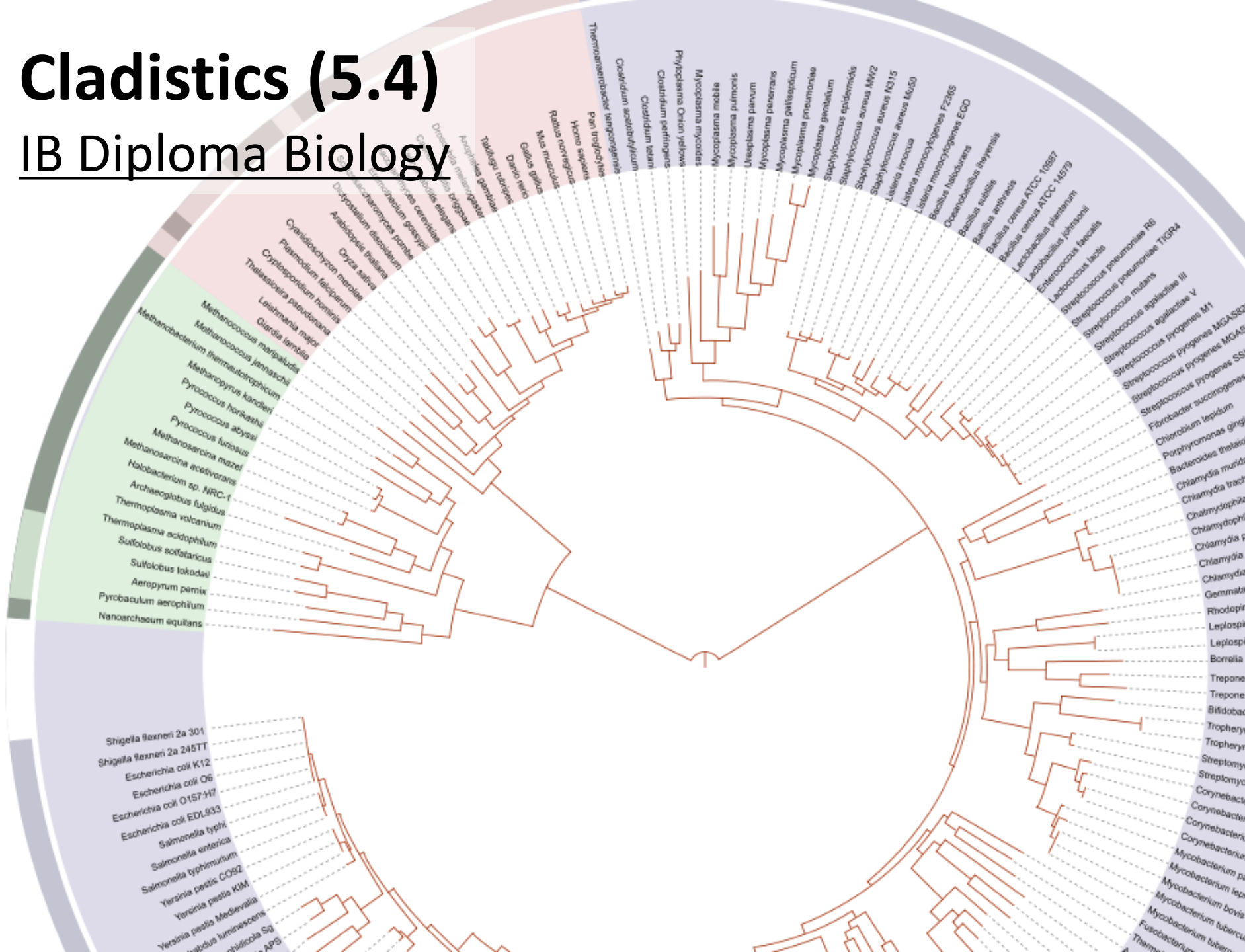


Cladistics (5.4)

IB Diploma Biology



Cladistics (From the ancient Greek for "branch") is a method of classifying species of organisms into groups called **clades**, which consist of an ancestor organism and all its descendants (and nothing else).

Wikipedia





For example, birds,
dinosaurs, crocodiles,
and all descendants
(living or extinct) of
their most recent
common ancestor
form a clade


Wikipedia



Mammals have the
unique homologous
characteristic of
producing milk

They form a **clade**





Likewise, birds share the
common characteristic of
feathers

They too form a **clade**



Tortoise



Lizard

Reptiles, as a group, consist of the crocodylians, lizards and snakes, tortoises and turtles and tuatara.

However, they are not a clade.

One of them is actually more closely related to birds.

Care to guess which one?



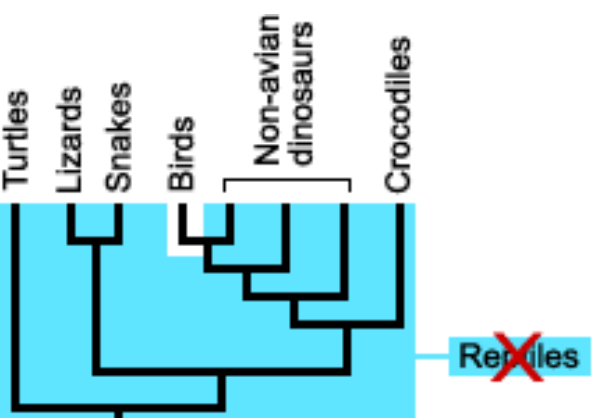
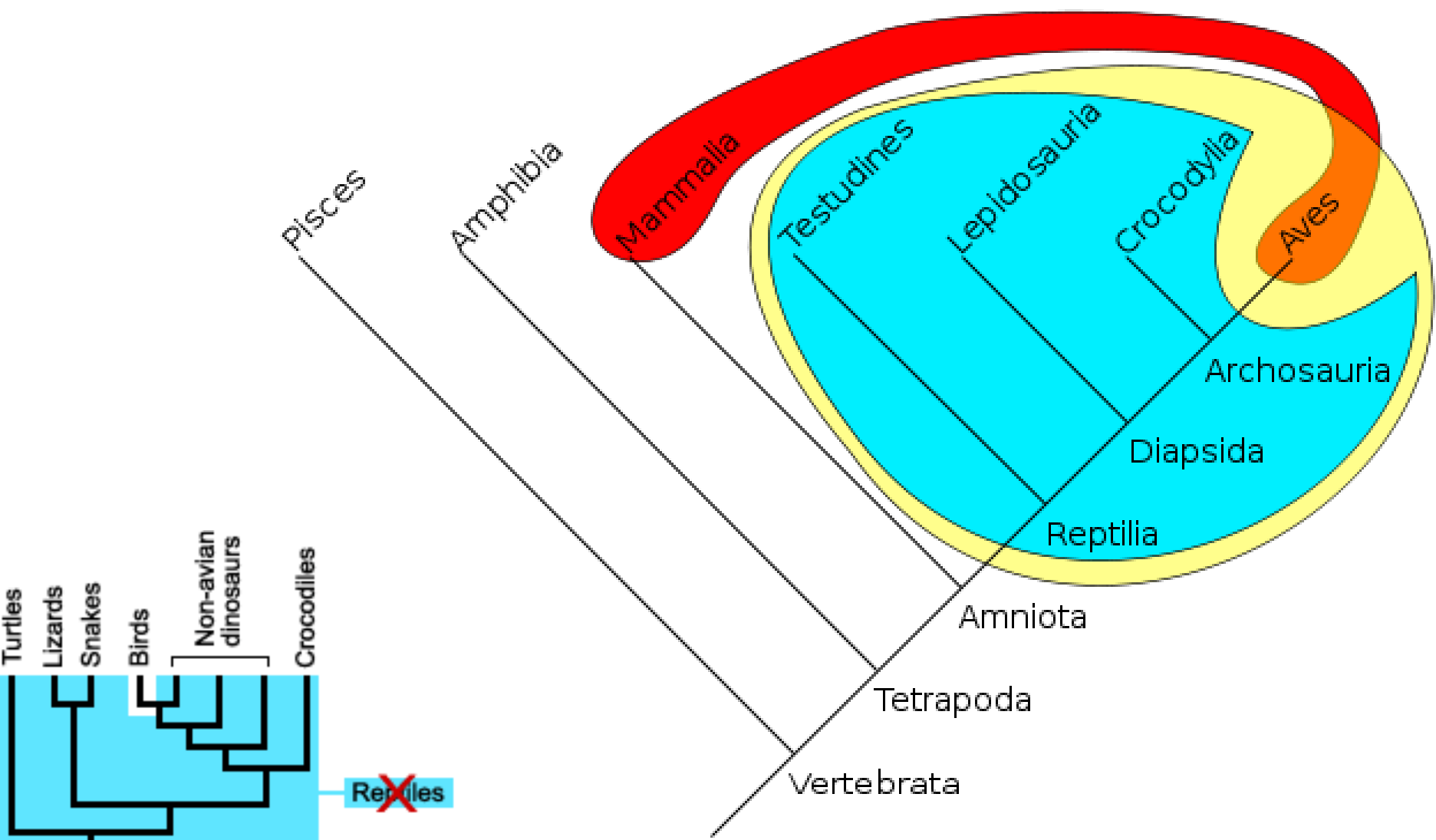
Crocodile

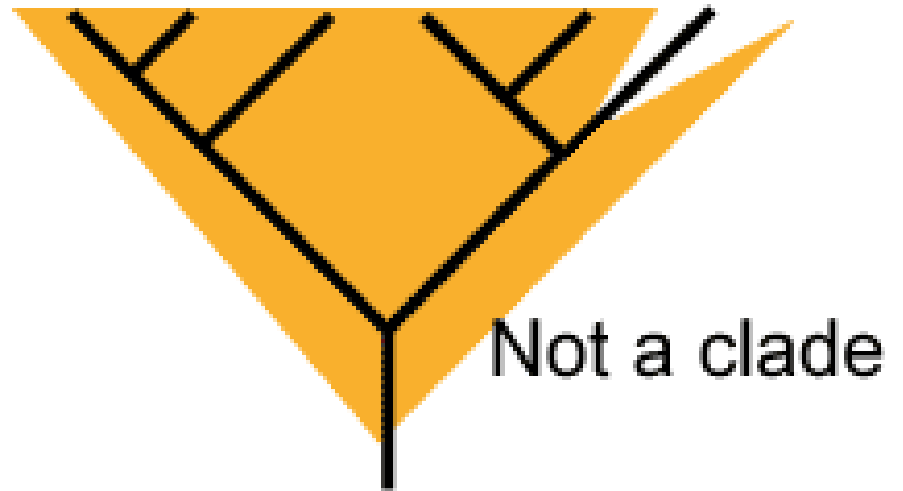
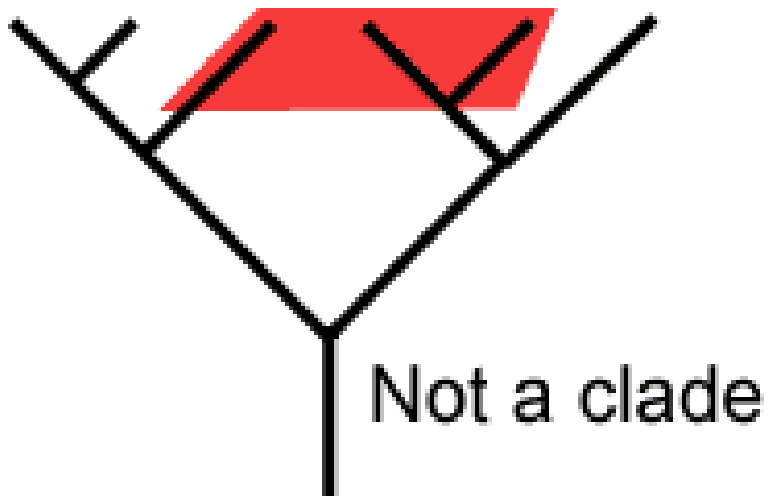
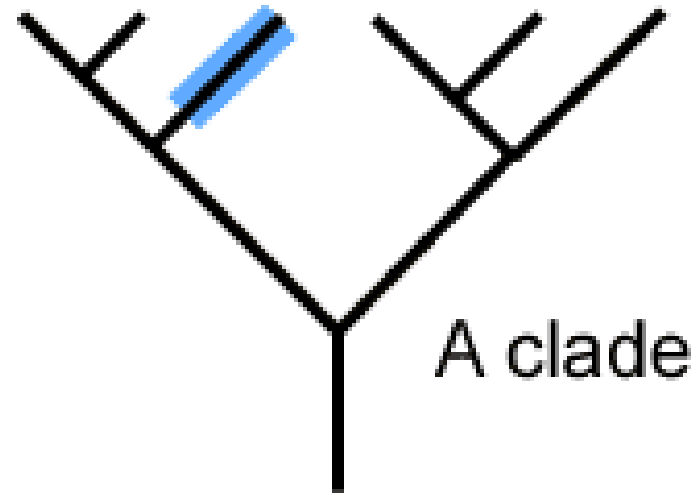
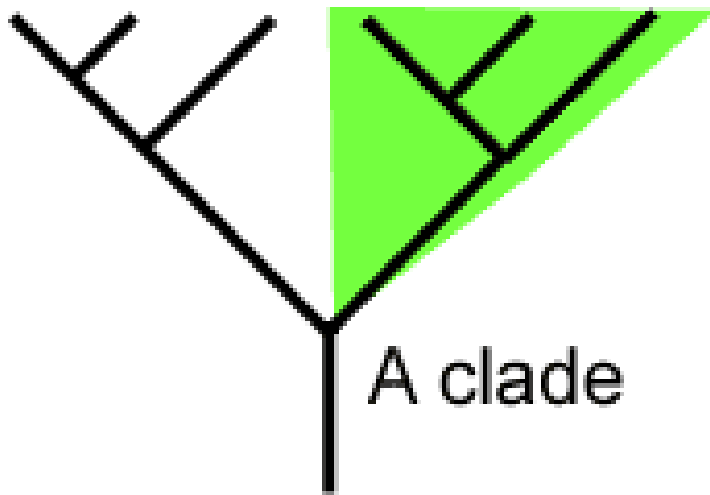


