# Scientific Computing for Biologists

## Lecture 10: Clustering I

Instructor: Paul M. Magwene

04 November 2014

# Outline of Lecture

- Distance and dissimilarity measures
  - Quantitative data
  - Dichotomous data
  - Qualitative data
- Hierarchical clustering
- Neighbor-joining
- Minimum Spanning Tree (MST)

# Similarity/Dissimilarity

## Intuition

Similarity is a measure of "likeness" between two entities of interest. Dissimilarity is the complement of similarity.

- Dissimilarities may be converted to similarities (and vise versa) by taking any monotonically decreasing function. For example:

$$s = 1 - d_{ij} \text{ (for } 0 \leq d_{ij} \leq 1)$$

- Dissimilarities are usually in range $0 \leq d_{ij} \leq C$ where $C$ is the maximum dissimilarity
- Distances are one measure of dissimilarity but distances are unbounded to the right

$$d_{ij} \in [0, \infty]$$

# Dissimilarity Measures for Quantitative Data

- Euclidean distance

$$d_{ij} = \left\{ \sum_{k=1}^{p} (x_{ik} - x_{jk})^2 \right\}^{1/2}$$

- Scaled Euclidean distance

$$d_{ij} = \left\{ \sum_{k=1}^{p} w_k^2 (x_{ik} - x_{jk})^2 \right\}^{1/2}$$

  where $w_k$ are suitable weight for the $k$-th variable, e.g. $\sigma_{x_k}^{-1}$ or $(max(x_k) - min(x_k))^{-1}$

- Manhattan (taxi cab, city block) distance

$$d_{ij} = \sum_{k=1}^{p} |x_{ik} - x_{jk}|$$

# Dissimilarity Measures for Quantitative Data, cont.

- Manhattan (taxi cab, city block) distance

$$d_{ij} = \sum_{k=1}^{p} |x_{ik} - x_{jk}|$$

- Chebychev distance

$$d_{ij} = max_k \left\{ |x_{ik} - x_{jk}| \right\}$$

- Minkowski Metric

$$d_{ij} = \left\{ \sum_{k=1}^{p} |x_{ik} - x_{jk}|^{\lambda} \right\}^{1/\lambda}$$

$\lambda = 1$ is Manhattan distance, $\lambda = 2$ is Euclidean distance,
$\lambda = \infty$ is Chebychev distance.

# More distance measures

- Canberra distance (weighted Manhattan distance)

$$d_{ij} = \sum_{k=1}^{p} \frac{|x_{ik} - x_{jk}|}{|x_{ik}| + |x_{jk}|}$$

- Cosine distance

$$d_{ij} = \frac{x_{i\cdot} \cdot x_{j\cdot}}{|x_{i\cdot}||x_{j\cdot}|}$$

  where $x_{j\cdot}$ and $x_{j\cdot}$ indicate the row vectors, representing objects $i$ and $j$

- Hamming distance

$$d_{ij} = \frac{\text{count}(x_{ik} \neq x_{jk})}{p}$$

# Metric Distance Functions

A non-negative function, $g(x, y)$, is metric if:

1. $g(x, y)$ satisifies the triangle inequality:

$$g(x, y) \leq g(x, z) + g(y, z)$$

2. symmetric:

$$g(x, y) = g(y, x)$$

3. $g(x, y) = 0$ only if $x = y$

# Dissimilarity Measures for Dichotomous Data

For each pair of objects (samples) of interest form a $2 \times 2$ contigency table:

| | 1 | 0 |
|---|---|---|
| 1 | $a$ | $b$ |
| 0 | $c$ | $d$ |

- Simple matching coefficient:

$$d_{ij} = 1 - \frac{a+d}{p} = \frac{b+c}{p}$$

- Jaccard's coefficient (ignores joint absence):

$$d_{ij} = \frac{b+c}{a+b+c}$$

- Czenkanowski coefficient:

$$d_{ij} = \frac{b+c}{2a+b+c}$$

# Dissimilarity Measures for Variables

Correlation provides a suitable measure of *similarity*. Common *dissimilarity* measures based on correlation include:

- $d_{kl} = 1 - r_{kl}$ if $r_{kl} = -1$ is taken to indicate maximum disagreement
- $d_{kl} = 1 - r_{kl}^2$ if $r_{kl} = 1$ and $r_{kl} = -1$ are treated equivalently (predictive power)
- Based on uncentered correlation:

$$d_{kl} = 1 - \frac{\sum_{i=1}^{n} x_{ik} x_{il}}{\sum_{i=1}^{n} x_{ik}^2 \sum_{i=1}^{n} x_{il}^2}$$

# Introduction to Clustering

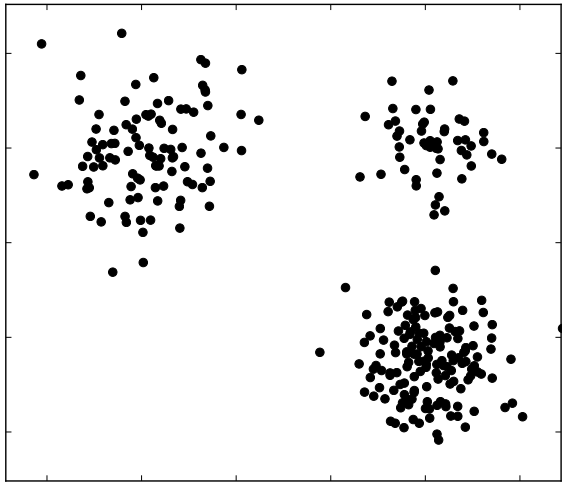
# Goal of Clustering

## Goal

Find “natural groups” in data

What’s a “natural group”?

- Patches of high density points surrounded by patches of lower density in the $p$-dimensional space defined by the variates.

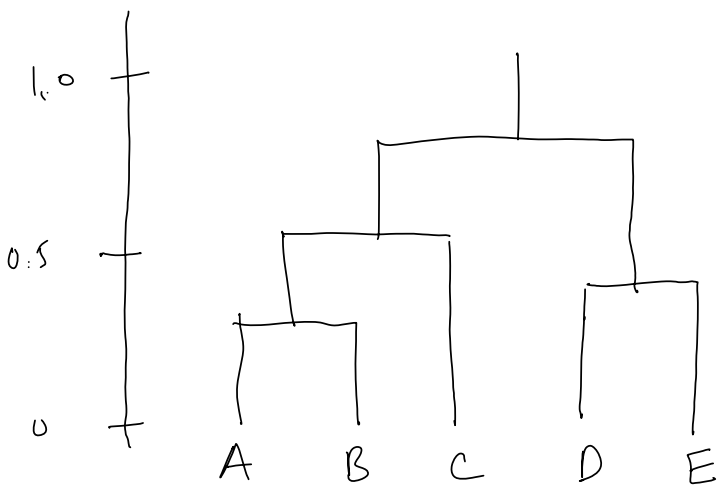


# Hierarchical Clustering

Agglomerative / Divisive methods

- In practice almost always agglomerative

For n data points define a set of n-1 joins that represent groupings of objects @ different levels of similarity



# Generic Algorithm for Agglomerative Hierarchical Clustering

1. Calculate a dissimilarity matrix for the $n$ items
2. Join the two nearest items, $i$ and $j$
3. Delete the $i$-th and $j$-th rows and columns of the dissimilarity matrix; and a new row/column that represents the dissimilarity of a new group $(i,j)$ to all other items
4. Repeat from step 2 until there is a single group

## Key Point

The different hierarchical clustering methods are determined by the function used to calculate the distance between groups in step 3.

# Single Linkage Clustering

## Group Distance Measure

Let $i$ and $j$ be groups, and $n_i$ and $n_j$ be the number of objects in the respective groups.

