

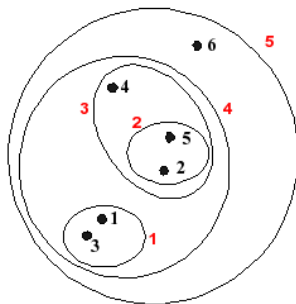
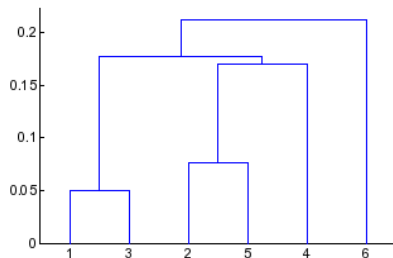
# STATS 415: Hierarchical Clustering

Prof. Liza Levina

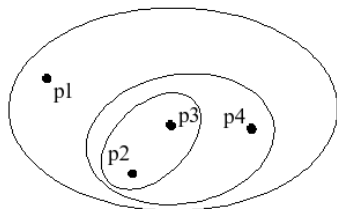
Department of Statistics, University of Michigan

# Hierarchical Clustering

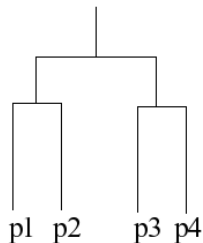
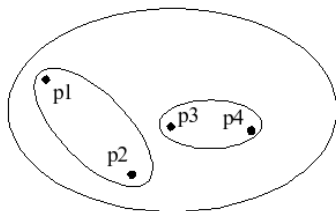
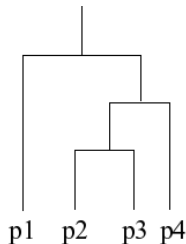
- A set of “**nested**” clusters organized as a hierarchical tree.
- Can be visualized as a **dendrogram** – a tree-like diagram that records the sequences of merges or splits.



# Examples



**Traditional Hierarchical Clustering**

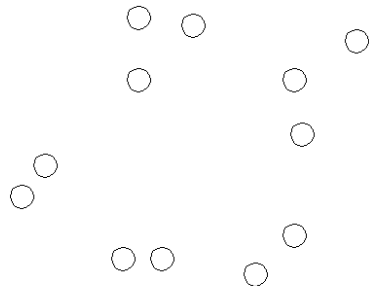


# Two types of hierarchical clustering

- Agglomerative
  - Start with the points as individual clusters
  - At each step, merge the closest pair of clusters until only one cluster (or  $K$  clusters) left
- Divisive
  - Start with one, all-inclusive cluster
  - At each step, split a cluster until each cluster contains a point (or there are  $K$  clusters)

# Start

Start with clusters of individual points and a dissimilarity matrix



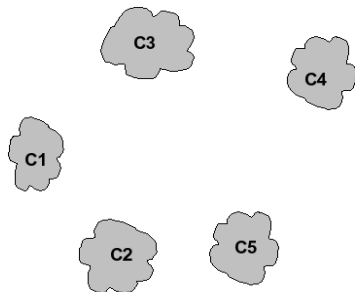
	p1	p2	p3	p4	p5	...
p1						
p2						
p3						
p4						
p5						
.						
.						
.						

**Proximity Matrix**



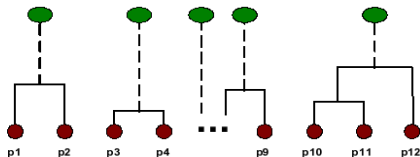
# Intermediate

After some merging steps, we have clusters:



	C1	C2	C3	C4	C5
C1					
C2					
C3					
C4					
C5					

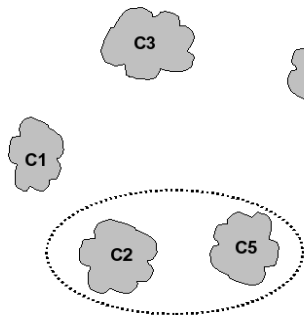
**Proximity Matrix**



# Take the next step

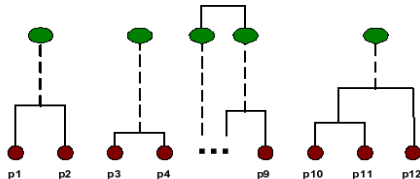
We want to merge two closest clusters:

- How do we determine which are closest?