Tuatara

<http://www.flickr.com/photos/audreyim529/155024495/>
http://www.flickr.com/photos/mg_muscapix/3288435589/
<http://www.flickr.com/photos/8363028@N08/2665814123/>
<http://www.flickr.com/photos/sidm/5253662054/>

- Monophyly
- Paraphyly
- Polyphyly



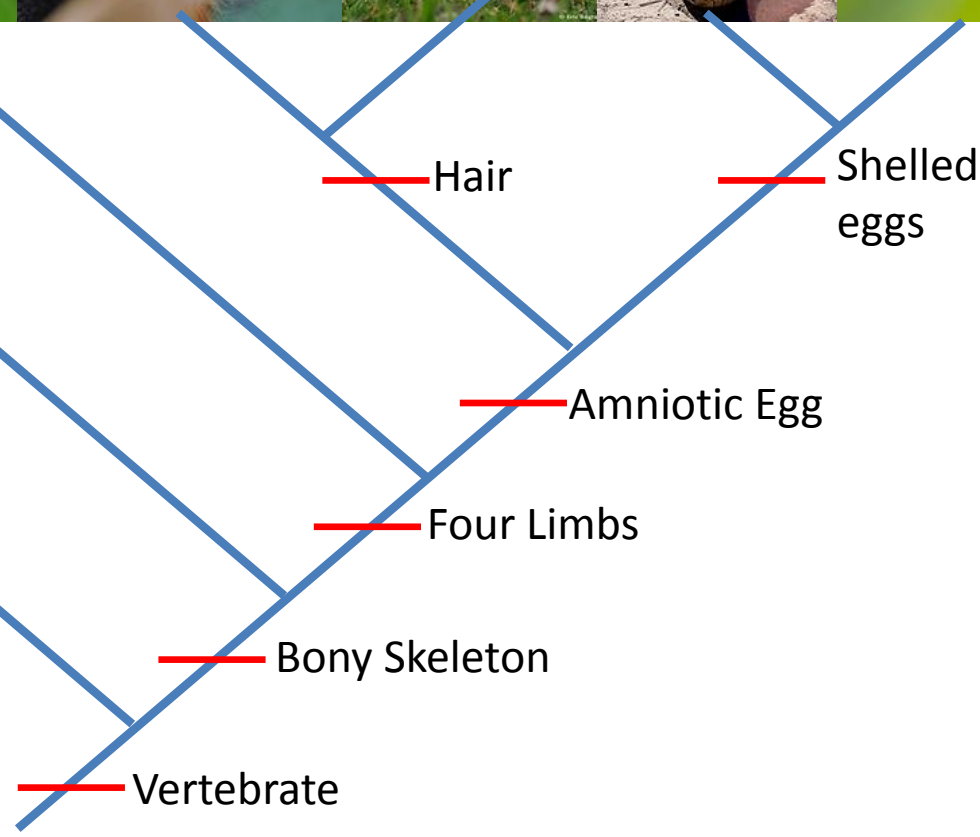


Characteristics change over time,
thus the amount of change can
help determine relationships

Groups of organisms are descended
from a common ancestor

Assumptions

There is a branching pattern in the
evolution of species and when a
split occurs, two distinct species
eventuate (**SPECIATION!**)



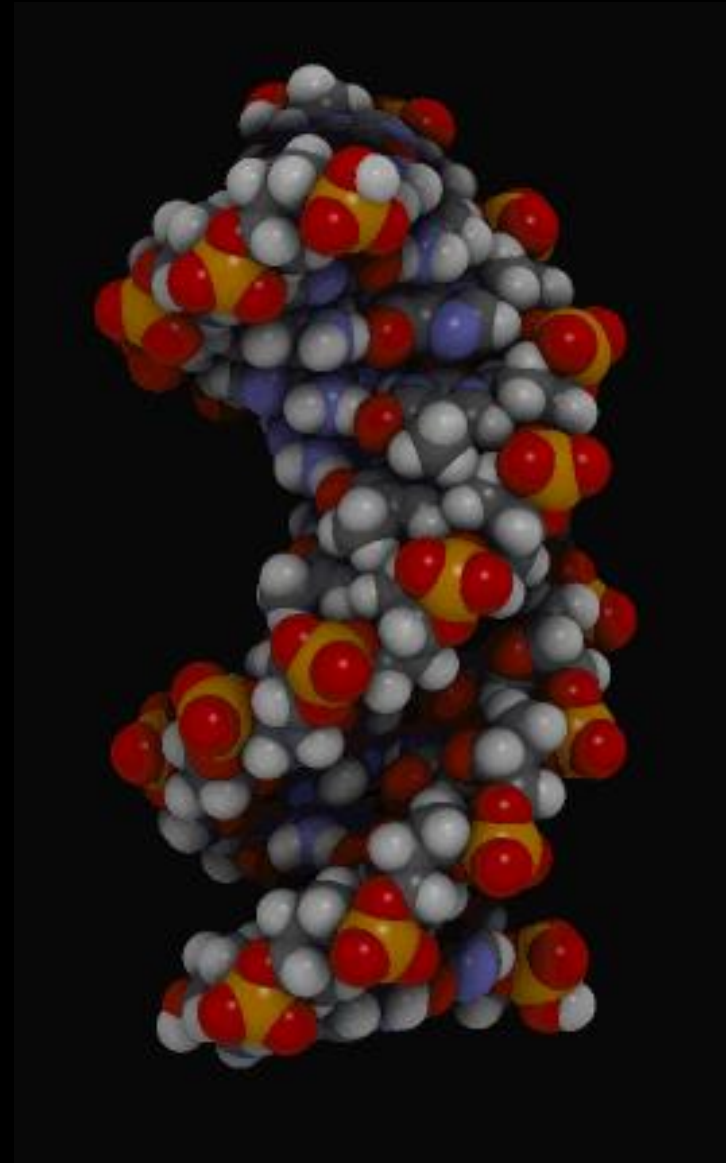
Each clade is determined by common characteristics of its members that are different from that of the other species from which it has diverged

These traits which tie the clades together
are called shared **derived characters**

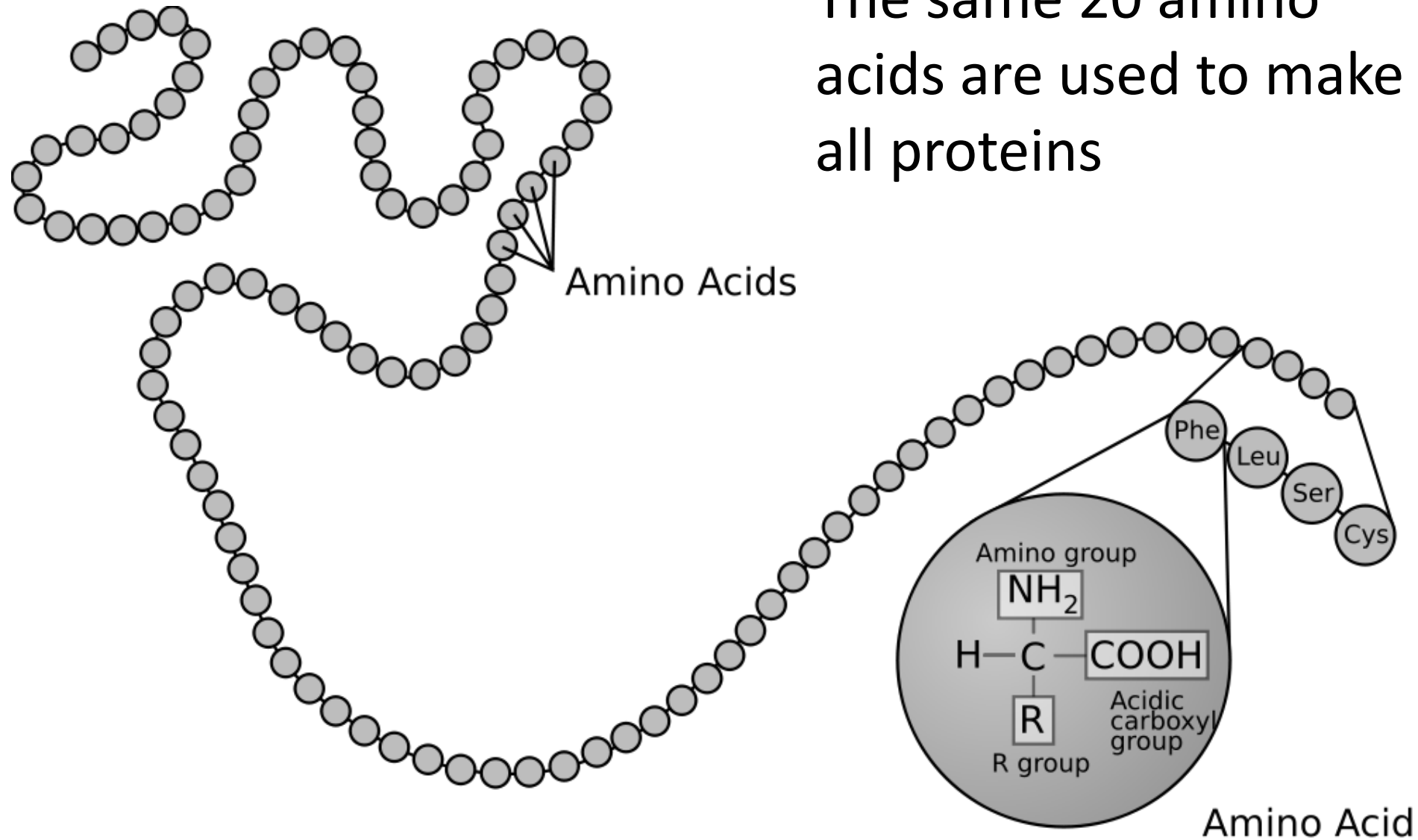
5.4.2 Evidence for which species are part of a clade can be obtained from the base sequences of a gene or the corresponding amino acid sequence of a protein.

