When $J(U,\Theta)$ is **minimized**?

CFO hard clustering algorithms

$$J(U,\Theta) = \sum_{i=1}^{N} \sum_{j=1}^{m} u_{ij} d(\mathbf{x}_i, \boldsymbol{\theta}_j) = \sum_{j=1}^{m} \sum_{\mathbf{x}_i \in C_j} d(\mathbf{x}_i, \boldsymbol{\theta}_j)$$

For fixed θ_j 's: When, for each x_i , only its distance from its closest representative is taken into account.

This suggests to define
$$u_{ij} = \begin{cases} 1, & if \ d(\mathbf{x_i}, \boldsymbol{\theta_j}) = min_{q=1,\dots,m} d(\mathbf{x_i}, \boldsymbol{\theta_q}) \\ 0, & otherwise \end{cases}$$

For fixed u_{ij} 's: Solve the following \underline{m} independent problems

$$min_{\theta_j} \sum_{\mathbf{x}_i \in C_j} d(\mathbf{x}_i, \boldsymbol{\theta}_j) \equiv min_{\theta_j} \sum_{i=1}^N u_{ij} d(\mathbf{x}_i, \boldsymbol{\theta}_j)$$

Thus, the Generalized Hard Algorithmic Scheme (GHAS) is given below

Generalized Hard Algorithmic Scheme (GHAS)

- Choose $\theta_i(0)$ as initial estimates for θ_i , i=1,...,m.
- t = 0
- Repeat

$$-t = t+1$$

$$- \text{ For } j = 1 \text{ to } m \text{ \% Parameter updating }$$
o Set
$$\theta_j(t) = argmin_{\theta_j} \sum\nolimits_{i=1}^N u_{ij}(t-1) \, d\big(\textbf{x}_i, \theta_j\big), j = 1, ..., m$$

$$- \text{ End {For-} } j \}$$

• Until a termination criterion is met.

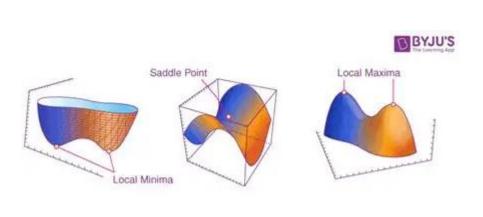
Generalized Hard Algorithmic Scheme (GHAS)

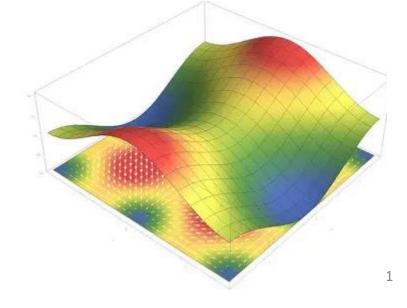
Remarks:

- In the update of each θ_j , only the vectors \mathbf{x}_i for which $u_{ij}(t-1)=1$ are used.
- GHAS may terminate when either
 - $-||\theta(t) \theta(t-1)|| < \varepsilon$ or
 - -U remains **unchanged** for two successive iterations.

The two-step optimization procedure in GHAS does not necessarily lead to a

local minimum of $J(U, \Theta)$.





Generalized Hard Algorithmic Scheme (GHAS)

The Isodata or k-Means or c-Means algorithm

General comments

- It is a special case of GHAS where
 - -Point representatives are used.
 - -The **squared** Euclidean distance is **employed**.
- The cost function $J(U,\Theta)$ becomes now

$$J(U,\Theta) = \sum_{i=1}^{N} \sum_{j=1}^{m} u_{ij} ||\mathbf{x}_i - \mathbf{\theta}_j||^2$$

- Applying GHAS in this case, it turns out that it converges to a minimum of the cost function.
- Isodata recovers clusters that are as compact as possible.
- For other choices of the distance (including the Euclidean), the algorithm converges but not necessarily to a minimum of $J(U, \Theta)$.

Generalized Hard Algorithmic Scheme (GHAS)

The Isodata or k-Means or c-Means algorithm

- Choose arbitrary initial estimates $m{ heta}_j(0)$ for the $m{ heta}_j$ s, j=1,...,m.
- t = 0
- Repeat

