

9 Phylogenetic tree

9.1 Introduction to phylogenetic trees

A phylogenetic provides additional views on the analysis of multiple sequences.

Elements of phylogenetic tree

- Terminal nodes: sequences, groups of genes, species, operational taxonomic units
- Internal nodes: hypothetical ancestral units
- Edges: often represent distances

Types of trees

- Cladogram or phylogram
- Bifurcating or multifurcating
- Rooted or unrooted

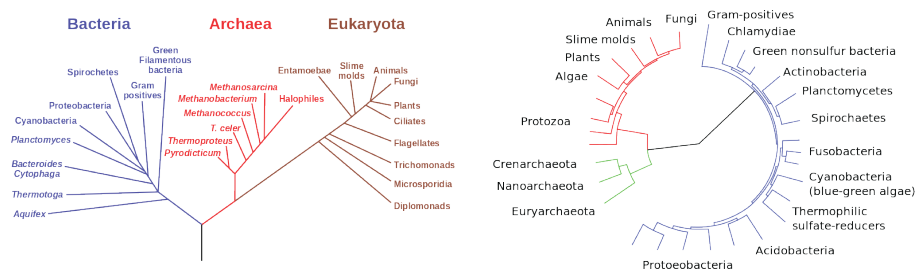


Figure 9.1: Phylogenetic trees (sources: TimVickers, Wikimedia Commons, NASA Astrobiology Institute, Wikimedia Commons))

Rooted and unrooted trees

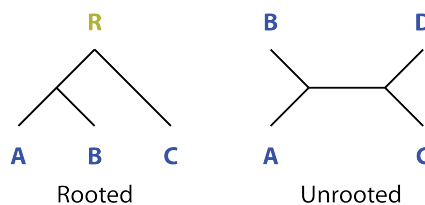


Figure 9.2: A rooted tree with three nodes and an unrooted tree with four nodes

Additive and ultrametric trees

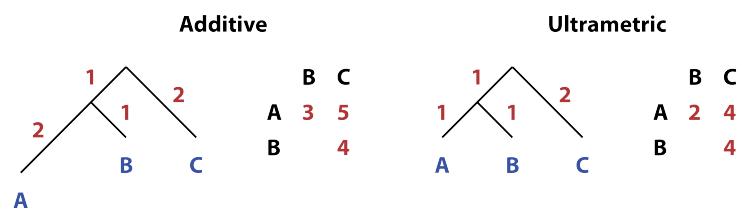


Figure 9.3: A rooted tree with three nodes and an unrooted tree with four nodes

An ultrametric tree is a special version of additive tree. It assumes that the distances from two sequences to their common ancestor are always equal.

Number of topologically different tree

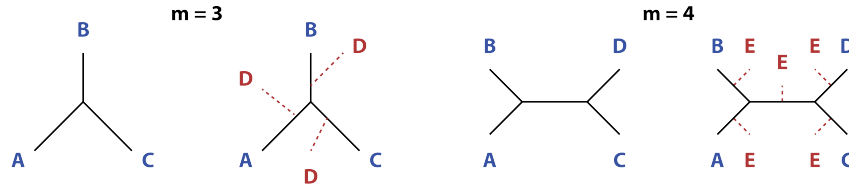


Figure 9.4: Adding one external node to unrooted trees

The number of all possible topologically different unrooted tree $T_{\text{unroot}}(m)$ can be obtained by the double factorial of $2m - 5$.

$$T_{\text{unroot}}(m) = (2m - 5)!! \equiv \frac{(2m - 5)!}{2^{m-3}(m - 3)!}$$

$T_{\text{root}}(m)$ can be calculated from $T_{\text{unroot}}(m)$.

$$T_{\text{root}}(m) = (m - 1) \times T_{\text{unroot}}(m)$$

Example of the number of unrooted tree

What is the number of all possible topologically different unrooted trees when $m = 7$?

$$T_{\text{unroot}}(7) = (2 \times 7 - 5)!! = 9!! = 1 \times 3 \times 5 \times 7 \times 9 = 945$$

or

$$T_{\text{unroot}}(7) = \frac{(2 \times 7 - 5)!}{2^{7-3}(7 - 3)!} = \frac{9!}{2^4(4)!} = 945$$

Exercise 9.1

1. Calculate the number of all possible topologically different unrooted trees when $m = 5$.
2. Construct an additive rooted tree for the distance matrix below. Estimate the edge values by trial and error.

	B	C
A	4	7
B		5

9.2 Tree reconstruction methods

A number of methods have been proposed to reconstruct a phylogenetic tree.

Two types of reconstruction methods

- Distance-based methods
- Character-based methods

Distance-based methods

A distance is a positive value with larger values indicating that two sequences are separated further.

- PGMA (pair-group method using arithmetic mean)
- Neighbor-joining (NJ)

Character-based methods

Character based methods rely on characters (amino acid/nucleotide letters) to reconstruct a tree.

- Maximum parsimony
- Maximum likelihood

Evaluation of reconstructed trees

Bootstrapping is one of the methods to test the robustness of a reconstructed tree by adding noises and comparing the results.

1. Randomly generate a pseudo MAS from the original MSA
2. Reconstruct a tree
3. Repeat the process
4. Compare the trees

9.3 Distance-based methods

PGMA (pair-group method using arithmetic mean) and neighbor-joining are two popular distance-based methods to reconstruct a phylogenetic tree.

