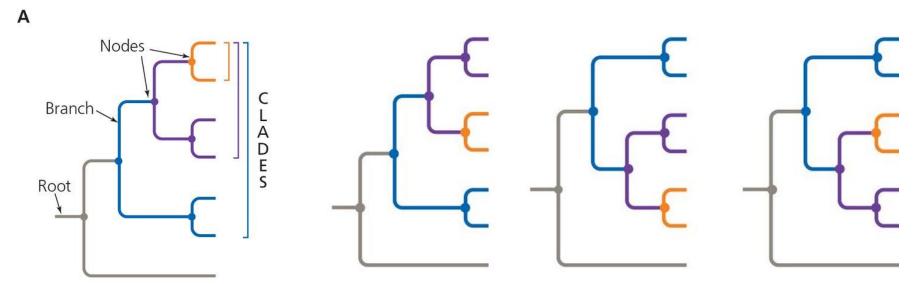
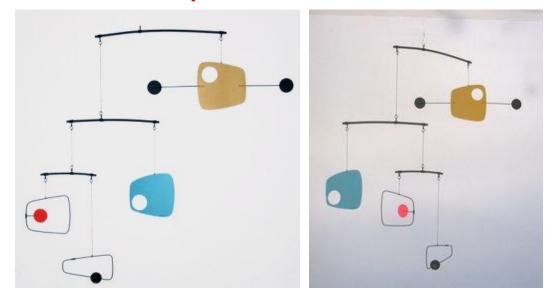
Tree thinking and and Building trees with characters

Taxa can be rotated around nodes



All four trees depict the same relationships!!

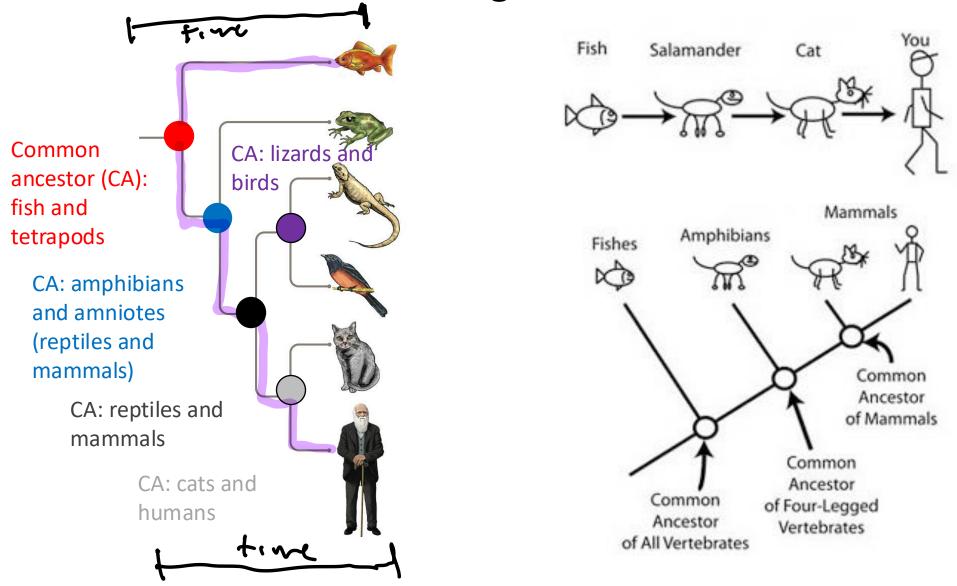


Reading a phylogenetic tree



- Rotate trues to see if they are comparable
- Rectangular treus, horizontal are easier to read _TE micci
- -Never ever read the taxa next to each other
- If we want to know the relationshop between two taxa we travel all the way to treir MRCA

Did humans evolve from frogs?



