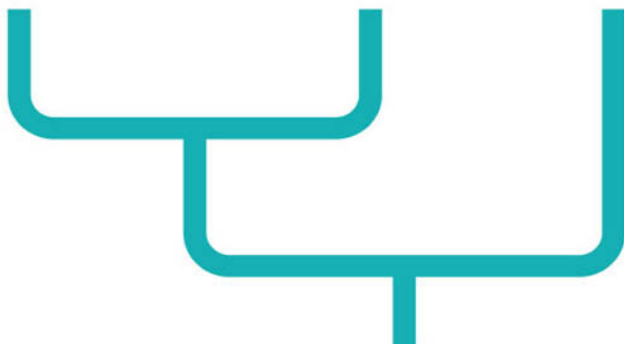


Chapter 26:

Phylogeny & Systematics



An unexpected family tree. What are the evolutionary relationships among a human, a mushroom, and a tulip?

Molecular systematics has revealed that —despite appearances—animals, including humans, and fungi, such as mushrooms, are more closely related to each other than either are to plants.

Phylogeny & Systematics

- **Phylogeny** = the evolutionary history of a species or group of species
 - ◆ To construct a phylogeny we use **systematics**, which classifies organisms based on common ancestries inferred from...
 - fossil records
 - morphological & biochemical resemblances
 - molecular evidence (*DNA/RNA Nucleotide & Protein Amino Acid Sequence comparisons*)
- **Systematics**
 - ◆ Classifying organisms and determining their evolutionary relationships
 - connects classification system to phylogeny by categorizing & naming organisms



2004-2005

Fossil record

- **Sedimentary rock are the richest source of fossils**
 - ◆ **This fossil record is a substantial, but an incomplete chronicle of evolutionary history**
 - ◆ incomplete historical document of biology
 - ◆ **history of life on Earth is punctuated by mass extinctions**

5000 year old ice mummy found on an Alpine ridge dividing Austria from Italy at 10,500 feet above sea level.



Paleontology

- The Field that studies fossils
 - ◆ fossils provide the strongest evidence of change
 - links past & current organisms

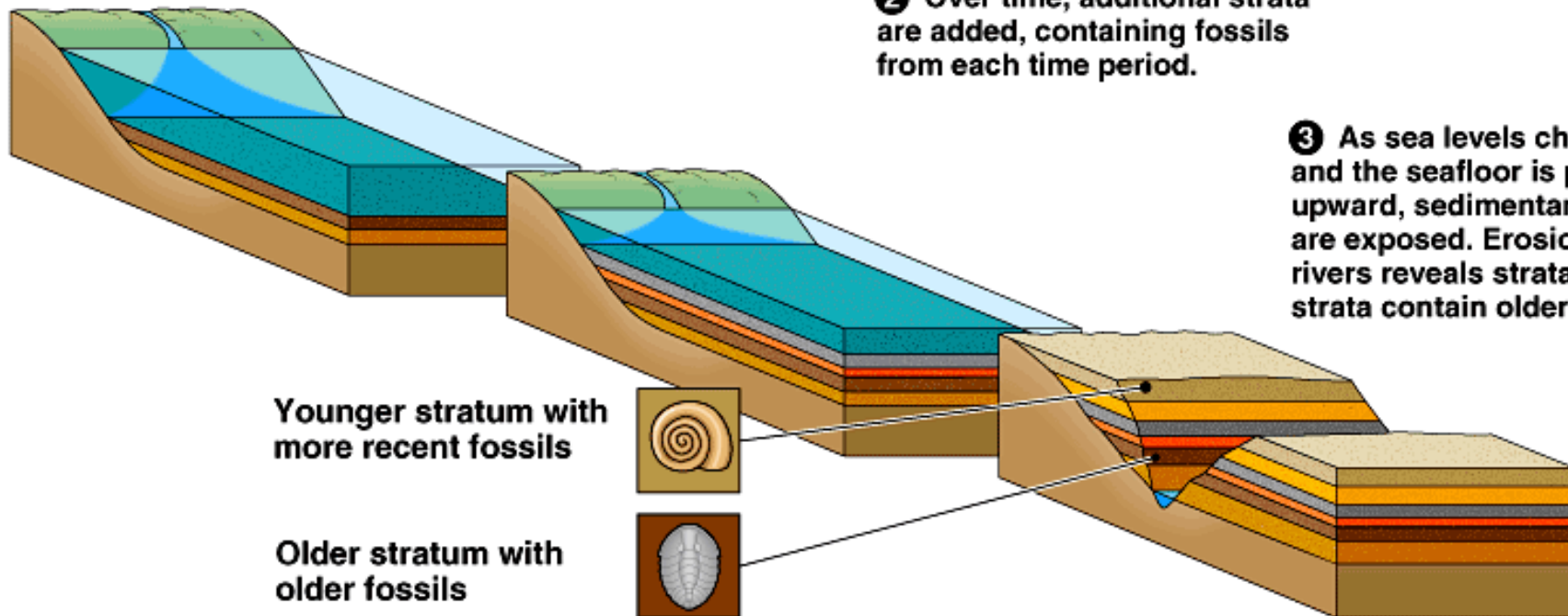


Woolly mammoth tusks

① Rivers bring sediment to the ocean. Sedimentary rocks containing fossils form on the ocean floor.

② Over time, additional strata are added, containing fossils from each time period.

③ As sea levels change and the seafloor is pushed upward, sedimentary rocks are exposed. Erosion by rivers reveals strata; older strata contain older fossils.



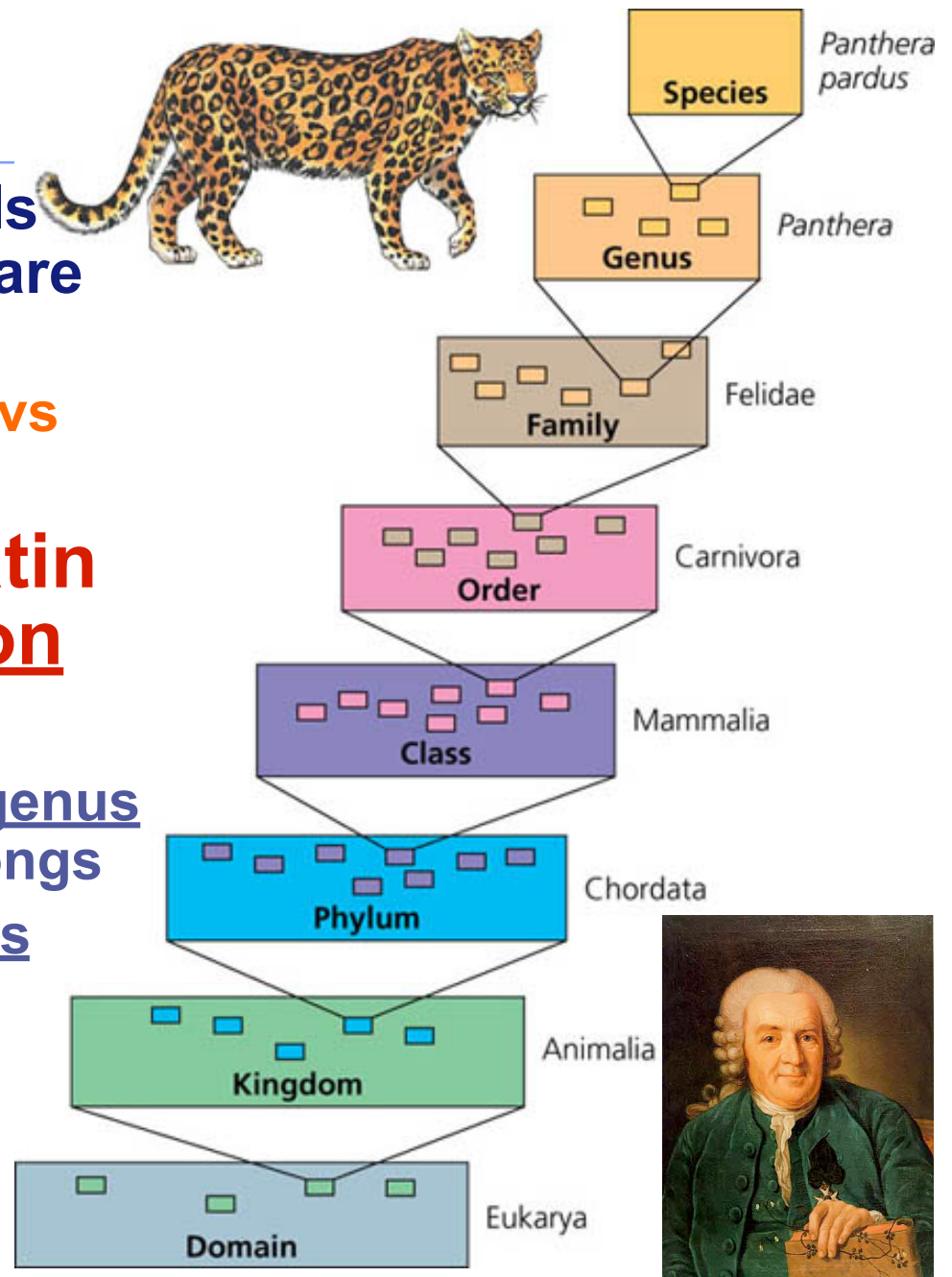
Fossils - may include the entire organism including soft tissue left overs, bones, mineralized tissues, or impressions/molds left behind by the body of the organisms



Systematics

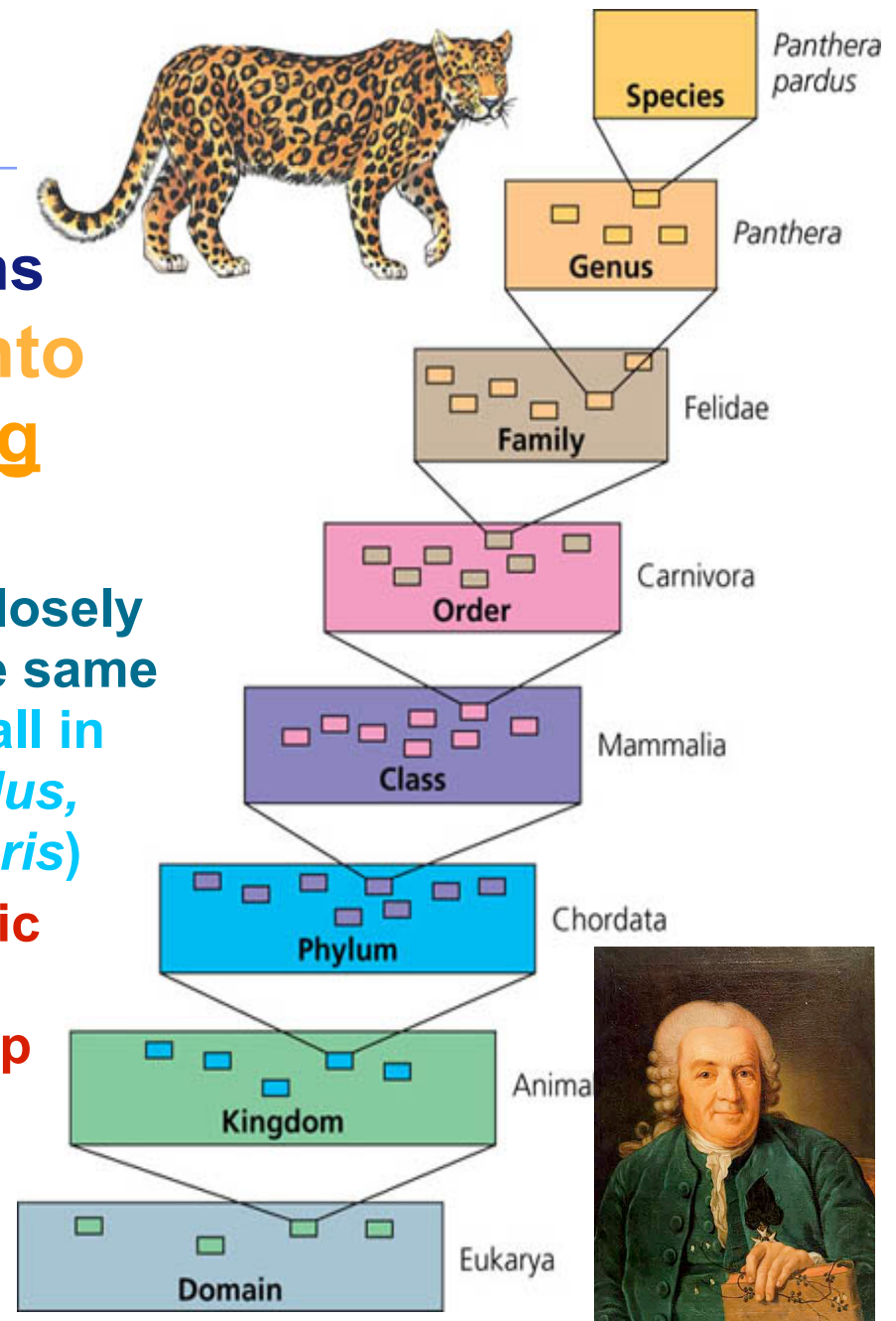
- classifying organisms

- Common names of animals can cause confusion and are ambiguous
 - ◆ i.e. monkey or jelly“fish” vs cray“fish”
- **Scientists use the Latin binomial classification system**
 - ◆ First part is the name of genus to which the species belongs
 - ◆ Second part is the species name
 - First letter of genus is capitalized
 - Entire binomial name is italicized



