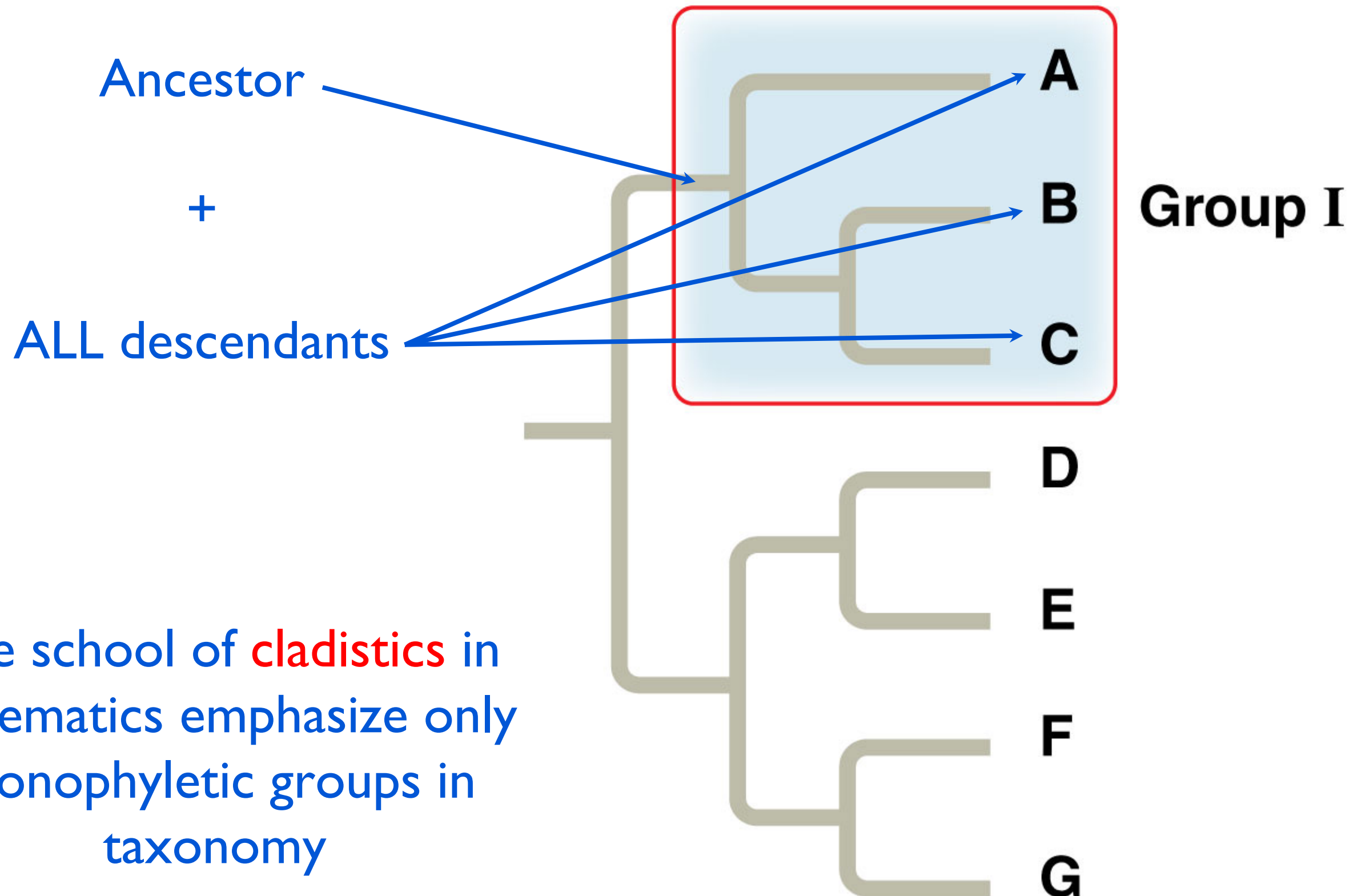


## (a) Monophyletic group (clade)



The school of **cladistics** in systematics emphasize only monophyletic groups in taxonomy

# 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 (14<sup>th</sup>.century)*

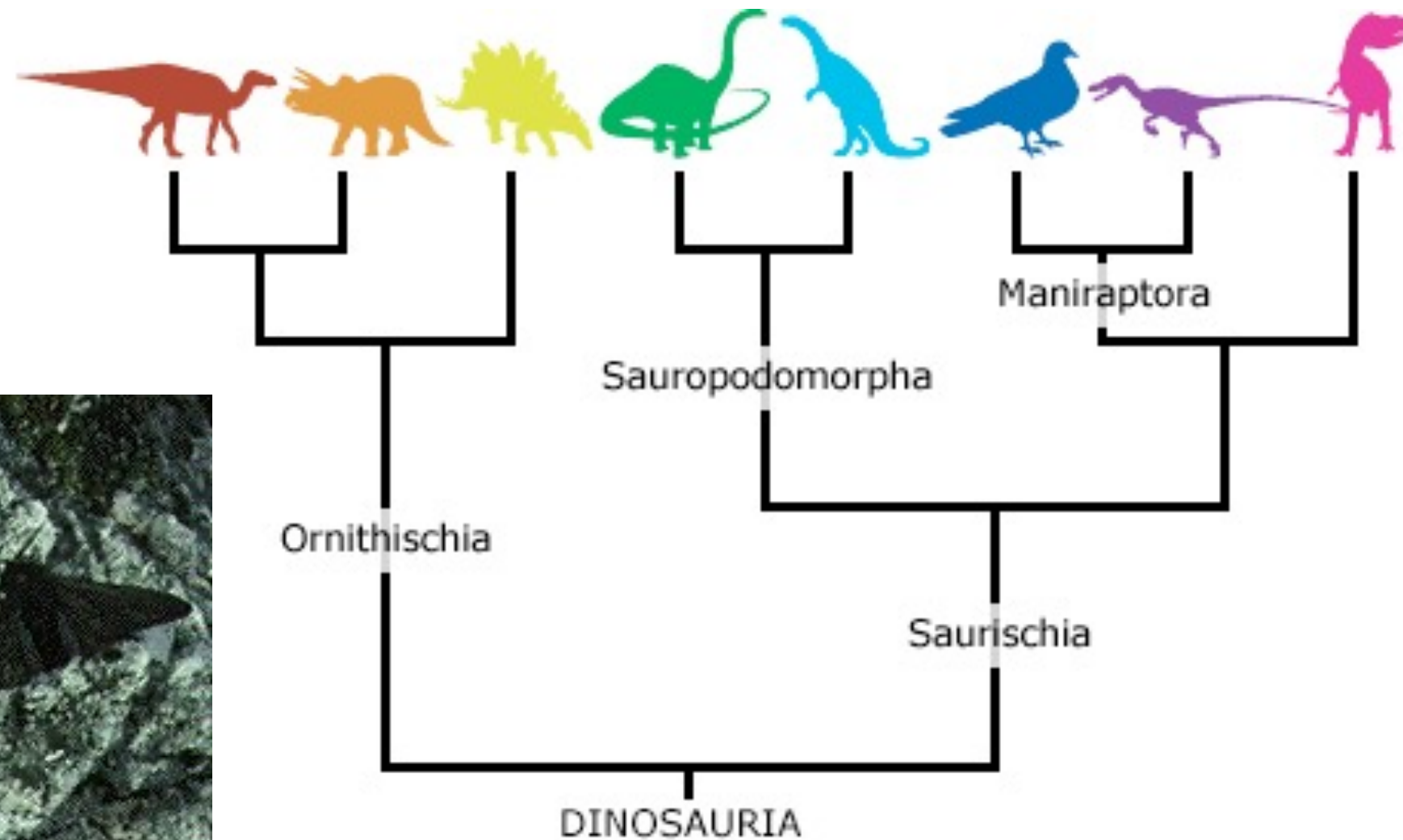
- ***Parsimony in phylogenetics*** – Phylogenetic tree (cladogram) that assumes the fewest steps more likely to be correct

# ***Microevolution vs. Macroevolution***



micro

vs.



DINOSAURIA

MACRO

***Branching points (nodes): speciation events***



# Characters (Traits) - Ancestral or Derived?

- **Analogous characters (homoplastic traits)**
- Traits that appear similar due to shared environment

## Homologous characters

- **Ancestral characters**
- characteristics inherited from ancestors, primitive traits (more accurately called plesiomorphies, or plesiomorphic traits)
- **Shared Derived characters (synapomorphies)**
- New characteristics relative to earlier forms
- Distinguishes from related ancestral species
- **Most useful for figuring out relationships**





# Characters (Traits) - Ancestral or Derived?

Are humans more closely related to vervet monkeys or gorillas?

