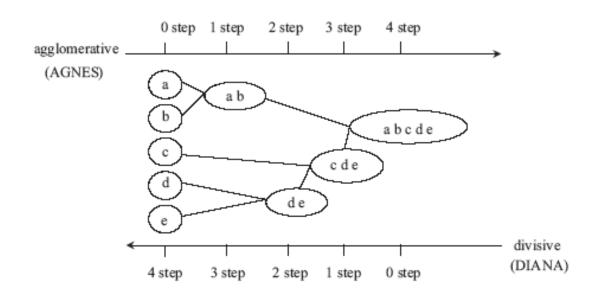
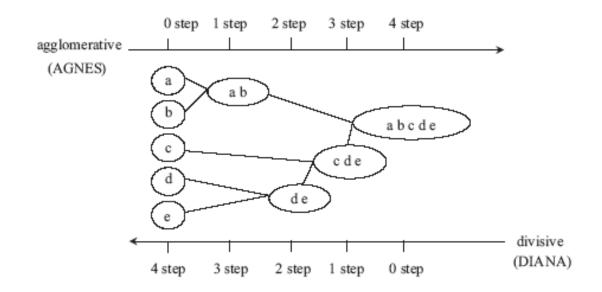
• They work by grouping data objects into a tree of clusters

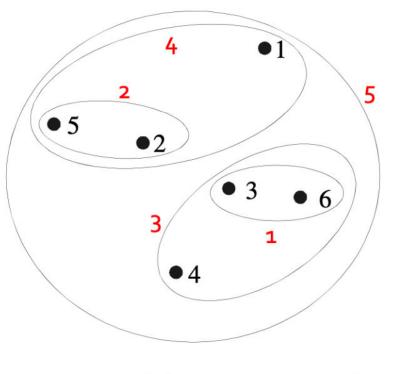


# Hierarchical Clustering Agglomerative

- It is a bottom-up strategy
- It first places each object in its own cluster
- Then merges these clusters into larger and larger clusters



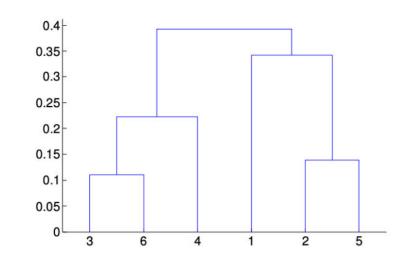
### Agglomerative



Nested Clusters

Dendrogram

|   | 1   | 2   | 3   | 4   | 5   | 6   |
|---|-----|-----|-----|-----|-----|-----|
| 1 | 0   | .24 | .22 | -37 | .34 | .23 |
| 2 | .24 | 0   | .15 | .20 | .14 | .25 |
| 3 | .22 | .15 | 0   | .15 | .28 | .11 |
| 4 | -37 | .20 | .15 | 0   | .29 | .22 |
| 5 | .34 | .14 | .28 | .29 | 0   | .39 |
| 6 | .23 | .25 | .11 | .22 | -39 | 0   |

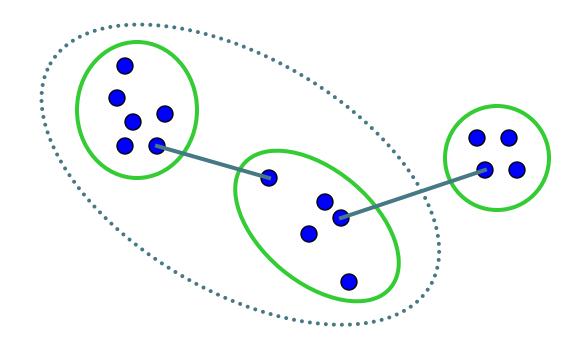


• The splitting and merging of clusters is based on distance measures

• Four widely used distance measures are

# Single Link

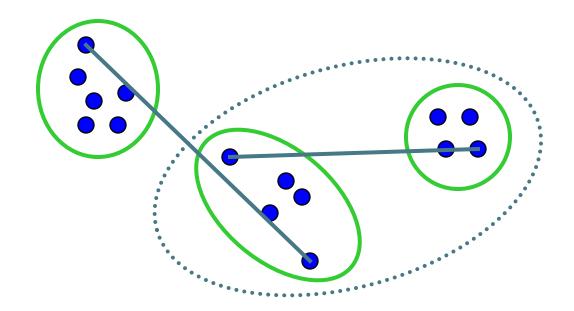
• cluster similarity = similarity of two most similar members