$$-t = t + 1$$

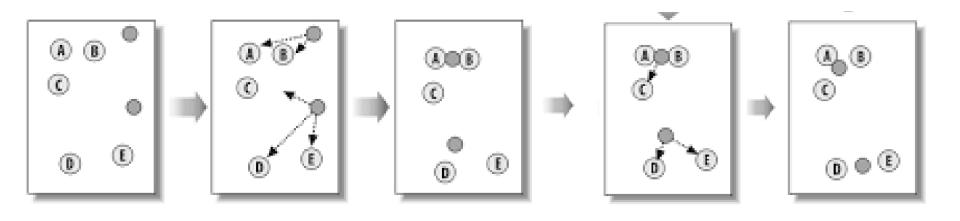
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- For j=1 to m % Parameter updating o Set  \pmb{\theta}_j(t) = \frac{\sum_{i=1}^N u_{ij}(t-1)\pmb{x}_i}{\sum_{i=1}^N u_{ij}(t-1)}, j=1,\dots,m  - End {For-j}
```

• Until no change in θ_i 's occurs between two successive iterations

The k-means case.

Choose arbitrary initial estimates $\theta_j(0)$ for the θ_j 's, j=1,...,m. Repeat

- $-\operatorname{For} i = 1 \text{ to } N \text{ Partition determination}$ $\operatorname{o Determine the closest representative, say } \boldsymbol{\theta}_j, \operatorname{for} \boldsymbol{x}_i$ $\operatorname{o Set} u_{ij} = 1 \text{ and } u_{iq} = 0, \ q = 1, \dots, m, \ q \neq j.$ $-\operatorname{End} \left\{ \operatorname{For} \right\}$ $-\operatorname{For} j = 1 \text{ to } m \text{ Parameter updating}$ $\operatorname{o Determine } \boldsymbol{\theta}_j \text{ as the mean of the vectors } \boldsymbol{x}_i \in X \text{ with } u_{ij} = 1.$ $-\operatorname{End} \left\{ \operatorname{For} \right\}$
- **Until** no change in θ_i s occurs between two successive iterations



Remarks

- ► It is a batch, single clustering algorithm
- \triangleright It is a hard clustering algorithm that uses point representatives θ_j for the clusters C_i .
- > It results from the optimization of the following cost function

$$J(U,\Theta) = \sum_{i=1}^{N} \sum_{j=1}^{m} u_{ij} ||\mathbf{x}_i - \mathbf{\theta}_j||^2$$

where $U = [u_{ij}]$ and $\Theta = \{\boldsymbol{\theta}_1, \dots, \boldsymbol{\theta}_m\}$

- It is of iterative nature.
- \triangleright Initially it places the representatives θ_i at random positions in space.
- ➤ It gradually moves the representatives towards the centers of the true clusters.
- \triangleright In practice, its time complexity is $O(q \cdot m \cdot N)$ (q is the number of iterations).
- \triangleright It requires the number of clusters m to be known a priori.

Generalized Hard Algorithmic Scheme (GHAS)

The Isodata or k-Means or c-Means algorithm

Example 1: (a) Consider three two-dimensional normal distributions with mean values:

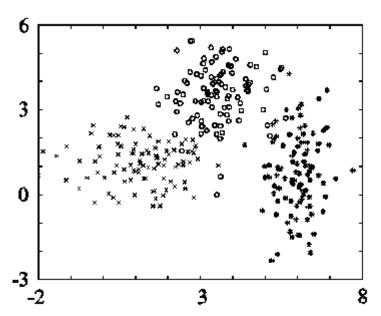
$$\mu_1 = [1,1]^T$$
, $\mu_2 = [3.5,3.5]^T$, $\mu_3 = [6,1]^T$

and respective covariance matrices

$$\Sigma_1 = \begin{bmatrix} 1 & -0.3 \\ -0.3 & 1 \end{bmatrix}, \Sigma_2 = \begin{bmatrix} 1 & 0.3 \\ 0.3 & 1 \end{bmatrix}, \Sigma_3 = \begin{bmatrix} 1 & 0.7 \\ 0.7 & 1 \end{bmatrix}$$

Generate a group of 100 vectors from each distribution. These form the data

set X.



Confusion matrix for the results of k-means.

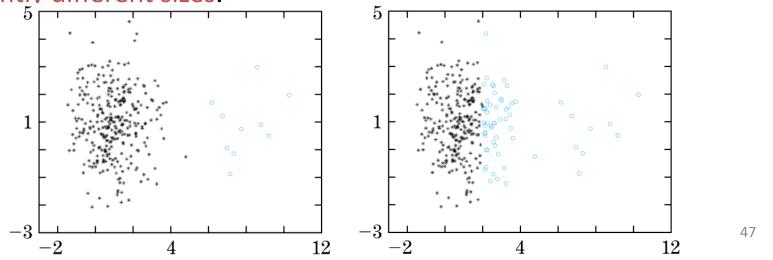
$$A = \begin{bmatrix} 94 & 3 & 3 \\ 0 & 100 & 0 \\ 9 & 0 & 91 \end{bmatrix}$$

Generalized Hard Algorithmic Scheme (GHAS)

The Isodata or k-Means or c-Means algorithm

Example 2: (i) Consider two 2-dimensional Gaussian distributions $N(\mu_1, \Sigma_1)$, $N(\mu_2, \Sigma_2)$, with $\mu_1 = [1, 1]^T$, $\mu_2 = [8, 1]^T$, $\Sigma_1 = 1.5I$ and $\Sigma_2 = I$. (ii) Generate 300 points from the 1st distribution and 10 points from the 2nd distribution. (iii) Set m = 2 and initialize randomly θ_i 's ($\theta_i = \mu_i$).

- > After convergence the large group has been split into two clusters.
- ➤ Its right part has been assigned to the same cluster with the points of the small group (see figure below).
- This indicates that k-means cannot deal accurately with clusters having significantly different sizes.



Generalized Hard Algorithmic Scheme (GHAS)

The Isodata or k-Means or c-Means algorithm

Remarks:

- *k*-means recovers compact clusters.
- The computational complexity of the k-means is O(Nmq), where q is the number of iterations required for convergence. In practice, m and q are significantly less than N, thus, k-means becomes eligible for processing large data sets.
- Sequential (online) versions of the k-means, where the updating of the representatives takes place immediately after the identification of the representative that lies closer to the current input vector \mathbf{x}_i , have also been proposed.
- A variant of the k-means results if the number of vectors in each cluster is constrained a priori.

Further remarks:

Some drawbacks of the original k-means accompanied with the variants of the k-means that deal with them are discussed next.

Generalized Hard Algorithmic Scheme (GHAS)

The Isodata or k-Means or c-Means algorithm

Drawback 1: Different initial partitions may lead k-means to produces different final clusterings, each one corresponding to a different local minimum of the cost function.

Strategies for facing drawback 1:

- <u>Single run methods</u>
 - –Use a sequential algorithm (discussed previously) to produce initial estimates for θ_i 's.
 - -Partition randomly the data set into m subsets and use their means as initial estimates for $\boldsymbol{\theta}_i$'s.
- Multiple run methods
 - -Create different partitions of X, run k-means for each one of them and select the best result (associated with the minimum cost function value).
- <u>Utilization of tools from stochastic optimization techniques</u> (simulated annealing, genetic algorithms etc).

Generalized Hard Algorithmic Scheme (GHAS)

The Isodata or k-Means or c-Means algorithm

Drawback 2: Knowledge of the number of clusters m is required a priori.

Strategies for facing drawback 2:

- Employ splitting, merging and/or discarding operations of the clusters resulting from k-means.
- Estimate *m* as follows:
 - -Run a **sequential** algorithm many times for different thresholds of dissimilarity Θ .
 - -Plot Θ versus the number of clusters and identify the largest plateau in the graph and set m equal to the value that corresponds to this plateau.

Generalized Hard Algorithmic Scheme (GHAS)

The Isodata or k-Means or c-Means algorithm

Drawback 2: Knowledge of the number of clusters m is required a priori.

Strategies for facing drawback 2 (cont.):

- Estimate *m* as follows:
 - -Run the k-means algorithm for different values of the number of clusters m.
 - For each of the resulting clusterings compute the value of J.
 - -Plot J versus the number of clusters m and identify the most significant knee in the graph. Its position indicates the number of physical clusters.



Generalized Hard Algorithmic Scheme (GHAS)

The Isodata or k-Means or c-Means algorithm

Drawback 3: k-means is sensitive to outliers and noise.

Strategies for facing drawback 3:

- Discard all "small" clusters (they are likely to be formed by outliers).
- Use a k-medoids algorithm (see below), where a cluster is represented by one of its points.