KEY POINT: No currently existing species is the ancestor of any other

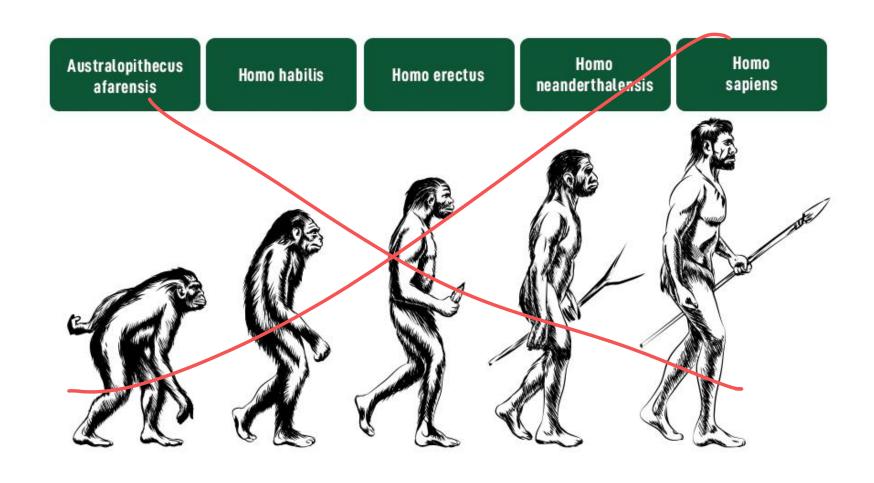
Reading a phylogenetic tree

- Freading relationships Linearly WRONG we do not come from cats nor from homo erectus

Terminology - tarly divergent lineage does not exist

- Living fossil does not exist. If we see a speciel is Living

Popular and incorrect view of evolution



Phylogenetic trees create new classifications

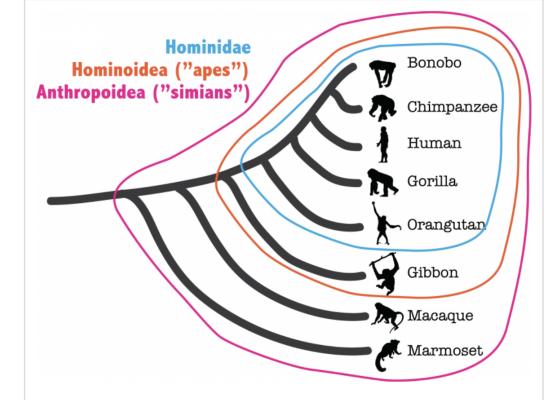


Figure 4: A cladogram with eight primate species. The different colored lines highlight nested groups – clades – of species. Clades include an ancestor species (which lived at the point where a line splits into two) and all its descendants. Hominidae is nested inside Hominoidea, which is in turn nested inside Anthropoidea. Biologists arrive at these groups by comparing species with respect to many of their characteristics, including at the DNA and protein level. Note that a human is as much of a simian as a macaque is, and an orangutan is as much of a hominid as a human is, but that a macaque is not a hominid.

Evolutionary biologists explain speciation



Source: Tim Allen/Twitter

We did not evolve from apes. We *are* apes. We did not evolve from chimps. We diverged from a common ancestor with chimps ~6-8

mya. = million years ago

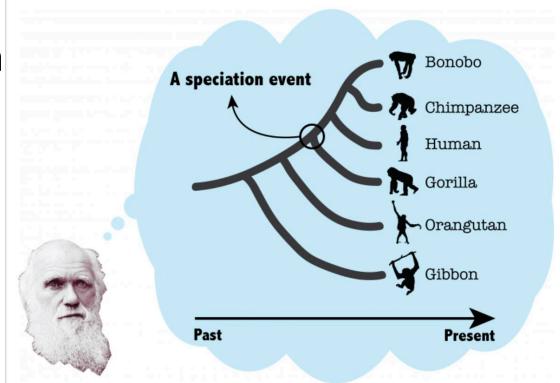
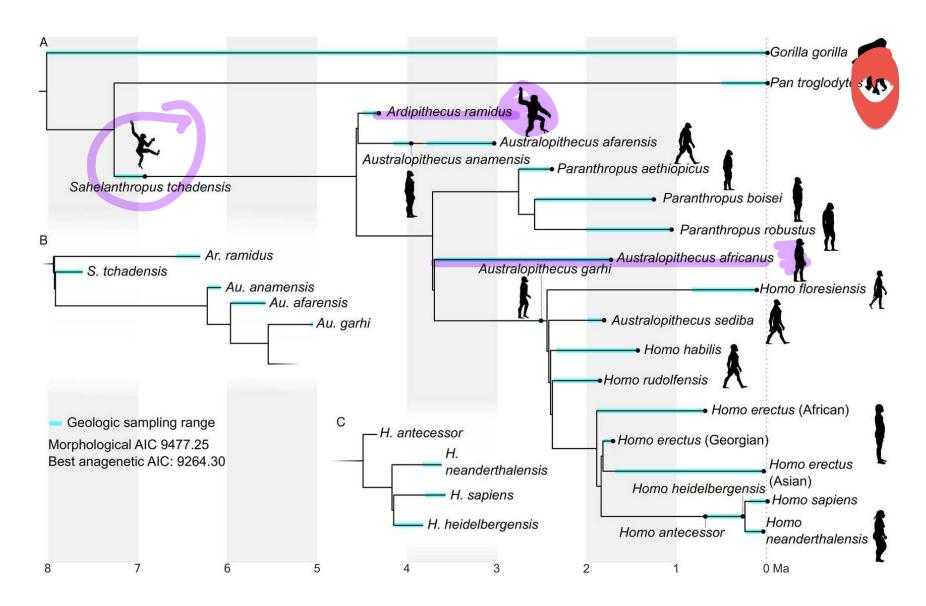


