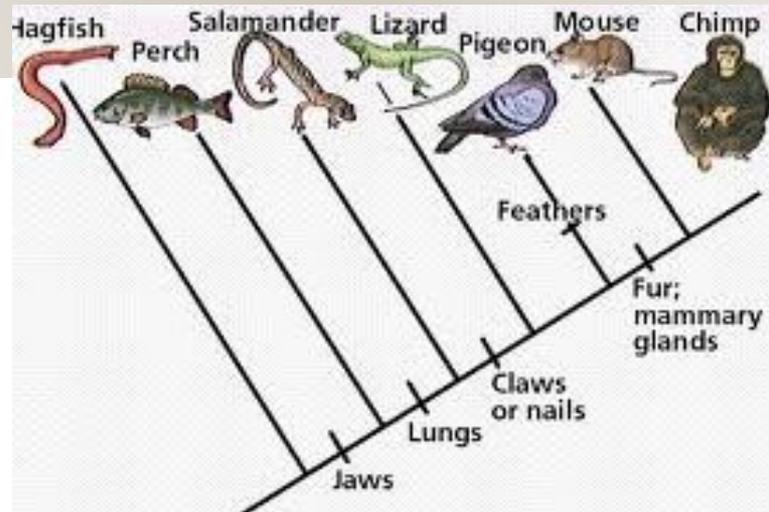


Phylogeny and Modern Taxonomy



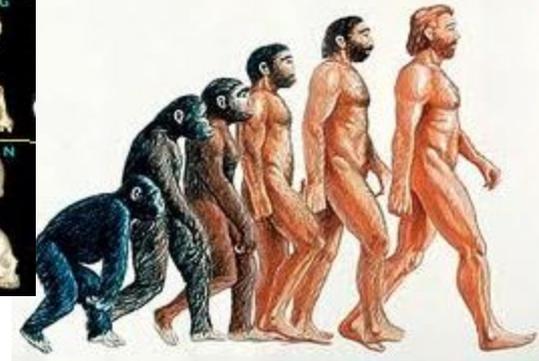
Recall:

Taxonomy

- the classification, identification and naming of organisms
- aims to group organisms according to a set of criteria (ex. how closely related they are to each other)
- Classifying a species by kingdom, phylum, and so on, is like placing students in a large school system. First a student might be identified by school, then by specific grade, and finally as a unique individual by name.



The leopard shares many characteristics with the lion—which belongs to the same genus—but far fewer characteristics with snails, sponges, or earthworms, though they are all members of the animal kingdom.



The Theory of Evolution

- All living things are descended from a common ancestor in the same way that family members are related to each other through a common ancestor.

THEREFORE we have a different type of taxonomy:

Phylogenetics – reconstructing the evolutionary relationships among organisms

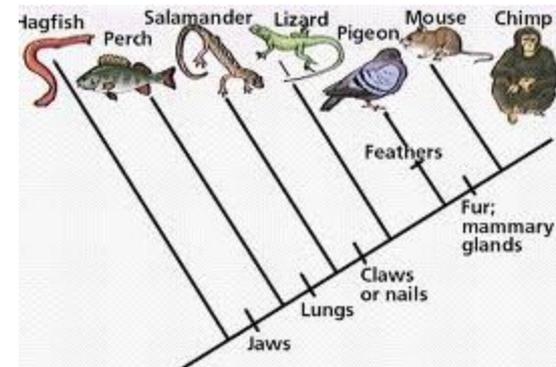
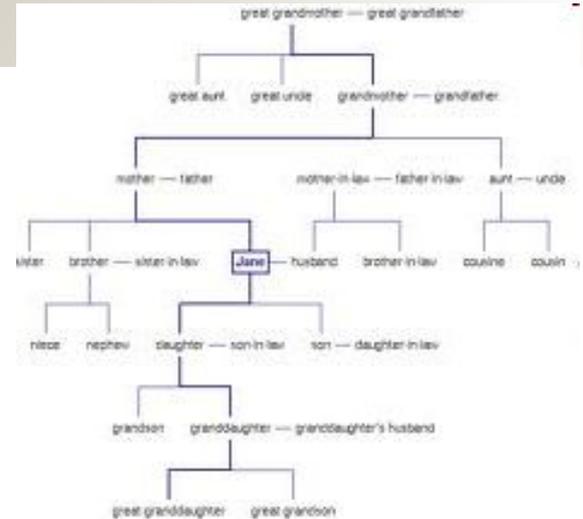
What is this study called?

