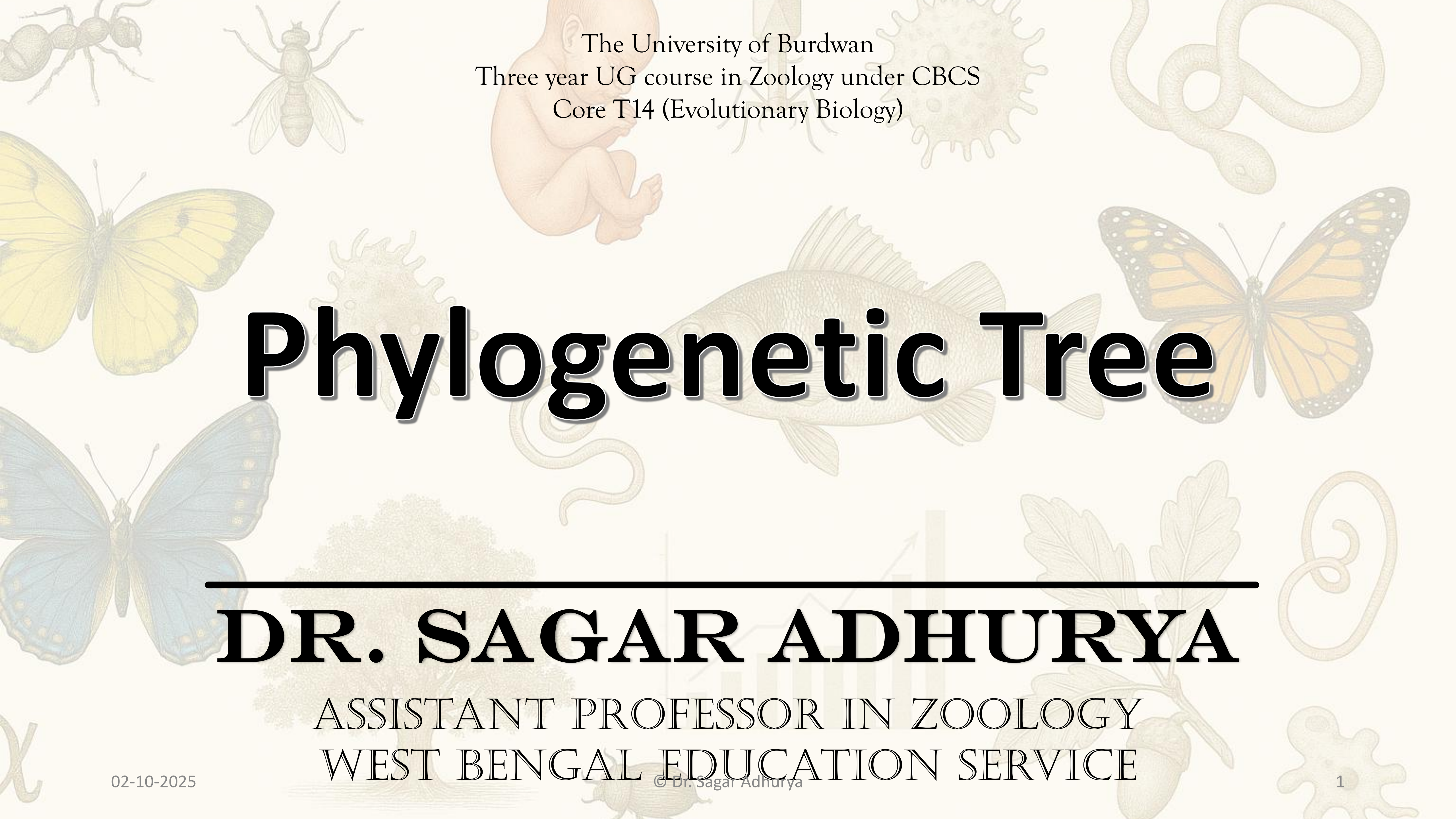


The University of Burdwan
Three year UG course in Zoology under CBCS
Core T14 (Evolutionary Biology)