Systematics

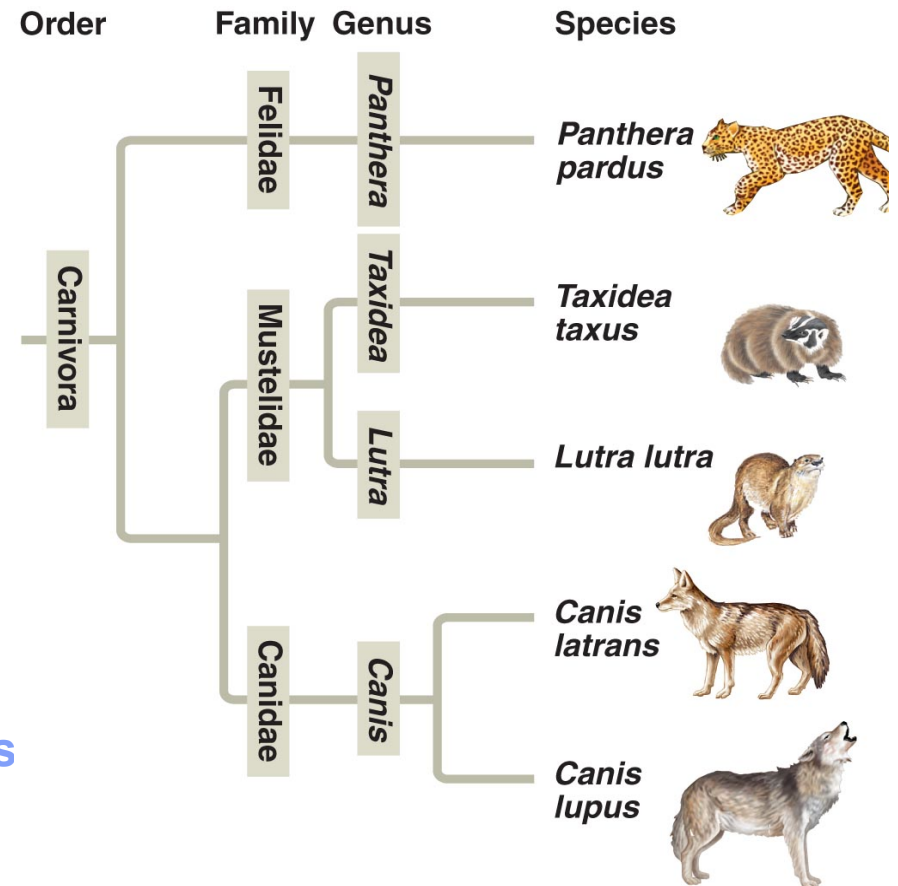
- Linnaeus came up with a system for naming organisms
 - ◆ He grouped species into hierarchy of increasing inclusive categories
 - Species that appear to be closely related are grouped into the same genus (jaguar, tiger, & lion all in same genus: *Panthera pardus*, *Panthera leo* & *Panthera tigris*)
 - Being in the same taxonomic unit does not tell you about the evolutionary relationship between the members of one grouping (ex: all the species in genus *Panthera*)



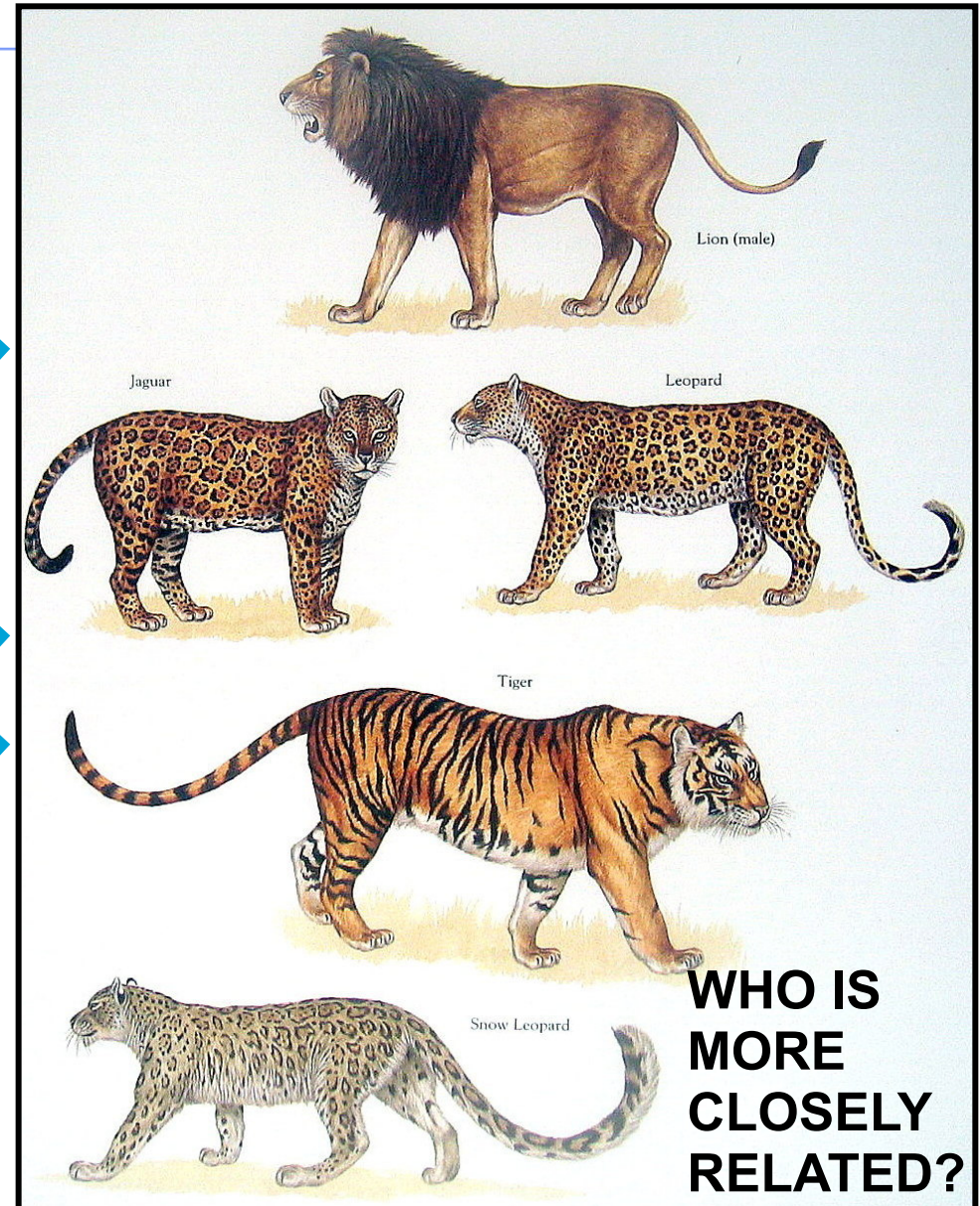
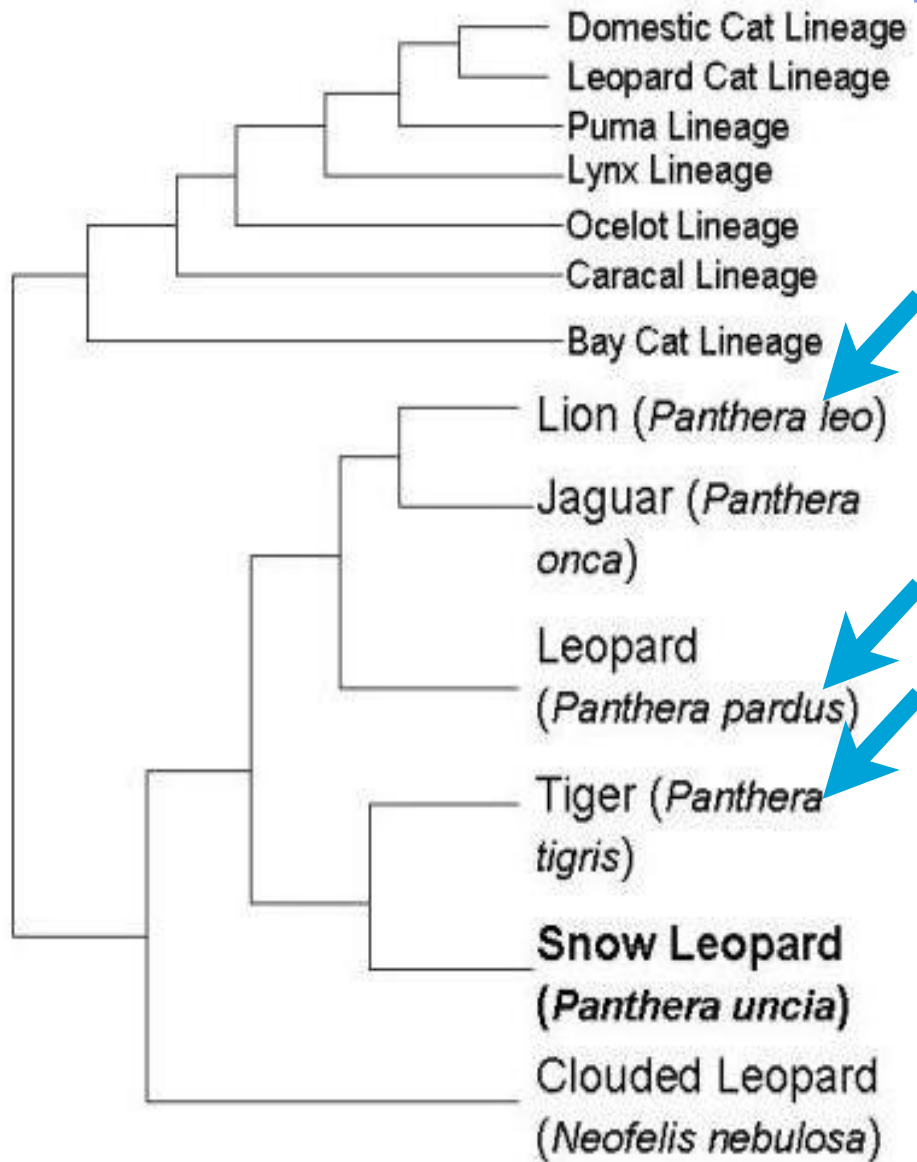
Looking for evolutionary relationships

- Organisms who share a close relative are more likely to share many genes, DNA sequences, metabolic pathways, embryological development patterns, and structural proteins

- ◆ The evolutionary history of a group of organisms can be represented in a branching diagram called a phylogenetic (evolutionary) tree.
 - This represents a hypothesis about evolutionary relationships



Phylogeny for *Panthera tigris*, *leo*, *pardus*

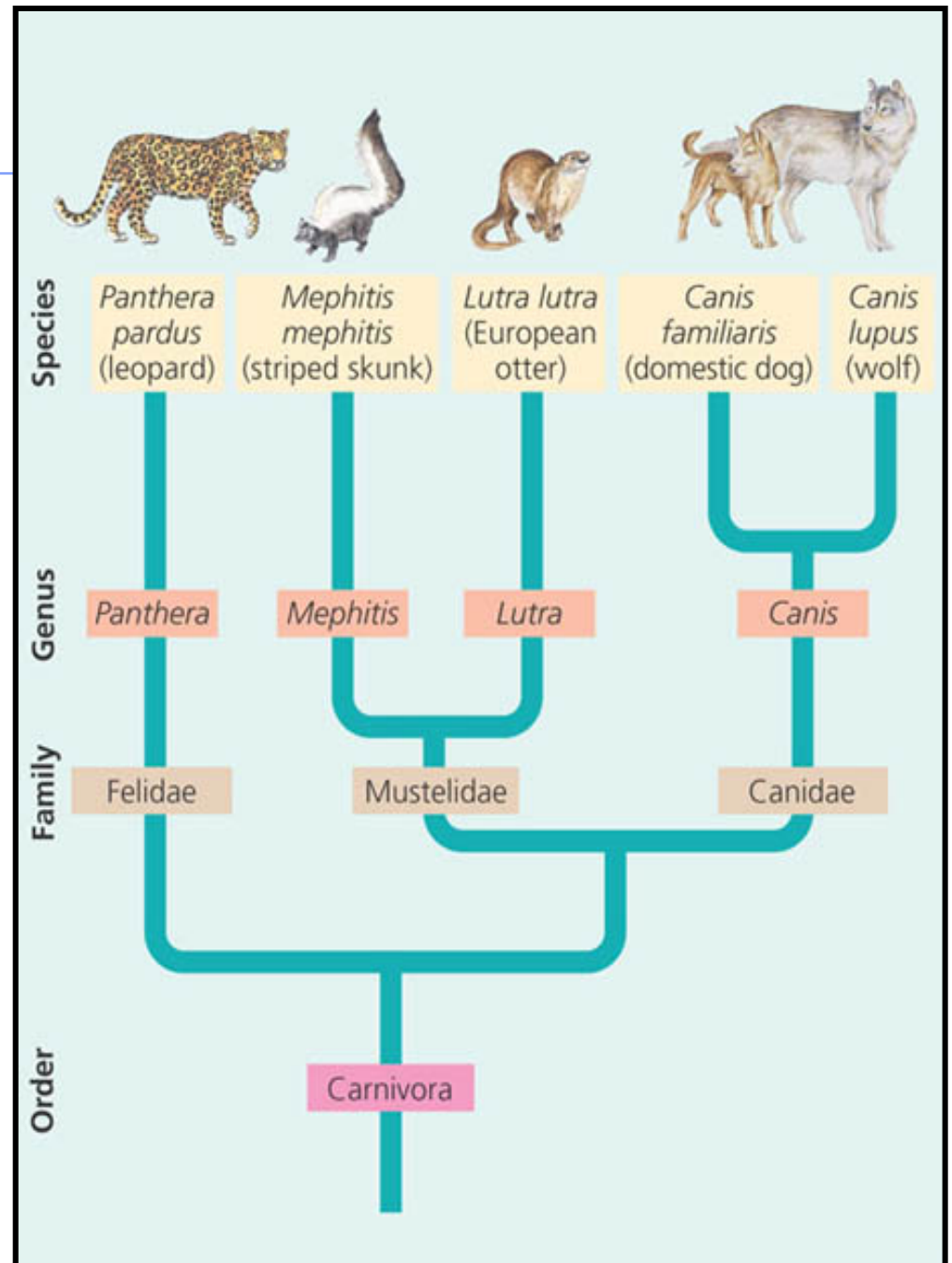


Building trees

- Ideally, there is a relationship between the classification into groups (*Linnean Classification System*) and the organisms phylogeny (*Evolutionary Relationships shown in a Tree*)

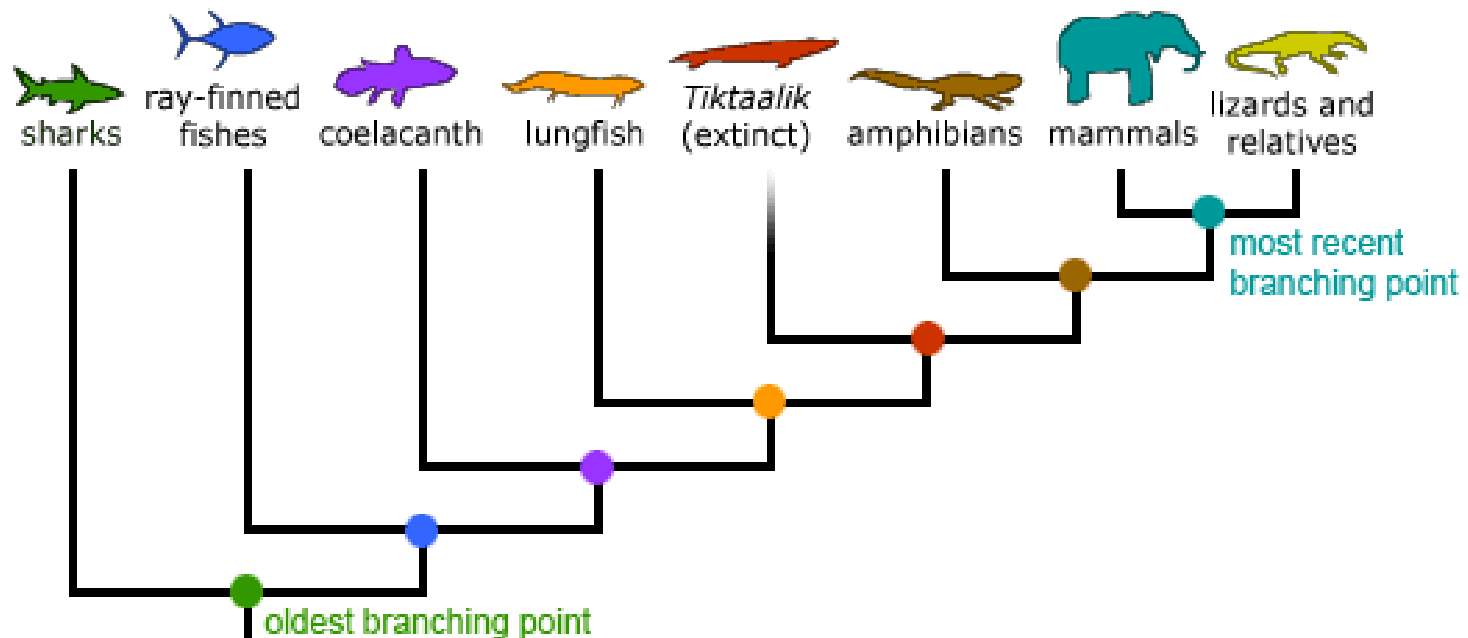
- ◆ If a mistake is noticed and the organism has been placed in a group to which it is not most closely related, the organisms may be reclassified and placed into a different genus or family etc..to more accurately reflects its evolutionary history.

