# **Clustering algorithms** Konstantinos Koutroumbas

# <u>Unit 8</u>

- Hierarchical clustering algorithms
  - \* Matrix theory-based
  - \* Graph theory-based

### Agglomerative Clustering Algorithms

According to the mathematical tools used for their expression, **agglomerative algorithms** are divided into:

- Algorithms based on matrix theory.
- Algorithms based on graph theory.

**NOTE:** In the sequel we consider only dissimilarity measures.

- > Algorithms based on matrix theory.
  - They take as input the  $N \times N$  dissimilarity matrix  $P_0 = P(X)$ .
  - At each level *t* where two clusters  $C_i$  and  $C_j$  are merged to  $C_q$ , the dissimilarity matrix  $P_t$  is extracted from  $P_{t-1}$  by:
    - -Deleting the two rows and columns of  $P_t$  that correspond to  $C_i$  and  $C_i$ .
    - -Adding a new row and a new column that contain the distances of newly formed  $C_q = C_i \cup C_j$  from each of the remaining clusters  $C_s$ , via a relation of the form

$$d(C_q, C_s) = f(d(C_i, C_s), d(C_j, C_s), d(C_i, C_j))$$

•A number of distance functions comply with the following update equation  $C_q = C_i \cup C_j$ 

 $d(C_q, C_s) = a_i d(C_i, C_s) + a_j (d(C_j, C_s) + bd(C_i, C_j) + c |d(C_i, C_s) - d(C_j, C_s)|$ (1)
Algorithms that follow the above equation are:

Single link (SL) algorithm ( $a_i = 1/2$ ,  $a_j = 1/2$ , b = 0, c = -1/2). In this case

 $d(C_q, C_s) = \min\{d(C_i, C_s), d(C_j, C_s)\}$  (2)

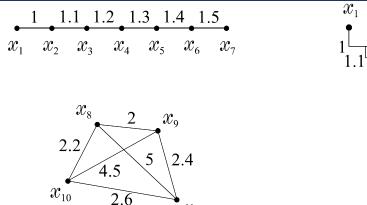
Complete link (CL) algorithm ( $a_i = 1/2$ ,  $a_j = 1/2$ , b = 0, c = 1/2). In this case

$$d(C_q, C_s) = \max\{d(C_i, C_s), d(C_j, C_s)\}$$

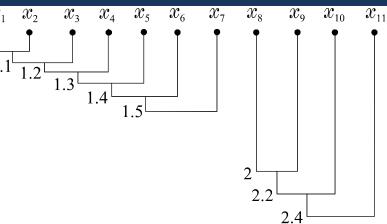
#### **Remarks:**

- Single link forms clusters at low dissimilarities while complete link forms clusters at high dissimilarities.
- Single link tends to form elongated clusters (*chaining effect* ) while complete link tends to form compact clusters.
- The rest algorithms are compromises between these two extremes.

**Example:** 



 $x_{11}$ 



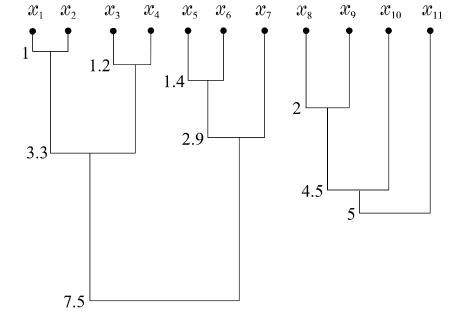


(b)

(a) The data set X.

(b) The single link algorithm dissimilarity dendrogram.

(c) The complete link algorithm dissimilarity dendrogram.



(c)

Weighted Pair Group Method Average (WPGMA)  $(a_i = 1/2, a_j = 1/2, b = 0, c = 0)$ . In this case:  $d(C_q, C_s) = a_i d(C_i, C_s) + a_j (d(C_j, C_s) + bd(C_i, C_j) + c|d(C_i, C_s) - d(C_j, C_s)|$   $d(C_q, C_s) = \frac{1}{2} (d(C_i, C_s) + d(C_j, C_s))$ 

➢ Unweighted Pair Group Method Average (UPGMA) ( $a_i = n_i/(n_i + n_j), a_j = n_j/(n_i + n_j), b = 0, c = 0$ , where  $n_i$  is the cardinality of  $C_i$ ). In this case:

$$d(C_q, C_s) = \frac{n_i}{n_i + n_j} d(C_i, C_s) + \frac{n_j}{n_i + n_j} d(C_j, C_s)$$

➢ Unweighted Pair Group Method Centroid (UPGMC) ( $a_i = n_i/(n_i + n_j)$ ,  $a_j = n_j/(n_i + n_j)$ ,  $b = -n_i n_j/(n_i + n_j)^2$ , c = 0). In this case:

$$d_{qs} = \frac{n_i}{n_i + n_j} d_{is} + \frac{n_j}{n_i + n_j} d_{js} - \frac{n_i n_j}{(n_i + n_j)^2} d_{ij}$$

For the UPGMC, if  $d_{ij}$  is defined as the squared Euclidean distance between the means of  $C_i$  and  $C_j$ , then it holds that  $d_{qs} = ||m_q - m_s||^2$ , where  $m_q$ ,  $m_s$  are the means of  $C_q$ ,  $C_s$ , respectively.

> Weighted Pair Group Method Centroid (WPGMC) ( $a_i = 1/2, a_j = 1/2, b =$ 

$$-1/4, c = 0$$
. In this case  

$$d_{qs} = \frac{1}{2}d_{is} + \frac{1}{2}d_{js} - \frac{1}{4}d_{ij}$$

$$d_{qs} = \frac{1}{2}d_{is} + \frac{1}{2}d_{js} - \frac{1}{4}d_{ij}$$

For WPGMC there are cases where  $d_{qs} \le \max\{d_{is}, d_{js}\}$  (crossover)

Ward or minimum variance algorithm. Here the distance d'<sub>ij</sub> between C<sub>i</sub> and C<sub>j</sub> is defined as

$$d'_{ij} = \frac{n_i n_j}{n_i + n_j} ||\boldsymbol{m}_i - \boldsymbol{m}_j||^2$$
 (3)

 $d'_{qs} \text{ can be expressed in terms of } d'_{is}, d'_{js}, d'_{ij} \text{ as}$  $d'_{qs} = \frac{n_i + n_s}{n_i + n_j + n_s} d'_{is} + \frac{n_j + n_s}{n_i + n_j + n_s} d'_{js} - \frac{n_s}{n_i + n_j + n_s} d'_{ij}$ 

