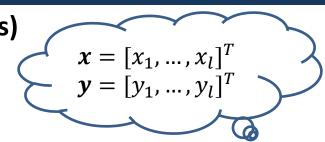
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Unit 3

- Proximity measures for mixed-valued vectors
- Fuzzy measures
- Missing data issue
- Short introduction to clustering algorithms
- Sequential clustering algorithms

(D) Mixed-valued vectors –similarity measures (SMs) Here some coordinates of the feature vectors are real-valued, while others are discrete-valued.



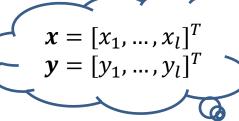
How to **measure** the proximity between x and y?

- Adopt a proximity measure suitable for real-valued vectors (only for ordinal discrete-valued features).
- Convert the real-valued features to discrete-valued ones (e.g., via quantization) and employ a discrete proximity measure (again, only for ordinal discrete-valued features).
- For the more general case where nominal, ordinal, interval-scaled and ratio-scaled features co-exist, we treat each one of them separately, as follows:

(D) Mixed-valued vectors –similarity measures (SMs)

The similarity between x and y is defined as:

$$s(x, y) = \frac{\sum_{k=1}^{l} s_k(x_k, y_k)}{\sum_{k=1}^{l} w_k}$$



where:

• $w_k = 0$, if at least one of x_k and y_k is undefined or (optionally) both x_k and y_k are equal to 0. Otherwise $w_k = 1$.

• If
$$x_k$$
 and y_k are binary, $s_k(x_k, y_k) = \begin{cases} 1, & if x_k = y_k = 1 \ (or \ x_k = y_k) \\ 0, & otherwise \end{cases}$

- If x_k and y_k are nominal or ordinal, $s_k(x_k, y_k) = \begin{cases} 1, & x_k = y_k \\ 0, & otherwise \end{cases}$
- If x_k and y_k are interval or ratio scaled-valued

$$s_k(x_k, y_k) = 1 - \frac{|x_k - y_k|}{r_k}$$
 measure. Other options can also be used.

This is the overlap can also be used.

where r_k is the width of the interval where the k-th coordinates of the vectors of X lie.

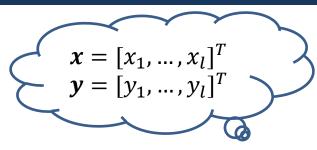
(D) Mixed-valued vectors –similarity measures (SMs)

Exercise 2: Consider the data set given in the following table. Each row corresponds to a vector and each column to a feature. The first three features are ratio scaled, the 4th one is nominal and the 5th one is ordinal. Utilizing the previous similarity measure, compute the similarities between any pair of feature vectors.

Company	1 st year budget	2 nd year budget	3 rd year budget	Activity abroad	Rate of services 0: not good 1: good 2: very good
1 (x ₁)	1.2	1.5	1.9	0	1
$2(x_2)$	0.3	0.4	0.6	0	0
$3(x_3)$	10	13	15	1	2
$4(x_4)$	6	6	7	1	1

Fuzzy measures – an alternative perspective

- Let $x \in [0,1]^l$.
- In this context, x_k is **not** the outcome of a measuring device.



- Rather, it **indicates** the degree to which x possesses the k-th characteristic.
- The closer the x_k to 1 (0), the **more likely** is that x possesses (does not possess) the k-th characteristic.
- As x_k approaches 0.5, the certainty about the possession or not of the *i*-th feature from x decreases.
- Let

$$\mathbf{x} = [x_1, x_2, ..., \mathbf{x}_k, ..., x_l]^T \in [0,1]^l$$

 $\mathbf{y} = [y_1, y_2, ..., \mathbf{y}_k, ..., y_l]^T \in [0,1]^l$

• A measure of similarity between x_k and y_k is the following $s(x_k, y_k) = \max(\min(1 - x_k, 1 - y_k), \min(x_k, y_k))$

Then, as measure of similarity between x and y we can use the following

$$s^{q}(\boldsymbol{x}, \boldsymbol{y}) = \left(\sum_{k=1}^{l} s(x_{k}, y_{k})^{q}\right)^{1/q}, q \in [1, +\infty)$$

Fuzzy measures – an alternative perspective

Exercise 3: Let l=3 and q=1.

