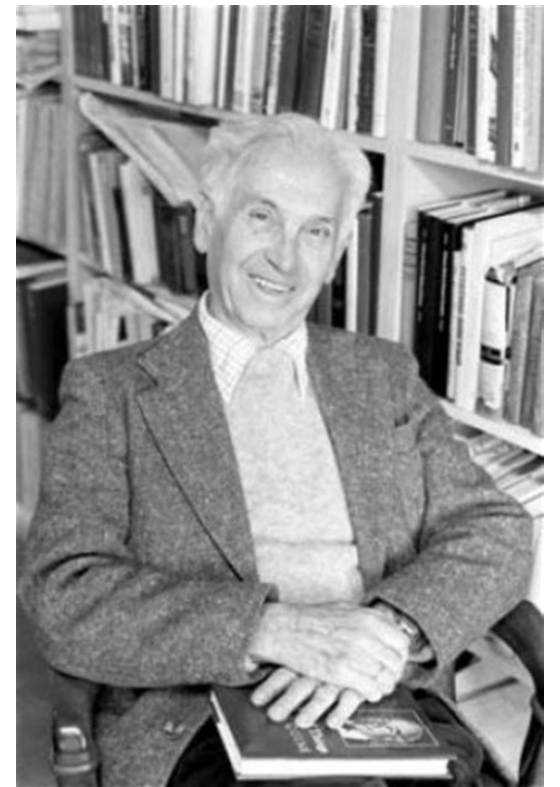


Species

The **biological species concept** by Ernst Mayr



- A species is a group of populations that can interbreed in nature and produce viable and fertile offspring
- Note: Some species might show morphological diversity (but with interbreeding), while other times isolated species can be almost indistinguishable (e.g. 2 spp. meadowlarks and 2 spp. gray treefrogs)



(a) Similarity between different species



(b) Diversity within a species

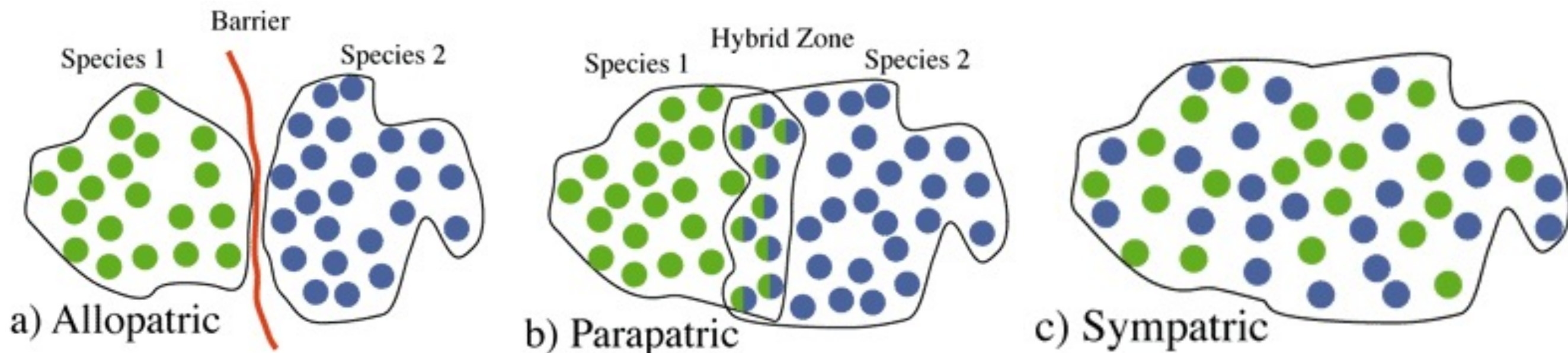
Three Traditional Models of Speciation (+polyploidy)

- Geographic relationship

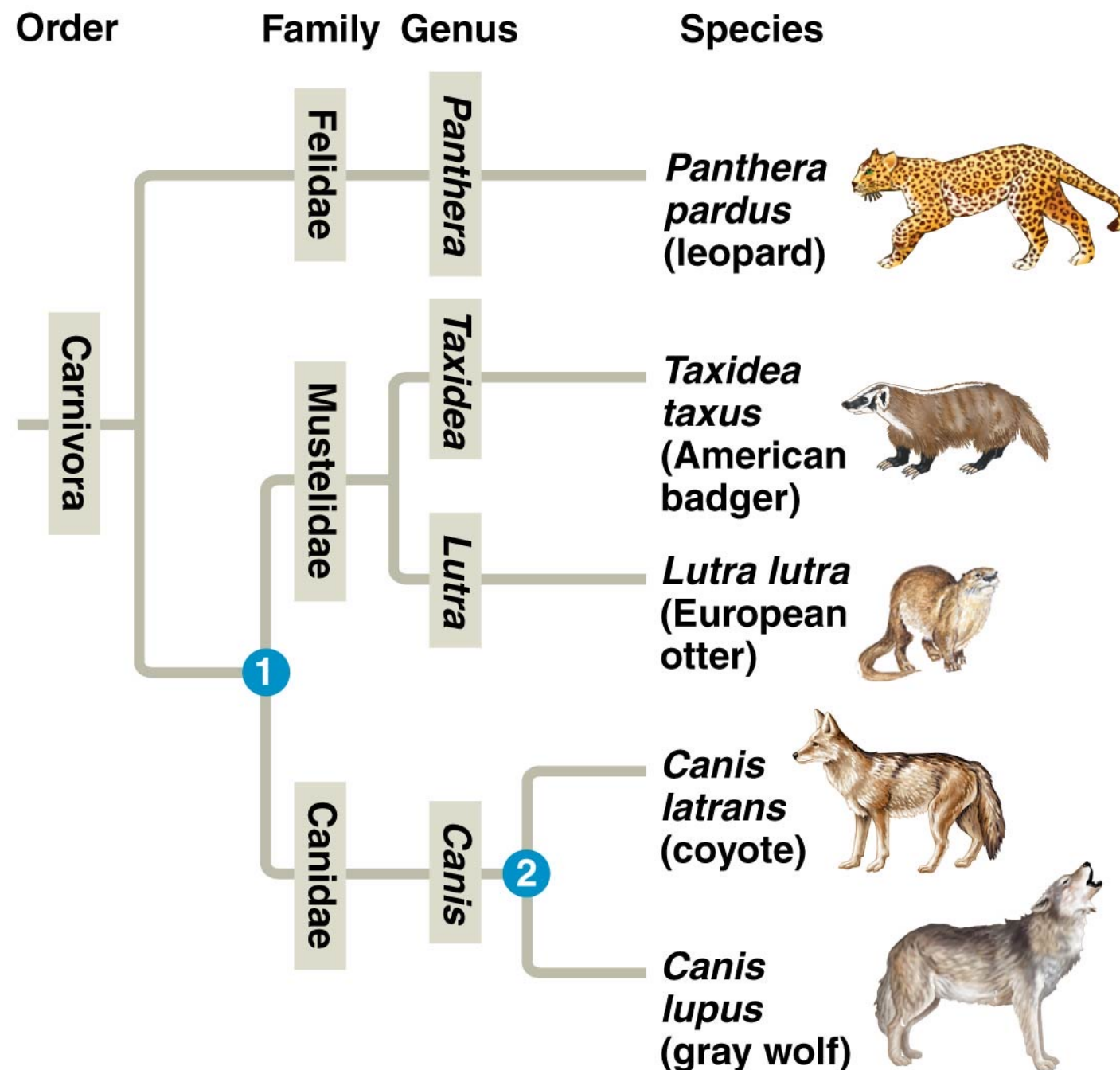
1. Allopatric speciation (vicariance)

