Chapter VIII.3: Hierarchical Clustering

1. Basic idea

- 1.1. Dendrograms
- **1.2. Agglomerative and divisive**

2. Cluster distances

- 2.1. Single link
- **2.2. Complete link**
- 2.3. Group average and Mean distance
- 2.4. Ward's method

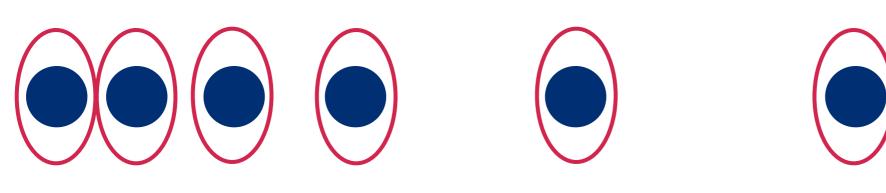
3. Discussion

- Create clustering for each number of clusters k = 1, 2, ..., n
- The clusterings must be **hierarchical**
 - -Every cluster of a *k*-clustering is a union of some clusters in an *l*-clustering for all l < k
 - I.e. for all *l*, and for all *k* > *l*, every cluster in an *l*-clustering is a subset of some cluster in *k*-clustering
- Example:

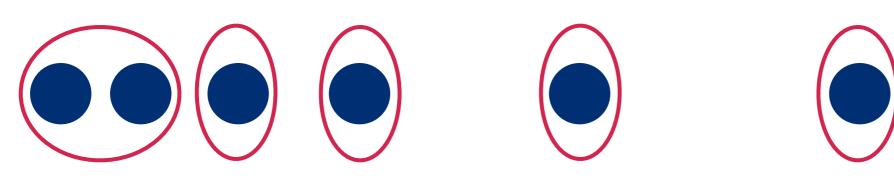
- Create clustering for each number of clusters k = 1, 2, ..., n
- The clusterings must be **hierarchical**
 - -Every cluster of a *k*-clustering is a union of some clusters in an *l*-clustering for all l < k
 - I.e. for all *l*, and for all *k* > *l*, every cluster in an *l*-clustering is a subset of some cluster in *k*-clustering

• Example:

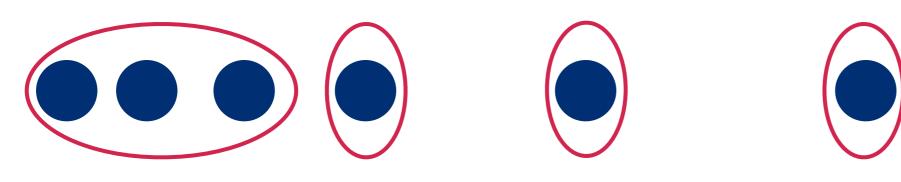
- Create clustering for each number of clusters k = 1, 2, ..., n
- The clusterings must be **hierarchical**
 - -Every cluster of a *k*-clustering is a union of some clusters in an *l*-clustering for all l < k
 - I.e. for all *l*, and for all *k* > *l*, every cluster in an *l*-clustering is a subset of some cluster in *k*-clustering
- Example:



- Create clustering for each number of clusters k = 1, 2, ..., n
- The clusterings must be **hierarchical**
 - -Every cluster of a *k*-clustering is a union of some clusters in an *l*-clustering for all l < k
 - I.e. for all *l*, and for all *k* > *l*, every cluster in an *l*-clustering is a subset of some cluster in *k*-clustering
- Example:

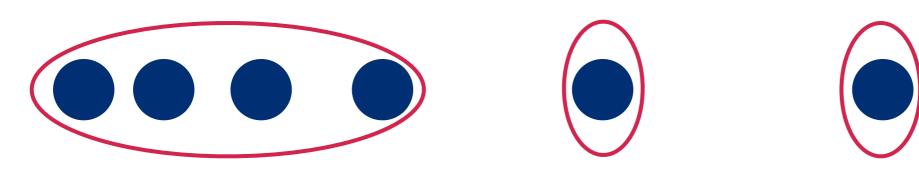


- Create clustering for each number of clusters k = 1, 2, ..., n
- The clusterings must be **hierarchical**
 - -Every cluster of a *k*-clustering is a union of some clusters in an *l*-clustering for all l < k
 - I.e. for all *l*, and for all *k* > *l*, every cluster in an *l*-clustering is a subset of some cluster in *k*-clustering
- Example:

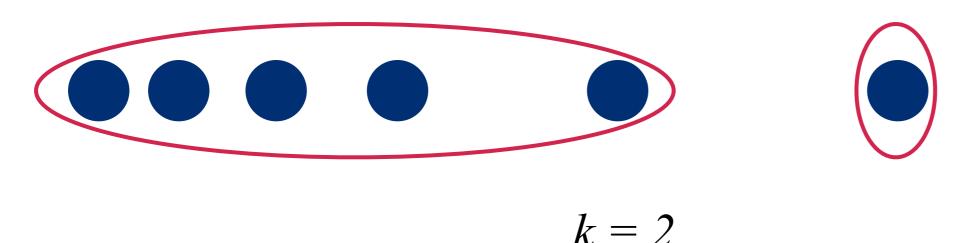


k = *4*

- Create clustering for each number of clusters k = 1, 2, ..., n
- The clusterings must be **hierarchical**
 - -Every cluster of a *k*-clustering is a union of some clusters in an *l*-clustering for all l < k
 - I.e. for all *l*, and for all *k* > *l*, every cluster in an *l*-clustering is a subset of some cluster in *k*-clustering
- Example:



- Create clustering for each number of clusters k = 1, 2, ..., n
- The clusterings must be **hierarchical**
 - -Every cluster of a *k*-clustering is a union of some clusters in an *l*-clustering for all l < k
 - I.e. for all *l*, and for all *k* > *l*, every cluster in an *l*-clustering is a subset of some cluster in *k*-clustering
- Example:

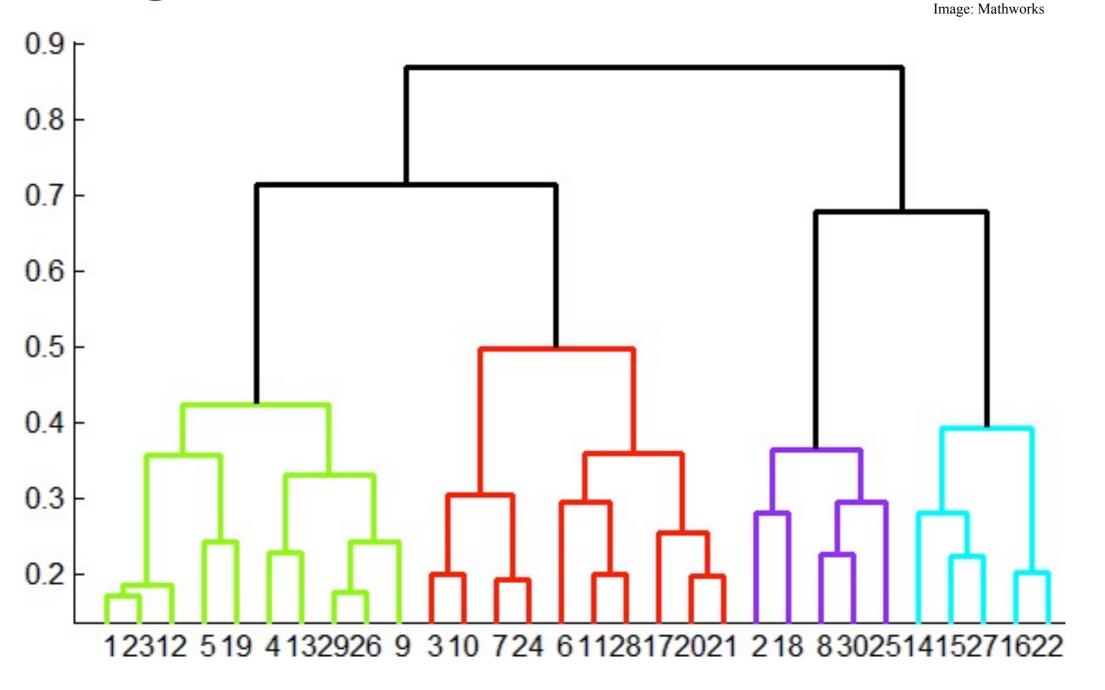


- Create clustering for each number of clusters k = 1, 2, ..., n
- The clusterings must be **hierarchical**
 - -Every cluster of a *k*-clustering is a union of some clusters in an *l*-clustering for all l < k
 - I.e. for all *l*, and for all *k* > *l*, every cluster in an *l*-clustering is a subset of some cluster in *k*-clustering
- Example:



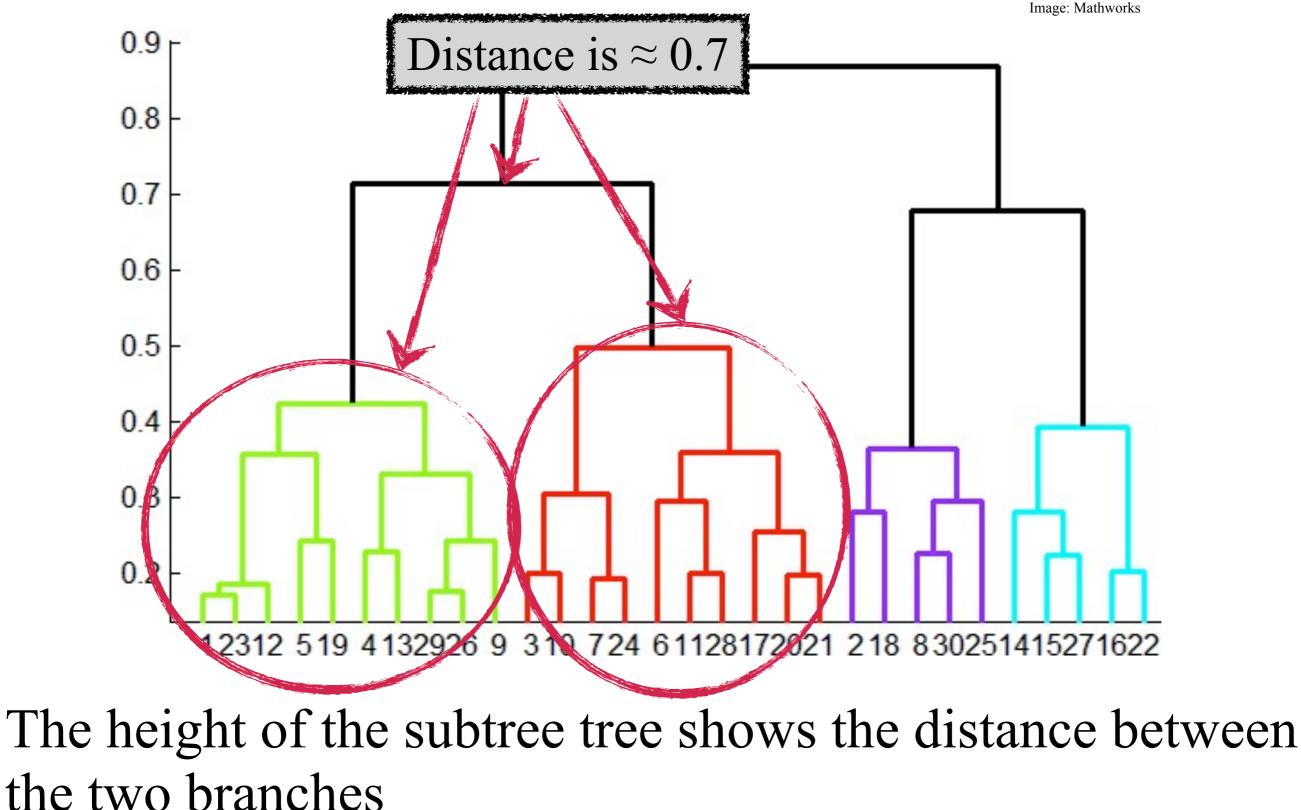
k = *1*

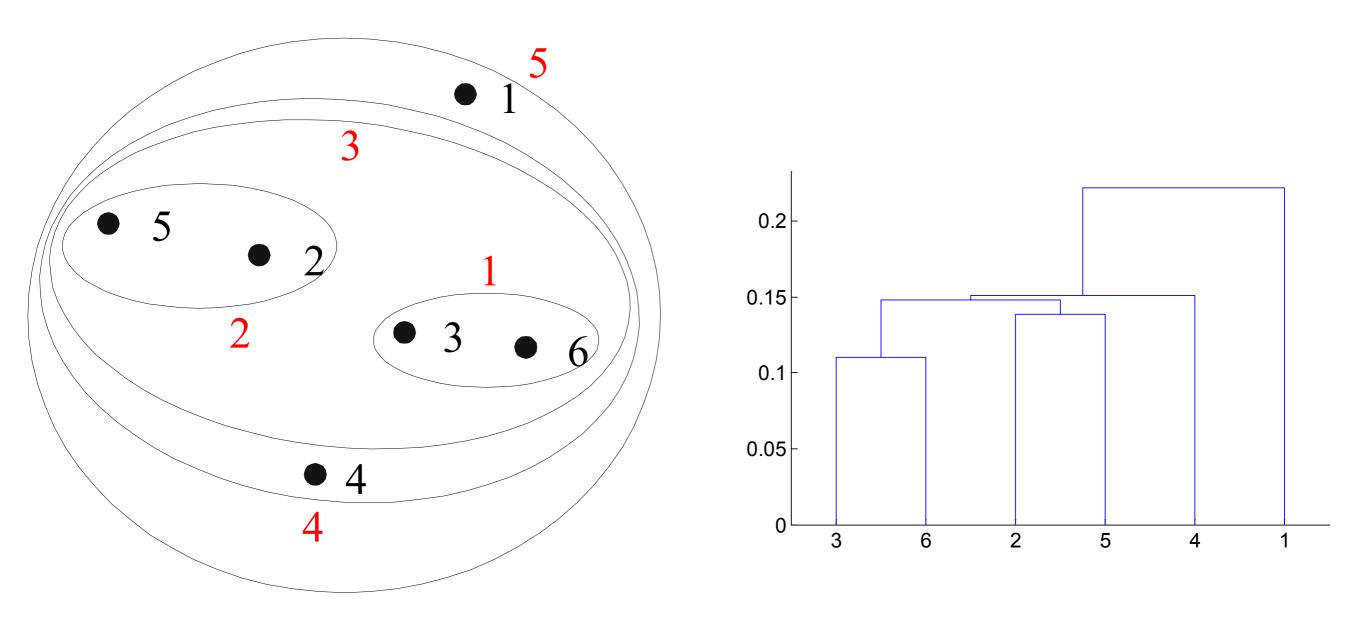
Dendrograms

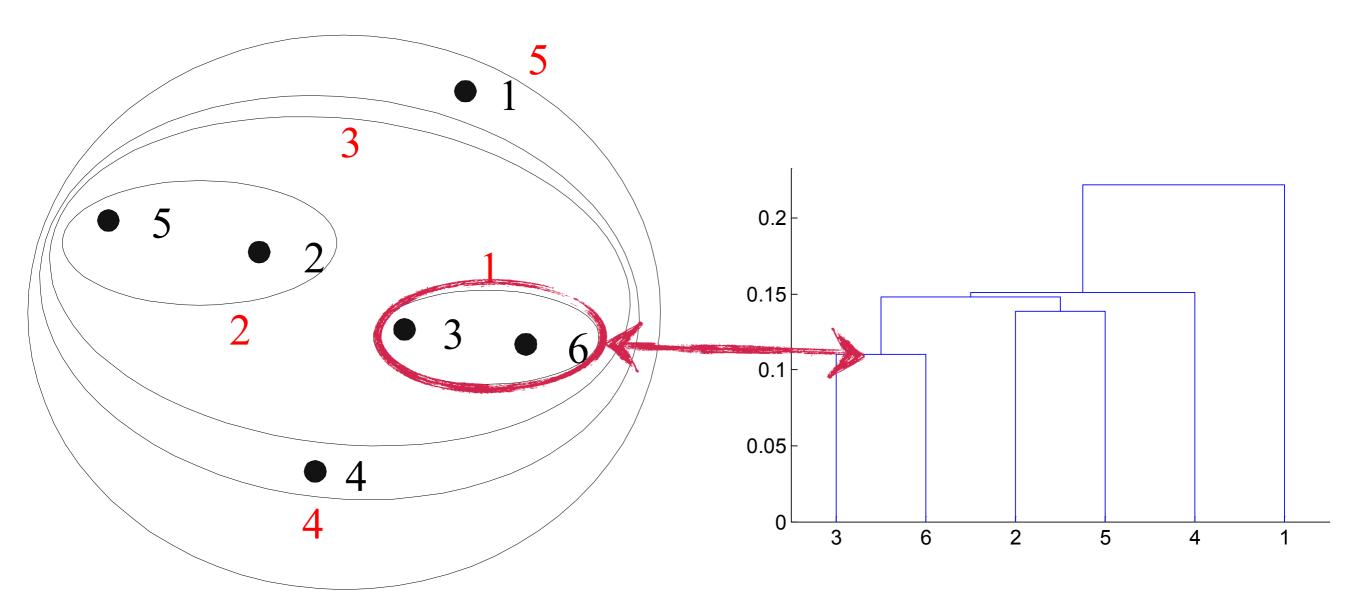


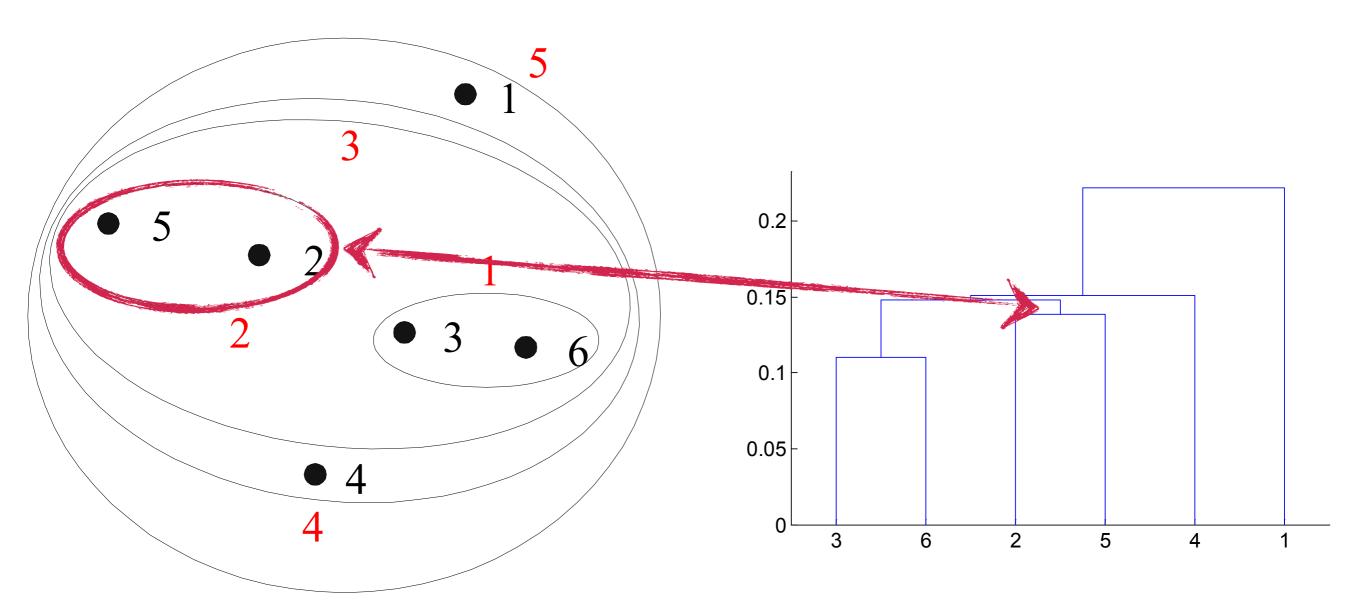
The height of the subtree tree shows the distance between the two branches