**Remark:** Ward's algorithm forms  $\Re_{t+1}$  by merging the two clusters that lead to the smallest possible increase of the total variance, i.e.,

$$E_t = \sum_{r=1}^{N-t} \sum_{x \in C_r} ||x - m_r||^2$$

**Example 3:** Consider the following dissimilarity matrix (Euclidean

distance)  

$$P_{0} = \begin{bmatrix} 0 & 1 & 2 & 26 & 37 \\ 1 & 0 & 3 & 25 & 36 \\ 2 & 3 & 0 & 16 & 25 \\ 26 & 25 & 16 & 0 & 1.5 \\ 37 & 36 & 25 & 1.5 & 0 \end{bmatrix}$$

 $\begin{aligned} &\mathcal{R}_{0} = \{ \{ \underline{x}_{1} \}, \{ \underline{x}_{2} \}, \{ \underline{x}_{3} \}, \{ \underline{x}_{4} \}, \{ \underline{x}_{5} \} \}, \\ &\mathcal{R}_{1} = \{ \{ \underline{x}_{1}, \underline{x}_{2} \}, \{ \underline{x}_{3} \}, \{ \underline{x}_{4} \}, \{ \underline{x}_{5} \} \}, \\ &\mathcal{R}_{2} = \{ \{ \underline{x}_{1}, \underline{x}_{2} \}, \{ \underline{x}_{3} \}, \{ \underline{x}_{4}, \underline{x}_{5} \} \}, \\ &\mathcal{R}_{3} = \{ \{ \underline{x}_{1}, \underline{x}_{2}, \underline{x}_{3} \}, \{ \underline{x}_{4}, \underline{x}_{5} \} \}, \\ &\mathcal{R}_{4} = \{ \{ \underline{x}_{1}, \underline{x}_{2}, \underline{x}_{3}, \underline{x}_{4}, \underline{x}_{5} \} \} \end{aligned}$ 

All the algorithms produce the same sequence of clusterings shown above, yet at different proximity levels:

	SL	CL	WPGMA	UPGMA	WPGMC	UPGMC	Ward
$\mathscr{R}_0$	0	0	0	0	0	0	0
$\mathscr{R}_1$	1	1	1	1	1	1	0.5
$\mathscr{R}_2$	1.5	1.5	1.5	1.5	1.5	1.5	0.75
$\Re_3$	2	3	2.5	2.5	2.25	2.25	1.5
$\mathscr{R}_4$	16	37	25.75	27.5	24.69	26.46	31.75

# **Example 3** (in detail): (a) The single-link case

 $(C_q = C_i \cup C_j, d(C_q, C_s) = \min(d(C_i, C_s), d(C_j, C_s))$ 

		{ <b>x</b> <sub>1</sub> }	$\{x_2\}$	$\{x_3\}$	$\{x_4\}$	${x_5}$			${x_1}$	${x_2}$	${x_3}$	$\{x_4\}$	${x_5}$
<i>P</i> <sub>0</sub> :	${x_1}$	0	1	2	26	37		{ <b>x</b> <sub>1</sub> }	0	1	2	26	37
	${x_2}$	1	0	3	25			${x_2}$	1	0	3	25	36
	${x_3}$	2	3	0	16	25	≽	{ <b>x</b> <sub>3</sub> }	2	3	0	16	25
	${x_4}$	26	25	16	0	1.5		${x_4}$	26	25	16	0	1.5
	${x_5}$	37	36	25	1.5	0		${x_5}$	37	36	25	1.5	0

 $d(\{x_1, x_2\}, \{x_3\}) = \min(d(\{x_1\}, \{x_3\}), d(\{x_2\}, \{x_3\})) = \min(2,3) = 2$ 

 $\frac{d(\{x_1, x_2\}, \{x_4\})}{\min(26, 25)} = 25$ 

 $\frac{d(\{x_1, x_2\}, \{x_5\})}{\min(37, 36)} = 36$ 

				~						d	l({ <b>x</b>
		$\{x_1, x_2\}$	${x_3}$	$\{x_4\}$	${x_5}$		$\{x_1, x_2\}$	${x_3}$	$\{x_4\}$	${x_5}$	m
	$\{x_1, x_2\}$	0	2	25	36	$\{x_1, x_2\}$	0	2	25	36	d(· m
<i>P</i> <sub>1</sub> :	$\{x_3\}$	2	0	16	25	${x_3}$	2	0	16	25	
	$\{\boldsymbol{x}_4\}$	25	16	0	1.5	$\{\boldsymbol{x}_4\}$	25	16	0	1.5	
	$\{x_{5}\}$	36	25	1.5	0	$\{x_{5}\}$	36	25	1.5	0	

 $d(\{x_1, x_2\}, \{x_4, x_5\}) = min(25, 36) = 25$  $d(\{x_3\}, \{x_4, x_5\}) =$ 

min(16,25) = 16

**Example 3 (in detail): (a)** The single-link case  $(C_q = C_i \cup C_j, d(C_q, C_s) = \min(d(C_i, C_s), d(C_j, C_s))$ 

		$\{x_1, x_2\}$	${x_3}$	$\{x_4, x_5\}$		$\{x_1, x_2\}$	${x_3}$	$\{x_4, x_5\}$
<b>D</b> .	$\{x_1, x_2\}$	0	2	25	$\{x_1, x_2\}$	0	2	25
12.	$\{x_1, x_2\}$ $\{x_3\}$	2	0	16	$\{x_3\}$	2	0	16
	$\{x_4, x_5\}$	25	16	0	$\{x_4, x_5\}$	25	16	0

 $d(\{x_1, x_2, x_3\}, \{x_4, x_5\}) = \min(25, 16) = 16$ 

		$\{x_1, x_2, x_3\}$	$\{x_4, x_5\}$			$\{x_1, x_2, x_3\}$	$\{x_4, x_5\}$
<i>P</i> <sub>3</sub> :	$\{x_1, x_2, x_3\}$	0	16	≽	$\{x_1, x_2, x_3\}$	0	16
	$\{x_4, x_5\}$	16	0		$\{x_4, x_5\}$	16	0