■ Phylogeny

(“evolutionary tree”)

- *the study of the evolutionary relatedness between, and among, species (entire populations of individuals)*

- these relationships are similar to a large family tree, but instead of tracing relationships between family members, phylogeny tracks relationships between *entire species*





These relationships can be presented in a:

■ **Phylogenetic tree**

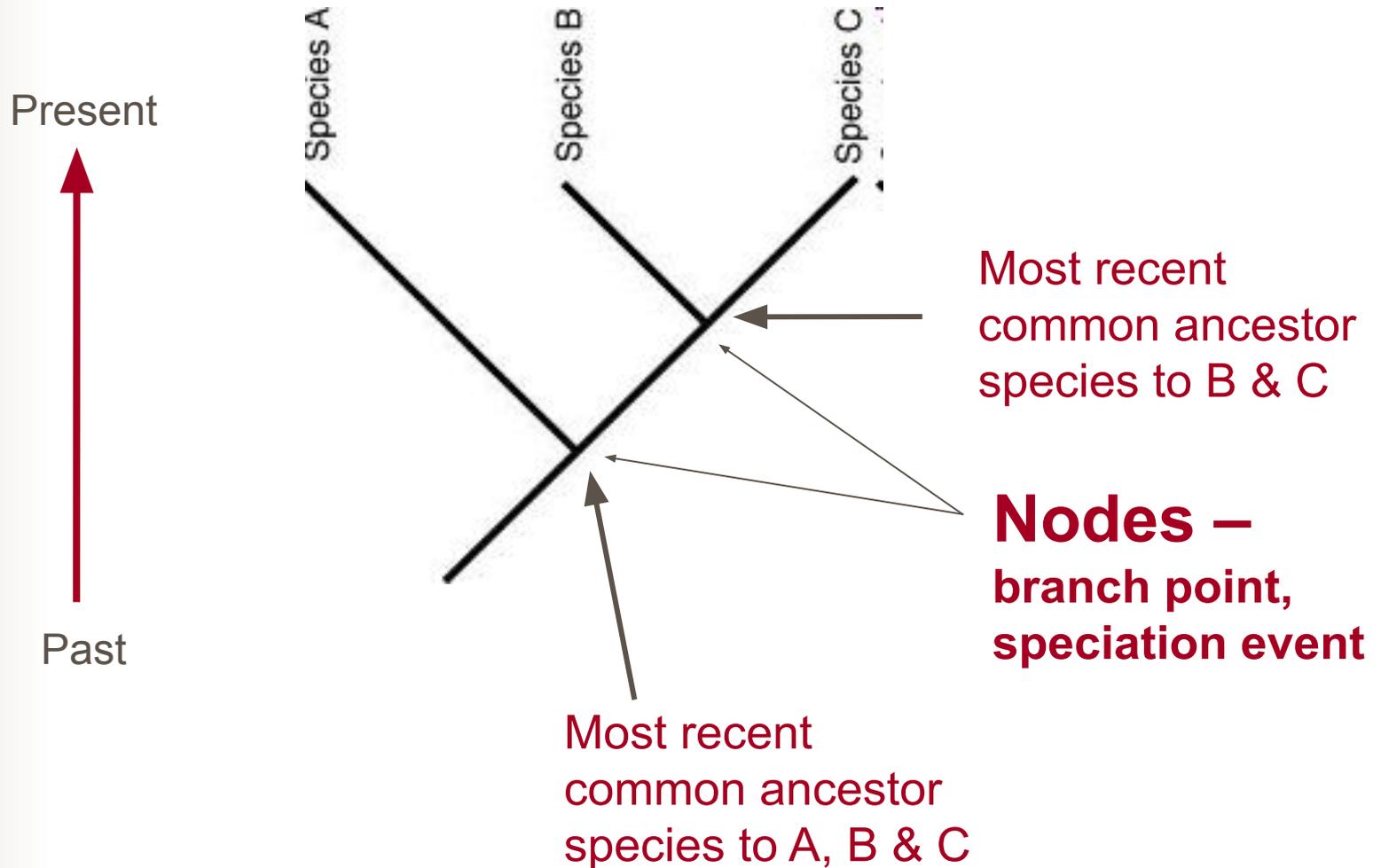
- *a branching diagram used to show evolutionary relationships between different species or groups*