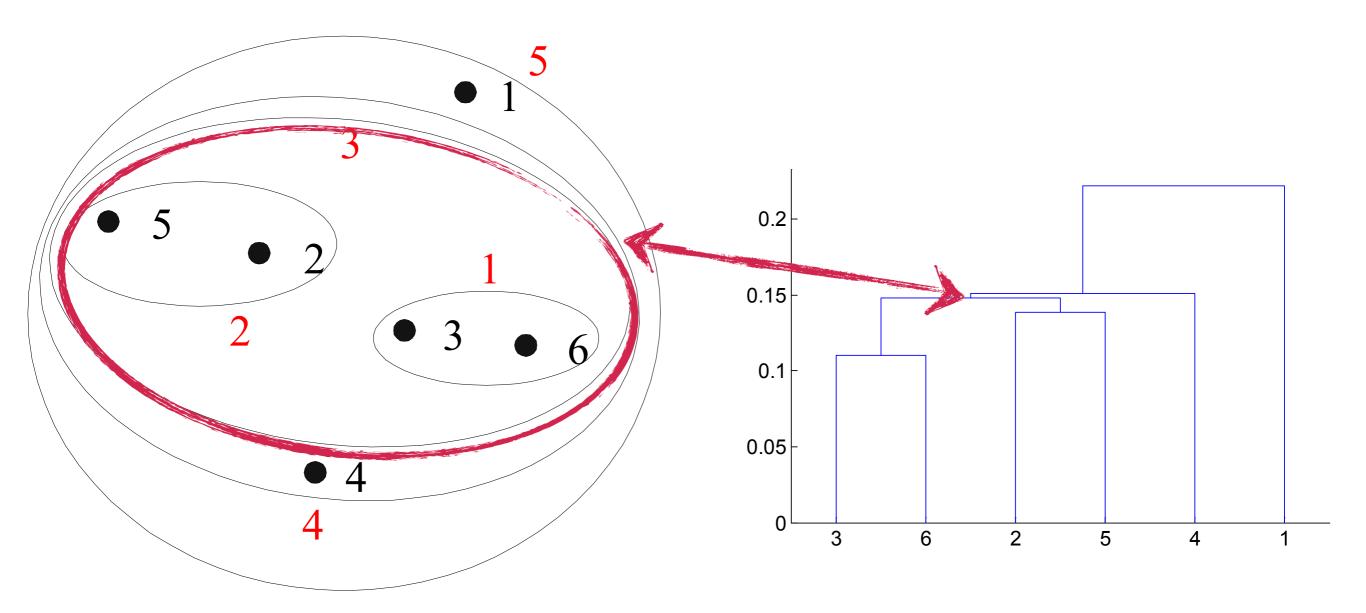
Dendrograms

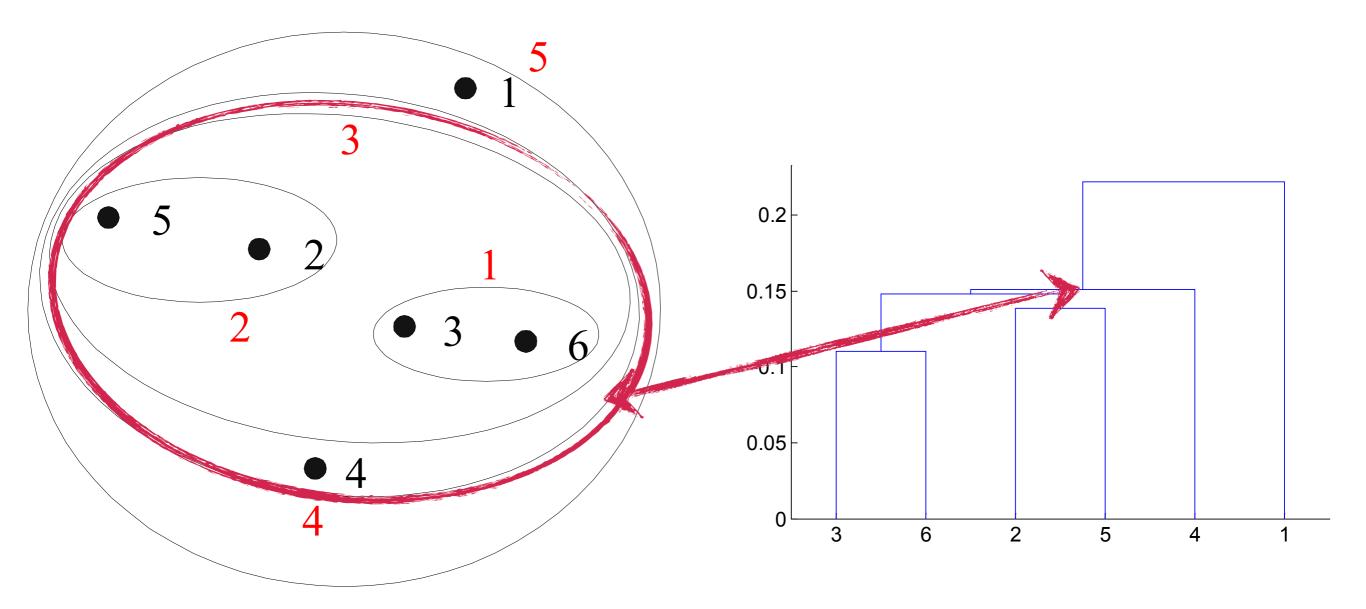


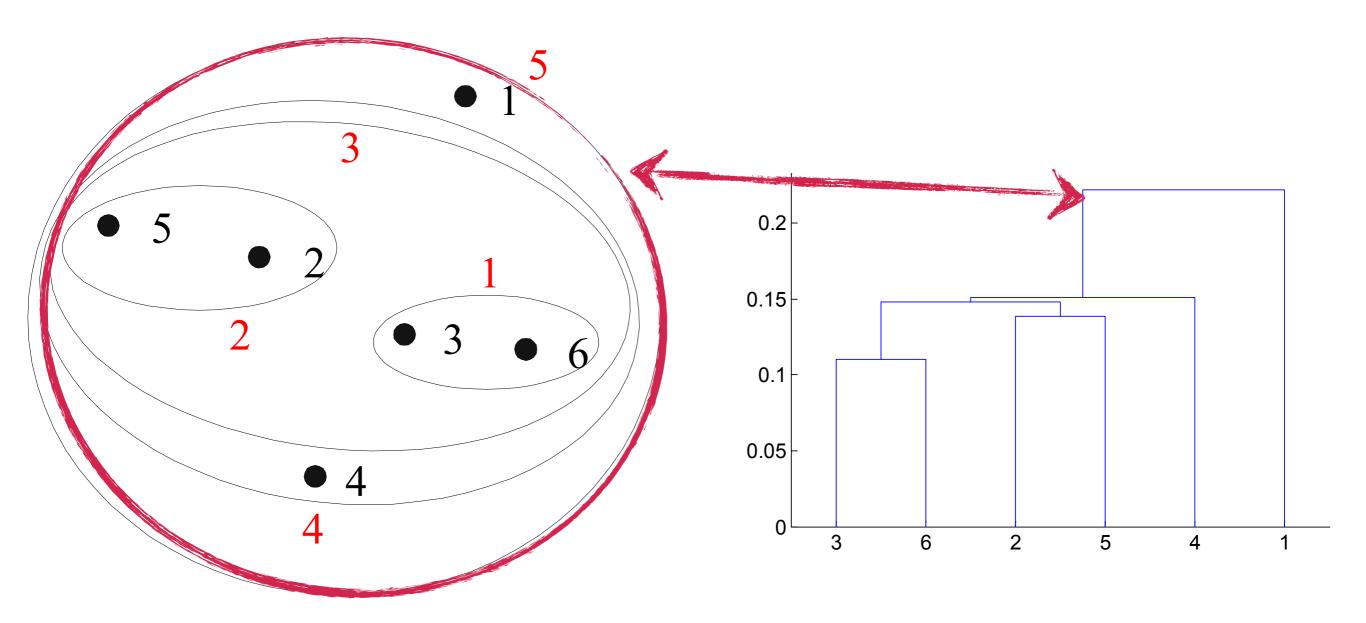


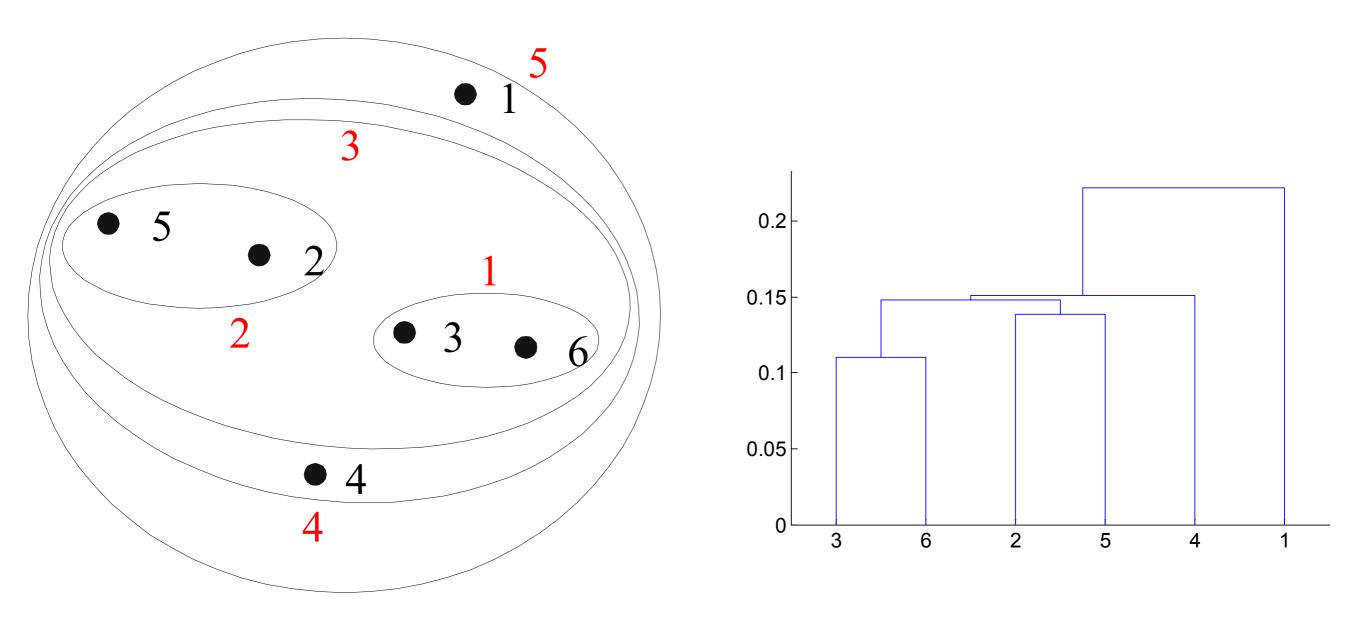








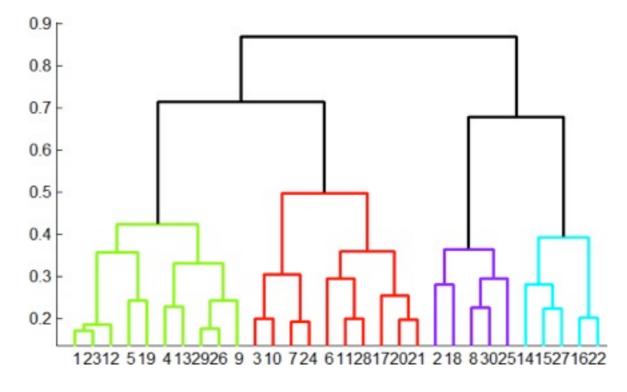




Dendrograms

- Dendrograms show the hierarchy of the clustering
- The number of clusters can be deduced from dendrogram
 - -Higher branches
- Outliers can be detected from dendrograms

-Single points that are far from others



Agglomerative and divisive

- Agglomerative: bottom-up
 - Start with *n* clusters
 - -Combine two closest points into a cluster of two elements
 - Combine two closest clusters into one bigger cluster
- Divisive: top-down
 - -Start with 1 cluster
 - -Divide the cluster into two
 - Divide the largest (per diameter) cluster into two smaller

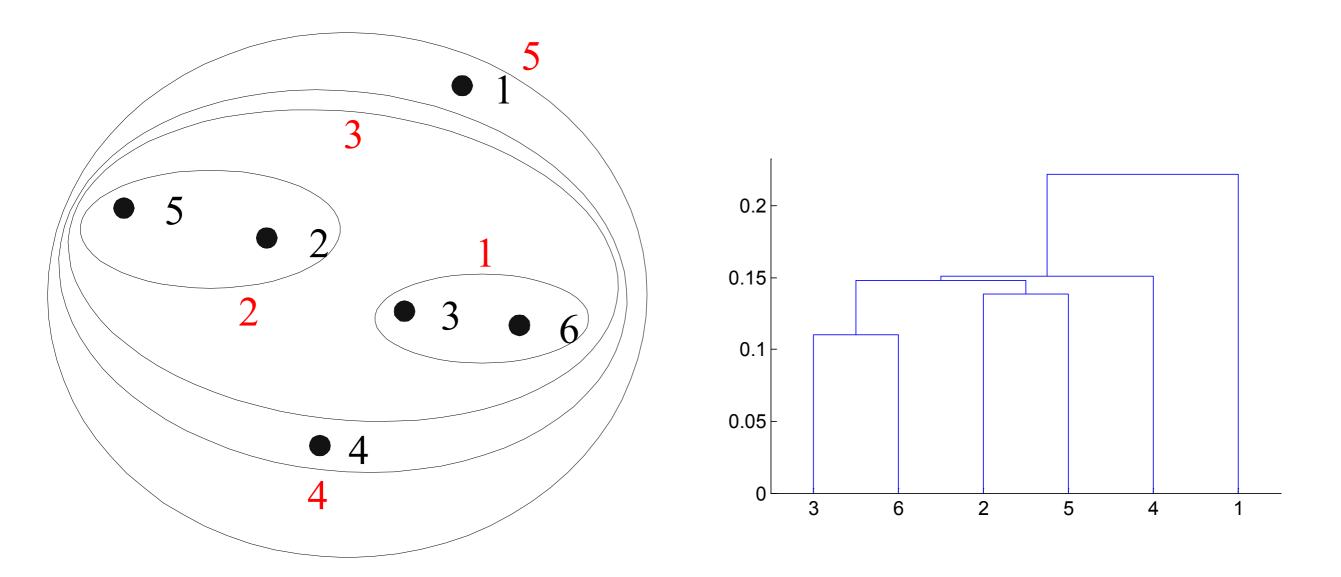
Cluster distances

- The distance between two points x and y is d(x,y)
- But what is the distance between two clusters?
- Many intuitive definitions no universal truth
 Different cluster distances yield different clusterings
 The selection of cluster distance depends on application
- Some distances between clusters *B* and *C*:
 - -minimum distance $d(B,C) = \min\{d(x,y) : x \in B \text{ and } y \in C\}$
 - -maximum distance $d(B,C) = \max\{d(x,y) : x \in B \text{ and } y \in C\}$
 - -average distance $d(B,C) = avg\{d(x,y) : x \in B \text{ and } y \in C\}$
 - distance of centroids $d(B,C) = d(\mu_B, \mu_C)$, where μ_B is the centroid of *B* and μ_C is the centroid of *C*