	C1	C2	C3	C4	C5
C1					
C2					
C3					
C4					
C5					

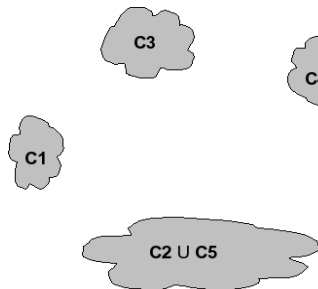
**Proximity Matrix**



# After Merging

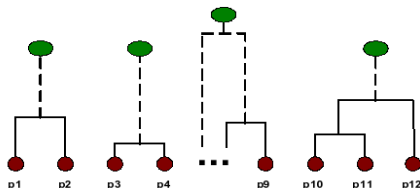
Let's say we merged C2 and C5.

- How do we update the dissimilarity matrix?



		C2 U C5		
	C1	C5	C3	C4
C1		?		
C2 U C5	?	?	?	?
C3		?		
C4		?		

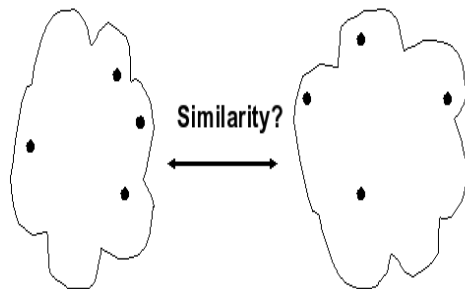
**Proximity Matrix**





# Dissimilarity between clusters

Answering both questions requires computing dissimilarity between clusters, not just pairs of points.



	p1	p2	p3	p4	p5	...
p1						
p2						
p3						
p4						
p5						
.						

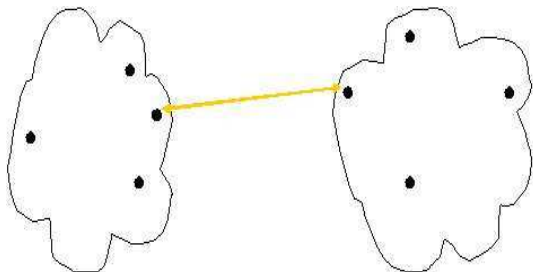
# Cluster dissimilarity measures

- Single linkage (min)
- Complete linkage (max)
- Average linkage
- Distance between centroids
- Other methods driven by various loss functions

# Single (min) linkage

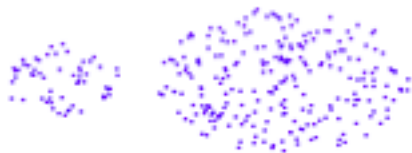
Distance between two nearest points:

$$d(C_1, C_2) = \min_{s,t} \{d(s,t) : s \in C_1, t \in C_2\}$$



# Strengths of min linkage

Can handle diverse shapes/sizes



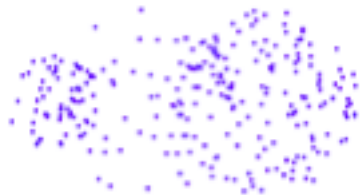
**Original Points**



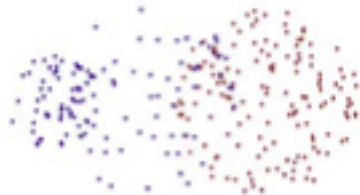
**Two Clusters**

# Weaknesses of min linkage

Sensitive to noise and outliers



**Original Points**

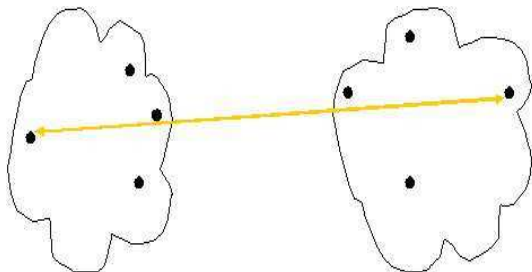


**Two Clusters**

# Complete (max) linkage

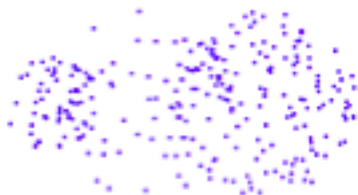
Distance between the **farthest** points

$$d(C_1, C_2) = \max_{s,t} \{d(s,t) : s \in C_1, t \in C_2\}$$

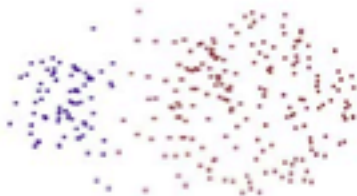


# Strengths of max linkage

Robust to noise and outliers



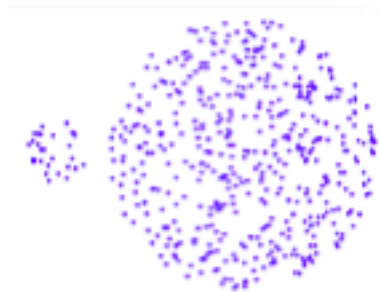
**Original Points**



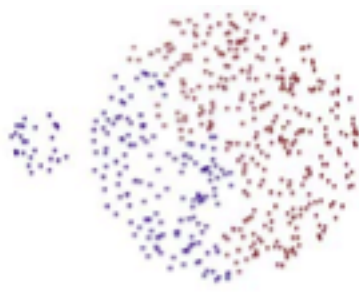
**Two Clusters**

# Weaknesses of max linkage

- Tendency towards breaking large clusters
- Preference for spherical clusters



**Original Points**



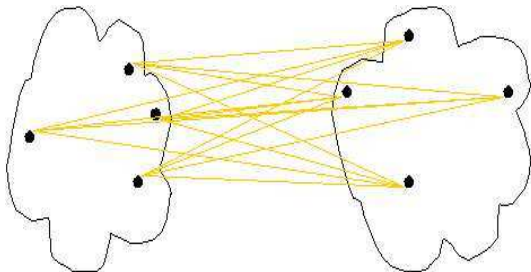
**Two Clusters**



# Average linkage

Average of distances between all pairs of points

$$d(C_1, C_2) = \frac{\sum_{s \in C_1} \sum_{t \in C_2} d(s, t)}{n_1 n_2}$$



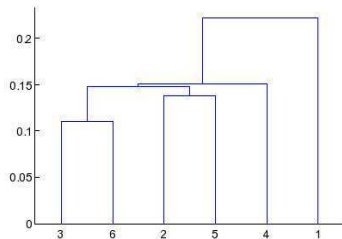
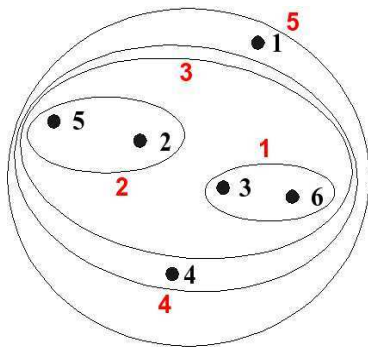
# Properties of average linkage clustering

- Compromise between min and max linkage clustering
- Less susceptible to noise and outliers than min linkage; but more so than max linkage
- Still has a preference for spherical clusters, but less so than max linkage
- In practice often ends up similar to one of them

