# Section 2 Unsupervised Learning: Hierarchical Clustering



Departament de Ciències Matemàtiques i Informàtica 11752 Aprendizaje Automático
11752 Machine Learning
Máster Universitario
en Sistemas Inteligentes

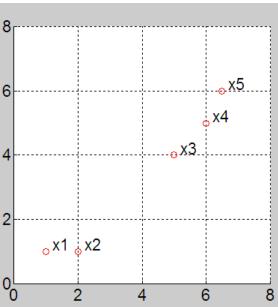
Alberto ORTIZ RODRÍGUEZ

#### Contents

- Introduction
- Agglomerative clustering
- Divisive clustering
- Selection of a good clustering

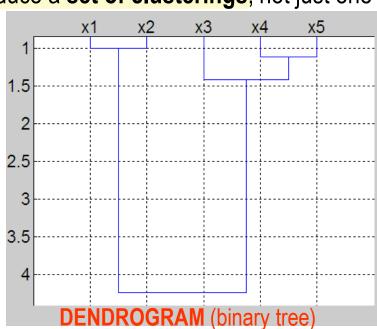
#### Introduction

Given a set of samples X, these algorithms produce a set of clusterings, not just one



 $R_0: \{x_1\}, \{x_2\}, \{x_3\}, \{x_4\}, \{x_5\}$   $R_1: \{x_1, x_2\}, \{x_3\}, \{x_4\}, \{x_5\}$   $R_2: \{x_1, x_2\}, \{x_3\}, \{x_4, x_5\}$   $R_3: \{x_1, x_2\}, \{x_3, x_4, x_5\}$   $R_4: \{x_1, x_2, x_3, x_4, x_5\}$ 

Actually, it is a hierarchy of clusterings, as they can be considered nested:  $R_0 \subset R_1 \subset R_2 \subset R_3 \subset R_4 \subset R_5$ 



- N samples ⇒ N-level hierarchy N execution steps
- Essentially, two sorts of hierarchical clustering algorithms:
  - **Agglomerative**  $\{x_1\}, \{x_2\}, \{x_3\}, \{x_4\}, \{x_5\} \rightarrow \{x_1, x_2, x_3, x_4, x_5\}$  (bottom-up process)
  - **Divisive**  $\{x_1, x_2, x_3, x_4, x_5\} \rightarrow \{x_1\}, \{x_2\}, \{x_3\}, \{x_4\}, \{x_5\}$  (top-down process)
  - both are just heuristic, not optimal, i.e. they do not optimize any objective function
  - a hierarchy of clusterings is produced even if there is no structure in the data

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#### Generic algorithm:

- (1)  $\mathcal{R}_0 = \{C_i = \{x_i\}, i = 1, \dots, N\}$
- (2) t = 0
- (3) repeat

(3.1) Choose the pair of clusters  $(C_r, C_s) \in \mathcal{R}_t \ (r \neq s)$  such that

$$\wp(C_r, C_s) = \begin{cases} \min_{i,j} \{\wp(C_i, C_j)\} & \text{$\wp$ is DM} \\ \max_{i,j} \{\wp(C_i, C_j)\} & \text{$\wp$ is SM} \end{cases}$$

(3.2) 
$$\mathcal{R}_{t+1} = (\mathcal{R}_t - \{C_r, C_s\}) \bigcup \{C_r \bigcup C_s\}$$

$$(3.3)$$
  $t = t + 1$ 

until all samples are in a single cluster

#### **OBSERVATIONS:**

- when two samples get in the same cluster, they keep together until the end
- there is no way to recover from a bad merge

• At the level **t**, there are **N-t** clusters, therefore, one has to analyze:

$$\binom{N-t}{2} = \frac{(N-t)!}{2!(N-t-2)!} = \frac{(N-t)(N-t-1)}{2}$$

clusters to find the best merge for level **t+1**.

 The number of merges which have to be considered up to the end of the process can be easily calculated:

$$\sum_{t=0}^{N-1} \binom{N-t}{2} = \sum_{k=1}^{N} \binom{k}{2} = \sum_{k=1}^{N} \frac{k(k-1)}{2} = \frac{1}{2} \left( \sum_{k=1}^{N} k^2 - \sum_{k=1}^{N} k \right)$$

$$= \frac{1}{2} \left( \frac{N(N-1)(2N-1)}{12} - \frac{N(N-1)}{2} \right)$$

$$= \frac{1}{2} \left( \frac{N(N-1)(2N-1)}{12} - \frac{N(N-1)}{2} \right)$$

$$\Rightarrow k = N - t = 1, 2, \dots, N$$

This gives an idea of the complexity of the process.

 From an implementation point of view, there are two main approaches of agglomerative clustering:



- based on matrix concepts
  - based on graph theory
  - We will consider the first approach. Some previous concepts first:
    - data matrix:

$$D(X) = \begin{bmatrix} x_{11} & x_{12} & \dots & x_{1L} \\ x_{21} & x_{22} & \dots & x_{2L} \\ \vdots & \vdots & & \vdots \\ x_{N1} & x_{N2} & \dots & x_{NL} \end{bmatrix} \begin{array}{c} x_1 \\ x_2 \\ \vdots \\ x_N \end{bmatrix}$$

• proximity matrix: (e.g. dissimilarity matrix) 
$$P(X) = \begin{bmatrix} \wp(x_1,x_1) & \wp(x_1,x_2) & \dots & \wp(x_1,x_N) \\ \wp(x_2,x_1) & \wp(x_2,x_2) & \dots & \wp(x_2,x_N) \\ \vdots & \vdots & & \vdots \\ \wp(x_N,x_1) & \wp(x_N,x_2) & \dots & \wp(x_N,x_N) \end{bmatrix}$$
 construction