UPGMA

UPGMA is an unweighted version of PGMA. It requires the evolutionary rate should be constant (ultrametric). Pairwise distances need to be pre-calculated, for instance, by DP.

- w : A new node
- u, v : Child nodes of w
- m_A The number of original sequences in subtree A
- $D_{A,B}$: Distance between sequences/subtrees A and B

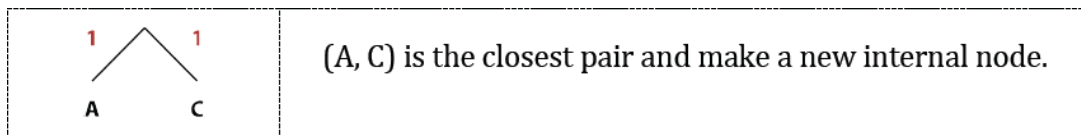
$$D_{w,x} = \frac{m_u D_{u,x} + m_v D_{v,x}}{m_u + m_v}$$

Example of UPGMA

Reconstruct a phylogenetic tree from the pre-calculated distances below.

	B	C	D
A	4	2	5
B		4	8
C			5

Step 1a. Find a pair with the closest distance



Step 1b. Recalculate the distances

$$d_{B,(AC)} = \frac{d_{B,A} + d_{B,C}}{2} = 4, \quad d_{D,(AC)} = \frac{d_{D,A} + d_{D,C}}{2} = 5$$

Step 1c. Update the distance matrix with a new node (AC)

	B	D
(AC)	4	5
B		8

Step 2a. Find a pair with the closest distance



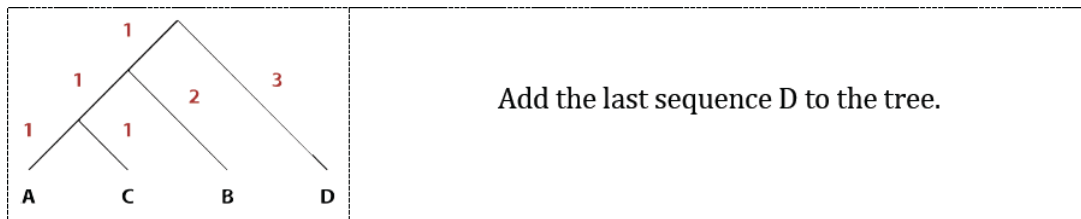
Step 2b. Recalculate the distance

$$d_{((AC)B),D} = \frac{2 \times d_{(AC),D} + d_{B,D}}{3} = 6$$

Step 2c. Update the distance matrix with a new node ((AC)B)

	D
((AC)B)	6

Step 3. Complete the tree



Evaluation on how well fitted to the original distances

Several criteria are available to find the best-fitted tree for a given distance matrix, such as the Cavalli-Sforza and Edwards criterion:

$$\sum_{i,j} (M_{i,j} - d_{i,j})^2$$

where $M_{i,j}$ and $d_{i,j}$ are respectively the original and the calculated pairwise distances.

Example of the Cavalli-Sforza and Edwards criterion

Original				Reconstructed			
	B	C	D		B	C	D
A	4	2	5	A	4	2	6
B		4	8	B		4	6
C			5	C			6

$$\sum_{i,j} (M_{i,j} - d_{i,j})^2 = 2((5 - 6)^2 + (8 - 6)^2 + (5 - 6)^2) = 12$$

WPGMA

WPGMA is a weighted version of PGMA.

$$D_{w,x} = \frac{D_{u,x} + D_{v,x}}{2}$$

Neighbor-joining (NJ) method

It starts with the initial tree and then selects two sequences which results in the smallest sum of edge lengths. It continues until there are no sequences to join. Unlike UPGMA, it does not require a constant evolutionary rate.

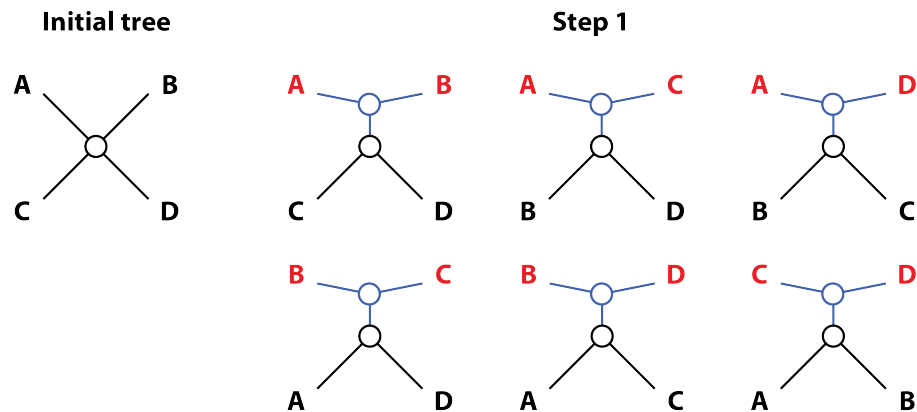


Figure 9.5: All possible combinations of adding one node to the four sequences

Exercise 9.2

1. Reconstruct a phylogenetic tree by using UPGMA and the following pre-calculated distances.

	B	C
A	2	3
B		5

2. Create the distance matrix of the reconstructed tree.

	B	C
A		
B		

3. Calculate the Cavalli-Sforza and Edwards criterion.