- This may mean having to revisit the scientific name of the organism



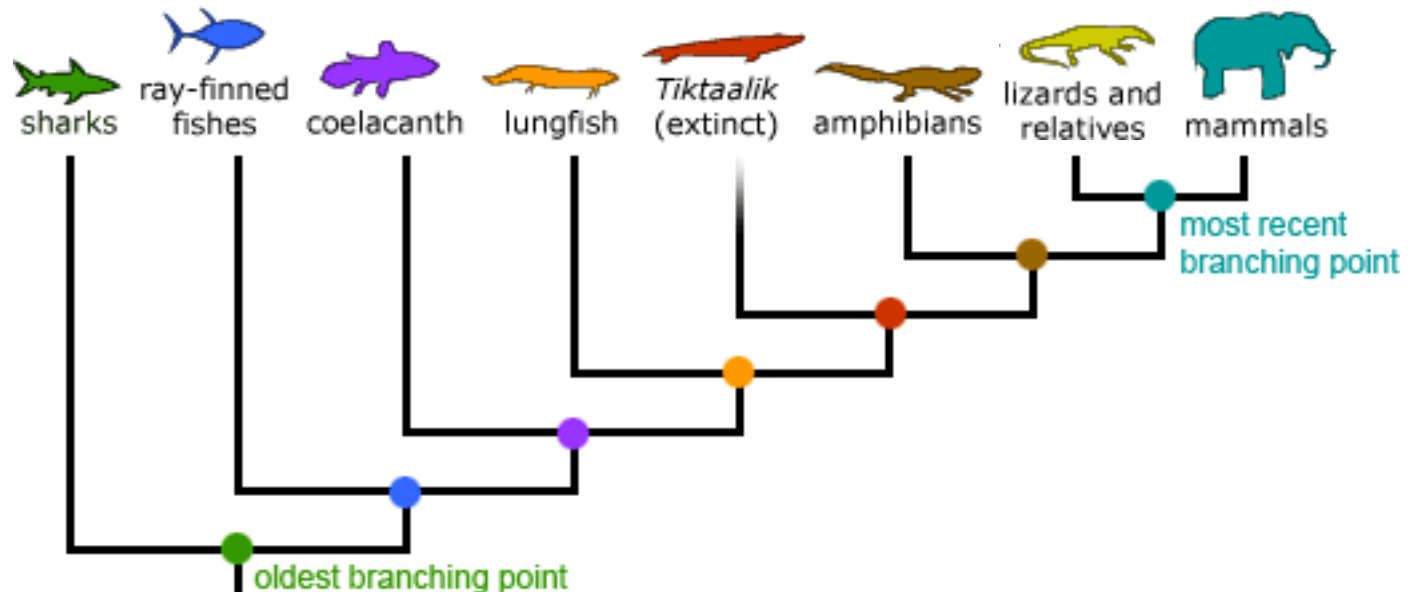
Building trees

- In a phylogenetic tree, a series of dichotomies or two way branch points are found.
 - ◆ Each **branch point** or **NODE** represents the divergence of two evolutionary lineages from a common ancestor.
 - A taxonomic unit is called a **taxon** or (taxa, plural)
 - ◆ In the example below, sharks, lungfish and mammals (each made of multiple species) are all different taxa
 - **Sister taxa share an immediate common ancestor or node**
 - ◆ Mammals and lizards (reptiles) are sister taxa



Building trees

- The turquoise dot is the branch point that represents the most recent common ancestor of mammals and reptiles (lizards etc).
- The brown dot represents the most recent common ancestor of all amphibians, mammal, and reptiles
 - ◆ **Note:** tree branches can be rotated around a branch point without changing their evolutionary relationship!!!

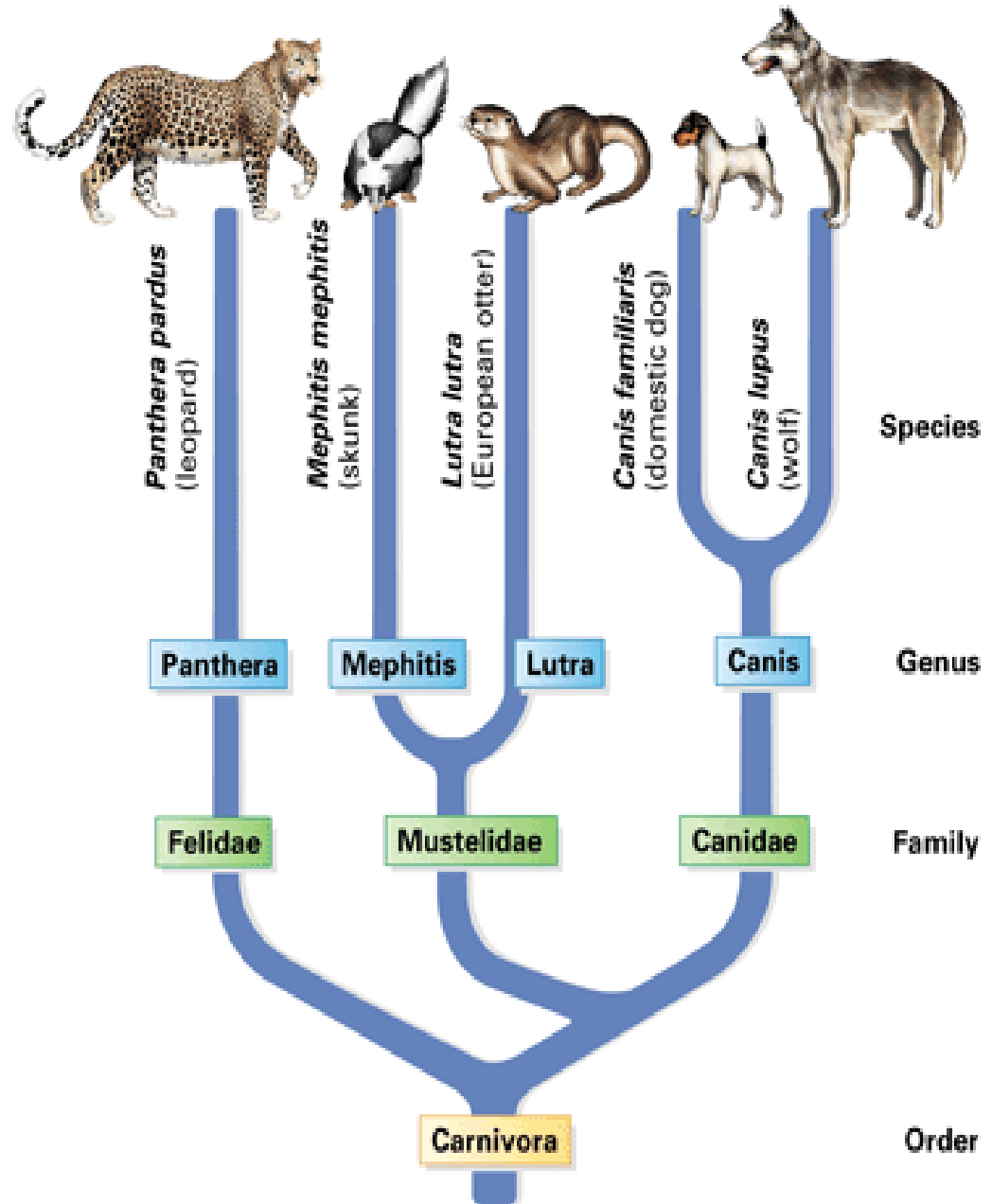


Building trees

Tracing possible evolutionary relationships between some of the taxa of the order Carnivora, a branch of the class Mammalia.

The skunk & otter are sister taxa and therefore each other's closest relatives.

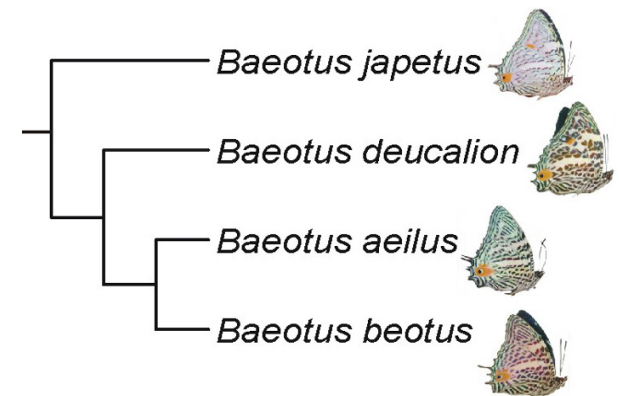
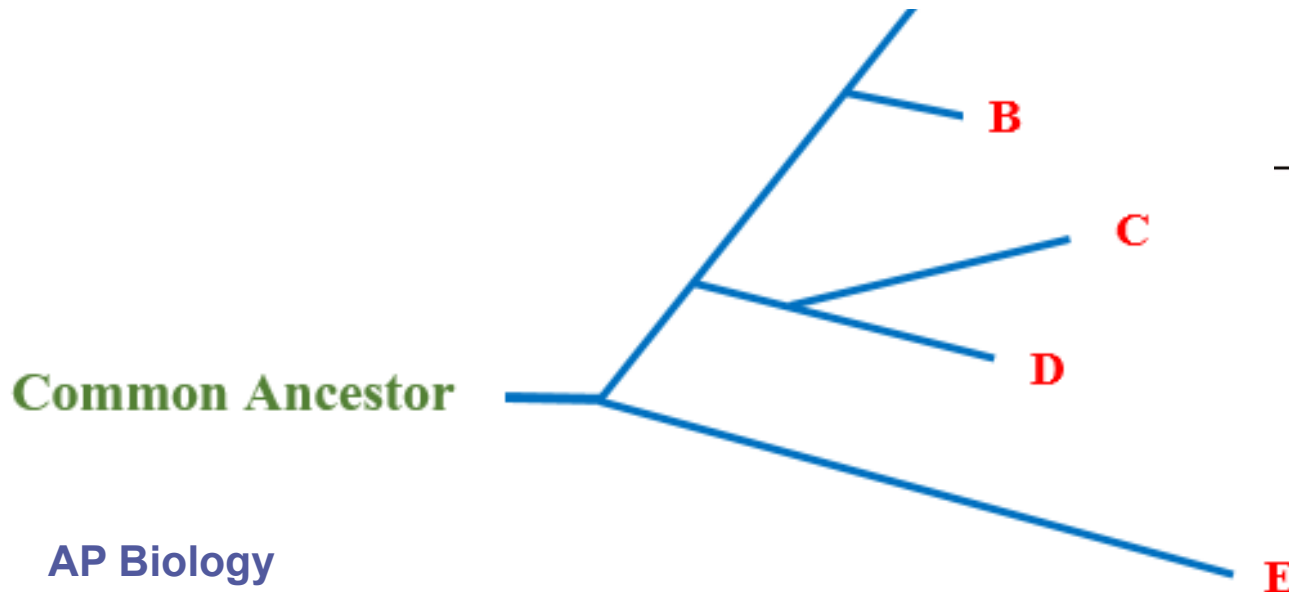
This tree is rooted: the lowest branch point represents the common ancestor of all taxa in this entire tree.



Rooted vs. Unrooted Trees

Rooted tree shows the most basal ancestor of the tree while **unrooted phylogenetic tree** does not show an ancestral root.

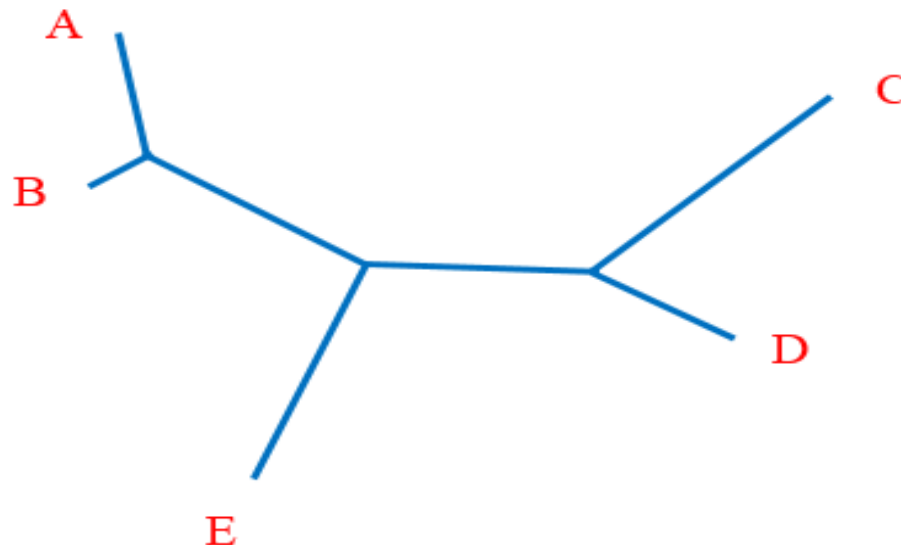
- A rooted phylogenetic tree serves as a useful diagram which shows the **evolutionary history**.
 - It has a basal node which is called the root, representing the common ancestor of all the groups of the tree.
 - The root of a tree is considered as the oldest point in the tree which represents the **last common ancestor** of all groups included in the tree.
 - A rooted tree shows the direction of evolutionary time.



Rooted vs. Unrooted Trees

Unrooted tree is a phylogenetic diagram which lacks a common ancestor or a basal node.