#### **Example**:

• given X = 
$$\{x_1, x_2, x_3, x_4, x_5\}$$
 such that  $D(X) = \begin{bmatrix} 1 & 1 \\ 2 & 1 \\ 5 & 4 \\ 6 & 5 \\ 6.5 & 6 \end{bmatrix}$   $\sqrt{(5-1)^2 + (4-1)^2} = 5$ 

- [1] Using the Euclidean distance, the proximity matrix (dissimilarity) is  $P(X) = \begin{bmatrix} 0.00 & 1.00 & 5.00 & 6.40 & 7.43 \\ 1.00 & 0.00 & 4.24 & 5.66 & 6.73 \\ 5.00 & 4.24 & 0.00 & 1.41 & 2.50 \\ 6.40 & 5.66 & 1.41 & 0.00 & 1.12 \\ 7.43 & 6.73 & 2.50 & 1.12 & 0.00 \end{bmatrix}$ • [1] Using the Euclidean distance, the

• [2] Using the **Tanimoto measure**, the proximity matrix (**similarity**) is 
$$P(X) = \begin{bmatrix} 1.00 & 0.75 & 0.26 & 0.21 & 0.18 \\ 0.75 & 1.00 & 0.44 & 0.35 & 0.30 \\ 0.26 & 0.44 & 1.00 & 0.96 & 0.90 \\ 0.21 & 0.35 & 0.96 & 1.00 & 0.98 \\ 0.18 & 0.30 & 0.90 & 0.98 & 1.00 \end{bmatrix}$$

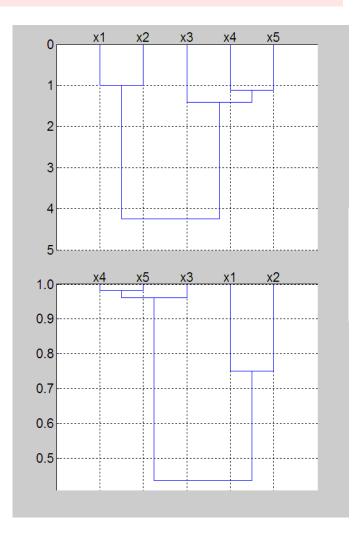
• Example: dendrograms for  $\wp(C_1,C_2)=\min/\max_{a\in C_1,b\in C_2}\wp(a,b)$ 

#### [1] proximity function: Euclidean distance (d<sub>2</sub>)

$$P(X) = \begin{bmatrix} 0.00 & 1.00 & 5.00 & 6.40 & 7.43 \\ 1.00 & 0.00 & 4.24 & 5.66 & 6.73 \\ 5.00 & 4.24 & 0.00 & 1.41 & 2.50 \\ 6.40 & 5.66 & 1.41 & 0.00 & 1.12 \\ 7.43 & 6.73 & 2.50 & 1.12 & 0.00 \end{bmatrix}$$

#### [2] proximity function: **Tanimoto similarity** $(s_T)$

$$P(X) = \begin{bmatrix} 1.00 & 0.75 & 0.26 & 0.21 & 0.18 \\ 0.75 & 1.00 & 0.44 & 0.35 & 0.30 \\ 0.26 & 0.44 & 1.00 & 0.96 & 0.90 \\ 0.21 & 0.35 & 0.96 & 1.00 & 0.98 \\ 0.18 & 0.30 & 0.90 & 0.98 & 1.00 \end{bmatrix}$$



## dissimilarity dendrogram

the sequence of mergings is different because

$$d_2 \neq 1 - s_T !!$$

similarity dendrogram

 $C_6 = \{x_1, x_2\}$ 

• **Example**: dendrogram for

$$\wp(C_1, C_2) = \min_{a \in C_1, b \in C_2} \wp(a, b)$$

$$P_0 = \begin{bmatrix} 0.00 & 1.00 & 5.00 & 6.40 & 7.43 \\ 1.00 & 0.00 & 4.24 & 5.66 & 6.73 \\ 5.00 & 4.24 & 0.00 & 1.41 & 2.50 \\ 6.40 & 5.66 & 1.41 & 0.00 & 1.12 \\ 7.43 & 6.73 & 2.50 & 1.12 & 0.00 \end{bmatrix}$$

$$P_1 = \begin{bmatrix} 0.00 & 1.00 & 5.00 & 6.40 & 7.43 & -- \\ 1.00 & 0.00 & 4.24 & 5.66 & 6.73 & -- \\ 5.00 & 4.24 & 0.00 & 1.41 & 2.50 & 4.24 \\ 6.40 & 5.66 & 1.41 & 0.00 & 1.12 & 5.66 \\ 7.43 & 6.73 & 2.50 & 1.12 & 0.00 & 6.73 \\ -- & -- & 4.24 & 5.66 & 6.73 & 0.00 \end{bmatrix}$$
(a)  $d(C_3, C_6)$  (b)  $d(C_4, C_6)$  (c)  $d(C_5, C_6)$ 