- hypothesized genealogy traced back to the last common ancestor (*i.e.*, the most recent) through hierarchical, dichotomous branching

■ **Cladistics**

- the principles that guide the production of phylogenetic trees, a.k.a., **cladograms**

How to read a phylogenetic tree:

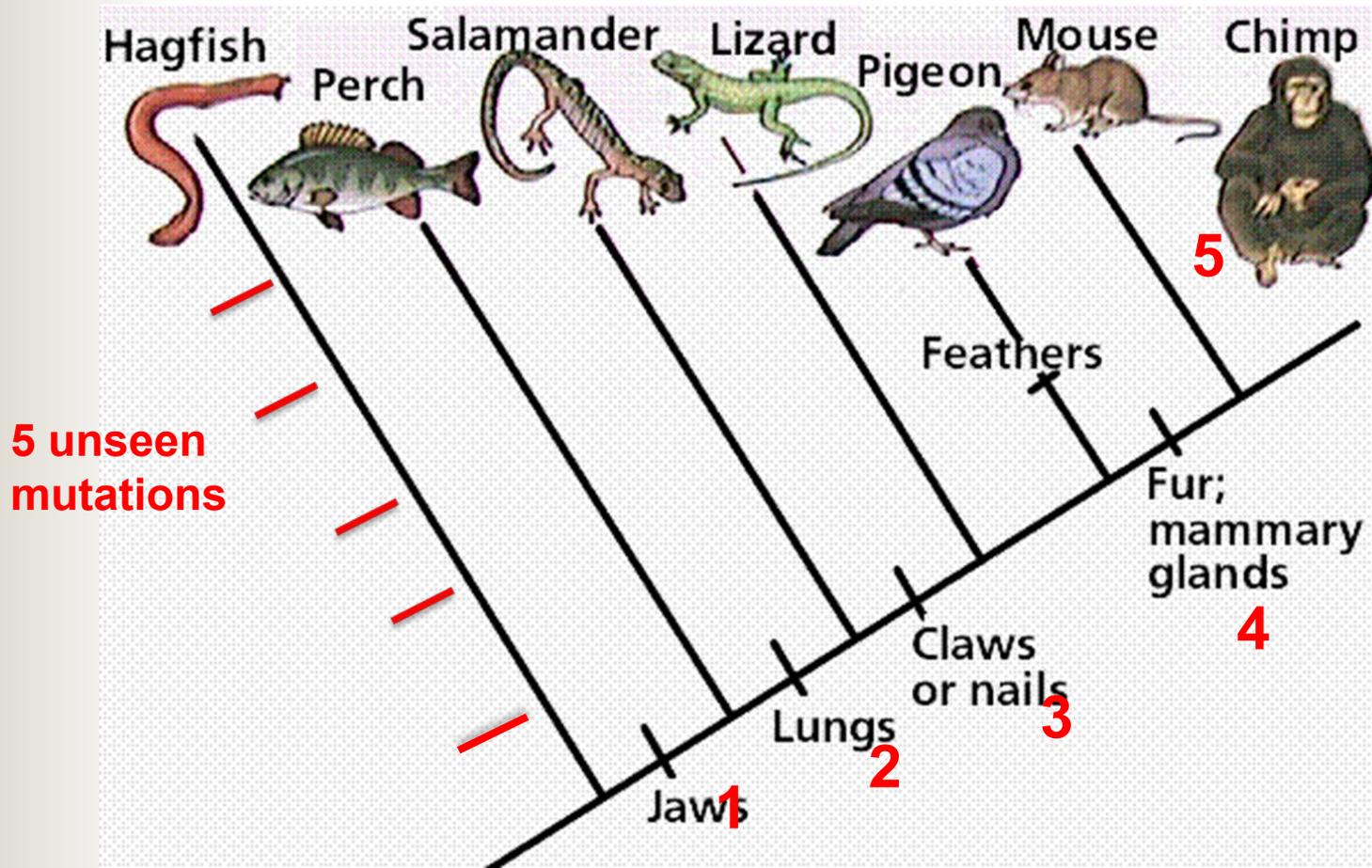




Note: all **living** species end up at the same point on the page while any **extinct** species would be written earlier.

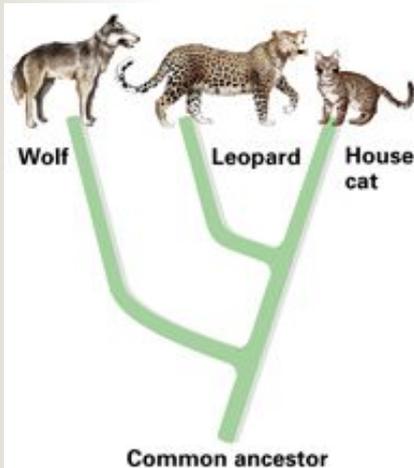