- All three have a vertebral column and mammary glands – these are an ancestral characters, and not useful for this specific problem (but useful if looking at a larger scale problem)
- Gorillas and humans share a larger brain and lack of a tail, these are **shared derived characters (synapomorphies)**, lacking in vervet monkeys, that indicate relationship



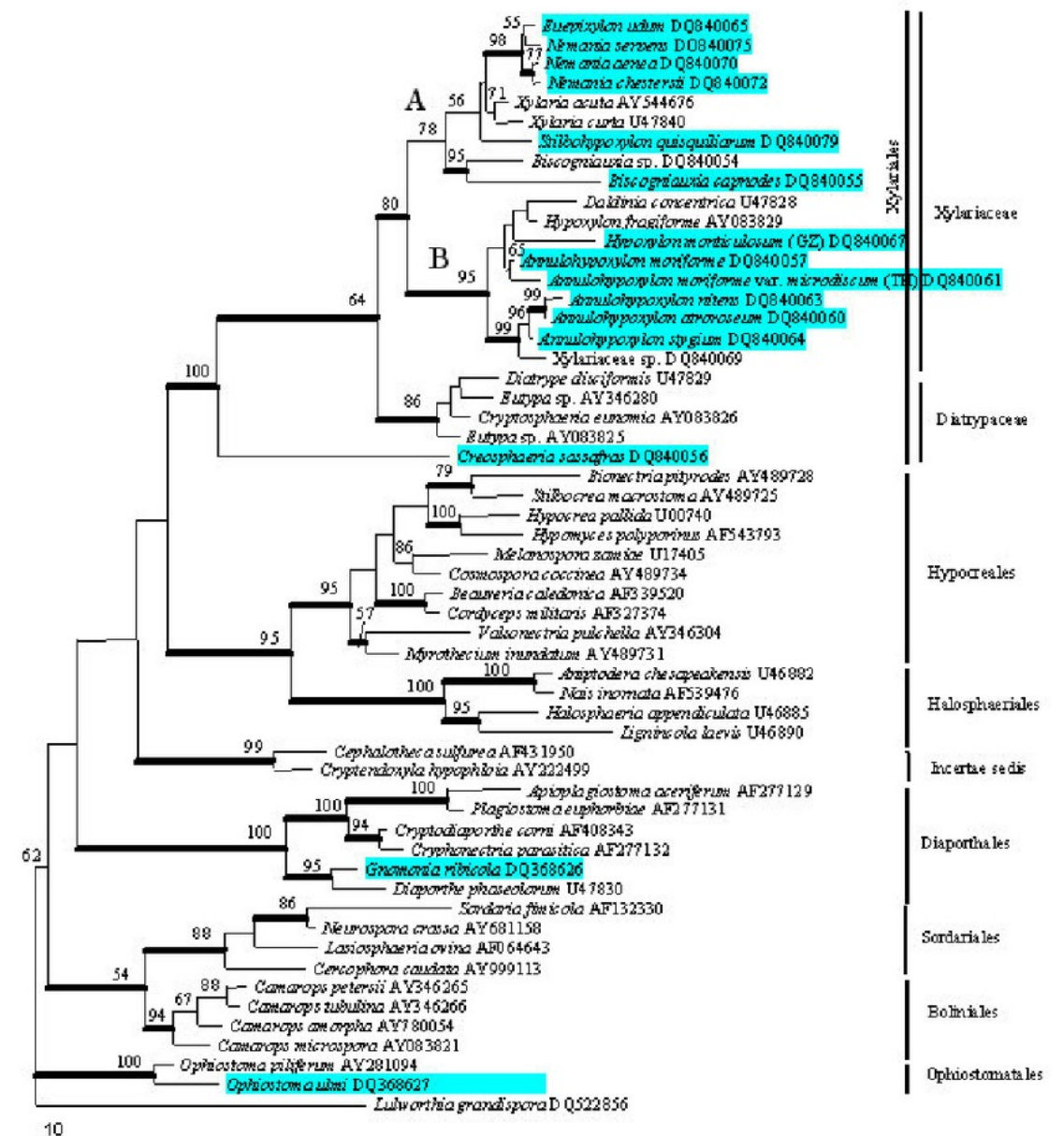
# Methods for finding the best cladograms

- Parsimony

Statistical methods:

- Maximum likelihood

- Bayesian inference







**Species I**



**Species II**



**Species III**

we want to build a tree for these three bird species.



**Species I**

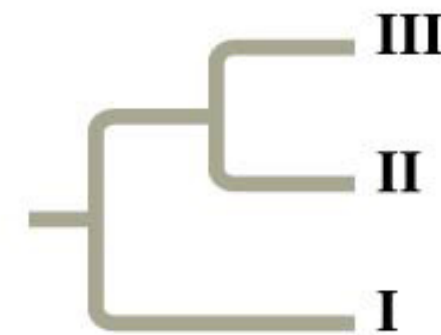
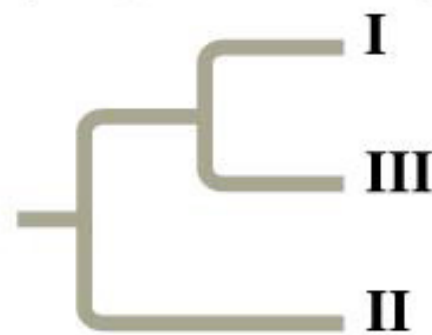
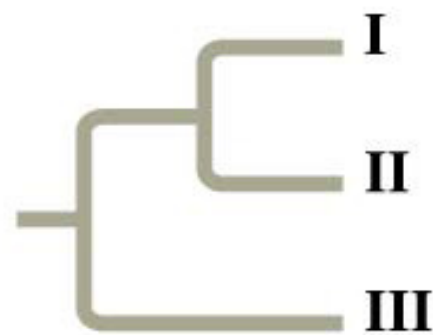


**Species II**



**Species III**

**Three phylogenetic hypotheses:**



	Site 1
Species I	C
Species II	C
Species III	A

We can test our hypotheses  
using molecular data.





Species I

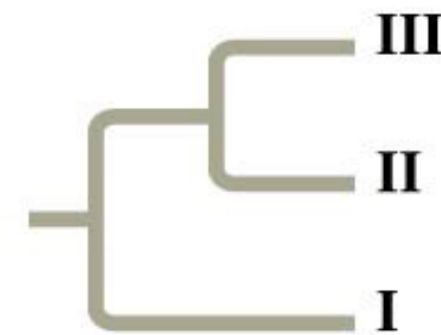
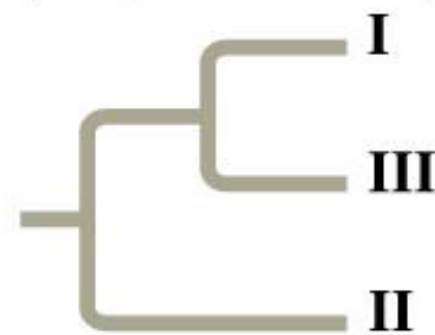
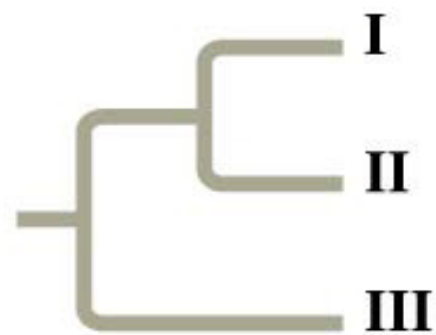


Species II



Species III

Three phylogenetic hypotheses:

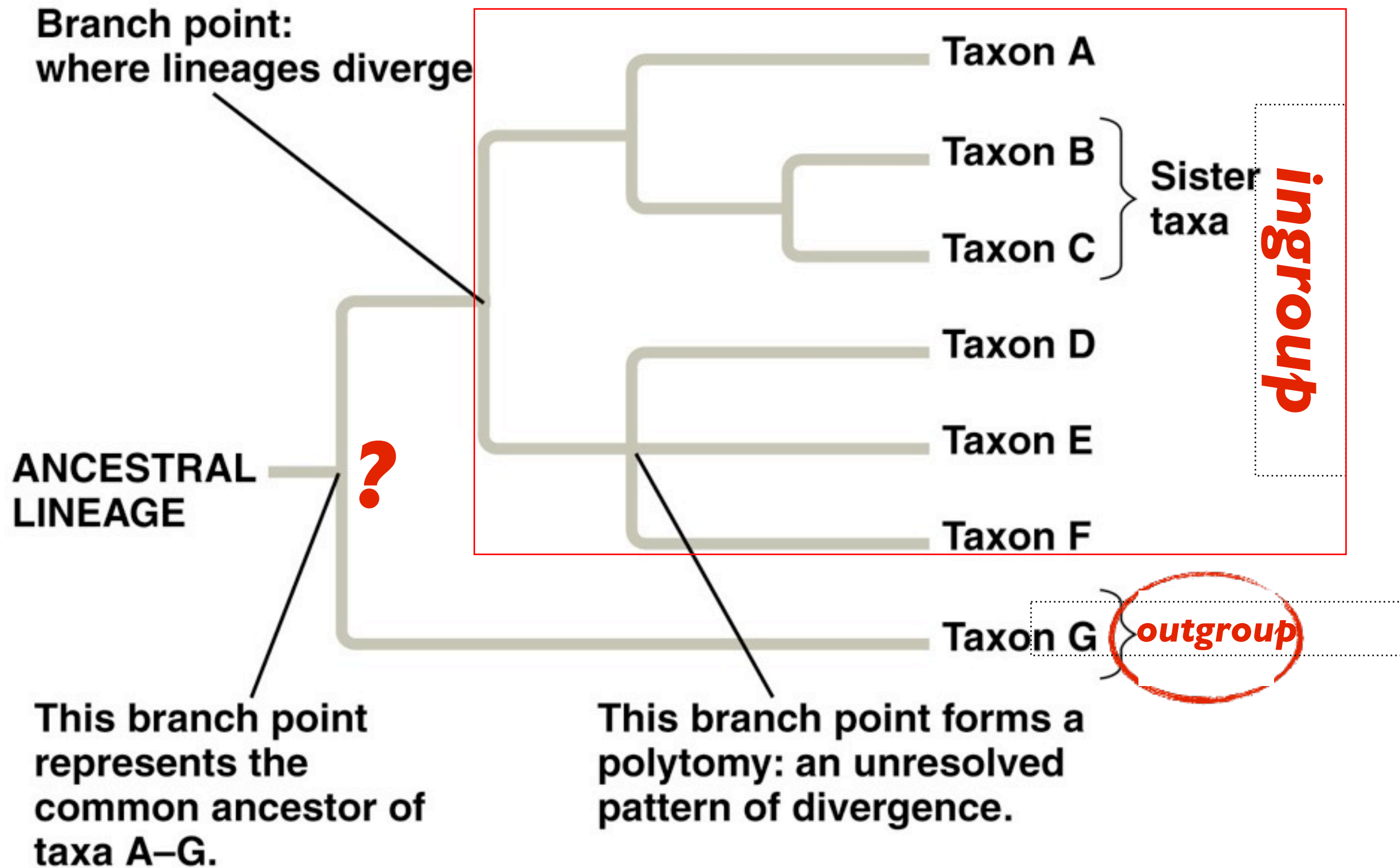


	Site 1
Species I	C
Species II	C
Species III	A

***What is ancestral?***

An **outgroup** tells us about the ancestral lineage that we compare to our **ingroup taxa**

-If we are studying the relationships of A-F, then G is an outgroup





Species I

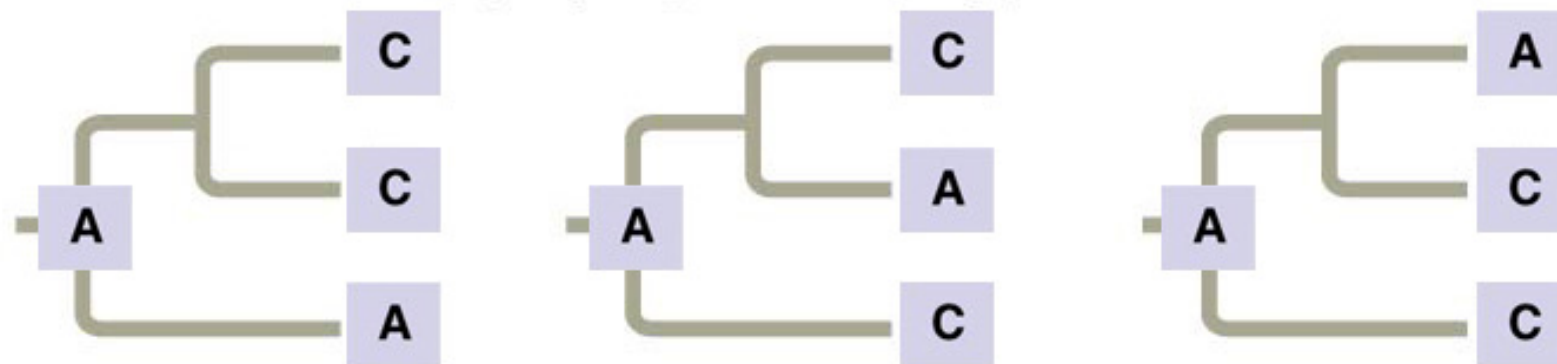


Species II



Species III

Three phylogenetic hypotheses:



	Site 1
Species I	C
Species II	C
Species III	A
Ancestral sequence	A

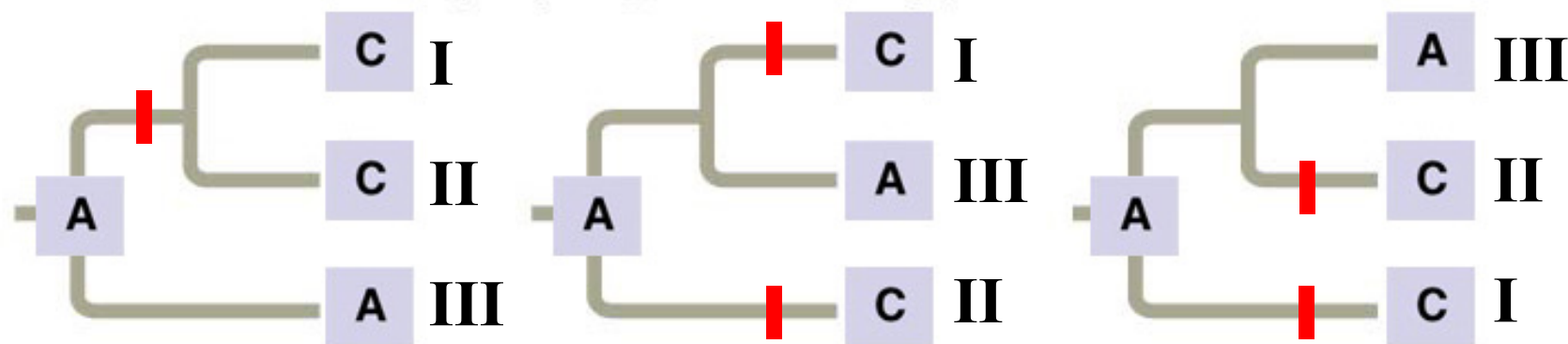
***Outgroup comparison  
indicates that the  
ancestral state is A***



## ***Maximum Parsimony:***

the best tree requires the fewest changes

Three phylogenetic hypotheses:



***The tree suggesting a relationship between species I and II has fewer evolutionary steps = more parsimonious***



Species I



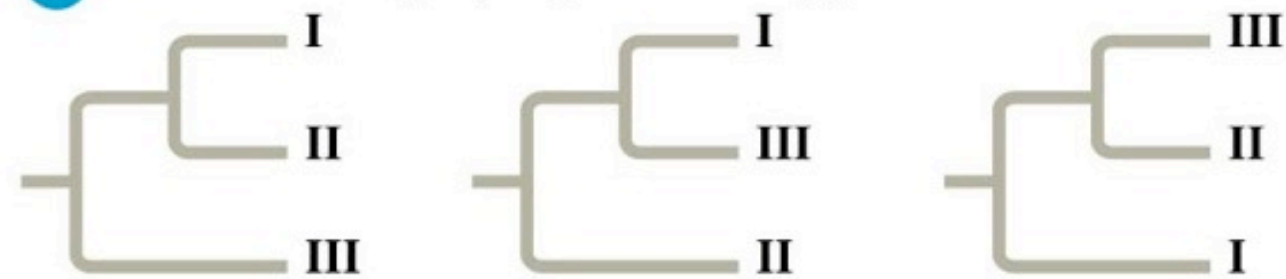
Species II



Species III

1

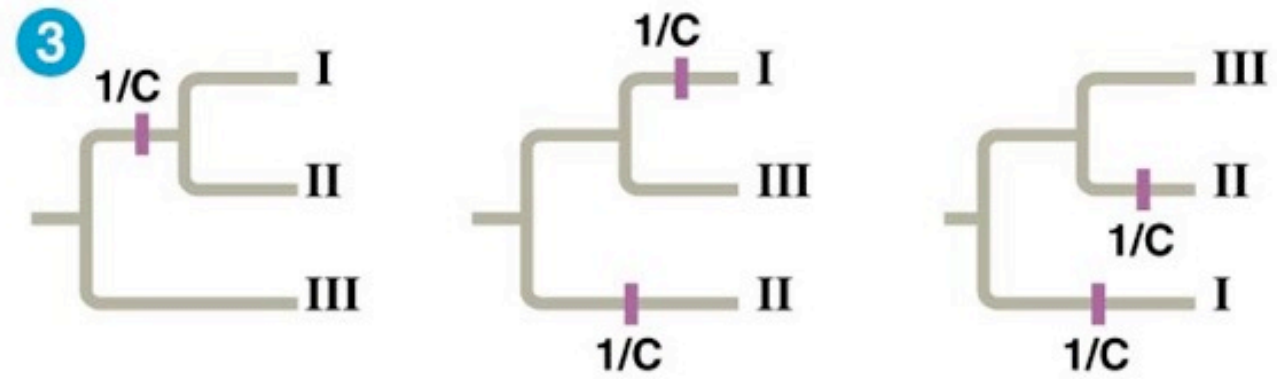
Three phylogenetic hypotheses:



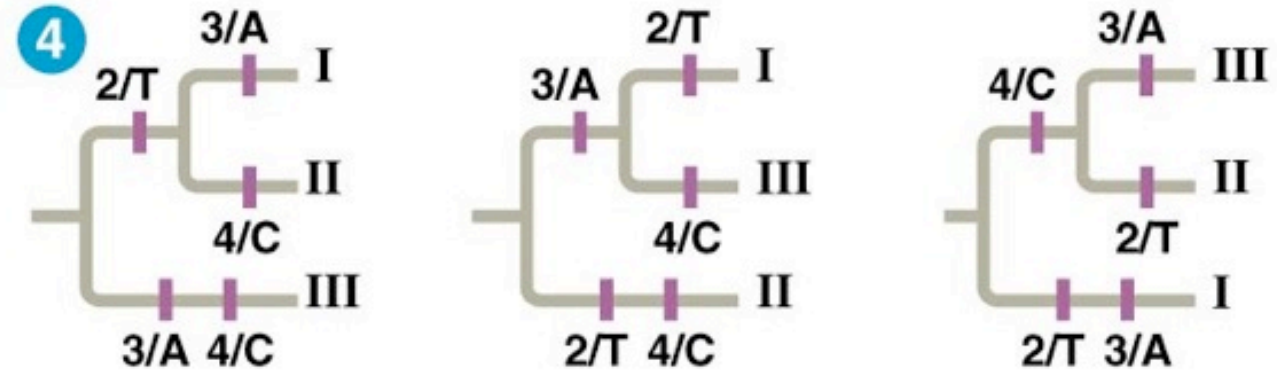
2

	Site			
	1	2	3	4
Species I	C	T	A	T
Species II	C	T	T	C
Species III	A	G	A	C
Ancestral sequence	A	G	T	T