$D_{ij}$ is the *smallest* of the $n_i n_j$ dissimilarities between each element of $i$ and each element of $j$

Properties of Single Linkage Clustering

- Invariant under monotonic transformation of the $d_{ij}$
- Unaffected by ties
- Provably nice asymptotic properties
- Disadvantage: susceptible to chaining

# Hierarchical Clustering, A worked Example

| | A | B | C | D | E |
|---|---|---|---|---|---|
| A | 0 | | | | |
| B | 4 | 0 | | | |
| C | 1 | 4 | 0 | | |
| D | 4 | 2 | 4 | 0 | |
| E | 5 | 5 | 3 | 4 | 0 |

Single Linkage

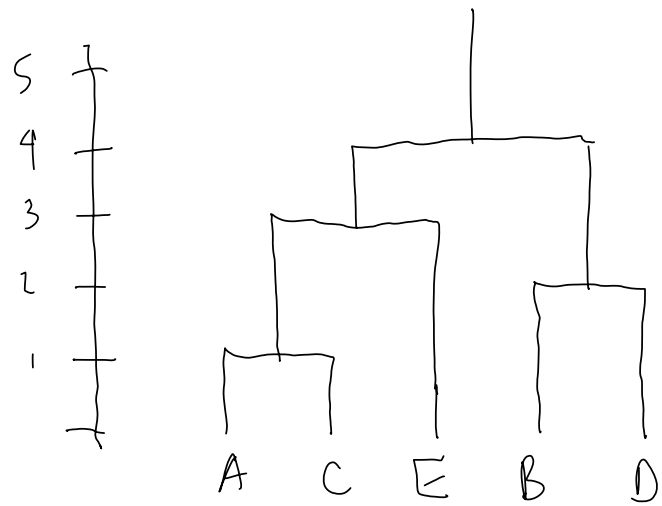
| | (A,C) | B | D | E |
|---|---|---|---|---|
| (A,C) | | | | |
| B | 4 | | | |
| D | 4 | 2 | 0 | |
| E | 3 | 5 | 4 | 0 |

| | (A,C) | (B,D) | E |
|---|---|---|---|
| (A,C) | 0 | | |
| (B,D) | 4 | 0 | |
| E | 3 | 4 | 0 |

# Worked Example, cont.

| | ((A, C), E) | (B, D) |
|---|---|---|
| ((A, C), E) | 0 | |
| (B, D) | 4 | 0 |

→ Only one Choice ((A, C), E), (B, D))




Single Linkage Clustering

# More Hierarchical Clustering Functions

Complete Linkage – $D_{ij}$ is the maximum of the $n_i n_j$ dissimilarities between the two groups.

Group Average Methods – $D_{ij}$ is the average of the $n_i n_j$ dissimilarities between the two group (UPGMA, WPGMA)

Centroid Method – $D_{ij}$ is the squared Euclidean distance between the centroids of groups $i$ and $j$

# Neighbor Joining

Originally described by Saitou and Nei, 1987.

**Goal**

Tries to create the (unrooted) tree topology with the least branch length (minimum-evolution criterion).

Basic algorithm:

1. Calculate matrix $Q$ (next slide) from the distance matrix
2. Find the pair of taxa in $Q$ with the lowest value; create a node on the tree that joins these two taxa (i.e. the closest neighbors)
3. Calculate the distance of each of the taxa in the pair to this new node
4. Calculate the distance of all taxa outside of this pair to the new node
5. Repeat from step 1 using the distances calculated in the previous step

# Neighbor Joining, cont.

$$Q_{ij} = (r - 2)d_{ij} - (R_i + R_j)$$

where $r$ is the number of taxa, $d_{ij}$ is the distance between taxa $i$ and $j$ and $R_k$ is the row sum over row $k$ of the distance matrix ($R_k = \sum_i d_{ik}$).

When nodes $i$ and $j$ are joined they are replaced by a node, $A$, with distance to a remaining node $k$ given by:

$$d_{Ak} = \frac{1}{2}(d_{ik} + d_{jk} - d_{ij})$$

# NJ example from Saitou and Nei 1987

**Table 1**
**Distance Matrix for the Tree in Figure 1**

| | OTU | | | | | | |
|---|---|---|---|---|---|---|---|
| OTU | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
| 2 .. | 7 | | | | | | |
| 3 .. | 8 | 5 | | | | | |
| 4 .. | 11 | 8 | 5 | | | | |
| 5 .. | 13 | 10 | 7 | 8 | | | |
| 6 .. | 16 | 13 | 10 | 11 | 5 | | |
| 7 .. | 13 | 10 | 7 | 8 | 6 | 9 | |
| 8 .. | 17 | 14 | 11 | 12 | 10 | 13 | 8 |