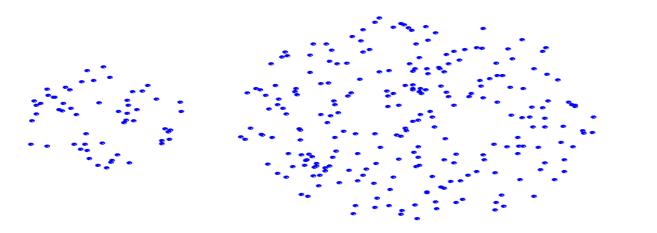
Single link

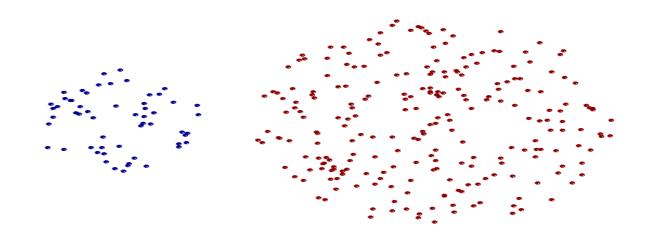
• The distance between two clusters is the distance between the closest points

 $-d(B,C) = \min\{d(x,y) : x \in B \text{ and } y \in C\}$



Strengths of single-link



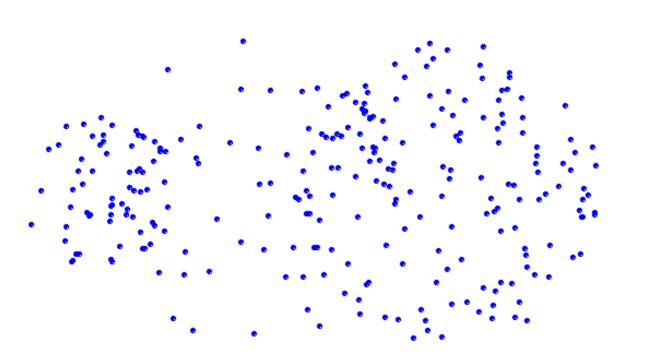


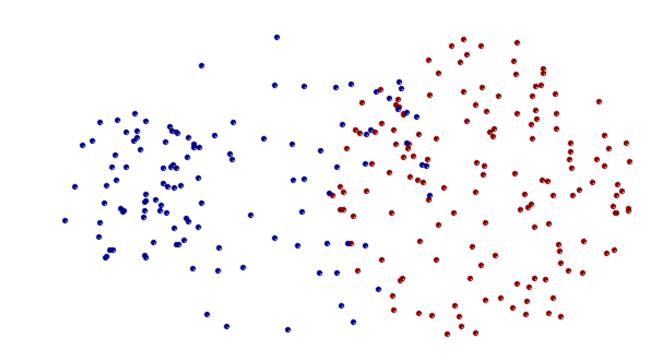
Original Points

Two Clusters

Can handle non-spherical clusters of unequal size

Weaknesses of single-link





Original Points

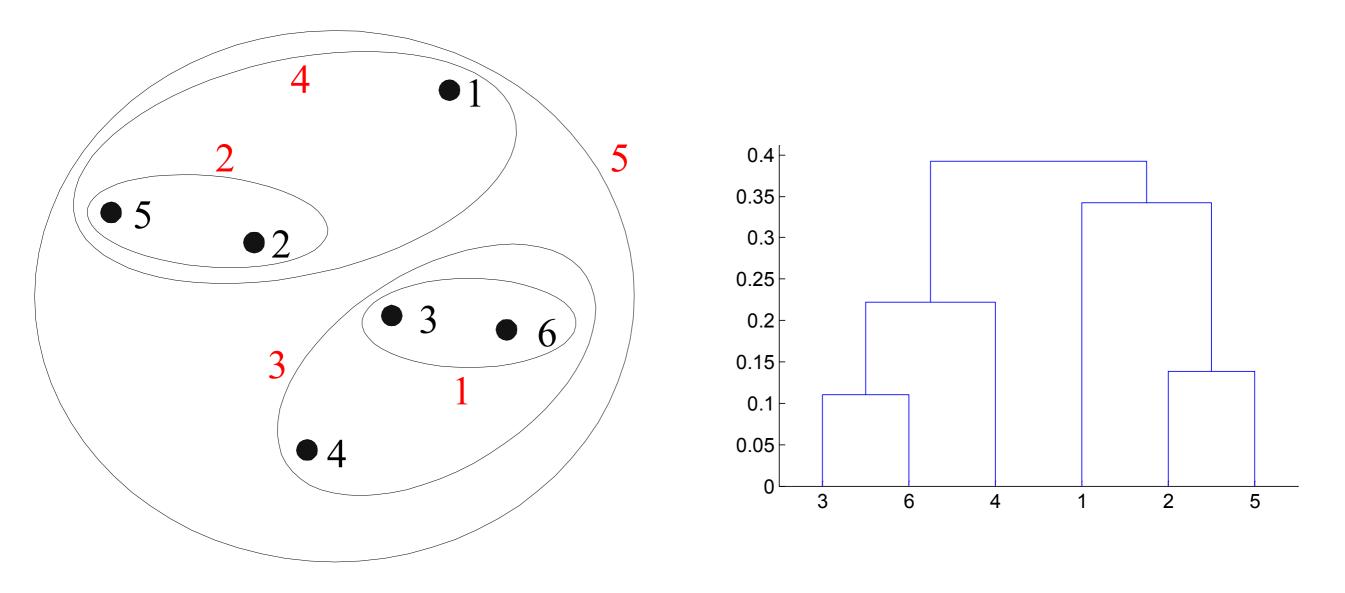
Two Clusters

- Sensitive to noise and outliers
- Produces elongated clusters

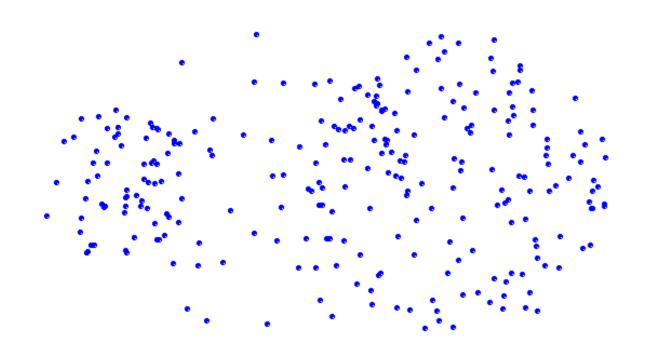
Complete link

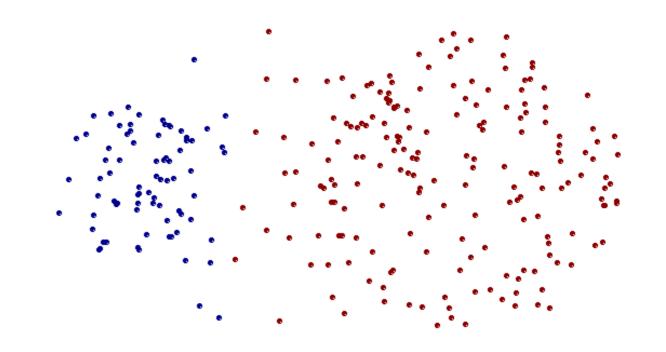
• The distance between the clusters is the distance between the furthest points

 $-d(B,C) = \max\{d(x,y) : x \in B \text{ and } y \in C\}$



Strengths of complete link



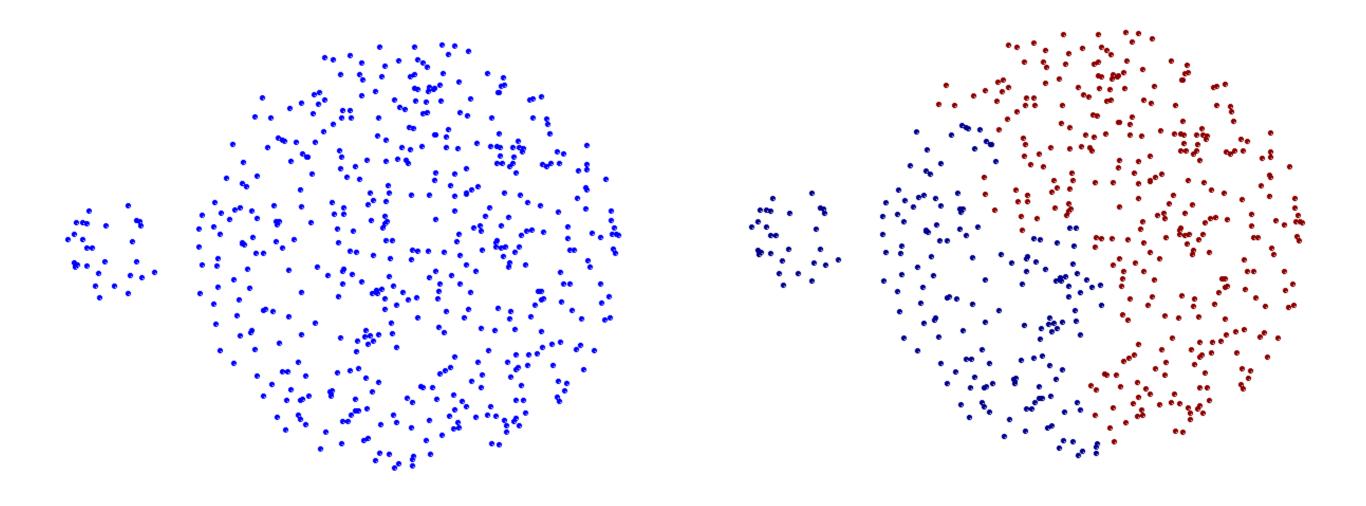


Original Points

Two Clusters

•Less susceptible to noise and outliers

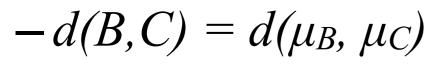
Weaknesses of complete link

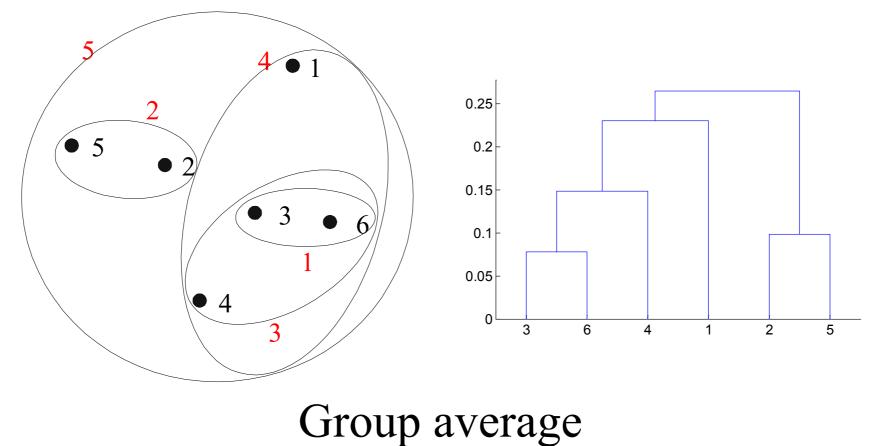


Breaks largest clustersBiased towards spherical clusters

Group average and Mean distance

- *Group average* is the average of pairwise distances $-d(B,C) = \arg\{d(x,y) : x \in B \text{ and } y \in C\}$ $= \sum_{x \in B, y \in C} d(x,y) / (|B| |C|)$
- Mean distance is the distance of the cluster centroids