All known organisms use DNA as genetic material

The genetic code is universal. Gene sequences inserted in different organisms express the same proteins



The same 20 amino acids are used to make all proteins



Look at these made up base sequences:

1) AATCGCCGAAGCTTTGCAATTTGCAA

2) AATCGCAGGAAGCTTTGCAATTTTCAA

3) AATCAACGAAGCTATGGATTTGCAA

4) AATCACCGAAGCTATGGATTTGCAA

Which two species are most closely related?

Compare the sequences

1) AATCGCCGAAGCTTTTGCATTTGCAA

2) AATCGC●AGAAGCTTTTGCATTT●CAA

3) AATC●A●CGAAGCT●ATGGATTTGCAA

4) AATC●ACCGAAGCT●ATGGATTTGCAA

● = Differences when compared to species 1)

3) and 4) have only one base pair difference and so therefore are the closest relatives

1) And 3) have the most differences (3bp) so are most distantly related

Taking the example of the protein **cytochrome c**. It is not identical in all species because single point mutations in the DNA that codes for it can lead to different amino acids making up the protein.

Both humans and chimpanzees have **identical** cytochrome c molecules, while rhesus monkeys share all but one of the amino acids.

This suggests that humans and chimpanzees are more closely related to each other than to rhesus monkeys.



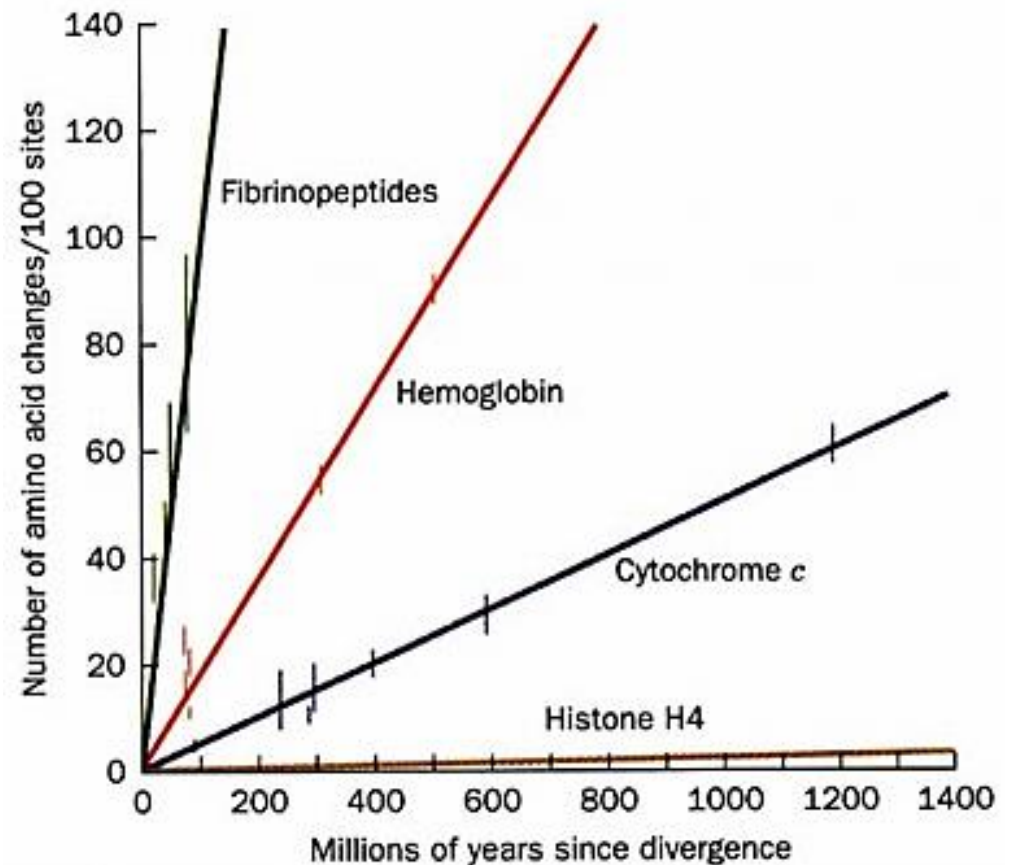
Morphology is only part of the story in cladistics. Genetics are the primary basis for grouping organisms into clades and determining likely paths of evolutionary descent

Ex: Crocodiles are more closely related to birds than lizards...



5.4.3 Sequence differences accumulate gradually so there is a positive correlation between the number of differences between two species and the time since they diverged from a common ancestor.

Mutations (DNA changes) occur at a relatively constant rate so they can be used as **molecular clocks** in which the number of genetic differences can predict how long ago two species diverged



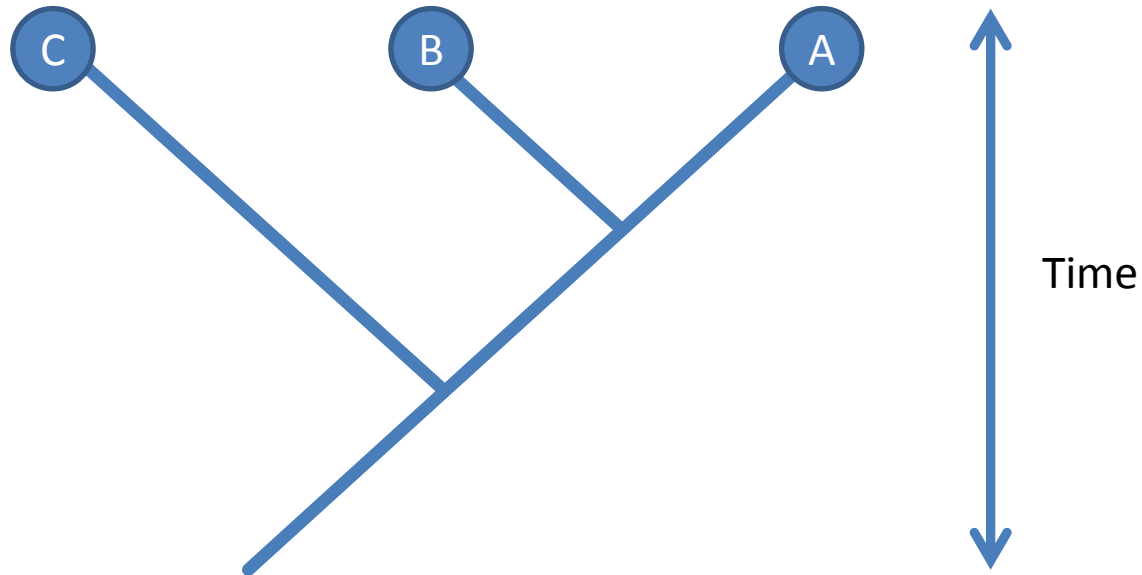
An **evolutionary clock** involves calculating the time since species diverged by comparing the number of differences in their DNA and/or protein sequences.

Scientists who originated the idea calibrated the amino acid differences in Hemoglobin with times derived from the fossil record.



The assumption is that these changes occur at a regular rate.
(which may not always be the case)

Therefore if species A had 5 differences from species B and 10 differences from species C, then the lineages for A and C must have split twice as long ago as for A and B



Homologous structures are inherited from a common ancestor



e.g. The fly on the previous page and the mosquito on this page have mouthparts adapted to their food sources but the basic components were inherited from a common ancestor

Other examples include pentadactyl limbs and finches' beaks

Analogous structures have similar form and function due to **convergent evolution**, they do not stem from a common ancestor



Bats...

...birds...



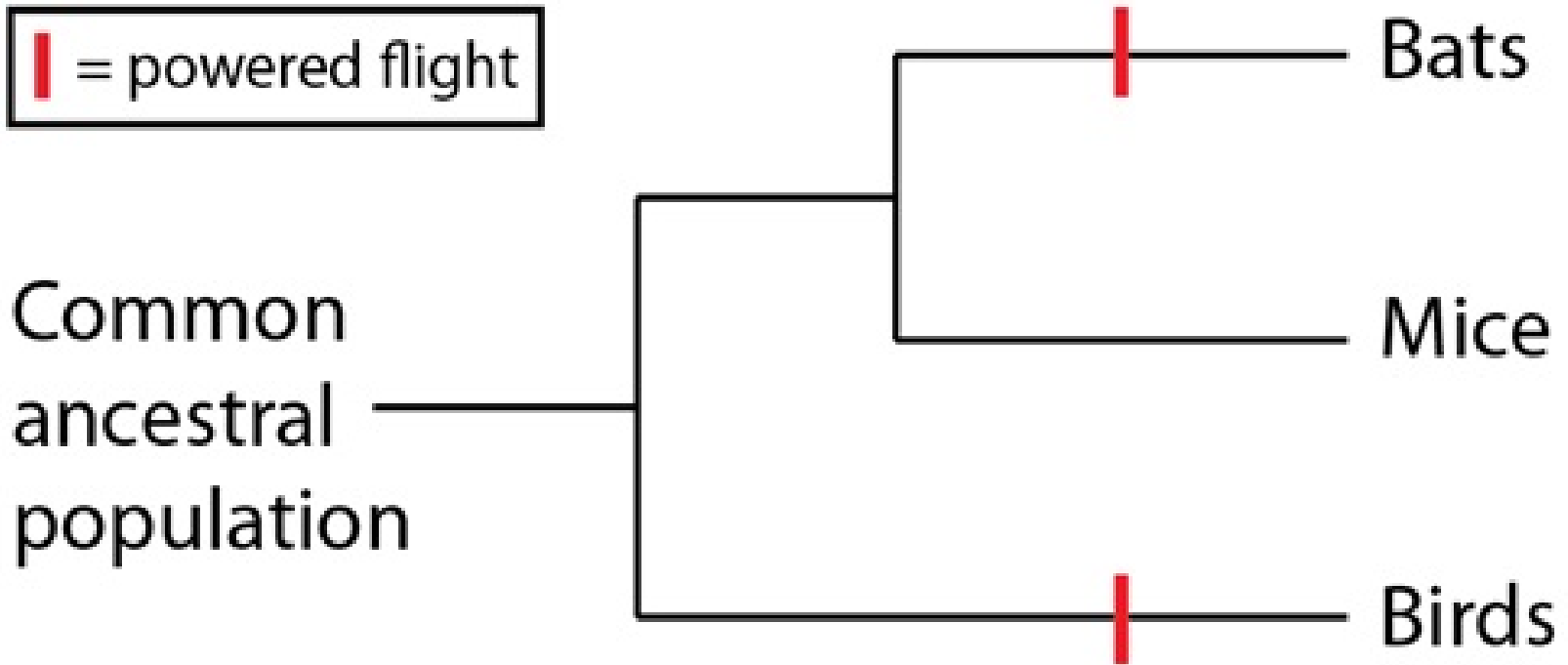
...and bugs all have wings for flight that evolved independently



Other examples include:

- Streamlined shape for dolphins , sharks and ichthyosaurs
- Long snout and tongue for capturing ants on the anteater and echidna

