Computing a tree

Genome 559: Introduction to Statistical and Computational Genomics

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Review

- A tree can be used to represent sequence relationships.

- A sequence tree has a topology and branch lengths (distances).

- The number of tree topologies grows very fast.

Distance tree methods

- Measure pairwise distance between each pair of sequences.

- Use a clustering method to build up a tree, starting with the closest pair.

	1	2	3	4	5	6
human	a	g	t	c	t	c
chimp	a	g	a	g	t	c
gorilla	c	g	g	c	a	g
orangutan	c	g	g	g	a	c

human - chimp has 2 changes out of 6 sites
human - orang has 4 changes of out 6 sites
etc.

Distance matrix from alignment

	human	chimp	gorilla	orang
human	0	2/6	4/6	4/6
chimp		0	5/6	3/6
gorilla			0	2/6
orang				0

(symmetrical, lower left not filled in)

Distance matrix methods

- Methods based on a set of pairwise sequence distances, typically from a multiple alignment.

- Try to build the tree that best matches the distances.

- Usual standard for "best match" is the least squares of the tree distances compared to the real pairwise distances:

Let D_m be the real distances and D_t be the tree distances.
Find the tree that minimizes:

$$\sum_{i=1}^{N} D_t - D_m \quad {}^2$$

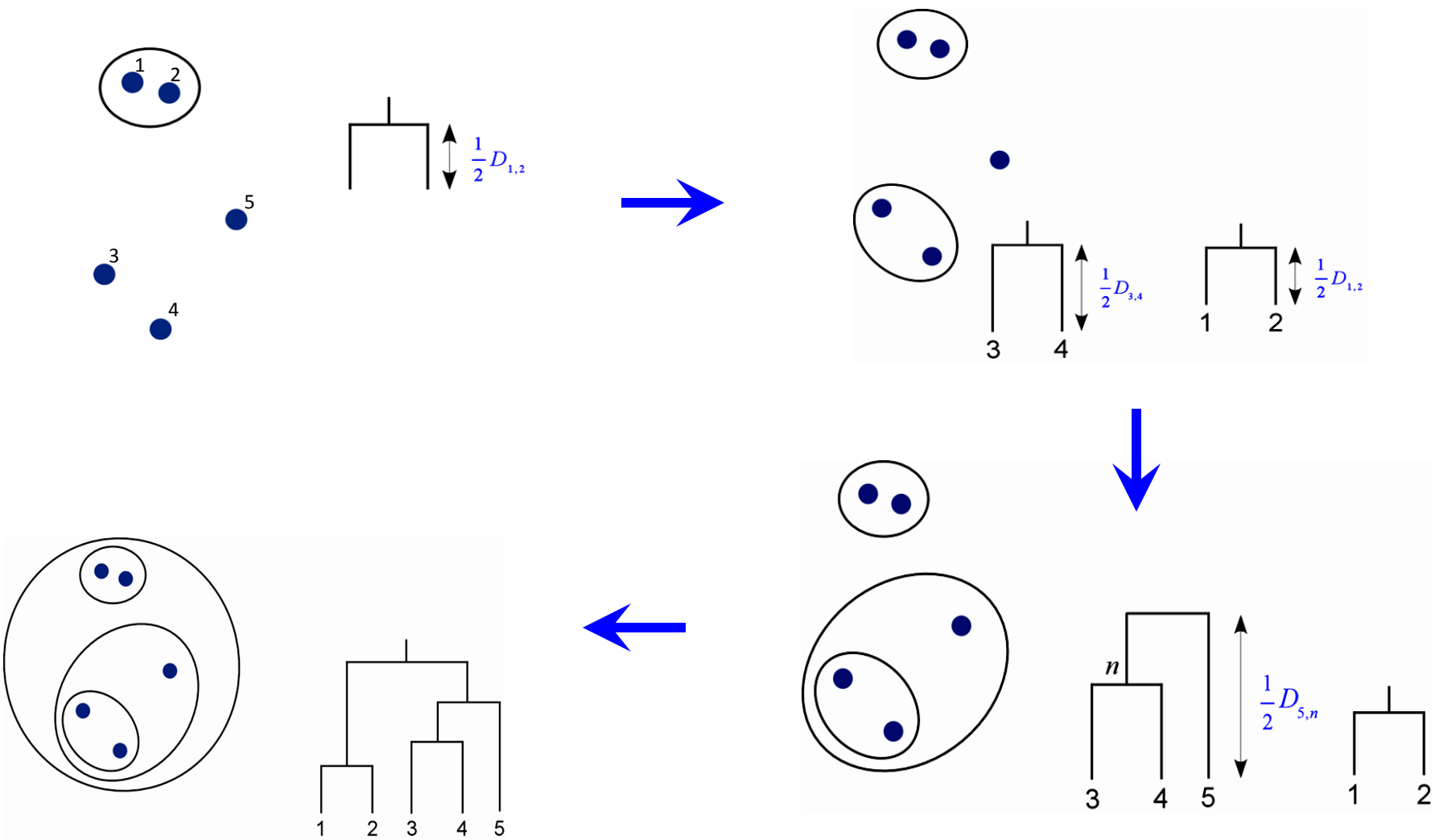
Enumerate and score all trees

- Enumerate every tree topology, fit least-squares best distances for each topology, keep best.

- Not used for distance trees - there is a much faster way to get very close to correct.