Minimum distance:  $d_{min}(C_i, C_j) = min_{p \in C_i, p' \in C_j} |p - p'|$ 

# Complete Link

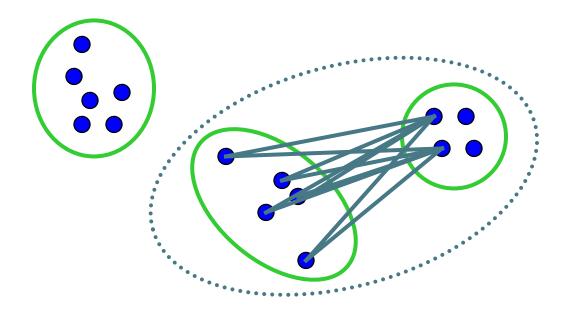
 cluster similarity = similarity of two least similar members



**Maximum** distance:  $d_{max}(C_i, C_j) = max_{p \in C_i, p' \in C_j} |p - p'|$ 

# **Group Average**

 cluster similarity = average similarity of all pairs



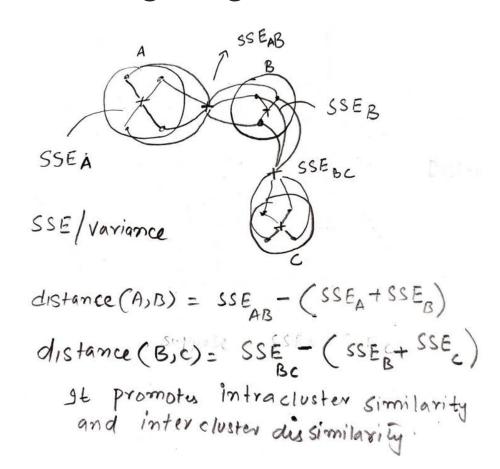
Average distance:  $d_{avg}(C_i, C_j) = \frac{1}{n_i n_j} \sum_{p \in C_i} \sum_{p' \in C_j} |p - p'|$ 

Mean distance:  $d_{mean}(C_i, C_j) = |m_i - m_j|$ 

where  $m_i$  is the mean data object of cluster  $C_i$ 

### **WARD**

• 'ward' minimizes the variance of the clusters being merged.



Example: Let us consider five data samples: A, B, C, D, and E

Let the inter-point distances between these examples be given by the following distance matrix.

$$A \quad B \quad C \quad D \quad E$$

$$A \quad 0$$

$$DM(1) = \begin{cases} B & 1 & 0 \\ C & 5 & 3 & 0 \\ D & 6 & 8 & 4 & 0 \\ E & 8 & 7 & 6 & 2 & 0 \end{cases}$$

Using the *nearest neighbor* measure, also known as the *single linkage* measure, we merge A and B to form a cluster, since they are closest.

Next we compute the distances between this cluster and the remaining examples. We can get these distances from the above distance matrix.

The values for these are as follows:

$$d(AB)C = min\{dAC, dBC\} = dBC = 3$$
  
 $d(AB)D = min\{dAD, dBD\} = dAD = 6$   
 $d(AB)E = min\{dAE, dBE\} = dBE = 7$ 

#### **Updated distance matrix**

$$AB \quad C \quad D \quad E$$

$$AB \quad 0$$

$$DM(2) = \begin{cases} C & 3 & 0 \\ D & 6 & 4 & 0 \\ E & 7 & 6 & 2 & 0 \end{cases}$$

Since the smallest entry in above distance matrix is 2, examples D and E are merged to form another cluster

#### **Updated distance matrix**

$$\mathbf{DM}(3) = \begin{pmatrix} AB & C & DE \\ AB & 0 \\ C & 3 & 0 \\ DE & 6 & 4 & 0 \end{pmatrix}$$

This matrix indicates that C should be merged with A and B.

At this stage we have only two clusters left that are joined to form a single cluster of five examples.

- Termination Condition
  - The user can specify the desired number of clusters as a termination condition
  - The quality of clusters can also be a termination condition

How to Choose the Number of Clusters: Lifetime Method

The *lifetime* of a cluster is defined as the absolute value of the difference between the dendrogram level at which it is created and the level at which it is absorbed into a larger cluster.

Using lifetime as a criterion, a user can search for cluster that have a large lifetime.

- The merge (or split) decisions are critical in these types of algorithms
- Once a merging (or splitting) of two clusters is made, it cannot be undone and furthering clustering proceeds on the basis of this decision