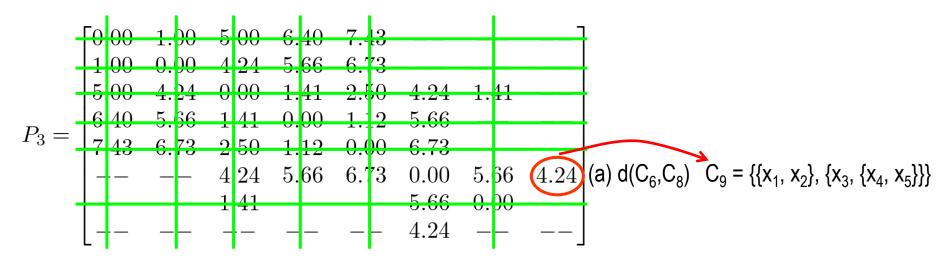
- (a) = min{d( $x_3, x_1$ )5.00, d( $x_3, x_2$ )4.24}
- (b) =  $\min\{d(x_4,x_1)6.40, d(x_4,x_2)5.66\}$
- (c) =  $\min\{d(x_5,x_1)7.43, d(x_5,x_2)6.73\}$



• Example: dendrogram for  $\wp(C_1,C_2)=\min_{a\in C_1,b\in C_2}\wp(a,b)$ 

(a) = 
$$\min\{d(x_3,x_4)1.41, d(x_3,x_5)2.50\}$$
  
(b) =  $\min\{d(x_1,x_4)6.40, d(x_1,x_5)7.43, d(x_2,x_4)5.66, d(x_2,x_5)6.73\}$ 

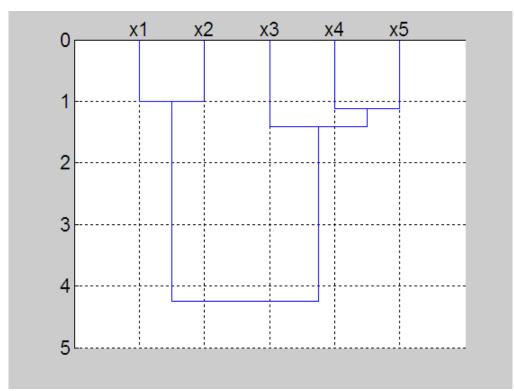
• Example: dendrogram for  $\wp(C_1,C_2)=\min_{a\in C_1,b\in C_2}\wp(a,b)$ 



(a) = min{d(
$$x_1, x_3$$
)5.00, d( $x_1, x_4$ )6.40, d( $x_1, x_5$ )7.43, d( $x_2, x_3$ )4.24, d( $x_2, x_4$ )5.66, d( $x_2, x_5$ )6.73}

• Example: dendrogram for  $\wp(C_1,C_2)=\min_{a\in C_1,b\in C_2}\wp(a,b)$ 

$$C_6 = \{x_1, x_2\} (1.00)$$
  
 $C_7 = \{x_4, x_5\} (1.12)$   
 $C_8 = \{x_3, \{x_4, x_5\}\} (1.41)$   
 $C_9 = \{\{x_1, x_2\}, \{x_3, \{x_4, x_5\}\}\} (4.24)$ 



- In this way, the clustering algorithm turns out to be as follows:
  - (1)  $\mathcal{R}_0 = \{C_i = \{x_i\}, i = 1, \dots, N\}$
  - (2) t = 0
  - (3) repetir
    - (3.1) Choose the pair of clusters  $(C_r, C_s) \in \mathcal{R}_t \ (r \neq s)$  such that:

$$P_t(r,s) = \begin{cases} \min_{i,j} P_t(i,j) & P_t \text{ is DM} \\ \max_{i,j} P_t(i,j) & P_t \text{ is SM} \end{cases}$$

- $(3.2) \mathcal{R}_{t+1} = (\mathcal{R}_t \{C_r, C_s\}) \bigcup \{C_r \bigcup C_s\}$
- (3.3) Calculate  $P_{t+1}$  from  $P_t$ :

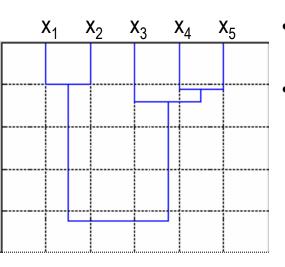
$$P_{t+1} = P_t$$

remove row and column r of  $P_{t+1}$ remove row and column s of  $P_{t+1}$ open new row and column  $P_{t+1}$  for  $C_q = \{C_r \bigcup C_s\}$ calculate  $P_{t+1}(\cdot, q)$  and  $P_{t+1}(q, \cdot)$ 

(3.4) t = t + 1

until all examples are in a single cluster

#### Additional remarks:



- (1)  $\mathcal{R}_0 = \{C_i = \{x_i\}, i = 1, \dots, N\}$
- (2) t = 0
- (3) repeat
  - (3.1) Choose the pair of clusters  $(C_r, C_s) \in \mathcal{R}_t \ (r \neq s)$  such that

$$\wp(C_r, C_s) = \begin{cases} \min_{i,j} \{\wp(C_i, C_j)\} & \text{$\wp$ is DM} \\ \max_{i,j} \{\wp(C_i, C_j)\} & \text{$\wp$ is SM} \end{cases}$$

- (3.2)  $\mathcal{R}_{t+1} = (\mathcal{R}_t \{C_r, C_s\}) \bigcup \{C_r \bigcup C_s\}$
- (3.3) t = t + 1

until all samples are in a single cluster

- the dendrogram strongly depends on the chosen proximity measure between clusters  $\wp(C_i, C_j)$
- the shape of the dendrogram itself indicates whether the clustering at a certain level is natural or not:
  - a great "jump" between levels suggests the existence of a non-natural merging
  - it is not necessary to build completely the dendrogram: one can stop at a certain level, before reaching a non-natural clustering, or when a certain number of clusters has been found
- regarding the adequateness of a merge, every step of the algorithm increases the **total variance of the clustering** E<sub>t</sub>, defined by:

$$E_t = \sum_{r \in \mathcal{R}_t} e_r^2$$
 [total variance of clustering  $\mathcal{R}_t$ ]

$$e_r^2 = \sum_{a \in C_r} \|a - \mu_r\|^2, \quad \mu_r = \frac{1}{n_r} \sum_{a \in C_r} a$$



