# STAT406- Methods of Statistical Learning Lecture 21

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#### Clustering

#### Dissimilarity measures

- $d(a, b) \ge 0$
- d(a, b) = 0 iff a = b
- d(a, b) = d(b, a)
- $d(\mathbf{a}, \mathbf{b}) \leq d(\mathbf{a}, \mathbf{d}) + d(\mathbf{d}, \mathbf{b})$

#### Clustering

#### Dissimilarity measures

• Euclidean distance –  $L_p$  distances

$$-d\left(\mathbf{a},\mathbf{b}\right) = \left[\sum_{j=1}^{k}\left|\mathbf{a}_{j}-\mathbf{b}_{j}\right|^{p}\right]^{1/p}$$

L<sub>∞</sub>

$$-d(\mathbf{a},\mathbf{b}) = \max_{1 \leq j \leq k} |\mathbf{a}_j - \mathbf{b}_j|$$

#### Clustering

#### When $a_j \in \{0, 1\}$

 We can use the number of matches / mismatches

	0	1
0	а	b
1	С	d

- (b+c)/k = proportion of mismatches
- 1 d/k = 1 proportion of 1-1 matches
- Presence is more significant than absence: "person likes Kenneth J. Harvey"

#### Agglomerative methods

- 1. Start with n clusters,  $C_1, \ldots, C_n$  each with one point
- 2. Find the pair of closest clusters,  $C_a$ ,  $C_b$
- 3. Merge them into  $C_{(ab)}$ , find  $d\left(C_{(ab)},C_{j}\right)$  for all other clusters  $C_{i}$
- 4. Repeat until all observations belong in one cluster

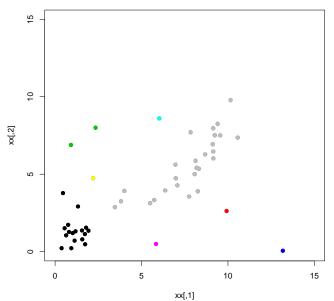
#### Agglomerative methods

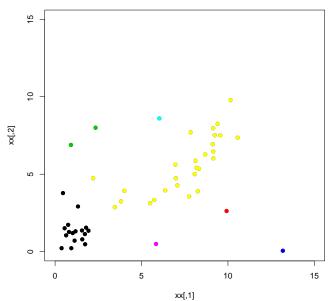
Different choices for  $d(C_{(ab)}, C_j)$ :

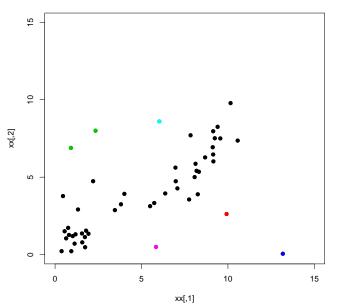
- Single linkage
- Complete linkage
- Average linkage
- Ward's "information" criterion

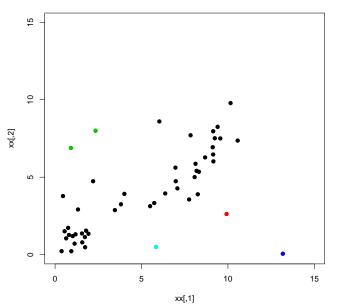
The **distance** between two **clusters** is the **minimum** distance between any **two elements**:

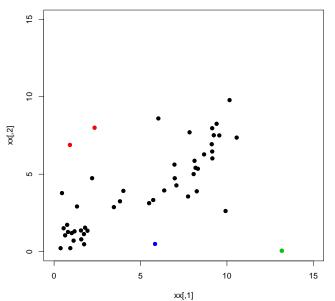
$$\mathcal{C}_1 = \{a_1, \dots, a_n\}$$
  $\mathcal{C}_2 = \{b_1, \dots, b_m\}$   $d(\mathcal{C}_1, \mathcal{C}_2) =$   $\min \{d(a_1, b_1), d(a_1, b_2), \dots, d(a_n, b_m)\}$ 