Drawback 4: *k*-means is not suitable for data with nominal (categorical) coordinates.

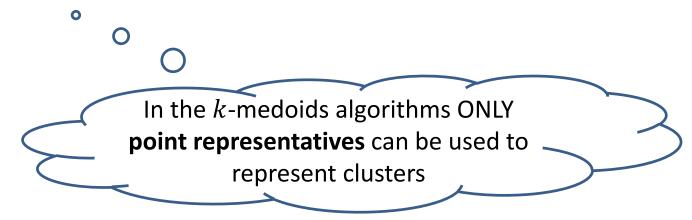
Strategies for facing drawback 4:

• Use a k-medoids algorithm.

Generalized Hard Algorithmic Scheme (GHAS)

<u>k-Medoids Algorithms</u>

- Each cluster is represented by a vector selected among the elements of X
 (medoid).
- A cluster contains
 - Its medoid
 - All vectors in X that
 - o Are not used as medoids in other clusters
 - o Lie closer to its medoid than the medoids representing other clusters.



Let

- Θ be the set of medoids of all clusters,
- I_{Θ} the set of indices of the points in X that constitute Θ and
- $I_{X-\Theta}$ the set of indices of the points that are not medoids.

Obtaining the set of medoids Θ that best represents the data set, X is equivalent to minimizing the following cost function

$$J(\Theta, U) = \sum_{i \in I_{X-\Theta}} \sum_{j \in I_{\Theta}} u_{ij} d(\mathbf{x}_i, \mathbf{x}_j)$$

with

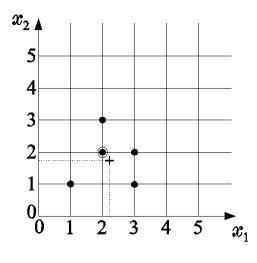
$$u_{ij} = \begin{cases} 1, & \text{if } d(\mathbf{x}_i, \mathbf{x}_j) = \min_{q \in I_{\Theta}} d(\mathbf{x}_i, \mathbf{x}_q), \\ 0, & \text{otherwise} \end{cases}, \quad i = 1, ..., N$$

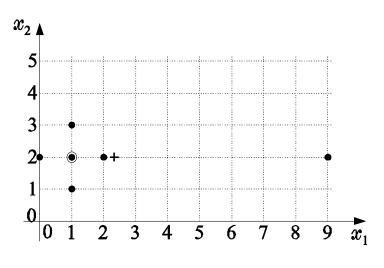
Generalized Hard Algorithmic Scheme (GHAS)

k-Medoids Algorithms

Example 3:

- (a) The five-point two-dimensional set stems from the discrete domain $D = \{1,2,3,4,...\} \times \{1,2,3,4,...\}$. Its medoid is the circled point and its mean is the "+" point, which does not belong to D.
- (b) In the six-point two-dimensional set, the point (9,2) can be considered as an outlier. While the outlier affects significantly the mean of the set, it does not affect its medoid.





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(a) (b)

Generalized Hard Algorithmic Scheme (GHAS)

Representing clusters with mean values vs representing clusters with

medoids

Mean Values	Medoids
1. Suited only for continuous domains	1. Suited for either cont. or discrete domains
2. Algorithms using means are sensitive to outliers	2. Algorithms using medoids are less sensitive to outliers
3. The mean possesses a clear geometrical and statistical meaning	3. The medoid has not a clear geometrical meaning
4. Algorithms using means are less computationally demanding	4. Algorithms using medoids are more computationally demanding

Generalized Hard Algorithmic Scheme (GHAS)

k-Medoids Algorithms

Algorithms to be considered

- PAM (Partitioning Around Medoids)
- CLARA (<u>Clustering LARge Applications</u>)
- CLARANS (Clustering Large Applications based on RANdomized Search)

The PAM algorithm

• The number of clusters m is **required** a *priori*.

Definitions-preliminaries

- Two <u>sets</u> of medoids Θ and Θ' , each one consisting of m elements, are called neighbors if they **share** m-1 elements.
- A set Θ of medoids with m elements can have m(N-m) neighbors.
- Let Θ_{ij} denote the neighbor of Θ that results if x_j , $j \in I_{X-\Theta}$ replaces x_i , $i \in I_{\Theta}$.
- Let $\Delta J_{ii} = J(\Theta_{ii}, U_{ii}) J(\Theta, U)$.

Generalized Hard Algorithmic Scheme (GHAS)

The PAM algorithm

- Determination of Θ that best represents the data
 - Generate a set Θ of m medoids, randomly selected out of X.
 - (A) Determine the neighbor Θ_{qr} , $q \in I_{\Theta}$, $r \in I_{X-\Theta}$ among the m(N-m) neighbors of Θ for which $\Delta J_{qr} = min_{i \in I_{\Theta}, j \in I_{X-\Theta}} \Delta J_{ij}$.
 - $-\operatorname{If} \Delta J_{qr} < 0 \text{ then} \bullet \bullet \bullet \\ \operatorname{o} \operatorname{Replace} \Theta \text{ by } \Theta_{qr} \bullet J(\Theta_{qr}, U_{qr}) J(\Theta, U) < 0 \\ \operatorname{o} \operatorname{Go} \operatorname{to} \text{ (A)}$
 - End
- Assignment of points to clusters
 - Assign each $x \in X \Theta$ to the cluster represented by the closest to x medoid.

Generalized Hard Algorithmic Scheme (GHAS)

The PAM algorithm

Computation of ΔJ_{ij} .

It is defined as:

$$\Delta J_{ij} = J(\Theta_{ij}, U_{ij}) - J(\Theta, U) = \sum_{S \in I_{X-\Theta_{ij}}} \sum_{t \in I_{\Theta_{ij}}} u_{st} d(\mathbf{x}_{s}, \mathbf{x}_{t}) - \sum_{S \in I_{X-\Theta}} \sum_{t \in I_{\Theta}} u_{st} d(\mathbf{x}_{s}, \mathbf{x}_{t})$$

$$\equiv \sum_{h \in I_{X-\Theta}} C_{hij}$$

where C_{hij} is the <u>difference in J, resulting from the (possible) assignment of the vector $x_h \in X - \Theta$ from the cluster it currently belongs to another, as a consequence of the replacement of $x_i \in \Theta$ by $x_i \in X - \Theta$.</u>

For the computation of C_{hij} associated with a specific $\mathbf{x}_h \in X - \Theta$ it is required

- The distance of x_h from its closest medoid in Θ
- The distance of x_h from its next to closest medoid in Θ .
- The distance of x_h from the newly inserted medoid in θ_{ij} , x_j .

Generalized Hard Algorithmic Scheme (GHAS)

The PAM algorithm (cont.)

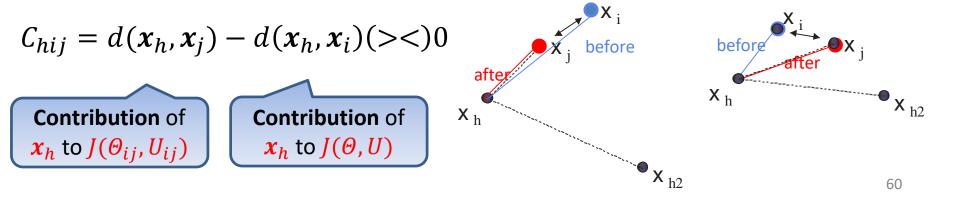
Computation of C_{hij} :

 x_h belongs to the cluster represented by x_i ($x_{h2} \in \Theta$ denotes the second closest to x_h representative) and $d(x_h, x_j) \ge d(x_h, x_{h2})$ ($\ge d(x_h, x_i)$). Then

$$C_{hij} = d(x_h, x_{h2}) - d(x_h, x_i) \ge 0$$
Contribution of x_h to $J(\Theta_{ij}, U_{ij})$
Contribution of x_h to $J(\Theta, U)$

$$x_h = \frac{1}{2} \sum_{k=1}^{N} x_k \cos J(\Theta, U)$$

 x_h belongs to the cluster represented by x_i ($x_{h2} \in \Theta$ denotes the second closest to x_h representative) and $d(x_h, x_j) \le d(x_h, x_{h2})$. Then

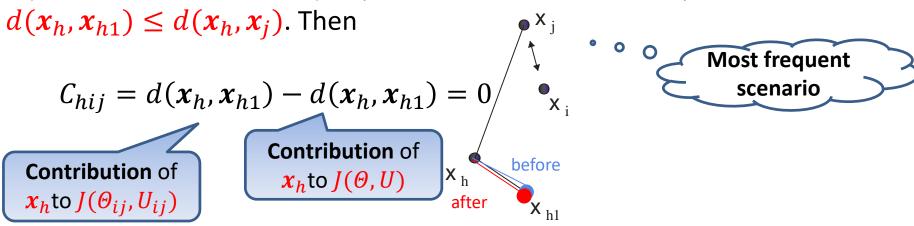


Generalized Hard Algorithmic Scheme (GHAS)

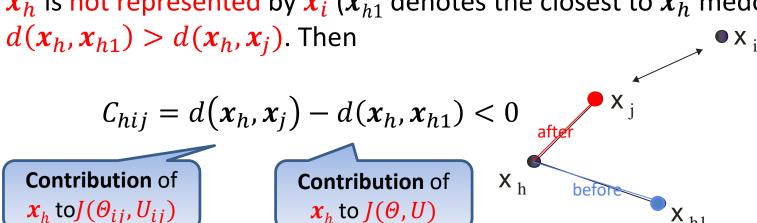
The PAM algorithm (cont.)

Computation of C_{hij} (cont.):

 x_h is not represented by x_i (x_{h1} denotes the closest to x_h medoid) and



 x_h is not represented by x_i (x_{h1} denotes the closest to x_h medoid) and



Generalized Hard Algorithmic Scheme (GHAS)

The PAM algorithm (cont.)

Remarks:

- Experimental results show the PAM works satisfactorily with small data sets.
- Its computational complexity is $O(m(N-m)^2)$. Unsuitable for large data sets.

Generalized Hard Algorithmic Scheme (GHAS)

The PAM algorithm (Example)

Data set:
$$X = \{x_1, x_2, x_3, x_4, x_5, x_6\}$$
, with

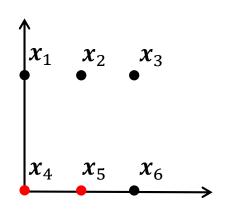
$$x_1 = [0,3]^T$$
, $x_2 = [1,3]^T$, $x_3 = [2,3]^T$, $x_4 = [0,0]^T$, $x_5 = [1,0]^T$, $x_6 = [2,0]^T$.

Set of medoids: $\Theta = \{x_4, x_5\}$

Computation of $\underline{I(\Theta,U)}$ (**Squared Euclidean distance** is considered):