- Increase of total variance from level t to level t+1:
  - Let us consider the merge between clusters C<sub>i</sub> and C<sub>i</sub> into cluster C<sub>q</sub> at level t+1
  - Then, the increment of total variance can be stated as:

$$\Delta E_{t+1}^{ij} = E_{t+1}^{ij} - E_t = \left(\sum_{r \neq q} e_r^2\right) + e_q^2 - \left(\left(\sum_{r \neq i, j} e_r^2\right) + e_i^2 + e_j^2\right) = e_q^2 - e_i^2 - e_j^2$$

– Taking into account that:

$$\begin{aligned} e_r^2 &= \sum_{a \in C_r} \|a - \mu_r\|^2 = \sum_{a \in C_r} (a - \mu_r)^T (a - \mu_r) \\ &= \sum_{a \in C_r} a^T a - 2 \sum_{a \in C_r} \mu_r^T a + \sum_{a \in C_r} \mu_r^T \mu_r \\ &= \sum_{a \in C_r} a^T a - 2 \mu_r^T (n_r \mu_r) + n_r (\mu_r^T \mu_r) \mathbf{1} \\ &= \sum_{a \in C_r} a^T a - n_r (\mu_r^T \mu_r) = \sum_{a \in C_r} \|a\|^2 - n_r \|\mu_r\|^2 \end{aligned}$$

- Increase of total variance from level t to level t+1:
  - Since  $C_{\alpha}$  is the merge of  $C_{i}$  and  $C_{i}$ , the increment of total variance is given by:

$$\Delta E_{t+1}^{ij} = \sum_{a \in C_q} ||a||^2 - n_q ||\mu_q||^2 - \left(\sum_{a \in C_i} ||a||^2 - n_i ||\mu_i||^2\right) - \left(\sum_{a \in C_j} ||a||^2 - n_j ||\mu_j||^2\right)$$
$$= n_i ||\mu_i||^2 + n_j ||\mu_j||^2 - n_q ||\mu_q||^2 = n_i (\mu_i^T \mu_i) + n_j (\mu_j^T \mu_j) - n_q (\mu_q^T \mu_q)$$

– Taking into account that:

$$n_q \mu_q = \sum_{a \in C_i} a + \sum_{b \in C_j} b = n_i \mu_i + n_j \mu_j \quad \text{and} \quad n_q = n_i + n_j$$

then we obtain:

$$\Delta E_{t+1}^{ij} = n_i(\mu_i^T \mu_i) + n_j(\mu_j^T \mu_j) - n_q \left(\frac{n_i}{n_q} \mu_i + \frac{n_j}{n_q} \mu_j\right)^T \left(\frac{n_i}{n_q} \mu_i + \frac{n_j}{n_q} \mu_j\right)$$

$$= \frac{n_i n_j}{n_i + n_j} \mu_i^T \mu_i + \frac{n_i n_j}{n_i + n_j} \mu_j^T \mu_j - 2 \frac{n_i n_j}{n_i + n_j} \mu_i^T \mu_j$$

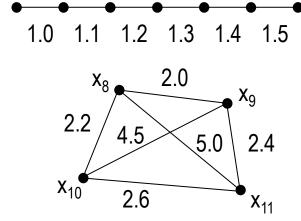
$$= \frac{n_i n_j}{n_i + n_j} (\mu_i - \mu_j)^T (\mu_i - \mu_j) = \boxed{\frac{n_i n_j}{n_i + n_j} \|\mu_i - \mu_j\|^2 = \Delta E_{t+1}^{ij} > 0}$$

- Agglomerative algorithms depending on the proximity function between clusters
  - Nearest neighbour (or single-link / single-linkage)
    - (3.1) Choose the pair of clusters  $(C_r, C_s) \in \mathcal{R}_t \ (r \neq s)$  such that:

$$\wp(C_r, C_s) = \begin{cases} \min_{i,j} \{\wp_{\min}(C_i, C_j) = \min_{a \in C_i, b \in C_j} \wp(a, b)\} & (\wp \text{ is DM}) \\ \max_{i,j} \{\wp_{\max}(C_i, C_j) = \max_{a \in C_i, b \in C_j} \wp(a, b)\} & (\wp \text{ is SM}) \end{cases}$$

favour elongated clusters (chain effect)

Example of application:





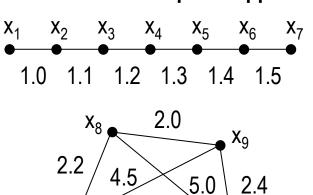
- Agglomerative algorithms depending on the proximity function between clusters
  - Farthest neighbour (or complete-link / complete-linkage)
    - (3.1) Choose the pair of clusters  $(C_r, C_s) \in \mathcal{R}_t \ (r \neq s)$  such that:

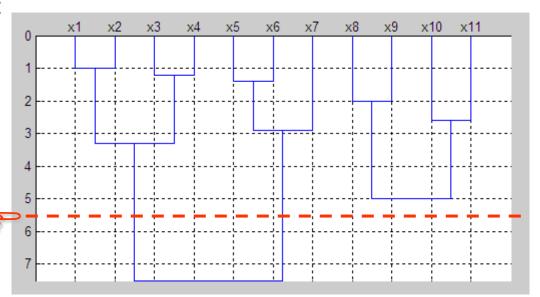
$$\wp(C_r, C_s) = \begin{cases} \min_{i,j} \{\wp_{\max}(C_i, C_j) = \max_{a \in C_i, b \in C_j} \wp(a, b)\} & (\wp \text{ is DM}) \\ \max_{i,j} \{\wp_{\min}(C_i, C_j) = \min_{a \in C_i, b \in C_j} \wp(a, b)\} & (\wp \text{ is SM}) \end{cases}$$

favour compact clusters (reduced diameter clusters)