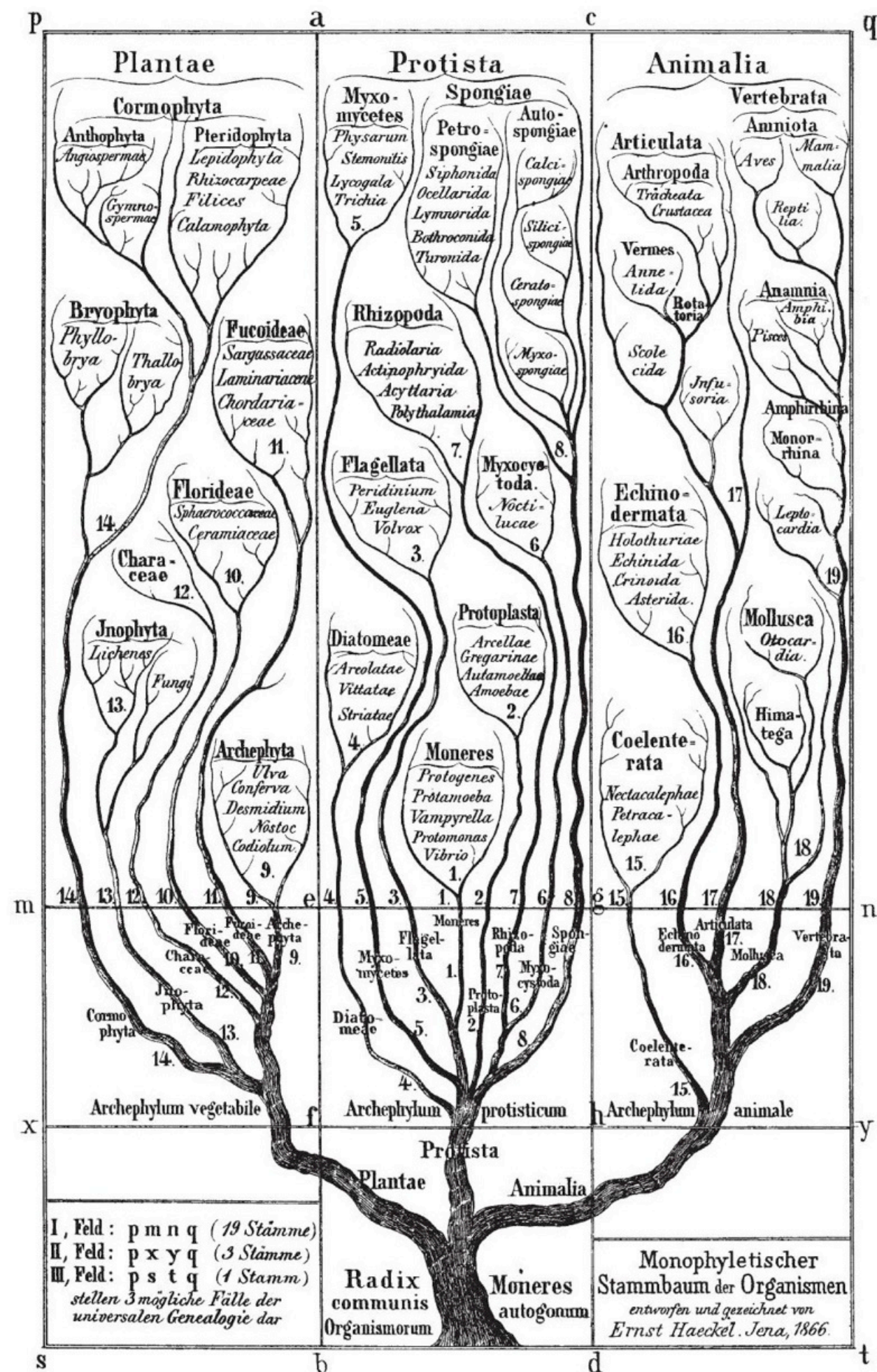
2. Parapatric speciation

3. Sympatric speciation



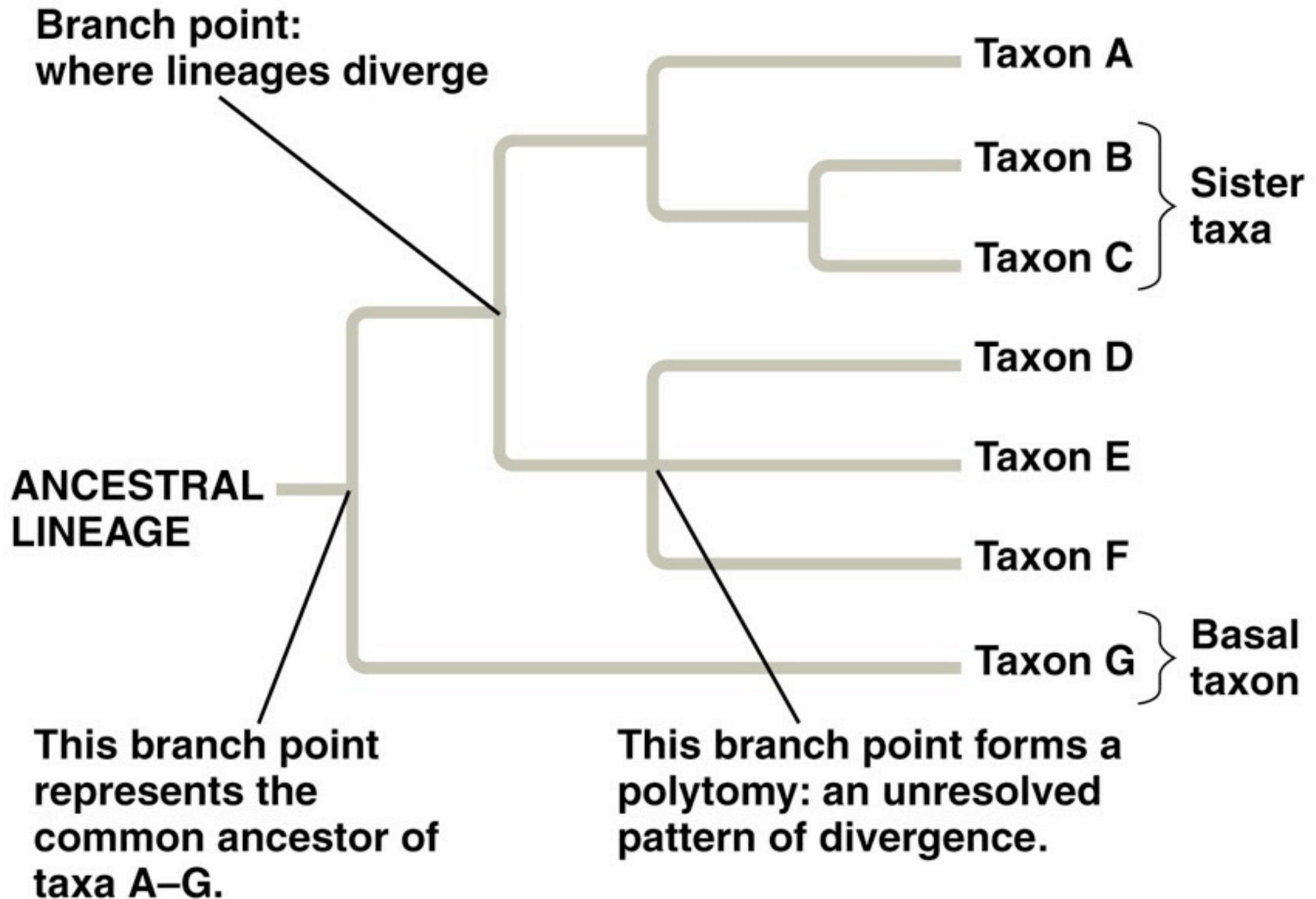
Phylogenetics & Systematics



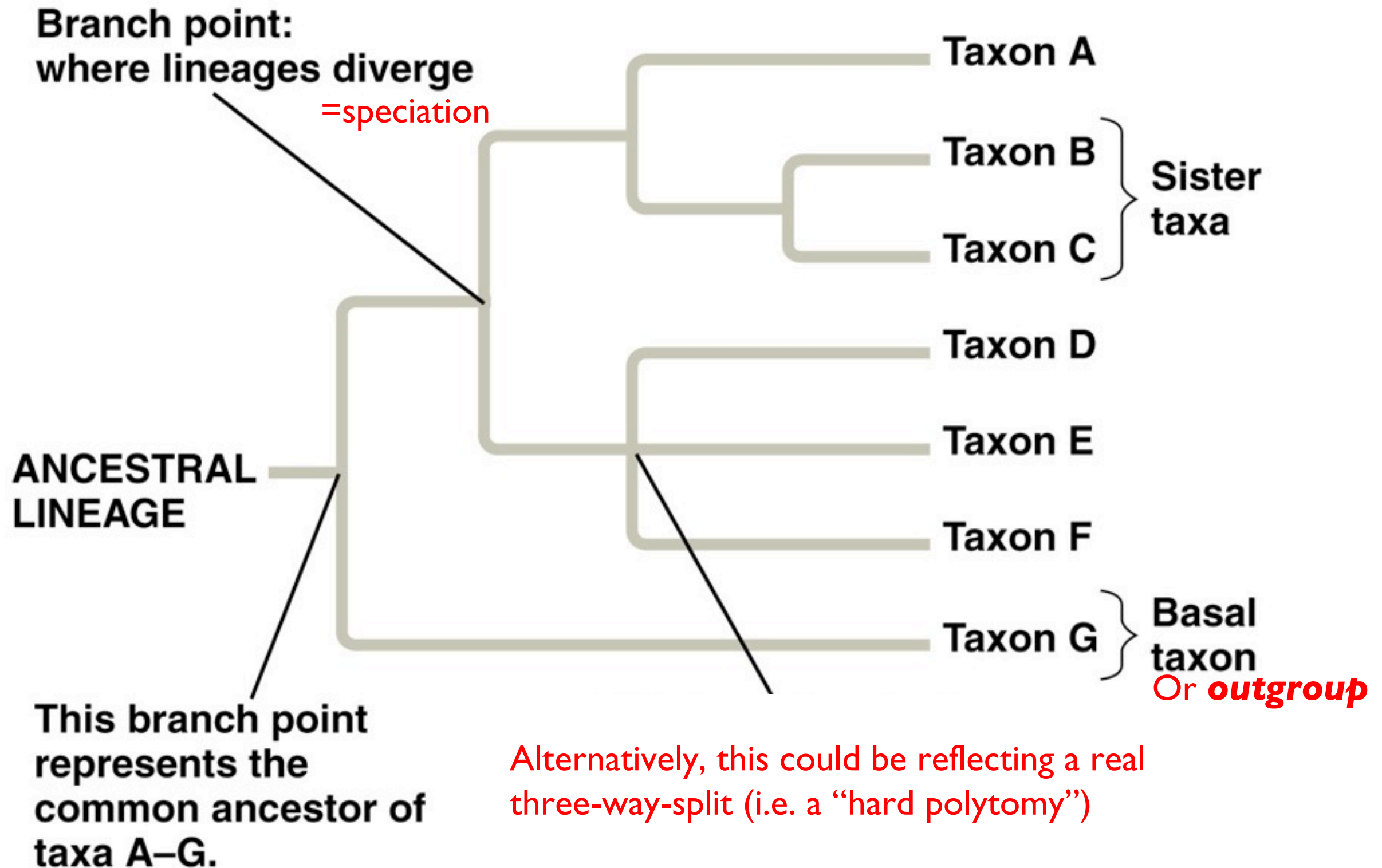


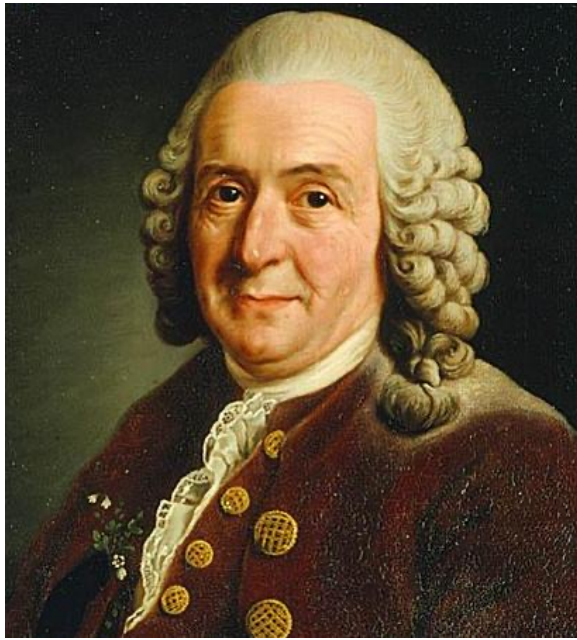
- Phylogenetics = the science of figuring out relationships between organisms
- Phylogeny = the evolutionary history of a species or group of related species
- Systematics = the science of classifying organisms based on their characteristics, taxonomy = part of systematics concerned with naming organisms