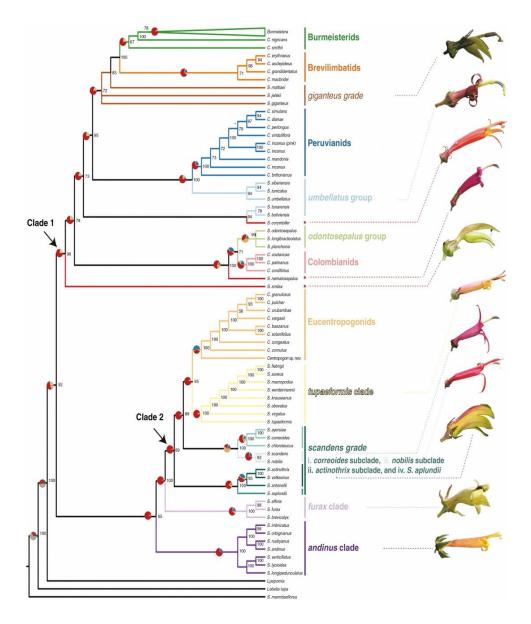
Figure 3: A diagram (also known as cladogram) that accurately depicts evolution. Two or more species originate from ancestral species due to speciation (or cladogenetic) events – when a line splits into two. By starting at the present and going backwards in time, it is clear that any one species finds a common ancestor with any other species at some point in the past. This means all species share some ancestor, and consequently are always related; this powerful idea is referred to as common descent, and was proposed by Charles Darwin and Alfred Russell Wallace. Modified from original, CCO (public domain).

Instead of showing Hominids descend with modification from common ancestor



Some Linnean classifications are not monophyletic once we have

learned about their DNA







Dr. Laura Lagomarsino Louisiana State University



S. odontosepalus S. longibracteolatus S. planchonis C. costaricae C. palmanus C. cordifolius S. nematosepalus * Colombianids * Colombianids * Colombianids

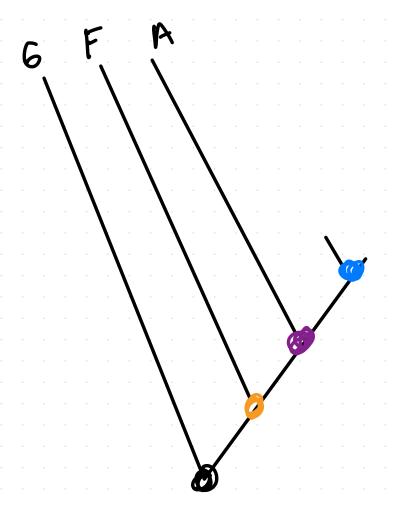
Linnean classifications often end up being not monophyletic

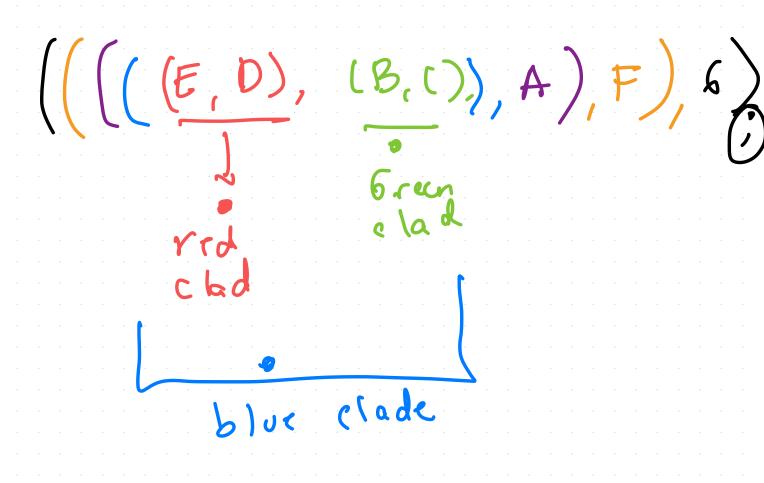


From our KY gardens Cardinal flower with Ruby-throated hummingbird



-tre Newick format \ ((A,B),C); (C, (A,B)); (C, (B, A));





Why phylogenetic trees and clades don't aggregate information easily?

