

Phylogeny

Bioinformatics Applications (PLPTH813)

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Outline

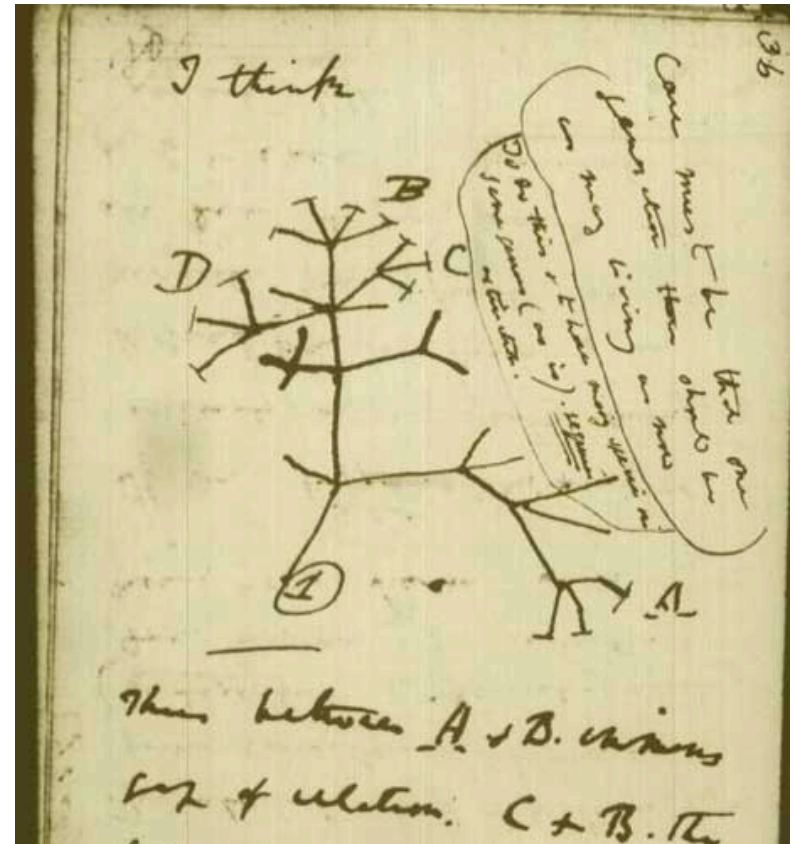
- Background
- Algorithms to build phylogeny
- Interpretation of phylogenetic trees

Tree of life

The **tree of life** is used to describe the relationships between organisms. Its use dates back to at least the early 1800s. It was employed by **Charles Darwin** to express the concept of the branching divergence of varieties and then species in a process of descent from common ancestors.

Ernst Haeckel coined the term **phylogeny** for the evolutionary relationships of species through time, and went further than Darwin in proposing phylogenetic histories of life. The modern development of this idea is called the **phylogenetic tree**.

- wikipedia



A page from Darwin's Notebook B showing his sketch of the tree of life

Evolution and Phylogeny

- Evolution is a process of change. At the molecular level, evolution is a process of mutation with selection.
- Molecular evolution is the study of changes in genes and proteins throughout different branches of the tree of life.
- Phylogeny is **the inference** of evolutionary relationships, providing **hypotheses** of past biological events.

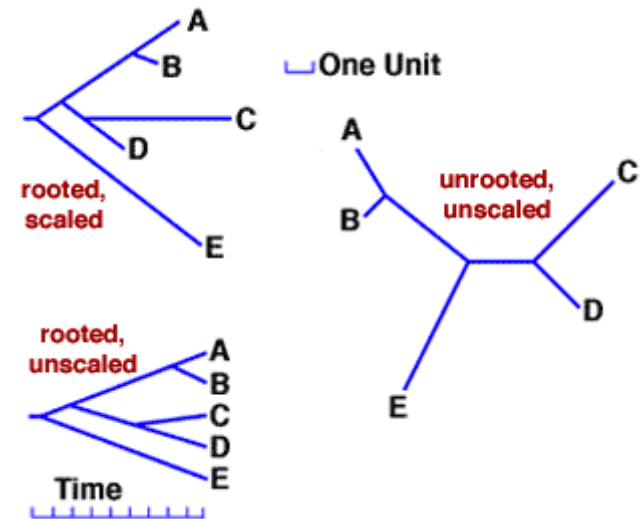
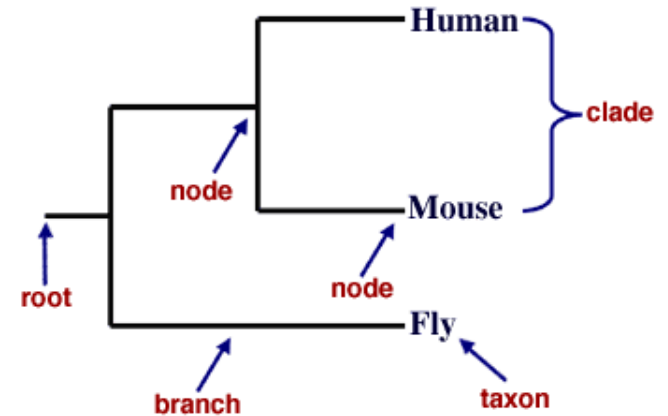
Applications of phylogenetic trees (examples)

1. to represent the relationships among species/isolates/varieties/genotypes/lines
2. to describe relationships among homologs in a gene family
3. to infer the evolutionary and epidemiological dynamics of pathogens
4. to classify metagenomic sequences

Nowadays, every biologist needs to know something about phylogenetic inference!

Tree components

- A phylogeny is a tree containing **nodes** that are connected by **braches (edges)**. The pattern of branching determines the tree's **topology**.
- **Root** represents a common ancestor of all taxa shown in the tree.
- **Rooted trees** are thus directional, since all taxa evolved from the root.
- **Unrooted trees** illustrate relationships only.