- Cladistics (Phylogenetic systematics) = classification of organisms based on their order of branching on an evolutionary tree

Phylogenetic tree (cladogram)



Phylogenetic tree (cladogram)





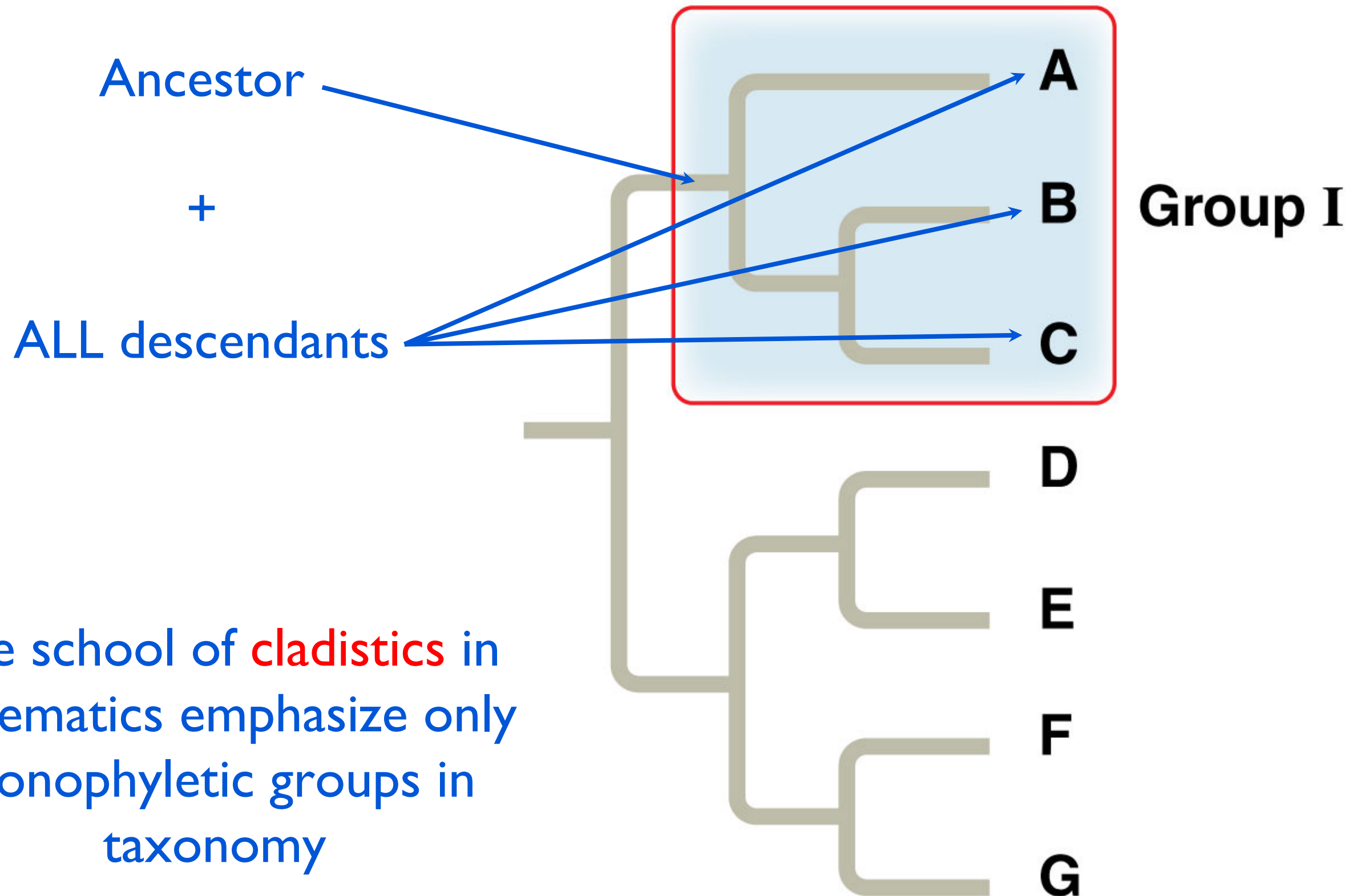
Linnaeus: 18th century taxonomy

- Includes two part format for scientific names (binomial nomenclature) and hierarchical classification system (e.g., Kingdom, Phylum, Class, Order, Family, Genus, Species)
- Still in use today (although Domain has been added as the most inclusive hierarchical category)
- Today, the Linnean system is used assuming the named taxa show some sort of relationship (usually monophyletic)