$P_4$ :		$\{x_1, x_2, x_3, x_4, x_5\}$
1	$\{x_1, x_2, x_3, x_4, x_5\}$	0

 $\mathcal{R}_{0} = \{ \{ \underline{x}_{1} \}, \{ \underline{x}_{2} \}, \{ \underline{x}_{3} \}, \{ \underline{x}_{4} \}, \{ \underline{x}_{5} \} \}, (\mathbf{0})$  $\mathcal{R}_{1} = \{ \{ \underline{x}_{1}, \underline{x}_{2} \}, \{ \underline{x}_{3} \}, \{ \underline{x}_{4} \}, \{ \underline{x}_{5} \} \}, (\mathbf{1})$  $\mathcal{R}_{2} = \{ \{ \underline{x}_{1}, \underline{x}_{2} \}, \{ \underline{x}_{3} \}, \{ \underline{x}_{4}, \underline{x}_{5} \} \}, (\mathbf{1}, \mathbf{5})$  $\mathcal{R}_{3} = \{ \{ \underline{x}_{1}, \underline{x}_{2}, \underline{x}_{3} \}, \{ \underline{x}_{4}, \underline{x}_{5} \} \}, (\mathbf{2})$  $\mathcal{R}_{4} = \{ \{ \underline{x}_{1}, \underline{x}_{2}, \underline{x}_{3}, \underline{x}_{4}, \underline{x}_{5} \} \}, (\mathbf{16})$ 

**Example 3 (in detail): (b)** The complete-link case  $(C_q = C_i \cup C_i, d(C_q, C_s) = \max(d(C_i, C_s), d(C_i, C_s))$ 

		$\{x_1\}$	$\{x_2\}$	$\{x_3\}$	${x_4}$	${x_5}$			${x_1}$	${x_{2}}$	$\{x_3\}$	${x_4}$	${x_5}$	
	${x_1}$	0	1	2	26	37		${x_1}$	0	1	2	26	37	
р	${x_2}$	1	0		25			${x_2}$			3	25	36	
0.	${x_3}$	2	3	0	16	25	≽	${x_3}$	2	3	0	16	25	
	${x_4}$	26	25	16	0	1.5		${x_4}$	26	25	16	0	1.5	
	${x_5}$	37	36	25	1.5	0		${x_5}$	37	36	25	1.5	0	

 $d(\{x_1, x_2\}, \{x_3\}) = \max(d(\{x_1\}, \{x_3\}), d(\{x_2\}, \{x_3\})) = \max(2,3) = 3$ 

 $d(\{x_1, x_2\}, \{x_4\}) = max(26, 25) = 26$ 

 $\frac{d(\{x_1, x_2\}, \{x_5\})}{\max(37, 36)} = 37$ 

 $\{x_1, x_2\}$  $\{\boldsymbol{x}_3\}$  $\{x_4\} | \{x_5\}$  $\{x_1, x_2\}$  $\{x_4\} | \{x_5\}$  $\{x_3\}$  $\{x_1, x_2\}$ 26 37  $\{x_1, x_2\}$ 37 0 3 3 26 0 *P*<sub>1</sub>:  $\{x_3\}$ 3 16 25  $\{x_3\}$ 3 25 0 0 16  $\{x_4\}$ 1.5 26 16 0 26 16 0 1.5  $\{\boldsymbol{x}_4\}$ 0  $\{x_{5}\}$ 25 1.5  ${x_5}$ 37 25 1.5 0 37

 $d(\{x_1, x_2\}, \{x_4, x_5\}) = \max(26, 37) = 37$ 

 $d(\{x_3\}, \{x_4, x_5\}) = max(16, 25) = 25$ 

**Example 3 (in detail): (b)** The complete-link case  $(C_q = C_i \cup C_j, d(C_q, C_s) = \max(d(C_i, C_s), d(C_j, C_s))$ 

		$\{x_1, x_2\}$	${x_3}$	$\{x_4, x_5\}$			$\{x_1, x_2\}$	${x_3}$	$\{x_4, x_5\}$
D.	$\{x_1, x_2\}$	0	3	37	~	$\{x_1, x_2\}$	0	3	37
12	$\{x_1, x_2\}$ $\{x_3\}$	0 <b>3</b>	0	25		${x_3}$	3	0	25
	$\{x_4, x_5\}$	37	25	0		$\{x_4, x_5\}$	37	25	0

 $d(\{x_1, x_2, x_3\}, \{x_4, x_5\}) = \max(37, 25) = 37$ 

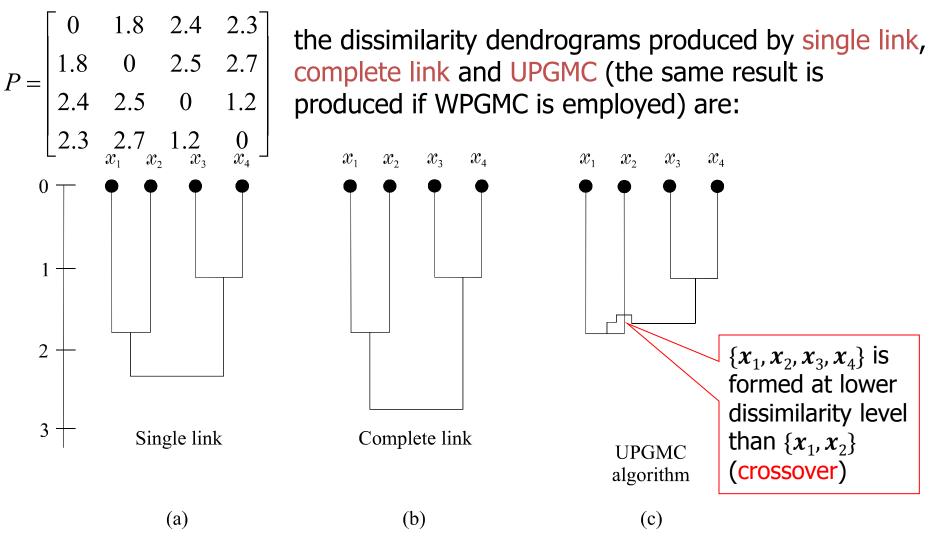
		$\{x_1, x_2, x_3\}$	$\{x_4, x_5\}$		$\{x_1, x_2, x_3\}$	$\{x_4, x_5\}$
<i>P</i> <sub>3</sub> :	$\{x_1, x_2, x_3\}$			$\{x_1, x_2, x_3\}$	0	37
	$\{x_4, x_5\}$	37	0	$\{x_4, x_5\}$	37	0