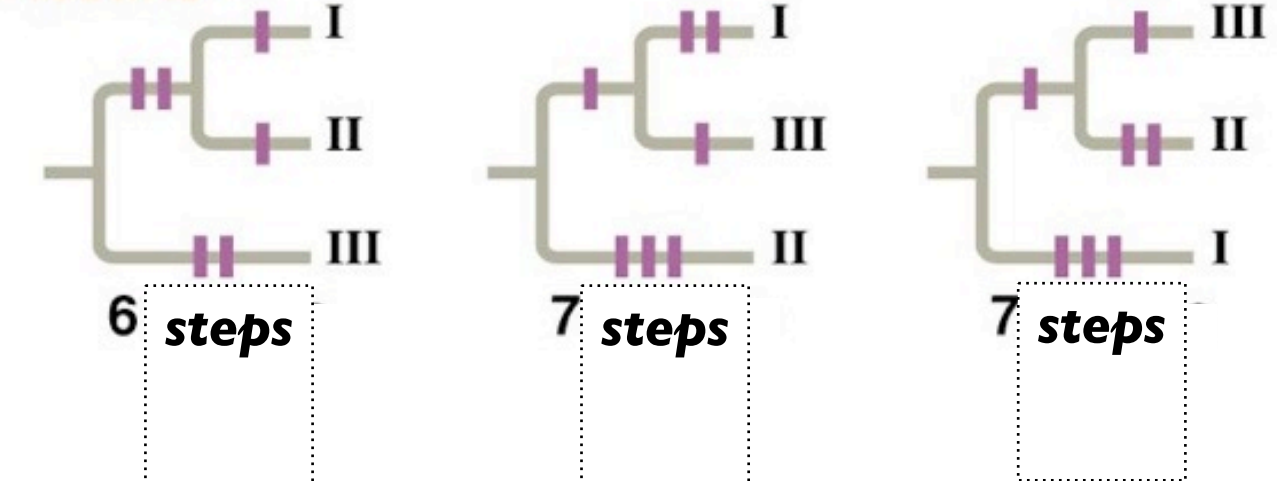
3



4

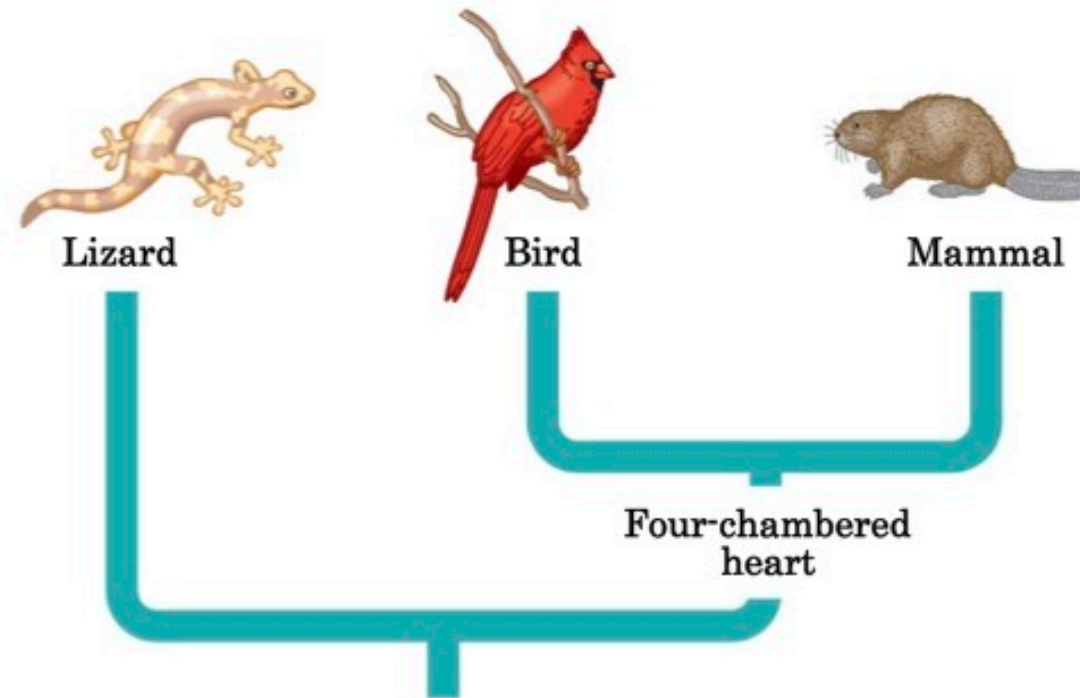


Results

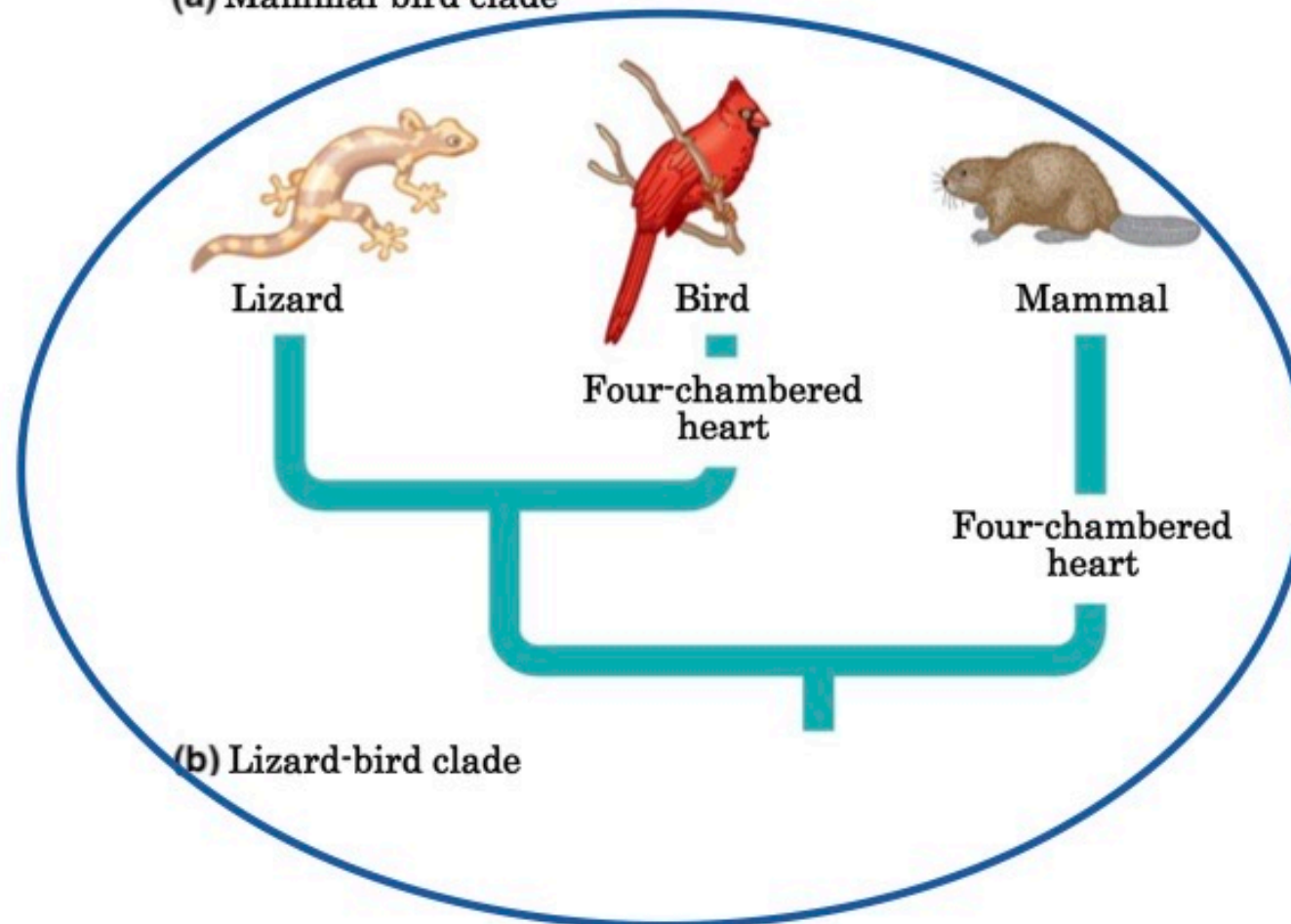


**In a parsimony analysis, we enter all the molecular or morphological data, and the computer (ideally) builds all possible trees and counts the number of steps. The fewest steps indicate the best phylogenetic hypothesis**

# However, is nature always parsimonious?



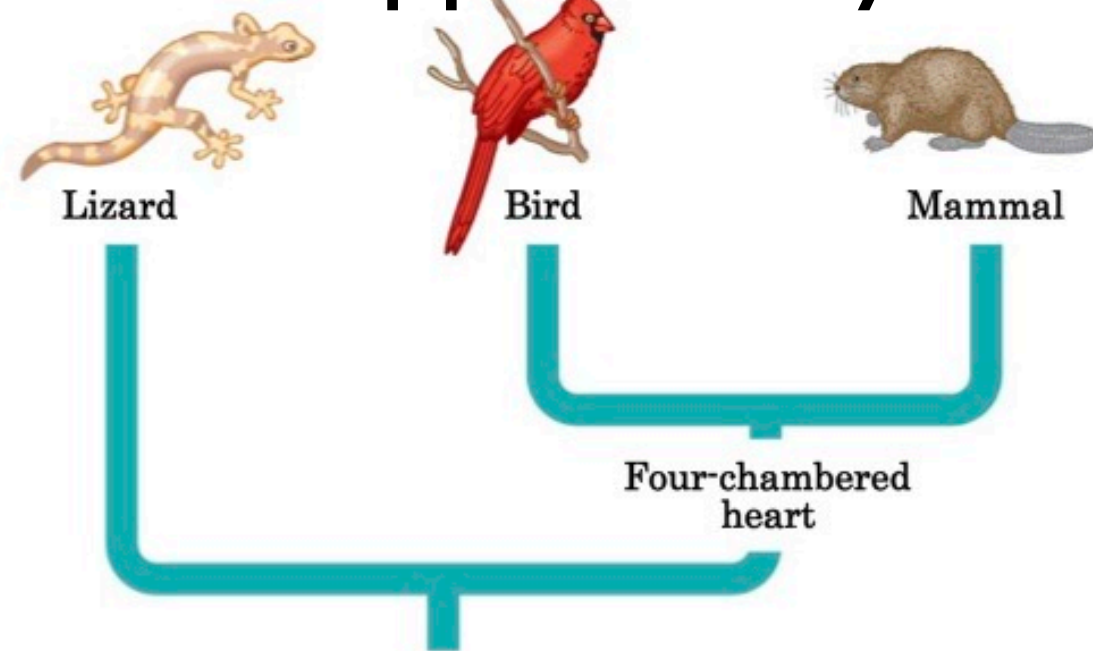
(a) Mammal-bird clade



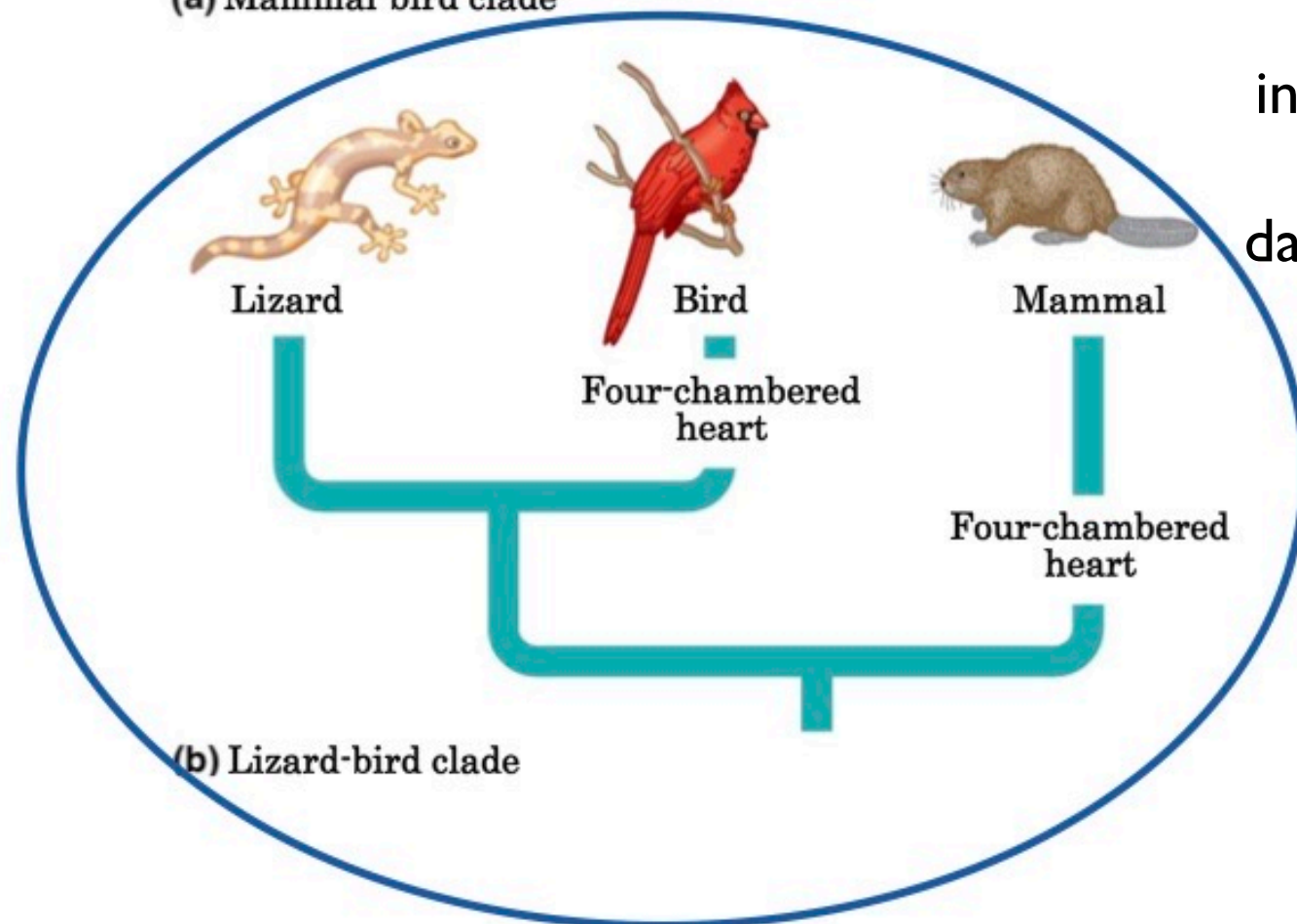
(b) Lizard-bird clade



The point is not that nature is parsimonious, but that hypotheses don't contain unnecessary complexity that is not supported by data