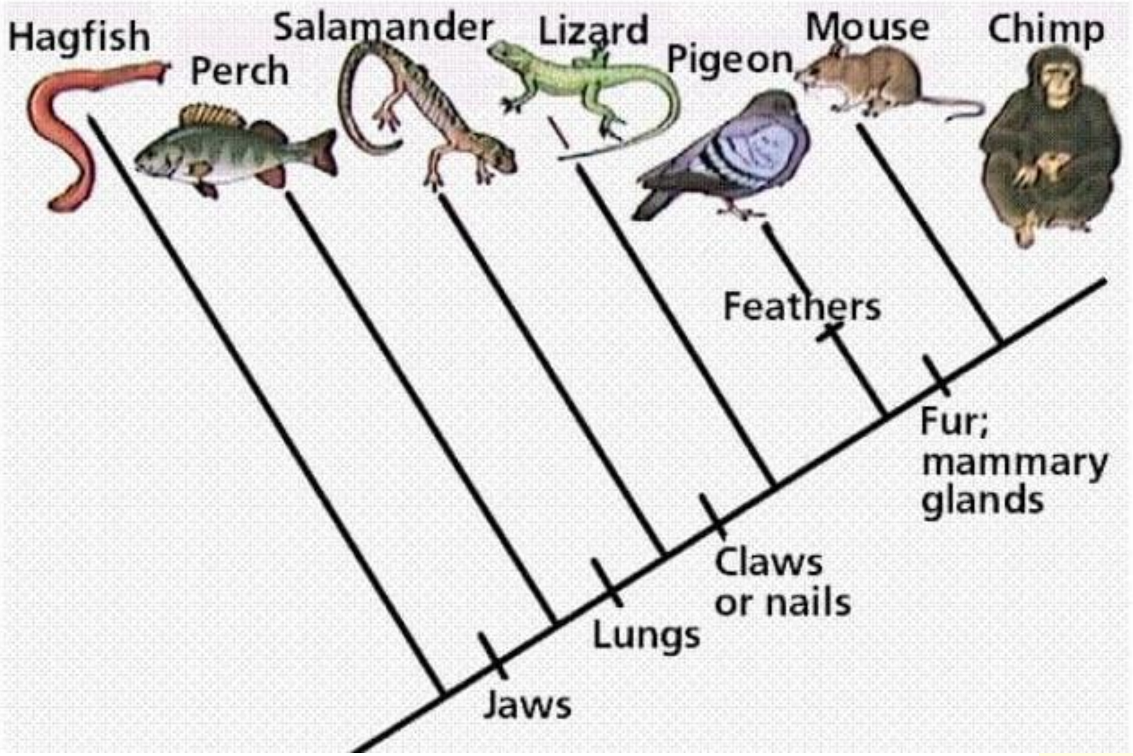
Phylogenetic Tree

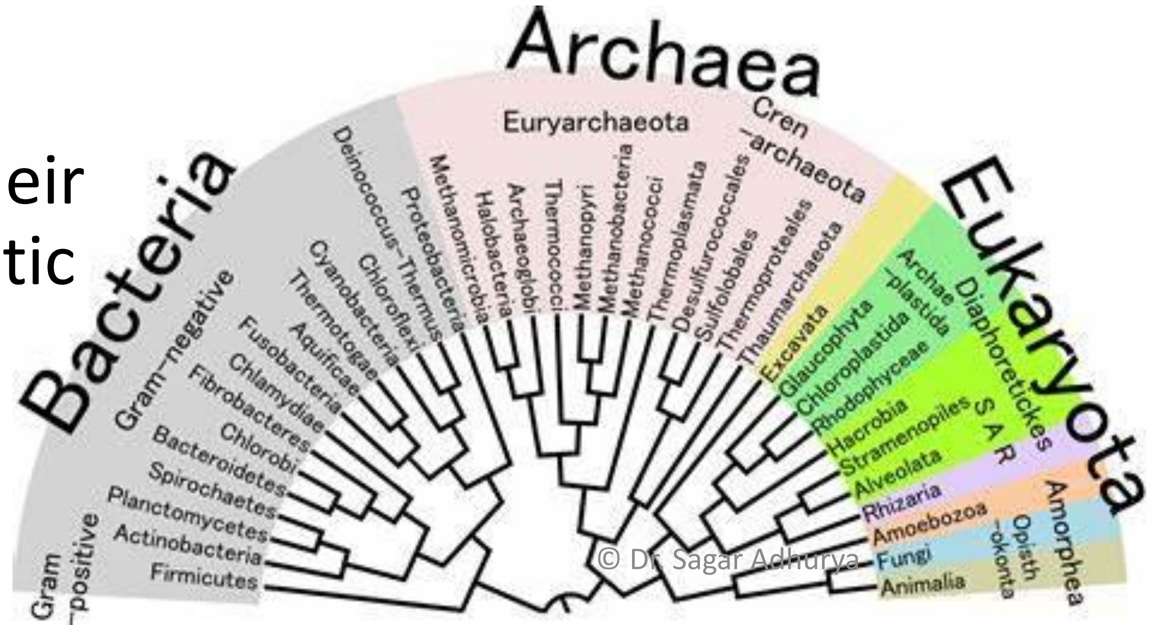
DR. SAGAR ADHURYA

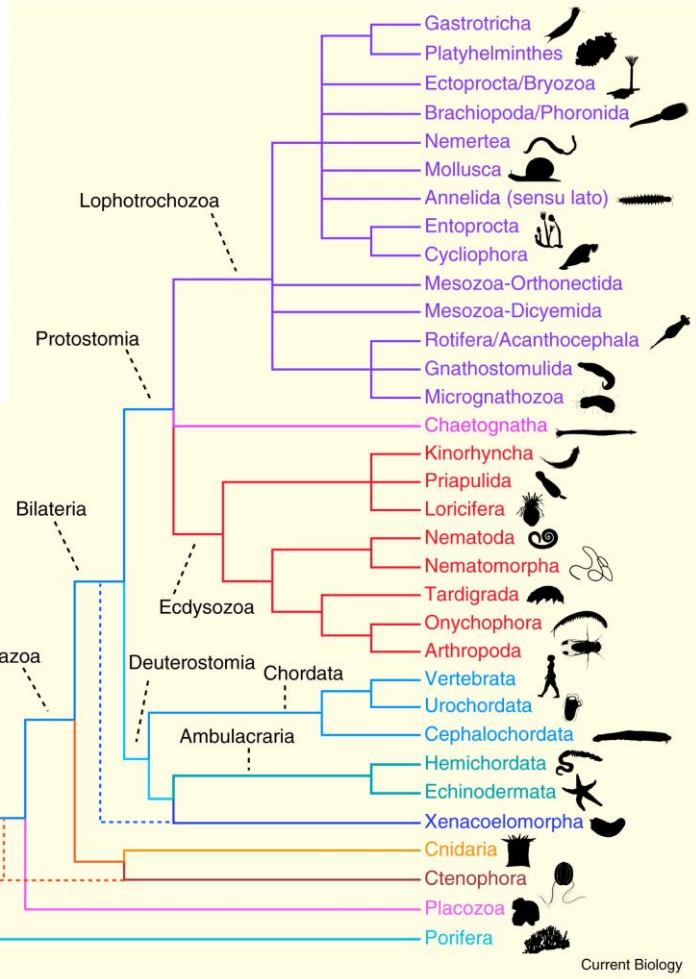
ASSISTANT PROFESSOR IN ZOOLOGY
WEST BENGAL EDUCATION SERVICE

Phylogenetic Tree

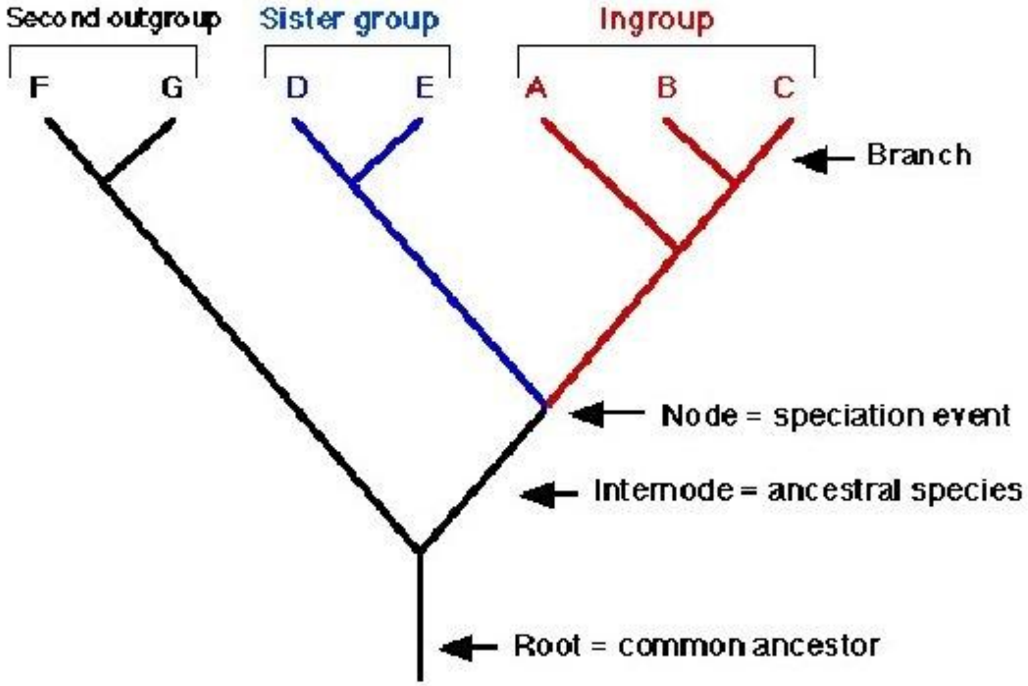
- It is a branching diagram showing the inferred evolutionary relationship among various entities, based upon similarities and differences in their physical or genetic characteristics.