An unrooted tree

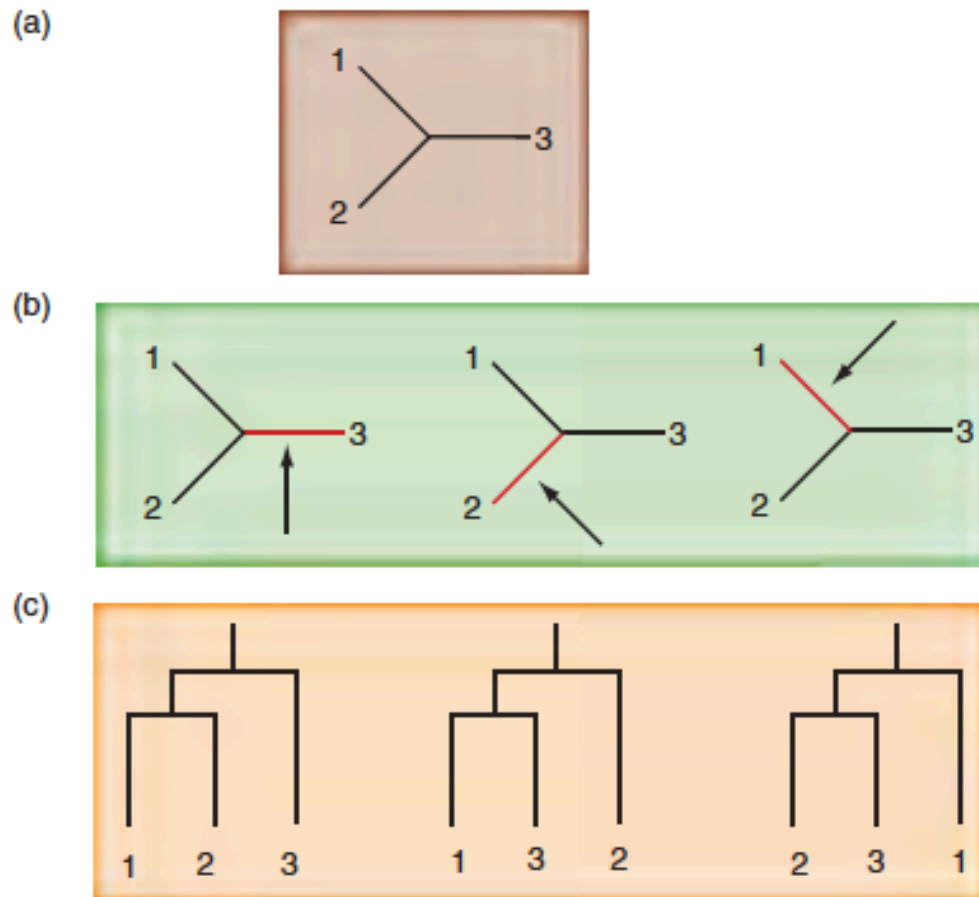
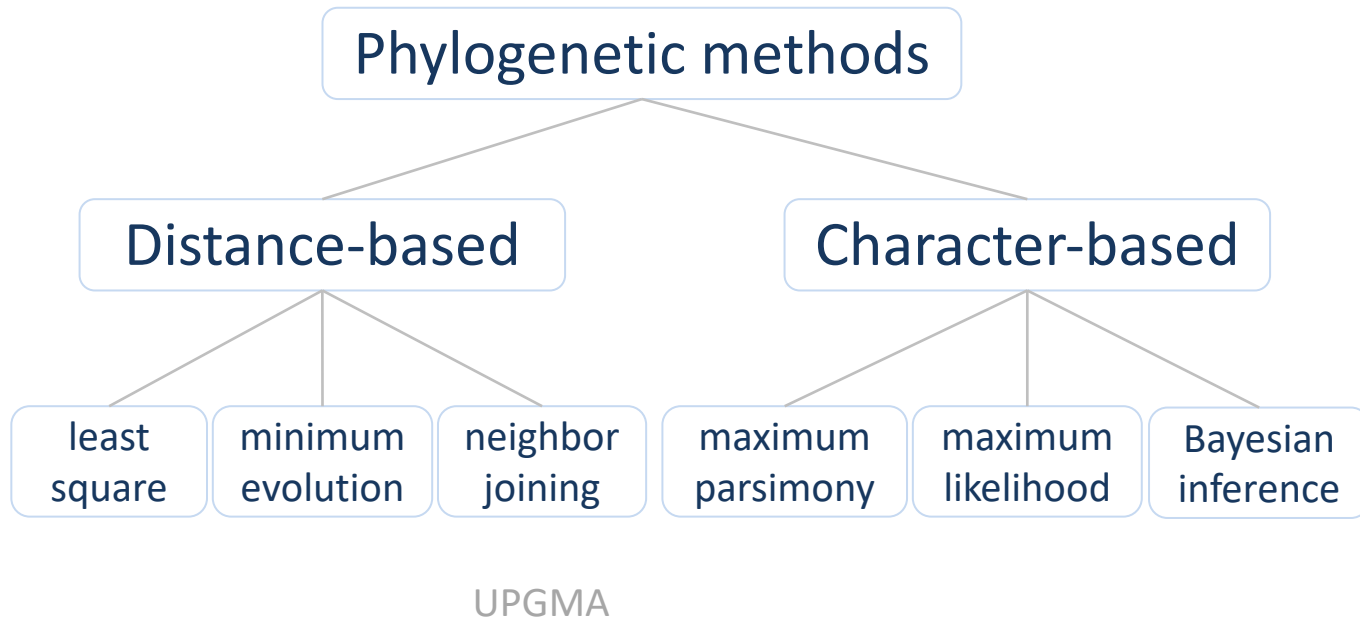


FIGURE 7.10 For three operational taxonomic units (such as three aligned protein sequences 1–3), there is (a) one possible unrooted tree. (b) Any of these edges may be used to select a root (see arrows), from which (c) three corresponding rooted trees are possible.

Approaches to construct phylogenetic trees



Distance-based method

- Distance calculation to build a distance matrix

A **distance matrix** is a table that indicates pairwise **dissimilarity**.

	A	B	C	D
A	0	3	4	6
B	3	0	5	7
C	4	5	0	6
D	6	7	6	0

	B	C	D
A	3	4	6
B		5	7
C			6

Distance between DNA sequences

- Distance (e.g., percentage of difference) between DNA sequences

A	ATTTGCGGTA
B	ATCTGCGATA
C	ATTGCCGTTT
D	TTCGCTGTTT



	A	B	C	D
A	0	0.2	0.4	0.7
B	0.2	0	0.5	0.6
C	0.4	0.5	0	0.3
D	0.7	0.6	0.3	0

example from Barbara Holland

e.g., DNA sequences

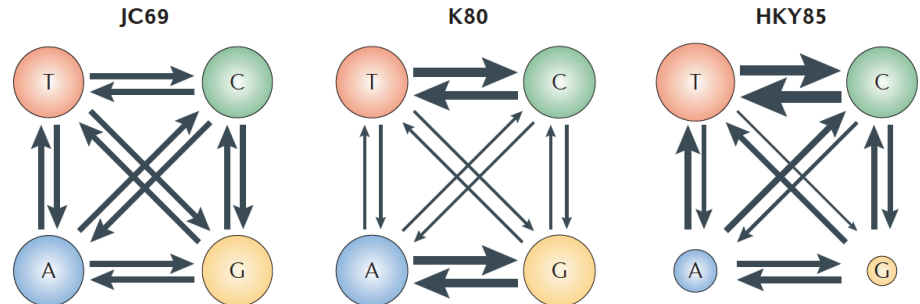
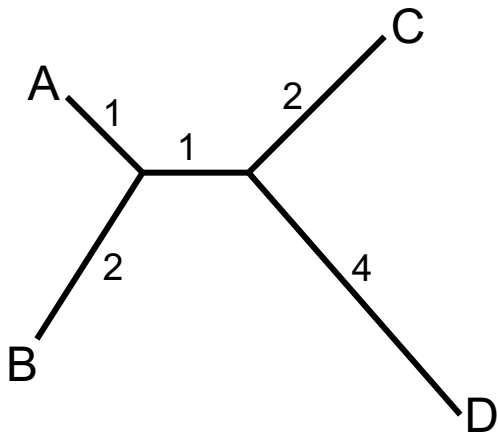