- (a) Consider the vectors $\mathbf{x_1} = [1,1,1]^T$, $\mathbf{x_2} = [0,0,1]^T$, $\mathbf{x_3} = [\frac{1}{2},\frac{1}{3},\frac{1}{4}]^T$, $\mathbf{x_4} = [\frac{1}{2},\frac{1}{2},\frac{1}{2}]^T$. Determine the similarities $s^1(\mathbf{x_i},\mathbf{x_i})$, i = 1,2,3,4.
- (b) Consider the vectors $\mathbf{y_1} = [\frac{3}{4}, \frac{3}{4}, \frac{3}{4}]^T$, $\mathbf{y_2} = [1,1,1]^T$, $\mathbf{y_3} = [\frac{1}{4}, \frac{1}{4}, \frac{1}{4}]^T$, $\mathbf{y_4} = [\frac{1}{2}, \frac{1}{2}, \frac{1}{2}]^T$. Determine the similarities $s^1(\mathbf{y_i}, \mathbf{y_j})$, i, j = 1,2,3,4, $i \neq j$.
- (c) Draw your conclusions.

Dynamic similarity measures

- These are useful for cases where the two vectors to be compared have different lengths.
- Such a situation may arise e.g., when comparing two strings stemming from two different texts.
- A simple example: The Edit distance.

Proximity measures between vectors – Missing data

Missing data

- For some vectors of the data set X, some features values are unknown.
- This issue arises very often in practice.
- It may be caused by a measurement device failure, inability to take measure due to specific physical conditions etc.
- Ways to *deal with this situation*:
 - ✓ Discard all vectors with missing values (not recommended for small data sets).
 - ✓ Find the <u>mean value</u> m_k of the available k-th feature values over that data set and substitute the missing k-th feature values with m_k .

Proximity measures between vectors – Missing data

Missing data

- Ways to deal with this situation:
 - ✓ **Define** $b_k = 0$, if **both** the *k-th* features x_k , y_k are **available** and 1 **otherwise**. Then

$$\wp(\mathbf{x}, \mathbf{y}) = \frac{l}{l - \sum_{k=1}^{l} b_k} \sum_{\substack{k: b_k = 0}} \phi(x_k, y_k)$$

where $\phi(x_k, y_k)$ denotes the proximity measure between two scalars x_k , y_k .

NOTE: The proximity is **based** only on the features for which both x_k , y_k are available.

✓ For the k-th feature, k = 1, 2, ..., l, find the average proximity $\phi_{avg}(k)$ among all available values along the feature vectors in X. Then

$$\wp(\mathbf{x}, \mathbf{y}) = \sum_{k=1}^{l} \psi(x_k, y_k),$$

where
$$\psi(x_k, y_k) = \begin{cases} \phi(x_k, y_k), & \text{if both } x_k, y_k \text{ are available} \\ \phi_{avg}(k), & \text{otherwise} \end{cases}$$

Proximity measures between vectors – Missing data

Missing data

Exercise 4: Consider the data set $X = \{x_1, x_2, x_3, x_4, x_5\}$, with $x_1 = [0,0]^T, x_2 = [1,*]^T, x_3 = [0,*]^T, x_4 = [2,2]^T, x_5 = [3,1]^T$ ("*" stands for missing values).

- (a) Compute the l_1 distances between all pairs of vectors, using all the four techniques for dealing with missing data.
- **(b)** In which of these techniques, the computed distances are dependent on the specific data set?