$$x_1 oup d(x_1, x_4) = 9 < 10 = d(x_1, x_5) oup u_{14} = 1, u_{15} = 0$$

 $x_2 oup d(x_2, x_4) = 10 > 9 = d(x_2, x_5) oup u_{24} = 0, u_{25} = 1$
 $x_3 oup d(x_3, x_4) = 13 > 10 = d(x_3, x_5) oup u_{34} = 0, u_{35} = 1$
 $x_4 oup d(x_4, x_4) = 0 < 1 = d(x_4, x_5) oup u_{44} = 1, u_{45} = 0$
 $x_5 oup d(x_5, x_4) = 1 > 0 = d(x_5, x_5) oup u_{54} = 0, u_{55} = 1$
 $x_6 oup d(x_6, x_4) = 2 > 1 = d(x_6, x_5) oup u_{64} = 0, u_{65} = 1$



$$J(\Theta, U) = \begin{array}{c} u_{24}d(x_2, x_4) + & u_{25}d(x_2, x_5) + \\ u_{34}d(x_3, x_4) + & u_{35}d(x_3, x_5) + \\ & u_{44}d(x_4, x_4) + & u_{45}d(x_4, x_5) + \\ & u_{54}d(x_5, x_4) + & u_{55}d(x_5, x_5) + \end{array}$$

$$u_{24}d(x_2, x_4) + u_{25}d(x_2, x_5) + 0 \cdot 10 + 1 \cdot 9 +$$

$$= u_{34}d(x_3, x_4) + u_{35}d(x_3, x_5) + = 0 \cdot 13 + 1 \cdot 10 +$$

 $u_{14}d(x_1,x_4) + u_{15}d(x_1,x_5) +$

$$1 \cdot 0 + 0 \cdot 1 + 0 \cdot 1 + 1 \cdot 0 +$$

 $1 \cdot 9 + 0 \cdot 10 +$

 $0 \cdot 10 + 1 \cdot 9 +$

$$u_{54}d(x_5, x_4) + u_{55}d(x_5, x_5) + 0 \cdot 1 + 1 \cdot 0 + u_{64}d(x_6, x_4) + u_{65}d(x_6, x_5)$$
 $0 \cdot 2 + 1 \cdot 1$

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Generalized Hard Algorithmic Scheme (GHAS)

The PAM algorithm (Example)

Data set: $X = \{x_1, x_2, x_3, x_4, x_5, x_6\}$, with

$$x_1 = [0,3]^T$$
, $x_2 = [1,3]^T$, $x_3 = [2,3]^T$, $x_4 = [0,0]^T$, $x_5 = [1,0]^T$, $x_6 = [2,0]^T$.

 $x_5 \leftrightarrow x_6$

Set of medoids: $\Theta = \{x_4, x_5\}$

$$\theta_{42} = \{x_2, x_5\}
J(\theta_{42}, U_{42}) = 4
\Delta J_{42} = 4 - 29 = -25$$

 $\Theta_{56} = \{\boldsymbol{x}_4, \boldsymbol{x}_6\}$

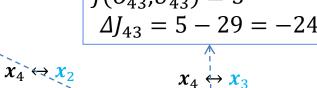
 $\Delta I_{56} = 29 - 29 = 0$

 $J(\Theta_{56}, U_{56}) = 29$

$$\Theta_{43} = \{x_3, x_5\}$$

$$J(\Theta_{43}, U_{43}) = 5$$

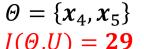
$$\Delta J_{43} = 5 - 29 = -24$$



$$\theta_{41} = \{x_1, x_5\}
J(\theta_{41}, U_{41}) = 5$$

$$x_4 \leftrightarrow x_1$$

$$J(\theta_{41}, \theta_{41}) = 5$$
$$\Delta J_{41} = 5 - 29 = -24$$



 $\chi_4 \leftrightarrow \chi_3$

$$J(\Theta,U) = \mathbf{29}$$

$$J(\Theta,U) = \mathbf{29}$$

 $x_5 \leftrightarrow x_3$

 $x_4 \leftrightarrow x_6$

$$\begin{array}{c}
x_5 \leftrightarrow x_1 \\
J(\Theta_{51}, U_{51}) = 6 \\
\Delta J_{51} = 6 - 29 = -23
\end{array}$$

$$x_5 \leftrightarrow x_2$$

$$\theta_{53} = \{x_4, x_3\}$$

$$J(\theta_{53}, U_{53}) = 5$$

$$\Delta J_{53} = 5 - 29 = -24$$

$$\Theta_{52} = \{x_4, x_2\}$$

$$J(\Theta_{52}, U_{52}) = 5$$

$$\Delta J_{52} = 5 - 29 = -24$$

 \boldsymbol{x}_2

 x_5 x_6

 $\Theta_{46} = \{x_6, x_5\}$

 $\Delta I_{46} = 29 - 29 = 0$

 $\Theta_{51} = \{\boldsymbol{x}_4, \boldsymbol{x}_1\}$

 $J(\Theta_{46}, U_{46}) = 29$

It is
$$\Delta J_{42} = min_{i \in I_{\Theta}, j \in I_{X-\Theta}} \Delta J_{ij} = -25 < 0$$

Thus, according to **PAM**, Θ will be **replaced** by Θ_{42} .

Generalized Hard Algorithmic Scheme (GHAS)

The PAM algorithm (Example)

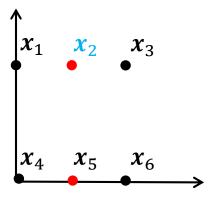
Data set: $X = \{x_1, x_2, x_3, x_4, x_5, x_6\}$, with $x_1 = [0,3]^T$, $x_2 = [1,3]^T$, $x_3 = [2,3]^T$, $x_4 = [0,0]^T$, $x_5 = [1,0]^T$, $x_6 = [2,0]^T$. Set of medoids: $\Theta_{42} = \{x_2, x_5\}$

Computation of
$$I(\Theta_{42}, U_{42})$$
 (Squared Euclidean distance is considered):

$$x_1 oup d(x_1, x_2) = 1 < 10 = d(x_1, x_5) oup u_{12} = 1, u_{15} = 0$$

 $x_2 oup d(x_2, x_2) = 0 < 9 = d(x_2, x_5) oup u_{22} = 1, u_{25} = 0$
 $x_3 oup d(x_3, x_2) = 1 < 10 = d(x_3, x_5) oup u_{32} = 1, u_{35} = 0$
 $x_4 oup d(x_4, x_2) = 10 > 1 = d(x_4, x_5) oup u_{42} = 0, u_{45} = 1$
 $x_5 oup d(x_5, x_2) = 9 > 0 = d(x_5, x_5) oup u_{52} = 0, u_{55} = 1$

$$x_6 \rightarrow d(x_6, x_2) = 10 > 1 = d(x_6, x_5) \rightarrow u_{62} = 0, u_{65} = 1$$



$$\frac{u_{12}d(x_1, x_2) + u_{15}d(x_1, x_5) +}{u_{22}d(x_2, x_2) + u_{25}d(x_2, x_5) +} = \frac{1 \cdot 1 + 0 \cdot 10 +}{1 \cdot 0 + 0 \cdot 9 +}$$

$$J(\Theta_{42}, U_{42}) = \frac{u_{32}d(x_3, x_2) +}{u_{35}d(x_3, x_2) +} = \frac{1 \cdot 1 +}{0 \cdot 10 +} = 4$$

$$\frac{u_{42}d(x_4, x_2) +}{u_{45}d(x_4, x_5) +} = \frac{1 \cdot 1 +}{0 \cdot 10 +} = 4$$

$$\frac{u_{52}d(x_5, x_2) +}{u_{55}d(x_5, x_5) +} = \frac{0 \cdot 10 +}{1 \cdot 0 +} = 4$$

$$\frac{u_{62}d(x_6, x_2) +}{u_{65}d(x_6, x_5)} = \frac{0 \cdot 10 +}{1 \cdot 0 +} = 65$$

Generalized Hard Algorithmic Scheme (GHAS)

The PAM algorithm (Example)

Data set:
$$X = \{x_1, x_2, x_3, x_4, x_5, x_6\}$$
, with

$$x_1 = [0,3]^T$$
, $x_2 = [1,3]^T$, $x_3 = [2,3]^T$, $x_4 = [0,0]^T$, $x_5 = [1,0]^T$, $x_6 = [2,0]^T$
Sets of medoids: $\Theta = \{x_4, x_5\}$, $\Theta_{42} = \{x_2, x_5\}$

Computation of ΔJ_{42} as

$$\Delta J_{42} = J(\Theta_{42}, U_{42}) - J(\Theta, U) = \sum_{h \in X - \Theta} C_{h42}$$
 (Sq. Eucl. dist. is used):

	Dist. from Closest repr. in $\Theta = \{x_4, x_5\}$	Dist. from Next closest repr. in $0 = \{x_4, x_5\}$	Dist. from closest repr. In $\Theta_{42} = \{x_2, x_5\}$	C_{h42}
x_1	9 (x4)	10 (x_5)	1 (x ₂)	1 - 9 = -8
\boldsymbol{x}_2	9 (x ₅)	10 (x_4)	0 (x ₂)	0 - 9 = -9
\boldsymbol{x}_3	10 (<i>x</i> ₅)	13 (<i>x</i> ₄)	1 (x ₂)	1-10=-9
x_4	0 (x4)	$1(x_5)$	$1(x_5)$	1 - 0 = 1
x_5	0 (x ₅)	1 (<i>x</i> ₄)	0 (x ₅)	0 - 0 = 0
\boldsymbol{x}_6	1 (x ₅)	$2(x_4)$	1 (<i>x</i> ₅)	1 - 1 = 0
ΔJ_{42}				-25

0]?	x_1	x ₂	x_3
			•
	x_4	x_5	x_6

Generalized Hard Algorithmic Scheme (GHAS)

The CLARA algorithm

- It is more suitable for large data sets.
- The strategy:
 - **Draw** randomly a sample X' of size N' from the entire data set.
 - Run the PAM algorithm to determine Θ' that best represents X'.
 - Use Θ' in the place of Θ to represent the entire data set X.
- The rationale:
 - Assuming that X' has been selected in a way representative of the statistical distribution of the data points in X, Θ' is expected to be a good approximation of Θ , which would have been produced if PAM were run on the entire X.
- The algorithm:
 - Draw s sample subsets of size N' from X, denoted by $X'_1, ..., X'_s$ (typically s = 5, N' = 40 + 2m).
 - Run PAM on each one of them and identify $\Theta'_1, \dots, \Theta'_{\varsigma}$.

- Choose the set
$$\Theta'_j$$
 that minimizes
$$J(\Theta, U) = \sum_{i \in I_{X-\Theta'}} \sum_{j \in I_{\Theta'}} u_{ij} d(\mathbf{x}_i, \mathbf{x}_j)$$

based on the entire data set X.

Generalized Hard Algorithmic Scheme (GHAS)

The CLARANS algorithm

- It is more suitable for large data sets.
- It follows the philosophy of PAM with the difference that only a randomly selected fraction q(< m(N-m)) of the neighbors of the current medoid set is considered.
- It performs several runs (s) starting from different initial choices for Θ .

The algorithm:

```
- For i=1 to s o Initialize randomly \Theta.

o (A) Select randomly q neighbors of \Theta.

o For j=1 to q

* If the present neighbor of \Theta is better than \Theta (in terms of J(\Theta,U)) then -- Set \Theta equal to its neighbor -- Go to (A)

* End If o End For o Set \Theta^i = \Theta
```

- End For
- **Select** the best Θ^i with respect to $J(\Theta, U)$.
- Based on Θ^i , assign each $\mathbf{x} \in X \Theta$ to the cluster whose representative is closest to \mathbf{x}

Generalized Hard Algorithmic Scheme (GHAS)

The CLARANS algorithm (cont.)

Remarks:

- CLARANS depends on q and s. Typically, s=2 and $q=\max(0.125m(N-m),250)$
- As q approaches m(N-m) CLARANS approaches PAM and the complexity increases.
- CLARANS can also be described in terms of graph theory concepts.
- CLARANS unravels better quality clusters than CLARA.
- In some cases, CLARA is significantly faster than CLARANS.
- CLARANS retains its quadratic computational nature and thus it is not appropriate for very large data sets.

Random variable (RV): It models the output of an experiment.

RV types:

- Discrete
- continuous

Discrete random variables:

- •A discrete RV x can take any value x from a finite or countably infinite set X.
- •X: sample space or state space.
- •Event: Any subset of X.
- •Elementary or simple event: A single element subset of X.
- •Example: Consider the die roll experiment. X={1,2,3,4,5,6}
- •Events: "Odd number", "number>3",("2", "5")

Elementary events

Discrete random variables (cont.):

- •Notation: Probability of the event $x=x\in X$: $P(x=x)\equiv P(x)$
- •P(.):A function called probability mass function (pmf) satisfying

✓
$$P(x) \ge 0, \forall x \in X$$

$$\checkmark \sum_{x \in X} P(x) = 1$$

Discrete random variables (cont.):

The case of more than one random variables: Definitions

Discrete RV	X	у
Sample space	$X=\{x_1,\ldots,x_{nx}\}$	$Y=\{y_1,\ldots,y_{ny}\}$

Joint probability: $P(x_i, y_i) \equiv P(x=x_i \text{ AND } y=y_i)$

•It corresponds to the case where x takes the value x_i AND y takes the value y_i , simultaneously.

Marginal probabilities: $P(x_i) \equiv P(x=x_i)$, $P(y_j) = P(y=y_j)$

•This terminology is used only when more than one rvs are involved.

Conditional probability: $P(x_i | y_j) \equiv P(x=x_i | y=y_j) = P(x_i, y_j) / P(y_j)$

•It corresponds to the case where x takes the value x_i given that y takes the value y_i .

Discrete random variables (cont.):

The case of more than one variables: Properties

Discrete RV	X	y
Sample space	$X = \{x_1, \dots, x_{nx}\}$	$\mathbf{Y} = \{y_1, \dots, y_{ny}\}$

Sum rule:
$$P(x) = \sum_{y \in Y} P(x, y), \quad \forall x \in X$$

Product rule: P(x, y) = P(x | y)P(y)

Statistical independence: P(x, y) = P(x)P(y)

A consequence: P(x | y) = P(x) P(y | x) = P(y)

Bayes rule: $P(y \mid x) = \frac{P(x \mid y)P(y)}{P(x)}$

or $P(y \mid x) = \frac{P(x \mid y)P(y)}{\sum_{y \in V} P(x \mid y)P(y)}$

It plays a key role in ML.

Continuous random variables:

- •A continuous RV x can take any value $x \in R$.
- •Sample space or state space: R
- •Events: $\{x \le x\}$, $\{x_1 < x \le x_2\}$, $\{x \ge x\}$

Corresponds to the probability mass function from the discrete case.

- •Cumulative distribution function (cdf): $F_x(x) = P(x \le x)$
- •It is $F_{x}(\infty) = P(x < \infty) = 1$

It assigns "mass" to events.

•Probability of events in terms of cdf:

$$\triangleright P(x \le x) = F_x(x)$$

$$P(x_1 < x \le x_2) = P(x \le x_2) - P(x \le x_1) = F_x(x_2) - F_x(x_1)$$

$$P(x \ge x) = P(x \le \infty) - P(x \le x) = 1 - P(x \le x) = 1 - F_x(x)$$

Continuous random variables (cont.):

•Assumption: $F_x(x)$ is continuous and differentiable.

•Probability density function (pdf):

$$p_{x}(x) = \frac{dF_{x}(x)}{dx}$$

It assigns "mass" to values.

•cdf in terms of pdf:

$$F_{\mathbf{x}}(x) = \int_{-\infty}^{x} p_{\mathbf{x}}(z) dz$$

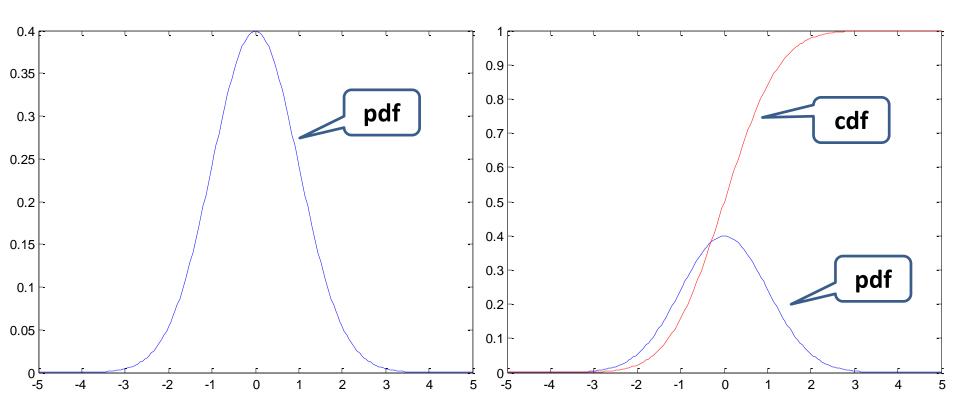
•Probability of events in terms of pdf:

$$\triangleright P(x \le x) = F_x(x) = \int_{-\infty}^x p_x(z) dz$$