Figure 1 | **Markov models of nucleotide substitution.** The thickness of the arrows indicates the substitution rates of the four nucleotides (T, C, A and G), and the sizes of the circles represent the nucleotide frequencies when the substitution process is in equilibrium. Note that both JC69 and K80 predict equal proportions of the four nucleotides.

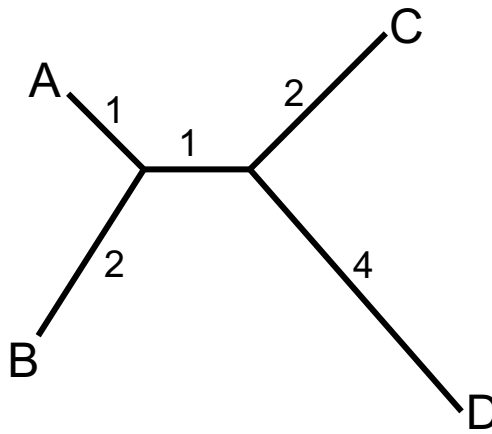
From distance matrix to a tree

	B	C	D
A	3	4	6
B		5	7
C			6

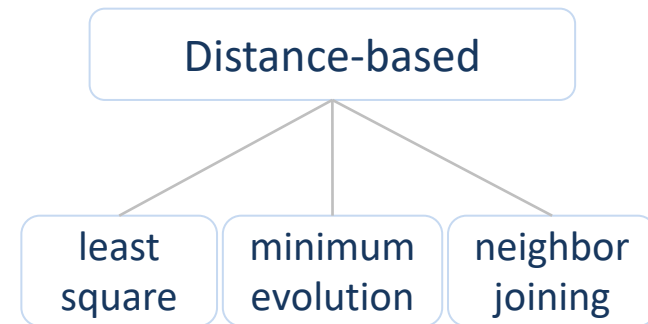


Perfect match

	B	C	D
A	3	4	7
B		4	7
C			6



No perfect matches



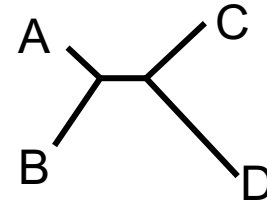
example from Barbara Holland

Distance-based method – least squares

- least squares

	B	C	D
A	3	4	7
B		4	7
C			6

1



	B	C	D
A	d_{AB}	d_{AC}	d_{AD}
B		d_{BC}	d_{BD}
C			d_{CD}

2

$$Q = \sum_{i=1}^s \sum_{j=1}^s (\hat{d}_{ij} - d_{ij})^2$$

3

$$Q_1, Q_2, Q_3, \dots$$

4

The tree with the smallest Q

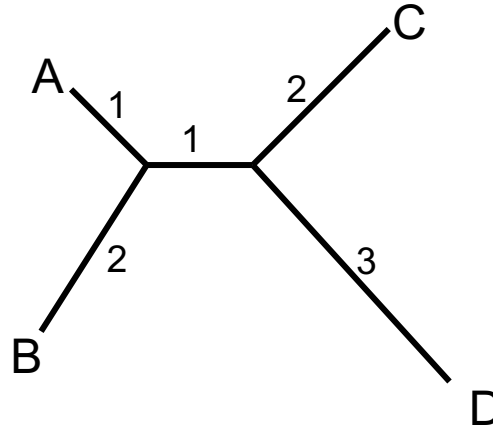
- 1) Given the distance matrix data, a tree is assumed and a new distance matrix is determined based on the tree
- 2) Determine Q values
- 3) Repeat 1 and 2 for all the possible trees
- 4) The tree with the smallest Q score is the least squares estimate of the true tree.

Distance-based method – least squares

- least squares

d_{ij}

	B	C	D
A	3	4	7
B		4	7
C			6



$d_{ij}(\text{hat})$

	B	C	D
A	3	4	5
B		5	6
C			5

1) Given the distance matrix data, a tree is assumed and a new distance matrix is determined based on the tree

2) Determine Q values

$$Q = \sum_{i=1}^s \sum_{j=1}^s (\hat{d}_{ij} - d_{ij})^2$$

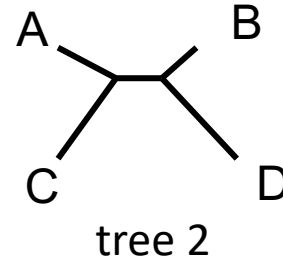
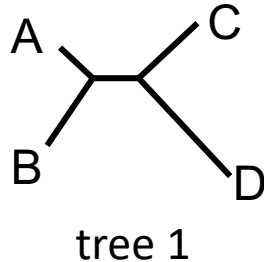
$$(3-3)^2 + (4-4)^2 + (5-7)^2 + (5-4)^2 + (6-7)^2 + (5-6)^2 = 7$$

Distance-based method – least squares

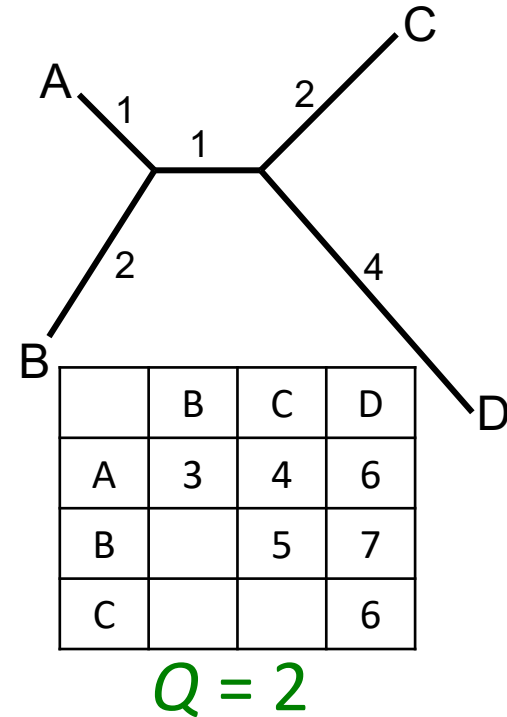
- least squares**

d_{ij}

	B	C	D
A	3	4	7
B		4	7
C			6



...



$$Q = \sum_{i=1}^s \sum_{j=1}^s (\hat{d}_{ij} - d_{ij})^2$$

- 1) Given the distance matrix data, a tree is assumed and a new distance matrix is determined based on the tree
- 2) Determine Q values
- 3) Repeat 1 and 2 for all the possible trees
- 4) The tree with the smallest Q score is the least squares estimate of the true tree.