The length of the line indicates how long it has been since the species **branched off**

Mutations are assumed to occur at a **constant** rate and so **all of** the species in this tree (hagfish to mammals) have undergone the **same** number of mutations □ **5**

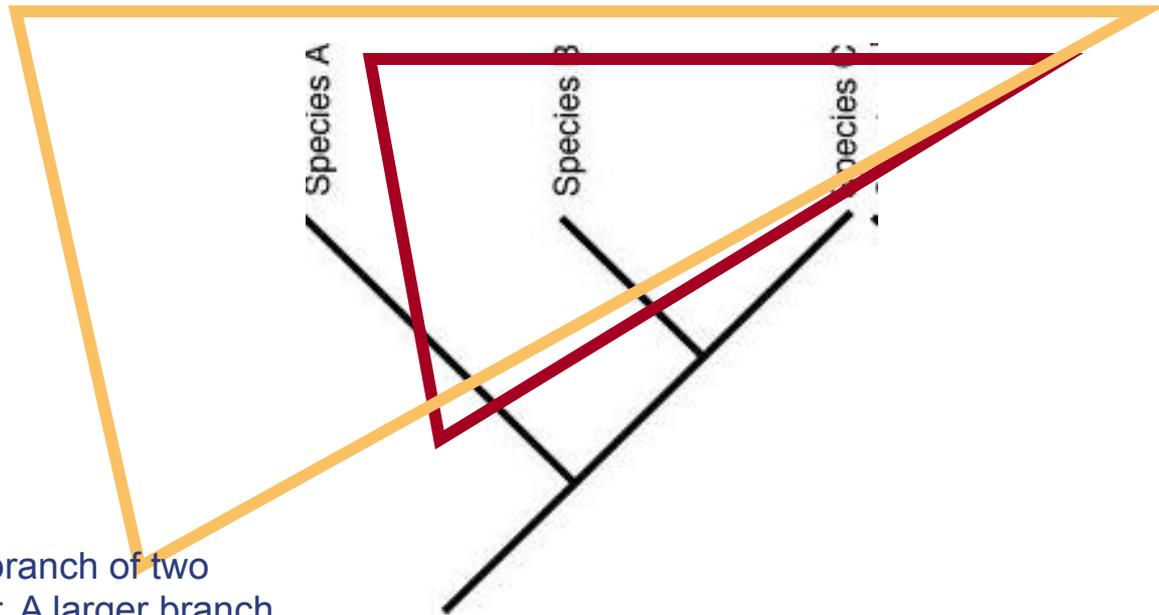


■ Clade

- *a taxonomic group that includes a single common ancestor and all its descendants*
- *each evolutionary branch in a phylogenetic tree*
- *Example: 2 clades exist in this tree*