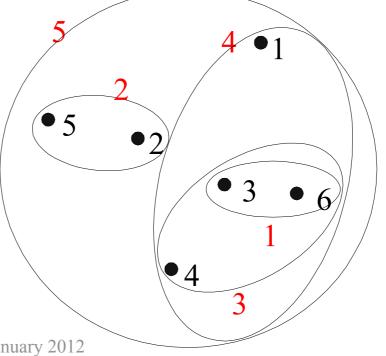


Properties of group average

- A compromise between single and complete link
- Less susceptible to noise and outliers
 - Similar to complete link
- Biased towards spherical clusters
 - -Similar to complete link

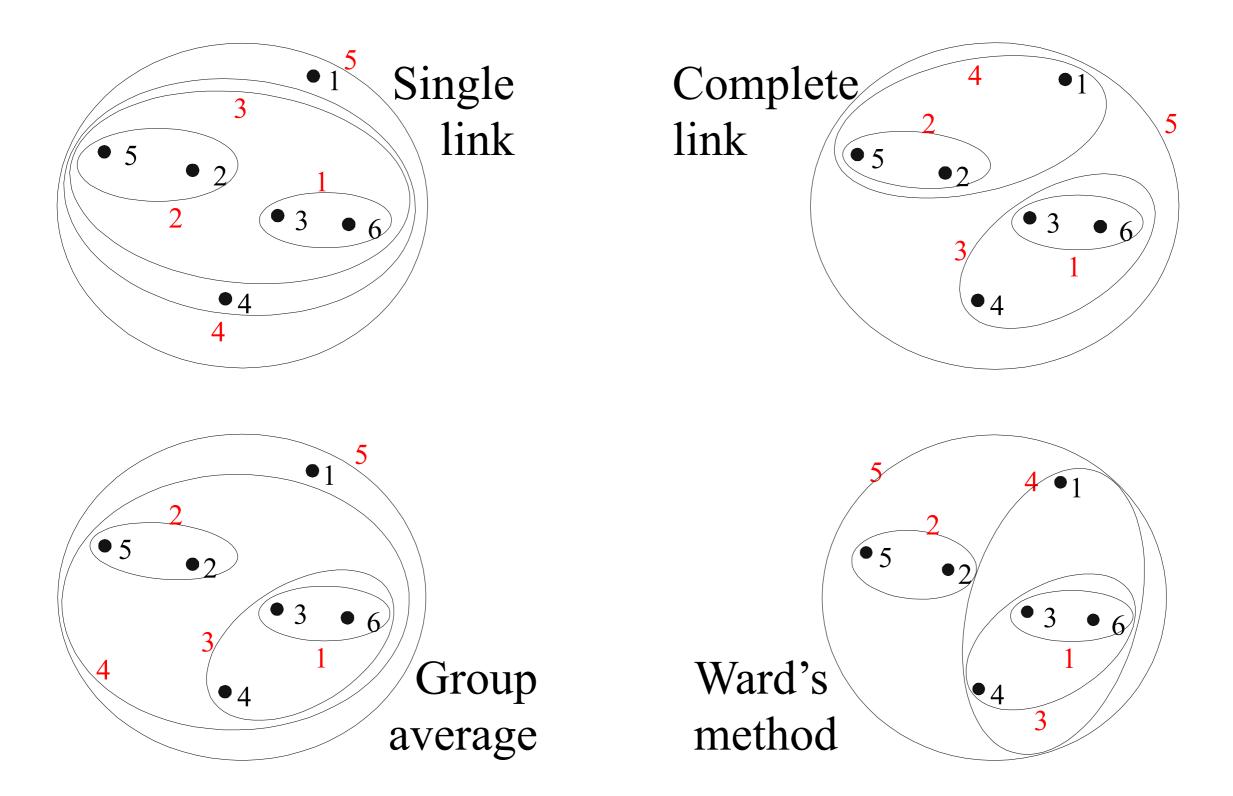
Ward's method

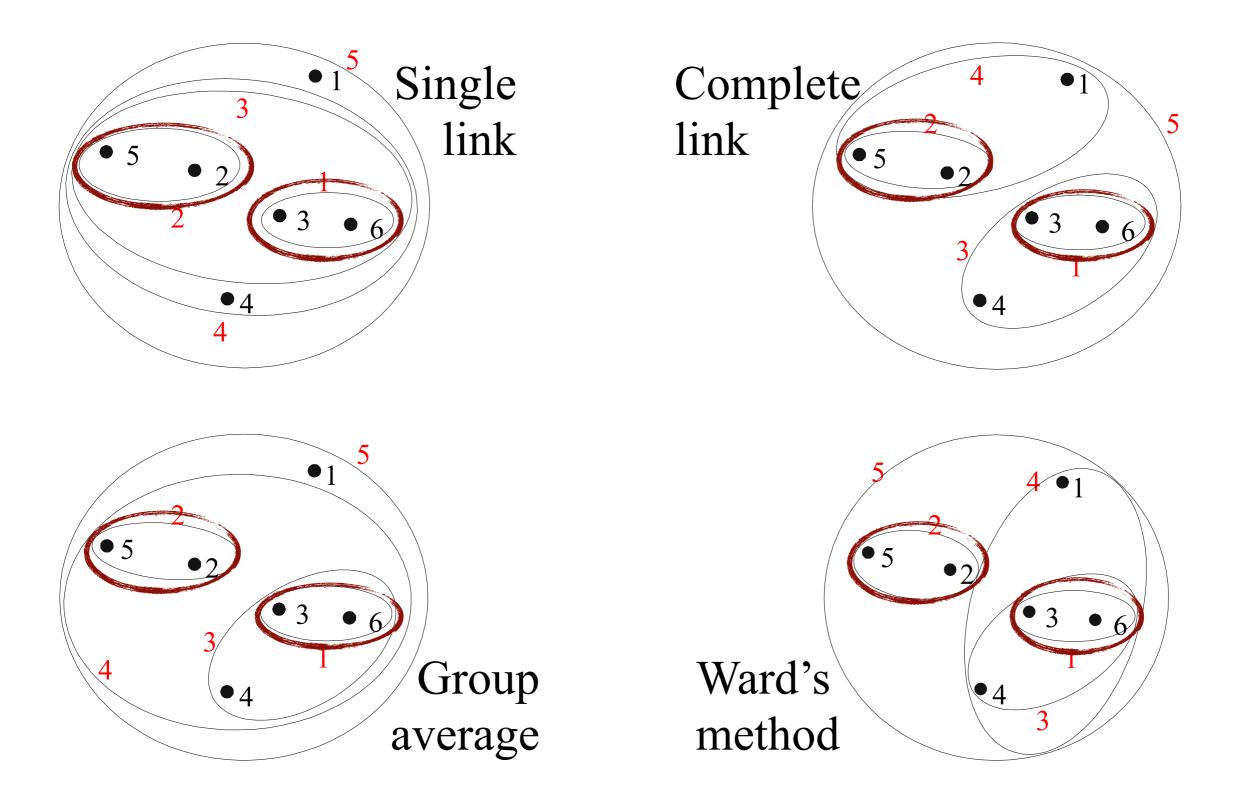
- Ward's distance between clusters A and B is the increase in sum of squared errors (SSE) when the two clusters are merged
 - -SSE for cluster A is $SSE_A = \sum_{x \in A} ||x \mu_A||^2$
 - Difference on merging clusters A and B to cluster C is then $d(A, B) = \Delta SSE_C = SSE_C - SSE_A - SSE_B$
 - -Equivalently, $d(A,B) = |A||B|/(|A|+|B|)||\mu_A \mu_B||^2$
 - Weighted mean distance