Distance-based method –minimum evolution

- **minimum evolution**

uses the tree length (which is the sum of branch lengths) instead of Q for tree selection. Under **the minimum evolution criterion**, shorter trees are more likely to be correct than longer trees are.

sum of $d_{ij}(\text{hat})$

	B	C	D
A	3	4	6
B		5	7
C			6

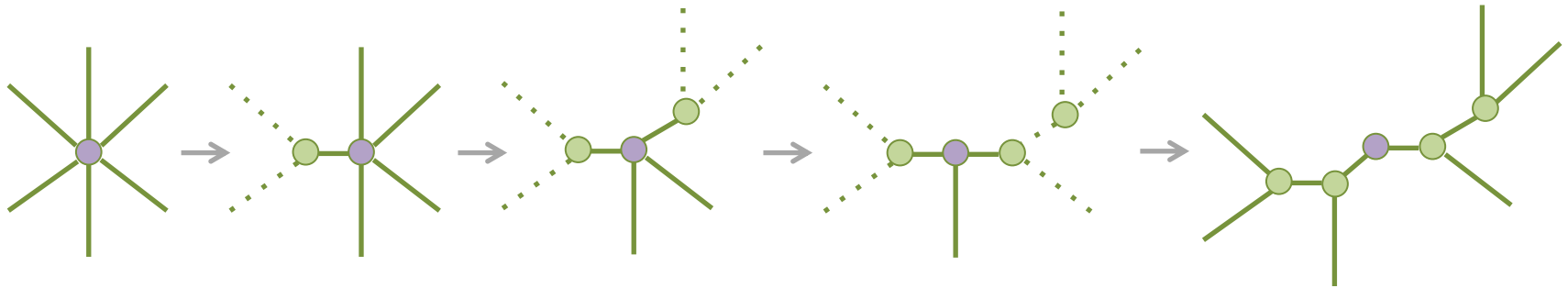
	B	C	D
A	3	4	5
B		5	6
C			5

$$3 + 4 + 6 + 5 + 7 + 6 = \mathbf{31} < 3 + 4 + 5 + 5 + 6 + 5 = \mathbf{28}$$

Distance-based method – neighbor joining

- **neighbor joining** (the most popular algorithm)
 - Find a close pair of leaves that are far from other leaves

The algorithm operates by starting with a **star tree** and successively choosing a **pair of taxa** to join together (based on the taxon distances), until a fully resolved tree is obtained.

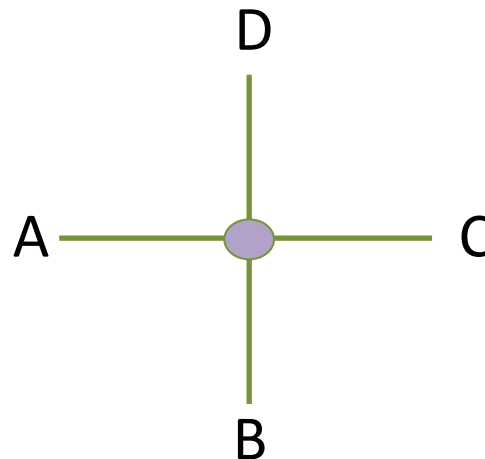


neighbor joining (NJ) procedure - I

Distance matrix (n=4)

	A	B	C	D
A	0	2	4	6
B		0	3	7
C			0	10
D				0

a star tree



neighbor joining (NJ) procedure - II

1. calculate Q (Q matrix)

$$Q(A, B) = (4 - 2)d(A, B) - \sum_{k=1}^4 d(A, k) - \sum_{k=1}^4 d(B, k)$$

$$Q_{AB} = (4-2)*2 - (2 + 4 + 6) - (2 + 3 + 7) = -20$$

k represents A, B, C, and D

Distance matrix (n=4)

	A	B	C	D
A	0	2	4	6
B		0	3	7
C			0	10
D				0

Q matrix

	A	B	C	D
A	0	-20		
B		0		
C			0	
D				0

neighbor joining (NJ) procedure - III

2. Find the lowest $Q_{i,j}$
3. i and j are joined to a newly node (e.g., AD)
4. The new node is connected to the central node.

Distance matrix (n=4)

	A	B	C	D
A	0	2	4	6
B		0	3	7
C			0	10
D				0

$$Q(i, j) = (n - 2)d(i, j) - \sum_{k=1}^n d(i, k) - \sum_{k=1}^n d(j, k)$$

$$Q_{AC} = (4-2)*4 - (2 + 4 + 6) - (4 + 3 + 9) = -20$$

$$Q_{AD} = (4-2)*6 - (2 + 4 + 6) - (6 + 7 + 9) = -22$$

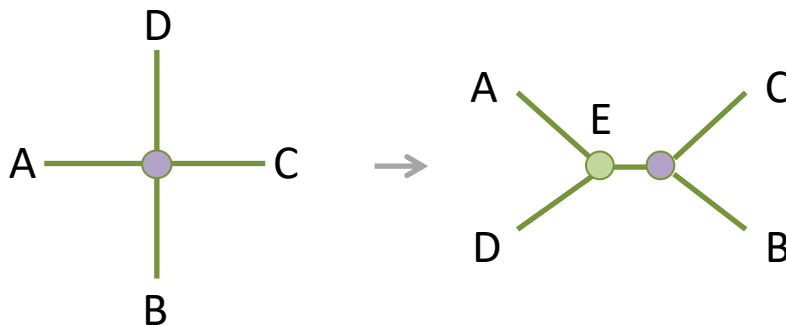
$$Q_{BC} = (4-2)*3 - (2 + 3 + 7) - (4 + 3 + 9) = -20$$

$$Q_{BD} = (4-2)*7 - (2 + 3 + 7) - (6 + 7 + 9) = -20$$

$$Q_{CD} = (4-2)*9 - (4 + 3 + 6) - (6 + 7 + 6) = -14$$

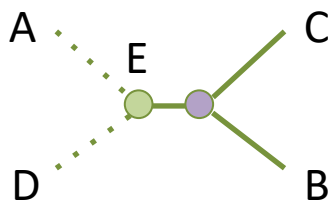
Q matrix

	A	B	C	D
A	0	-20	-20	-22
B		0	-20	-20
C			0	-14
D				0



neighbor joining (NJ) procedure - IV

5. Calculate the distance from each of the taxa in the pair to this new node.


$$\delta(A, E) = \frac{1}{2} d(A, D) + \frac{1}{2(n-2)} \left[\sum_{k=1}^n d(A, k) - \sum_{k=1}^n d(D, k) \right]$$
$$\delta(D, E) = d(A, D) - \delta(A, E)$$

k represents A, B, C, and D

Taxa A and D are the paired taxa and E is the newly created node. The branches joining A and E and D and E , and their lengths, $\delta(A, E)$ and $\delta(D, E)$ are part of the tree which is gradually being created.