$P_4$ :		$\{x_1, x_2, x_3, x_4, x_5\}$
1	$\{x_1, x_2, x_3, x_4, x_5\}$	0

 $\mathcal{R}_{0} = \{ \{ \underline{x}_{1} \}, \{ \underline{x}_{2} \}, \{ \underline{x}_{3} \}, \{ \underline{x}_{4} \}, \{ \underline{x}_{5} \} \}, (\mathbf{0})$  $\mathcal{R}_{1} = \{ \{ \underline{x}_{1}, \underline{x}_{2} \}, \{ \underline{x}_{3} \}, \{ \underline{x}_{4} \}, \{ \underline{x}_{5} \} \}, (\mathbf{1})$  $\mathcal{R}_{2} = \{ \{ \underline{x}_{1}, \underline{x}_{2} \}, \{ \underline{x}_{3} \}, \{ \underline{x}_{4}, \underline{x}_{5} \} \}, (\mathbf{1}, \mathbf{5})$  $\mathcal{R}_{3} = \{ \{ \underline{x}_{1}, \underline{x}_{2}, \underline{x}_{3} \}, \{ \underline{x}_{4}, \underline{x}_{5} \} \}, (\mathbf{3})$  $\mathcal{R}_{4} = \{ \{ \underline{x}_{1}, \underline{x}_{2}, \underline{x}_{3}, \underline{x}_{4}, \underline{x}_{5} \} \}, (\mathbf{37})$ 

#### Monotonicity and crossover:

For the following dissimilarity matrix



 $\{x_1\}$ 

0

1.8

2.05

 ${x_2} {x_3, x_4}$ 

1.8

0

2.3

2.05

2.3

0

#### **Example (in detail):** The WPGMC case

$$(C_q = C_i \cup C_j, d_{qs} = \frac{1}{2}d_{is} + \frac{1}{2}d_{js} - \frac{1}{4}d_{ij})$$

 $\{x_2\}$   $\{x_3, x_4\}$ 

1.8

0

2.3

2.05

2.3

0

 ${x_1}$ 

0

1.8

2.05

 ${x_1}$ 

 $\{x_{2}\}$ 

 $\{x_3, x_4\}$ 

 $P_1$ :

		{ <i>x</i> <sub>1</sub> }	${x_2}$	$\{x_3\}$	$\{x_4\}$			${x_1}$	$\{x_2\}$	$\{x_3\}$	$\{x_4\}$
	${x_1}$	0	1.8	2.4	2.3		${x_1}$	0	1.8	2.4	2.3
<i>P</i> <sub>0</sub> :	${x_2}$	1.8	0	2.5	2.7	≽	${x_2}$	1.8	0	2.5	2.7
	${x_3}$	2.4	2.5	0	1.2		${x_3}$	2.4	2.5	0	1.2
	${x_4}$	2.3	2.7	1.2	0		$\{x_4\}$	2.3	2.7	1.2	0

$$d_{(3,4),1} = \frac{1}{2}d_{3,1} + \frac{1}{2}d_{4,1} - \frac{1}{4}d_{3,4}$$
  
=  $\frac{1}{2}2.4 + \frac{1}{2}2.3 - \frac{1}{4}1.2 = 2.05$   
$$d_{(3,4),2} = \frac{1}{2}d_{3,2} + \frac{1}{2}d_{4,2} - \frac{1}{4}d_{3,4}$$
  
=  $\frac{1}{2}2.5 + \frac{1}{2}2.7 - \frac{1}{4}1.2 = 2.3$ 

 $\mathcal{R}_0 = \{\{\underline{x}_1\}, \{\underline{x}_2\}, \{\underline{x}_3\}, \{\underline{x}_4\}\}, (\mathbf{0})$  $\mathcal{R}_{1} = \{ \{ \underline{x}_{1} \}, \{ \underline{x}_{2} \}, \{ \underline{x}_{3}, \underline{x}_{4} \} \}, (\mathbf{1}, \mathbf{2})$  $\Re_2 = \{ \{ \underline{x}_1, \underline{x}_2 \}, \{ \underline{x}_3, \underline{x}_4 \} \}, (1.8)$  $\Re_3 = \{ \{ \underline{x}_1, \underline{x}_2, \underline{x}_3, \underline{x}_4 \} \}, (1.275 \text{ !!})$ 

 $d_{(1,2),(3,4)} = \frac{1}{2}d_{1,(3,4)} + \frac{1}{2}d_{2,(3,4)} - \frac{1}{4}d_{1,2}$  $+\frac{1}{2}2.3 - \frac{1}{4}1.8 = 1.275$ 

ת		$\{x_1, x_2\}$	$\{x_3, x_4\}$		=	$=\frac{1}{2}2.05+\frac{1}{2}2.3-\frac{1}{2}$
<i>P</i> <sub>2</sub> :	$\{x_1, x_2\}$	0	1.275			
	$\{x_3, x_4\}$	1.275	0	$\rightarrow P_3$ :		$\{x_1, x_2, x_3, x_4\}$
				* 3 *	$\{x_1, x_2, x_3, x_4\}$	0

 ${x_1}$ 

 ${x_2}$ 

 $\{x_3, x_4\}$ 

#### Monotonicity condition:

If clusters  $C_i$  and  $C_j$  are selected to be merged in cluster  $C_q$ , at the *t*th level of the hierarchy, the condition

 $d(C_q, C_k) \ge d(C_i, C_j)$ 

must hold for all  $C_k$ ,  $k \neq i, j, q$ .

In other words, the monotonicity condition implies that a clustering is formed at higher dissimilarity level than any of its components.

#### **Remarks:**

- Monotonicity is a property that is exclusively related to the clustering algorithm and not to the (initial) proximity matrix.
- An algorithm that does not satisfy the monotonicity condition, does not necessarily produce dendrograms with crossovers.
- Single link, complete link, UPGMA, WPGMA and the Ward's algorithm satisfy the monotonicity condition, while UPGMC and WPGMC do not satisfy it.

#### Complexity issues:

- GAS requires, in general,  $O(N^3)$  operations.
- More efficient implementations require  $O(N^2 \log N)$  computational time.
- For a class of widely used algorithms, implementations that require  $O(N^2)$  computational time and  $O(N^2)$  or O(N) storage have also been proposed.
- Parallel implementations on SIMD machines have also been considered.