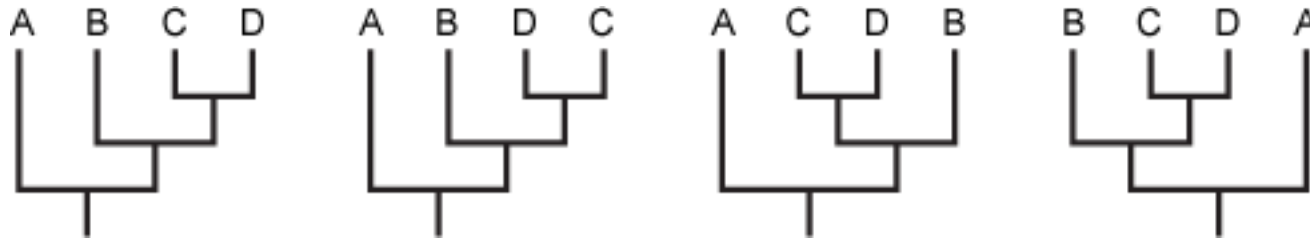
- This tree does not indicate the origin of evolution of the groups, depicting only the relationship between organisms irrespective of the direction of the evolutionary time line.
 - This tree has no basal node or root representing the common ancestor of all the groups in the tree.
 - It is difficult to study the evolutionary relationships of the groups with respect to time
 - Does not specify an evolutionary relationship between organisms



To extant species did not evolve from each other

- Are all these phylogenies the same?

YES

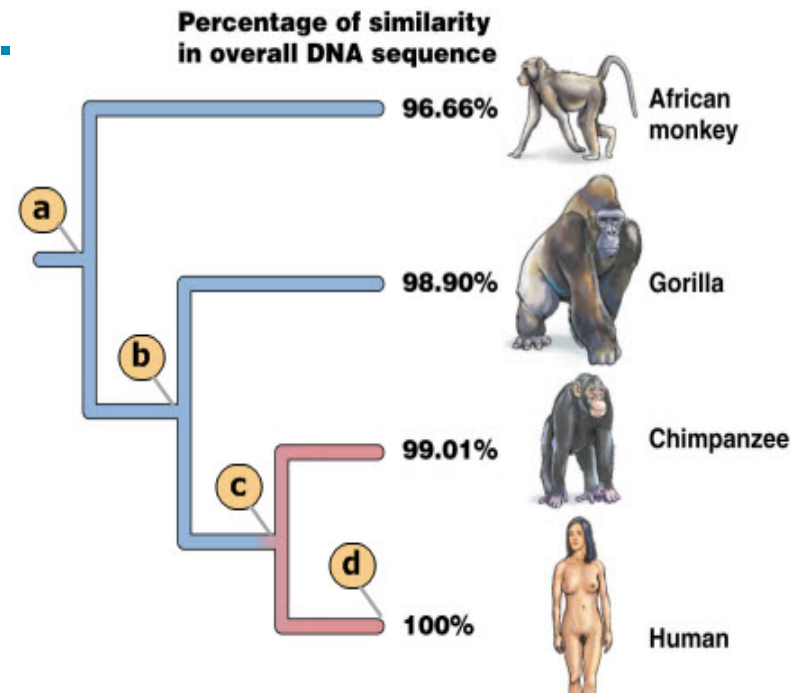


- One **CANNOT** assume that a taxon on a phylogenetic tree evolved from the taxon next to it.

- ◆ C did not evolve from D... (or B or A for that matter).

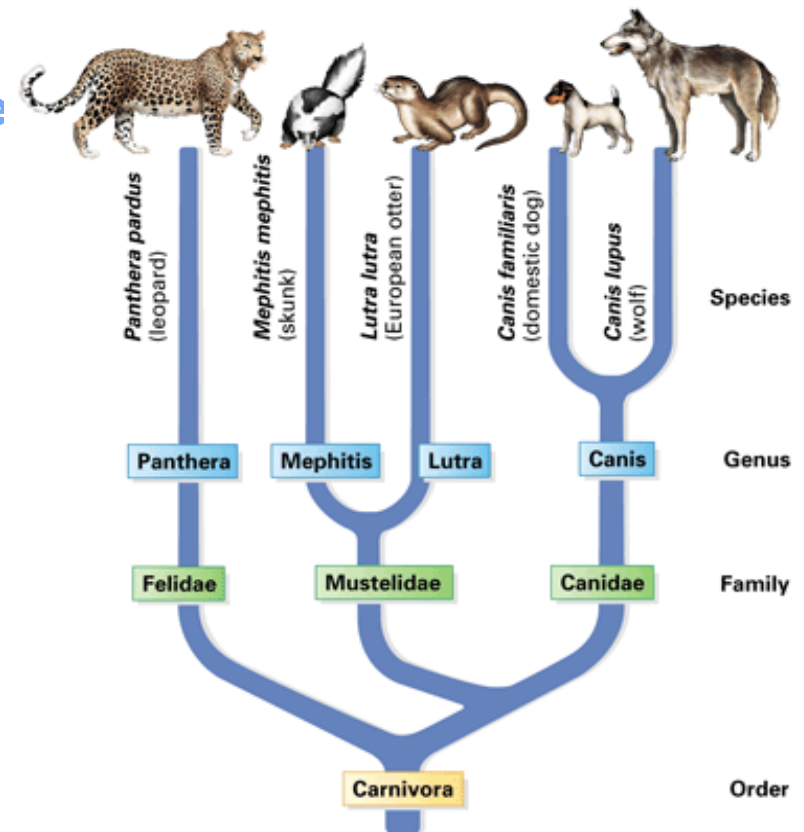
- **BOTH evolved from a Common Ancestor.**

- Human did not evolve from modern day chimps



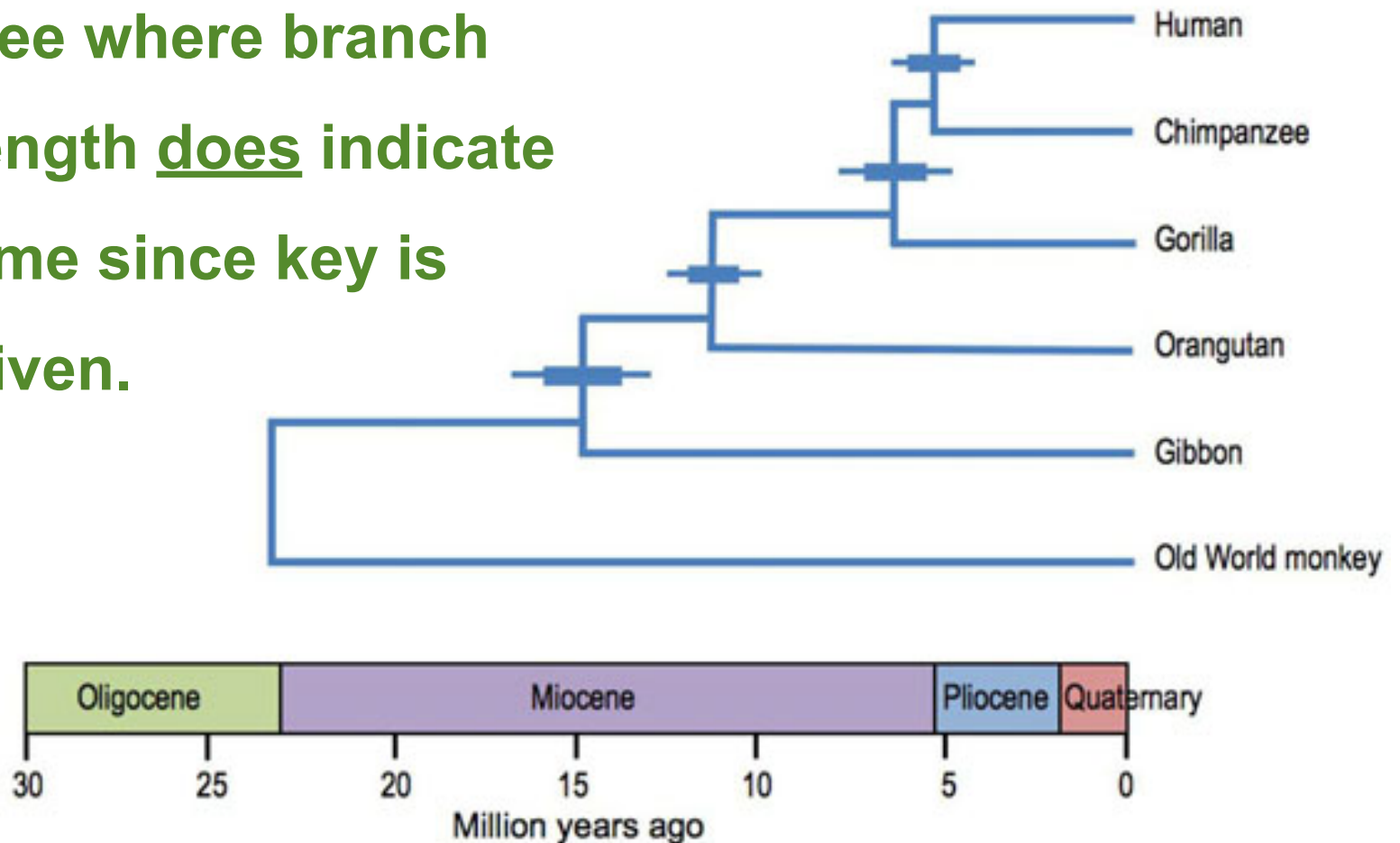
Branch length may or may not indicate the amount of time that has passed

- Unless a tree has dates, one cannot assume that the position of a branch point indicates the time of speciation.
 - ◆ Ex: Here, one cannot assume the skunk evolved prior to wolf.
 - All we can say is that the most recent common ancestor of the wolf and otter lived before the most recent common ancestor the work and coyote
- Don't assume branch length is proportional to time or amount of genetic change this info is given

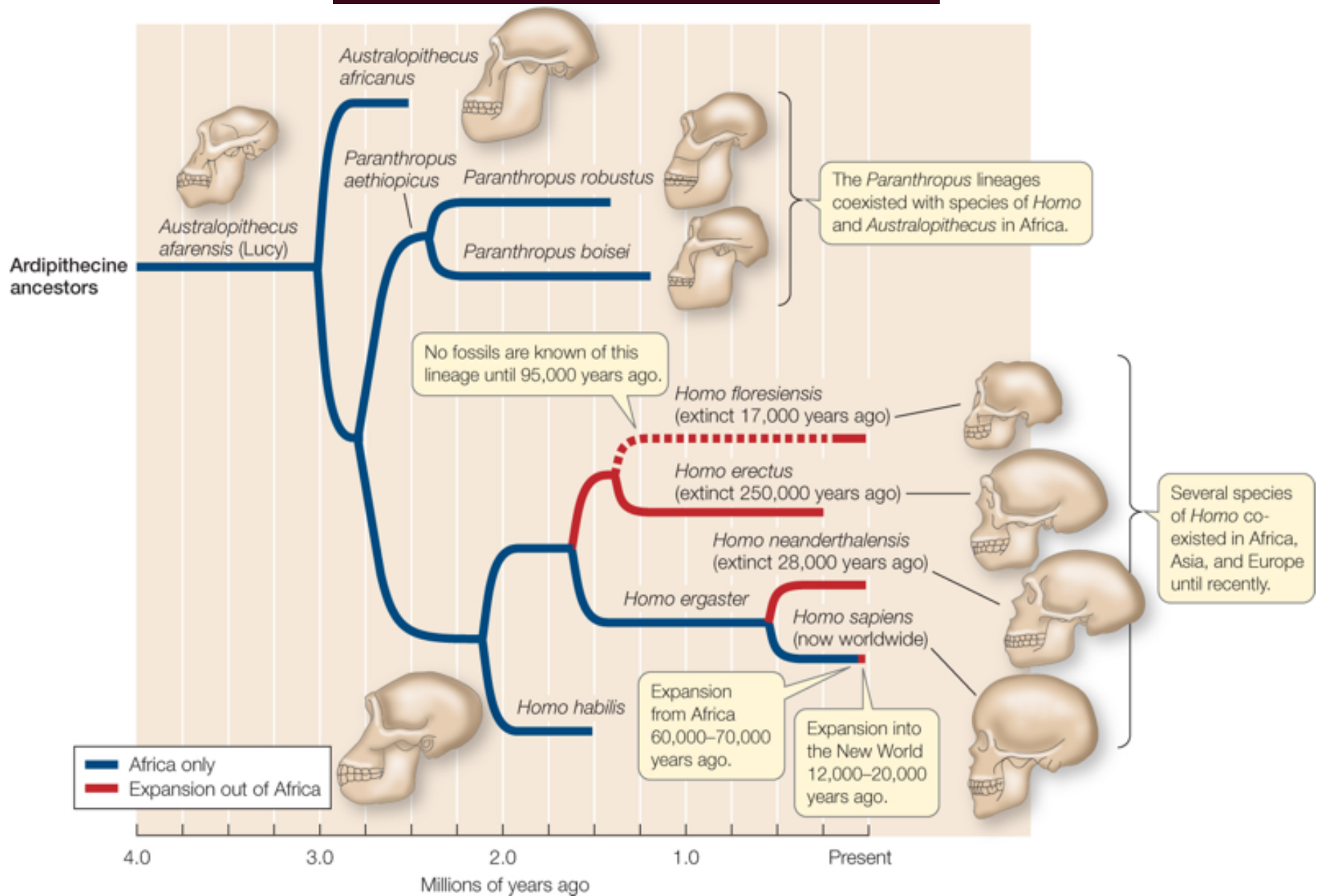


Additional Information can be given...

Here's a phylogenetic tree where branch length does indicate time since key is given.