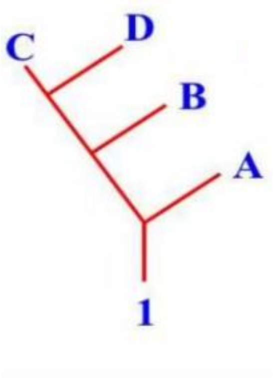
Structure


Second outgroup
Sister group
Ingroup
F
G
D
E
A
B
C
Branch
Node = speciation event
Internode = ancestral species
Root = common ancestor

Rooted vs unrooted tree

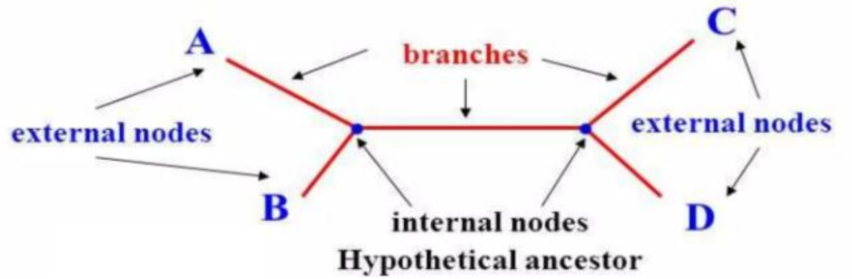
Rooted Tree

- A rooted tree is used to make inferences about the most common ancestor of the terminal species.



Unrooted tree

- An unrooted tree is used to make an illustration about the leaves or branches, but not the assumption about terminal species.



Approaches to classifying organisms

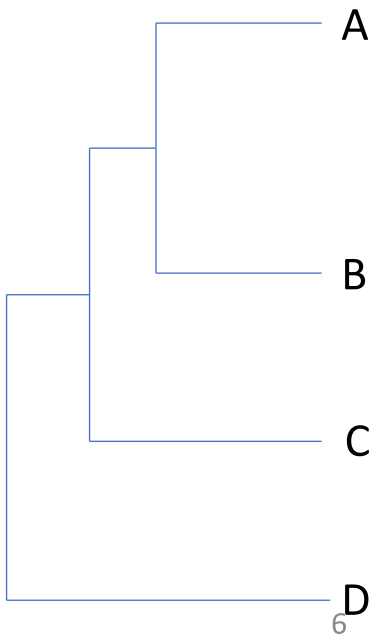
	Phenetics	**Cladistics**
Definition	Phenetics is a method of classifying organisms based on structural and morphological characteristics those are observable (phenotypical characters)	Cladistics is a method of classifying organisms based on their ancestry and evolutionary relationship
Characteristics considered	Morphological characters	Evolutionary relationships, genetic similarity and ancestry
Use of trees to describe relationships	Phenogram	Cladogram
Accuracy	Low	High
Reproducibility	Low	High

Phenetics

- This method classifies species based on their observable characters.
- This characters are called Operational Taxonomic Unit (OTU).
- Depending upon presences or absence of the character (OTU), the value 1 (presence) and 0 (absence) is assigned against that.
- Then the similarity coefficient is calculated.
- Depending upon the value of the similarity coefficient the phenogram is constructed and relationships among different species are established.

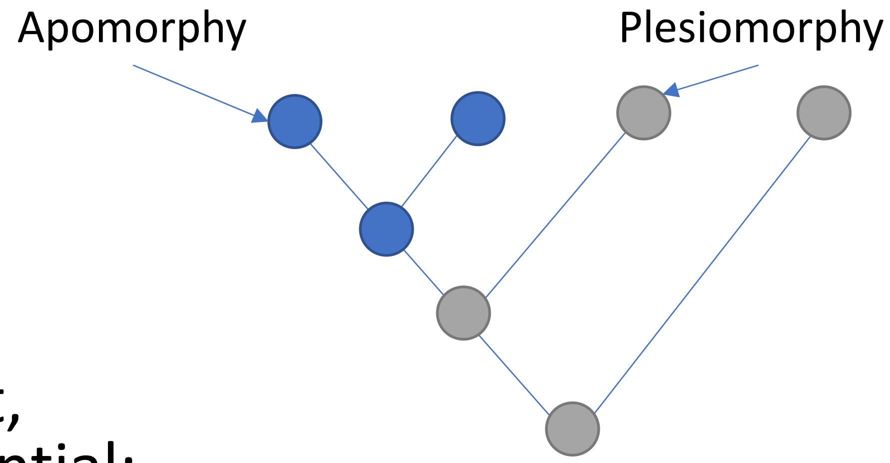
OTU	A	B	C	D
1	0	1	1	1
2	1	0	1	0
3	0	1	1	0
4	.	.	.	.
5	.	.	.	.
6	.	.	.	.
7	.	.	.	.

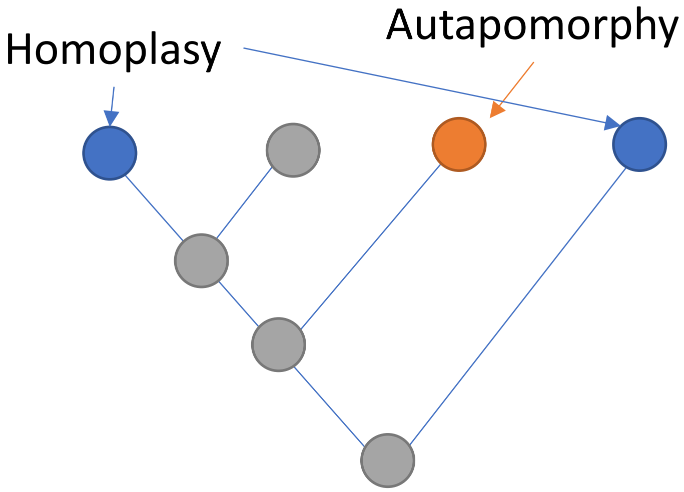
	A	B	C	D
A	1			
B	0.8	1		
C	0.5	0.5	1	
D	0.4	0.6	0.4	1