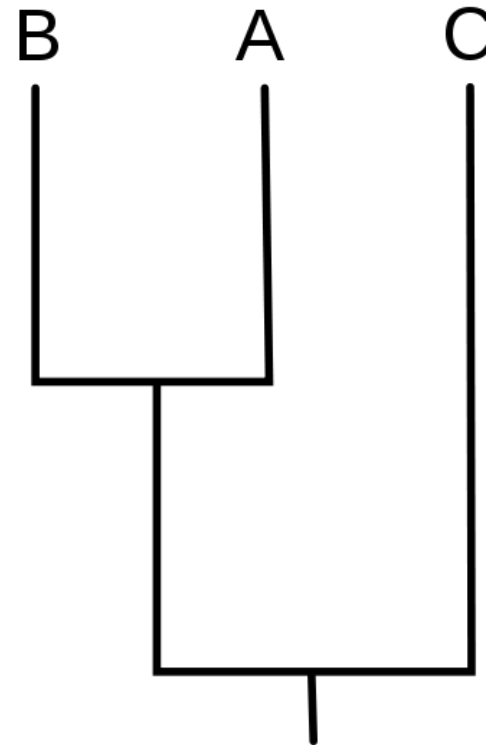
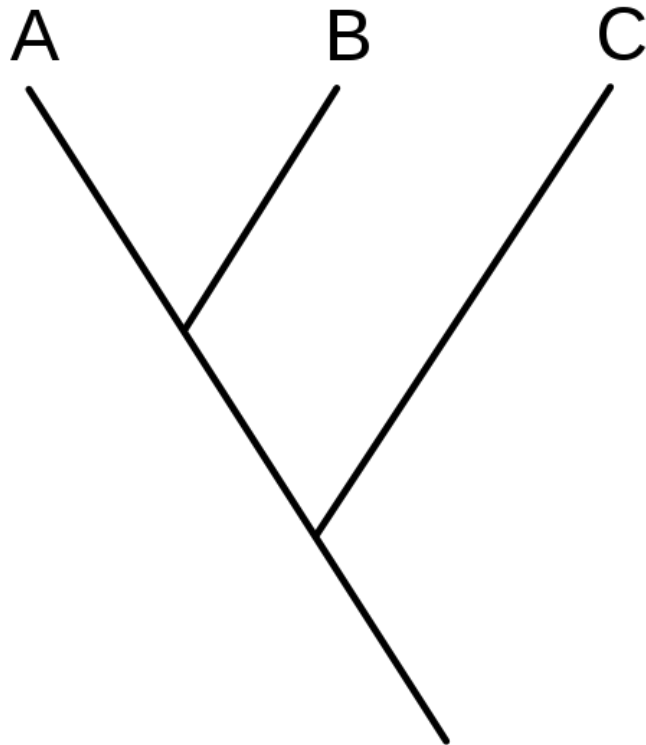
I = powered flight

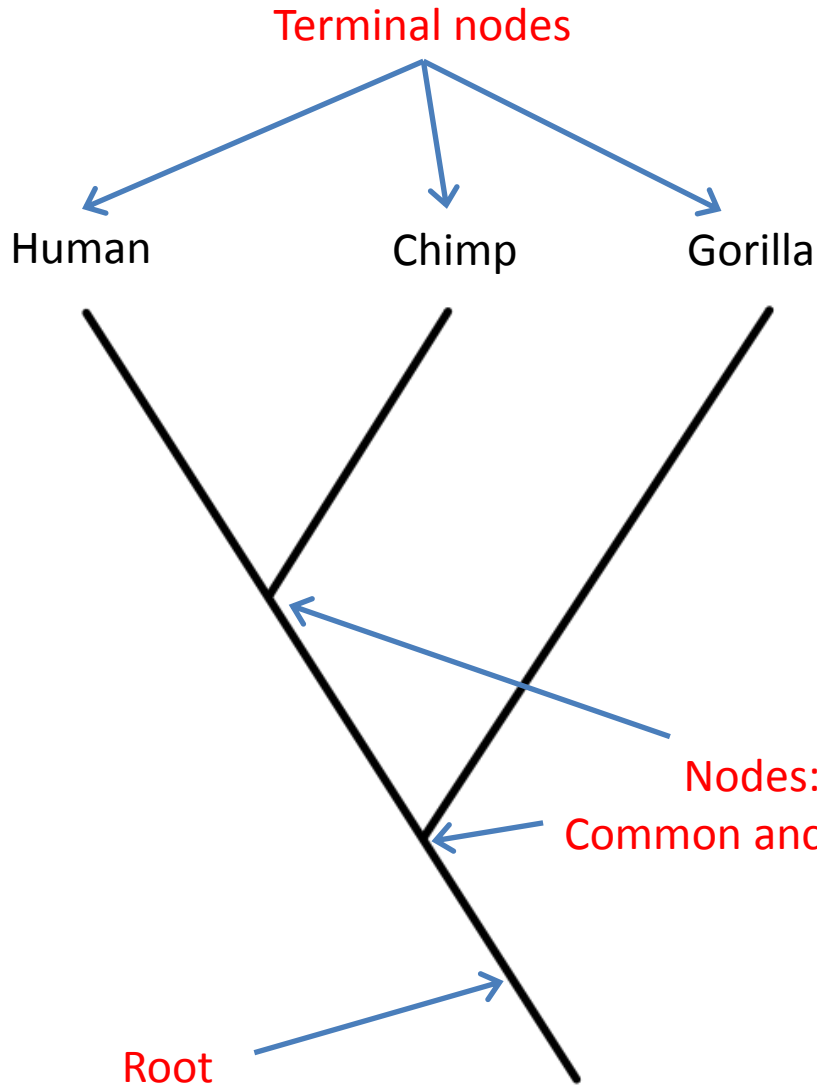


- **What is more likely?**
- A. the common ancestor to bats/mice/birds had powered flight, and mice lost the ability to fly
- B. powered flight evolved twice, independently in bats and birds

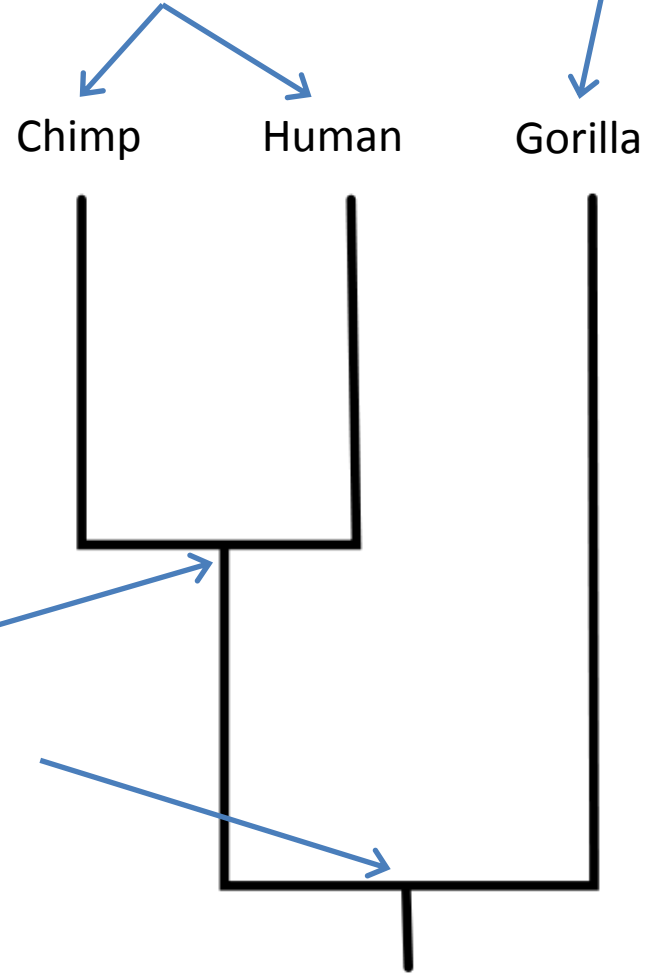
5.4.5 Cladograms are tree diagrams that show the most probable sequence of divergence in clades.

- These two cladograms are **identical** (although they don't look it)
- The shape and the order of the **terminal nodes** does not matter.
- The only information to be gathered from the cladograms below is the order of nesting of **sister clades** and the relative relatedness of species





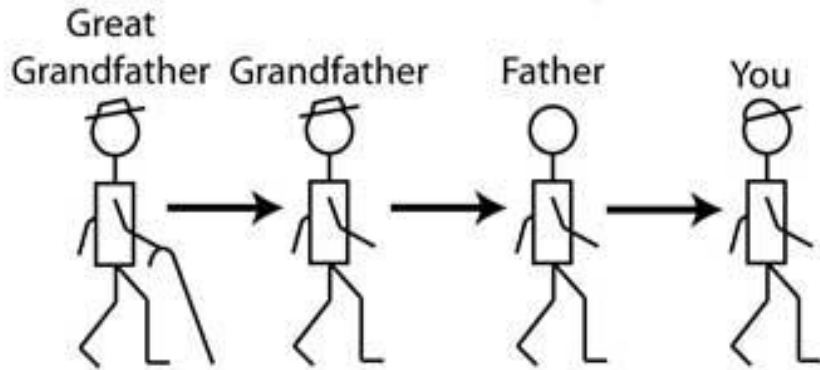
Sister clades: have a common ancestor



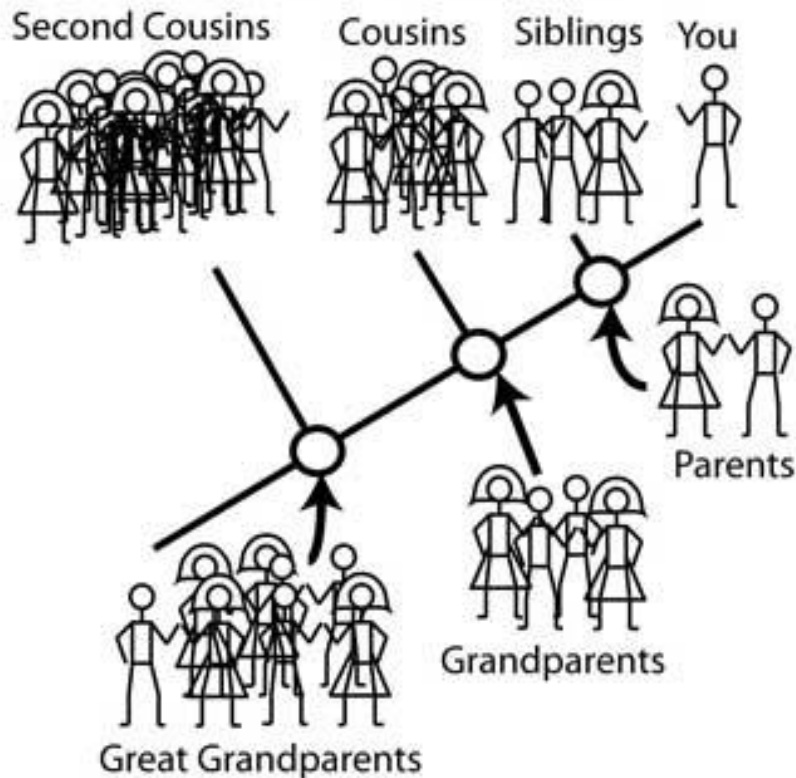
Out group: Defines the ancestral characters