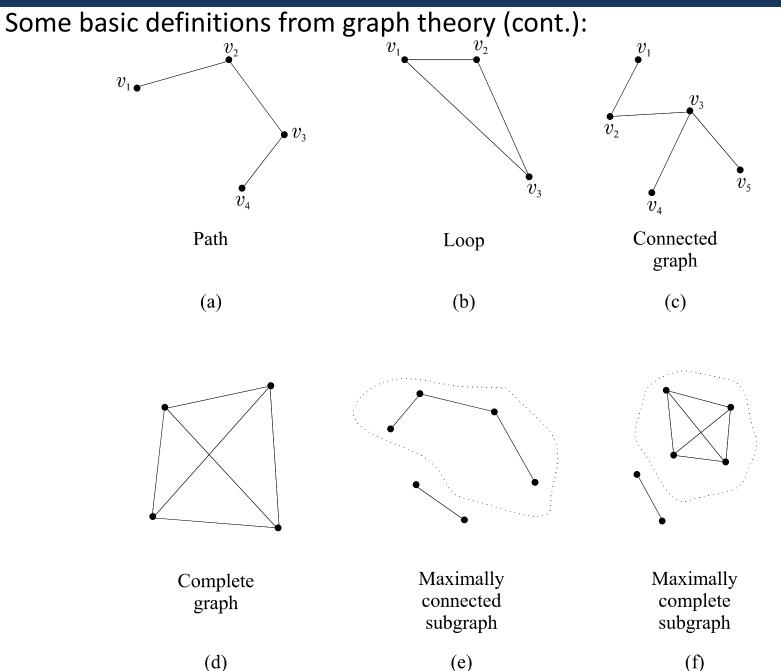
Some basic definitions from graph theory:

- A graph, G, is defined as an ordered pair G = (V, E), where  $V = \{v_i, i = 1, ..., N\}$  is a set of vertices and E is a set of edges connecting some pairs of vertices. An edge connecting  $v_i$  and  $v_j$  is denoted by  $e_{ij}$  or  $(v_i, v_j)$ .
- A graph is called undirected if there is no direction assigned to any of its edges. Otherwise, we deal with directed graphs.
- A graph is called unweighted if there is no cost associated with any of its edges. Otherwise, we deal with weighted graphs.
- A path in G between vertices  $v_{i_1}$  and  $v_{i_n}$  is a sequence of vertices and edges of the form  $v_{i_1}e_{i_1i_2}v_{i_2} \dots v_{i_{n-1}}e_{i_{n-1}i_n}v_{i_n}$ .
- A loop in G is a path where  $v_{i_1}$  and  $v_{i_n}$  coincide.
- A subgraph G' = (V', E') of G = (V, E) is a graph with  $V' \subseteq V$  and  $E' \subseteq E_1$ , where  $E_1$  is a subset of E containing edges that connect vertices of V'. Every graph is a subgraph to itself.

Some basic definitions from graph theory (cont.):

- A connected subgraph G' = (V', E') is a subgraph where there exists at least one path connecting any pair of vertices in V'.
- A complete subgraph G' = (V', E') is a subgraph where for any pair of vertices in V' there exists an edge in E' connecting them.
- A maximally connected subgraph of G is a connected subgraph G' of G that contains as many vertices of G as possible.
- A maximally complete subgraph of G is a complete subgraph G' of G that contains as many vertices of G as possible.

Examples for the above, are shown in the following figure.

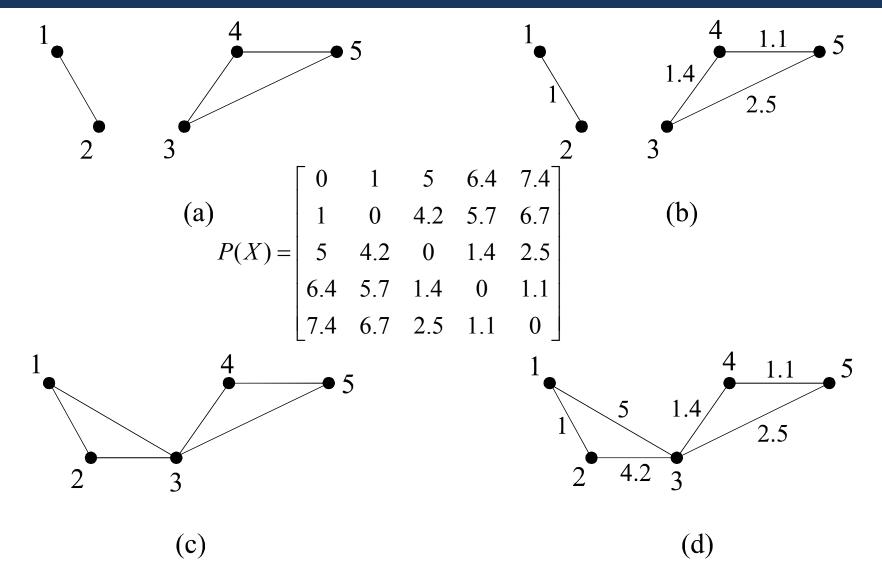


**NOTE:** In the framework of clustering, each vertex of a graph corresponds to a feature vector.

Useful **tools** for the algorithms based on graph theory are the threshold graph and the proximity graph.

- •A threshold graph G(a) (a is the threshold parameter)
- -is an undirected, unweighted graph with N nodes, each one corresponding to a vector of X.
- -No self-loops or multiple edges between any two vertices are encountered.
- -The set of edges of G(a) contains those edges  $(v_i, v_j)$  for which the distance  $d(x_i, x_j)$  between the vectors corresponding to  $v_i$  and  $v_j$  is less than or equal to a.

•A proximity graph  $G_p(a)$  is a threshold graph G(a), all of whose edges  $(v_i, v_j)$  are weighted with the proximity measure  $d(x_i, x_j)$ .



(a) The threshold graph G(3), (b) the proximity (dissimilarity) graph  $G_p(3)$ , (c) the threshold graph G(5), (d) the dissimilarity graph  $G_p(5)$ , for the dissimilarity matrix P(X) shown above.