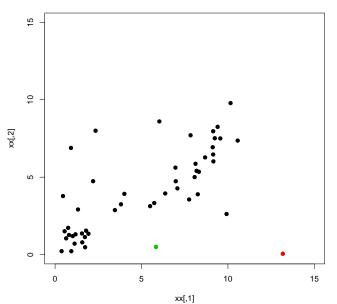


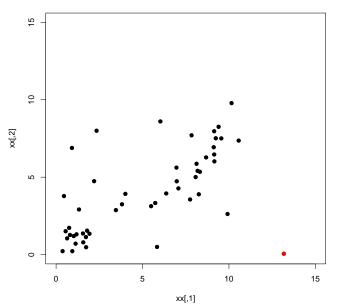


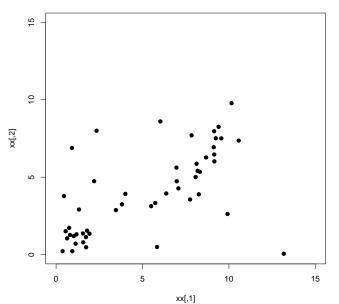






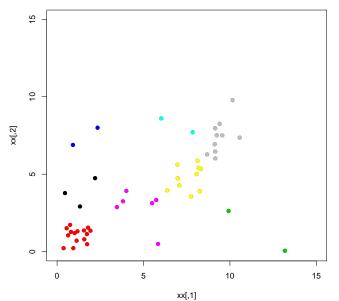


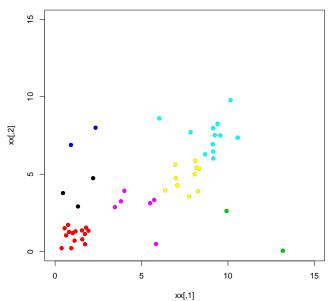


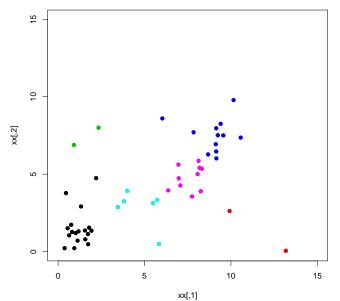


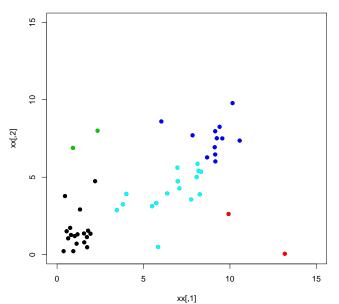
The **distance** between two **clusters** is the **maximum** distance between any **two elements**:

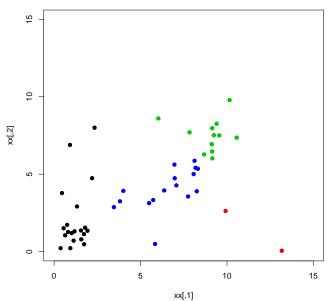
$$\mathcal{C}_1 = \{a_1, \dots, a_n\}$$
  $\mathcal{C}_2 = \{b_1, \dots, b_m\}$   $d(\mathcal{C}_1, \mathcal{C}_2) = \max \{d(a_1, b_1), d(a_1, b_2), \dots, d(a_n, b_m)\}$ 

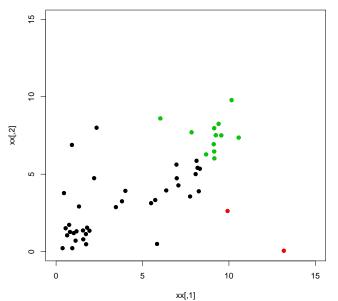


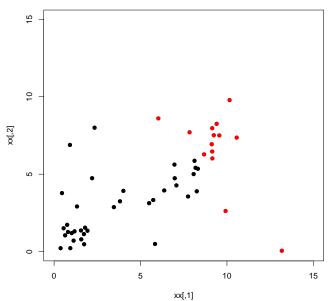


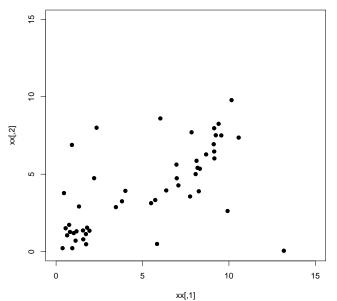






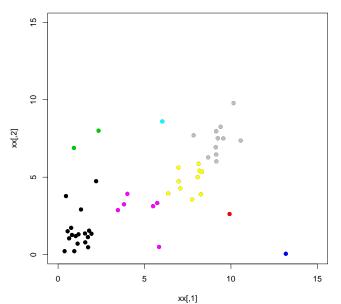


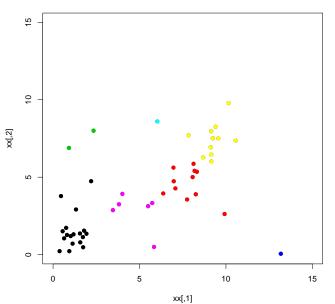


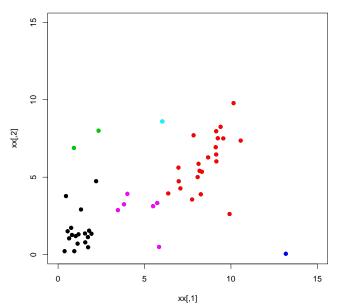


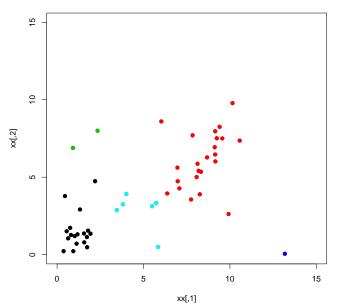
The **distance** between two **clusters** is the **average** of all pairwise distances between any **two elements**:

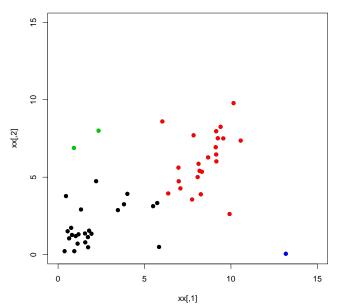
$$C_1 = \{a_1, \dots, a_n\} \qquad C_2 = \{b_1, \dots, b_m\}$$
$$d(C_1, C_2) = \frac{1}{n m} \sum_{i=1}^n \sum_{j=1}^m d(a_j, b_j)$$

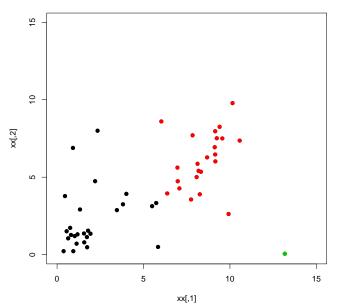


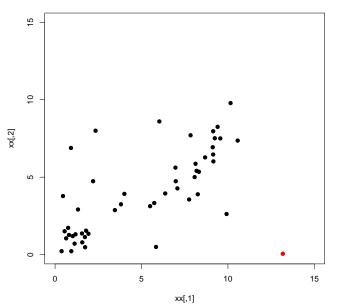


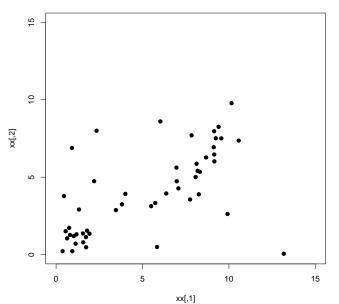












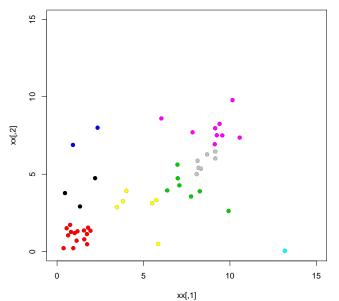
#### Ward's information criterion

A different merging criterion. Merge those two clusters that would result in the smallest increase in "within cluster sum of squares"

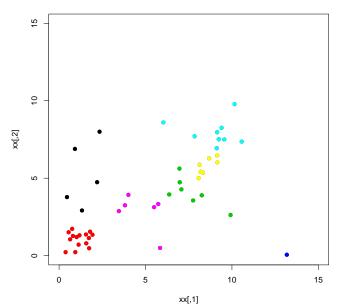
$$SS(C_r) = \sum_{i \in C_r} \sum_{i \in C_r} d^2(\mathbf{X}_i, \mathbf{X}_j)$$