Nodes:
Common ancestors

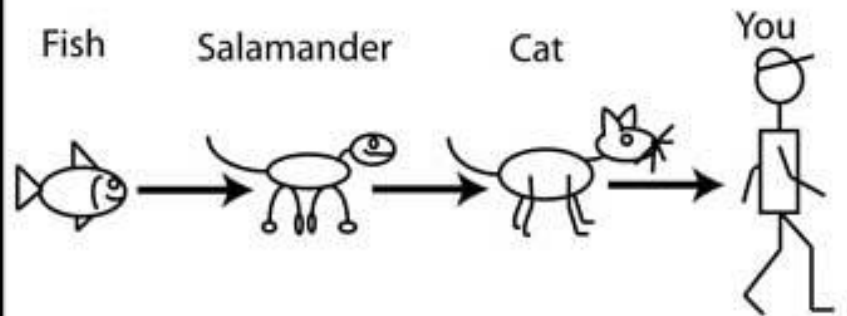
This is NOT Your Family Tree



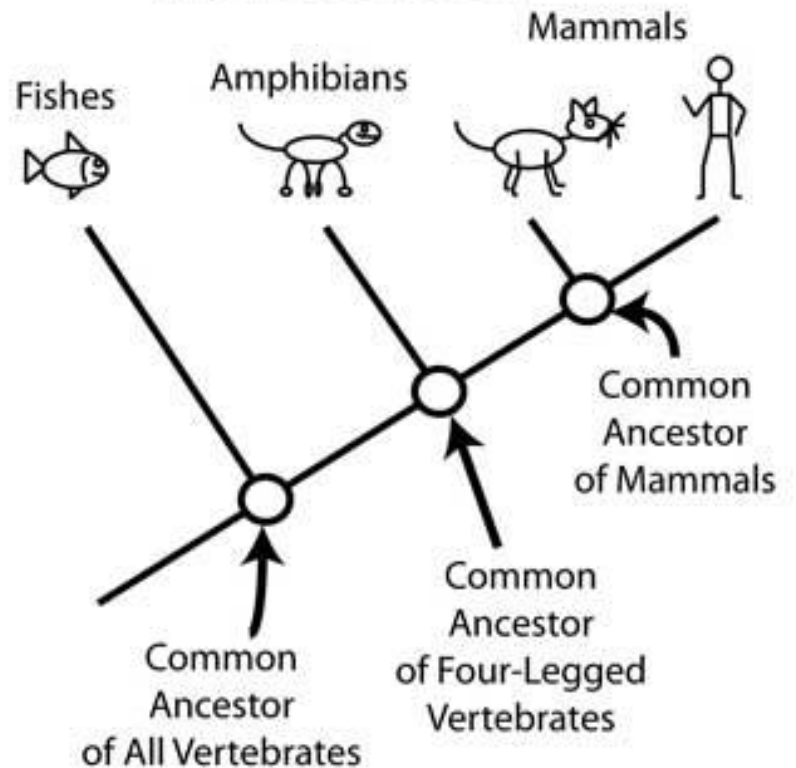
This is Your Family Tree



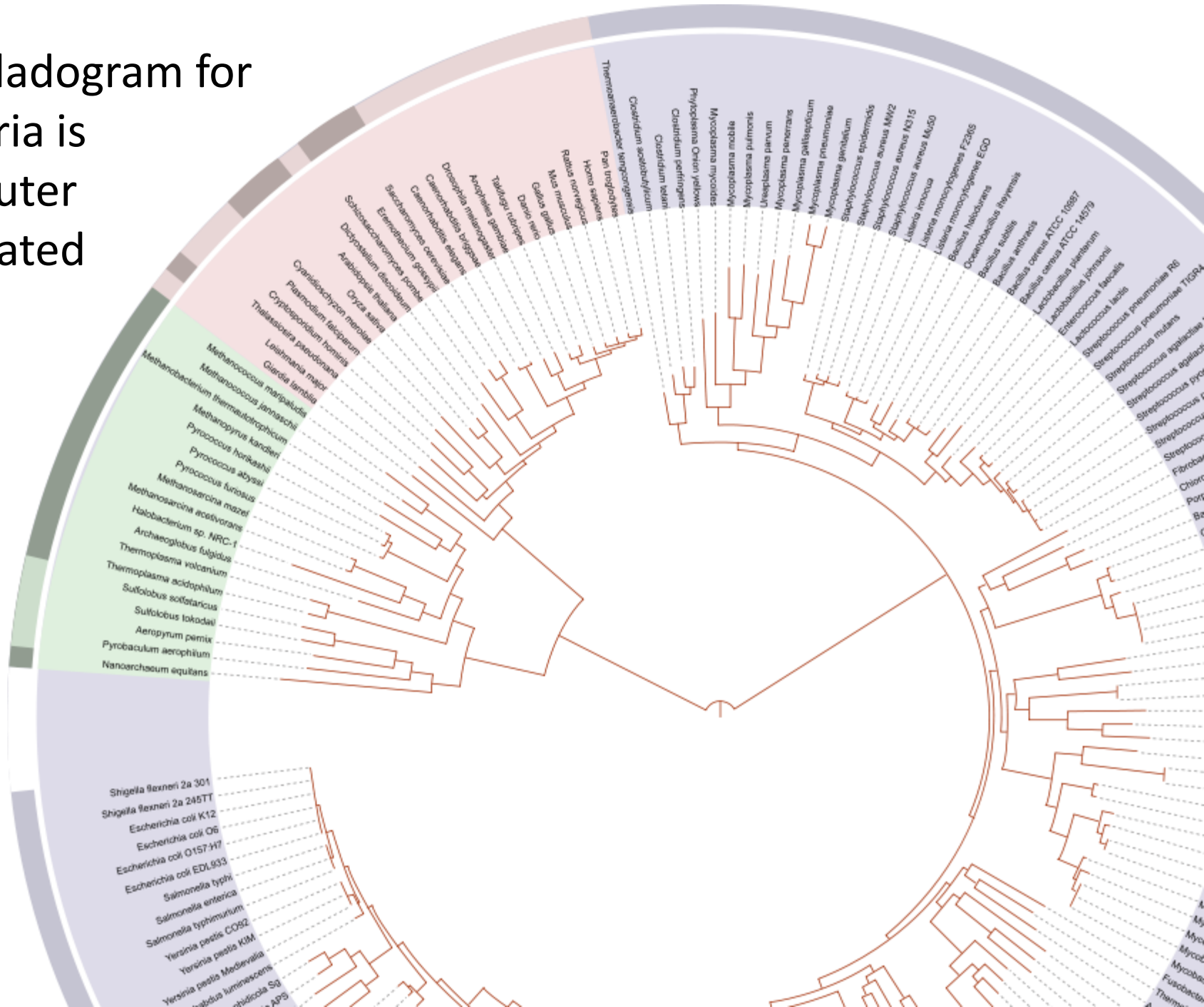
This is NOT Evolution



This is Evolution



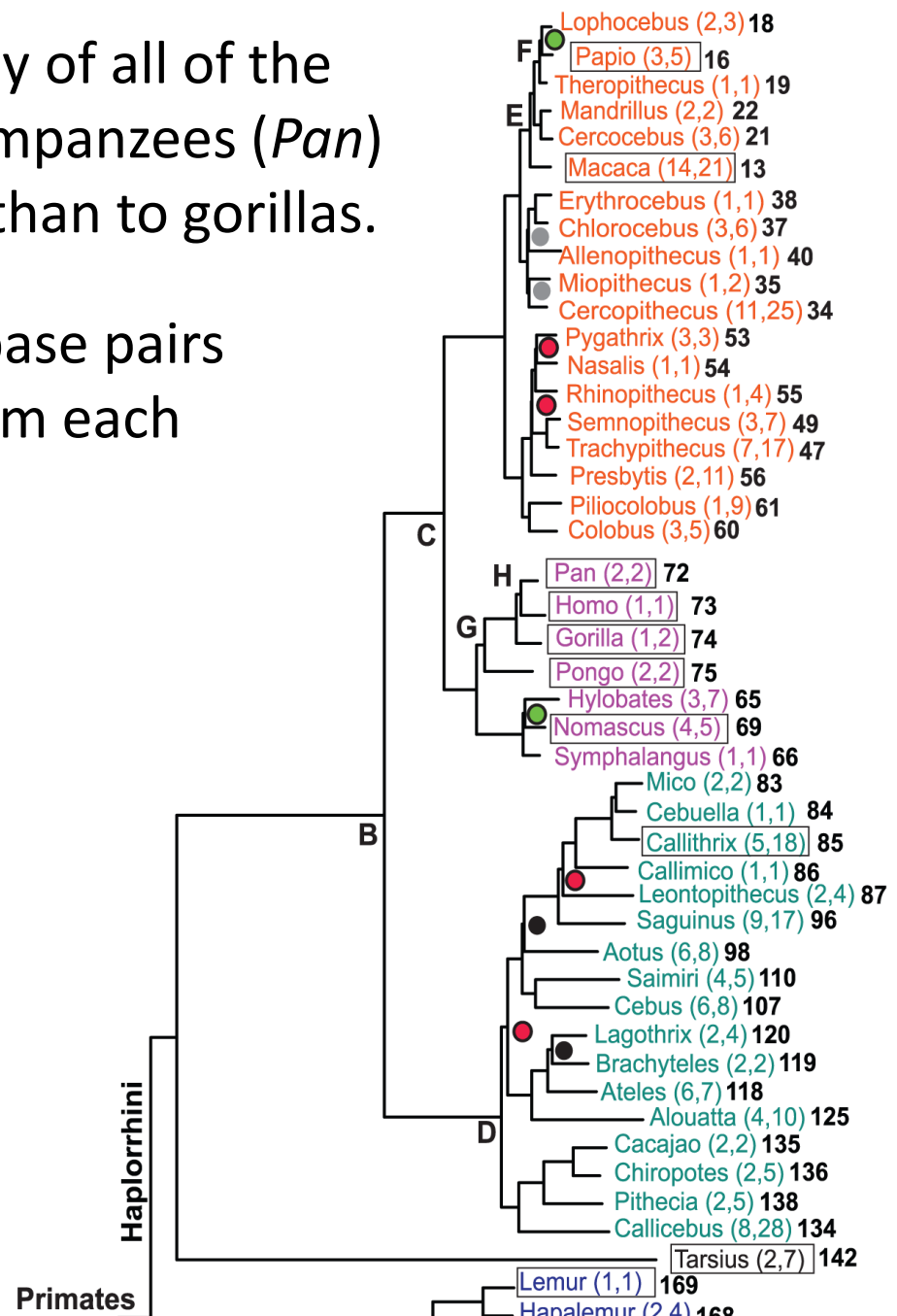
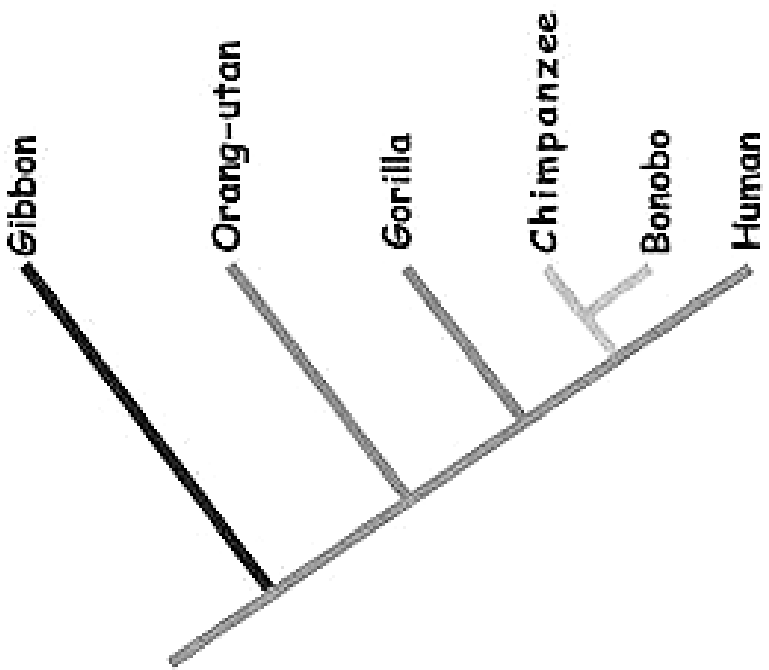
This cladogram for bacteria is computer generated



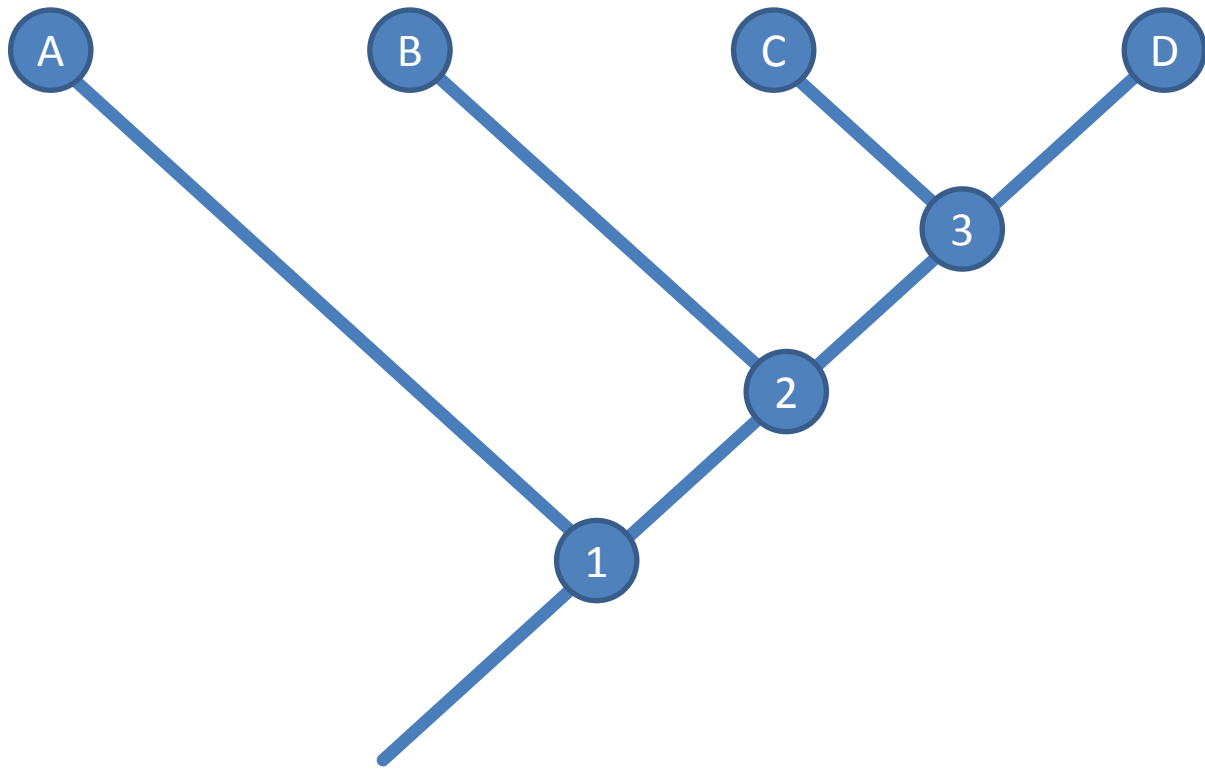
5.4.7 Analyze cladograms including humans and other primates.