Taxonomic tips

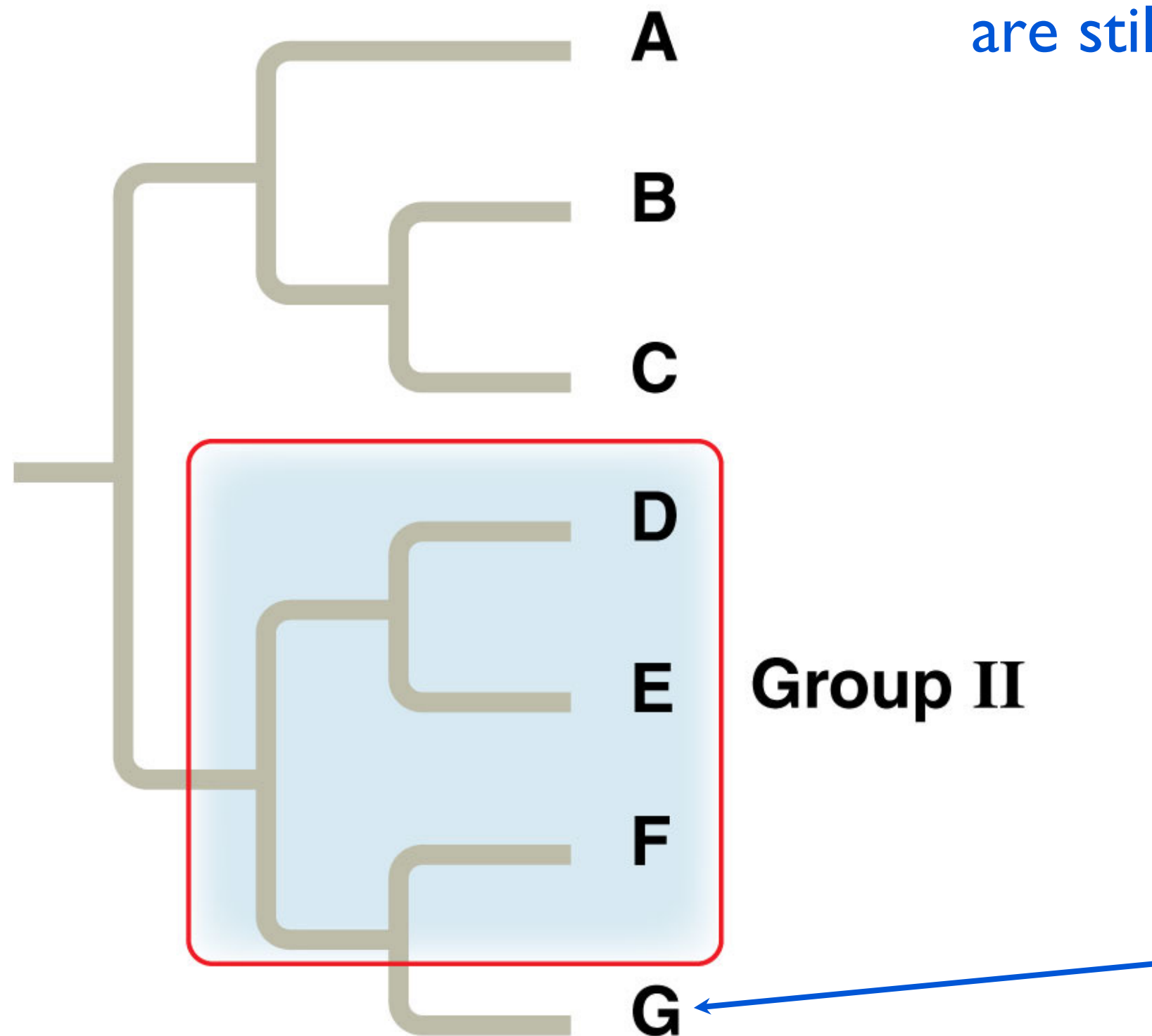
- ‘Species’ is both the singular and the plural form (there is no such thing as a ‘specie’)
- ‘Genus’ is singular, ‘genera’ is plural
- In a binomial species name, the first letter of the genus only is capitalized, e.g., *Homo sapiens*, **not** *Homo Sapiens* (and the ‘s’ is not plural)
- The entire binomial is *italicized*, or less commonly, underlined

(a) Monophyletic group (clade)