- Called Neighbor-Joining algorithm, one of a general class called hierarchical clustering algorithms.

Sequential clustering approach (UPGMA)



Sequential clustering algorithm

1) generate a table of pairwise sequence distances and assign each sequence to a list of N tree nodes.

2) look through the current list of nodes (initially these will all be leaf "nodes") for the pair with the smallest distance.

3) merge the closest pair, remove the pair of nodes from the list and add the merged node to the list.

4) repeat until there is only one node left - it is the root.

$$D_{n1,n2} = \frac{1}{N} \sum_i \sum_j d_{ij}$$

where i is each leaf of $n1$ (node1), j is each leaf of $n2$ (node2),

and N is the number of distances summed

(in words, this is the arithmetic average of the distances between all the leaves in one node and all the leaves in the other node)

Neighbor-Joining Algorithm (side note)

Essentially as for UPGMA, but correction for distance to other leaves is made.

Specifically, for sets of leaves ***i*** and ***j***, we denote the set of all <u>other</u> leaves as L, and the size of that set as $|L|$, and we compute the corrected distance D_{ij} as:

$$D_{ij} = d_{ij} - (r_i + r_j)$$

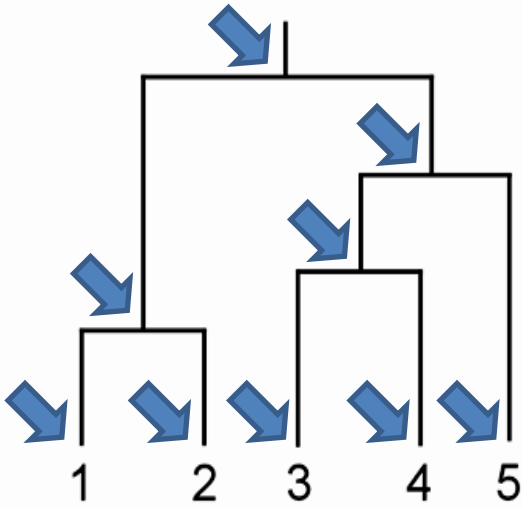
where

$$r_i = \frac{1}{|L|} \sum_{k \in L} d_{ik}$$

(the mean distance from
i to all 'other' leaves)

Data structure for a tree

```
class TreeNode:
    <parent node>
    <left-child node>
    <right-child node>
    <distance to parent>
```