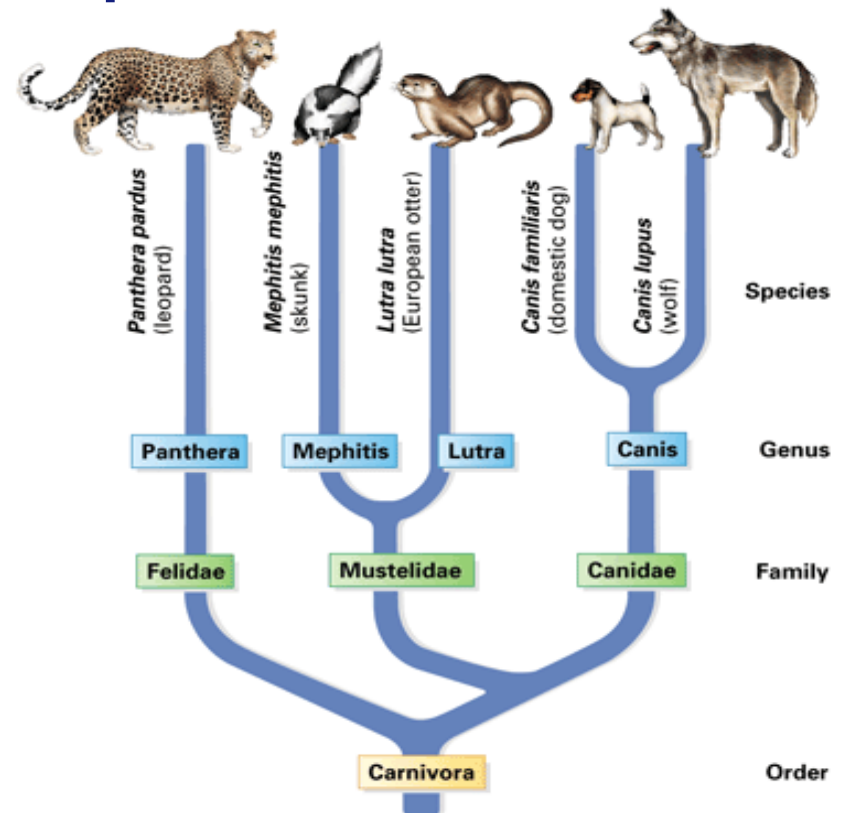


Hominid Evolution



Building trees

- To build a phylogenetic tree, information must be obtained about any kind of feature such as morphology, behavior, genes/DNA sequences, protein amino acid sequences, or biochemistry.
 - ◆ You must focus on features that results from common ancestry to reflect evolutionary relationships.



Beware when building trees...

- To build a tree one can use morphological & molecular homologies

- ◆ group based on similarities based on shared ancestries

- bone structure
- DNA or amino acid sequences

- ◆ beware of analogous structures though!!!
(aka homoplasies)

- These are due to convergent evolution rather than shared common ancestry

- ◆ These moles look the same externally, their reproductive systems and internal anatomy are dissimilar. They are not very closely related.



marsupial mole - mammal
(masupials = young complete their embryonic development in a pouch outside the mother)



placental mole - mammal
(eutharians = young complete embryonic development in the uterus within the mothers body)

Beware when building trees...

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marsupial mole - mammal
(masupials = young complete their embryonic development in a pouch outside the mother)

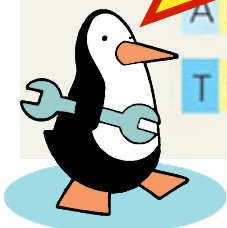


placental mole - mammal
(eutharians = young complete embryonic development in the uterus within the mothers body)

Molecular homologies can provide strong evidence for evolutionary relationships

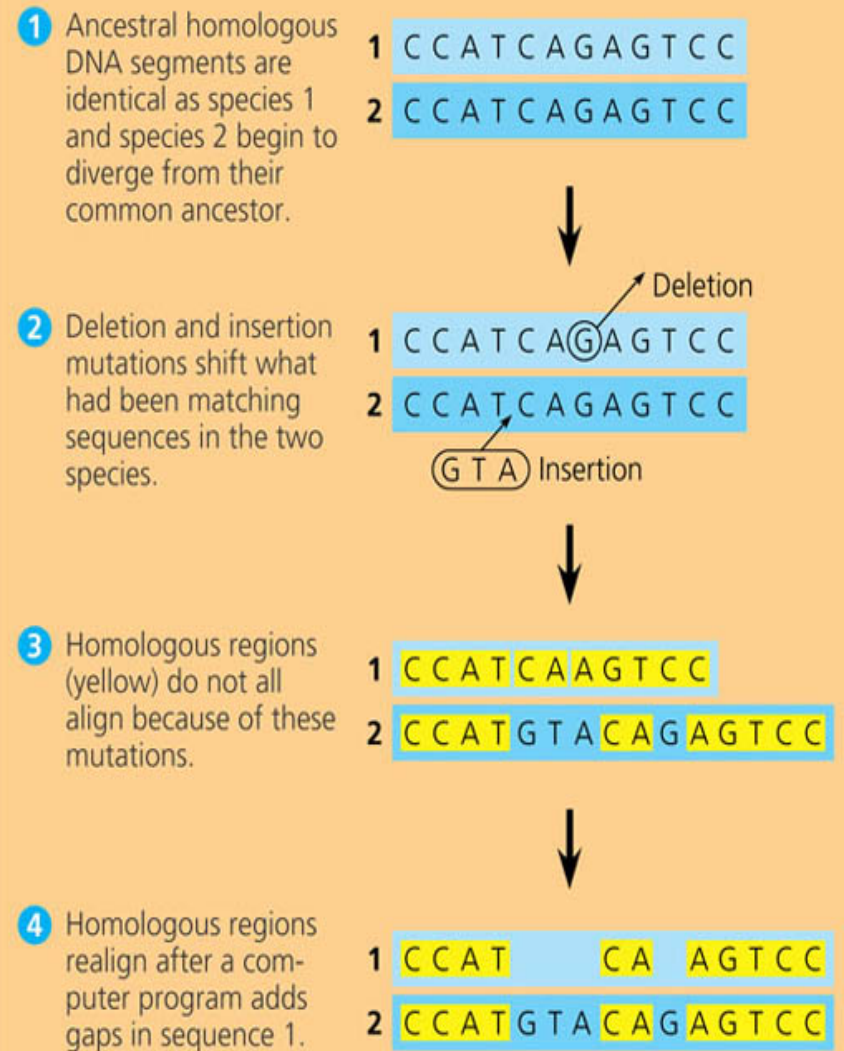
- **To build a phylogeny one can align DNA sequences**
 - ◆ **more bases in common = more closely related**
 - **analyzed by software**

Morphological (anatomical) divergences between related species may be great while their genetic divergence is still small or **VICE VERSA!**



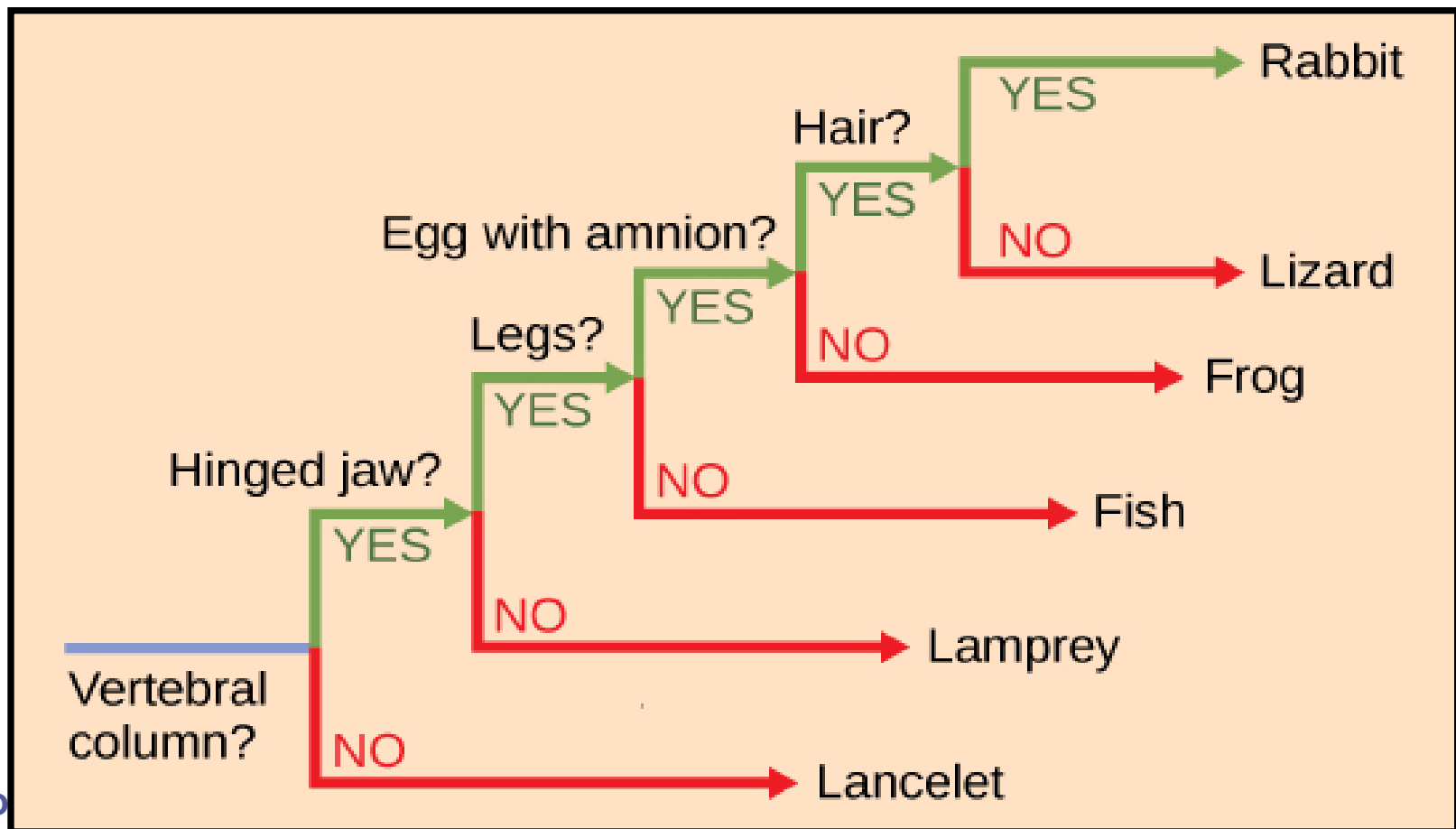
ACGGATAGTCCACTAGGCACTA
TCACCGACAGGTCTTTGACTAG

beware of relying just on morphological homologies



Building trees

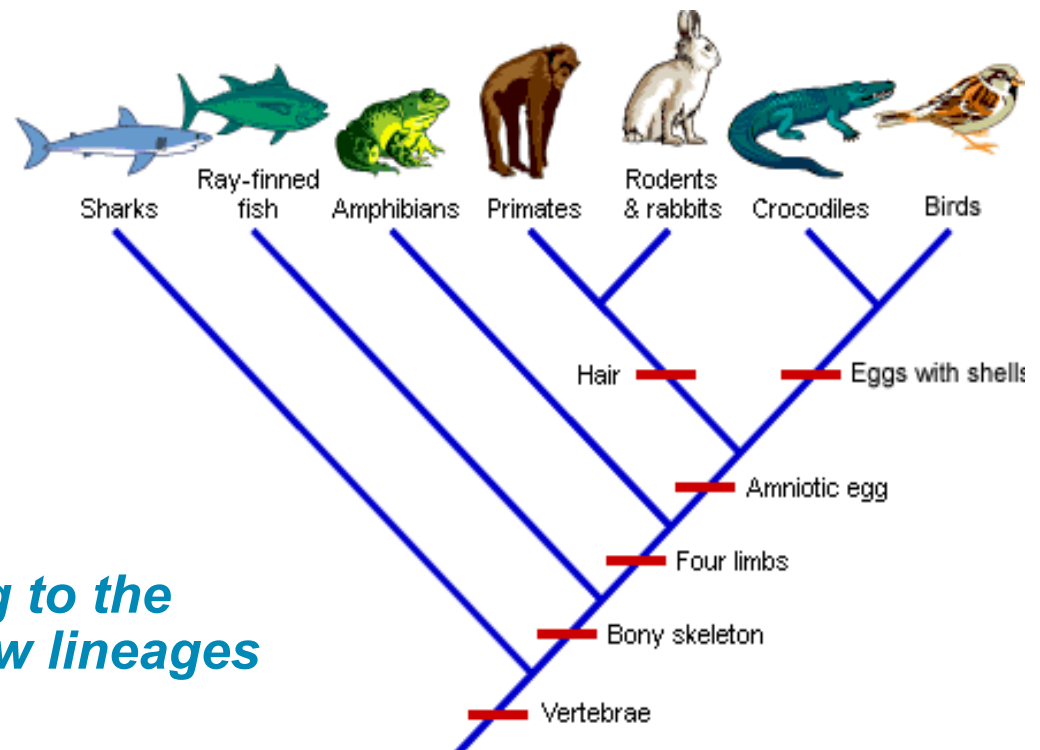
- Descendants of a common ancestor are expected to share certain homologous structures (*including homologous structures known as vestigial structures*)



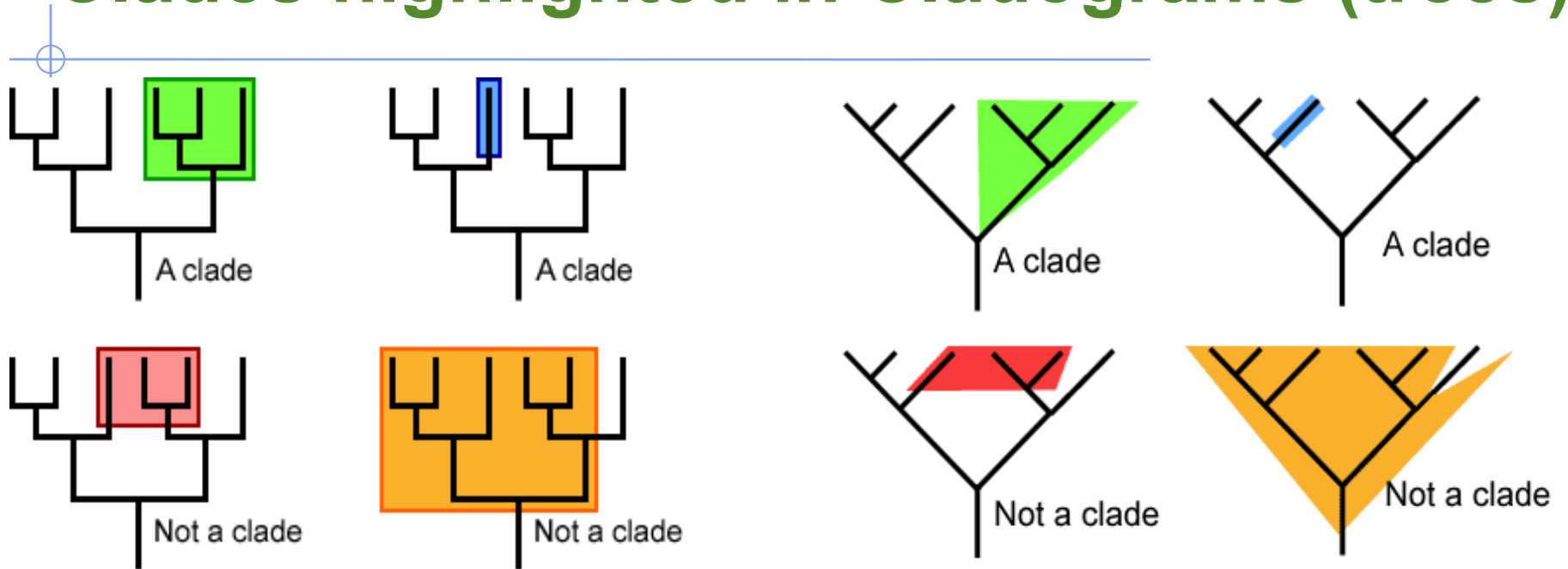
Cladistics

- In the systematic approach known as cladistics, common ancestry (not morphology or other) is the primary criterion used to classify organisms.
 - ◆ Species are placed into groups called clades within a cladogram (tree)
 - A clad includes an ancestral species and all of its descendants
 - ◆ Clades are nested within larger clades