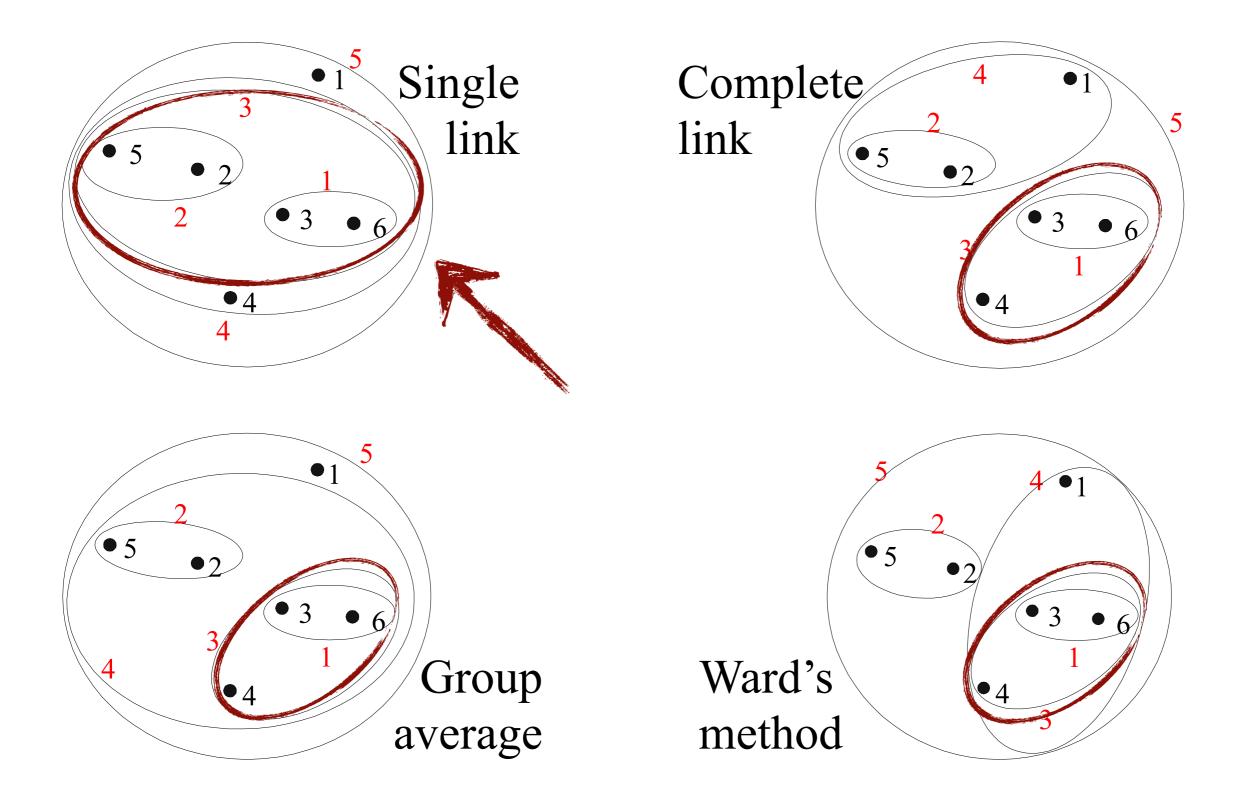


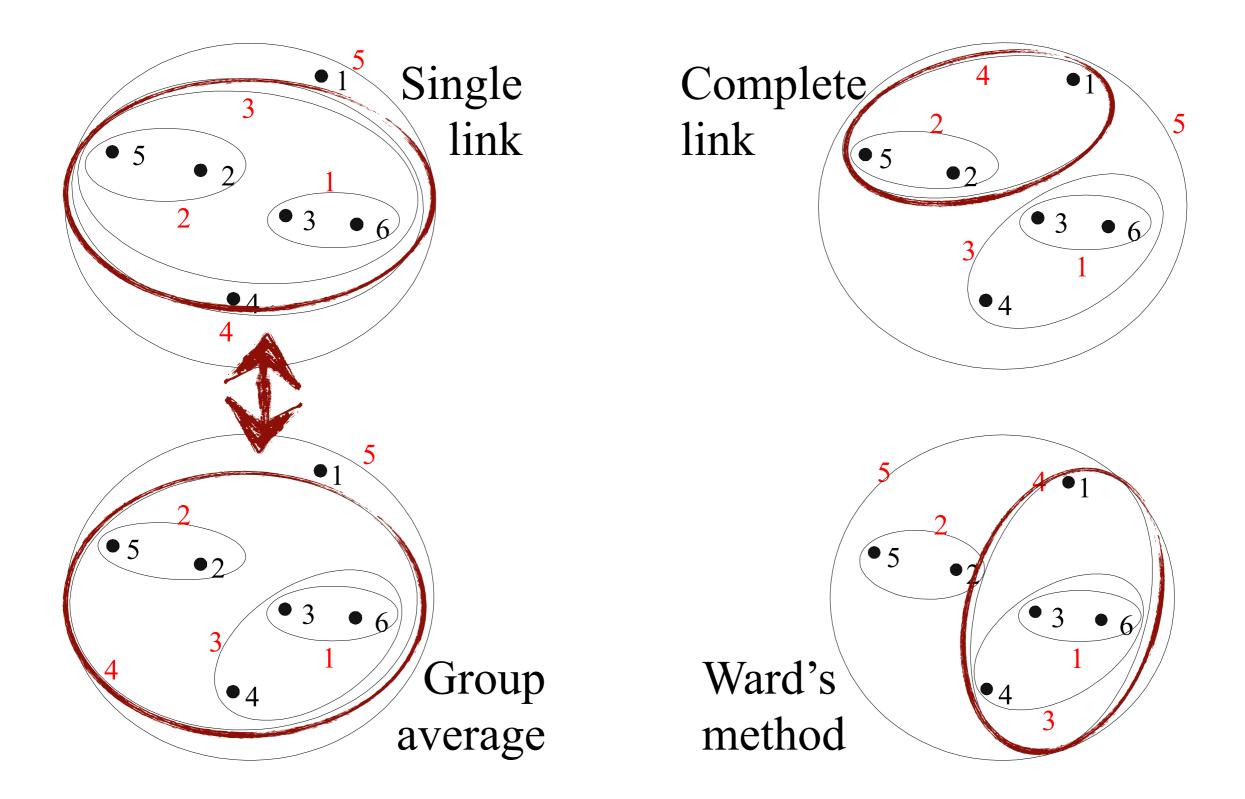
Discussion on Ward's method

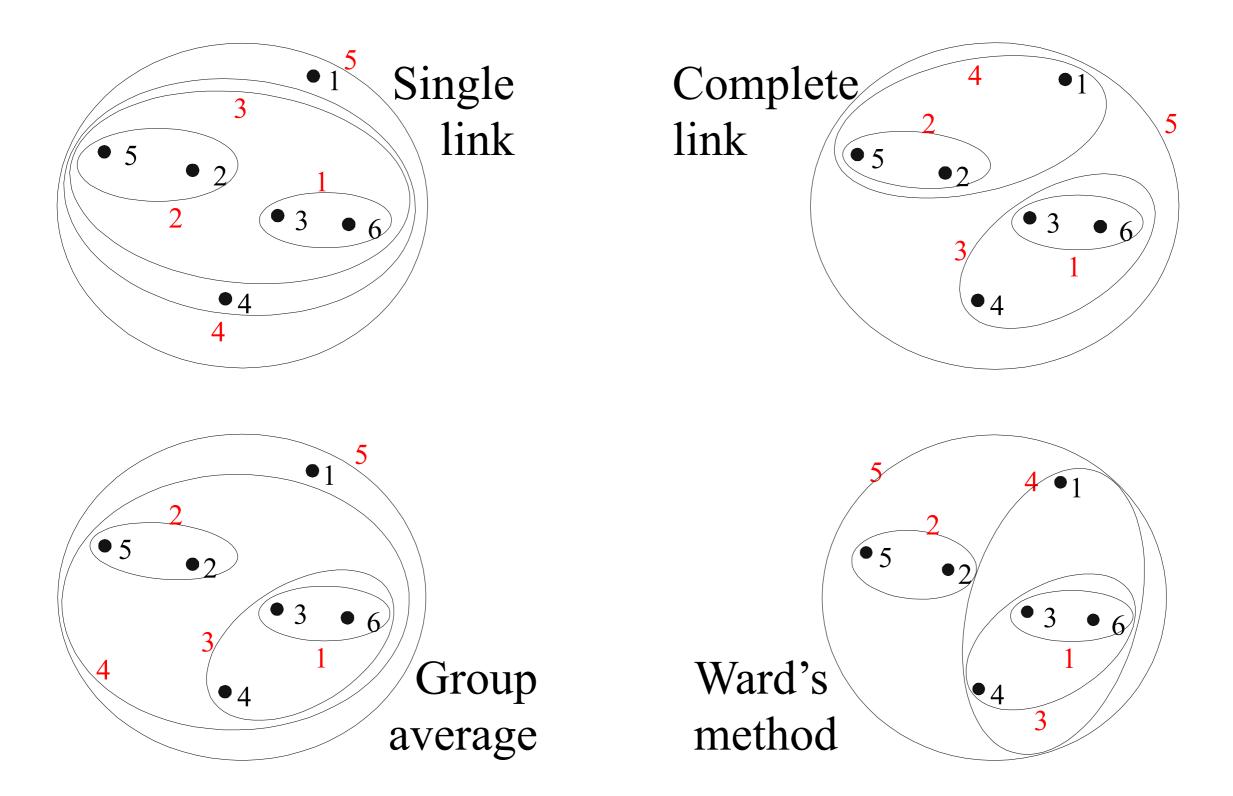
- Less susceptible to noise and outliers
- Biased towards spherical clusters
- Hierarchical analogue of *k*-means
 - -Hence many shared pros and cons
 - Can be used to initialize *k*-means











Lance–Williams formula

- After merging clusters A and B into cluster C, we need to compute C's distance to other clusters Z
- Lance–Williams formula provides a general equation for this

 $d(C,Z) = \alpha_A d(A,Z) + \alpha_B d(B,Z) + \beta d(A,B) + \gamma |d(A,Z) - d(B,Z)|$

	αΑ	α	β	γ
Single link	1/2	1/2	0	-1/2
Complete link	1/2	1/2	0	1/2
Group average	A /(A + B)	B /(A + B)	0	0
Mean distance	A /(A + B)	B /(A + B)	- A B /(A + B) ²	0
Ward's method	(A + Z)/(A + B + Z)	(B + Z)/(A + B + Z)	- Z /(A + B + Z)	0

Computational complexity

- Takes $O(n^3)$ time in most cases
 - -n steps
 - In each step, n^2 distance matrix must be updated and searched
- $O(n^2 \log(n))$ time for some approaches using appropriate data structures
 - -Keep distances in a heap
 - -Each step takes $O(n \log n)$ time
- $O(n^2)$ space complexity
 - -Have to store the distance matrix

Chapter VIII.4: Co-clustering

- **1. Clustering written with matrices**
- 2. Co-clustering definition
- 3. Algorithms

Clustering written with matrices

- Let *x*₁, *x*₂, ..., *x*_n be the *m*-dimensional vectors (data points) we want to cluster
- Write these as an *n*-by-*m* matrix *X*
 - Each data point is one row of X
- The exclusive representative clustering can be re-written using two matrices
 - Matrix C (cluster assignment matrix) has n rows and k columns
 - Each row of *C* has *exactly* one element 1 while others are 0
 - Matrix *M* (mean matrix) has *k* rows and *m* columns
 - Each row of *M* corresponds to a centroid of a cluster
- Loss function (SSE) is now $\|\mathbf{X} \mathbf{C}\mathbf{M}\|_2^2$



X 1	1	3
X 2	2	2
X 3	3	4
X 4	2	1
X 5	4	3

X 1	1	3
X 2	2	2
X 3	3	4
X 4	2	1
X 5	4	3

$$\mathbf{X} = \begin{pmatrix} 1 & 3 \\ 2 & 2 \\ 3 & 4 \\ 2 & 1 \\ 4 & 3 \end{pmatrix}$$

X 1	1	3
X2	2	2
X 3	3	4
X 4	2	1
X 5	4	3

$$\mathbf{X} = \begin{pmatrix} 1 & 3 \\ 2 & 2 \\ 3 & 4 \\ 2 & 1 \\ 4 & 3 \end{pmatrix}$$

$$C_1 = \{x_1, x_2, x_4\}$$

$$C_2 = \{x_3, x_5\}$$

X1

X2 X3 X4 X5

 C_1 C_2

1 2 3 2 4	3 2 4 1 3		X =	$\begin{pmatrix} 1\\ 2\\ 3\\ 2\\ 4 \end{pmatrix}$	$3 \\ 2 \\ 4 \\ 1 \\ 3$	/1	$0\rangle$
${x_1, :}$ ${x_3, :}$		4}		,	C	 $ \begin{bmatrix} 1\\ 0\\ 1\\ 0 \end{bmatrix} $	$\begin{array}{c} 0\\ 1\\ 0\\ 1 \end{array}$

X 1	1	3
X 2	2	2
X 3	3	4
X 4	2	1
X 5	4	3

$$C_1 = \{x_1, x_2, x_4\}$$

$$C_2 = \{x_3, x_5\}$$

 $\mu l = (1.66, 2)$ $\mu 2 = (3.5, 3.5)$

$$\mathbf{X} = \begin{pmatrix} 1 & 3 \\ 2 & 2 \\ 3 & 4 \\ 2 & 1 \\ 4 & 3 \end{pmatrix} \begin{pmatrix} 1 & 0 \\ 1 & 0 \\ 1 & 0 \\ 0 & 1 \\ 1 & 0 \\ 0 & 1 \end{pmatrix}$$