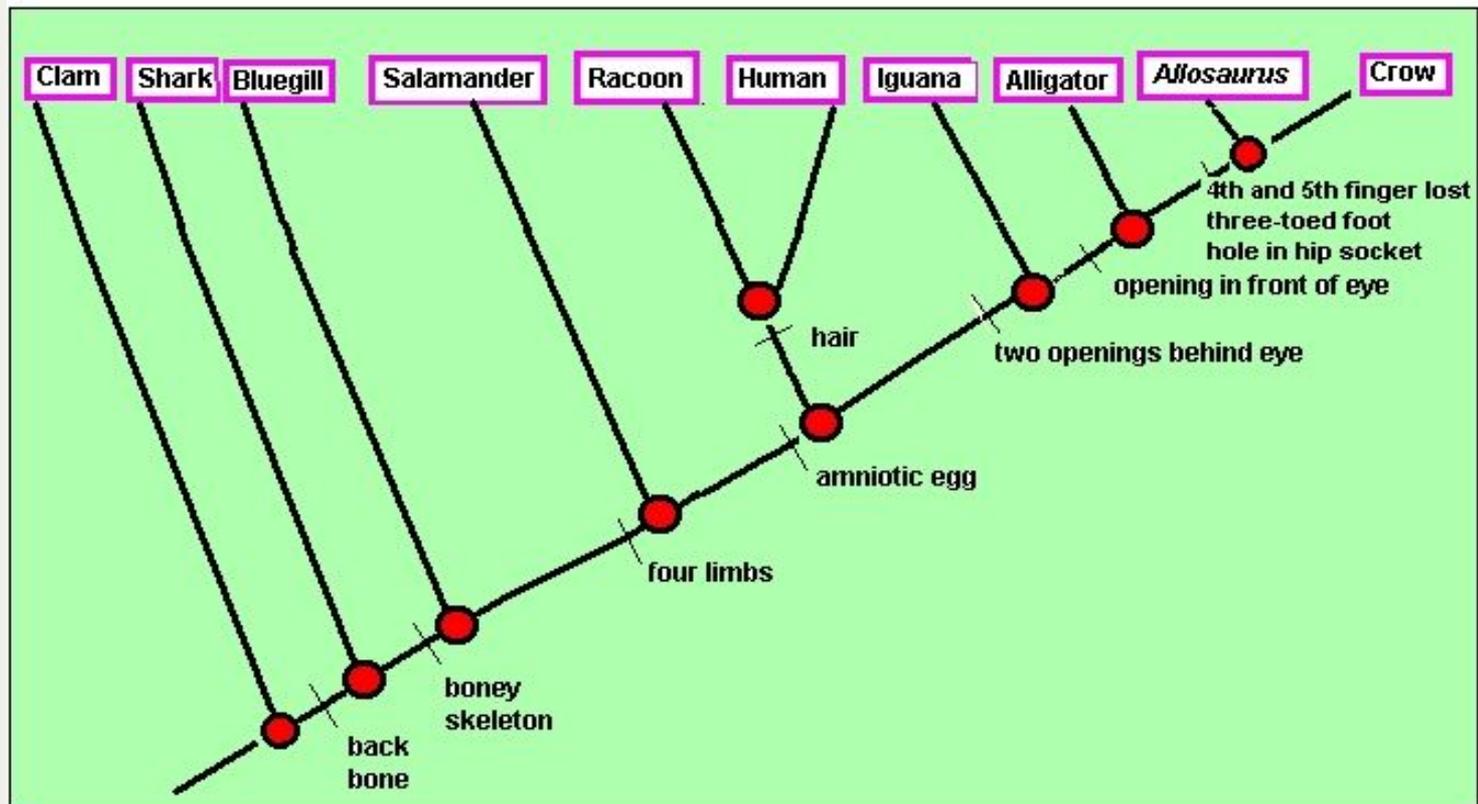


Leopards and house cats compose a branch of two species that share a common ancestor. A larger branch that also includes wolves has a common ancestor that would have lived longer ago than the ancestor of leopards and house cats.