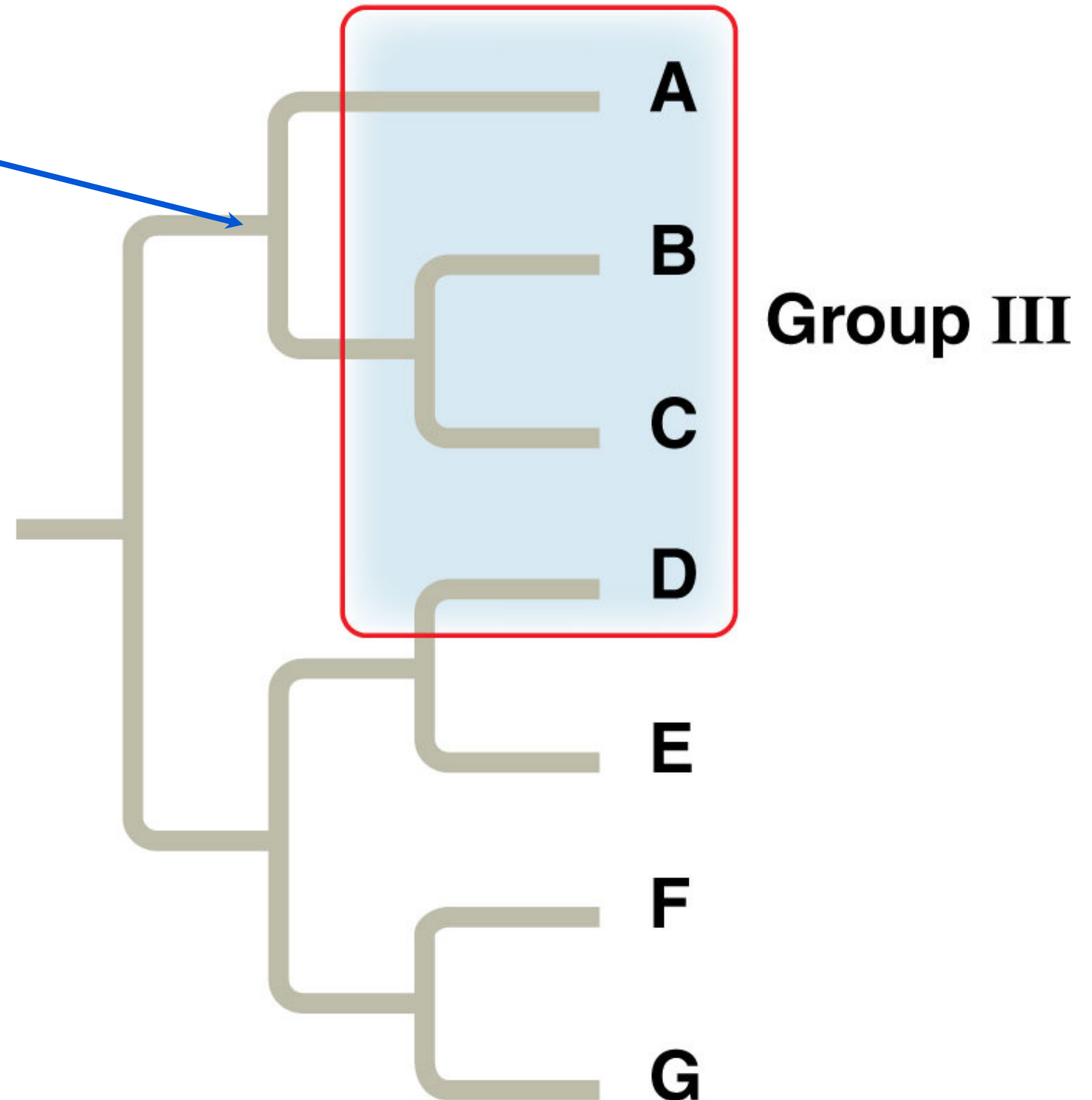
(b) Paraphyletic group

Some paraphyletic groups are still used in naming taxa



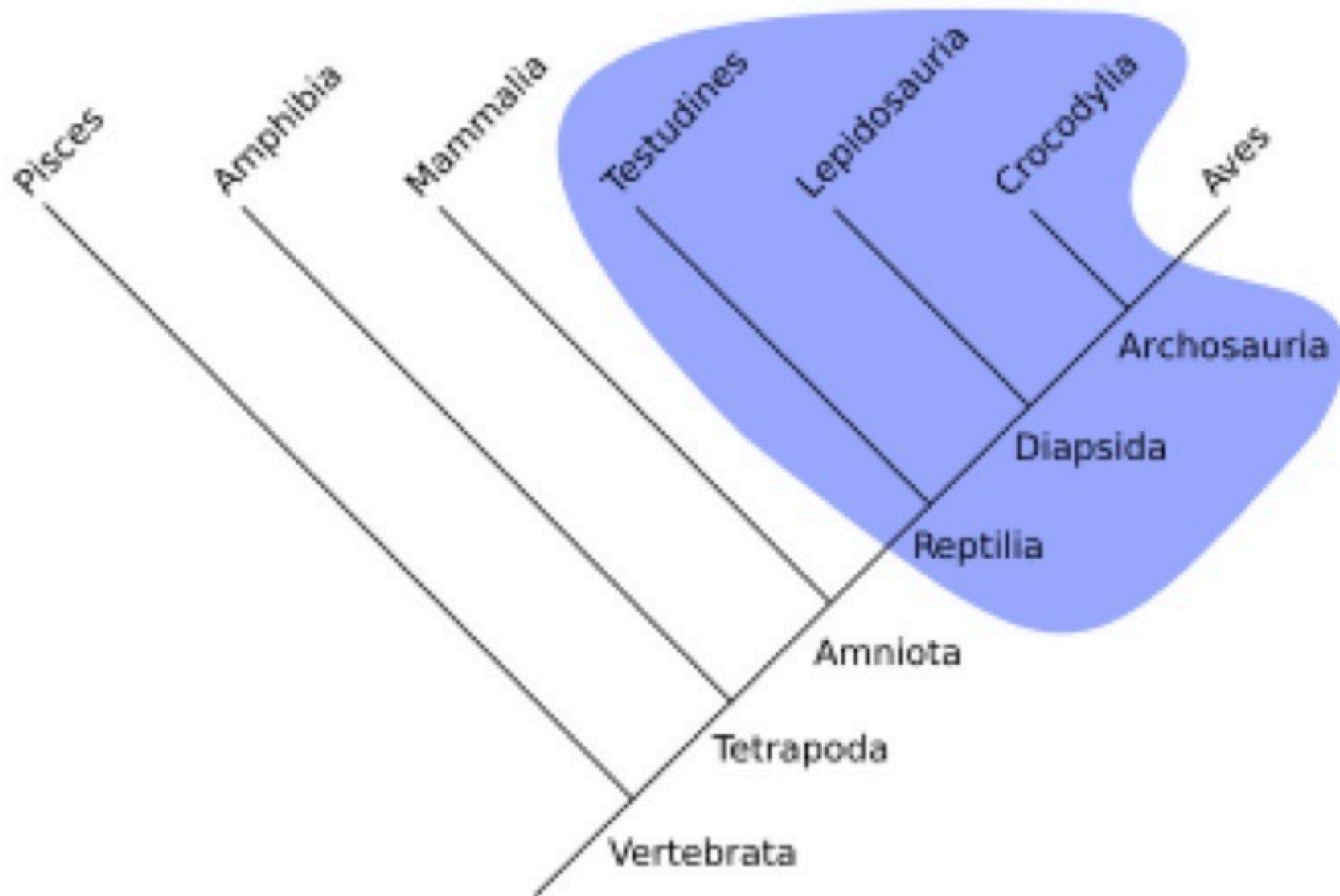
(c) Polyphyletic group

Ancestor
not included

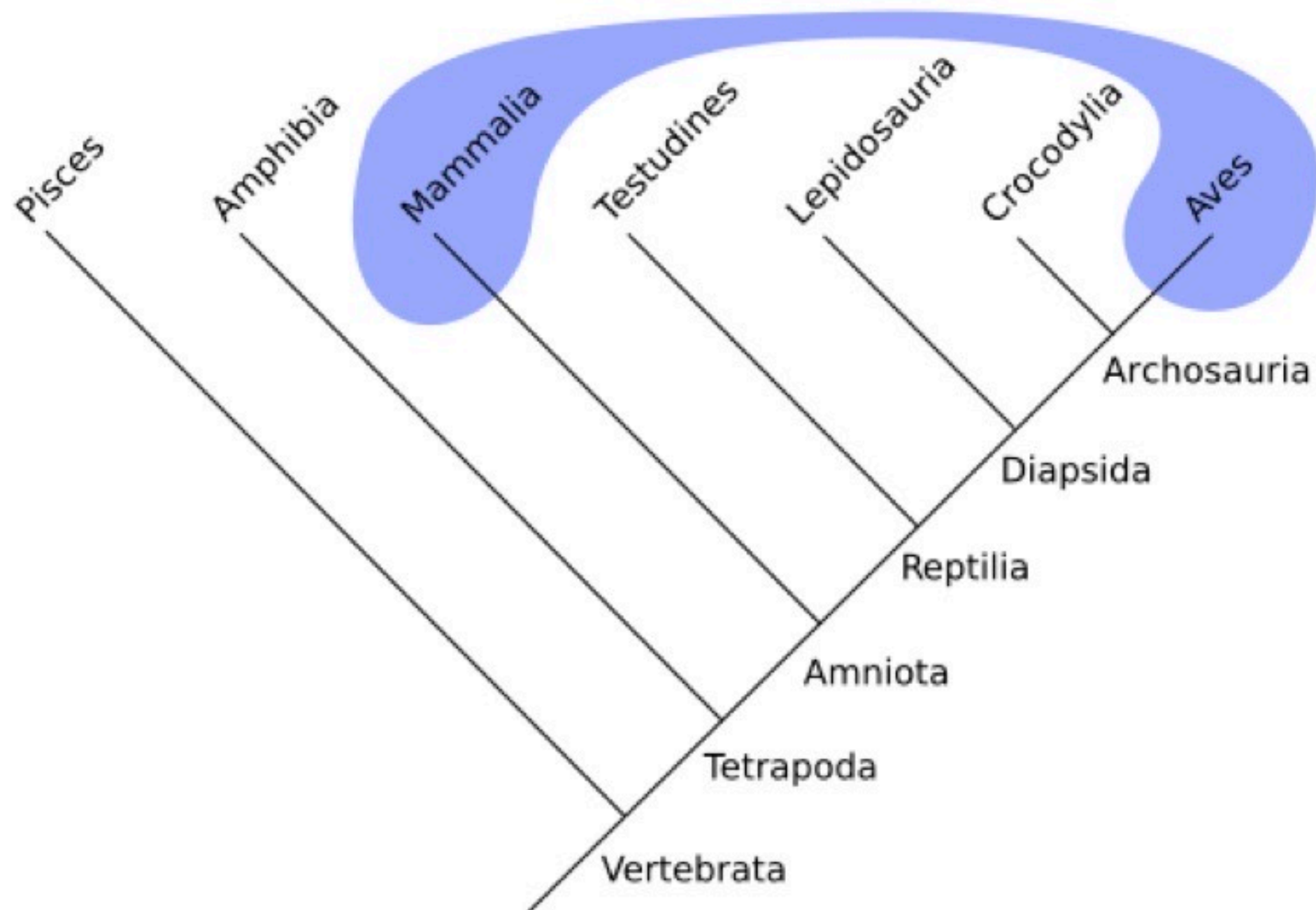


Polyphyletic groups are
avoided in modern
taxonomy

The class Reptilia is paraphyletic (as traditionally defined)



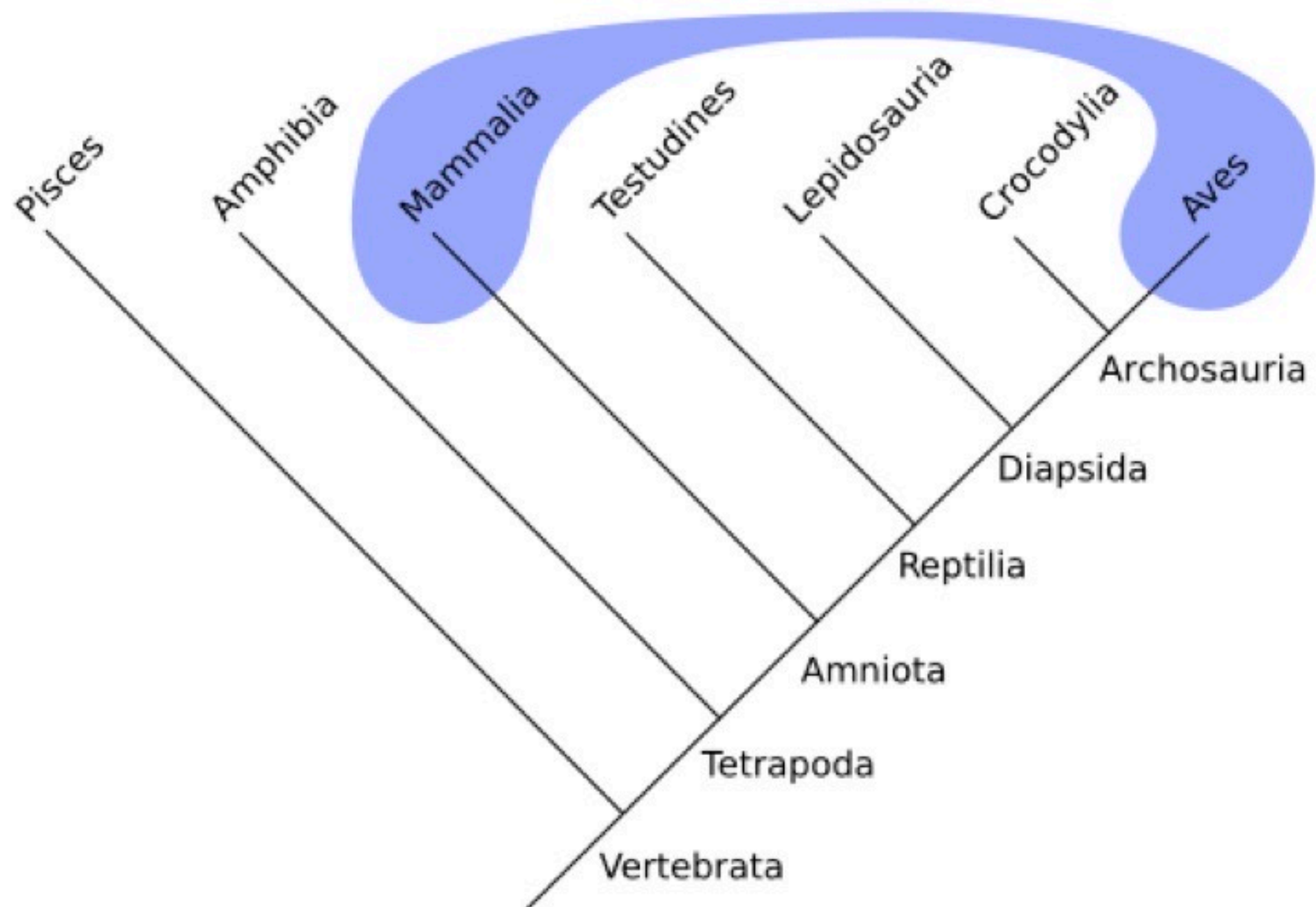
Systematists: 'Warm-blooded animals' are polyphyletic