Cladistics

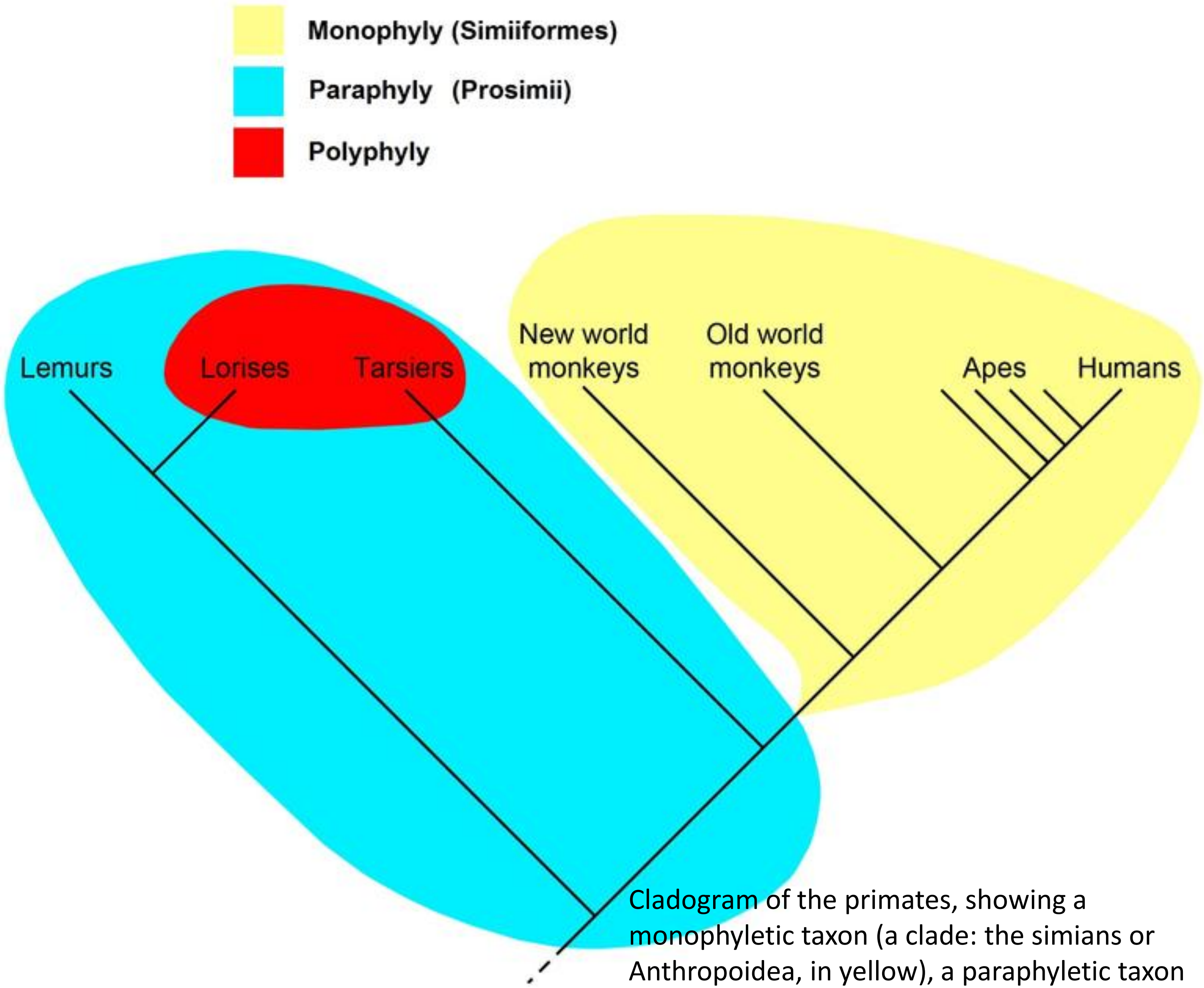
- In cladistics the relationships are based on shared derived characters.
- Before understanding the cladogram development, understanding about some terminologies are essential:
  - **Apomorphic character:** derived character
  - **Plesiomorphic character:** ancestral character
  - **Synapomorphy:** Shared-derived character
  - **Synplesiomorphy:** Shared-ancestral character
  - **Autapomorphy:** Derived character state restricted to a single lineage.
  - **Homoplasy:** A character state that independently evolved multiple time. Homoplasious character is a result of convergent evolution.





Monophyly

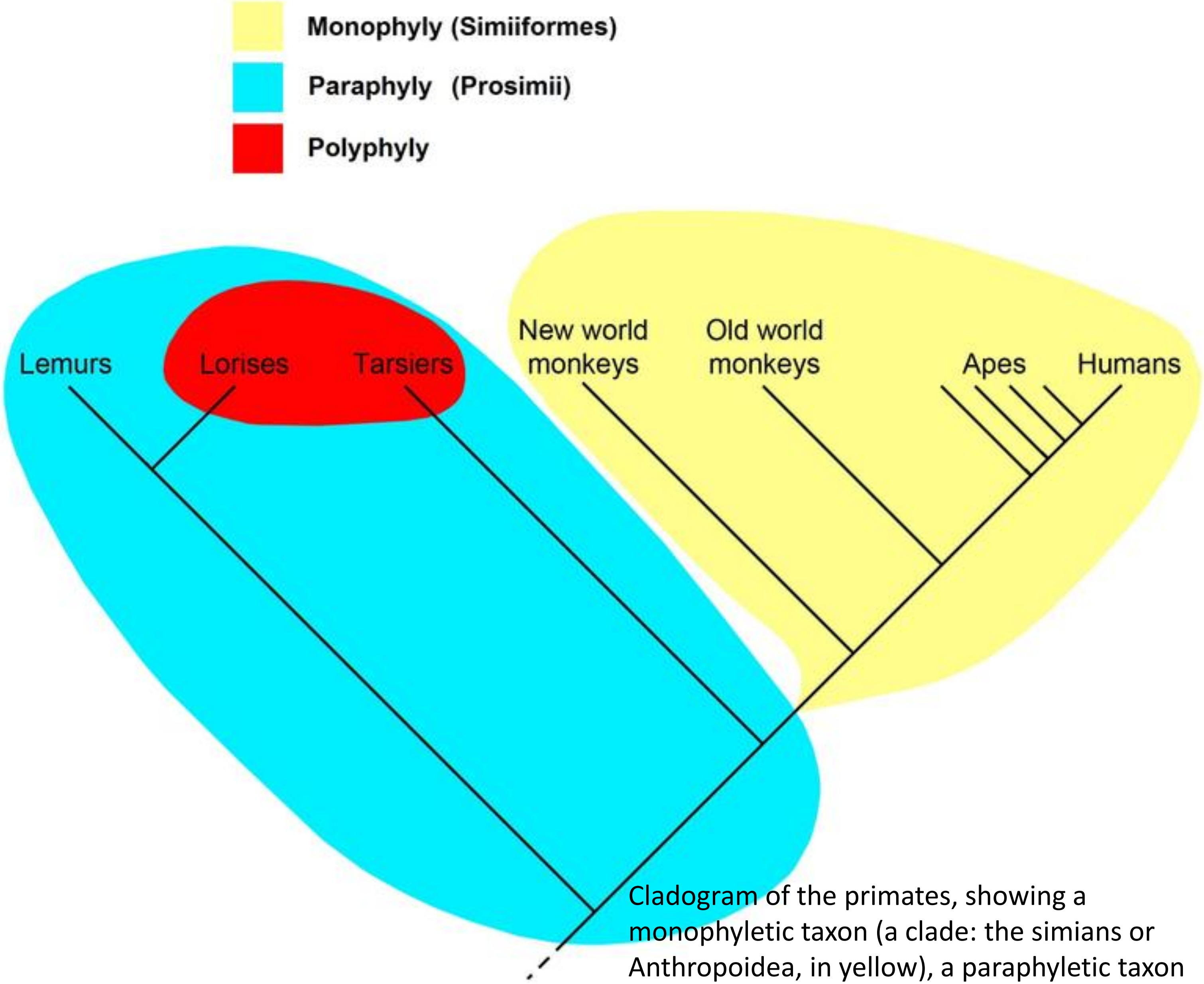
- **Clade** or **monophyletic taxa** includes all descendants from a near common ancestors.
- A clade is characterized by one or more apomorphies: derived character states present in the first member of the taxon, inherited by its descendants (unless secondarily lost), and not inherited by any other taxa.