## Toy example: dissimilarity matrix

	P1	P2	P3	P4	P5	P6
P1	0.000	0.234	0.216	0.368	0.342	0.235
P2	0.234	0.000	0.145	0.194	0.143	0.243
P3	0.216	0.145	0.000	0.158	0.285	0.102
P4	0.368	0.194	0.158	0.000	0.284	0.220
P5	0.342	0.143	0.285	0.284	0.000	0.386
P6	0.235	0.243	0.102	0.220	0.386	0.000

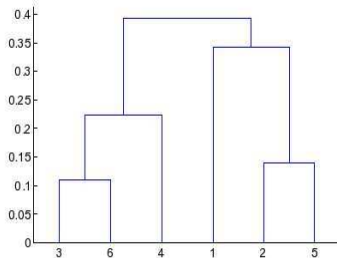
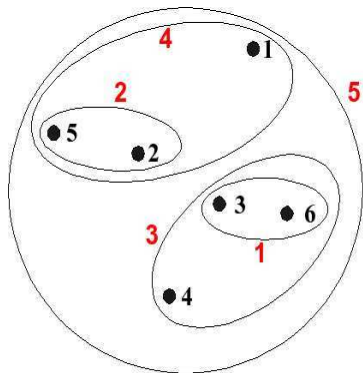
# Toy example: min linkage



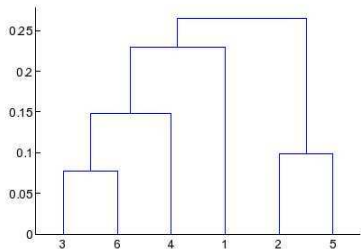
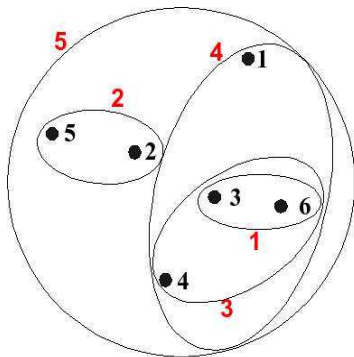
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P4	0.368	0.194	0.158	0.000	0.284	0.220
P5	0.342	0.143	0.285	0.284	0.000	0.386
P6	0.235	0.243	0.102	0.220	0.386	0.000

# Toy example: complete linkage

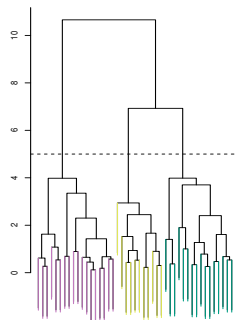
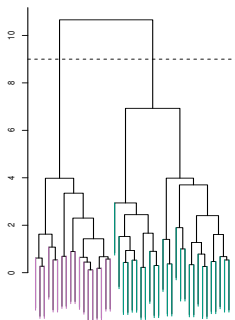
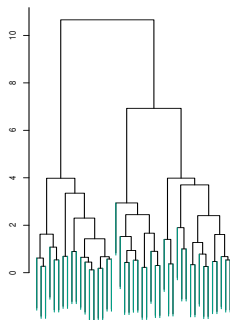


# Toy example: average linkage



# Choosing Clusters

- To choose clusters we draw lines across the dendrogram
- We can form any number of clusters depending on where we draw the line, from  $K = 1$  to  $K = n$





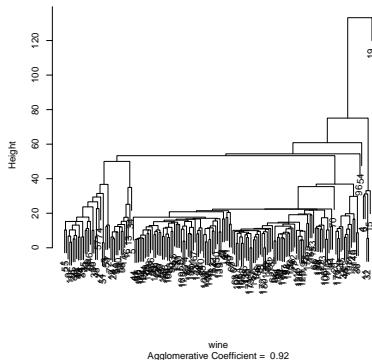
# Example: the wine data

180 wines, 13 variables

- 1) Alcohol
- 2) Malic acid
- 3) Ash
- 4) Alcalinity of ash
- 5) Magnesium
- 6) Total phenols
- 7) Flavanoids
- 8) Nonflavanoid phenols
- 9) Proanthocyanins
- 10) Color intensity
- 11) Hue
- 12) OD280/OD315 of diluted wines
- 13) Proline