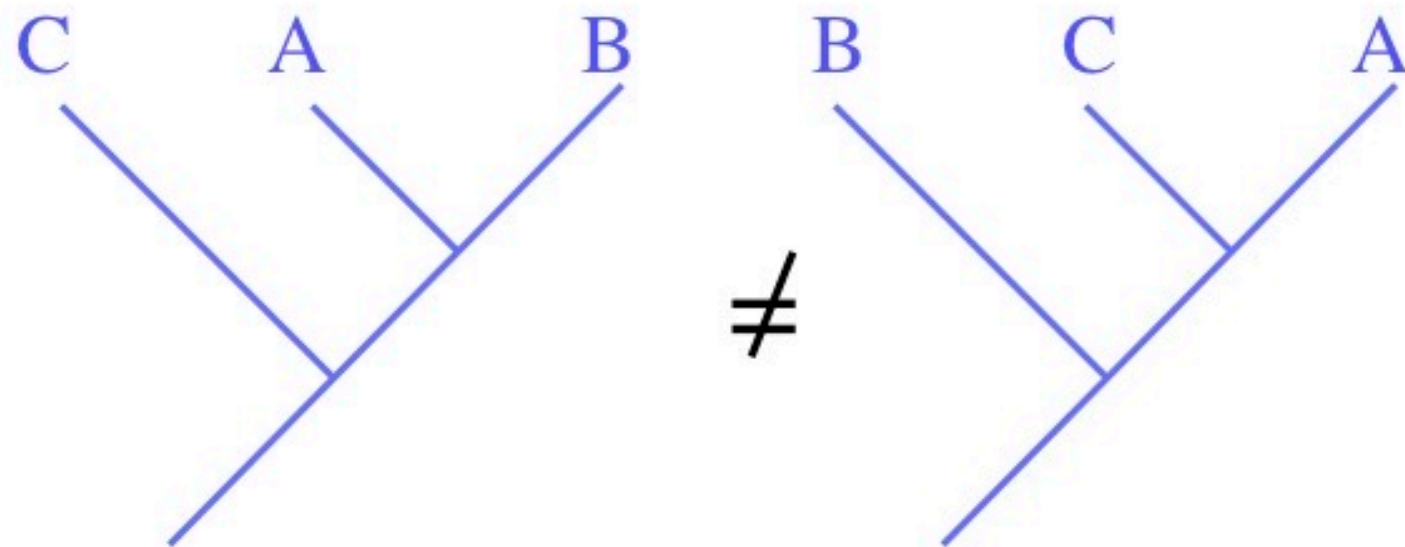
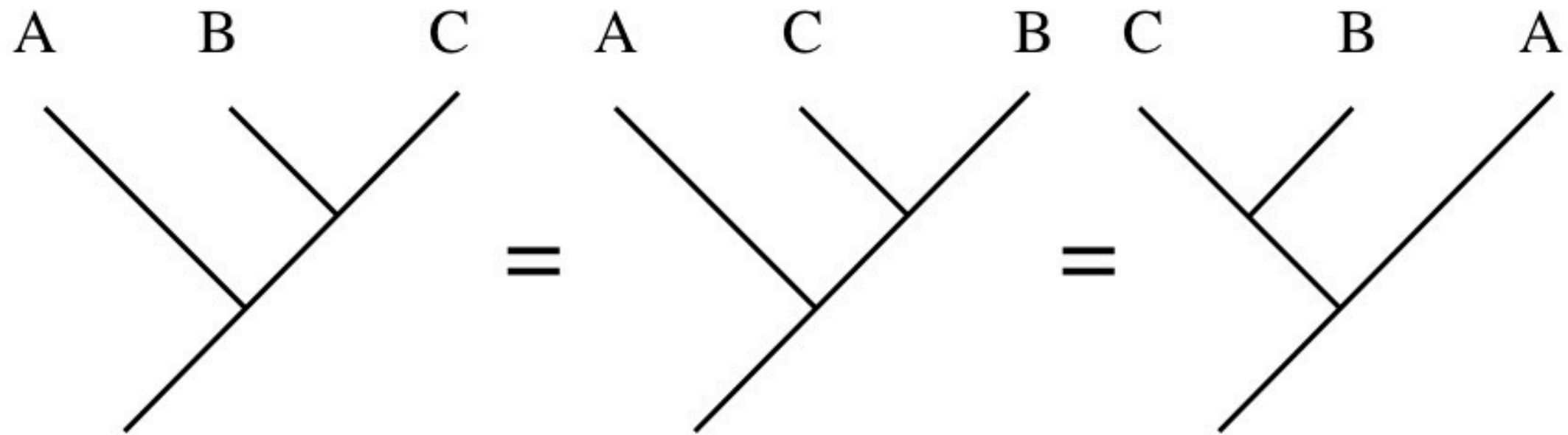
Systematists:

~~‘Warm-blooded animals’~~

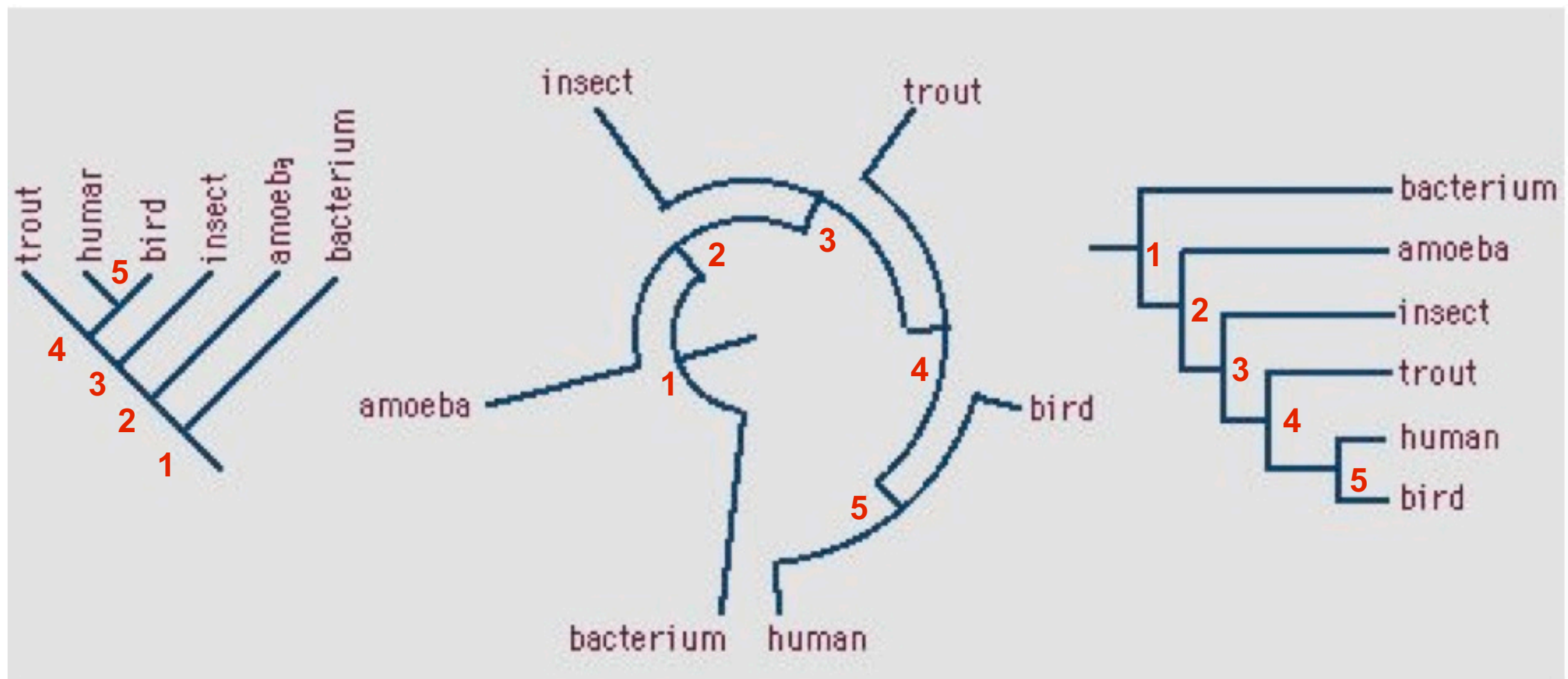
are polyphyletic



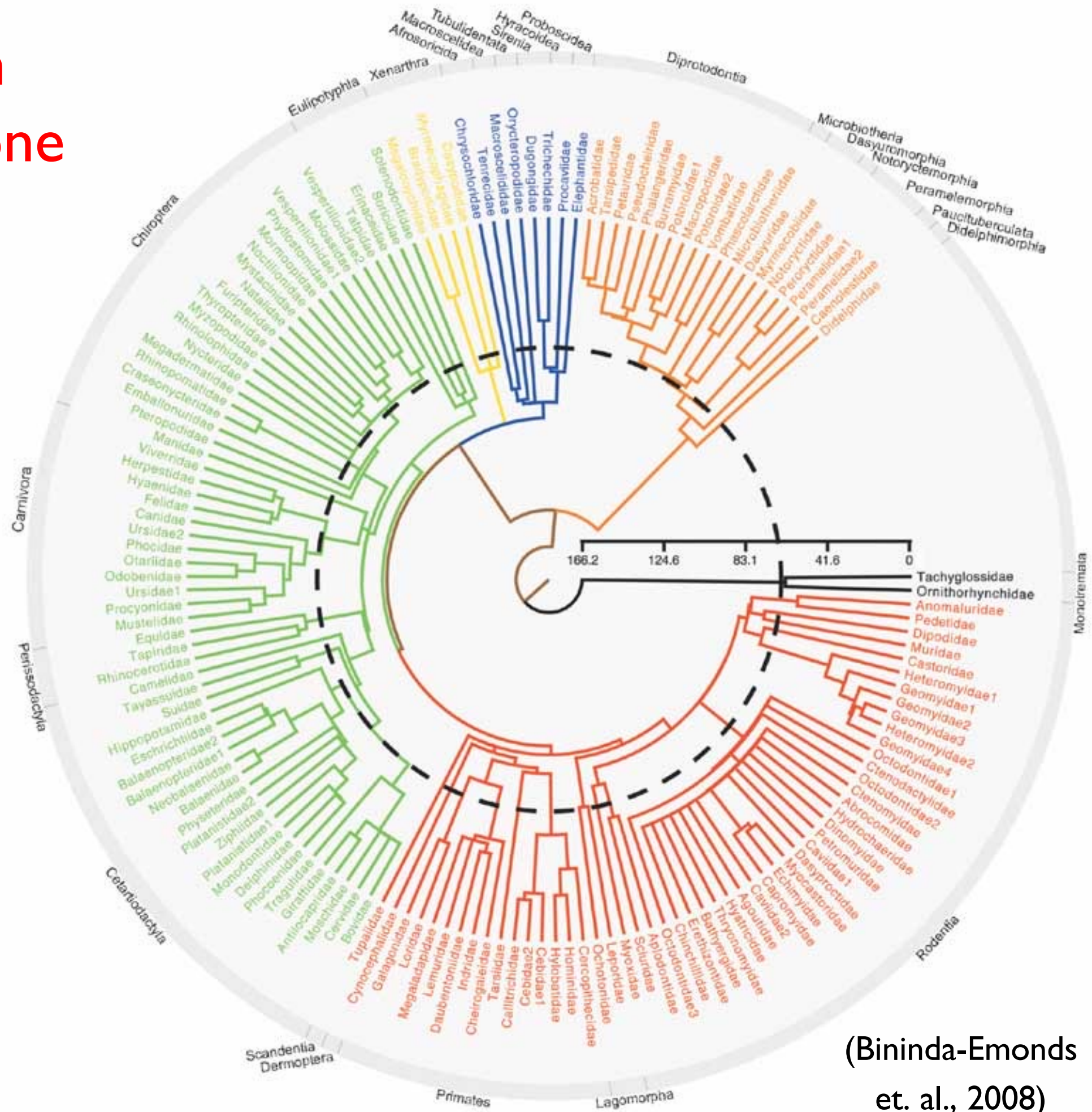
Branches can be rotated around nodes



These three phylogenies are equivalent



All mammalian families in one tree

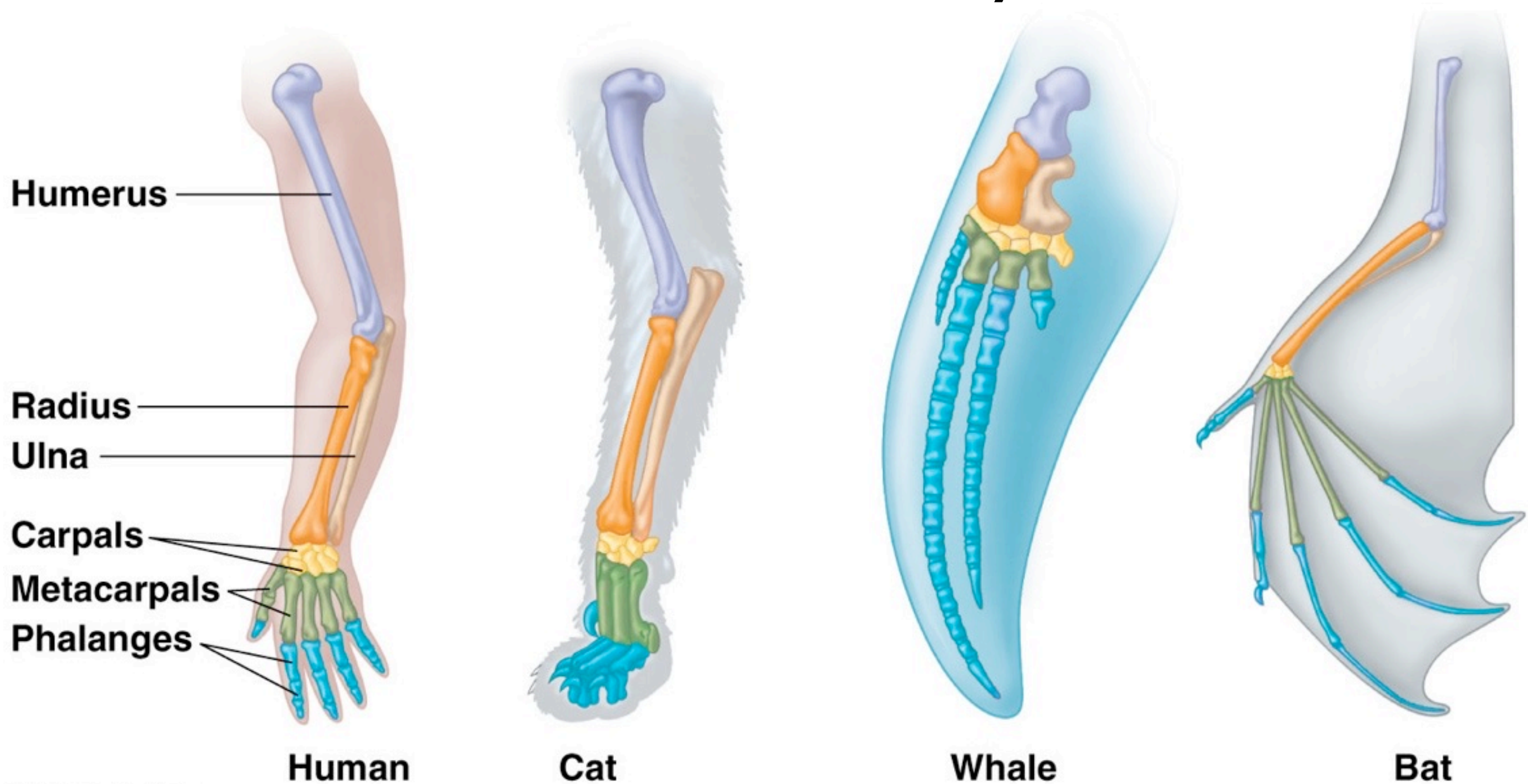


(Bininda-Emonds
et. al., 2008)

Phylogenies can be inferred from morphological and molecular homologies...