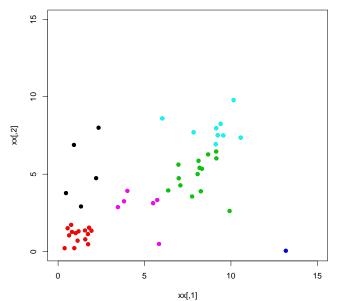
Total SS 
$$= \sum_{r} SS(C_r)$$

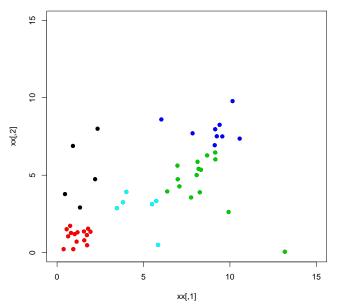
#### Ward's information criterion

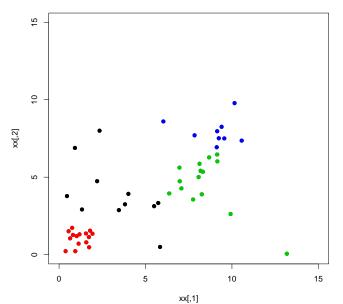


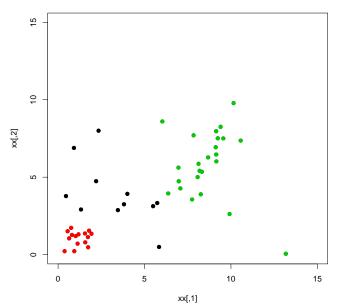
#### Ward's information criterion

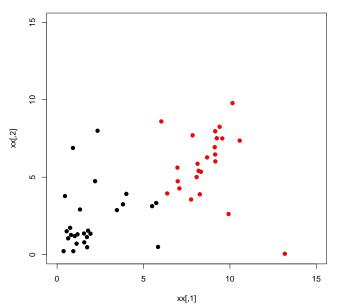


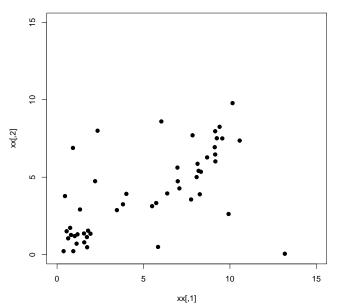












#### Languages

TABLE 12.3 NUMERALS IN 11 LANGUAGES

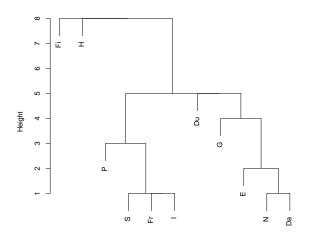
English (E)	Norwegian (N)	Danish (Da)	Dutch (Du)	German (G)	French (Fr)	Spanish (Sp)	Italian (I)	Polish (P)	Hungarian (H)	Finnish (Fi)
one	en	en	een	eins	un	uno	uno	jeden	egy	yksi
two	to	to	twee	zwei	deux	dos	due	dwa	ketto	kaksi
three	tre	tre	drie	drei	trois	tres	tre	trzy	harom	kolme
four	fire	fire	vier	vier	quatre	cuatro	quattro	cztery	negy	neua
five	fem	fem	vijf	funf	cinq	cinco	cinque	piec	ot	viisi
six	seks	seks	zes	sechs	six	seis	sei	szesc	hat	kuusi
seven	sju	syv	zeven	sieben	sept	siete	sette	siedem	het	seitseman
eight	atte	otte	acht	acht	huit	ocho	otto	osiem	nyolc	kahdeksan
nine	ni	ni	negen	neun	neuf	nueve	nove	dziewiec	kilenc	yhdeksan
ten	ti	ti	tien	zehn	dix	diez	dieci	dziesiec	tiz	kymmenei

## Languages - Dissimilarities

	Е	Ν	Da	Du	G	Fr	S	I	Р	Н	Fi
Е											
Ν	2										
Da	2	1									
Du	7	5	6								
G	6	4	5	5							
Fr	6		6	9	7						
S	6	6	5	9	7	2					
	6	6	5	9	7	1	1				
Р	7	7	6	10	8	5	3	4			
Н	9	8	8	8	9	10	10	10	10		
Fi	9	9	9	9	9	9	9	9	9	8	

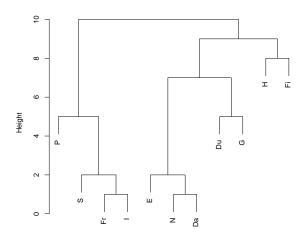
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# Languages - Single linkage



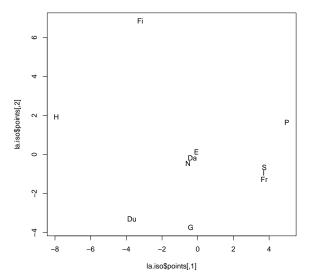
as.dist(a.la) hclust (\*, "single")

# Languages - Complete linkage

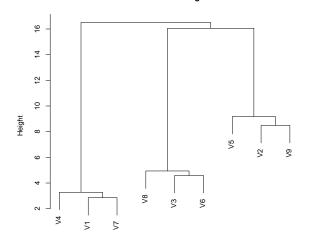


as.dist(a.la) hclust (\*, "complete")