neighbor joining (NJ) procedure - V

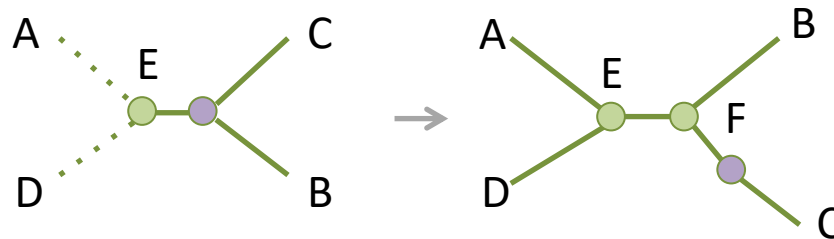
6. Calculate the distance from each of the taxa outside of this pair to the new node.
7. Repeat 1-4 until resolving all

Updated distance matrix

	E	B	C
E	0		
B		0	
C			0

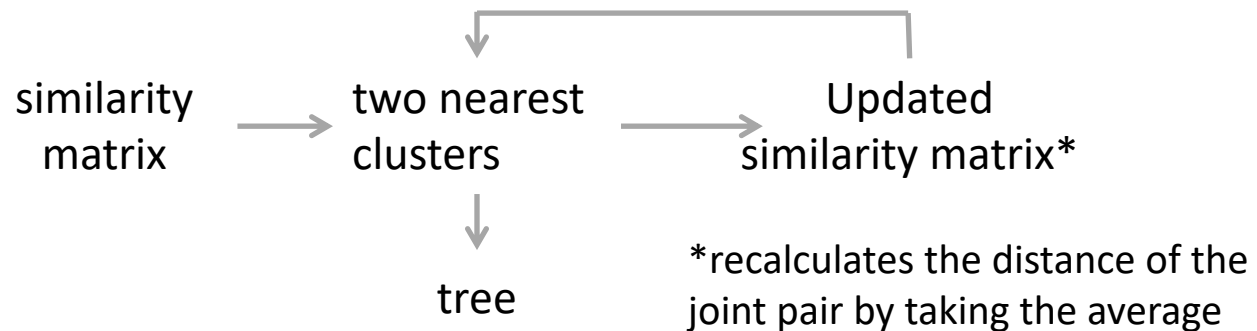
$$d(E, k) = \frac{1}{2} [d(A, k) + d(D, k) - d(A, D)]$$

k represents B and C



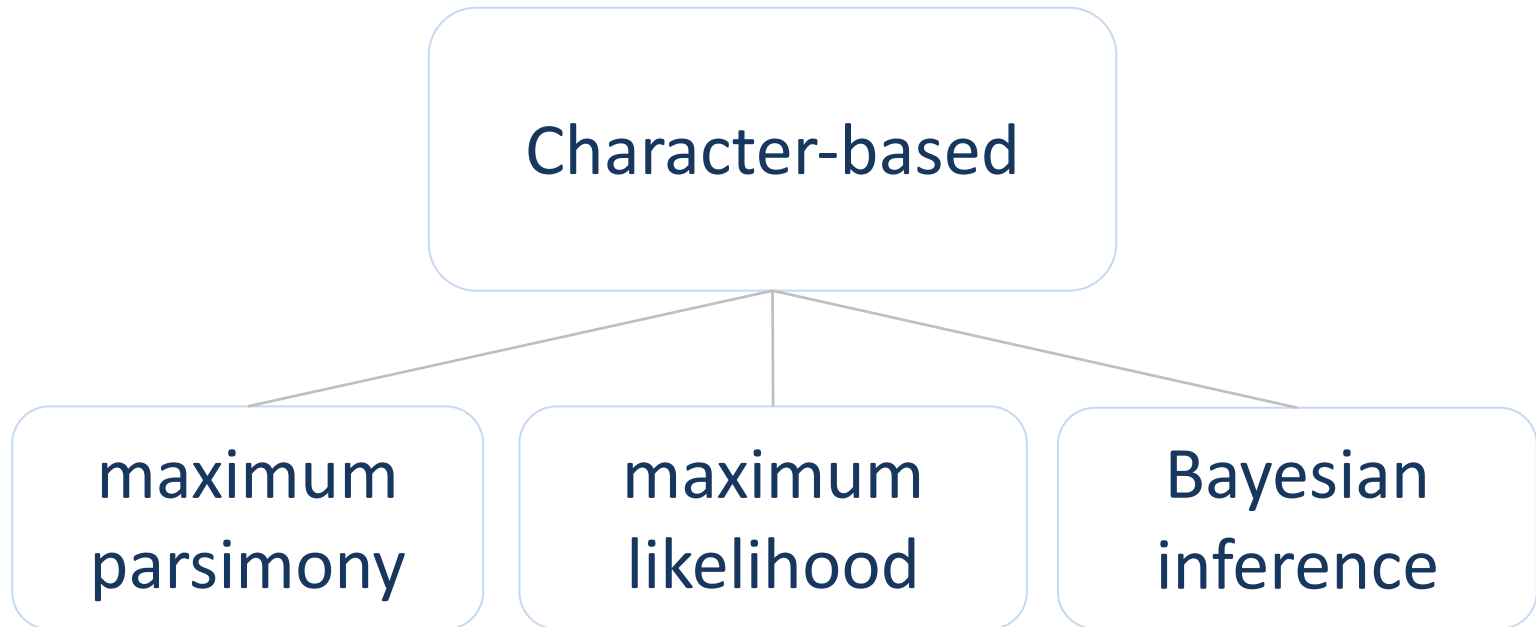
UPGMA (unweighted pair group method with arithmetic mean)

- UPGMA is a simple agglomerative (bottom-up) hierarchical clustering method, constructing a rooted tree.
- Based on a (dis)similarity matrix, at each step, the nearest two clusters are combined into a higher-level cluster.