• Example of application:

**X**<sub>11</sub>





 $X_{10}$ 

- Agglomerative algorithms depending on the proximity function between clusters
  - NN and FN algorithms are at the **opposite ends of the spectrum** of measures cluster-to-cluster  $\wp\left(C_i,\,C_i\right)$
  - Other algorithms, with intermediate behaviours, result for other distances: (3.1) Choose the pair of **clusters**  $(C_r, C_s) \in \mathcal{R}_t$   $(r \neq s)$  such that:

$$\wp(C_r, C_s) = \begin{cases} \min_{i,j} \{\wp(C_i, C_j)\} & (\wp \text{ is DM}) \\ \max_{i,j} \{\wp(C_i, C_j)\} & (\wp \text{ is SM}) \end{cases}$$

$$\wp_{\text{avg}}(C_i, C_j) = \frac{1}{n_i n_j} \sum_{a \in C_i} \sum_{b \in C_j} \wp(a, b) \quad (\text{average linkage alg.})$$

$$\wp_{\text{mean}}(C_i, C_j) = \wp(\mu_i, \mu_j)$$

$$\wp_{\text{ward}}(C_i, C_j) = \sqrt{\frac{n_i n_j}{n_i + n_j}} \wp(\mu_i, \mu_j)$$

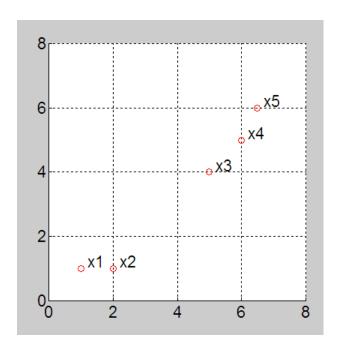
- Agglomerative algorithms depending on the proximity function between clusters
  - In particular:

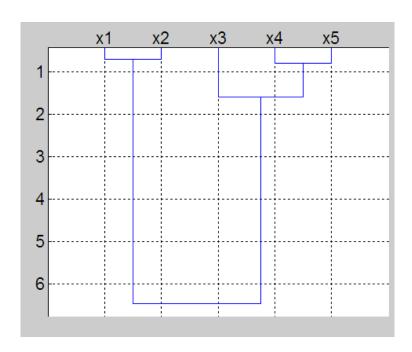
$$\wp_{\text{ward}}(C_i, C_j) = \sqrt{\frac{n_i n_j}{n_i + n_j}} \wp(\mu_i, \mu_j)$$

leads to the minimum total variance increase between steps if  $\wp(\mu_i, \mu_j) = ||\mu_i - \mu_j||$ :

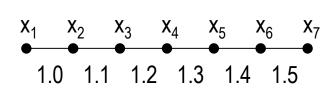
- The algorithm chooses the pair of clusters that minimize  $\sqrt{rac{n_i n_j}{n_i + n_j}} \|\mu_i \mu_j\|$  and we have already seen that  $\Delta E_{t+1}^{ij} = rac{n_i n_j}{n_i + n_i} \|\mu_i \mu_j\|^2$ .
- Because of this, this algorithm is termed algorithm (of agglomerative hierarchical clustering) of minimum variance.
- At a practical level, this algorithm **favours the fusion of small clusters with large clusters** against fusing large or medium-size *clusters*, because of the involvement of cluster sizes in the proximity measure.

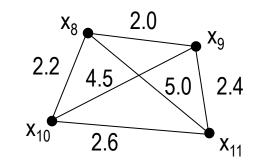
- Agglomerative algorithms depending on the proximity function between clusters
  - Example (of Ward distance use):

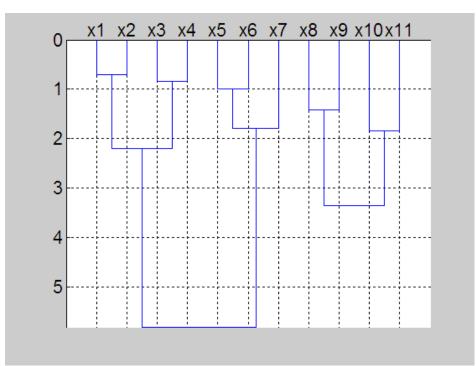




- Agglomerative algorithms depending on the proximity function between clusters
  - Example (of Ward distance use):







 In clear cases (compact and well separated clusters), all alternatives lead to the same results. Differences appear for extreme cases.