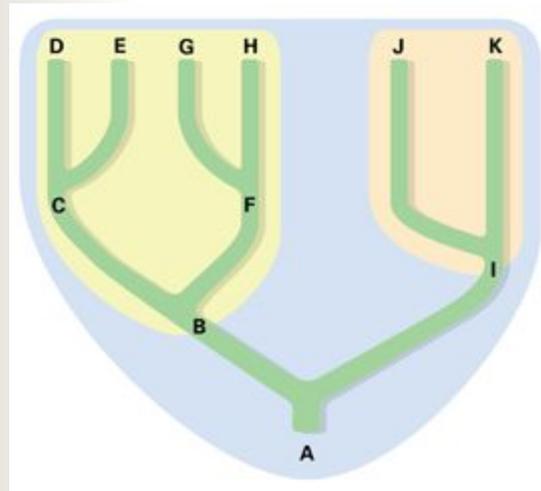
Small clades – small number of species that share a very recent common ancestor

Large clades – “super clades”
includes all species that share a
common distant ancestor

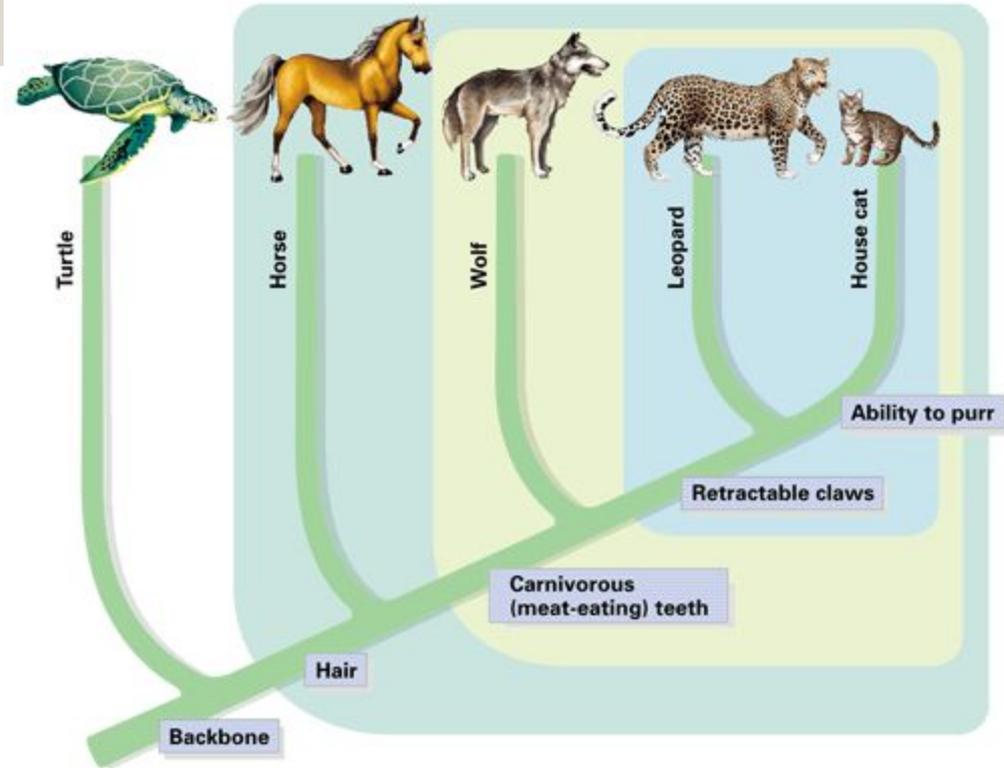


Common ancestor species

Other Examples:



Each shaded area in the phylogenetic tree highlights one clade, such as the yellow area including species B through H.