Cladogram of the primates, showing a monophyletic taxon (a clade: the simians or Anthropoidea, in yellow), a paraphyletic taxon (the prosimians, in blue, including the red patch), and a polyphyletic taxon (the nocturnal primates – the lorises and the tarsiers – in red)

Paraphyly

- In taxonomy, a group is **paraphyletic** if it consists of the group's last common ancestor and all its descendants, but excluding a few—typically only one or two—monophyletic subgroups.
- The group is said to be paraphyletic with respect to the excluded subgroups. In contrast, a monophyletic group (a clade) includes a common ancestor and all of its descendants.
- A paraphyletic assemblage is characterized by one or more **plesiomorphies**: character states inherited from ancestors but not present in all of their descendants.



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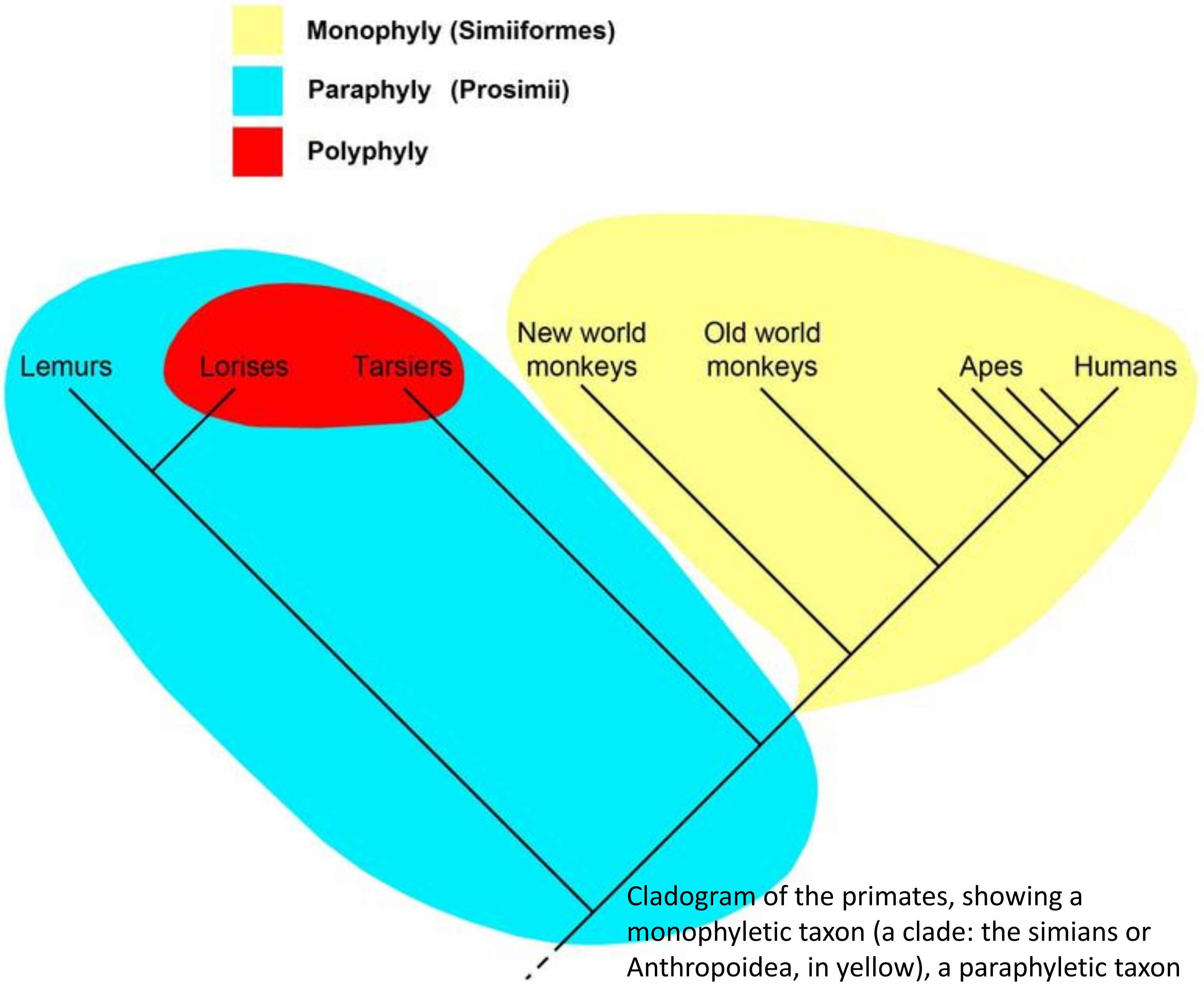
Polyphyly

- A polyphyletic group or assemblage is a set of organisms, that have been grouped together based on characteristics that do not imply that they share a common ancestor that is not also the common ancestor of many other taxa (of course, if "life" is monophyletic, then any set of organisms shares a common ancestor at some point back in the root of the tree).
- The term is often applied to groups that share similar features known as **homoplasies**, which are explained as a result of convergent evolution.



