

Bioinformatics II:

Building Phylogenies using different methods

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Review!

- What is a phylogenetics tree?
- It is a diagram inferred evolutionary relationships between a set of organism phylogenetic from Drains notebook.
- It reflects the process of descent with modification a process (from ancestors to descendant).
- Note:
- A little of sequences and species can be solved by hand.
- But we need a computational statistics to figure out the big groups.

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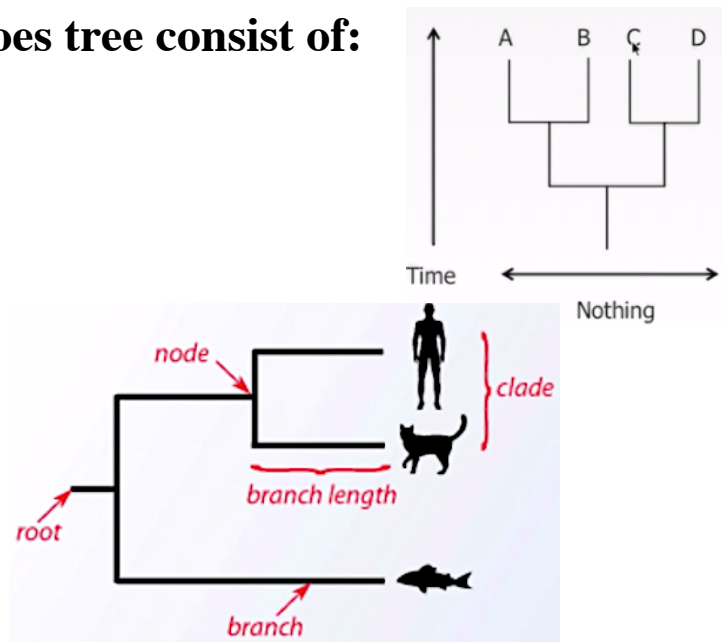
How does the phylogenetic tree describe the evolutionary relationship?

- By using large DNA sets to build tree underlying **principle and logic** sequences.
- The sequences are separated by shorter evolutionary distance which are expected to be similar to one another than sequences separated over longer distances.

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What does tree consist of:

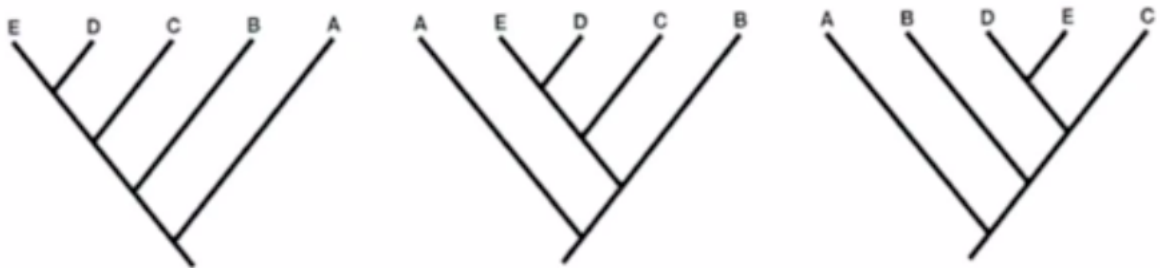
1. Root: where tree begins.
2. branch represent different species.
3. Node to separate the branches.
4. Tips of the tree (called leaves as in a plant tree).
5. There are 2D of the tree:
6. The length of the branch to the tips tells the time over.
7. The other dimension does not tell any things about the relationships.



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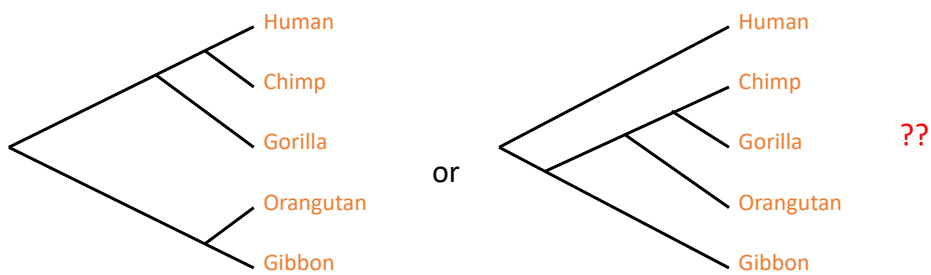
How can a tree describe the same evolutionary history for the following cladograms?