(a) Mammal-bird clade



(b) Lizard-bird clade

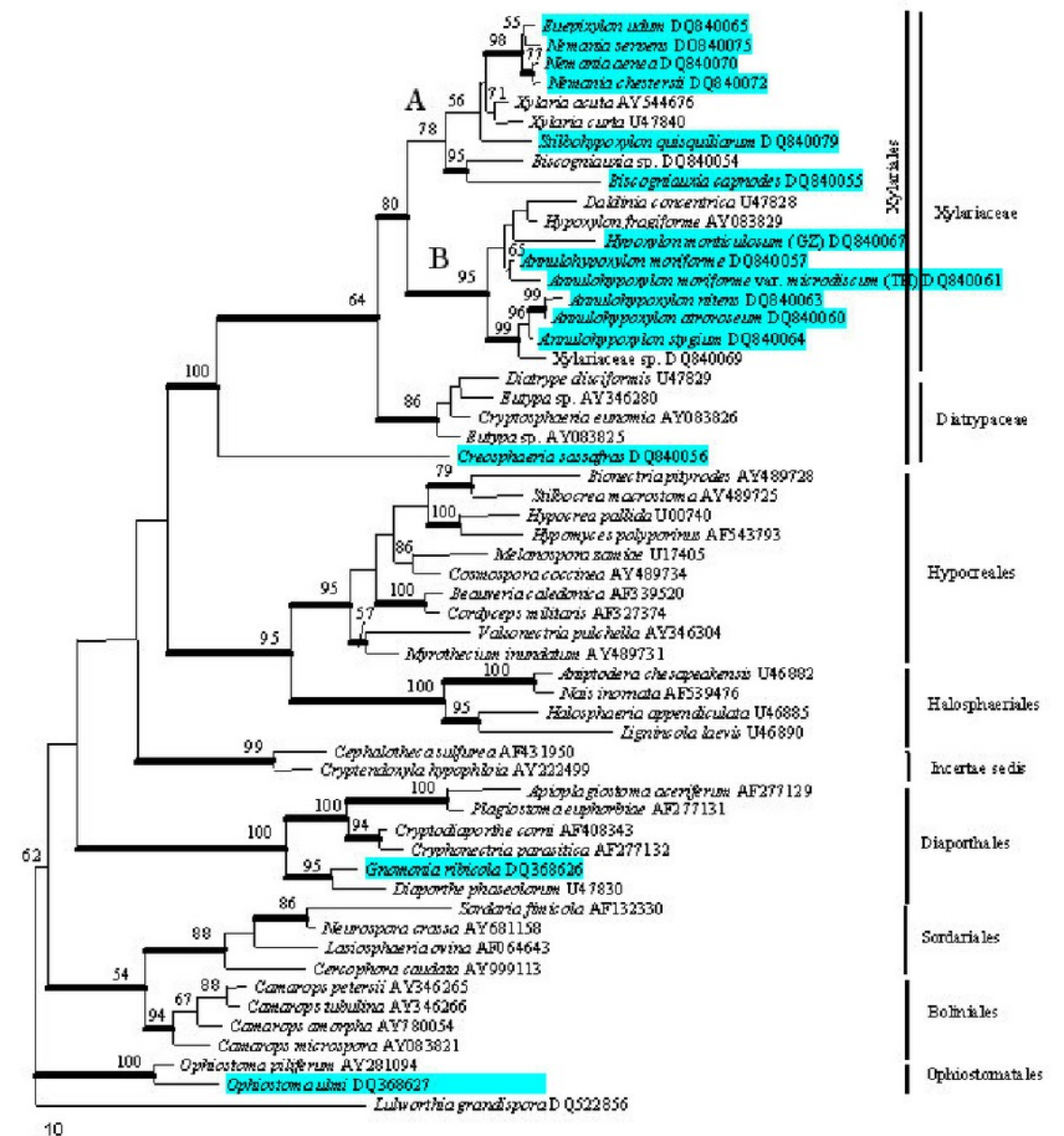
If the four-chambered heart was all we knew about these animals, then our best hypothesis would indeed be that birds and mammals are related, however, added information (fossils, skeletal anatomy, new molecular data) show that they are not

# Methods for finding the best cladograms

- **Parsimony** – picks the tree(s) with the fewest evolutionary steps

Statistical methods:

- **Maximum likelihood**
- **Bayesian inference**

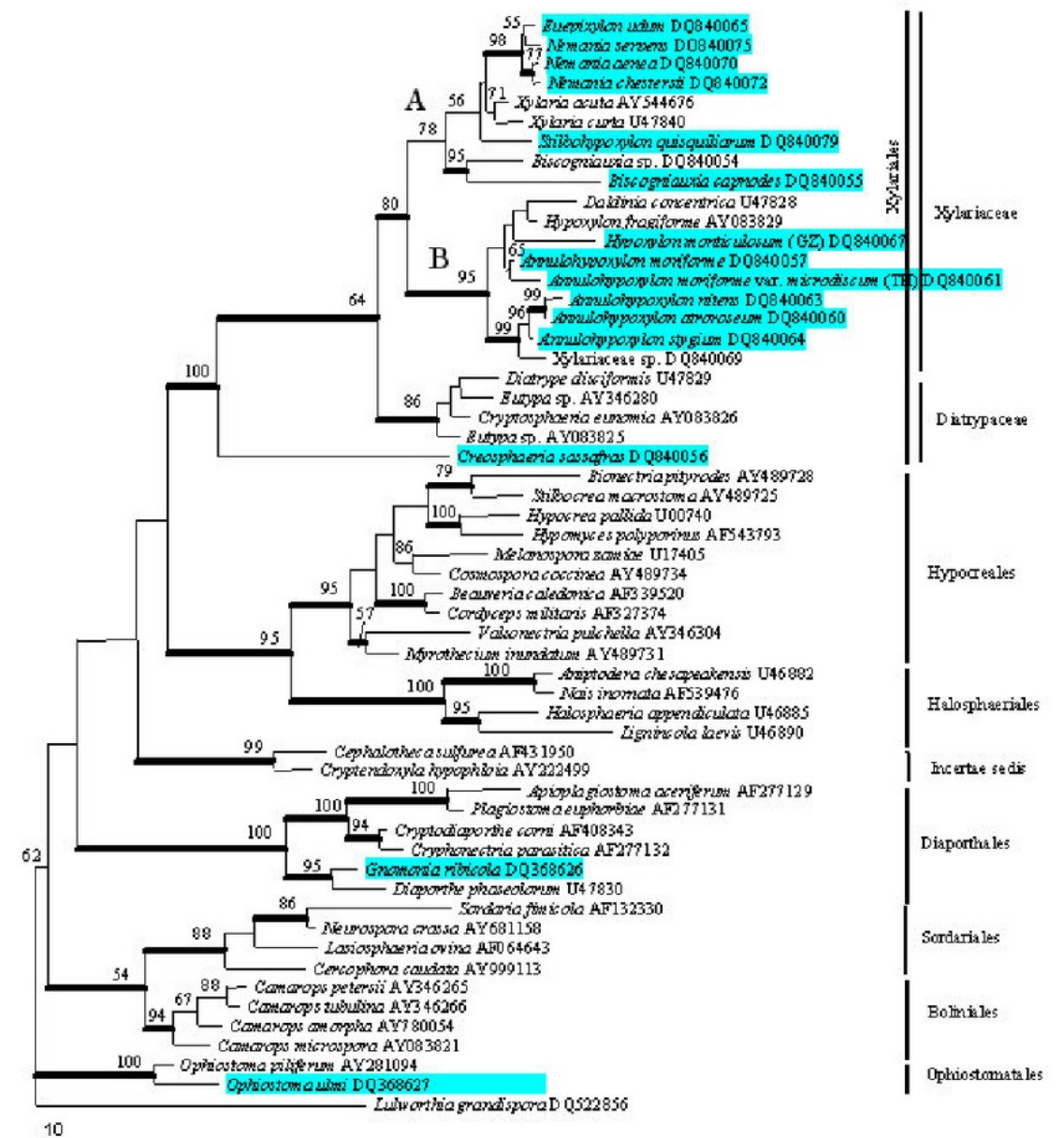


# Methods for finding the best cladograms

Statistical methods give clade support values:

- Maximum likelihood
- Bayesian inference

–Insert model on likelihood for e.g. base substitutions  
 –calculates how well each tree, and each branch, fits the data (ideally checking all possible trees)  
 –computationally demanding  
 (Bayesian inference even more so that Maximum Likelihood, but some say more theoretically sound)