$$P(x_1 < x \le x_2) = P(x \le x_2) - P(x \le x_1) = F_x(x_2) - F_x(x_1) = \int_{x_1}^{x_2} p_x(x) dx$$

$$P(x \ge x) = P(x \le \infty) - P(x \le x) = 1 - P(x \le x) = 1 - F_x(x) = \int_{-\infty}^{x} p_x(z) dz$$

Continuous random variables (cont.):



Continuous random variables (cont.):

•Since
$$P(-\infty < x < +\infty) = 1$$
 it is:
$$\int_{-\infty}^{+\infty} p_x(x) dx = 1$$

•It is
$$P(x < x \le x + \Delta x) = \int_{x}^{x + \Delta x} p_x(z) dz \approx p_x(x) \Delta x$$

As
$$\Delta x \rightarrow 0$$
, $P(x < x < x + \Delta x) = P(x = x) = 0$.

The probability of a continuous rv to take a single value is zero.

The case of more than one variables:

Continuous RV	X	у
Sample space	R	R

NOTE: All rules stated for the probability mass function in the discrete case are stated for the pdf in the continuous case.

Product rule

$$p(x, y) = p(x | y)p(y)$$

We drop the name of rv from the subscript of
$$p$$
.

Sum rule
$$p(x) = \int_{-\infty}^{+\infty} p(x, y) dy$$

Useful quantities related to (continuous) rvs:

•Mean (expected) value of a rv x: $E[x] = \int_{-\infty}^{+\infty} xp(x)dx$

$$E[x] = \int_{-\infty}^{+\infty} x p(x) dx$$

For discrete rv's, the integrals become summations.

- •Variance of a rv x: $\sigma_{x}^{2} = \int_{-\infty}^{+\infty} (x E[x])^{2} p(x) dx = E[(x E(x))^{2}]$
- •Mean (expected) value of a function of an rv x : $E[f(x)] = \int_{-\infty}^{+\infty} f(x)p(x)dx$
- •Mean of a function of two rv's x, y: $E_{x,y}[f(x,y)] = \int_{-\infty}^{+\infty} f(x,y) p(x,y) dxdy$
- $E[y \mid x] = \int_{-\infty}^{+\infty} y p(y \mid x) dy$ •Conditional mean of an rv y given x = x:
- •It is $E_{x,y}[f(x,y)] = E_x[E_{y|x}[f(x,y)]]$
- •Covariance between two rvs x and y: cov(x, y) = E[(x E[x])(y E[y])]
- Correlation between two rv's x and y: $r_{xy} \equiv E(xy) = cov(x, y) + E[x]E[y]$
- Correlation coefficient $r_{xy} = \frac{E[x-E[x])(y-E[y])}{\sigma_x\sigma_y}$

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Random vectors

- •A collection of rvs: $\mathbf{x} = [x_1, x_2, ... x_l]^T$
- •Probability density function (pdf) of x: The joint pdf of $x_1, x_2, ... x_l$. $p(x) = p(x_1, x_2, ...x_l)$

•Covariance matrix of
$$\mathbf{x}$$
:
$$cov(\mathbf{x}) = E[(\mathbf{x} - E[\mathbf{x}])(\mathbf{x} - E[\mathbf{x}])^{\mathrm{T}}] = \begin{bmatrix} cov(\mathbf{x}_1, \mathbf{x}_1) & \cdots & cov(\mathbf{x}_1, \mathbf{x}_l) \\ \vdots & \ddots & \vdots \\ cov(\mathbf{x}_l, \mathbf{x}_1) & \cdots & cov(\mathbf{x}_l, \mathbf{x}_l) \end{bmatrix}$$

•Correlation matrix of
$$\mathbf{x}$$
: $R_{\mathbf{x}} = \mathbf{E}[\mathbf{x}\mathbf{x}^{\mathrm{T}}] = \begin{bmatrix} \mathbf{E}(\mathbf{x}_{1}\mathbf{x}_{1}) & \cdots & \mathbf{E}(\mathbf{x}_{1}\mathbf{x}_{l}) \\ \vdots & \ddots & \vdots \\ \mathbf{E}(\mathbf{x}_{l}\mathbf{x}_{1}) & \cdots & \mathbf{E}(\mathbf{x}_{l}\mathbf{x}_{l}) \end{bmatrix}$

•It is
$$R_{\mathbf{x}} \equiv E[\mathbf{x}\mathbf{x}^{\mathrm{T}}] = \text{cov}(\mathbf{x}) + E[\mathbf{x}]E[\mathbf{x}^{\mathrm{T}}]$$
 Exercise: Prove this identity

Random vectors (cont.)

Exercise: Prove these statements

•Remark: Both R_x and cov(x) are symmetric and positive definite lxl matrices.

A square matrix A is symmetric iff $A^T = A$. A square matrix

A is positive

definite iff $z^TAz>0$, $\forall z \in \mathbb{R}^l$.

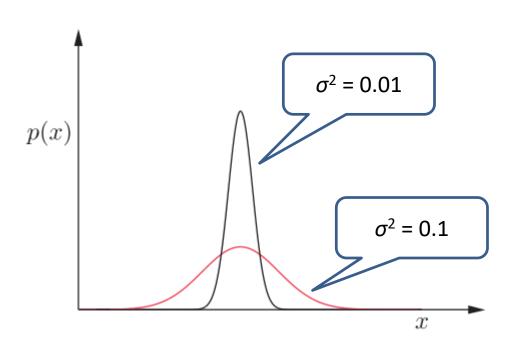
•One dim. normal (Gaussian) distribution $x \sim N(\mu, \sigma^2)$ or $N(x \mid \mu, \sigma^2)$:

- ■Sample space: *R*
- It is

$$p(x) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp(-\frac{(x-\mu)^2}{2\sigma^2})$$

$$\geq$$
E[x]= μ

$$> \sigma_x^2 = \sigma^2.$$



• Multi dim. normal (Gaussian) distribution $x \sim N(\mu, \Sigma)$ or $N(x|\mu, \Sigma)$:

- ■l-dim. case
- It is

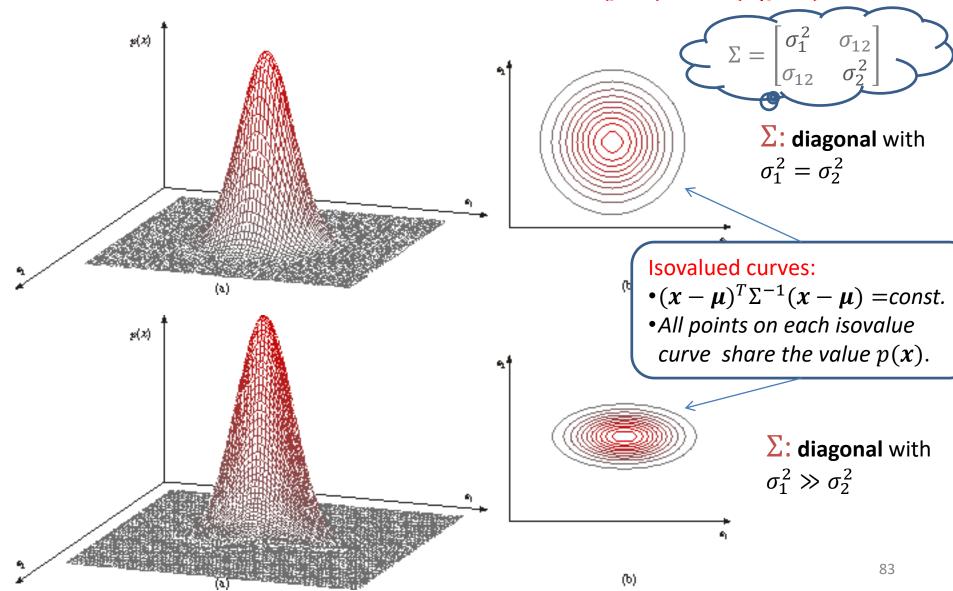
$$p(x) = \frac{1}{(2\pi)^{l/2} |\Sigma|^{1/2}} \exp\left(-\frac{(x-\mu)^T \Sigma^{-1} (x-\mu)}{2}\right)$$

$$\triangleright E[\mathbf{x}] = \boldsymbol{\mu}$$

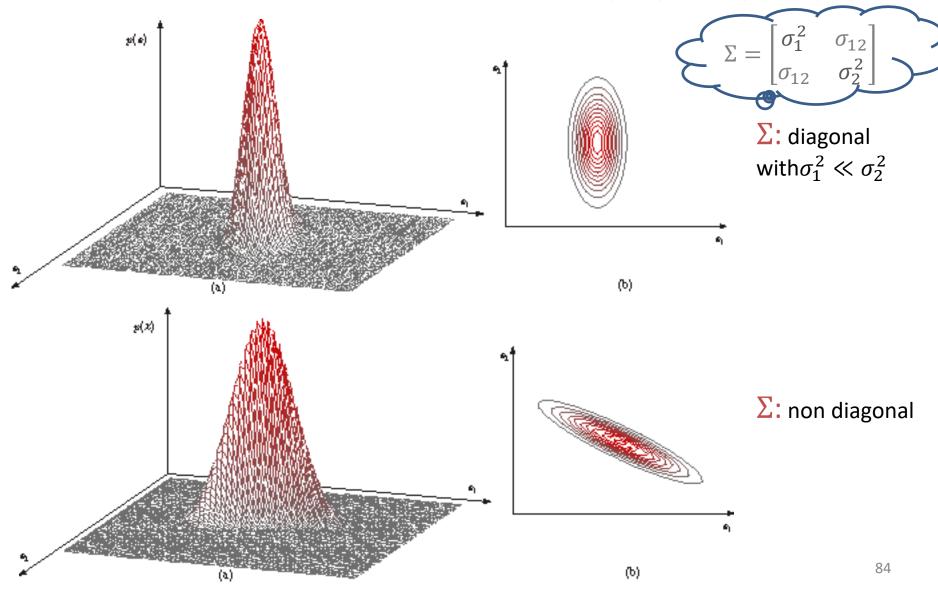
$$\succ cov(\mathbf{x}) = \Sigma.$$

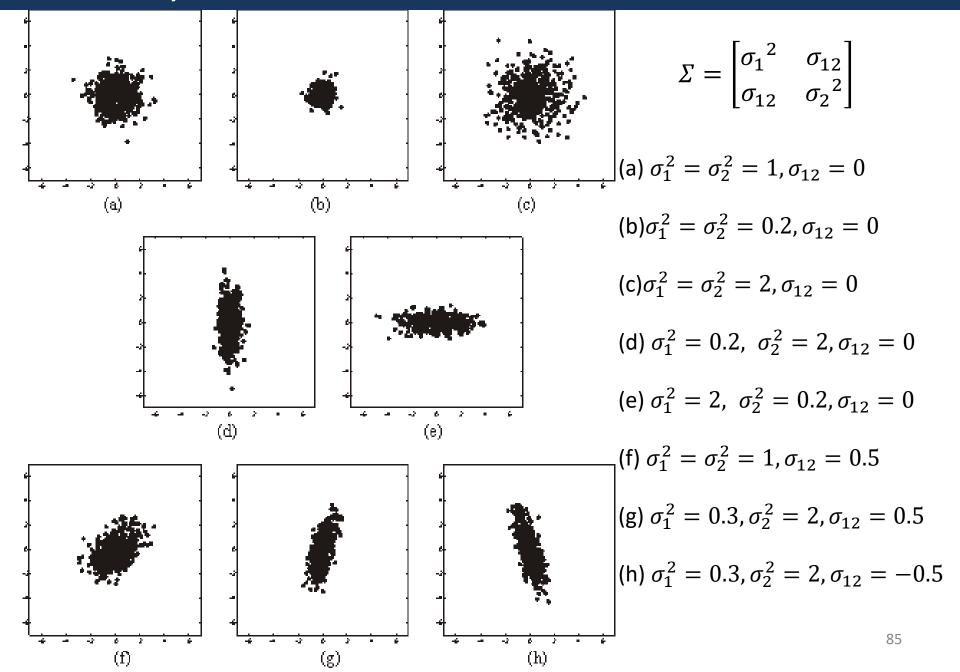
(*) For the 2-d case