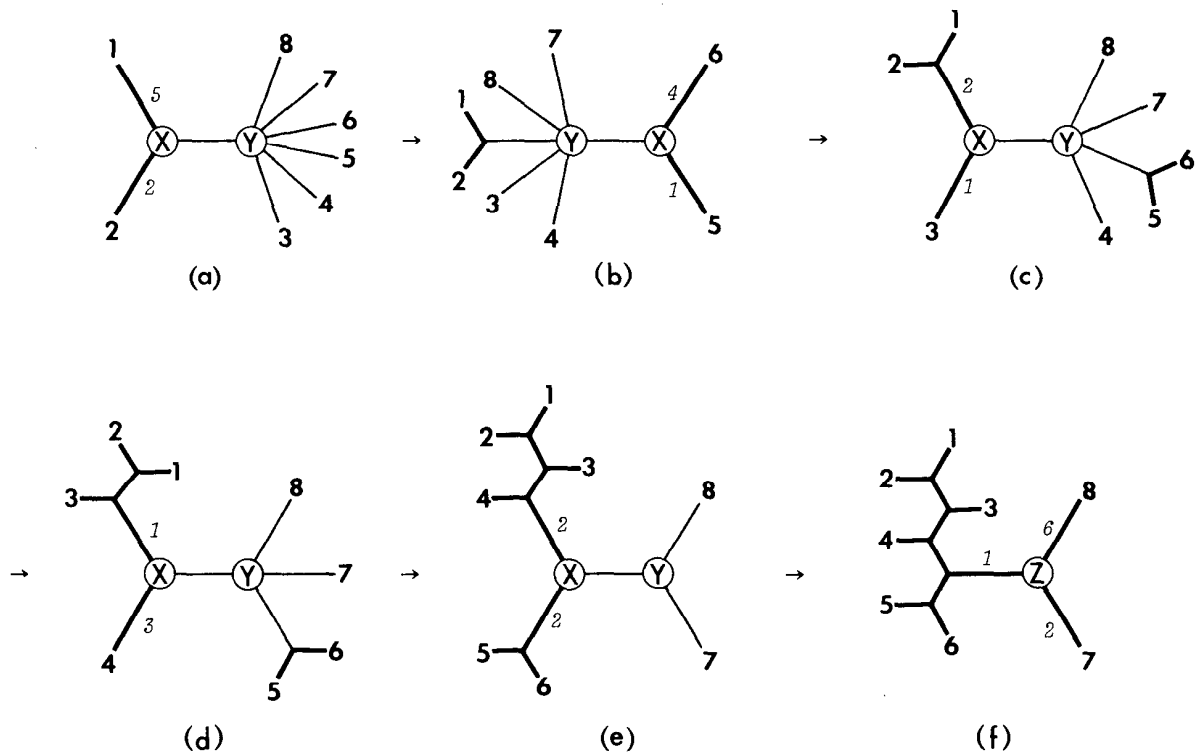



FIG. 3.—Application of the neighbor-joining method to the distance matrix of table 1. Italic numbers are branch lengths, and branches with thicker lines indicate that their lengths have been determined.

# Minimum Spanning Tree

**Goal**

Construct a tree that connects all points in the data set and whose total length is minimized.