 $\mathbf{X} = \begin{pmatrix} 1 & 3 \\ 2 & 2 \\ 3 & 4 \\ 2 & 1 \\ 4 & 3 \end{pmatrix}$ $\mathbf{X} = \begin{pmatrix} 1 & 3 \\ 2 & 2 \\ 3 & 4 \\ 2 & 1 \\ 4 & 3 \end{pmatrix}$ $\mathbf{C} = \begin{pmatrix} 1 & 0 \\ 1 & 0 \\ 0 & 1 \\ 1 & 0 \\ 0 & 1 \end{pmatrix}$ **X**1 **X**2 Х3 **X**4 **X**5 $C_1 = \{x_1, x_2, x_4\}$ $C_2 = \{x_3, x_5\}$ $\mathbf{M} = \begin{pmatrix} 1.66 & 2\\ 3.5 & 3.5 \end{pmatrix}$ $\mu l = (1.66, 2)$ $\mu 2 = (3.5, 3.5)$

 $\mathbf{X} = \begin{pmatrix} 1 & 3 \\ 2 & 2 \\ 3 & 4 \\ 2 & 1 \\ 4 & 3 \end{pmatrix}$ $\mathbf{C} = \begin{pmatrix} 1 & 0 \\ 1 & 0 \\ 0 & 1 \\ 1 & 0 \\ 0 & 1 \end{pmatrix}$ 1 3 **X**1 2 4 1 2 **X**2 3 **X**3 2 **X**4 3 4 **X**5 $C_1 = \{x_1, x_2, x_4\}$ $C_2 = \{x_3, x_5\}$ $\mathbf{M} = \begin{pmatrix} 1.66 & 2\\ 3.5 & 3.5 \end{pmatrix}$ $\mathbf{CM} = \begin{pmatrix} 1.66 & 2\\ 1.66 & 2\\ 3.5 & 3.5\\ 1.66 & 2\\ 3.5 & 3.5 \end{pmatrix}$ $\mu l = (1.66, 2)$ $\mu 2 = (3.5, 3.5)$

1 3 **X**1 2 2 **X**2 4 3 **X**3 2 **X**4 3 4 **X**5 $C_1 = \{x_1, x_2, x_4\}$ $C_2 = \{x_3, x_5\}$ $\mathbf{X} - \mathbf{C}\mathbf{M} = \begin{pmatrix} -0.66 & 1\\ 0.33 & 0\\ -0.5 & 0.5\\ 0.33 & -1\\ 0.5 & -0.5 \end{pmatrix}$ $\mathbf{M} = \begin{pmatrix} 1.66 & 2\\ 3.5 & 3.5 \end{pmatrix}$ $\mu l = (1.66, 2)$ $\mu 2 = (3.5, 3.5)$

Co-clustering definition

- The same way we clustered X, we can also cluster X^T – This clusters the dimensions, not the data points
- An (*k*,*l*)-**co-clustering** of *X* is partitioning of rows of *X* into *k* clusters and columns of *X* into *l* clusters
 - Row cluster *I* and column cluster *J* define a (combinatorial) **sub-matrix** X_{IJ}
 - Element x_{ij} belongs to this sub-matrix if $i \in I$ and $j \in J$
 - Each sub-matrix X_{IJ} is represented by single value μ_{ij}
- Let *R* be the *n*-by-*k* row cluster assignment matrix and *C* the *m*-by-*l* column cluster assignment matrix and *M* = (μ_{ij}) the *k*-by-*l* mean matrix

 The *loss function* is ||X RMC^T||²₂

$$\mathbf{X} = \begin{pmatrix} 1 & 3 & 2 \\ 2 & 2 & 1 \\ 0 & 1 & 0 \\ 4 & 3 & 5 \end{pmatrix}$$

$$\mathbf{X} = \begin{pmatrix} 1 & 3 & 2 \\ 2 & 2 & 1 \\ 0 & 1 & 0 \\ 4 & 3 & 5 \end{pmatrix}$$
$$\mathbf{R} = \begin{pmatrix} 1 & 0 & 0 \\ 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix}$$

 $\mathbf{C}^{\mathsf{T}} = \begin{pmatrix} 1 & 0 & 1 \\ 0 & 1 & 0 \end{pmatrix}$

$$\mathbf{X} = \begin{pmatrix} 1 & 3 & 2 \\ 2 & 2 & 1 \\ 0 & 1 & 0 \\ 4 & 3 & 5 \end{pmatrix}$$
$$\mathbf{R} = \begin{pmatrix} 1 & 0 & 0 \\ 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix} \qquad \mathbf{M} = \begin{pmatrix} 1.5 & 2.5 \\ 0 & 1 \\ 4.5 & 3 \end{pmatrix} \qquad \mathbf{C}^{\mathsf{T}} = \begin{pmatrix} 1 & 0 & 1 \\ 0 & 1 & 0 \end{pmatrix}$$

$$\mathbf{X} = \begin{pmatrix} 1 & 3 & 2 \\ 2 & 2 & 1 \\ 0 & 1 & 0 \\ 4 & 3 & 5 \end{pmatrix}$$
$$\mathbf{R} = \begin{pmatrix} 1 & 0 & 0 \\ 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix} \qquad \mathbf{M} = \begin{pmatrix} 1.5 & 2.5 \\ 0 & 1 \\ 4.5 & 3 \end{pmatrix} \qquad \mathbf{C}^{\mathsf{T}} = \begin{pmatrix} 1 & 0 & 1 \\ 0 & 1 & 0 \end{pmatrix}$$

$$\mathbf{X} = \begin{pmatrix} 1 & 3 & 2 \\ 2 & 2 & 1 \\ 0 & 1 & 0 \\ 4 & 3 & 5 \end{pmatrix}$$
$$\mathbf{R} = \begin{pmatrix} 1 & 0 & 0 \\ 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix} \qquad \mathbf{M} = \begin{pmatrix} 1.5 & 2.5 \\ 0 & 1 \\ 4.5 & 3 \end{pmatrix} \qquad \mathbf{C}^{\mathsf{T}} = \begin{pmatrix} 1 & 0 & 1 \\ 0 & 1 & 0 \end{pmatrix}$$

$$\mathbf{X} = \begin{pmatrix} 1 & 3 & 2 \\ 2 & 2 & 1 \\ 0 & 1 & 0 \\ 4 & 3 & 5 \end{pmatrix}$$
$$\mathbf{R} = \begin{pmatrix} 1 & 0 & 0 \\ 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix} \qquad \mathbf{M} = \begin{pmatrix} 1.5 & 2.5 \\ 0 & 1 \\ 4.5 & 3 \end{pmatrix} \qquad \mathbf{C}^{\mathsf{T}} = \begin{pmatrix} 1 & 0 & 1 \\ 0 & 1 & 0 \end{pmatrix}$$

$$\mathbf{X} = \begin{pmatrix} 1 & 3 & 2 \\ 2 & 2 & 1 \\ 0 & 1 & 0 \\ 4 & 3 & 5 \end{pmatrix}$$
$$\mathbf{R} = \begin{pmatrix} 1 & 0 & 0 \\ 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix} \qquad \mathbf{M} = \begin{pmatrix} 1.5 & 2.5 \\ 0 & 1 \\ 4.5 & 3 \end{pmatrix} \qquad \mathbf{C}^{\mathsf{T}} = \begin{pmatrix} 1 & 0 & 1 \\ 0 & 1 & 0 \end{pmatrix}$$

$$\mathbf{X} = \begin{pmatrix} 1 & 3 & 2 \\ 2 & 2 & 1 \\ 0 & 1 & 0 \\ 4 & 3 & 5 \end{pmatrix}$$
$$\mathbf{R} = \begin{pmatrix} 1 & 0 & 0 \\ 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix} \qquad \mathbf{M} = \begin{pmatrix} 1.5 & 2.5 \\ 0 & 1 \\ 4.5 & 3 \end{pmatrix} \qquad \mathbf{C}^{\mathsf{T}} = \begin{pmatrix} 1 & 0 & 1 \\ 0 & 1 & 0 \end{pmatrix}$$

$$\mathbf{X} = \begin{pmatrix} 1 & 3 & 2 \\ 2 & 2 & 1 \\ 0 & 1 & 0 \\ 4 & \mathbf{3} & 5 \end{pmatrix}$$
$$\mathbf{R} = \begin{pmatrix} 1 & 0 & 0 \\ 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix} \qquad \mathbf{M} = \begin{pmatrix} 1.5 & 2.5 \\ 0 & 1 \\ 4.5 & \mathbf{3} \end{pmatrix} \qquad \mathbf{C}^{\mathsf{T}} = \begin{pmatrix} 1 & 0 & 1 \\ 0 & 1 & 0 \end{pmatrix}$$

$$\mathbf{X} = \begin{pmatrix} 1 & 3 & 2 \\ 2 & 2 & 1 \\ 0 & 1 & 0 \\ 4 & 3 & 5 \end{pmatrix}$$
$$\mathbf{R} = \begin{pmatrix} 1 & 0 & 0 \\ 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix} \qquad \mathbf{M} = \begin{pmatrix} 1.5 & 2.5 \\ 0 & 1 \\ 4.5 & 3 \end{pmatrix} \qquad \mathbf{C}^{\mathsf{T}} = \begin{pmatrix} 1 & 0 & 1 \\ 0 & 1 & 0 \end{pmatrix}$$

$$\mathbf{X} = \begin{pmatrix} 1 & 3 & 2 \\ 2 & 2 & 1 \\ 0 & 1 & 0 \\ 4 & 3 & 5 \end{pmatrix} \quad \mathbf{RMC}^{\mathsf{T}} = \begin{pmatrix} 1.5 & 2.5 & 1.5 \\ 1.5 & 2.5 & 1.5 \\ 0 & 1 & 0 \\ 4.5 & 3 & 4.5 \end{pmatrix}$$

$$\mathbf{R} = \begin{pmatrix} 1 & 0 & 0 \\ 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix} \qquad \mathbf{M} = \begin{pmatrix} 1.5 & 2.5 \\ 0 & 1 \\ 4.5 & 3 \end{pmatrix} \qquad \mathbf{C}^{\mathsf{T}} = \begin{pmatrix} 1 & 0 & 1 \\ 0 & 1 & 0 \end{pmatrix}$$