Traits evolve

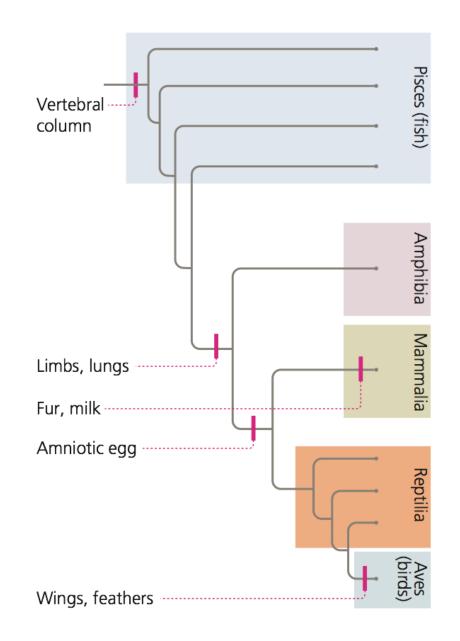
DNA differences (multiple gene stories)

Why phylogenetic trees and clades don't aggregate information easily?



Traits mapped onto trees: terminology

- Character or Trait: Comparable phenotype across multiple species
- Character state: a particular value if a character (presence/absence; shape; #; etc)
- **Homoplasy:** A character state that evolved more than once in evolutionary history



Parsimonious (simplistic) way to interpret a trait

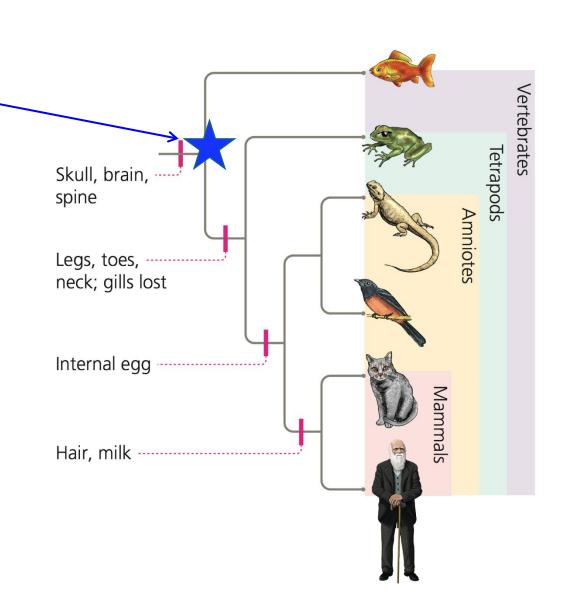
Traits inferred to be in the common ancestor at the adjacent node

Traits that appear deeper (earlier) in the phylogeny tend to be

widespread among taxa than later-appearing traits:

More

Less



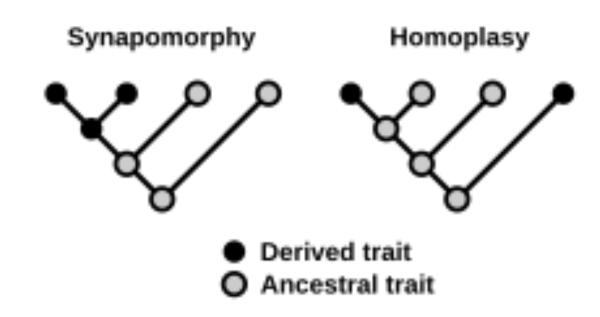
Important Definitions

Synapomorphy

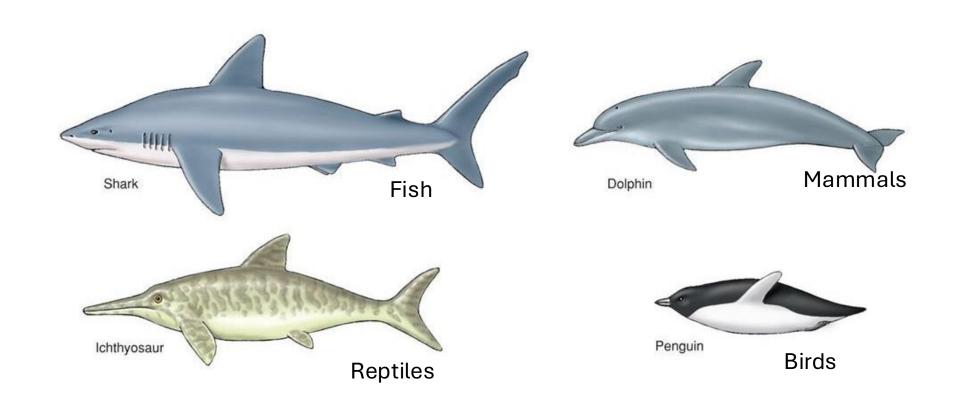
a characteristic present in an a common ancestor and shared exclusively (in more or less modified form) by its descendants

Homoplasy

Traits that evolved in different species, which resemble each other and have the same functions, but did not have a common ancestral origin



Homoplasy misleads phylogenetic inference



Early phylogenies relied on morphological characters



Characters and character states for an analysis of carnivorans

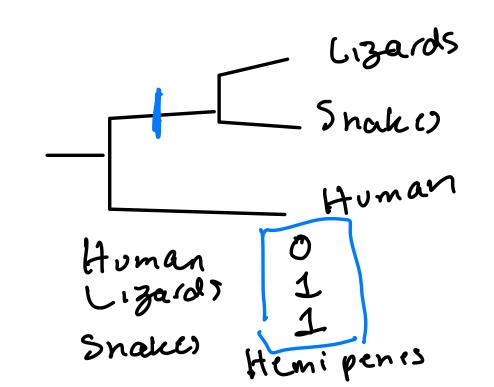
#	Character	State
1	Complexity of the cooling surfaces in the nose (maxilloturbinals)	0 = Minimally branched 1 = Highly branched
2	Bony spur by the auditory bulla (paraoccipital process)	0 = Straight and projecting 1 = Cupped around auditory bulla
3	Number of lower incisors	0 = 2 lower incisors 1 = 3 lower incisors
4	Upper molar 1	0 = Present 1 = Absent
5	Baculum (bone within the penis)	0 = Absent 1 = Present
6	Tail	0 = Elongated 1 = Short

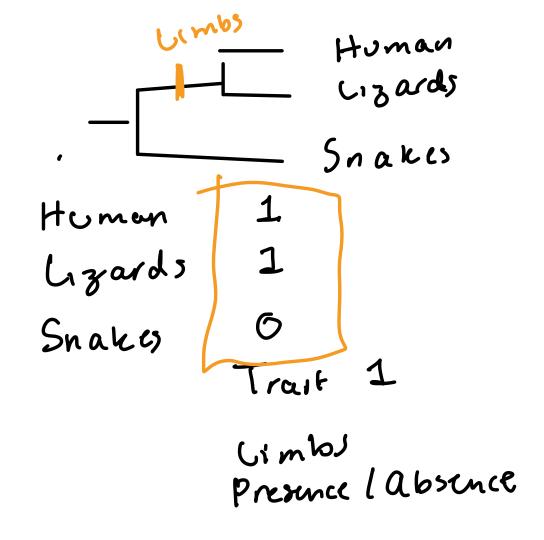
Character: any trait you can "score" in an organism (DNA base pair, skeletal element, physiological trait, behavior, habitat).

Types of inferences

Logical einstevence-

Statistical inference-





Parsimony analysis in practice...

TABLE 9.1 The Huge Number of Possible Tree Topologies

# of Taxa	# Unrooted trees	# Rooted trees	
# of Taxa 1 2 3 4 5 6 7 8 9	# Unrooted trees 1 1 1 1 3 15 105 945 10,395 135,135 2,027,025	# Rooted trees 1 1 1 3 15 105 945 10,395 135,135 2,027,025 34,459,425	Even with computers, trees cannot be exhaustively searched for most analyses so these programs employ algorithms to efficiently search "tree space"
11 12 13	34,459,425 654,729,075 13,749,310,575	654,729,075 13,749,310,575 316,234,143,225	