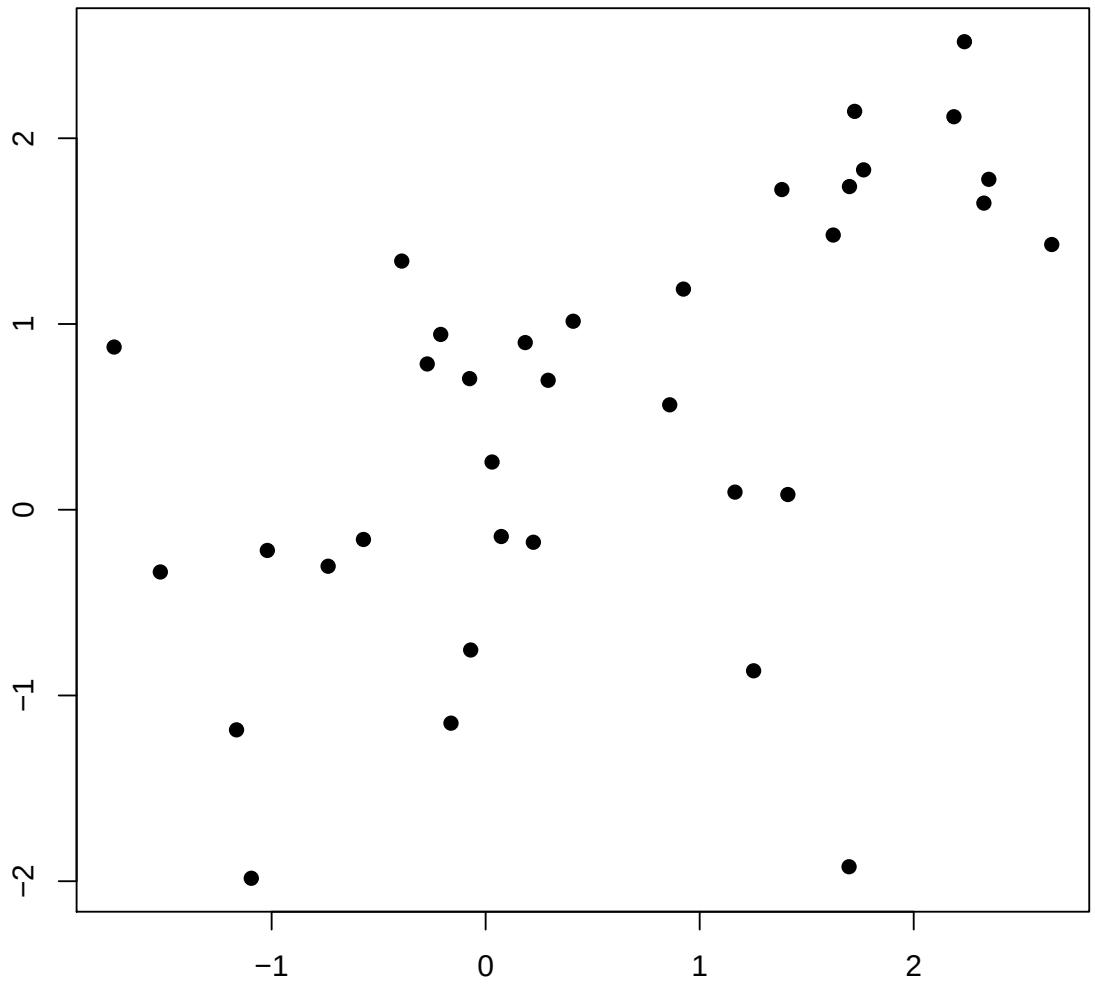
*Statistical applications*

- highlights close neighbors in a data set
- useful check for distortions produced by projection techniques
- tests of normality