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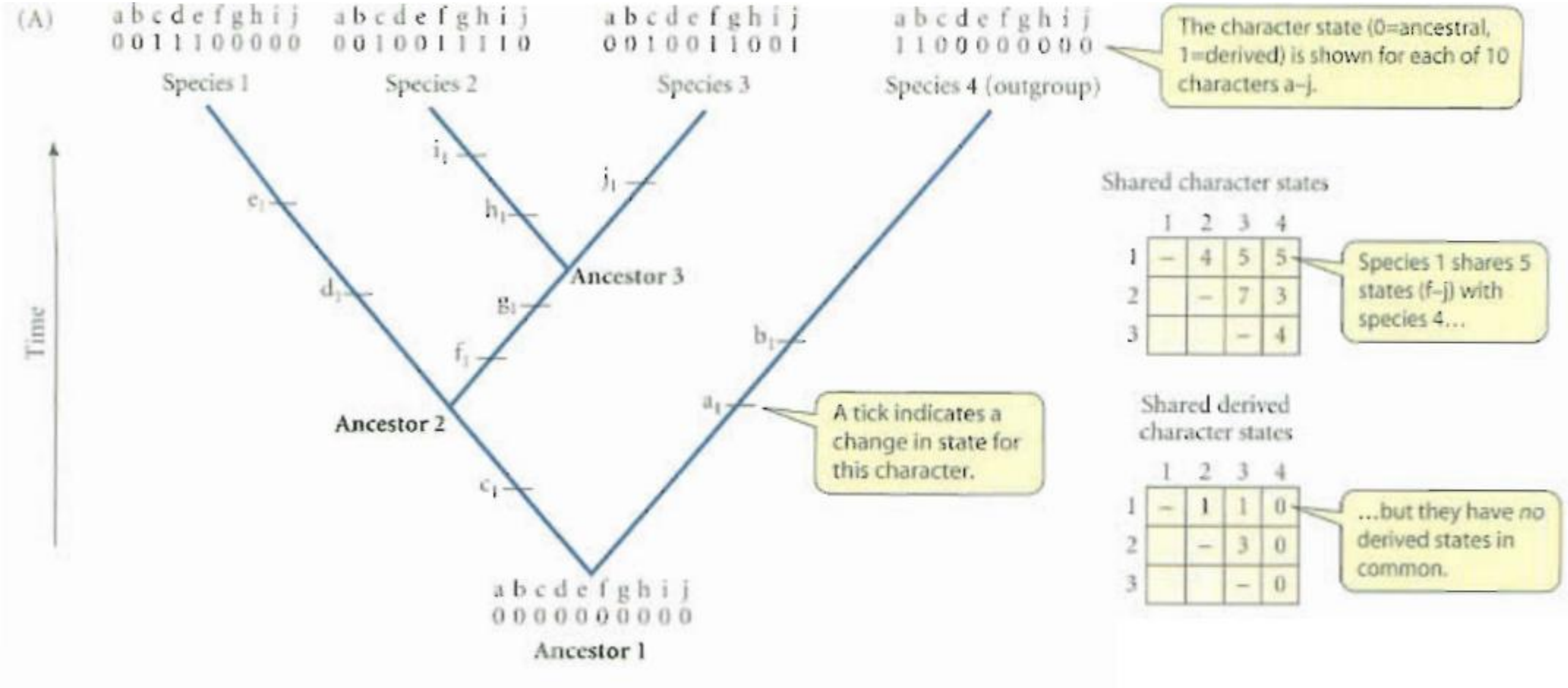
Phenetics vs cladistics



The character state (0=ancestral, 1=derived) is shown for each of 10 characters a–j.

A tick indicates a change in state for this character.

Shared character states

	1	2	3	4
1	–	4	5	5
2		–	7	3
3			–	4

Species 1 shares 5 states (f–j) with species 4…

Shared derived character states

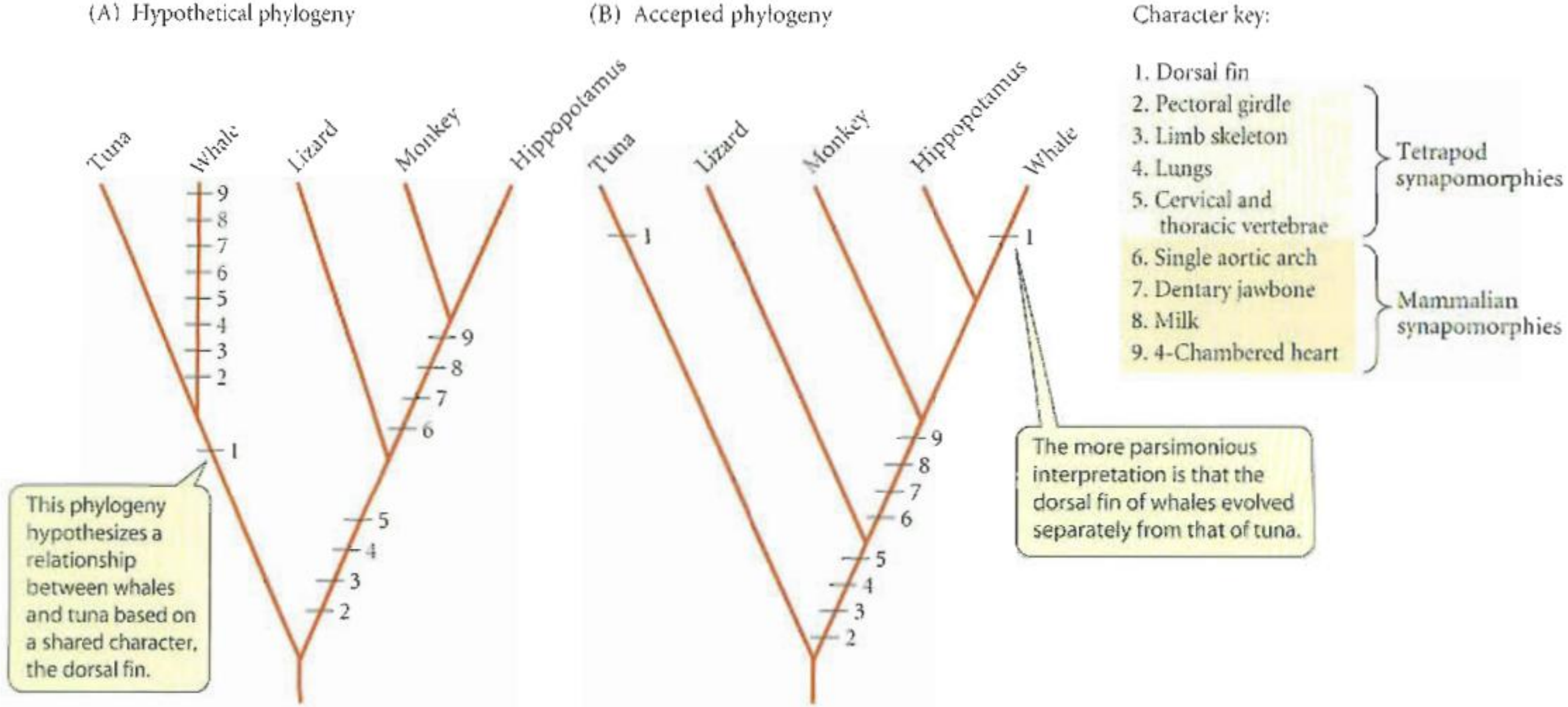
	1	2	3	4
1	–	1	1	0
2		–	3	0
3			–	0

…but they have *no* derived states in common.