Homologies show developmental, phenotypic, and genetic similarities due to shared ancestry



Caution:

- **Convergent Evolution can lead to *analogous (homoplastic)* traits:**
 - Similar, analogous, trait that evolved independently in each lineage (*homoplasy*)
 - Brought on by natural selection due to similar environment ***rather than*** shared ancestry

E.g. most monkeys eat fruits, but howler monkeys and colobus monkeys have independently evolved complex stomachs to handle a folivorous diet

Howler
Monkey



Colobus
Monkey

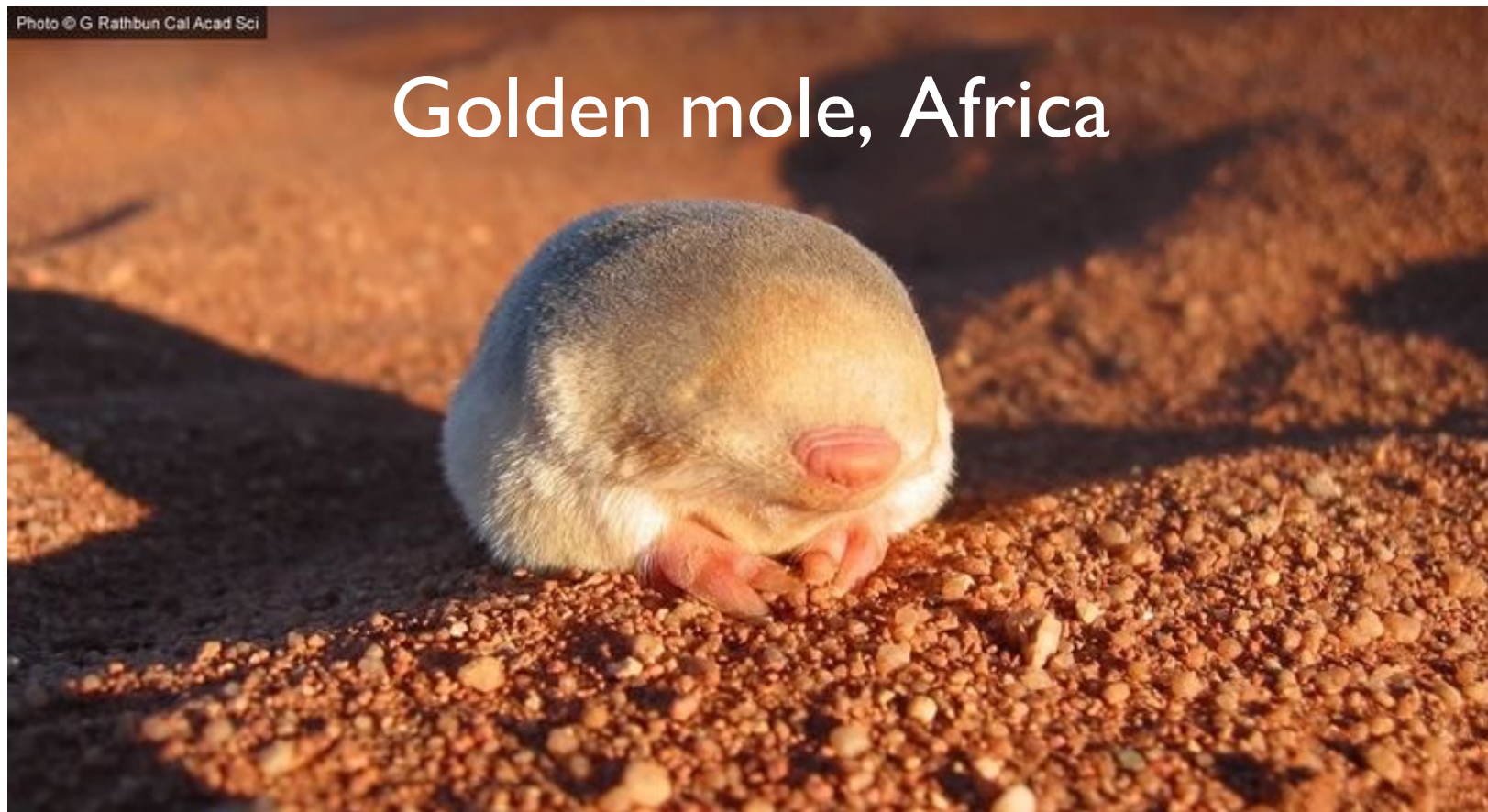


Homoplasy: Analogous (or convergent) characteristics

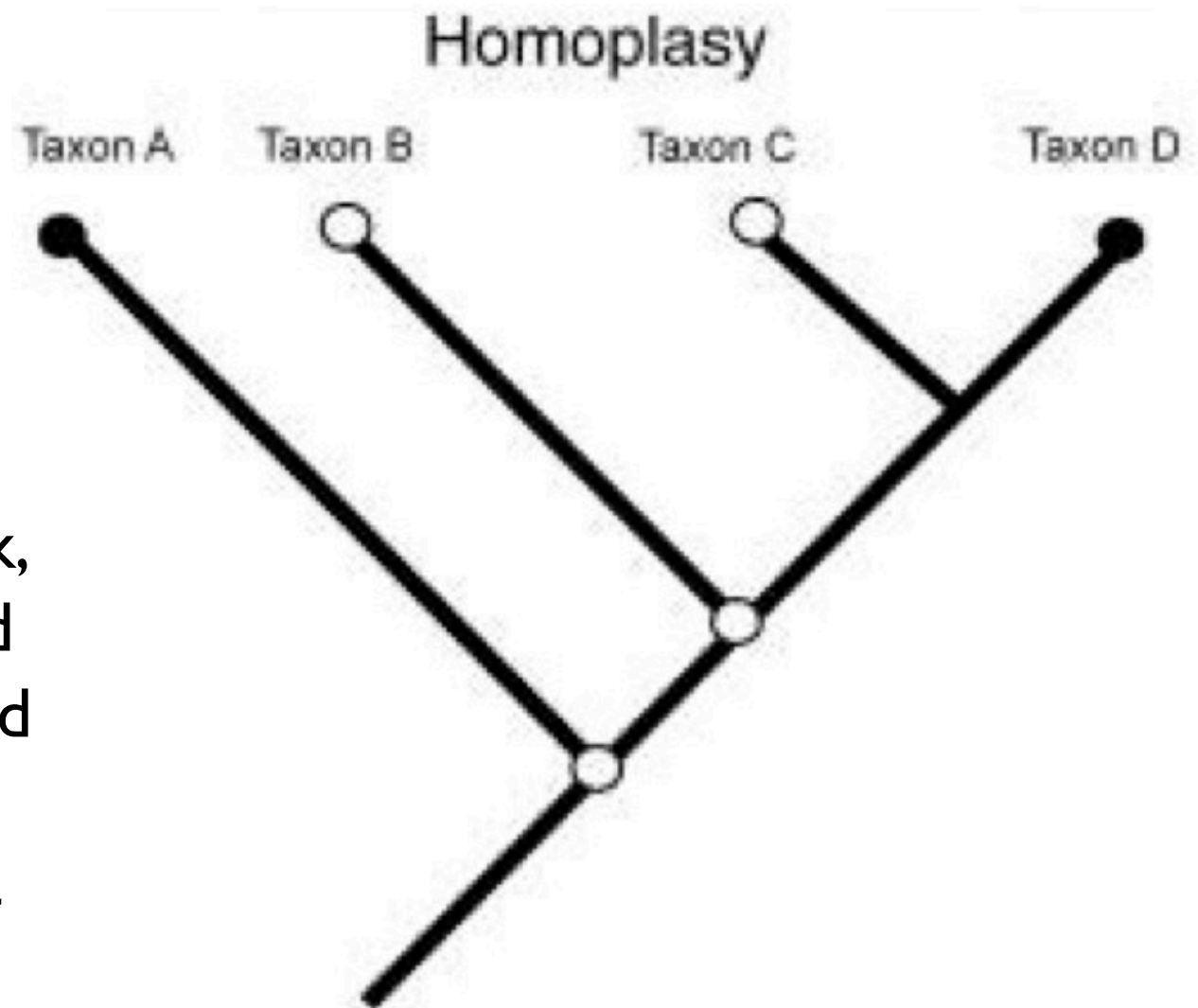
Marsupial mole, Australia



Golden mole, Africa



- In a phylogenetic analysis, analogous morphologies or molecular sequences that evolved independently are called homoplasies (homoplastic characters)



e.g., Taxon A and D are both black, but the last common ancestor and taxa B and C are white. Taxa A and D share a trait not because their common ancestor possessed that trait, but because they each have independently converged on the trait

The diagram shows two DNA sequences aligned horizontally. The top sequence is A C G G A T A G T C C A C T A G G C A C T A. The bottom sequence is T C A C C G A C A G G T C T T T G A C T A G. Vertical yellow bars highlight the mismatched bases at positions 2, 7, 10, 13, 16, and 19. In the top sequence, the highlighted bases are C, A, C, G, and C. In the bottom sequence, the highlighted bases are C, A, C, T, and G.

Position	Top Sequence	Bottom Sequence
1	A	T
2	C	C
3	G	A
4	G	C
5	A	C
6	T	G
7	A	A
8	G	G
9	T	T
10	C	C
11	C	A
12	A	G
13	C	T
14	T	T
15	A	T
16	G	G
17	C	A
18	A	C
19	C	T
20	T	A

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Molecular homoplasy: statistical tools have been developed to determine whether DNA sequences that share a certain fraction of their bases do so because they are **homologous** or **homoplastic**

How to distinguish relationships given these issues?

- Phylogenetic trees based on many traits and/or extensive molecular data (e.g. many genes)
- Relationships among living forms can be compared to fossil evidence (or vice versa) –Example: birds & mammals
- Numerous characters can be analyzed using concepts such as ***Parsimony***

Parsimony

- Occam's Razor – (Parsimony in Science) when you have two competing hypotheses that make the same predictions, the simpler hypothesis is more likely to be correct. (Cut away unnecessarily complex ideas and “ad hoc” assumptions)



William of Ockham (14th.century)

- ***Parsimony in phylogenetics*** – Phylogenetic tree (cladogram) that assumes the fewest steps more likely to be correct