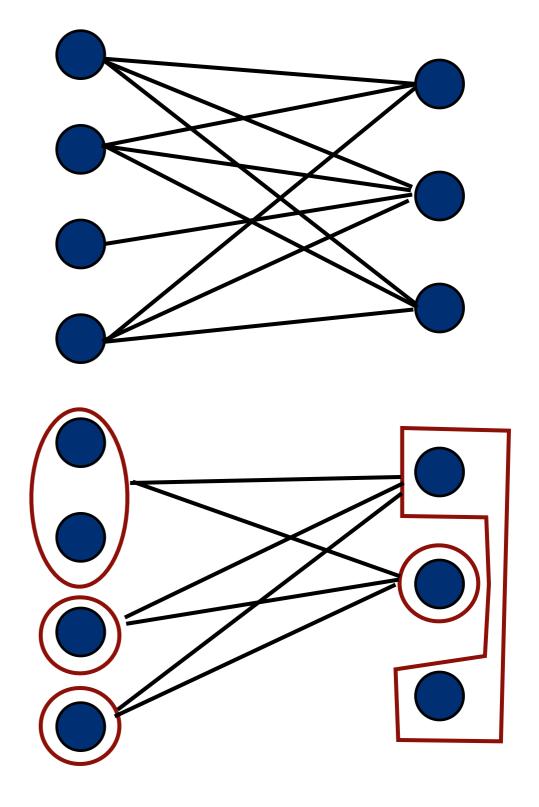
$$\mathbf{X} = \begin{pmatrix} 1 & 3 & 2 \\ 2 & 2 & 1 \\ 0 & 1 & 0 \\ 4 & 3 & 5 \end{pmatrix} - \mathbf{RMC}^{\mathsf{T}} = \begin{pmatrix} 1.5 & 2.5 & 1.5 \\ 1.5 & 2.5 & 1.5 \\ 0 & 1 & 0 \\ 4.5 & 3 & 4.5 \end{pmatrix} \middle| = \begin{pmatrix} 0.5 & 0.5 & 0.5 \\ 0.5 & 0.5 & 0.5 \\ 0 & 0 & 0 \\ 0.5 & 0 & 0.5 \end{pmatrix}$$
$$\mathbf{R} = \begin{pmatrix} 1 & 0 & 0 \\ 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix} \quad \mathbf{M} = \begin{pmatrix} 1.5 & 2.5 \\ 0 & 1 \\ 4.5 & 3 \end{pmatrix} \quad \mathbf{C}^{\mathsf{T}} = \begin{pmatrix} 1 & 0 & 1 \\ 0 & 1 & 0 \end{pmatrix}$$

Co-clustering and bipartite graphs

- A graph G=(V,E) is bipartite if its set of vertices can be partitioned into two sets, L and R, such that all edges in E have one end in L and other in R
- Any *n*-by-*m* matrix can be considered as a *weighted bipartite graph*
 - -Rows correspond to vertices in L
 - -Columns correspond to vertices in R
 - -Edge (i,j) has weight x_{ij}
- A co-clustering now clusters vertices in *L* and vertices in *R* and replaces edges in *E* with edges between the clusters having weights μ_{IJ}

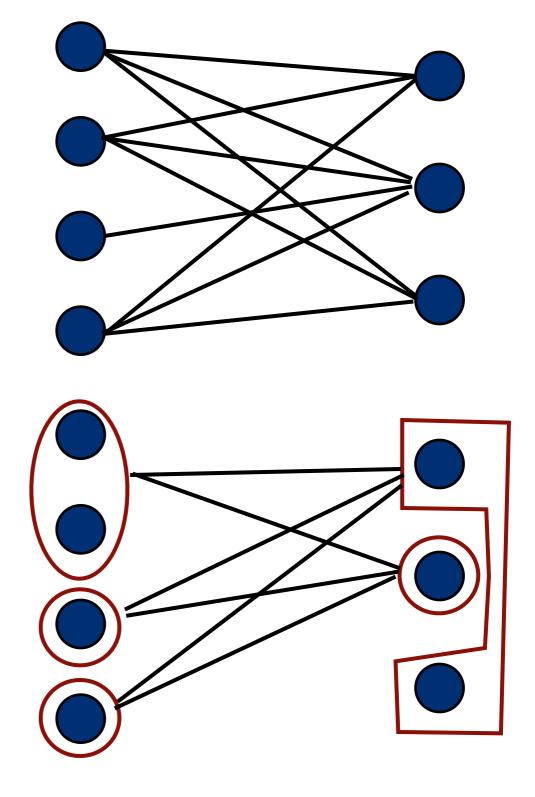


$$\mathbf{X} = \begin{pmatrix} 1 & 3 & 2 \\ 2 & 2 & 1 \\ 0 & 1 & 0 \\ 4 & 3 & 5 \end{pmatrix}$$





$$\mathbf{X} = \begin{pmatrix} 1 & 3 & 2 \\ 2 & 2 & 1 \\ 0 & 1 & 0 \\ 4 & 3 & 5 \end{pmatrix}$$



$$\mathbf{RMC}^{\mathsf{T}} = \begin{pmatrix} 1.5 & 2.5 & 1.5 \\ 1.5 & 2.5 & 1.5 \\ 0 & 1 & 0 \\ 4.5 & 3 & 4.5 \end{pmatrix}$$

Algorithm

- **1. input** data matrix X and two integers k and l
- 2. Cluster the rows of X to R (using e.g. k-means)
- **3.** Cluster the columns of X to C
- 4. Let $M = (\mu_{IJ}), \mu_{IJ} = (|I| |J|)^{-1} \sum_{i \in I, j \in J} x_{ij}$
- **5. return** *R*, *C*, and *M*

Chapter VIII.5: Discussion and clustering applications

- 1. Local and global patterns
- 2. Kleinberg's impossibility theorem
- **3. Example clustering applications**

Local and global patterns

- The quality of an association rule depends only on the rule itself
- The quality of a cluster depends on all the clusters in the clustering
 - Singleton clusters have the least SSE, but having *k*-1 singletons and one big cluster typically gives high total SSE
- Association rules are *local* patterns
 Their goodness depends only on the local part of the data
- Clusters are *global* patterns
 The overall quality depends also on points not in the cluster

Kleinberg's impossibility theorem

- A *clustering function* is a function f that takes a distance matrix D and returns a partition Γ
 - -We expect nothing on the type of points
 - -Distance is given using an implicit distance matrix
 - The number of clusters is defined somehow by the clustering function (build-in constant or something else)
 - -For example, an algorithm returning a *k*-means clustering to k=10 clusters could be one clustering function
- Idea: list some properties any clustering function should satisfy and show that none can satisfy them all

Three properties

- Scale-invariance
 - -Clustering does not change if we multiply the distances $-f(D) = f(\alpha D)$ for any $\alpha > 0$
- Richness
 - -For any partition Γ, there is a distance matrix *D* such that $f(D) = \Gamma$
- Consistency
 - The clustering does not change if we move points in the same cluster closer to each other and points in different clusters further away from each other

Impossibility result

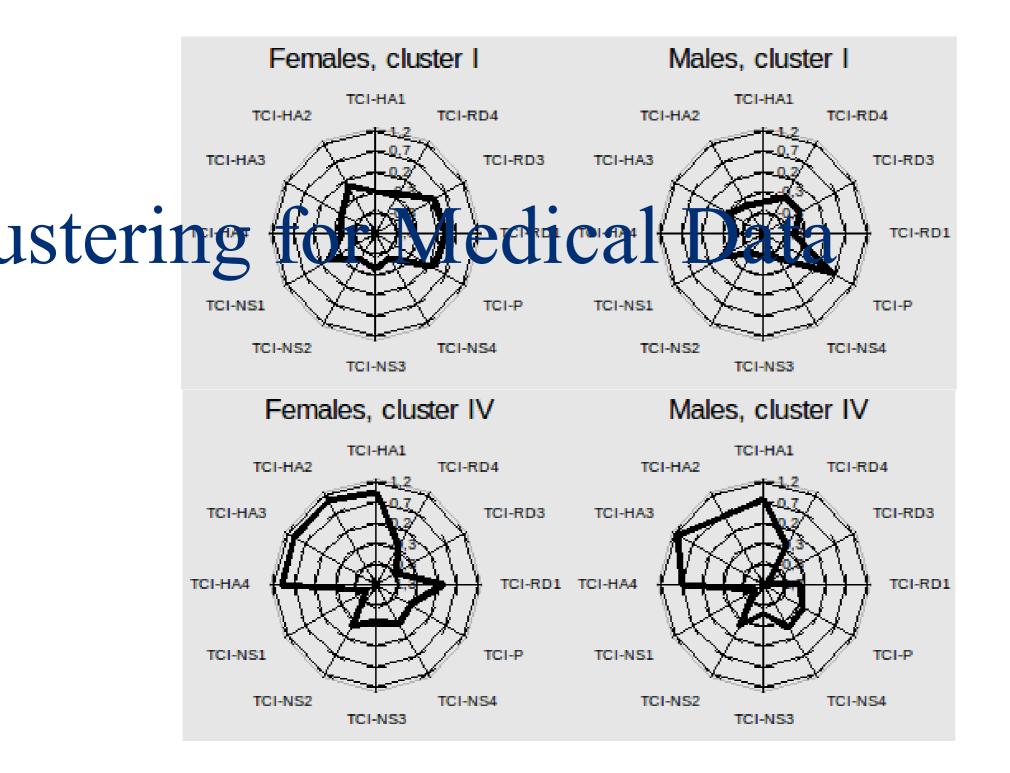
Theorem [Kleinberg '02]. There does not exist any clustering function *f* that satisfies all three properties.

- Single-link hierarchical clustering that stops at *k* < *n* clusters satisfies scale-invariance and consistency
- Single-link clustering that stops when the link length is some predefined fraction of maximum pairwise distance satisfies scale-invariance and richness
- Single-link that stops when the link length is longer than some predefined length satisfies richness and consistency

Some clustering applications

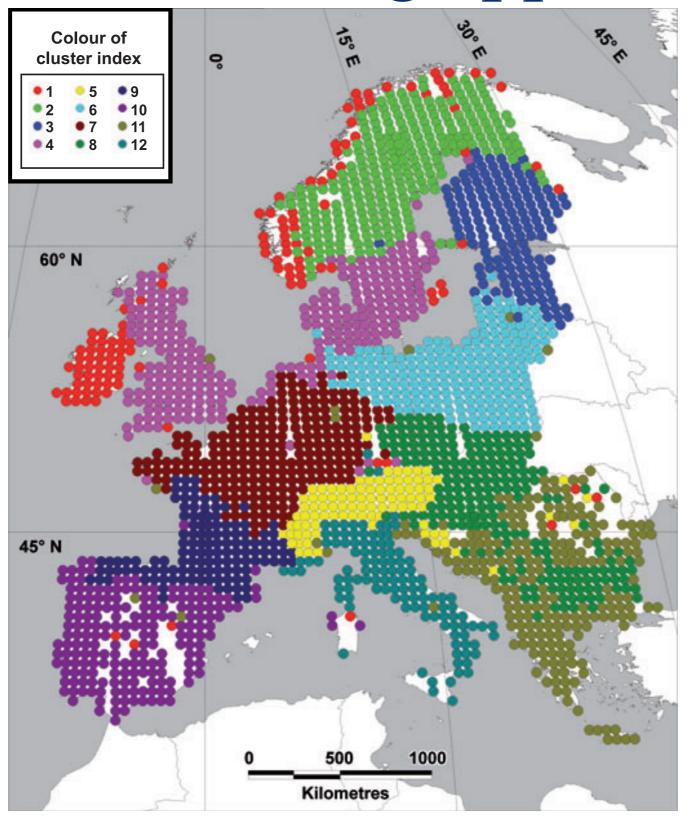
- Biology
 - -Creation of phylogenies (relations between organisms)
 - Inferring population structures from clusterings of DNA data
 - -Analysis of genes and cellular processes (co-clustering)
- Business
 - -Grouping of consumers into market segments
- Computer science
 - -Pre-processing step to reduce computation (representativebased methods)
 - -Automatic discovery of similar items

More clustering applications



Wessman: Clustering methods in the analysis of complex diseases

Even more clustering applications



Heikinheimo et al.: Clustering of European mammals, 2007