More definitions:

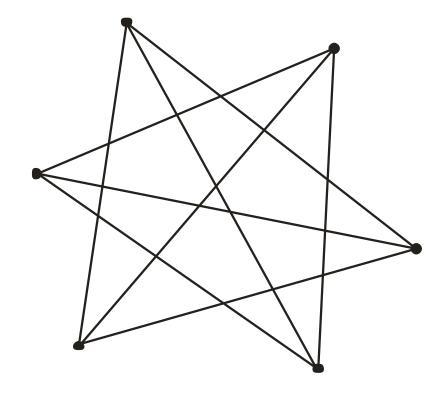
- In this framework, we consider graphs *G*, of *N* nodes, where each node corresponds to a vector of *X*.
- Valid clusters are connected components of G that satisfy an additional graph property h(k).

Typical graph properties for a connected component (subgraph) G' of G are:

•Node connectivity: The largest integer k such that all pairs of nodes of G' are joined by at least k paths having no nodes in common.

•Edge connectivity: The largest integer k such that all pairs of nodes are joined by at least k paths having no edges in common.

•Node degree: The largest integer k such that each node has at least k incident edges.



- Node connectivity : 3
- Edge connectivity : 3
- Node degree : 3

- Proximity function in the graph theory framework
  - The **proximity function**  $g_{h(k)}(C_r, C_s)$  between two clusters is **defined** in terms of
  - -a proximity measure between vectors (nodes)
  - -certain constraints imposed by property h(k) on the subgraphs that are formed.

In mathematical language:

 $g_{h(k)}(C_r, C_s) =$  $min \sum_{x_u \in C_r, x_v \in C_s} \begin{cases} d(x_u, x_v) \equiv a : the G(a) subgraph defined by C_r \cup C_s is \\ (a) connected and either (b1) has the property h(k) or (b2) is complete \end{cases}$ (4)

or

 $g_{h(k)}(C_r, C_s)$  equals to the smallest possible value *a* such that in the G(a) subgraph defined by  $C_r \cup C_s$  is (a) connected and either (b1) has the property h(k) or (b2) is complete.

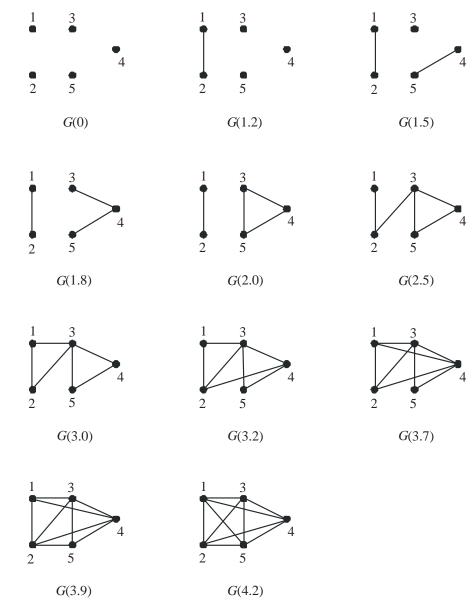
Example: For the dissimilarity matrix,

$$P = \begin{bmatrix} 0 & 1.2 & 3 & 3.7 & 4.2 \\ 1.2 & 0 & 2.5 & 3.2 & 3.9 \\ 3 & 2.5 & 0 & 1.8 & 2.0 \\ 3.7 & 3.2 & 1.8 & 0 & 1.5 \\ 4.2 & 3.9 & 2.0 & 1.5 & 0 \end{bmatrix}$$

all possible G(a) graphs are shown next.

Assuming that h(2) is the node connectivity property, it is

 $\begin{array}{l} g_h(\{x_1\},\{x_2\}) = 1.2 \text{ (complete)} \\ g_h(\{x_1\},\{x_5\}) = 4.2 \text{ (complete)} \\ g_h(\{x_1,x_2\},\{x_3\}) = 3 \text{ (compl.-}h(2) \text{ )} \\ g_h(\{x_1,x_2\},\{x_3,x_5\}) = 3.9 \text{ (}h(2)\text{ )} \end{array}$ 



Graph theory-based algorithmic scheme (GTAS): It is the GAS in the context of graph theory. In the context of GTAS, the definition of the proximity between the clusters is based on graph theory concepts. Thus

Generalized Agglomerative Scheme (GAS)

- Initialization
  - Choose  $\Re_0 = \{\{x_1\}, \dots, \{x_N\}\}$
  - t = 0
- Repeat
  - t = t + 1
  - **Choose**  $(C_i, C_j)$  in  $\Re_{t-1}$  such that

 $g_{h(k)}(C_i, C_j) = \begin{cases} \min_{r,s} g_{h(k)}(C_r, C_s), & \text{for disim. functions} \\ \max_{r,s} g_{h(k)}(C_r, C_s), & \text{for sim. functions} \end{cases}$ 

- Define  $C_q = C_i \cup C_j$  and produce  $\Re_t = (\Re_{t-1} \{C_i, C_j\}) \cup \{C_q\}$
- Until all vectors lie in a single cluster.

• Single link (SL) algorithm. Here

 $g_{h(k)}(C_r, C_s) = \min_{x_u \in C_r, x_v \in C_s} \{d(x_u, x_v) \equiv a: the G(a) subgraph defined by C_r \cup C_s is connected\} \\ \equiv \min_{x \in C_r, y \in C_s} d(x, y) \text{ (why?)}$ 

#### • Remarks:

- -No property h(k) or completeness is required.
- -The SL stemming from the graph theory is exactly the same with the SL stemming from the matrix theory.
- Complete link (CL) algorithm. Here

 $g_{h(k)}(C_r, C_s) = \min_{x_u \in C_r, x_v \in C_s} \{d(x_u, x_v) \equiv a: the G(a) subgraph defined by C_r \cup C_s is complete \} \\ \equiv \max_{x \in C_r, y \in C_s} d(x, y) \text{ (why?)}$ 

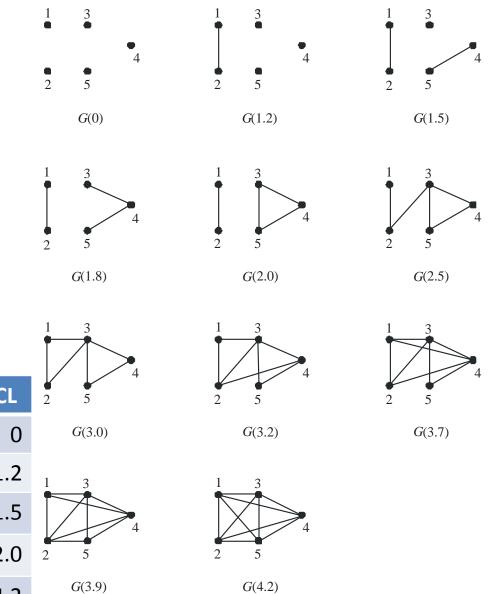
- Remarks:
- -No property h(k) is required.
- -The CL stemming from graph theory is exactly the same with the CL stemming from matrix theory.