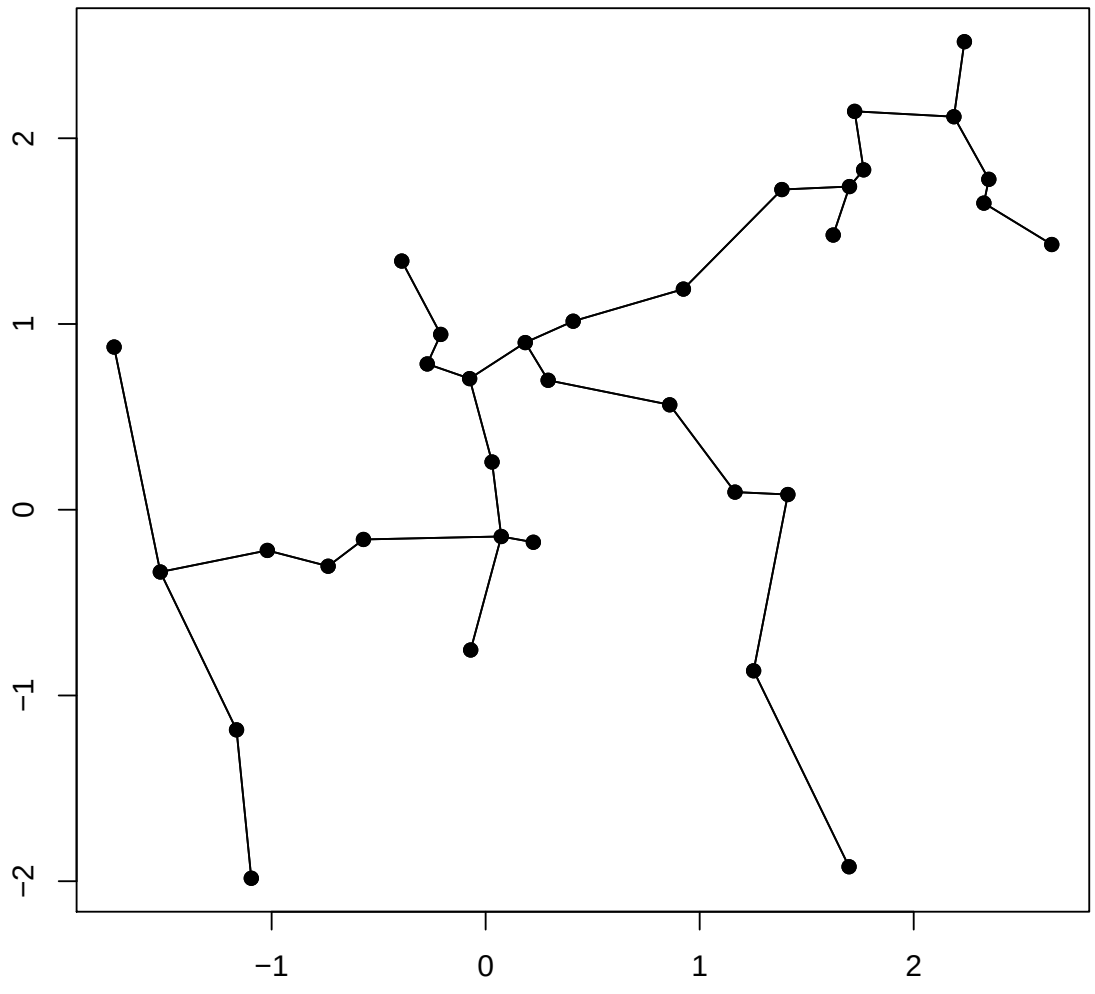
*Other applications*

- urban planning/engineering
- circuit design

# Example Data Set



# Minimum Spanning Tree: Example



# Relationship between MST and Single Linkage Clustering

- Cut a single linkage dendrogram at height, $\delta \dashrightarrow$ clusters
- Remove all edges in the MST with length $\geq \delta \dashrightarrow$ subgraphs corresponding to the same clusters

# A Generic MST Algorithm

**Input**: dissimilarity matrix, $\boldsymbol{D}$, between each object (point) of interest

1. Create a graph, G, where $V = \{v_1, \ldots, v_n\}$ and $E = \{\}$ ($E$ initially empty)
2. Find the smallest dissimilarity, $d_{ij}$ where (i,j) is not in $E$.
3. Add (i,j) to $E$ if (i,j) does not create a cycle
4. Repeat from step 2 until every vertex is included in at least one edge

Not particularly efficient algorithm, but simple. More efficient algorithms for finding MSTs include Kruskal's Algorithm and Prim's algorithm.

# Applications of the MST

MST tends to highlight close neighbors; can be used to look for distortions associated with projections to lower dimensional spaces.

## Using the MST to look for Projection Distortion

- Calculate the MST based on dissimilarity in a high-dimensional space
- Draw the MST edges among points in the projection space (e.g. MDS or PCA)
- MST edges that cross highlight geometric relationships among points that are not well represented by the projection