- UPGMA assumption: the distances from the root to every branch tip are equal.

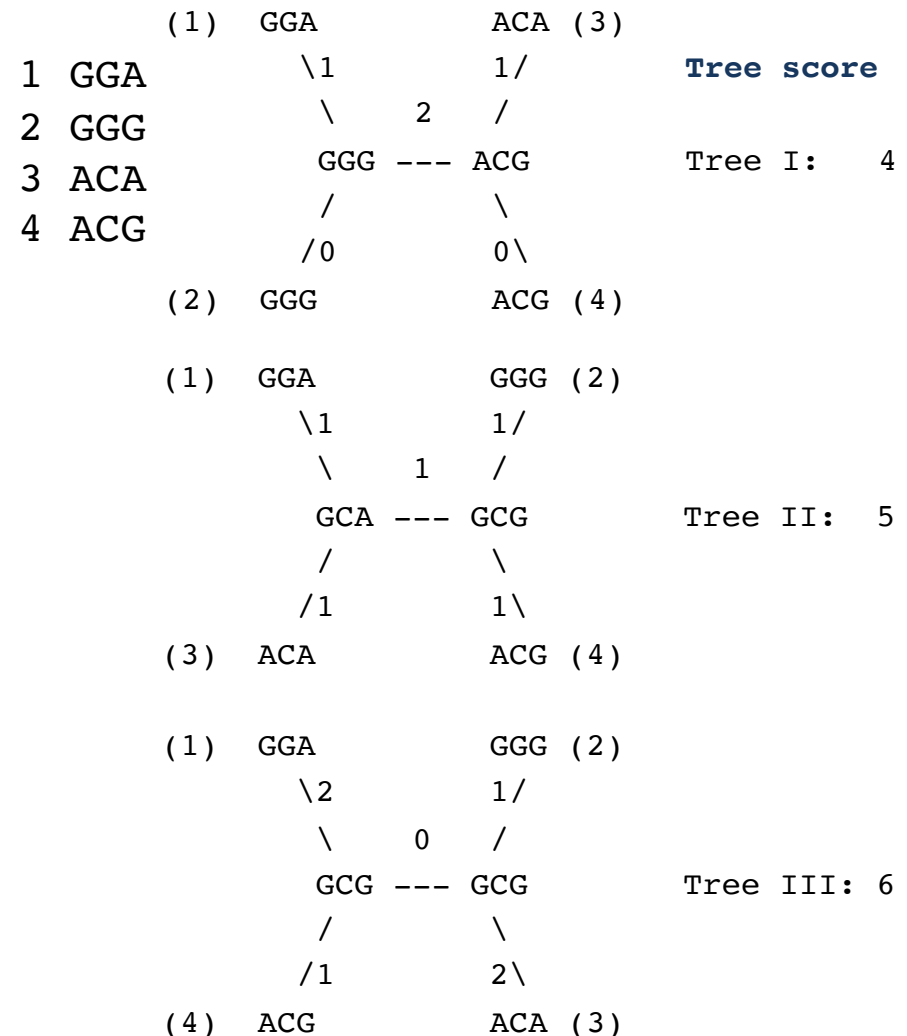
Character-based methods



character-based method - maximum parsimony

The **maximum parsimony** method minimizes the number of changes on a phylogenetic tree by assigning character states to interior nodes on the tree.

The **character length** is the minimum number of changes required for that site, whereas the **tree score** is the sum of character lengths over all sites. The **maximum parsimony tree** is the tree that minimizes the tree score.



maximum likelihood

- **maximum likelihood**

The maximum likelihood estimates (MLEs) of parameters are the parameter values that maximize the likelihood.

The tree is a model, whereas branch lengths on the given tree and substitution parameters are parameters in the model.

$P(\text{Data} | \text{Model})$: the probability or likelihood of observing the data given the model

1. optimization of branch lengths to calculate the tree likelihood, $P(\text{Data} | \text{Model})$, for each candidate tree
2. a search in the tree space for the tree with the maximum likelihood.

Bayesian inference methods

- Bayesian inference methods

$$P(T, \theta | D) = \frac{P(T, \theta) P(D | T, \theta)}{P(D)}$$

where $P(T, \theta)$ is the **prior probability** for tree T and parameter θ , $P(D | T, \theta)$ is the likelihood or probability of the data given the tree and parameter, and $P(T, \theta | D)$ is the **posterior probability**.

the posterior probability of a tree is simply the probability that the tree is correct