# Wine data: min linkage clustering

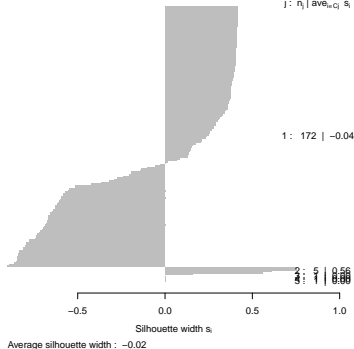
Dendrogram of `agnes(x = wine, diss = F, method = "single")`



Silhouette plot of `(x = cutree(wine.single, k = 5), dist = diss_wine)`

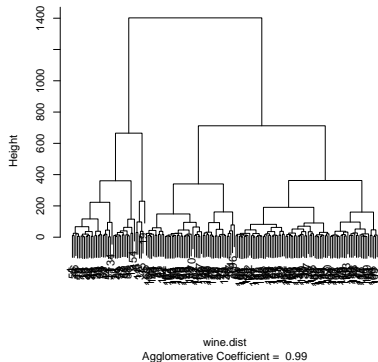
n = 180

5 clusters  $C_j$   
 $j: n_j | \text{ave}_{w(C_j)} s_j$

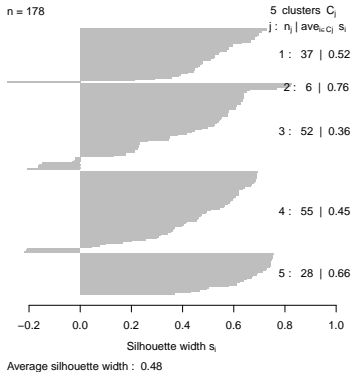


# Wine data: max linkage clustering

Dendrogram of `agnes(x = wine.dist, method = "complete")`

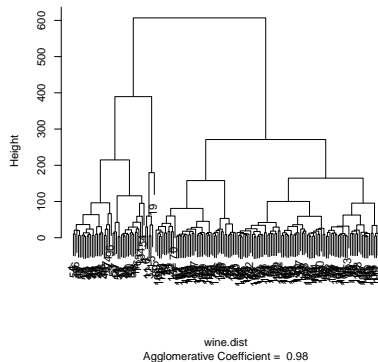


Silhouette plot of `(x = cutree(wine.agnes, k = 5), dist = dai`

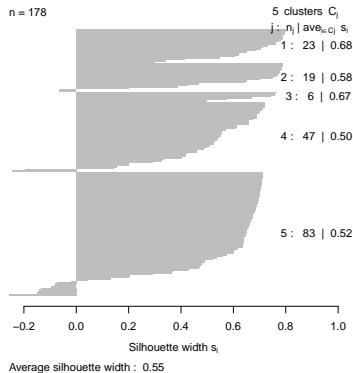


# Wine data: average linkage clustering

Dendrogram of `agnes(x = wine.dist, method = "average")`



Silhouette plot of `(x = cutree(wine.agnes, k = 5), dist = dai`



# Wine data example summary

- All methods but single linkage are similar; this is not uncommon
- The silhouette plot tends to give better visual assessment than the dendrogram
- The agglomerative coefficient tends to be not as informative as the silhouette width

# Advantages of hierarchical clustering

- Gives a family of possible solutions; any number of clusters can be obtained by “cutting” the dendrogram at the appropriate level
- Computationally fast
- Does not require raw data, only distances (or dissimilarities) between points

# Disadvantages of hierarchical clustering

- No global optimization criterion, greedy algorithm
- No objective way to choose where to stop (“cut” the tree)
- Different ways of measuring distance between clusters can give rise to very different solutions