Parsimony analysis

- **Parsimony:** Simplest explanation, requiring fewest undocumented assumption, should be preferred over more complicated hypothesis that require more assumptions for which evidences are lacking.
- **Principle of parsimony in phylogenetic analysis:** Among the various phylogenetic trees that can be imagined for a group of taxa, the best estimate of the true phylogeny is the one that requires us to postulate the fewest evolutionary changes.
- **The best phylogenetic hypothesis is the one that requires us to postulate the fewest homoplasious changes.**

Maximum parsimony



(A) Hypothetical phylogeny

(B) Accepted phylogeny

Character key:

1. Dorsal fin
2. Pectoral girdle
3. Limb skeleton
4. Lungs
5. Cervical and thoracic vertebrae
6. Single aortic arch
7. Dentary jawbone
8. Milk
9. 4-Chambered heart

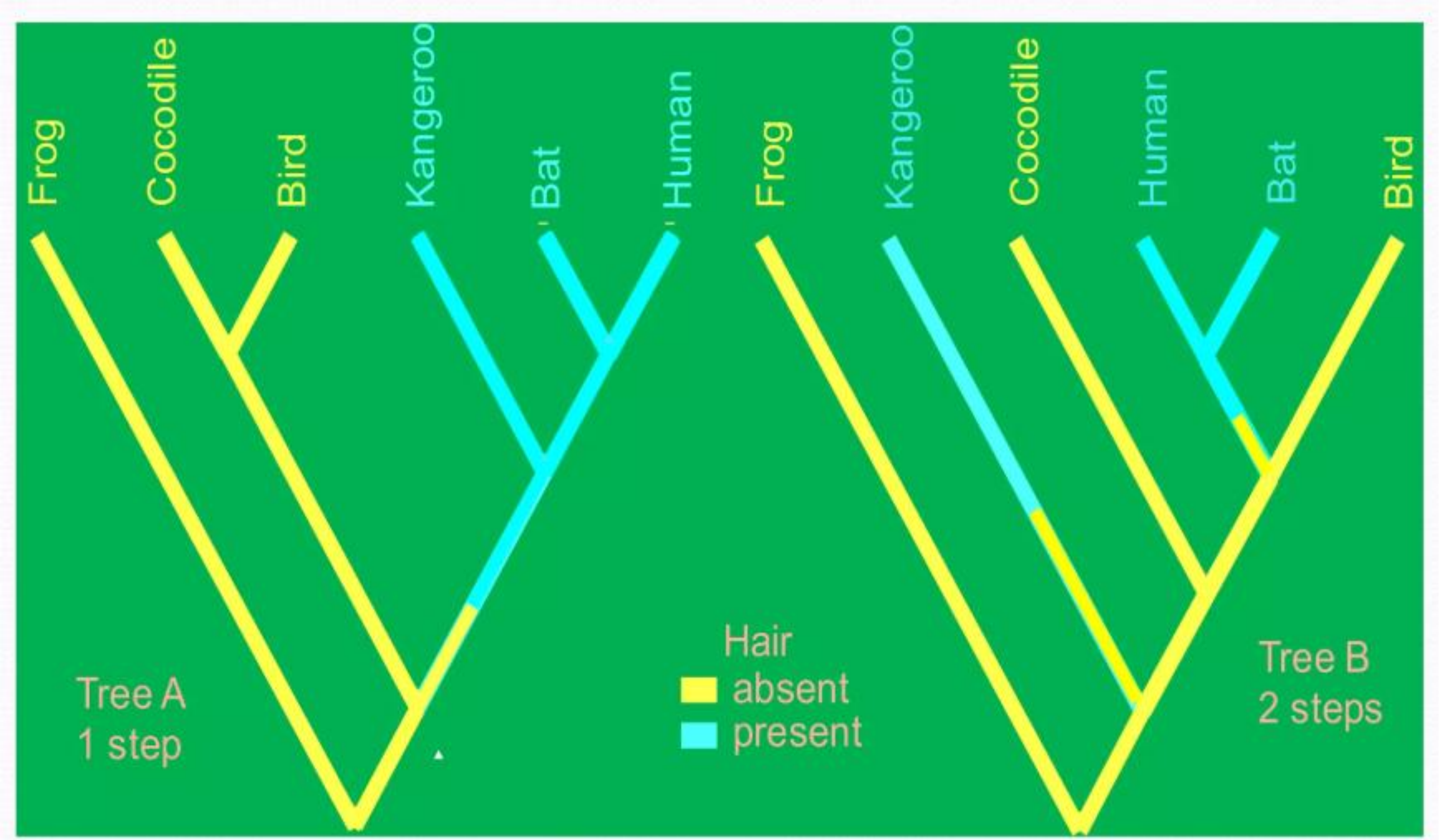
Tetrapod synapomorphies (2–5)