- The cladogram shows the same length of time.
- Just variations on each others by spinning tree around different that it has.



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An example: Describe evolutionary relationships between species



Cannot be known with certainty!

Nevertheless, phylogenies can be useful

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Applications of Phylogenetic Analysis

1. Inferring function:

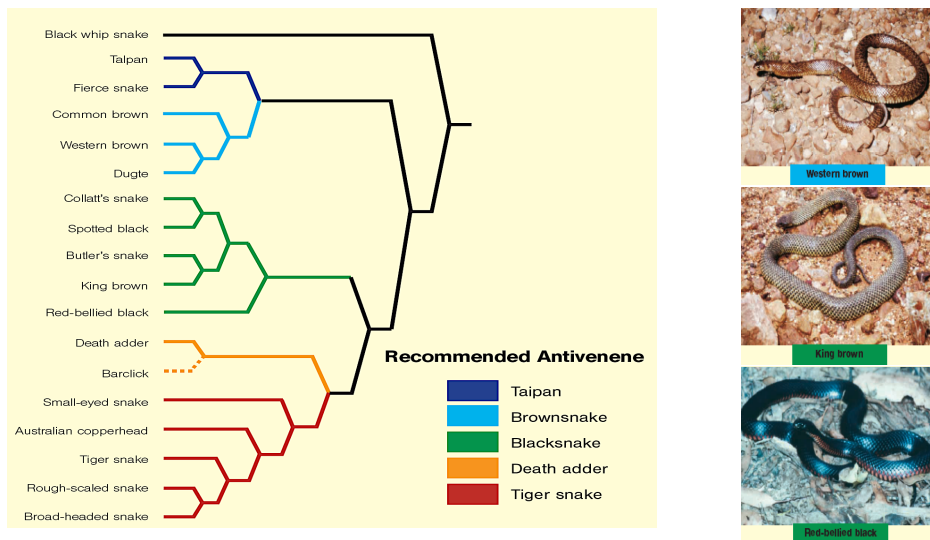
-Closely related sequences occupy neighboring branches of tree.

Tracking (following) changes in rapidly evolving populations (e.g., viruses)

Which genes are under selection?

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Discovering Snake Antivenin



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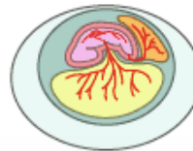
Reconstructing trees: A simple example: step 1

- **Choose the taxa.** You decide to study the major clades of vertebrates shown in the leftmost column of the table below. (Note that many vertebrate lineages are excluded from this example for the sake of simplicity.)

Taxa: a classification group.
Or Taxon

	Vertebrae?	Bony skeleton?	Four limbs?	Amniotic egg?*	Hair?	Two post-orbital fenestrae? **
Sharks and relatives	YES	no	no	no	no	no
Ray-finned fishes	YES	YES	no	no	no	no
Amphibians	YES	YES	YES	no	no	no
Primates	YES	YES	YES	YES	YES	no
Rodents and rabbits	YES	YES	YES	YES	YES	no
Crocodiles and relatives	YES	YES	YES	YES	no	YES
Dinosaurs and birds	YES	YES	YES	YES	no	YES

* **amniotic egg:**
an egg in which the embryo is surrounded by the moisture-retaining amnion membrane