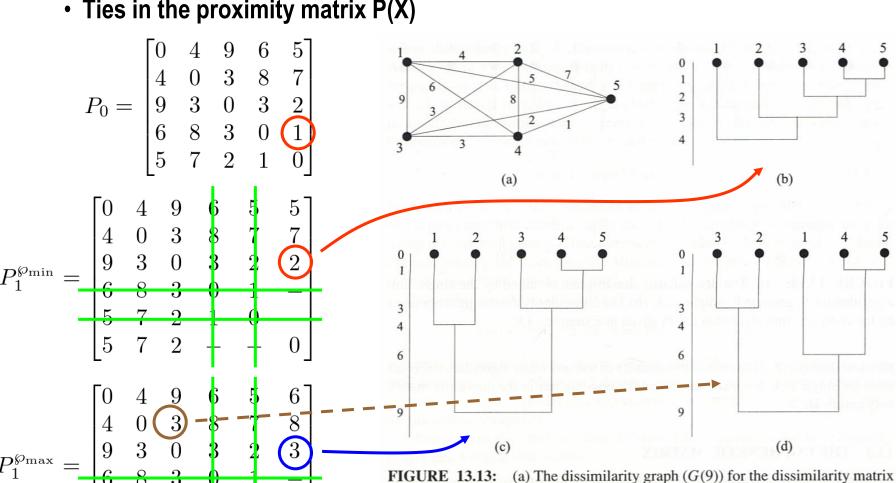
#### Monotonicity

- If the clustering algorithm selects clusters  $C_i$  y  $C_j$  to build a new cluster  $C_q$  so that  $d(C_q, C_k)$  ≥  $d(C_i, C_j)$ ,  $\forall k \neq i$ , j, q, then the resulting dendrogram is said to be **monotonous**
- If monotonicity holds, clusters are created at higher dissimilarity levels than its constituents



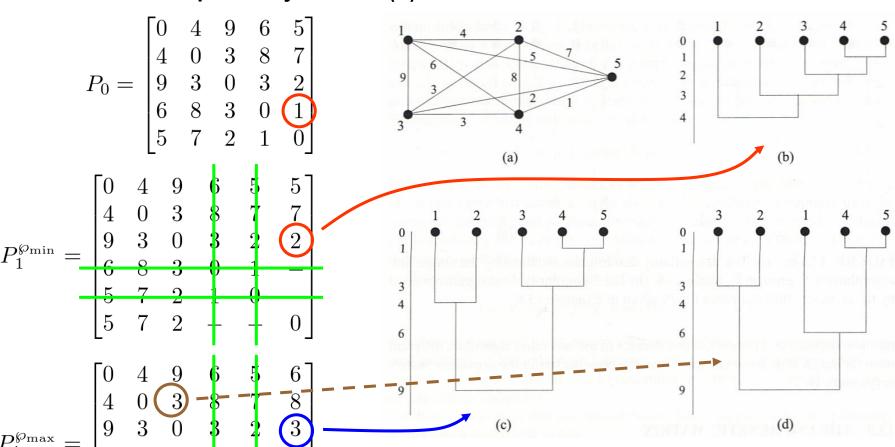
- $\wp_{\min}$ ,  $\wp_{\max}$ ,  $\wp_{\text{avg}}$  and  $\wp_{\text{ward}}$  can be proved to always give rise to monotonous dendrograms.
- Monotonicity has been considered to be necessary for a clustering algorithm to be useful.

#### Ties in the proximity matrix P(X)



given in Example 13.8. (b) The dissimilarity dendrogram obtained by the single link algorithm. (c) The dissimilarity dendrogram obtained by the complete link algorithm when edge (3, 4) is considered first. (d) The dissimilarity dendrogram obtained by the complete link algorithm when edge (2, 3) is considered first.

#### Ties in the proximity matrix P(X)



• All agglomerative algorithms are more or less affected by this defect, although the **nearest neighbour algorithm** seems to be the least affected.

Alberto Ortiz / EPS (last update 11/01/2024)

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#### **Divisive Clustering**

#### • Generic algorithm:

- (1)  $\mathcal{R}_0 = \{X\}$
- (2) t = 0
- (3) repeat
  - (3.1) for all clusters  $C_q$  of  $\mathcal{R}_t$ :

Find  $C_r^q$  and  $C_s^q$  s.t.  $C_q = C_r^q \bigcup C_s^q$ ,  $C_r^q \cap C_s^q = \emptyset$  and

$$\wp(C_r^q, C_s^q) = \begin{cases} \max_{i,j} \{\wp(C_i, C_j)\} & (\wp \text{ is DM}) \\ \min_{i,j} \{\wp(C_i, C_j)\} & (\wp \text{ is SM}) \end{cases}$$

end

(3.2) Find the cluster  $C_{q*}$  whose splitting is the best

$$(3.3) \mathcal{R}_{t+1} = (\mathcal{R}_t - \{C_{q*}\}) \bigcup \{C_r^{q*}, C_s^{q*}\}$$

$$(3.4)$$
  $t = t + 1$ 

until all samples are in a different cluster

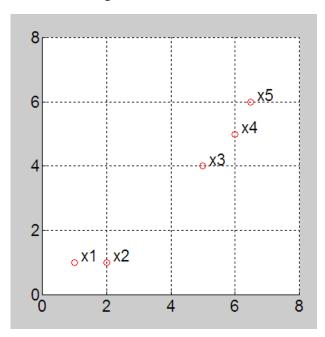
- Very high cost at the computational level
- Different alternatives available, which try to reduce the cost of (3.1)

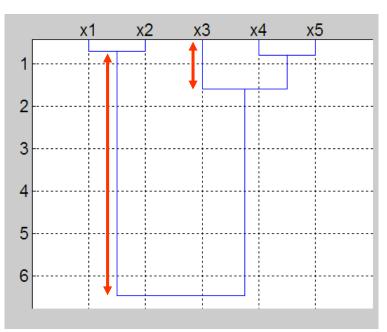
#### Contents

- Introduction
- Agglomerative clustering
- Divisive clustering
- Selection of a good clustering

## Selection of a good clustering (in the hierarchy)

- We turn our attention to the determination of a good clustering within a given hierarchy. This can help to identify the natural structure of the data.
- 1. Find in the dendrogram clusters with a long lifetime:
  - lifetime of a cluster = absolute diference between the proximity level at which a cluster is generated and the level at which it is absorbed