Example: For the dissimilarity matrix,

$$P = \begin{bmatrix} 0 & 1.2 & 3 & 3.7 & 4.2 \\ 1.2 & 0 & 2.5 & 3.2 & 3.9 \\ 3 & 2.5 & 0 & 1.8 & 2.0 \\ 3.7 & 3.2 & 1.8 & 0 & 1.5 \\ 4.2 & 3.9 & 2.0 & 1.5 & 0 \end{bmatrix}$$

SL and CL produce the same hierarchy of clusterings at the levels given in the table.

Clustering	SL	CL	2 5 4
$\mathfrak{R}_0 = \{\{\boldsymbol{x}_1\}, \{\boldsymbol{x}_2\}, \{\boldsymbol{x}_3\}, \{\boldsymbol{x}_4\}, \{\boldsymbol{x}_5\}\}$		0	
$\Re_1 = \{\{x_1, x_2\}, \{x_3\}, \{x_4\}, \{x_5\}\}$		1.2	
$\mathfrak{R}_{2} = \{\{x_{1}, x_{2}\}, \{x_{3}\}, \{x_{4}, x_{5}\}\}$	1.5	1.5	
$\Re_3 = \{\{x_1, x_2\}, \{x_3, x_4, x_5\}\}$	1.8	2.0	2 5
$\Re_4 = \{\{x_1, x_2, x_3, x_4, x_5\}\}$	2.5	4.2	<i>G</i> (3.9)



#### **Remarks:**

- SL poses the weakest possible graph condition (connectivity) for the formation of a cluster, while CL poses the strongest possible graph condition (completeness) for the formation of a cluster.
- A variety of graph theory-based algorithms, that lie between these two extremes result for various choices of h(k).
  - -For k = 1 all these algorithms collapse to the single link algorithm.
  - -As k increases, the resulting subgraphs approach completeness.

#### <u>Clustering algorithms based on the Minimum Spanning Tree (MST)</u> Definitions:

Spanning Tree: It is a connected graph (containing all the vertices of the graph), with no loops (only one path connects any two vertices).

- Weight of a Spanning Tree: The sum of the weights of its edges (provided a weight has been assigned to each one of them).
- Minimum Spanning Tree (MST): A spanning tree with the smallest weight among the spanning trees connecting all the vertices of the graph.

#### **Remarks:**

- The MST has N 1 edges.
- When all the weights are different from each other, the MST is unique.
   Otherwise, it may not be unique.
- > Employing the GTAS and substituting  $g_{h(k)}(C_r, C_s)$  with

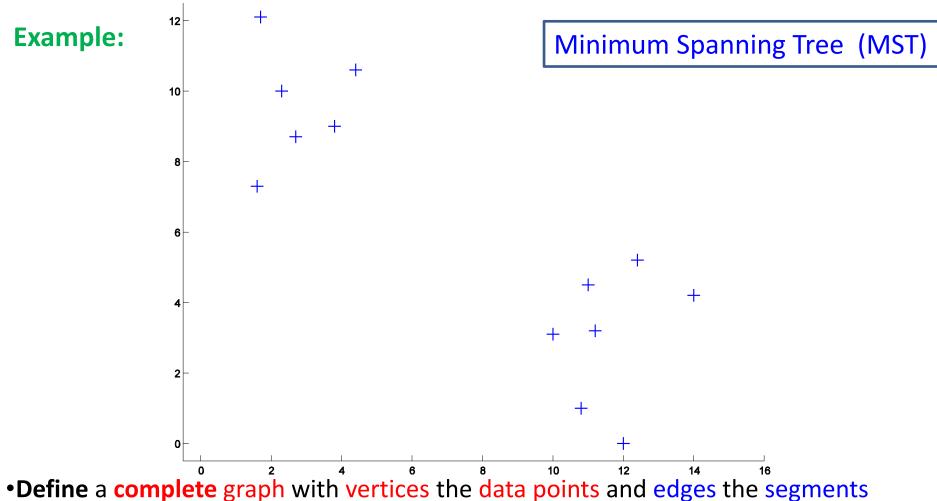
$$g(C_r, C_s) = min_{ij}\{w_{ij}: x_i \in C_r, x_j \in C_s\}$$
  
where  $w_{ij} = d(x_i, x_j)$ , we can determine the MST.

On the other hand, a hierarchy of clusterings may be obtained by the MST as follows:

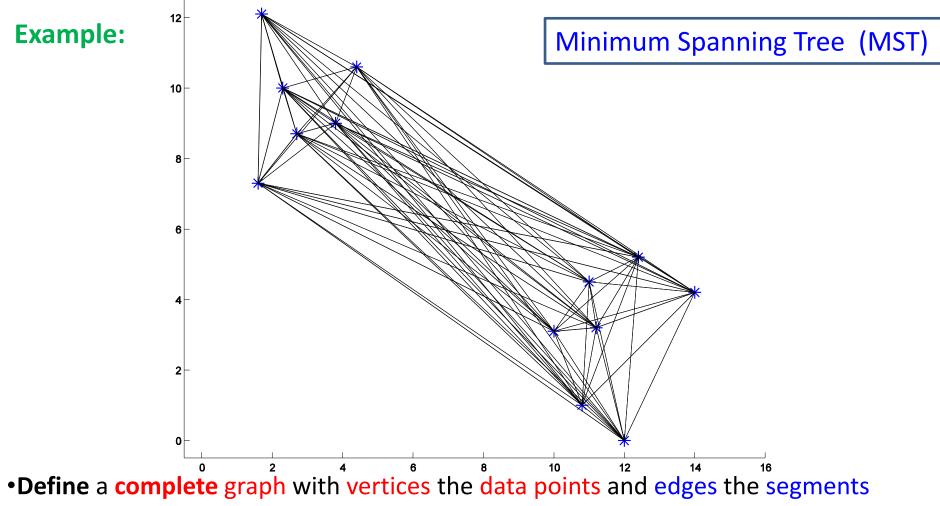
The clustering  $\Re_t$  at the t —th level is the set of connected components of the MST, when only its t smallest weights are considered.