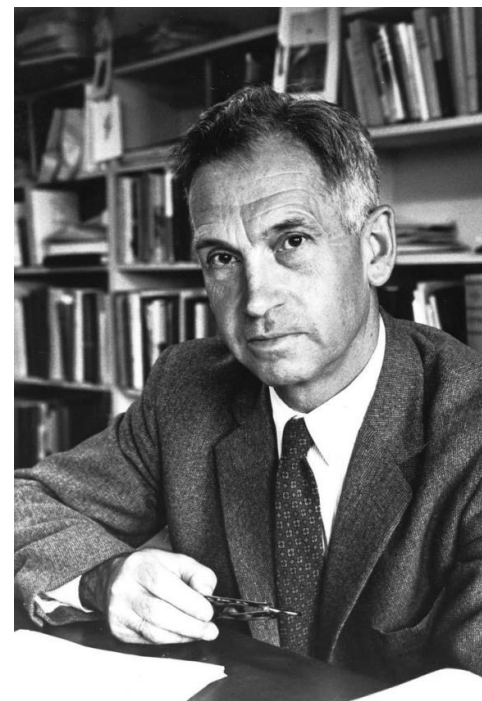
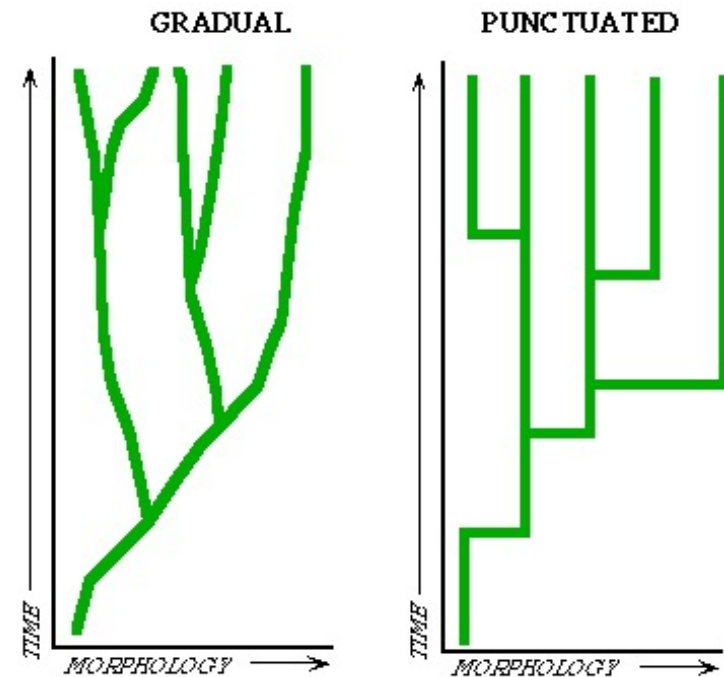


# Major Models of Macroevolution

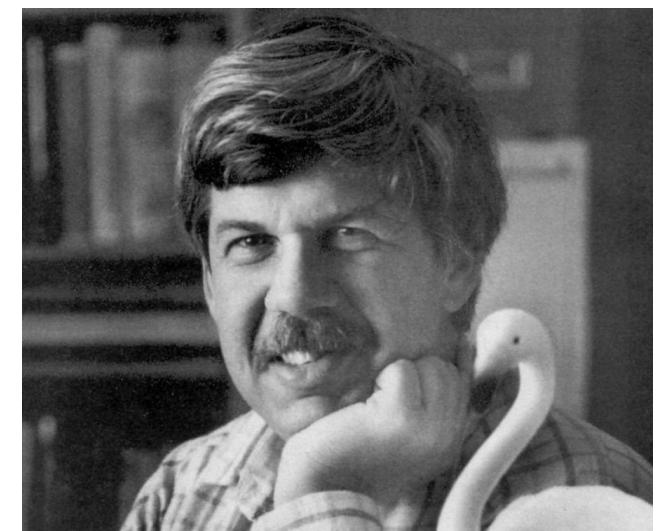
- Gradualism (e.g. Darwin, Mayr)

VS

- Punctuated equilibria (Gould, Eldredge)
  - Stasis “punctuated” by rapid change



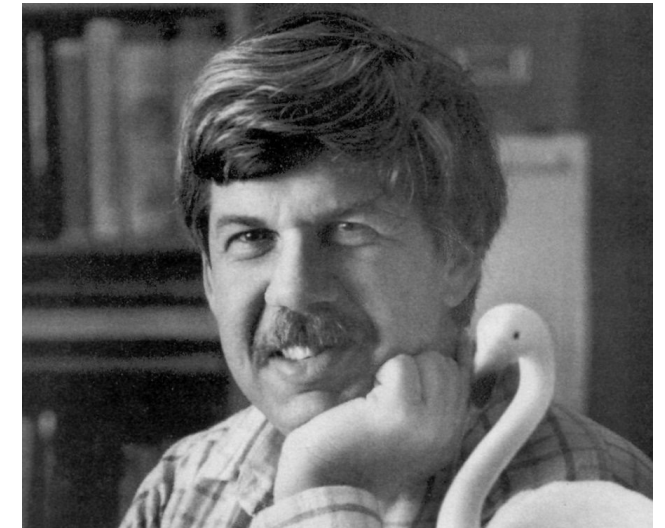
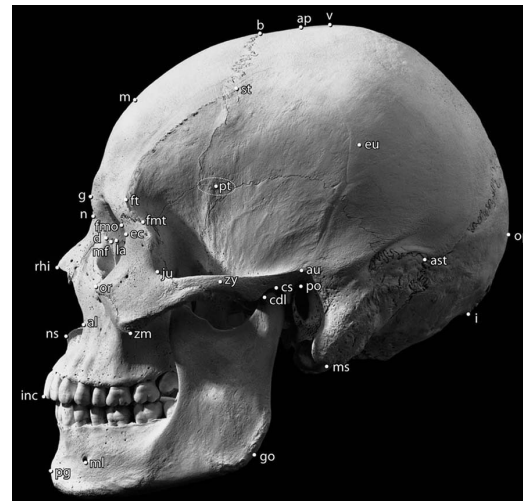
Ernst Mayr



Stephen Jay Gould

# Not everything in nature is adaptive

- Some features might be the byproduct of selection for other features
- Also, some features are vestigial
- E.g. human chin?
- Iridescence of golden mole fur?



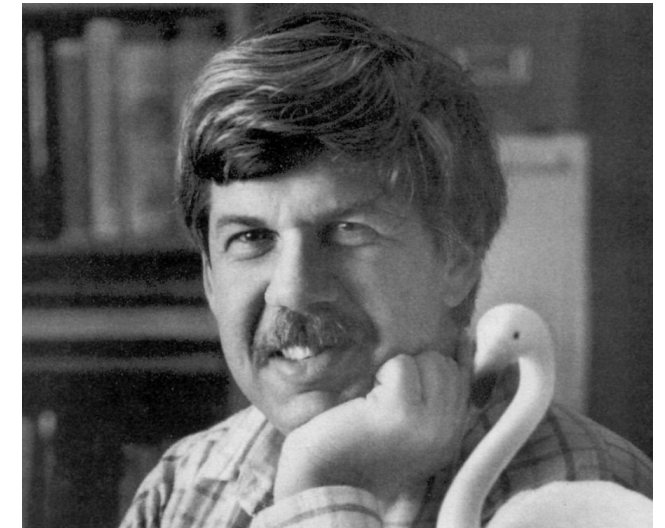
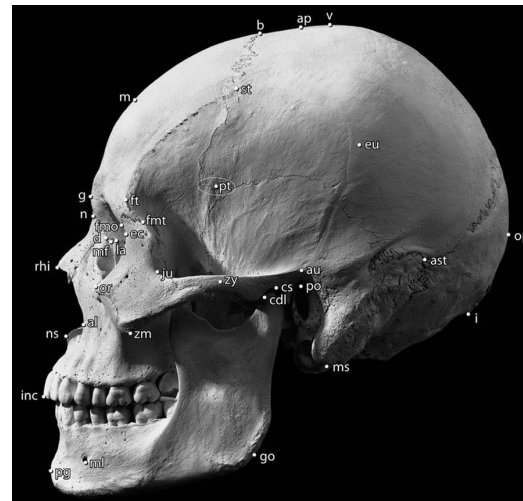
Stephen Jay Gould





# Not everything in nature is adaptive

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- E.g. human chin?
- Iridescence of golden mole fur?