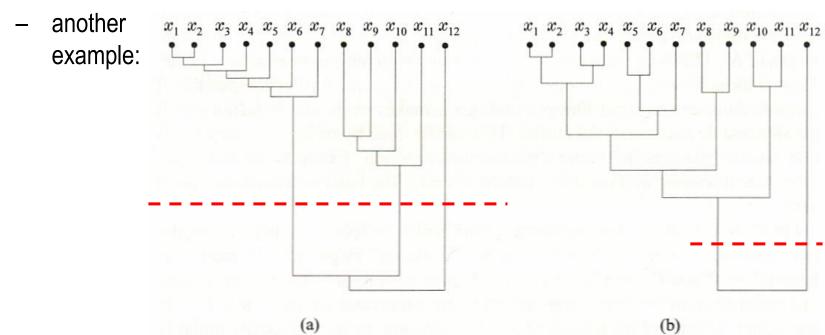




 $\Rightarrow$  final clustering should be:  $\{x_1, x_2\}, \{x_3, x_4, x_5\}$ 

#### Selection of best clustering

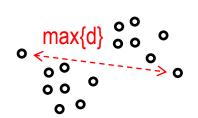
- 1. Find in the dendrogram clusters with a **long lifetime**:
  - lifetime of a cluster = absolute difference between the proximity level at which a cluster is generated and the level at which it is absorbed



## Selection of best clustering

#### 2. Stop before a low-quality cluster results:

Determine the disimilarity within a cluster by means of an appropriate measure **h**. Several possibilities:



$$\max\{d\} \circ \circ \circ \circ \qquad h_1(C) = \max\{d(x,y), \ x,y \in C\} \qquad -\text{diameter of C}$$
 
$$h_2(C) = \max\{d(x,y), \ x,y \in C\} \qquad -\text{robust to outliers}$$
 
$$h_3(C) = \frac{2}{n_C(n_C-1)} \sum_{x \neq y \in C} d(x,y)$$

 In this way, every time a cluster is going to be created, one can check its internal dissimilarity and decide not to create it if it is above a threshold  $\tau$ , and the process is stopped:

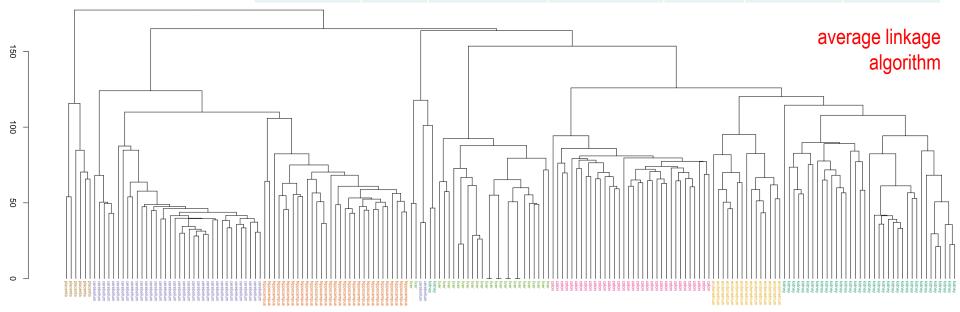
$$C_q = C_i \bigcup C_j \in \mathcal{R}_{t+1} : h(C_q) > \tau \Rightarrow \text{ STOP at level } t$$

- It is usually useful to define  $\tau = \mu + \lambda \sigma$ , where  $\mu$  is the average distance among elements of X and  $\sigma$  is the standard deviation.
- Typically, it is easier to set  $\lambda$  than  $\tau$ .