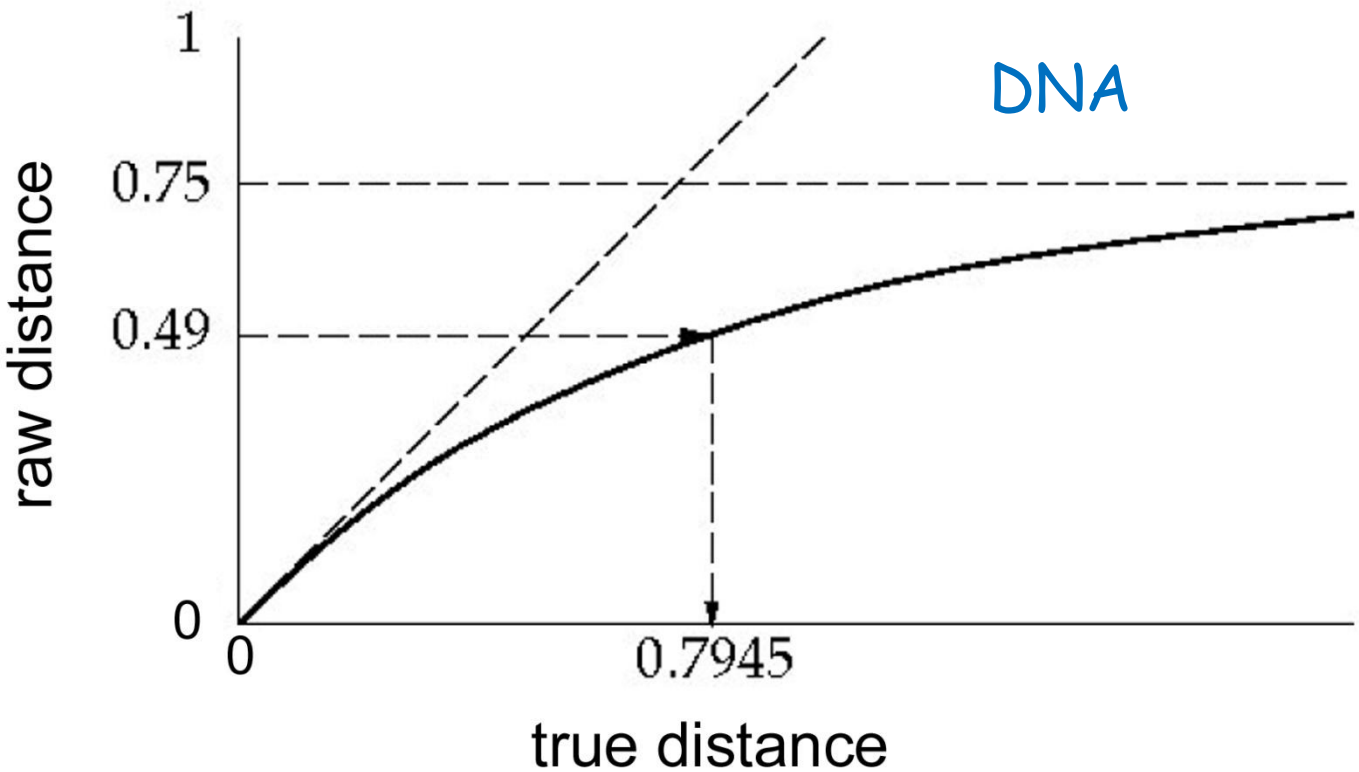
The tree itself is made up of `TreeNode` objects, each of which is connected to other `TreeNode` objects based on its three attributes.

How do we know a node is a leaf? A root?

Raw distance correction

- As two DNA sequences diverge, it is easy to see that their maximum raw distance is ~0.75 (assuming equal nt frequencies).

- This graph shows evolutionary distance related to raw distance:



Mutational models for DNA

- Jukes-Cantor (JC) - all mutations equally likely.

- Kimura 2-parameter (K2P) - transitions and transversions have separate rates.

- Generalized Time Reversible (GTR) - all changes may have separate rates.

(Models similar to GTR are also available for protein)

Jukes-Cantor

	G	A	T	C
G	1-3α	α	α	α
A	α	1-3α	α	α
T	α	α	1-3α	α
C	α	α	α	1-3α

Kimura 2-parameter

	purines		pyrimidines	
	G	**A**	**T**	**C**
G	1-α-2β	α	β	β
A	α	1-α-2β	β	β
T	β	β	1-α-2β	α
C	β	β	α	1-α-2β

Jukes-Cantor model - distance correction

Jukes-Cantor model:

$$D = -\frac{3}{4}\ln(1 - \frac{4}{3}D_{raw})$$

D_{raw} is the raw distance (what we directly measure)

D is the corrected distance (what we want)

ln is natural log

Distance trees - summary

- Convert each pairwise raw distance to a corrected distance.

- Build tree as before (UPGMA or neighbor-joining).

- Notice that these methods don't consider all tree topologies - they are very fast, even for large trees.