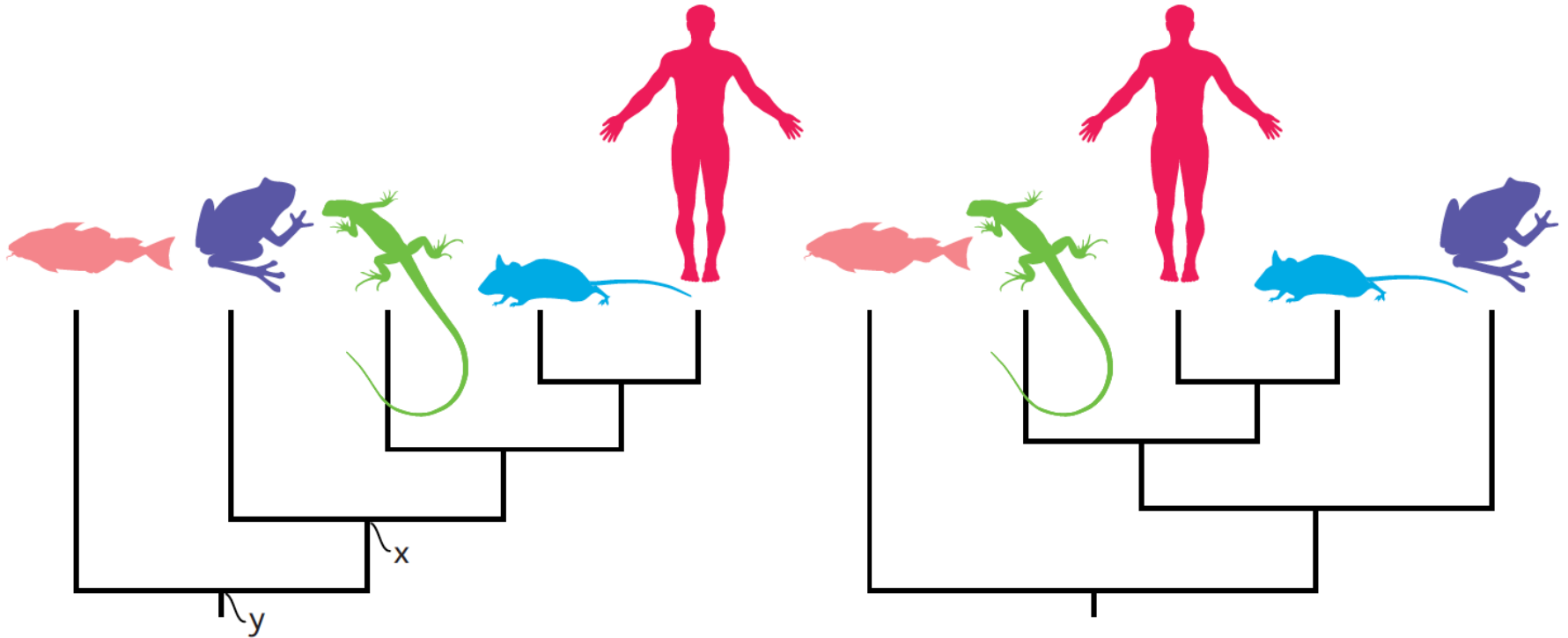
Strengths and weaknesses

Table 2 | **A summary of strengths and weaknesses of different tree reconstruction methods**

Strengths	Weaknesses
<i>Parsimony methods</i>	
<ul style="list-style-type: none"> • Simplicity and intuitive appeal • The only framework appropriate for some data (such as SINES and LINES) 	<ul style="list-style-type: none"> • Assumptions are implicit and poorly understood • Lack of a model makes it nearly impossible to incorporate our knowledge of sequence evolution • Branch lengths are substantially underestimated when substitution rates are high • Maximum parsimony may suffer from long-branch attraction
<i>Distance methods</i>	
<ul style="list-style-type: none"> • Fast computational speed • <u>Can be applied to any type of data as long as a genetic distance can be defined</u> • Models for distance calculation can be chosen to fit data 	<ul style="list-style-type: none"> • Most distance methods, such as neighbour joining, do not consider variances of distance estimates • <u>Distance calculation is problematic when sequences are divergent and involve many alignment gaps</u> • Negative branch lengths are not meaningful
<i>Likelihood methods</i>	
<ul style="list-style-type: none"> • Can use complex substitution models to approach biological reality • Powerful framework for estimating parameters and testing hypotheses 	<ul style="list-style-type: none"> • Maximum likelihood iteration involves heavy computation • The topology is not a parameter so that it is difficult to apply maximum likelihood theory for its estimation. Bootstrap proportions are hard to interpret
<i>Bayesian methods</i>	
<ul style="list-style-type: none"> • Can use realistic substitution models, as in maximum likelihood • Prior probability allows the incorporation of information or expert knowledge • Posterior probabilities for trees and clades have easy interpretations 	<ul style="list-style-type: none"> • Markov chain Monte Carlo (MCMC) involves heavy computation • In large data sets, MCMC convergence and mixing problems can be hard to identify or rectify • Uninformative prior probabilities may be difficult to specify. Multidimensional priors may have undue influence on the posterior without the investigator's knowledge • Posterior probabilities often appear too high • Model selection involves challenging computation^{138,139}

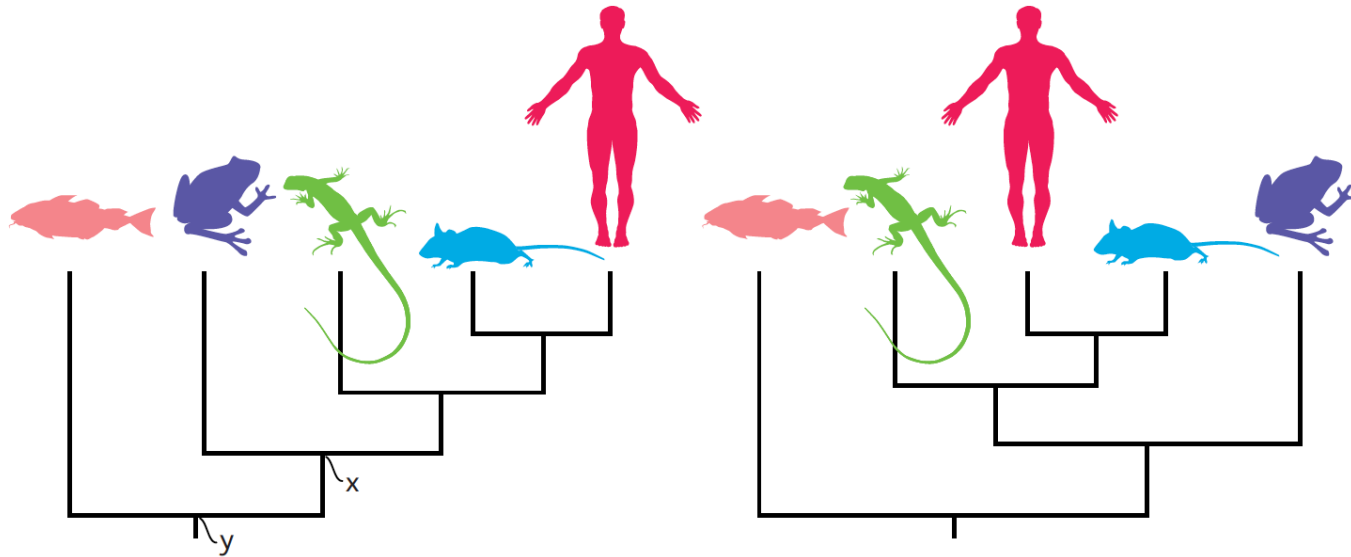
Which tree is correct?

“just as beginning students in geography need to be taught how to read maps, so beginning students in biology should be taught how to read trees and to understand what trees communicate.” - Robert O’Hara



The more recently species share a common ancestor, the more closely related they are.

Interpretation of a tree

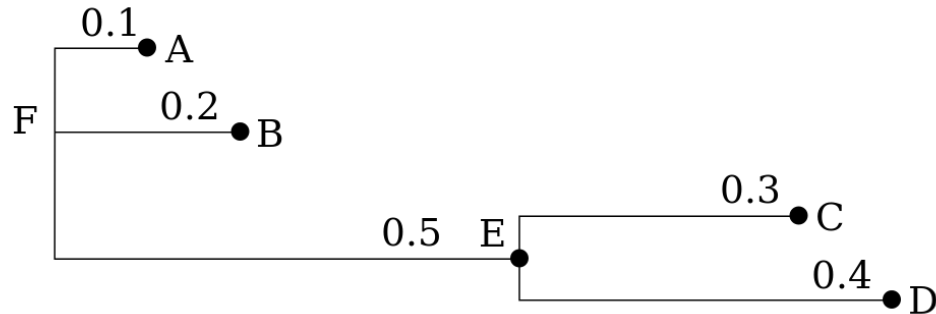


The correct way to read a tree is as a set of hierarchically nested groups, known as ***clades***.