$$\Sigma = \begin{bmatrix} \sigma_1^2 & \sigma_{12} \\ \sigma_{12} & \sigma_2^2 \end{bmatrix}$$

•Multi dim. normal (Gaussian) distribution $x \sim N(\mu, \Sigma)$ or $N(x|\mu, \Sigma)$:



•Multi dim. normal (Gaussian) distribution $x \sim N(\mu, \Sigma)$ or $N(x|\mu, \Sigma)$:





Continuous RV distributions (cont.)

•Multi dim. normal (Gaussian) distribution $x \sim N(\mu, \Sigma)$ or $N(x | \mu, \Sigma)$:

From 1-dim. \rightarrow 2-dim. case.

■1-dim. case:
$$p(x) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left(-\frac{(x-\mu)^2}{2\sigma^2}\right) = \frac{1}{(2\pi)^{1/2}\sigma} \exp\left(-\frac{(x-\mu)\sigma^{-2}(x-\mu)}{2}\right)$$

- A first extension to the 2-dim. case (independent rv's):
- $p(x_1, x_2) = p_1(x_1) \cdot p_2(x_2) =$

$$= \frac{1}{(2\pi)^{1/2} \cdot \sigma_1} \exp\left(-\frac{(x_1 - \mu_1)\sigma_1^{-2}(x_1 - \mu_1)}{2}\right) \cdot \frac{1}{(2\pi)^{1/2} \cdot \sigma_2} \exp\left(-\frac{(x_2 - \mu_2)\sigma_2^{-2}(x_2 - \mu_2)}{2}\right) =$$

$$\frac{1}{(2\pi)|\Sigma|^{1/2}} \exp\left(-\frac{(x-\mu)^T \Sigma^{-1}(x-\mu)}{2}\right)$$

$$x = \begin{bmatrix} x_1 \\ x_2 \end{bmatrix}, \mu = \begin{bmatrix} \mu_1 \\ \mu_2 \end{bmatrix}$$

$$\Sigma = \begin{bmatrix} \sigma_1^2 & \mathbf{0} \\ \mathbf{0} & \sigma_2^2 \end{bmatrix}$$

- The final extension to the 2-dim. case (dependent rv's): $x = \begin{bmatrix} x_1 \\ x_2 \end{bmatrix}, \mu = \begin{bmatrix} \mu_1 \\ \mu_2 \end{bmatrix}$ $\Sigma = \begin{bmatrix} \sigma_1^2 & \sigma_{12} \\ \sigma_{12} & \sigma_2^2 \end{bmatrix}$
- $p(x_1, x_2) = \frac{1}{(2\pi)^{|\Sigma|^{1/2}}} \exp\left(-\frac{(x-\mu)^T \Sigma^{-1} (x-\mu)}{2}\right)$

$$\Sigma = \begin{bmatrix} \sigma_1^2 & \sigma_{12} \\ \sigma_{12} & \sigma_2^2 \end{bmatrix}$$

•Multi dim. normal (Gaussian) distribution $x \sim N(\mu, \Sigma)$ or $N(x \mid \mu, \Sigma)$:

Properties

1. If the covariance matrix Σ is diagonal, then, the rv's $x_1, ..., x_l$ comprising x are statistically independent. It is

$$p(\mathbf{x}) = \prod_{i=1}^{l} p_i(x_i) = \prod_{i=1}^{l} \frac{1}{\sqrt{2\pi\sigma_i^2}} exp\left(-\frac{(x_i - \mu_i)^2}{2\sigma_i^2}\right)$$

2. Central limit theorem:

Let:

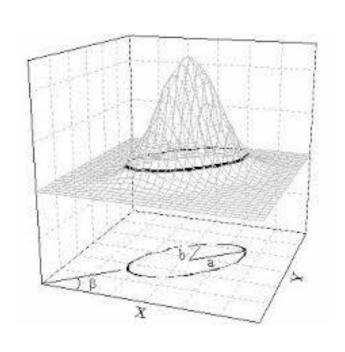
- $\mathbf{x_1}, \dots, \mathbf{x_r}$ independent rvs following different distributions
- • μ_i , σ_i^2 mean and variance of x_i .
- ■Define $\mathbf{x} = \mathbf{x}_1 + \dots + \mathbf{x}_r$, $\boldsymbol{\mu} = \mu_1 + \dots + \mu_r$, $\boldsymbol{\sigma}^2 = \sigma_1^2 + \dots + \sigma_r^2$.
- ■Define $\mathbf{z} = (\mathbf{x} \mu)/\sigma$.

Then

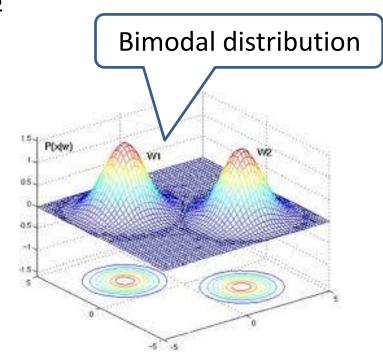
$$\mathbf{p}(z)$$
 → $N(z|0,1)$, as $r\to\infty$

Continuous RV distributions (cont.)

Other examples of multi-dimensional pdfs



Two-dim. pdfs



Likelihood function

- Let $X = \{x_1, x_2, ..., x_N\}$ a set of independent data vectors
- Let $p_{\theta}(\cdot)$ be a pdf belonging to a known parametric set of pdf functions of parameter vector $\boldsymbol{\theta}$.
- $p(\mathbf{x}) = p_{\theta}(\mathbf{x}) \equiv p(\mathbf{x}; \boldsymbol{\theta}).$

Examples:

- ightharpoonup If $p_{\theta}(x)$ is normal distribution parameterized on the mean vector μ , θ will simply be μ .
- ightharpoonup If $p_{\theta}(x)$ is normal distribution parameterized on both the <u>mean vector</u> μ and the <u>cov. matrix</u> Σ , θ will contain the coordinates of both μ and Σ .

Likelihood function of
$$\boldsymbol{\theta}$$
 wrt \boldsymbol{X} : $p(X;\boldsymbol{\theta}) = p(\boldsymbol{x}_1,...,\boldsymbol{x}_N;\boldsymbol{\theta}) = \prod_{i=1}^N p(\boldsymbol{x}_i;\boldsymbol{\theta})$

Log-likelihood function of θ wrt X:

$$L(\boldsymbol{\theta}) = \ln p(X; \boldsymbol{\theta}) = \ln p(\boldsymbol{x}_1, \dots, \boldsymbol{x}_N; \boldsymbol{\theta}) = \sum_{i=1}^{N} \ln p(\boldsymbol{x}_i; \boldsymbol{\theta})$$

Likelihood function

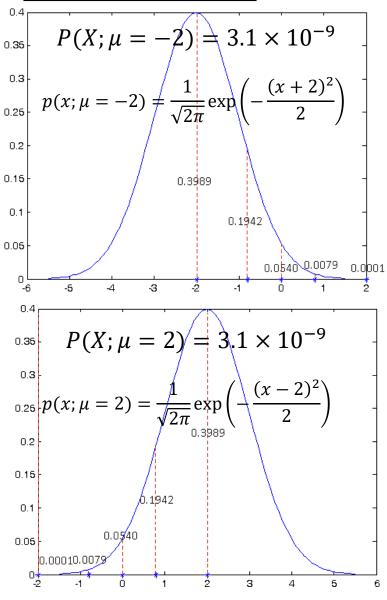
Example:

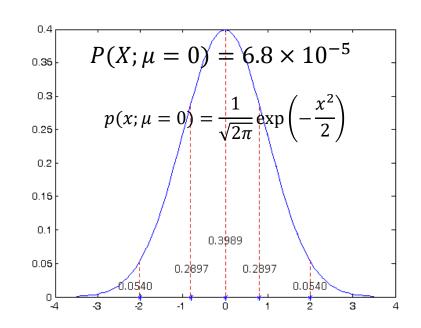
 $\bullet X = \{-2, -1, 0, 1, 2\}$

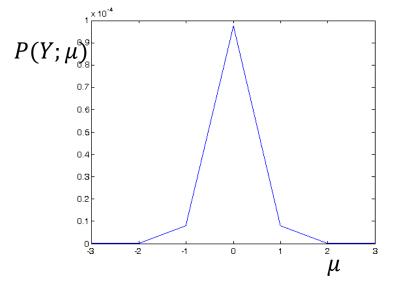