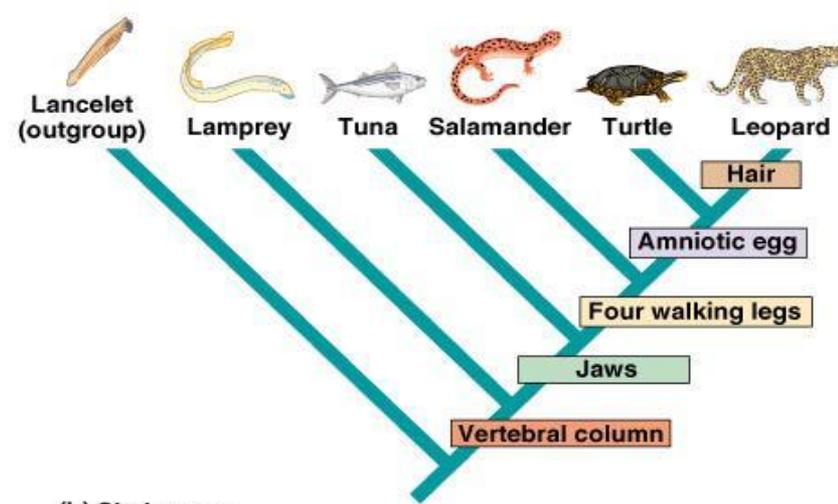


This cladogram shows how derived characters can be used to identify clades among certain vertebrates (animals with backbones). All the species shown here share a common ancestor that had a backbone. (Each clade is actually defined by several derived characters, not just one.)

How Cladograms are made:

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
Jaws	0	0	1	1	1	1
Vertebral column (backbone)	0	1	1	1	1	1

(a) Character table



(b) Cladogram

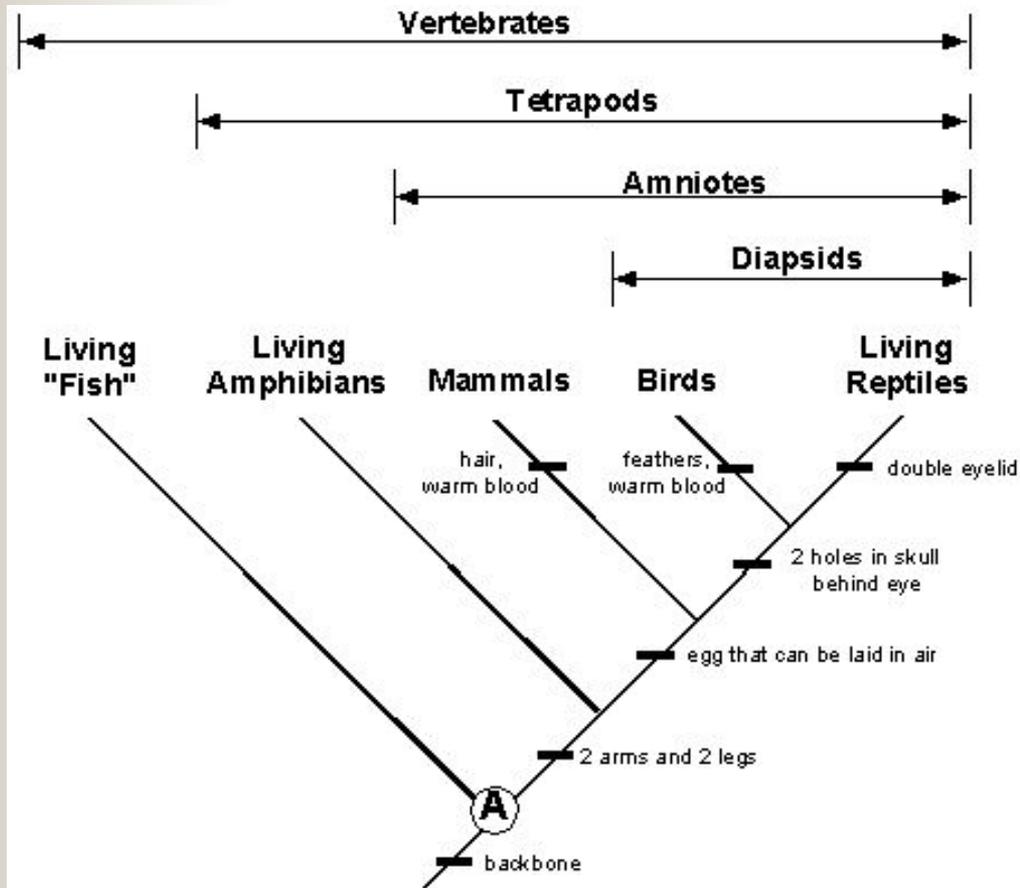
CHARACTERS →	Backbone	Jaws	4 Limbs	Amniotic Egg	Mammary Glands	Opposable Thumbs	Upright Posture
TAXA ↓							
Amphioxus (outgroup)	0	0	0	0	0	0	0
Lamprey	1	0	0	0	0	0	0
Sunfish	1	1	0	0	0	0	0
Newt	1	1	1	0	0	0	0
Lizard	1	1	1	1	0	0	0
Bear	1	1	1	1	1	0	0
Chimpanzee	1	1	1	1	1	1	0
Human	1	1	1	1	1	1	1