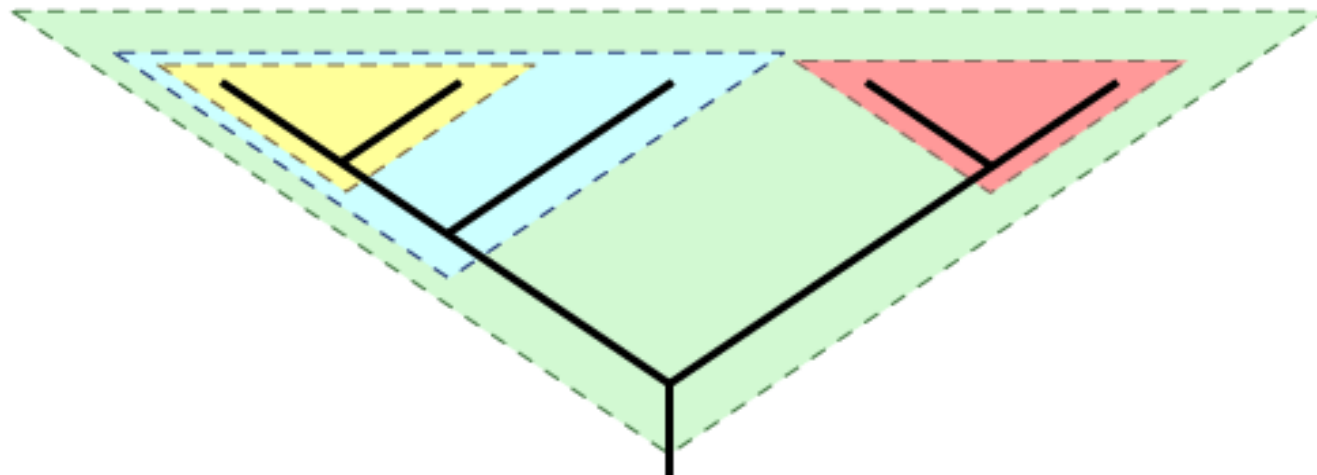
Classifying organisms according to the order in which adaptations in new lineages arise along a phylogenetic tree



Clades highlighted in Cladograms (trees)

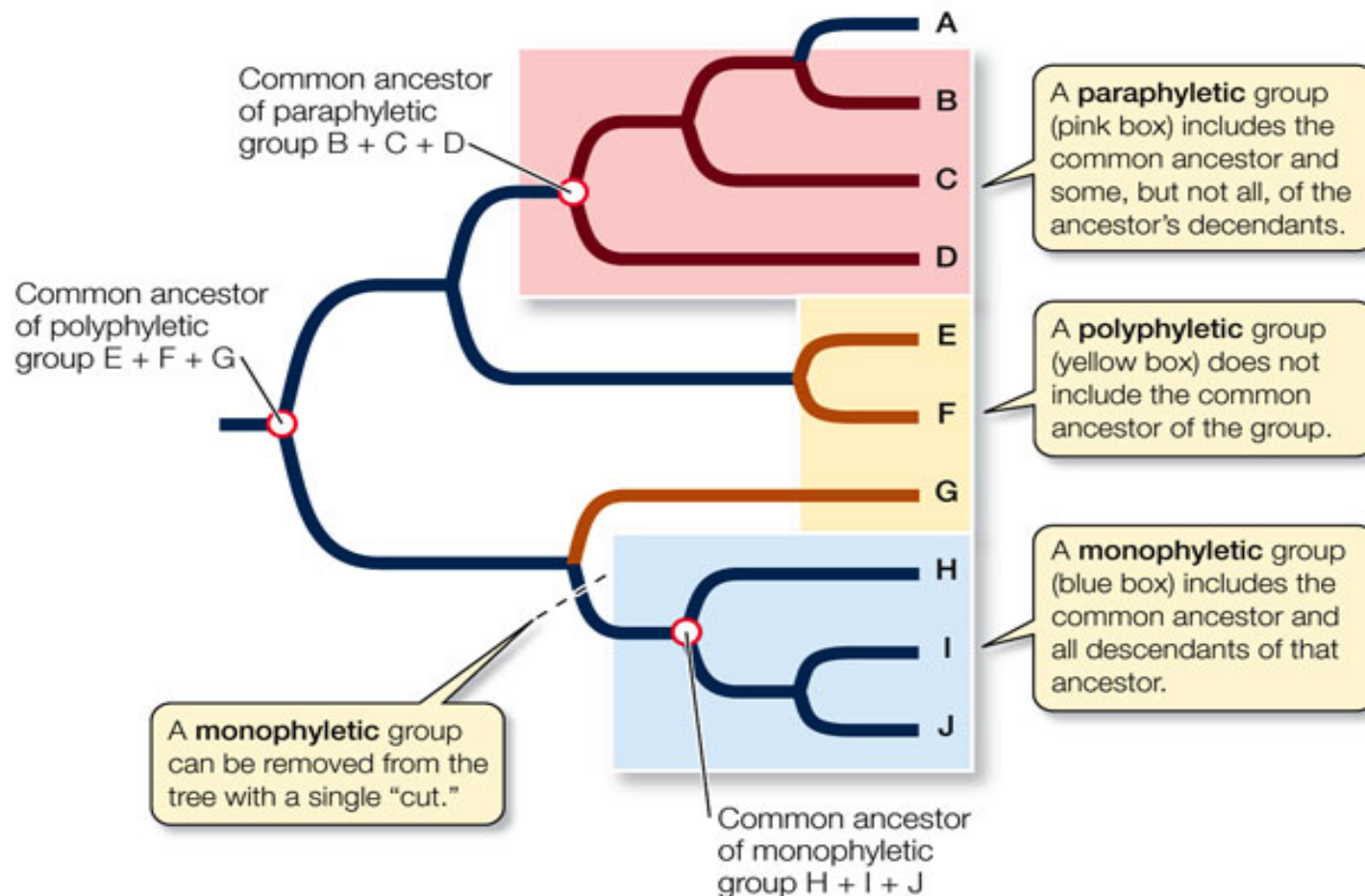


Each of these highlighted areas is a clade:



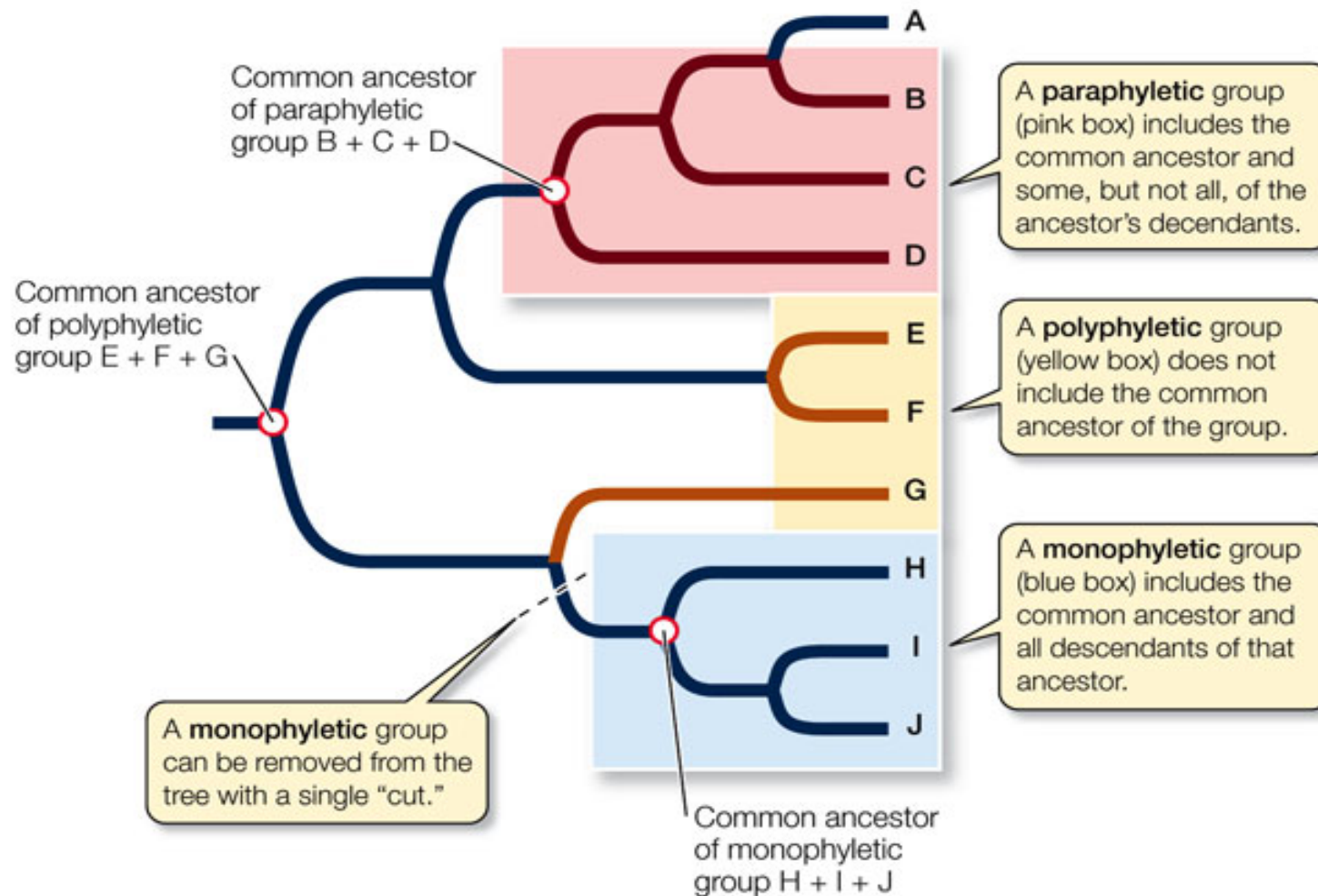
Taxa and other Groups vs Clades

- Taxons from other phylogenetic trees that are not cladograms are only equivalent to a clade if the clade is **monophyletic** (*Greek for “single tribe”*)



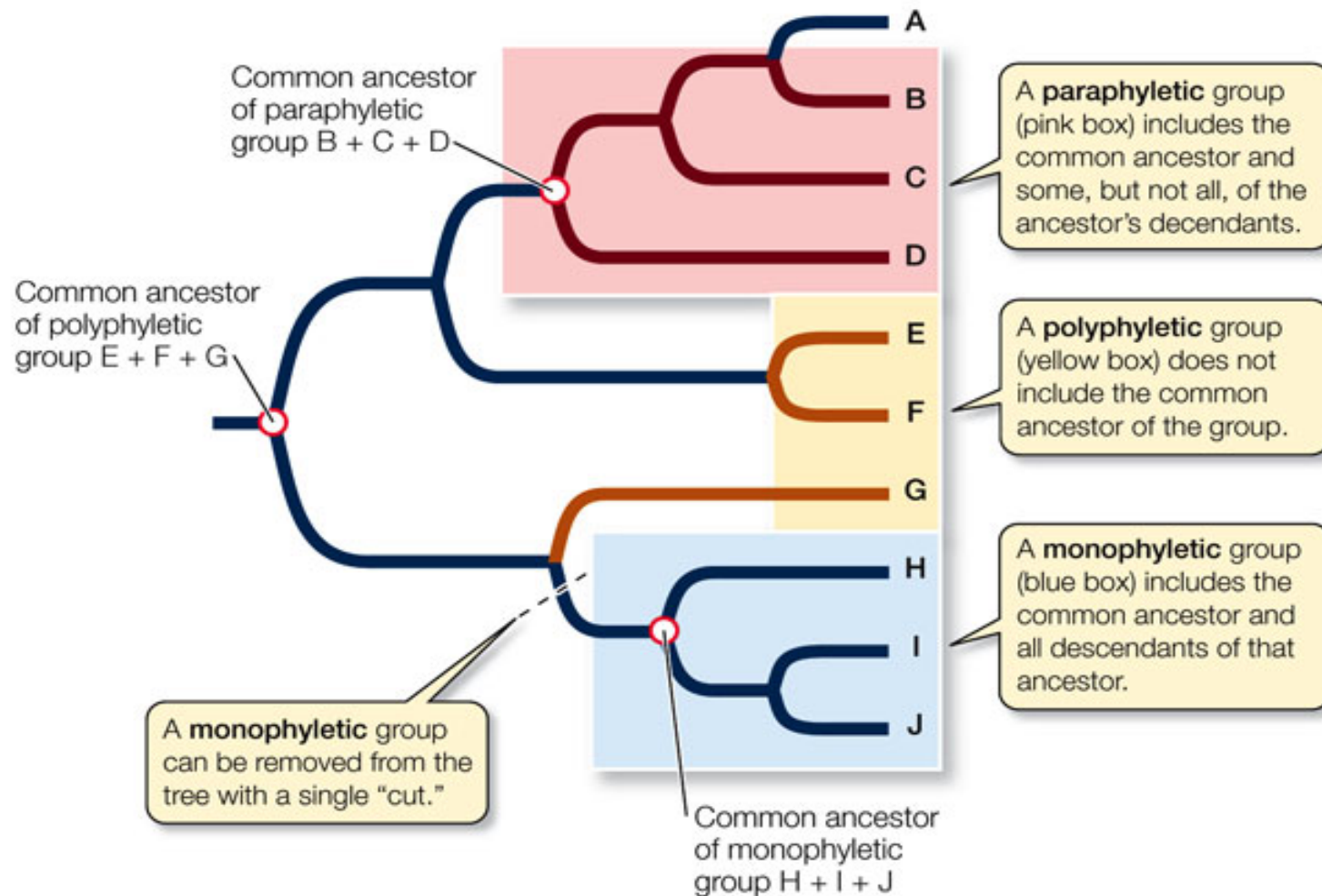
Groups within the Cladogram

- **Paraphyletic** groups consist of an ancestral species and some but not all descendants (*Greek for “beside the tribe”*)