#### Remark:

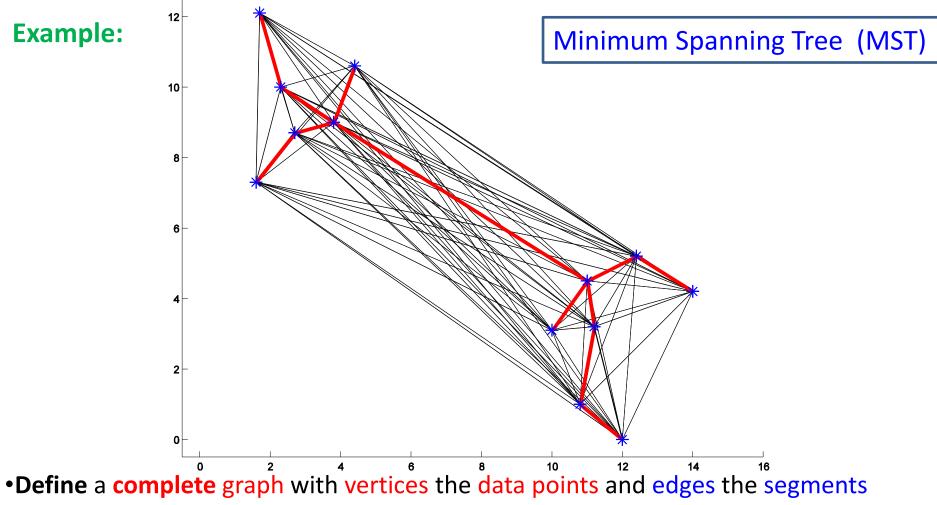
The hierarchy produced by MST is the same with that produced by the single link algorithm, at least when all  $w_{ij}$ 's are different from each other.



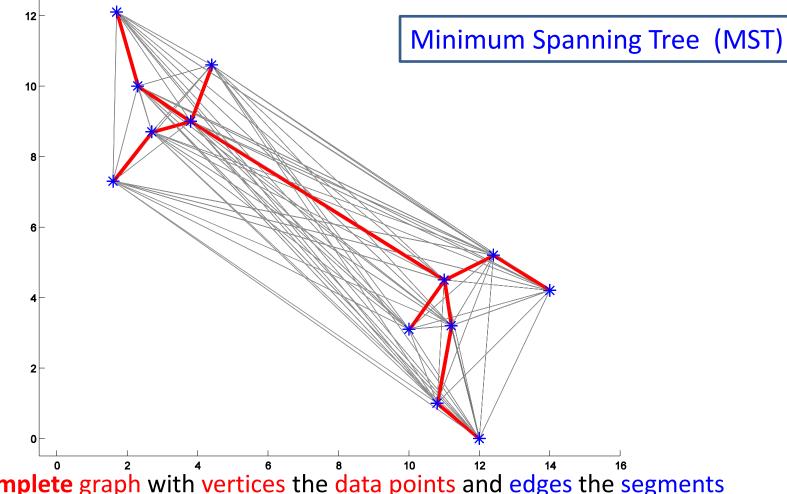
- •Define a complete graph with vertices the data points and edges the segments connecting every pair of vertices.
- •Weight each edge by the distance between its two end-points.
- •Define the MST of the graph.



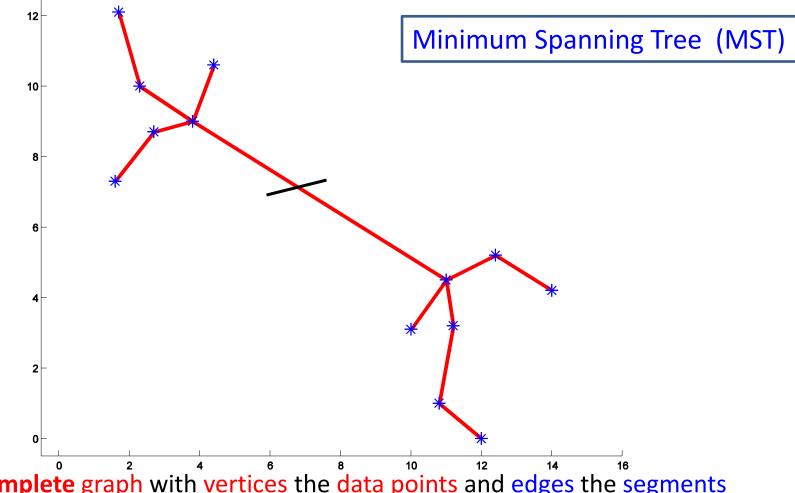
- connecting every pair of vertices.
- •Weight each edge by the distance between its two end-points.
- •Define the MST of the graph.



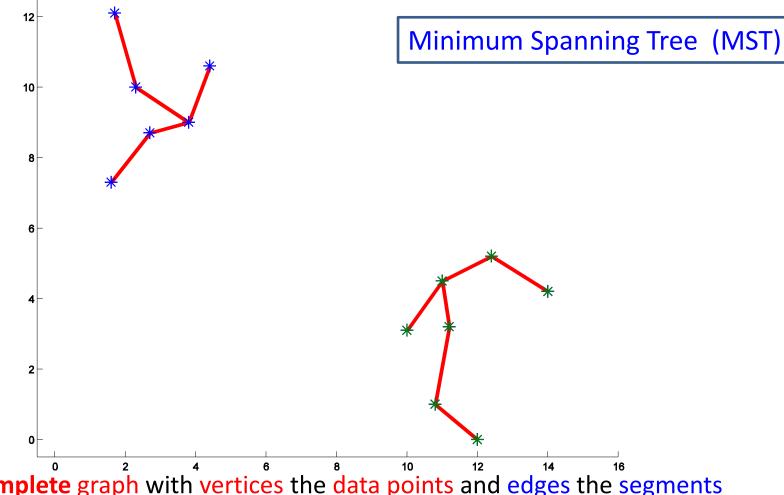
- connecting every pair of vertices.
- •Weight each edge by the distance between its two end-points.
- •Define the MST of the graph.



- •Define a complete graph with vertices the data points and edges the segments connecting every pair of vertices.
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- •Define a complete graph with vertices the data points and edges the segments connecting every pair of vertices.
- •Weight each edge by the distance between its two end-points.
- •Define the MST of the graph.
- •**Retaining** the edges with the *t* smallest weights, the resulting connected components define the clusters of the  $\Re_t$  clustering.