- $p(x) = \frac{1}{\sqrt{2\pi}} \exp(-\frac{(x-\mu)^2}{2})$
- •Consider the parametric set of normal distributions of unit variance, parameterized on μ .
- •The likelihood of μ wrt X is

$$p(X; \mu) = p(-2, -1, 0, 1, 2; \mu) = \frac{1}{\sqrt{2\pi}} \exp\left(-\frac{(-2-\mu)^2}{2}\right) \frac{1}{\sqrt{2\pi}} \exp\left(-\frac{(-1-\mu)^2}{2}\right) \frac{1}{\sqrt{2\pi}} \exp\left(-\frac{(0-\mu)^2}{2}\right) \frac{1}{\sqrt{2\pi}} \exp\left(-\frac{(1-\mu)^2}{2}\right) \frac{1}{\sqrt{2\pi}} \exp\left(-\frac{(2-\mu)^2}{2}\right)$$

Likelihood function







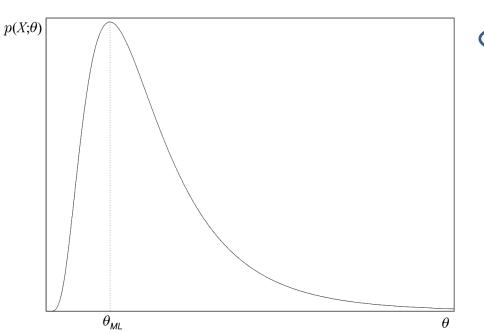
Probabilistic CFO clustering algorithms

Maximum likelihood (ML) method:

Given a set of independent data vectors $Y = \{x_1, x_2, ..., x_N\}$, estimate the parameter vector θ as the maximum of the likelihood $(p(Y; \theta))$ or the log-likelihood $(L(\theta))$ function.

$$\widehat{\boldsymbol{\theta}}_{ML} = argmax_{\boldsymbol{\theta}} \ p(Y; \boldsymbol{\theta}) \longrightarrow$$

$$\widehat{\boldsymbol{\theta}}_{ML} = \operatorname{argmax}_{\boldsymbol{\theta}} p(Y; \boldsymbol{\theta}) \rightarrow \widehat{\boldsymbol{\theta}}_{ML} : \frac{\partial L(\boldsymbol{\theta})}{\partial \boldsymbol{\theta}} = \sum_{\kappa=1}^{N} \frac{1}{p(\boldsymbol{x}_{k}; \boldsymbol{\theta})} \frac{\partial p(\boldsymbol{x}_{k}; \boldsymbol{\theta})}{\partial \boldsymbol{\theta}} = \mathbf{0}$$



Since In(·) is an increasing function, $p(Y; \theta)$ and $L(\theta)$ share the same maxima.

Probabilistic CFO clustering algorithms

Maximum likelihood (ML) method:

Assuming that

- the chosen model $p(x; \theta)$ is correct and
- there exists a true parameter θ_o ,

the ML estimator

- (a) is asymptotically unbiased $lim_{N\to\infty}E[\widehat{\boldsymbol{\theta}}_{ML}]=\boldsymbol{\theta}_o$
- (b) is asymptotically consistent $\lim_{N\to\infty} Prob\{\|\widehat{\boldsymbol{\theta}}_{ML} \boldsymbol{\theta}_o\|\} = 0$
- (c) is asymptotically efficient (it achieves the Cramer-Rao lower bound)

The **pdf** of the ML estimator approaches the normal distribution with mean θ_0 , as $N \rightarrow \infty$.

Maximum likelihood method

Example 1:

- -Let Y be a set of N (independent from each other) data points, \mathbf{x}_i , $i=1,\ldots,N$, generated by a normal distribution $p(\mathbf{x}; \boldsymbol{\theta})$ of known covariance matrix and unknown mean.
- -Determine the ML estimate of the mean μ of $p(x; \theta)$, based on Y.

Solution:

- -The unknown parameter vector in this case is the mean vector μ , i.e. $\theta \equiv \mu$.
- -It is

$$p(\mathbf{x}; \boldsymbol{\theta}) \equiv p(\mathbf{x}; \boldsymbol{\mu}) = \frac{1}{(2\pi)^{l/2} |\Sigma|^{1/2}} \cdot exp\left(-\frac{1}{2}(\mathbf{x} - \boldsymbol{\mu})^T \Sigma^{-1}(\mathbf{x} - \boldsymbol{\mu})\right) \Longrightarrow$$

$$\ln p(\mathbf{x}; \boldsymbol{\mu}) = \ln \frac{1}{(2\pi)^{l/2} |\Sigma|^{1/2}} - \frac{1}{2} (\mathbf{x} - \boldsymbol{\mu})^T \Sigma^{-1} (\mathbf{x} - \boldsymbol{\mu}) = C - \frac{1}{2} (\mathbf{x} - \boldsymbol{\mu})^T \Sigma^{-1} (\mathbf{x} - \boldsymbol{\mu})$$

Then

$$L(\boldsymbol{\mu}) = \sum_{i=1}^{N} \ln p(\boldsymbol{x}_i; \boldsymbol{\mu}) = NC - \frac{1}{2} \sum_{i=1}^{N} (\boldsymbol{x}_i - \boldsymbol{\mu})^T \Sigma^{-1} (\boldsymbol{x}_i - \boldsymbol{\mu})$$

Maximum likelihood method

Example 1 (cont.):

Setting the gradient of $L(\mu)$ wrt μ equal to 0 we have

$$\frac{\partial L(\boldsymbol{\mu})}{\partial \boldsymbol{\mu}} = \frac{\partial}{\partial \boldsymbol{\mu}} \left(NC - \frac{1}{2} \sum_{i=1}^{N} (\boldsymbol{x}_i - \boldsymbol{\mu})^T \Sigma^{-1} (\boldsymbol{x}_i - \boldsymbol{\mu}) \right) = \mathbf{0} \iff$$

$$\sum_{i=1}^{N} \Sigma^{-1}(x_i - \mu) = \mathbf{0} \Leftrightarrow \sum_{i=1}^{N} (x_i - \mu) = \mathbf{0} \Leftrightarrow \sum_{i=1}^{N} x_i - N\mu = \mathbf{0}$$

$$\mu_{ML} = \frac{1}{N} \sum_{i=1}^{N} x_i$$

Remark: The ML estimate for the covariance matrix is

$$\Sigma_{ML} = \frac{1}{N} \sum_{i=1}^{N} (\boldsymbol{x}_i - \boldsymbol{\mu}) (\boldsymbol{x}_i - \boldsymbol{\mu})^T$$