Flat file formats for phylogenetic trees

- **Newick:** Newick files are simply text files that consist of one or more tree descriptions in the Newick notation.
- **Nexus:** Nexus is widely used in phylogenetics and can contain trees in Newick notation and furthermore also information about taxa and phylogenetic data sets such as sequence alignments.
- **phyloXML:** phyloXML is a XML format for the analysis, exchange, and storage of phylogenetic trees (or networks) and associated data. It allows to store much more information about the tree nodes.

an example of the Newick format



Newick file:

```
(,,(,))  
(A,B,(C,D))  
(A,B,(C,D)E)F  
(:0.1,:0.2,(:0.3,:0.4):0.5)  
(:0.1,:0.2,(:0.3,:0.4):0.5):0.0  
(A:0.1,B:0.2,(C:0.3,D:0.4):0.5)  
(A:0.1,B:0.2,(C:0.3,D:0.4)E:0.5)F  
((B:0.2,(C:0.3,D:0.4)E:0.5)F:0.1)A
```

Notes:

no nodes are named

leaf nodes are named

all nodes are named

all but root node have a distance to parent

all have a distance to parent

distances and leaf names (popular)

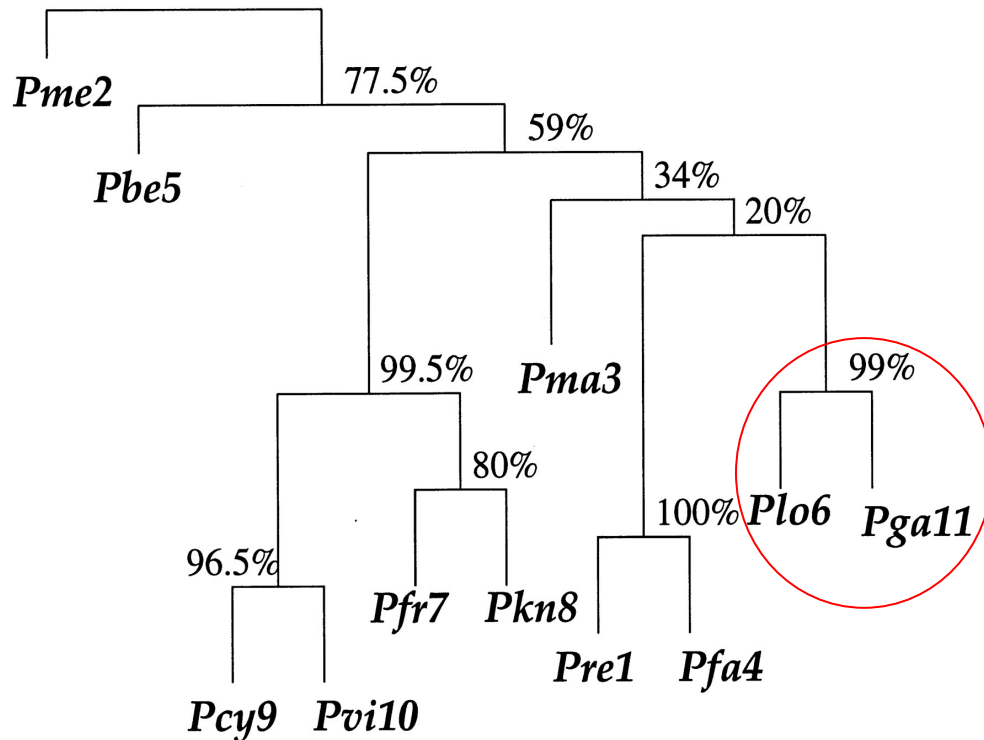
distances and all names

a tree rooted on a leaf node (rare)

Outgroup rooting

- Many methods (NJ) construct unrooted tree. An outgroup can be introduced to identify the “root”. Although the inferred tree for all species is still unrooted, the root is believed to be located along the branch that leads to the outgroup so that the tree for the ingroup species is rooted. This strategy is called outgroup rooting.
- A good outgroup needs to satisfy:
 1. not a member of the ingroup
 2. close related to the ingroup

Tree evaluation: Bootstrap analysis



Bootstrapping measures how consistently the data support given taxon bipartitions (Hedges, 1992).

Plo6 and *Pga11* are grouped together in 99% bootstrap replicates.

* B = 200 bootstrap replications.

An R package - ape

Analysis of Phylogenetics and Evolution ("ape") is an R software package for use in molecular evolution and phylogenetics.

Table 1. Special functions available in APE 1.1

Application	Available commands
Input/output	<code>read.dna</code> , <code>write.dna</code> , <code>read.nexus</code> , <code>write.nexus</code> , <code>read.tree</code> , <code>write.tree</code> , <code>read.GenBank</code>
Graphics	<code>add.scale.bar</code> , <code>plot.mst</code> , <code>plot.phylo</code> , <code>plot.skyline</code> , <code>lines.skyline</code> , <code>ltt.plot</code>
Tree manipulation	<code>bind.tree</code> , <code>drop.tip</code> , <code>is.binary.tree</code> , <code>is.ultrametric</code>
Comparative method	<code>compar.gee</code> , <code>compar.lynch</code> , <code>pic</code> , <code>v cv.phylo</code>
Diversification	<code>birthdeath</code> , <code>cherry</code> , <code>diversi.gof</code> , <code>diversi.time</code> , <code>gamma.stat</code>
Population genetics	<code>branching.times</code> , <code>coalescent.intervals</code> , <code>collapsed.intervals</code> , <code>find.skyline.epsilon</code> , <code>heterozygosity</code> , <code>skylineplot</code> , <code>skyline</code> , <code>theta.h</code> , <code>theta.k</code> , <code>theta.s</code>
Molecular dating	<code>chronogram</code> , <code>ratogram</code> , <code>NPRS.criterion</code>
Miscellaneous	<code>all.equal.phylo</code> , <code>balance</code> , <code>base.freq</code> , <code>dist.dna</code> , <code>dist.gene</code> , <code>dist.phylo</code> , <code>GC.content</code> , <code>klastorin</code> , <code>mantel.test</code> , <code>mst</code> , <code>summary.phylo</code>
Data sets	<code>bird.families</code> , <code>bird.orders</code> , <code>hivtree</code> , <code>landplants</code> , <code>opsin</code> , <code>woodmouse</code> , <code>xenarthra</code>

References

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Baum *et al.* The tree-thinking challenge, 2005, Science, 310:979-980