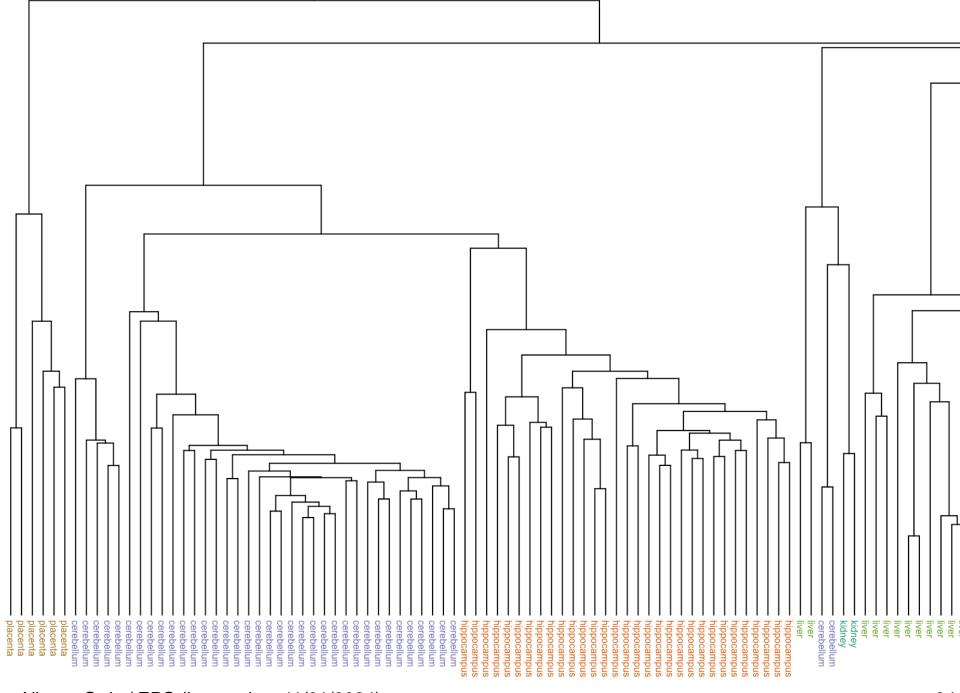
#### Example

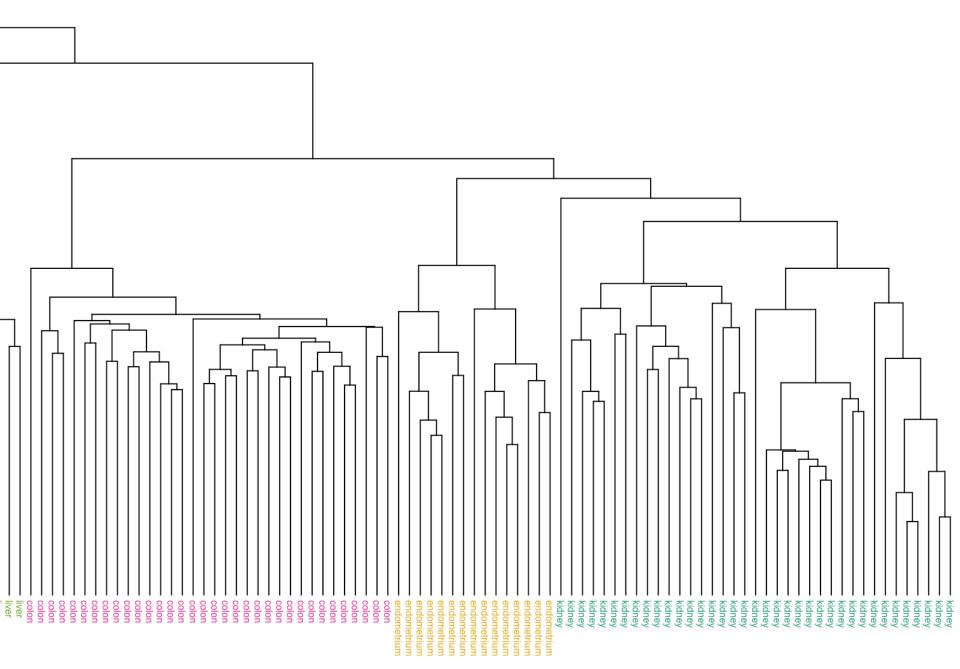
- <u>Example</u>: gene expression profiling of human tissues
  - Each row is a gene expression profile and each column is a different gene. The column names are the gene symbols. The outcome is a character vector representing the tissue.
  - Subset of the original dataset comprising 22.215 samples
  - 189 samples chosen at random, with L = 500

-	7 tissues:	cerebellum	colon	endometrium	hippocampus	kidney	liver	placenta
	189 =	38	34	15	31	39	26	6



source: https://github.com/genomicsclass/tissuesGeneExpression

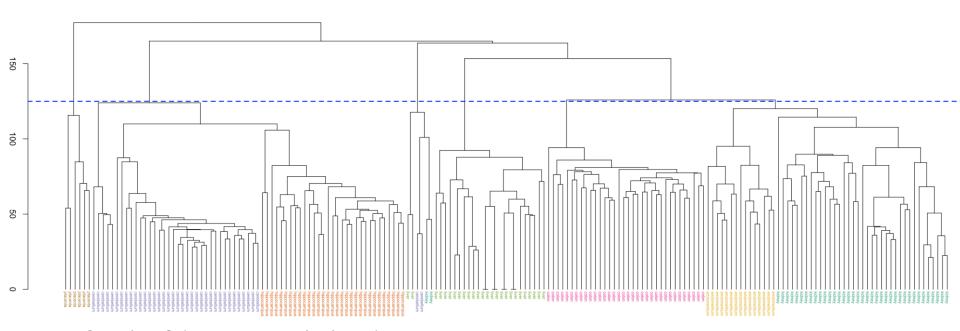




#### Example

## "Cutting" the dendrogram cluster tissue 6 at height = 125: 1.cerebellum 36 ## 2.colon 34 3.endometrium 15 contingency table → 4.hippocampus (or contingency matrix) 5.kidney 37 6.liver 24 2

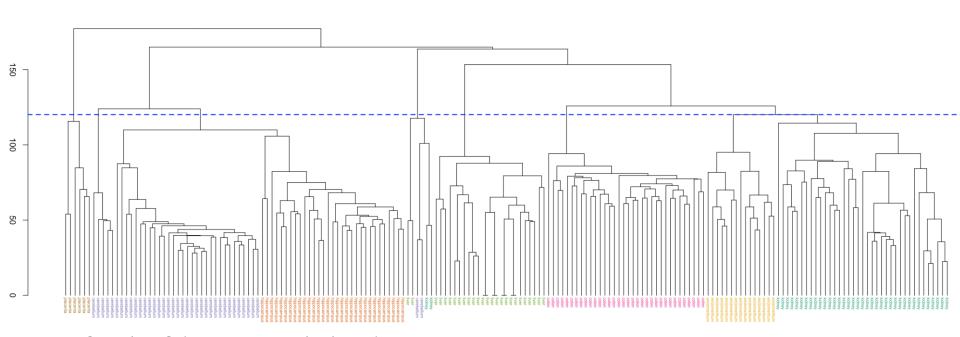
7.placenta



#### Example

 "Cutting" the dendrogram so as to have 8 clusters:

```
##
                            cluster
   tissue
                                          8
  1.cerebellum
                     31
##
  2.colon
                      0
                        34
   3.endometrium
                                  15
   4.hippocampus
   5.kidney
                  37
   6.liver
                            24
  7.placenta
```



# Section 2 Unsupervised Learning: Hierarchical Clustering



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