This is part of a molecular phylogeny of all of the living primates. It clearly shows chimpanzees (*Pan*) as more closely related to humans than to gorillas.

It was made by comparing 34,927 base pairs sequenced from 54 genes taken from each of a single species in each genus.



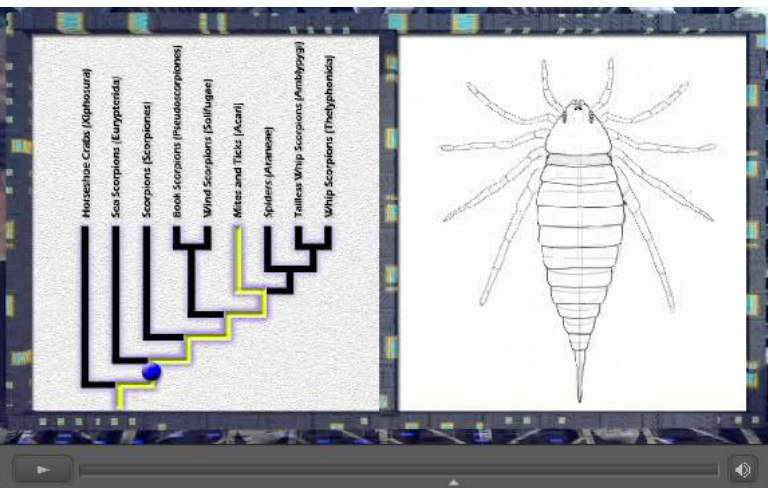
5.4.9 Analyze cladograms to deduce evolutionary relationships.

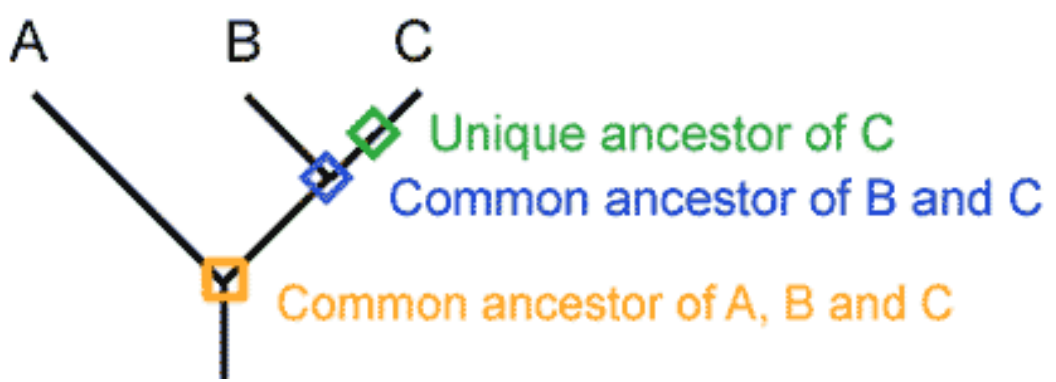
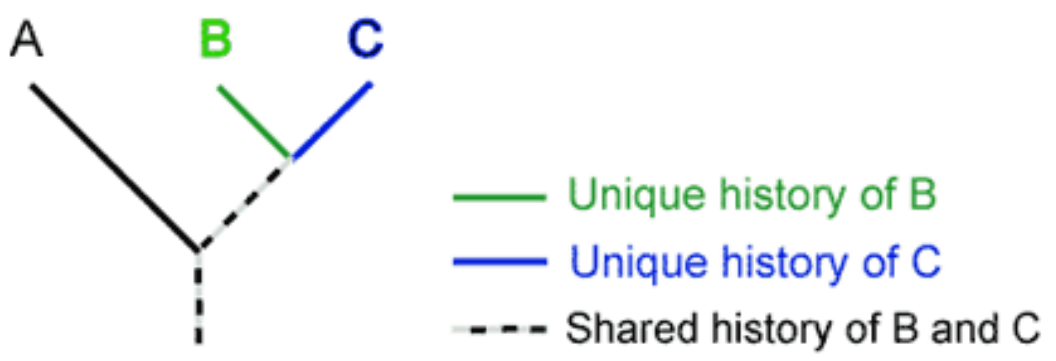
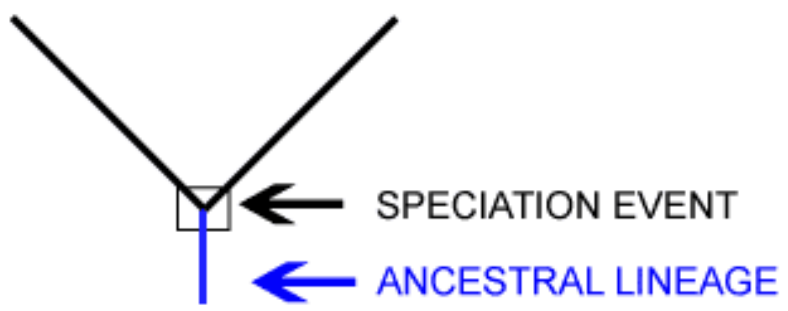
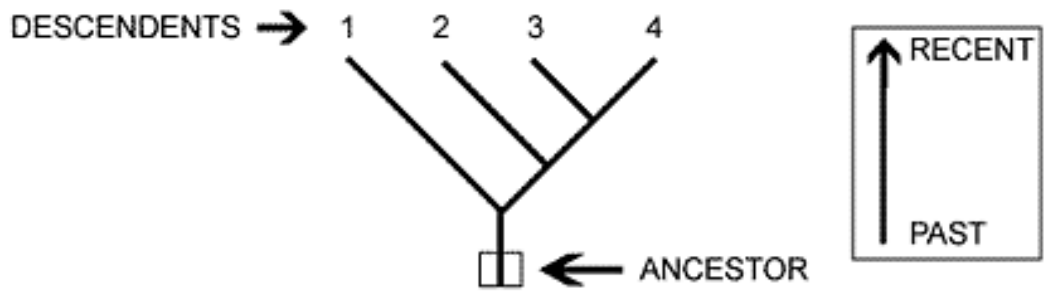


Which two species are most closely-related by evolution?

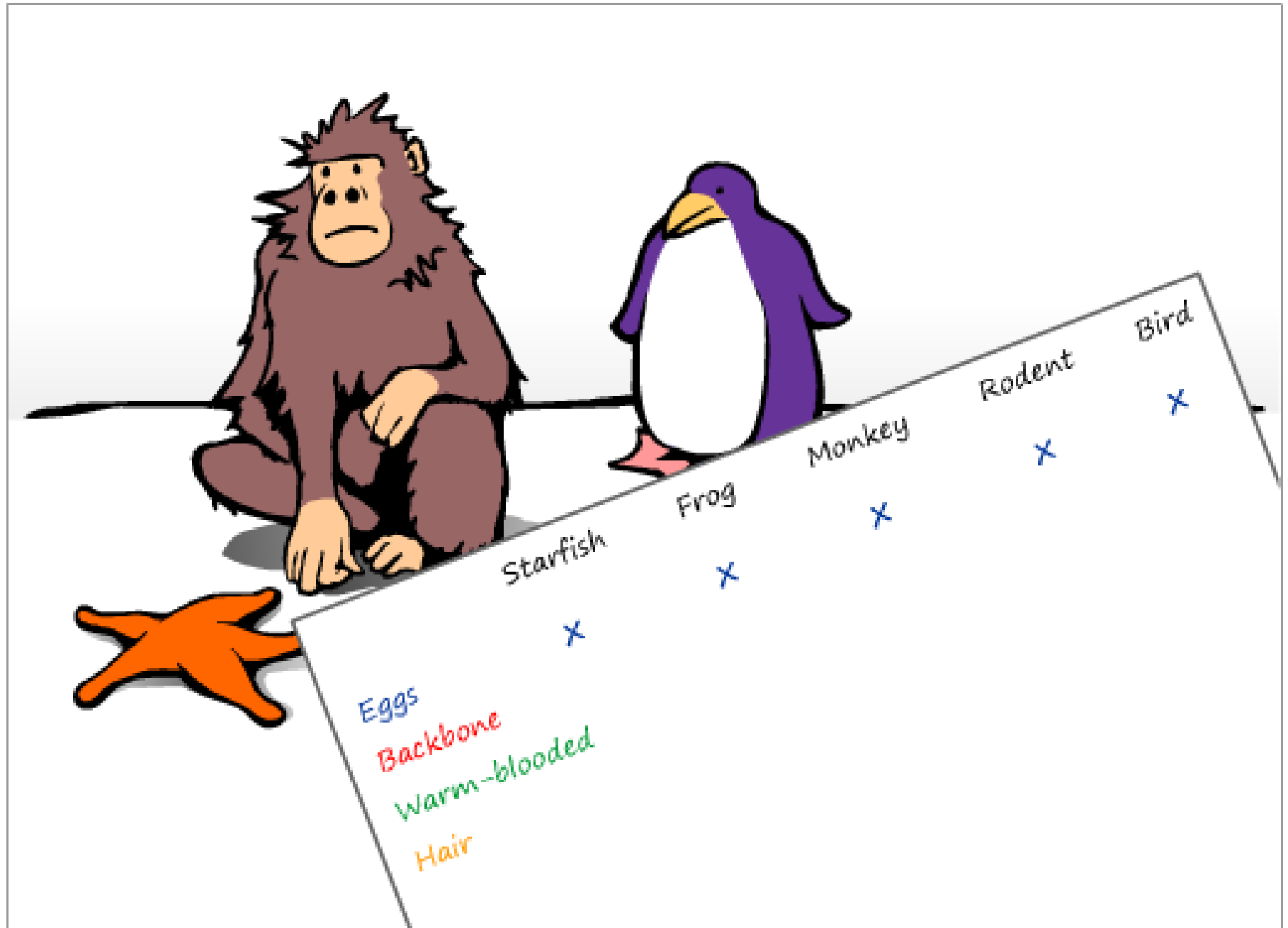
Which node represents the earliest speciation / divergence?

Which species is D more closely related to; A or B?