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

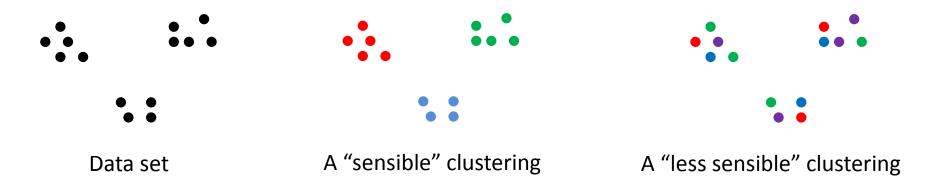
Examples:

- 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 (BSAS)

• $m = 1 \setminus \{\text{number of clusters}\}$ $X = \{x_1, \dots, x_N\} \longrightarrow$ $\bullet C_m = \{x_1\}$ • 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 (BSAS)

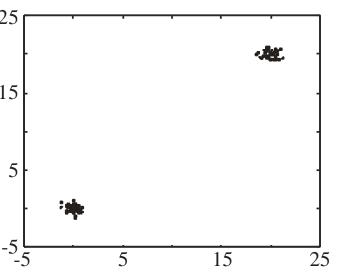
Remarks:

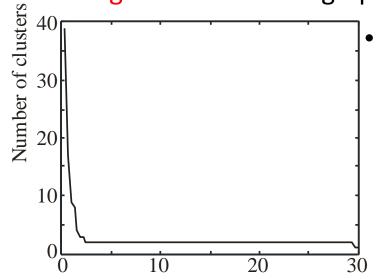
- The order of presentation of the data in the algorithm plays important role in the clustering results. Different order of presentation may lead to totally different clustering results, in terms of the number of clusters as well as the clusters themselves.
- The clustering results depend on the choice of the value of Θ .
- In BSAS the decision for a vector 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.

Basic Sequential Clustering Algorithm (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.





• Consider as final clustering, the clustering that results for the Θ in the middle of the widest flat region.

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).

- ullet In MBSAS, a decision for a vector $oldsymbol{x}$ 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

-Stop

End {if}

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The problem of closeness of clusters: "In all the above algorithms it may happen that two formed clusters lie very close to each other". (they may be parts of the same physical cluster)
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A simple merging procedure

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(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 \setminus \{M_1 \text{ is a user-defined threshold } \setminus \} —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)
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Refinement stages

The problem of sensitivity to the order of data presentation:

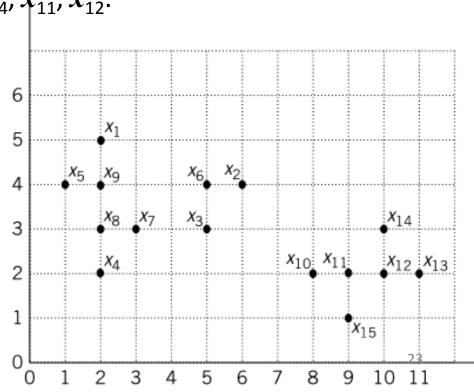
"A vector \underline{x} may have been assigned to a cluster C_i at the current stage but another cluster C_i may be formed at a later stage that lies closer to \underline{x} "

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 $C_j=\{x_i{\in}X\colon b(i)=j\}$ -If necessary, update representatives
- End {for}

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.



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 $\mathbf{m}_1 = [0, 0]^T$, $\mathbf{m}_2 = [4, 0]^T$, $m_3 = [0, 4]^T$, $m_4 = [5, 4]^T$, 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 $\Theta_{min}=0.25rac{d_{min}+d_{max}}{2}$, $\Theta_{max}=1.75rac{d_{min}+d_{max}}{2}$ and $s=rac{\Theta_{min}+\Theta_{max}}{n_{\Theta}}$, n_{Θ} is the number of successive values of Θ that will be considered. Use $n_{\Theta} = 50.$

24

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 ${\pmb m}_{tot}$ 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 $\{\theta_{min}, \theta_{min} + s, ..., \theta_{max}\}$ 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.