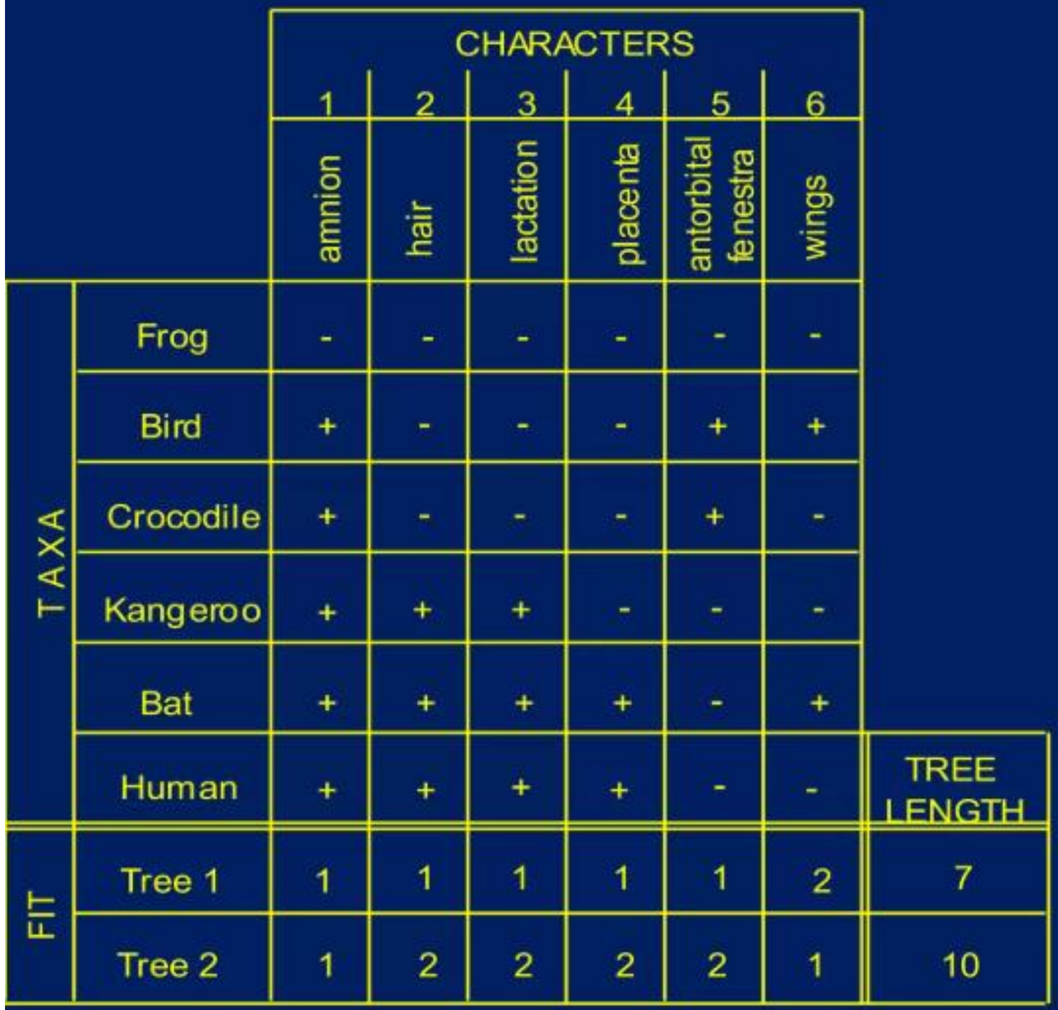
Mammalian synapomorphies (6–9)

This phylogeny hypothesizes a relationship between whales and tuna based on a shared character, the dorsal fin.

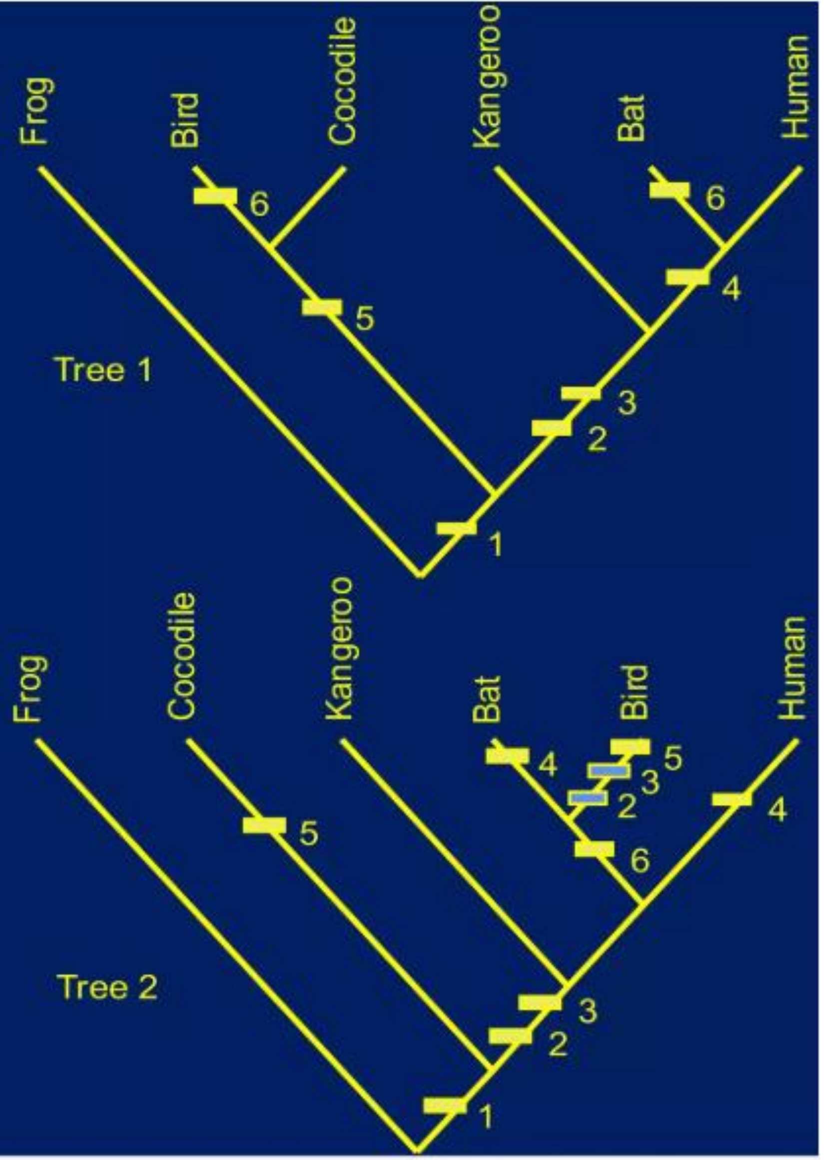
The more parsimonious interpretation is that the dorsal fin of whales evolved separately from that of tuna.

Maximum Parsimony





		CHARACTERS 1 amnion	2 hair	3 lactation	4 placenta	5 antorbital fenestra	6 wings	TREE LENGTH
TAXA	Frog	-	-	-	-	-	-	
	Bird	+	-	-	-	+	+	
	Crocodile	+	-	-	-	+	-	
	Kangeroo	+	+	+	-	-	-	
	Bat	+	+	+	+	-	+	
	Human	+	+	+	+	-	-	
FIT	Tree 1	1	1	1	1	1	2	7
	Tree 2	1	2	2	2	2	1	10



Of these two trees, Tree 1 has the shortest length and is the most parsimonious

Both trees require some homoplasy (extra steps)

Advantages of Parsimony

- Simple and easily understandable.
- Does not seem to depend on explicit models of evolution
- Gives both trees and the associated hypothesis of character evolution
- Good statistical properties when amount of change are small.

Disadvantages

- May lead to the delusion that you know exactly what happened in evolution, in detail.
- Underestimates branch length.
- Models of evolution are implicit – the behaviour of the method is not well understood.
- Not model – so people thinks it makes no assumptions