Groups within a Cladogram

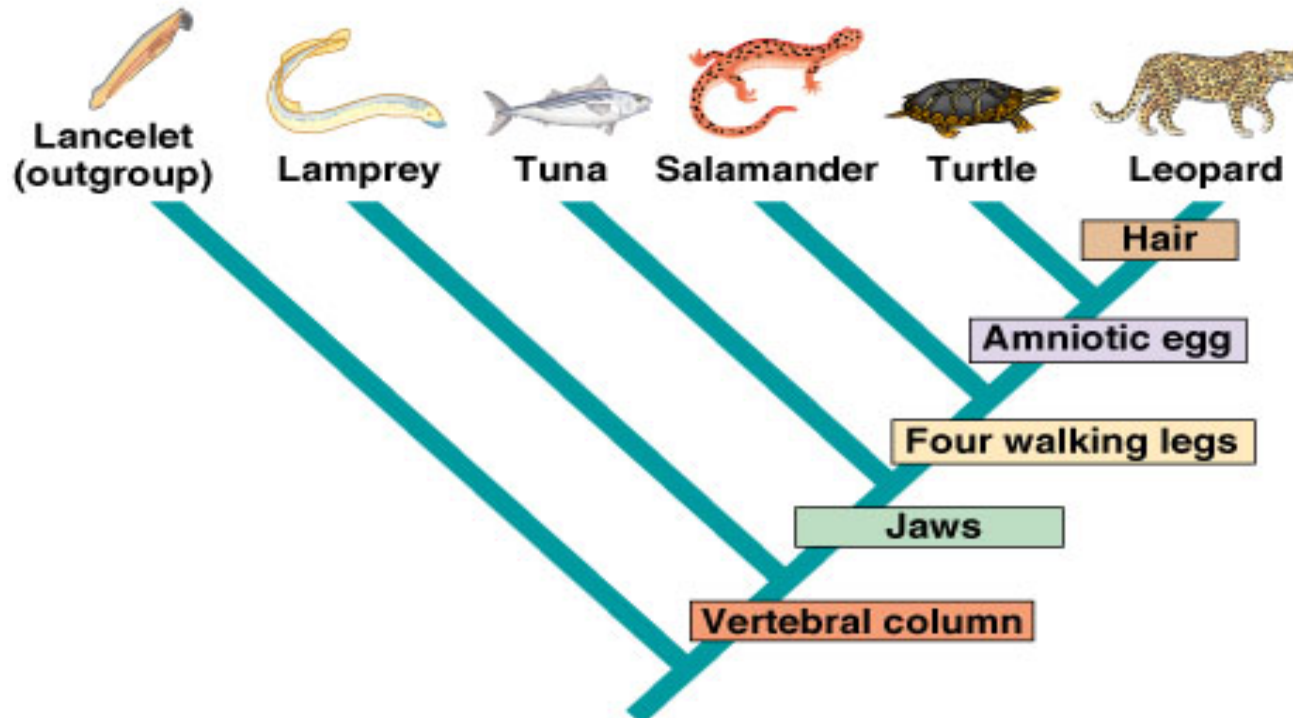
- **Polyphyletic** (*“many tribes”*) groups include taxa with different common ancestors.





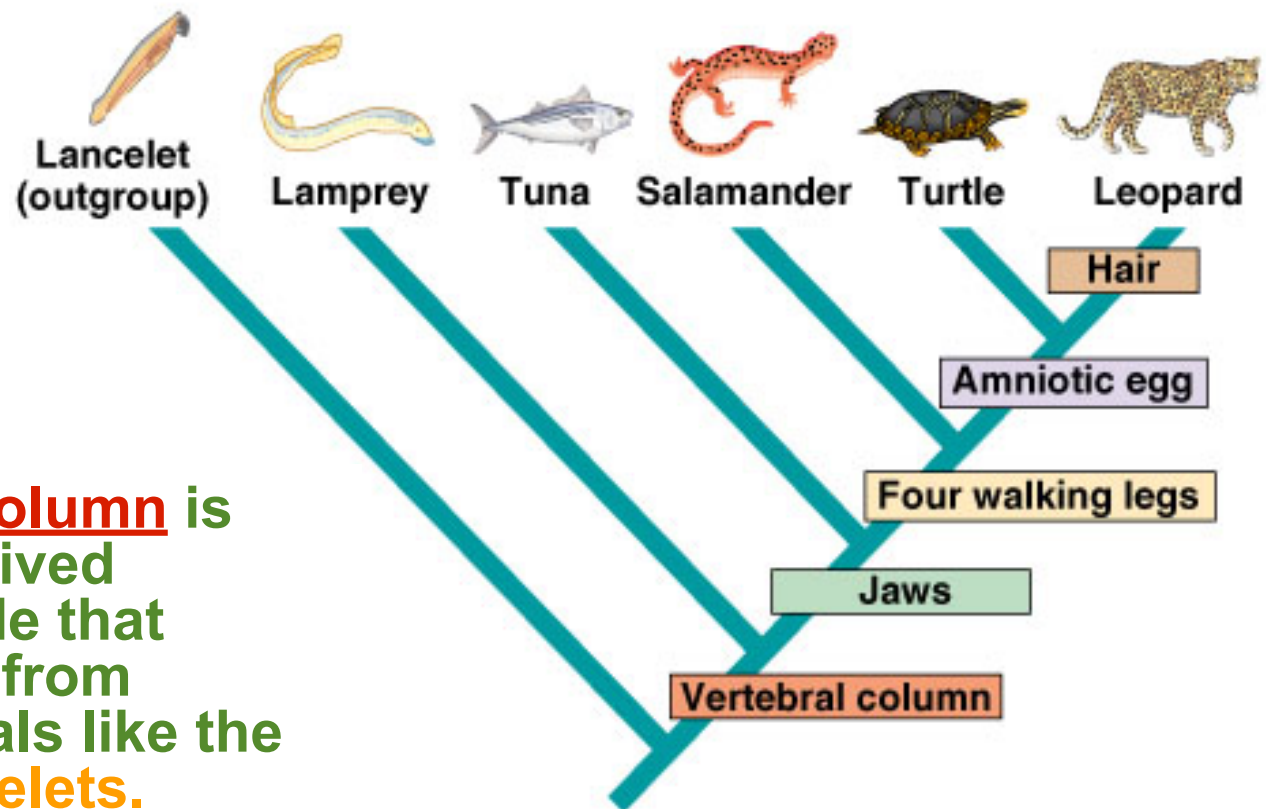
Understanding Cladograms

- Cladograms are **built off inherited homologies**
 - ◆ Cladograms show patterns of shared inherited characteristics
 - **Shared ancestral character** = a character that originated in an ancestor of the taxon
 - ◆ Ex: the backbone is shared by all vertebrates not just mammals.
The backbone is a shared ancestral character of mammals



Understanding Cladograms

- **Shared derived character** = an evolutionary novelty unique to a particular clade
 - ◆ Ex: hair is a characteristic unique to mammals only

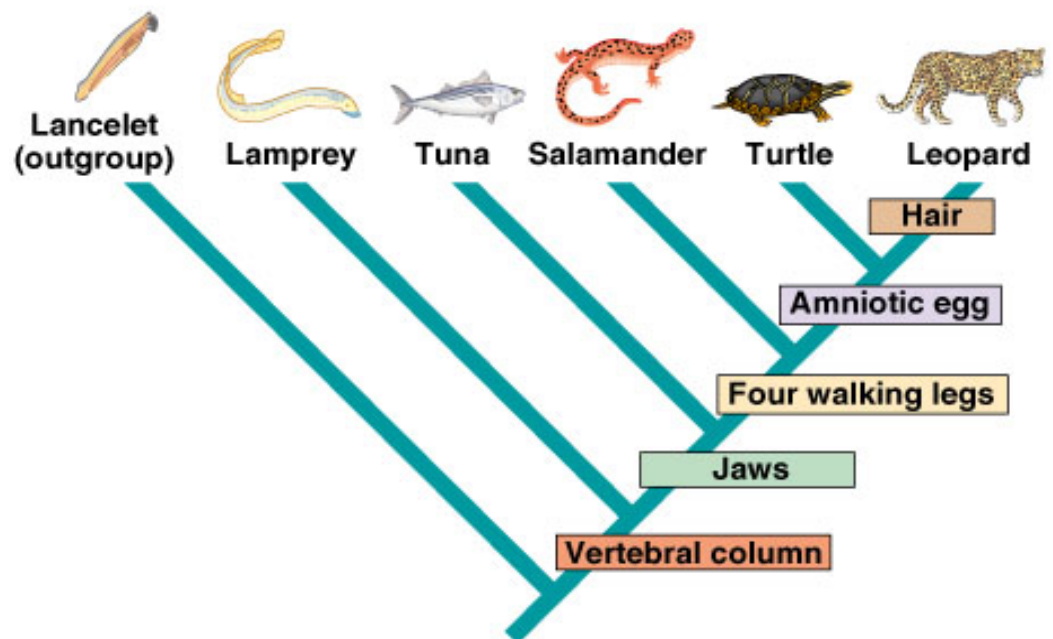
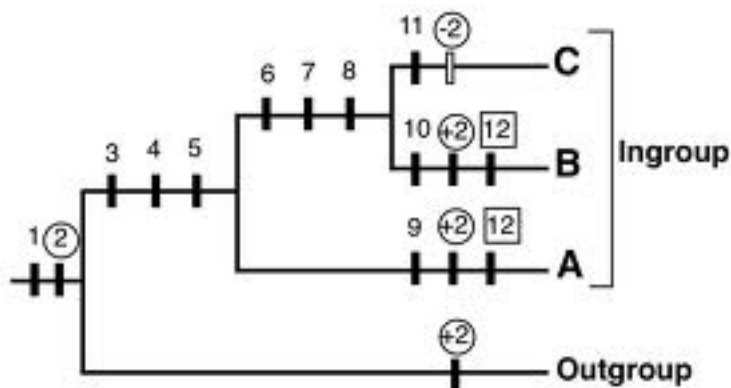


Having a **vertebral column** is though a shared derived character of the clade that includes everything from lamprey's to mammals like the leopard **but not lancelets.**

Understanding Cladograms

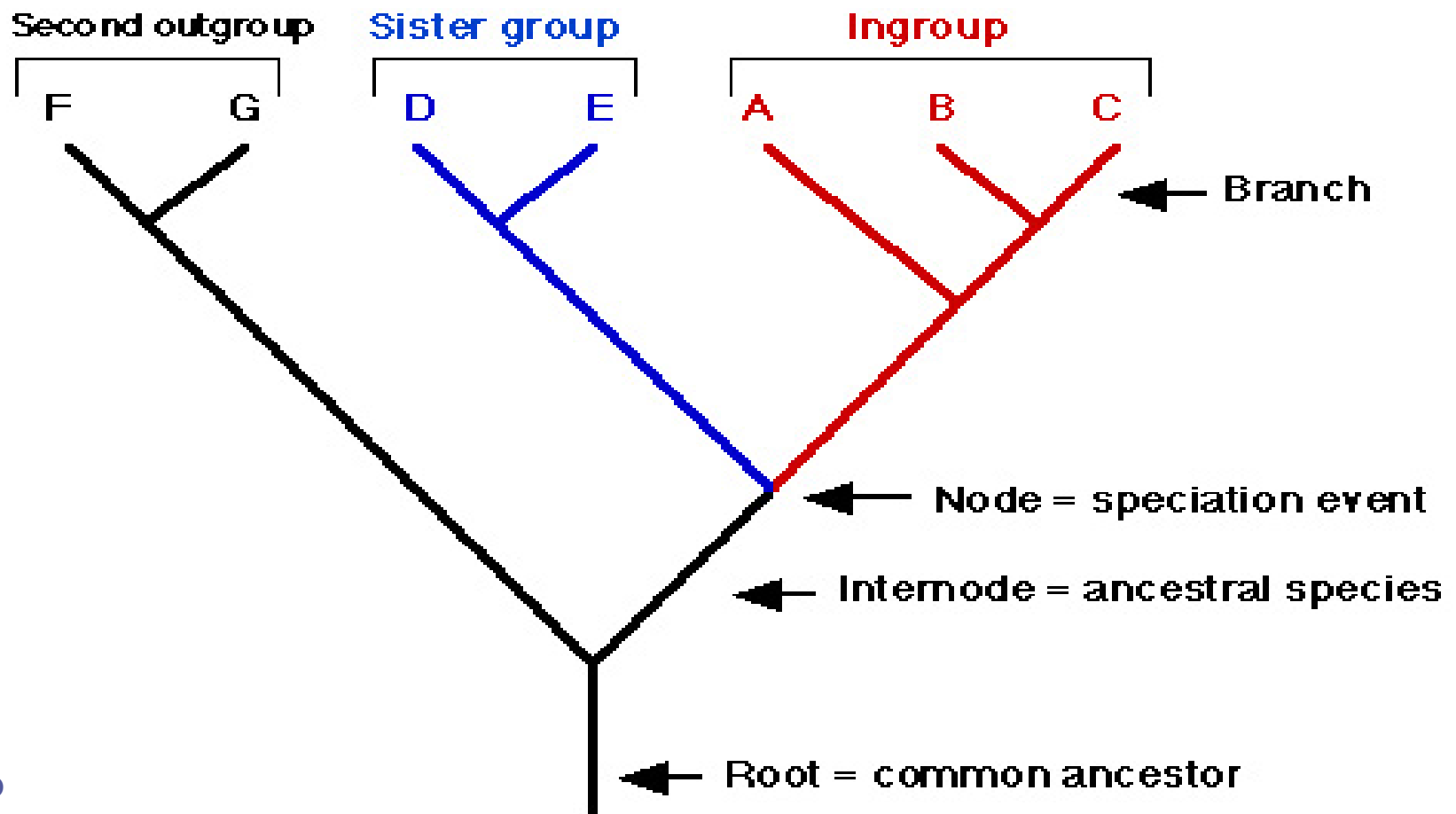
■ Outgroups and Ingroups

- ◆ Ingroup - the species or group species we are studying
- ◆ Outgroup - A species or group of species from an evolutionary lineage that is known to have diverged before the lineage that includes the species we are studying
(i.e. the *ingroup*)
 - With respect to mammals, the turtle is the outgroup and the leopard the ingroup



Summing up the Terms in Trees

- This cladogram has two outgroups (black & blue) and the ingroup in red, which includes the species that share a particular derived characteristic

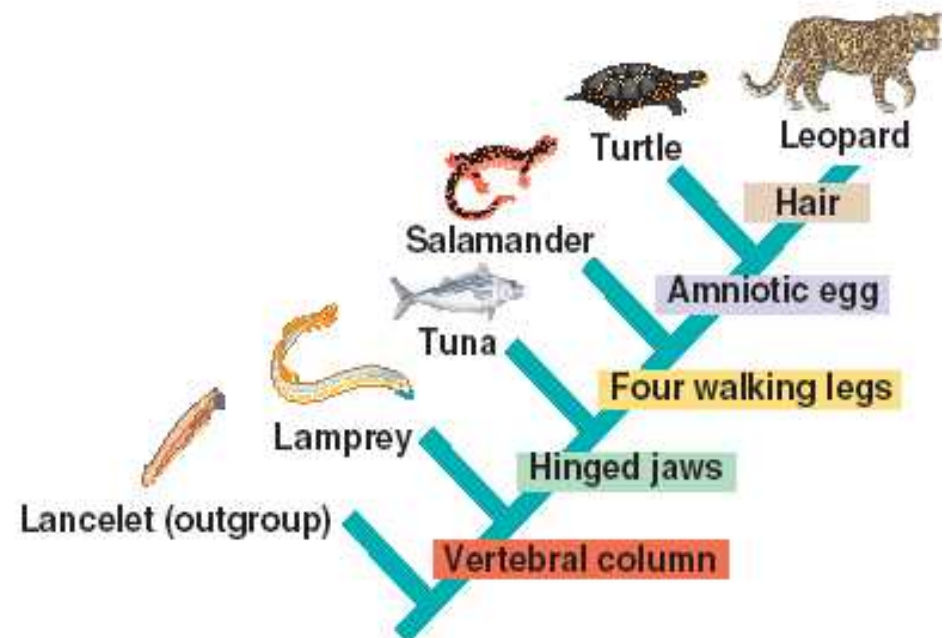


Building Cladograms

- It is useful to build a character table in order to build a cladogram (see below)
 - ◆ Each clade should include all the species that share a particular derived character.