# Languages - 2D representation via Multidimensional Scaling

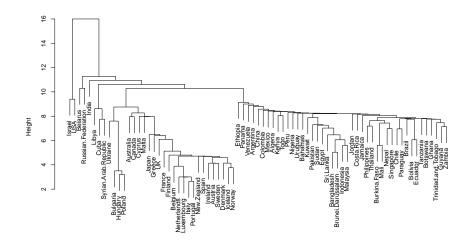


# Breweries - Single linkage

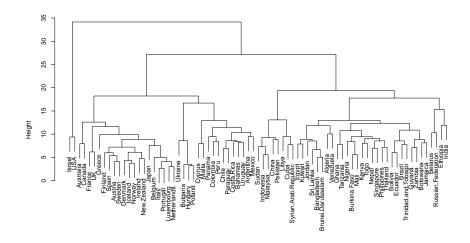


a.dis hclust (\*, "single")

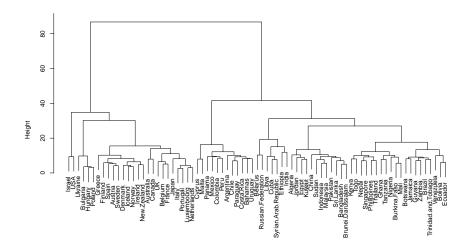
## UN Votes - Single linkage



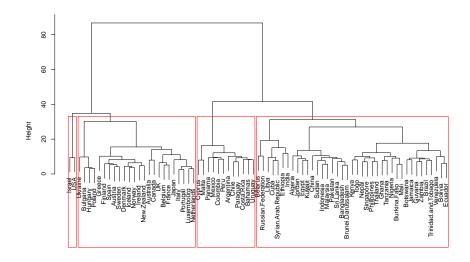
#### **UN Votes - Complete linkage**



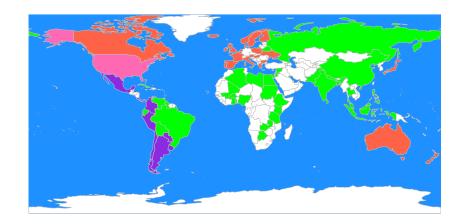
### UN Votes - Ward linkage



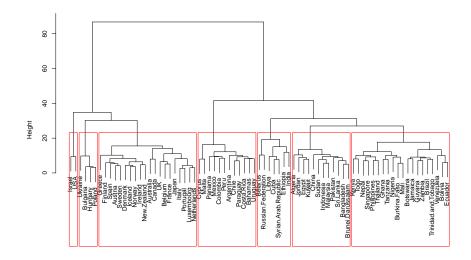
### UN Votes - Ward linkage



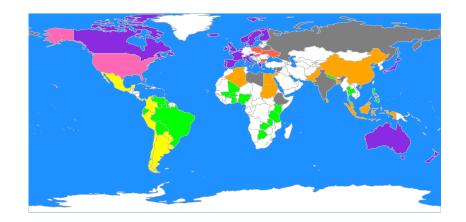
#### UN Votes - hierarchical - K=4



### UN Votes - Ward linkage



#### UN Votes - hierarchical - K=7

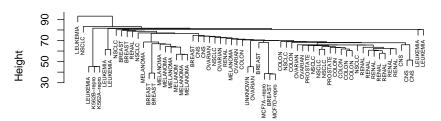


#### Cancer example

- Gene expression for 64 samples
- There are 6830 genes
- $X_1, X_2, \ldots, X_{64} \in \mathbb{R}^{6830}$
- We do know the label of each sample (which tissue this sample came from)
- The real problem is then "variable selection"

## Cancer example - Single

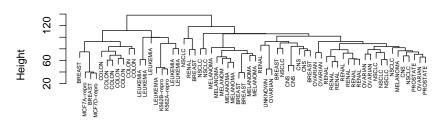
#### **Cluster Dendrogram**



nci.dis hclust (\*, "single")

#### Cancer example - Complete

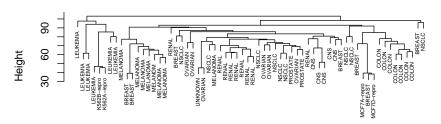
#### **Cluster Dendrogram**



nci.dis hclust (\*, "complete")

## Cancer example - Average

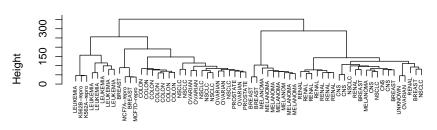
#### **Cluster Dendrogram**



nci.dis hclust (\*, "average")

## Cancer example - Ward

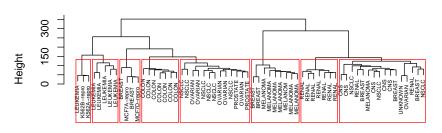
#### **Cluster Dendrogram**



nci.dis hclust (\*, "ward")

# Cancer example - Ward - 8 clusters

#### **Cluster Dendrogram**



nci.dis hclust (\*, "ward")