How to Build a Cladogram



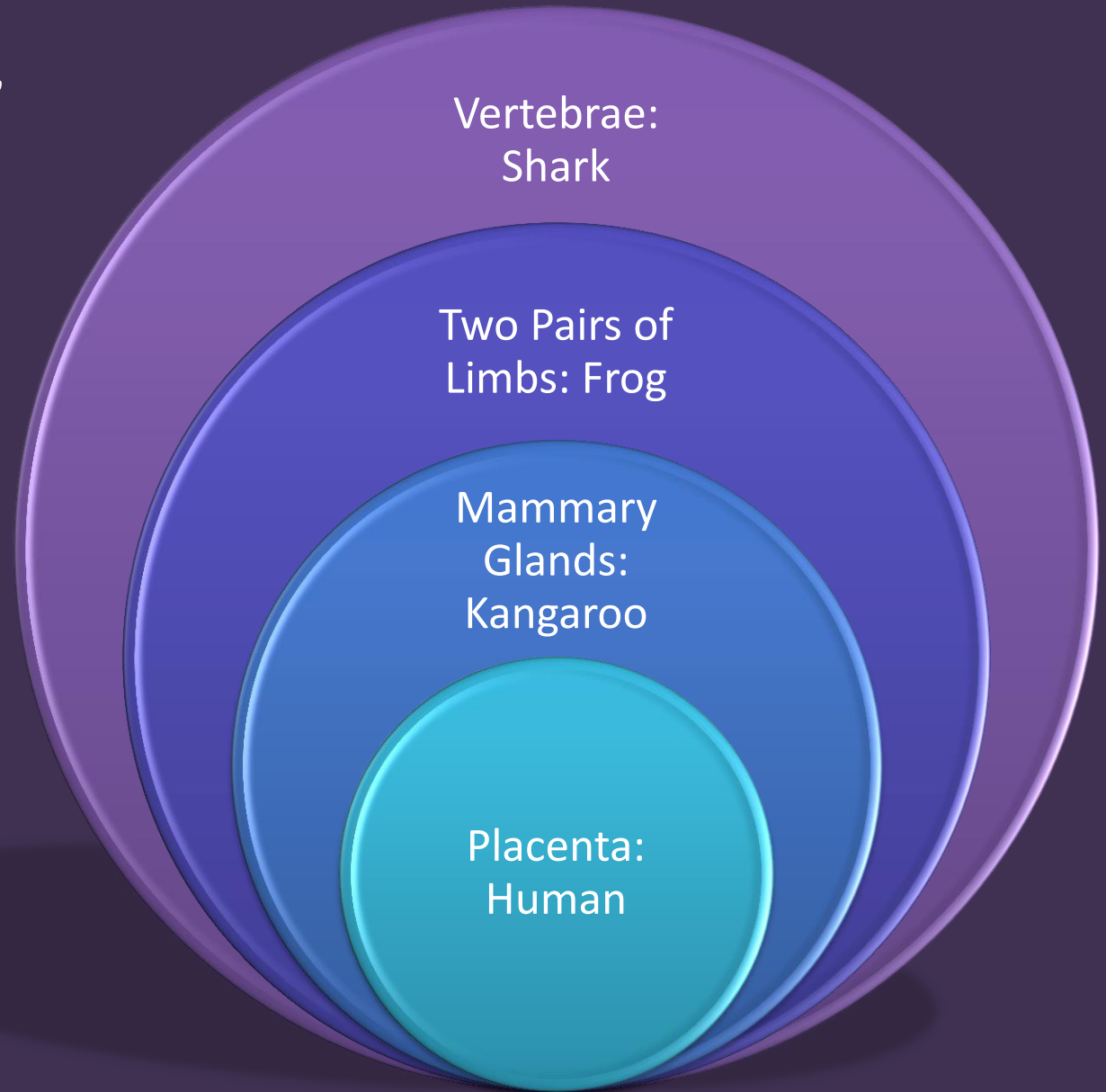
1) Compile a table of the characters being compared

Characters	Shark	Frog	Kangaroo	Human
Vertebrae	X	X	X	X
Two pairs of limbs		X	X	X
Mammary glands			X	X
Placenta				X

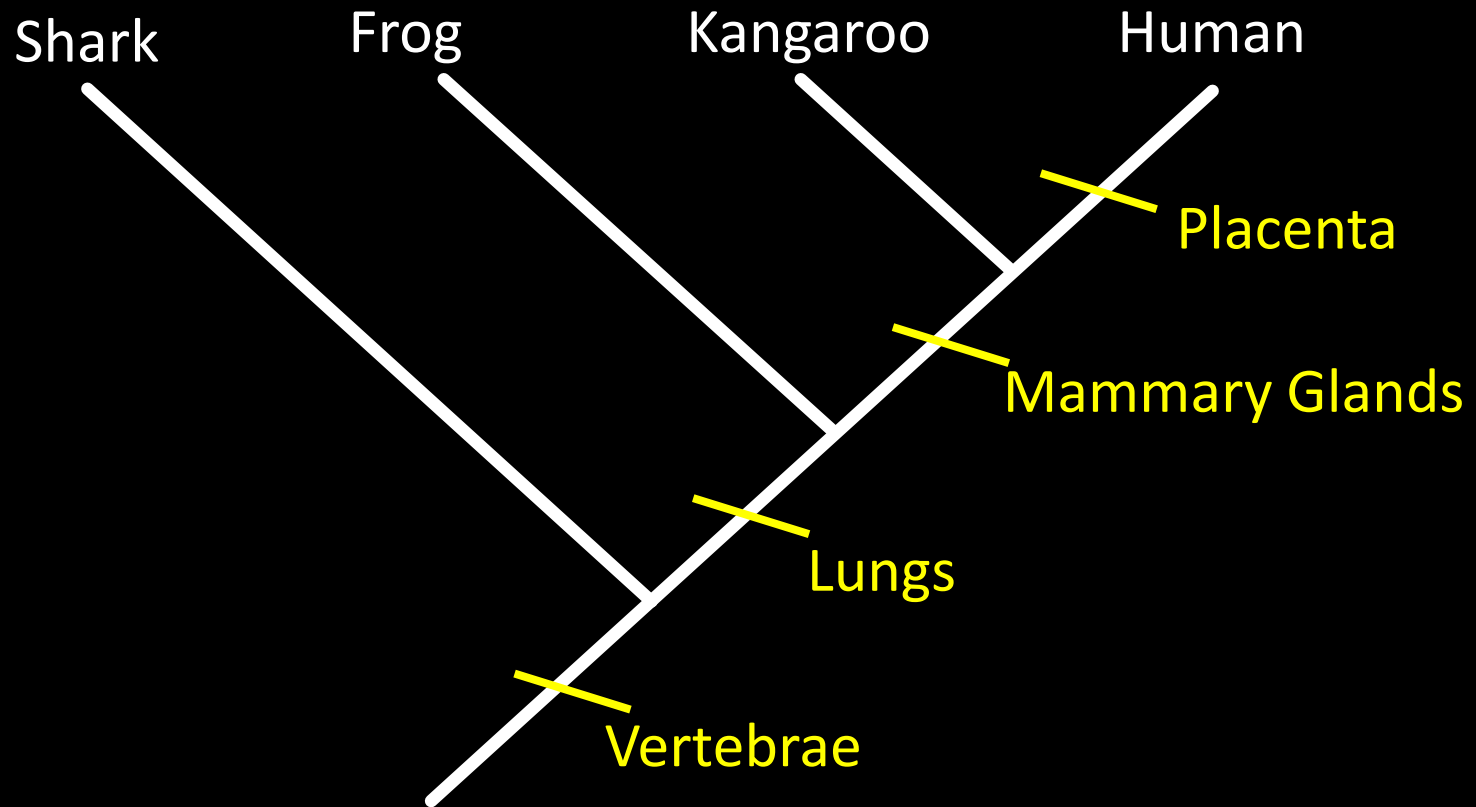
Modified from:

<http://www.bu.edu/gk12/eric/cladogram.pdf>

2) Use the data to construct a Venn diagram, Start with the characteristic shared by all taxa in the biggest circle and work inwards



3) Convert the Venn diagram into a cladogram



It should look
something
like this:

Cells with flagella: Sponge

Symmetry: Jellyfish

Bilateral symmetry: Flatworm

Mesoderm

Head develops first

Anus develops first

Segmented Body:
Earthworm

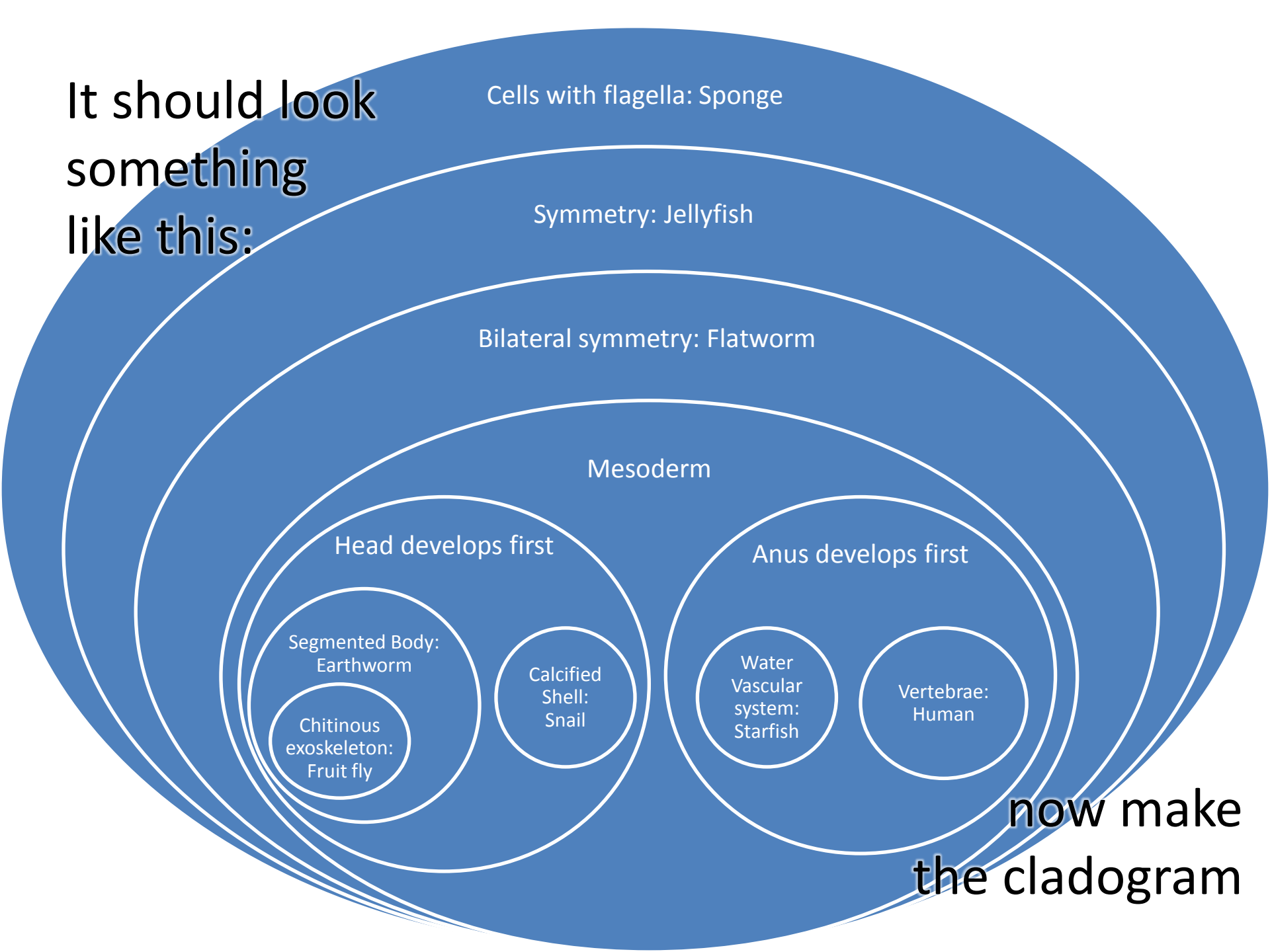
Calcified
Shell:
Snail

Chitinous
exoskeleton:
Fruit fly

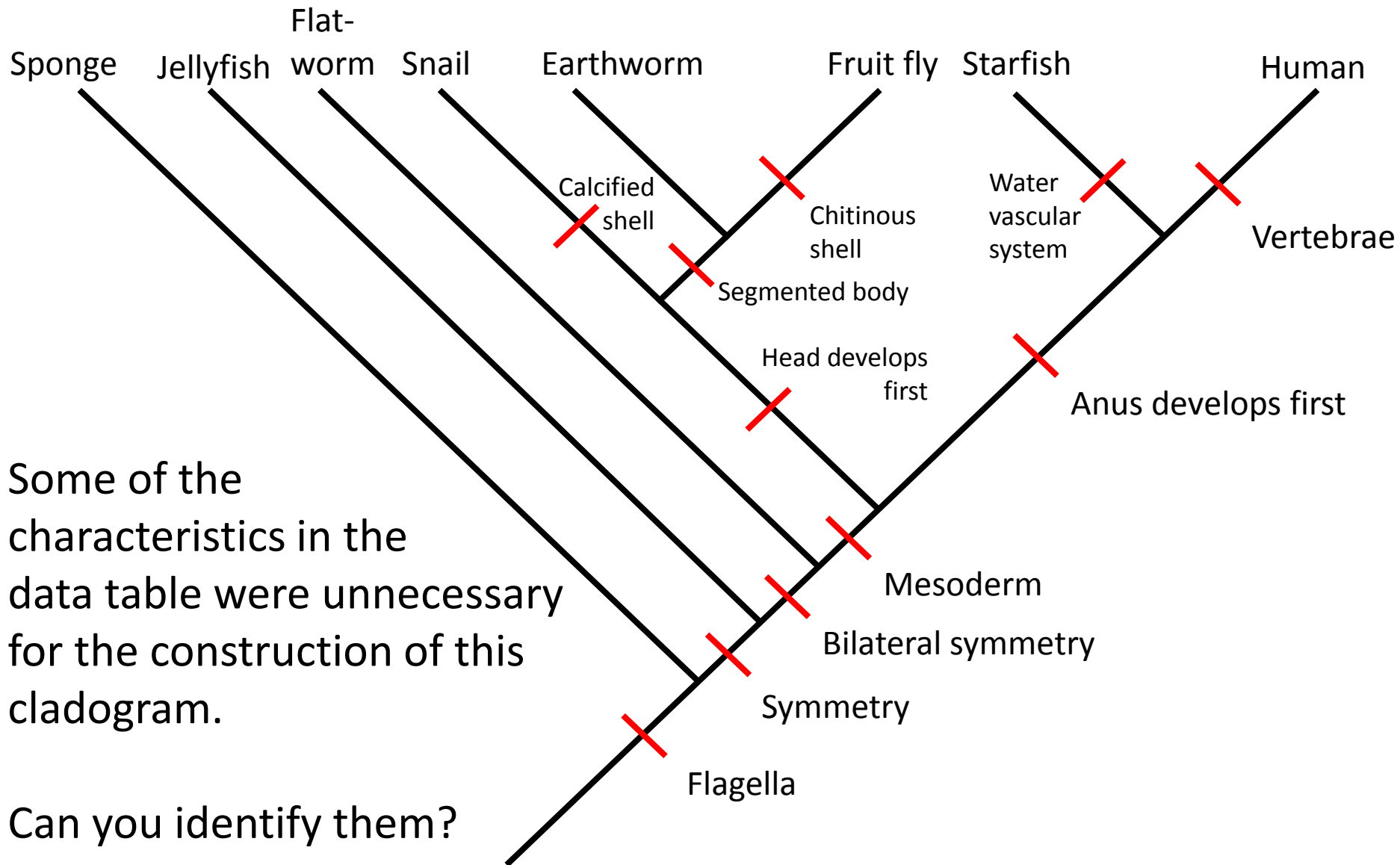
Water
Vascular
system:
Starfish

Vertebrae:
Human

now make
the cladogram



It should look something like this:



Some of the characteristics in the data table were unnecessary for the construction of this cladogram.

Can you identify them?

5.4.6 Evidence from cladistics has shown that classification of some groups based on structure did not correspond with the evolutionary origins of a group or species.

Evolutionary Links

Classification allows us to see evolutionary relationships. Organisms that are grouped together share a lot of similar features (homologous structures). These shared characteristics help us see how organisms have evolved from a common ancestor. HOWEVER, morphology has its limitations in terms of evolutionary classification and DNA/ Amino Acid evidence is now far more accurate and trustworthy...



e.g. Llamas were originally compared to sheep but a study of their genetics later placed them in the camel family

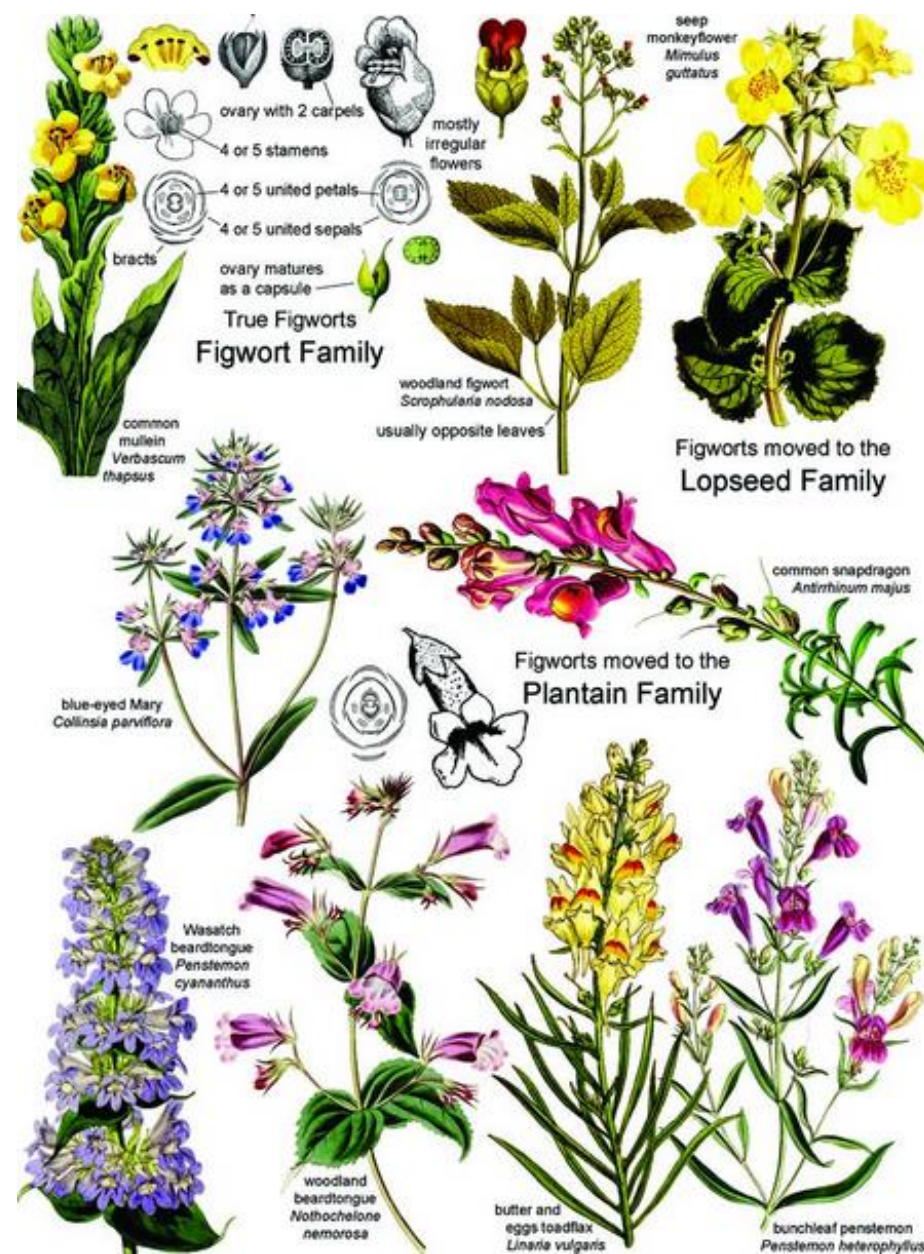


5.4.8 Discuss reclassification of the figwort family using evidence from cladistics.

- Until recently, Figworts were the 8th largest family of angiosperms (flowering plants). It grew from 16 genera in 1789 to 275 genera
- Taxonomists recently examined chloroplast genes and found the 5000 figwort species should be split into 5 different clades rather than just one

Figwort Family Breaks Up: Read All About It

by Pomona Belvedere



- Less than half of the original species remain in the Figwort family; now only the 36th largest among angiosperms
- Reclassification was helpful since old Figwort family was too large and dissimilar to be a helpful grouping

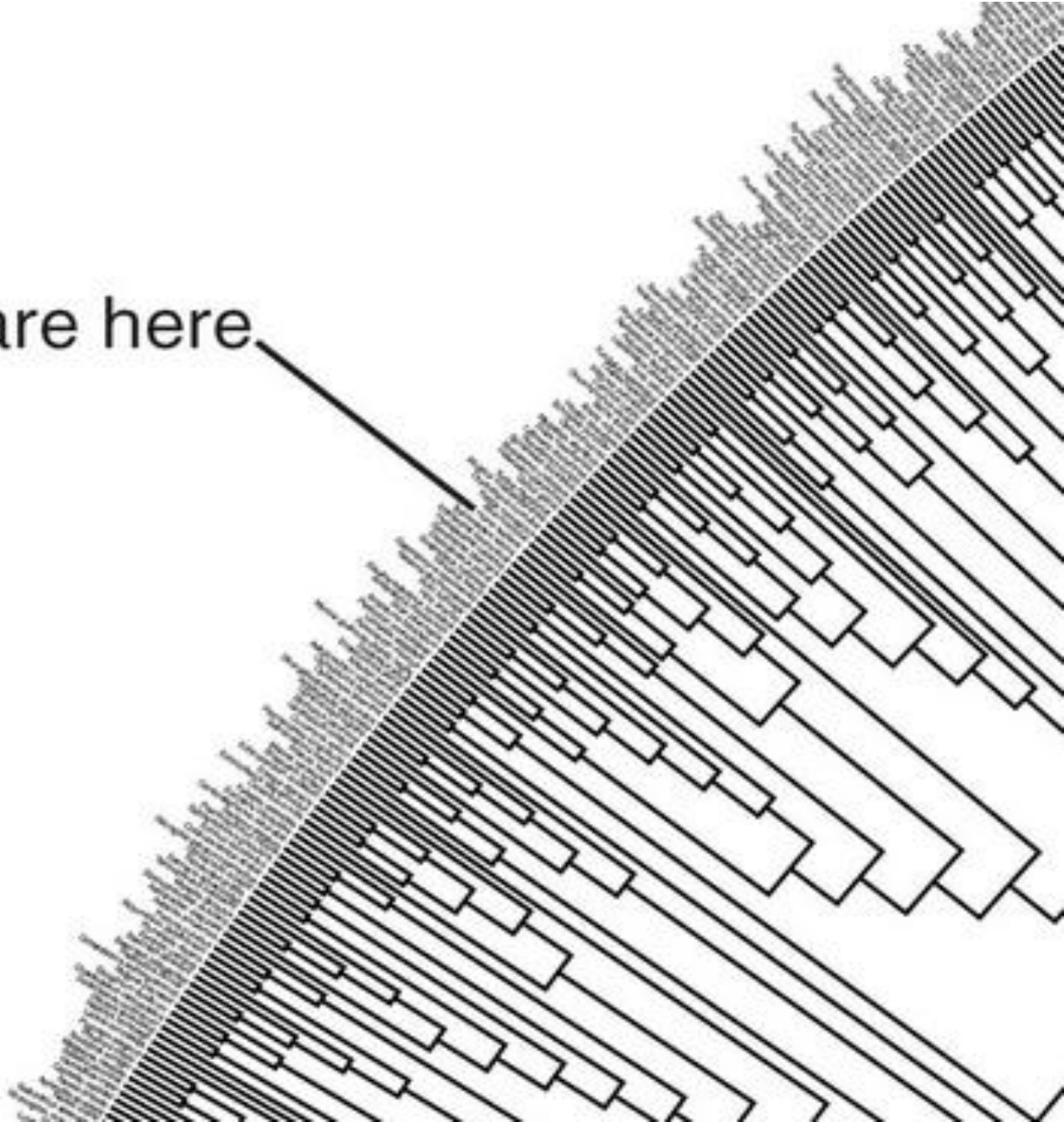


No longer a Figwort. Sad 😞

It's all connected...

Tree of Life

You are here



Bibliography / Acknowledgments

BioNinja

Your one-stop biology resource



[Jason de Nys](#)



[Chris Paine](#)