CHARACTERS	TAXA					
	Lancelet (outgroup)	Lamprey	Tuna	Salamander	Turtle	Leopard
Hair	0	0	0	0	0	1
Amniotic (shelled) egg	0	0	0	0	1	1
Four walking legs	0	0	0	1	1	1
Hinged jaws	0	0	1	1	1	1
Vertebral column (backbone)	0	1	1	1	1	1

(a) Character table

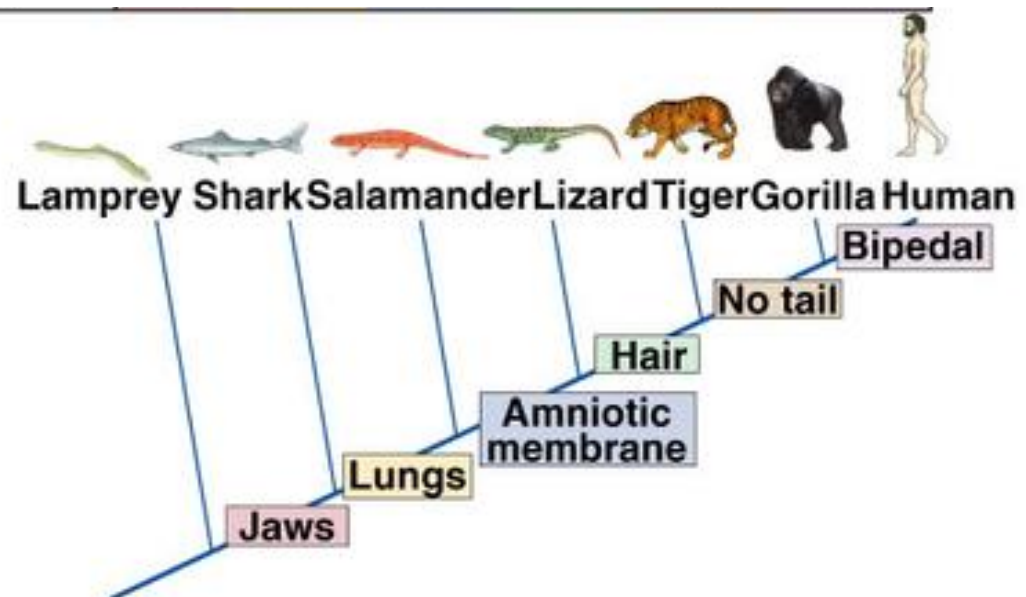


(b) Cladogram

Use the following Character Tables to find the Shared Derived Characters of Clades and build a cladogram.

Traits: Organism	Jaws	Lungs	Amniotic membrane	Hair	No tail	Bipedal
Lamprey	0	0	0	0	0	0
Shark	1	0	0	0	0	0
Salamander	1	1	0	0	0	0
Lizard	1	1	1	0	0	0
Tiger	1	1	1	1	0	0
Gorilla	1	1	1	1	1	0
Human	1	1	1	1	1	1

- What does the cladogram look like?



Molecular Systematics

- When hypothesizing phylogenies using molecular data sometimes many trees can be drawn for the same info. Therefore we...
 - ◆ **Always apply principle of maximum parsimony**
 - Use the simplest explanation
 - Construct the cladogram using the fewest evolutionary events that explain data (the base DNA changes for example)

hypothetical bird species



Species I



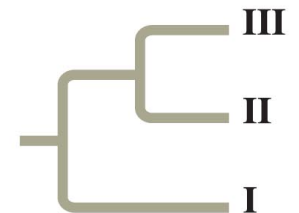
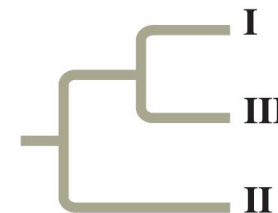
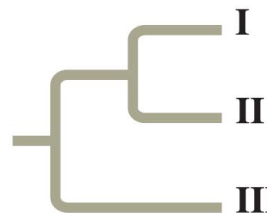
Species II



Species III

There are 3 possible
phylogenies
(there are 12 more)

Three phylogenetic hypotheses:



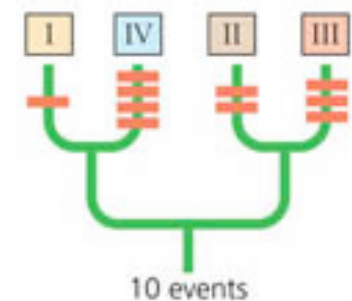
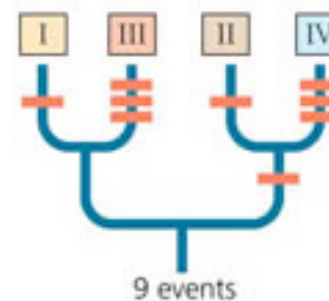
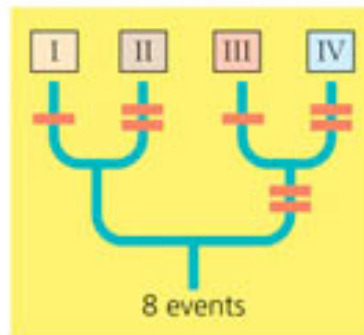
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Parsimony

- Which phylogeny is the best out of these three?

RESULTS

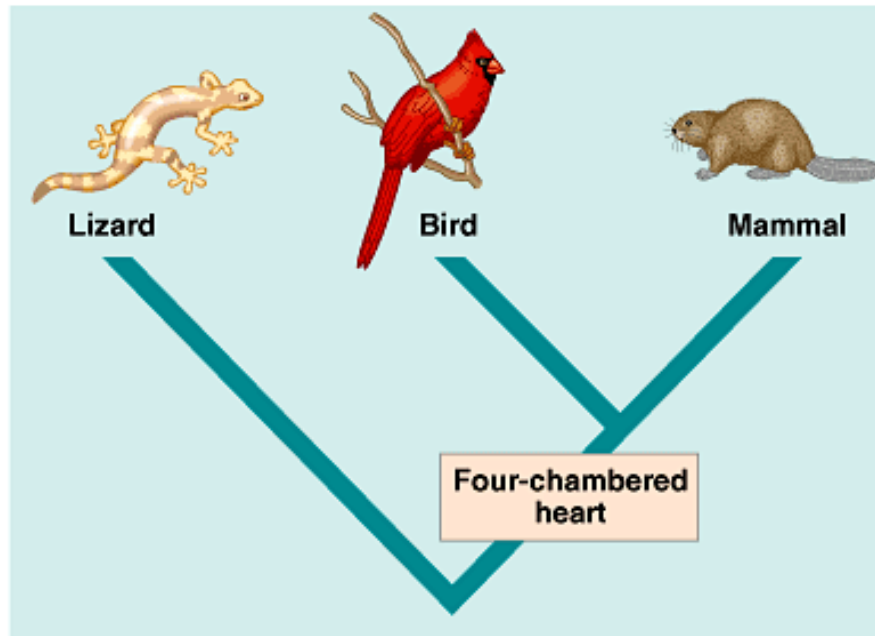
To identify the most parsimonious tree, we total all the base-change events noted in steps 3–6 (don't forget to include the changes for site 1, on the facing page). We conclude that the first tree is the most parsimonious of these three possible phylogenies. (But now we must complete our search by investigating the 12 other possible trees.)



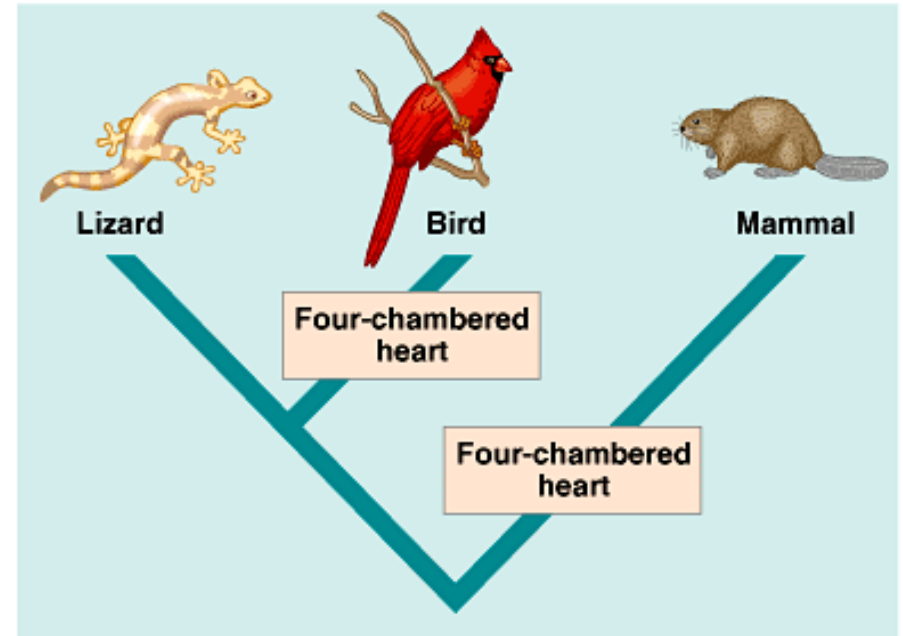
- When deciding which tree is the best hypothesis, choose the “tree” that explains the data invoking the fewest number of evolutionary events like DNA base changes/mutations

◆ Here, tree one is considered most parsimonious out of the three possible phylogenies...

Parsimony & analogy vs. homology



(a) Mammal–bird clade



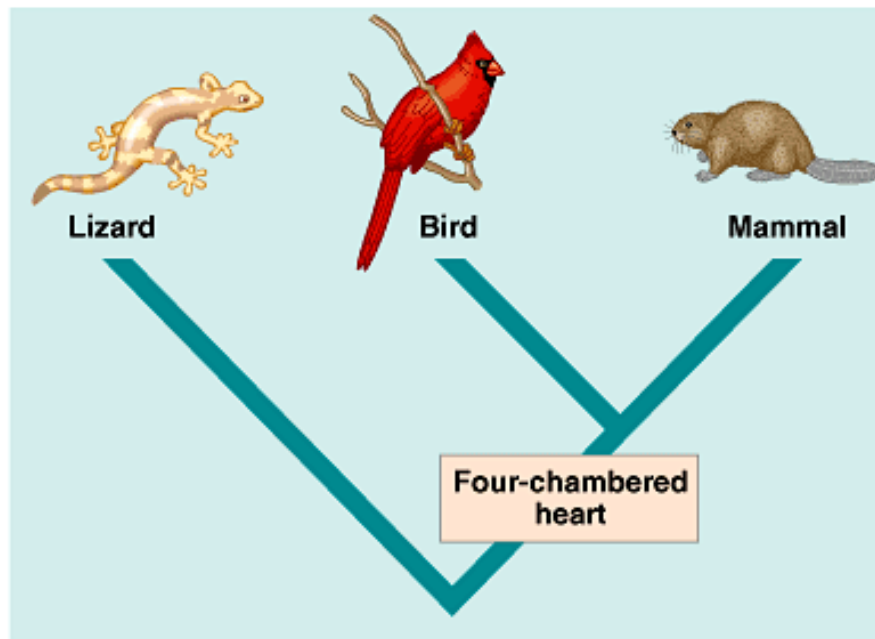
(b) Lizard–bird clade

Phylogenetic trees are hypotheses!!!

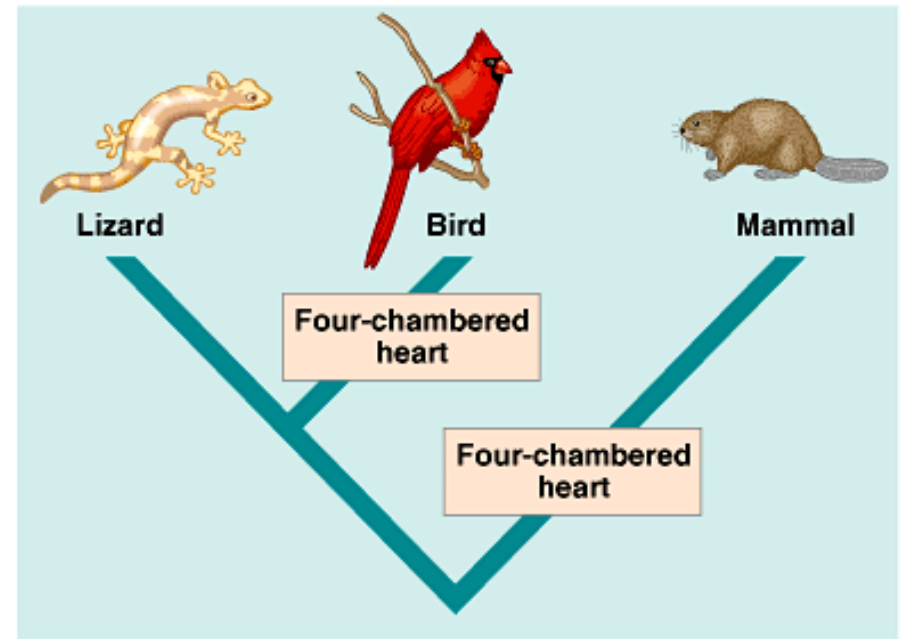
- Which is the most parsimonious tree?

If the four chambered heart is a homology then tree 1 may be a good hypothesis.

Parsimony & analogy vs. homology



(a) Mammal–bird clade



(b) Lizard–bird clade

DNA comparisons however reveal that aves' DNA (bird) is less similar to that of placental mammals than reptilia's DNA is to mammals.

The argument that birds evolved from reptiles is partially based on the belief that the four-chambered heart was formed in both birds and mammals due to convergent evolution (rather than a trait from a direct common ancestor).