Stephen Jay Gould





# Evidence used in study of Macroevolution

- **Biogeography** plus molecular data (e.g. chimpanzees & bonobos)
- Fossils - morphological change – transitional fossils
- Fossils - **adaptive radiations** after extinction events
- Fossils plus molecular data: **molecular clock**



# Molecular clock

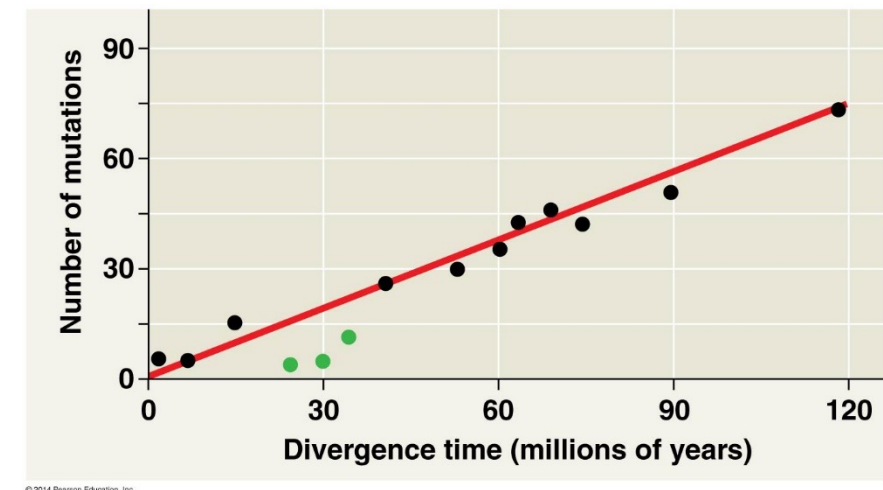
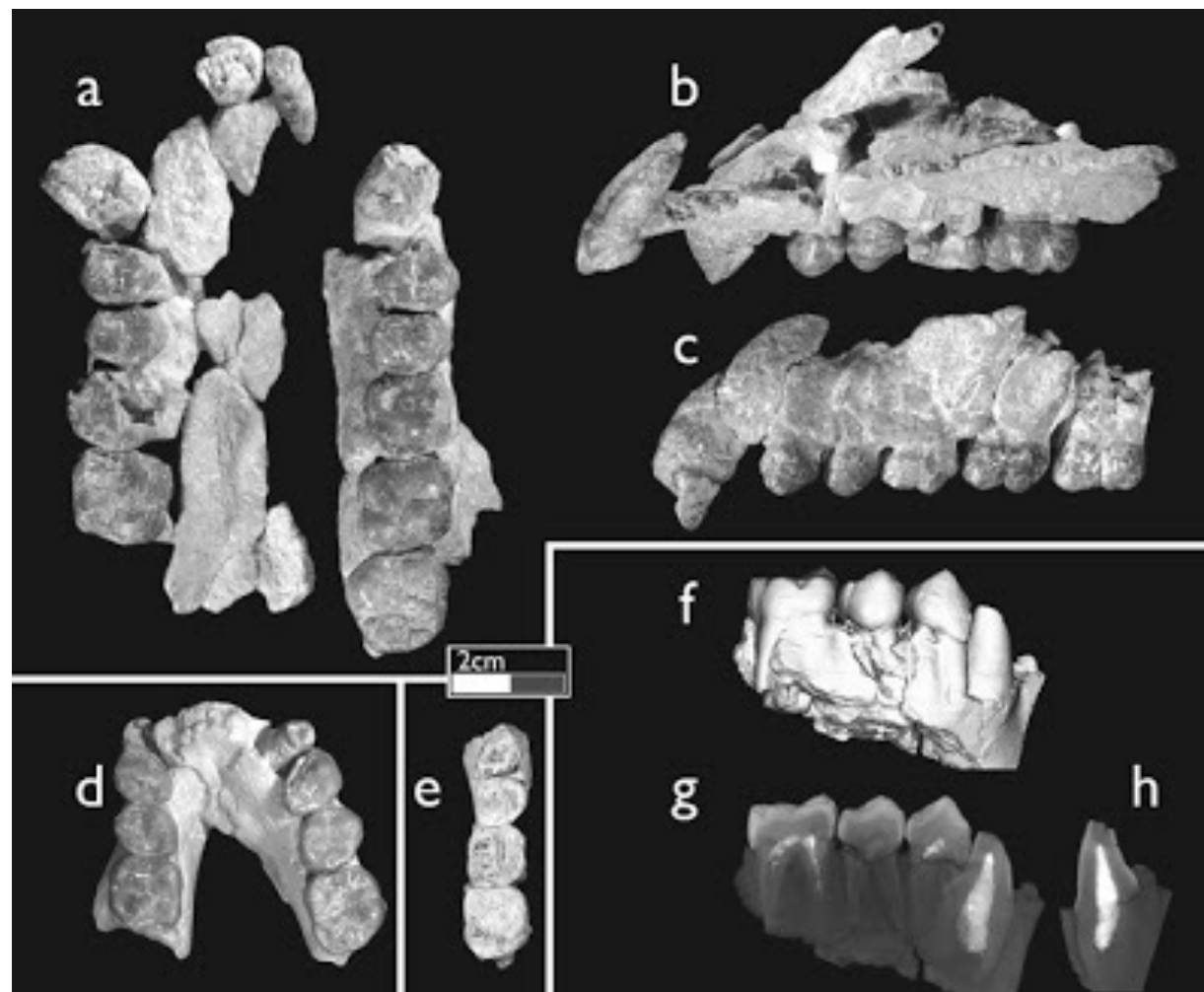
- How do we estimate the time of divergence of two lineages?
- Molecular clock studies use both fossil and molecular data



# Molecular clock

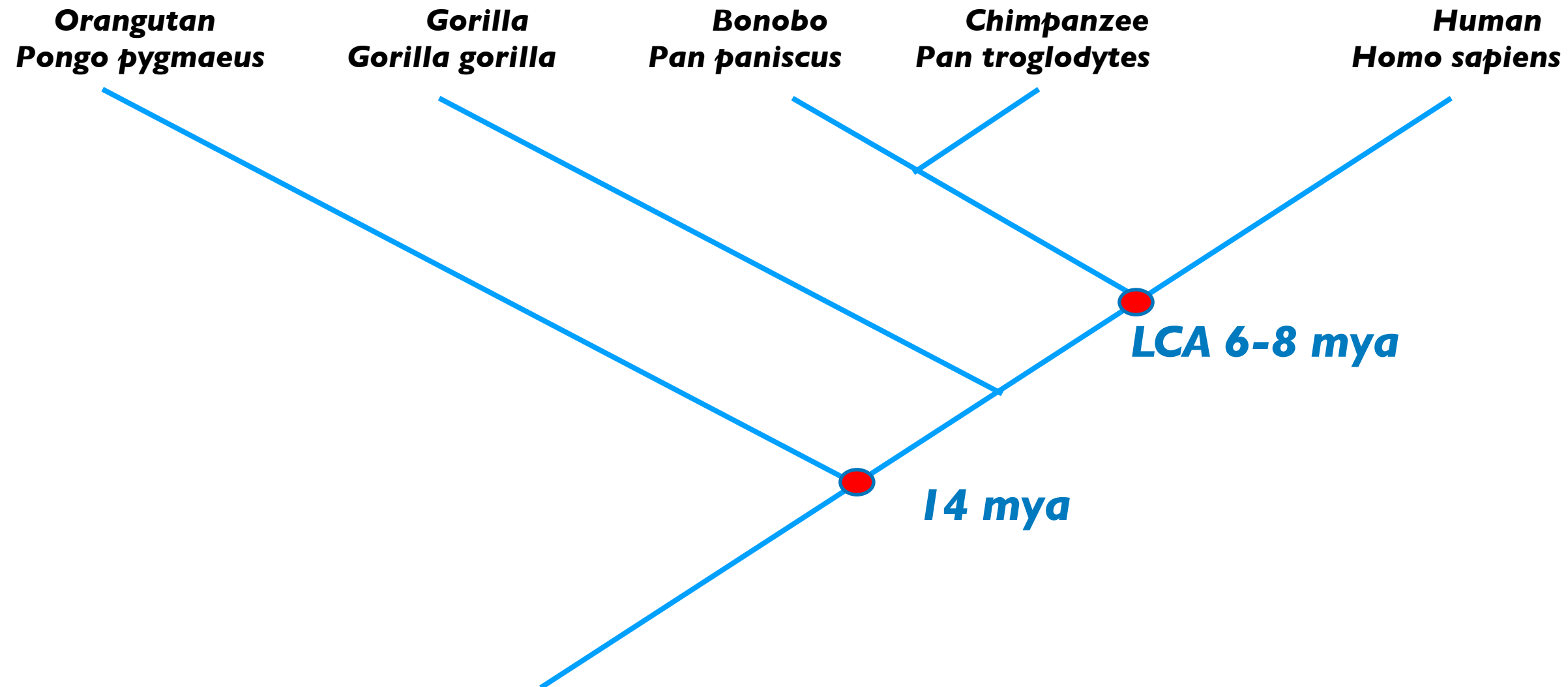
- Some parts of the genome will accumulate changes (mutations) at a relatively steady rate
- The speed of accumulation depends on the part of DNA under study (some fast, some slow)
- The “clock” is calibrated using the fossil record (e.g. orangutan fossils have been securely dated for apes), or the accumulation of mutations over generations

orangutan-  
like fossils





# Molecular clock



- By using the known age of the orangutan split, plus info on orangutan DNA, we know the rate of mutations in certain parts of the ape genome
  - Count known differences in DNA between humans and chimps
- The data indicates a date of the split between *Pan* and *Homo* at about 6-8 mya