Completed Cladogram

The completed cladogram doesn't necessarily tell us anything about evolutionary time. It only tells us which groups are most closely/distantly related.



Review:



1. How many clades are represented in this tree?
2. Which characteristic is located the "furthest back in time"?
3. Which characteristic links the living reptiles and living amphibians?
4. Are living reptiles more closely related to birds or mammals? Why?
5. Where is the most common ancestor located of all the species?

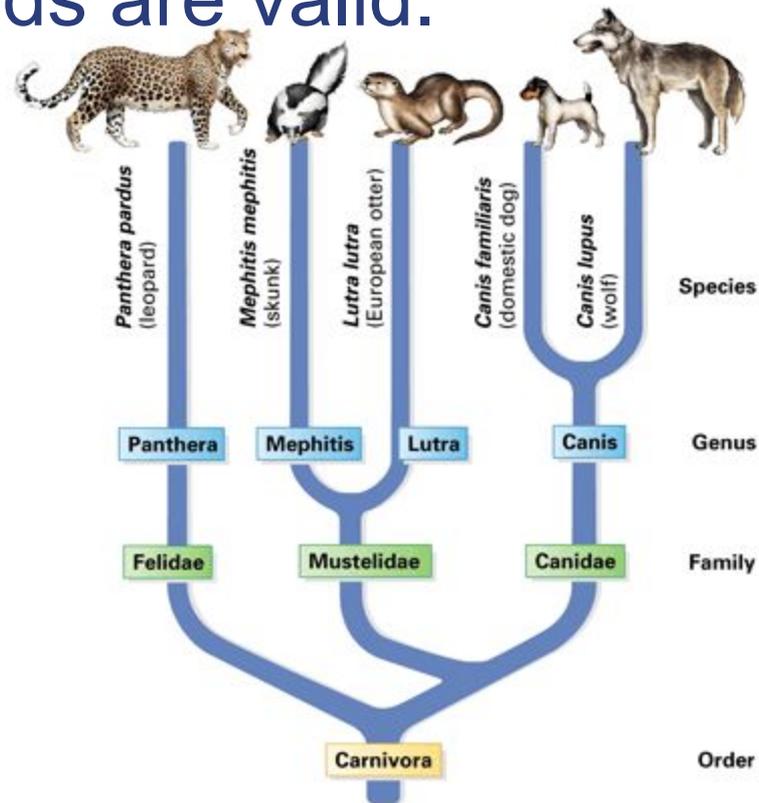
REVIEW

2 types of taxonomy:

- 1) **Traditional classification (taxonomic tradition)**
 - hierarchical classification system by Linnaeus
 - groups species primarily by observed morphological (physical) characteristics

- 2) **Phylogenetic analyses (cladistic hypotheses)**
 - “modern taxonomy”
 - organisms are grouped based on evolutionary relatedness/pathways (***not*** taxonomic ranks)

Note: Taxonomic groups often reflect true clades, so both methods are valid.



In a phylogenetic tree, each branch point represents a common ancestor of the species above that point. In this diagram, the branches are labeled to reinforce how taxonomy reflects the branching pattern of evolution.



Acknowledgements:

- <http://knight.noble-hs.sad60.k12.me.us/content/exploringLife/text/chapter15/concept15.4.html>
- Ross Koning from **plantphys.info**