** **post-orbital fenestrae:**
holes in the skull behind the eye



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Step 2 & step 3

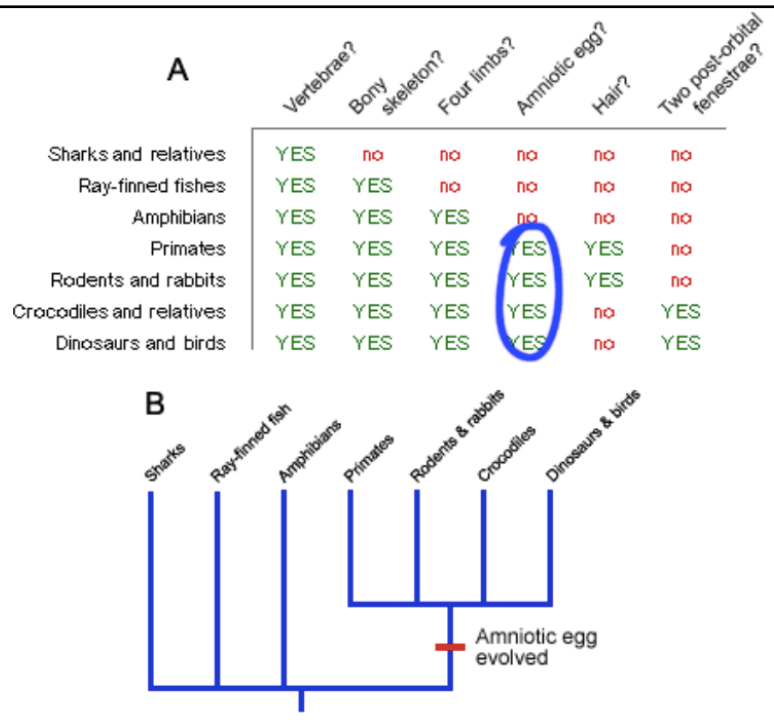
- **Determine the characters.** After studying the vertebrates, you select a set of traits, which seem to be homologies, and build the following data table to record your observations.
- (Note that many relevant vertebrate characters are excluded from this example for the sake of simplicity.)
- **Determine the polarity of characters.** From studying [fossils](#) and outgroups closely related to the vertebrate clade, you hypothesize that the ancestor of vertebrates had none of these features.

	Vertebrae?	Bony skeleton?	Four limbs?	Amniotic egg?	Hair?	Two post-orbital fenestrae?
Ancestor	no	no	no	no	no	no

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Step 4

- **Group taxa by traits** . We might start out by examining the egg character. We focus in on the group of lineages that share the **traits** form of this character, an amniotic egg (A.) and hypothesize that they form a clade (B):



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Then,

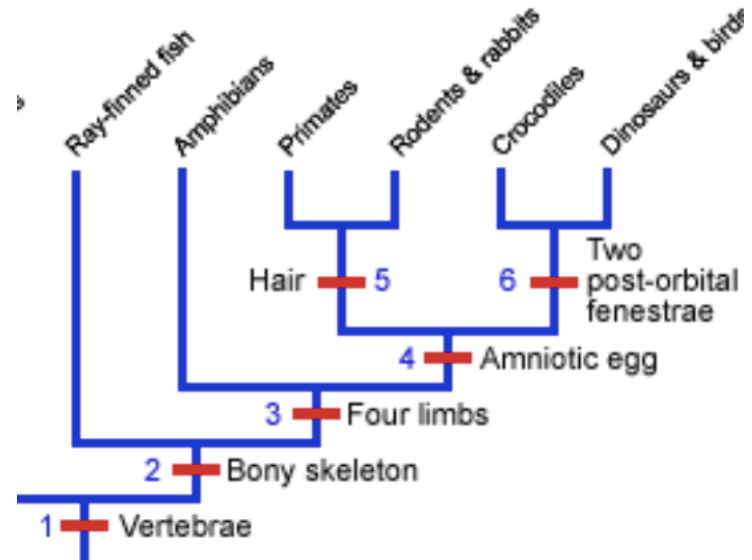
- We go through the whole table like this, grouping clades according to traits



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Step 5

- **Work out conflicts that arise.** There are no conflicts here. Every group is a subset of another group (see C).
- **Build your tree.** Based on the groupings above, you produce this tree:



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Step 7

- **You have made a phylogeny.**
- Of course, this was just an example of the tree-building process.
- Phylogenetic trees are generally based on many more characters and often involve more lineages.

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What are the common Methods to build a phylogenetic tree?

1. Distance-based measures: (UPGMA and NJ methods)
2. Character Based Methods: (Parsimony: straightforward method and Maximum likelihood). They are statistical measures.
3. Additional Method (Quartets Based and Disc Covering) (we are NOT going to study).