



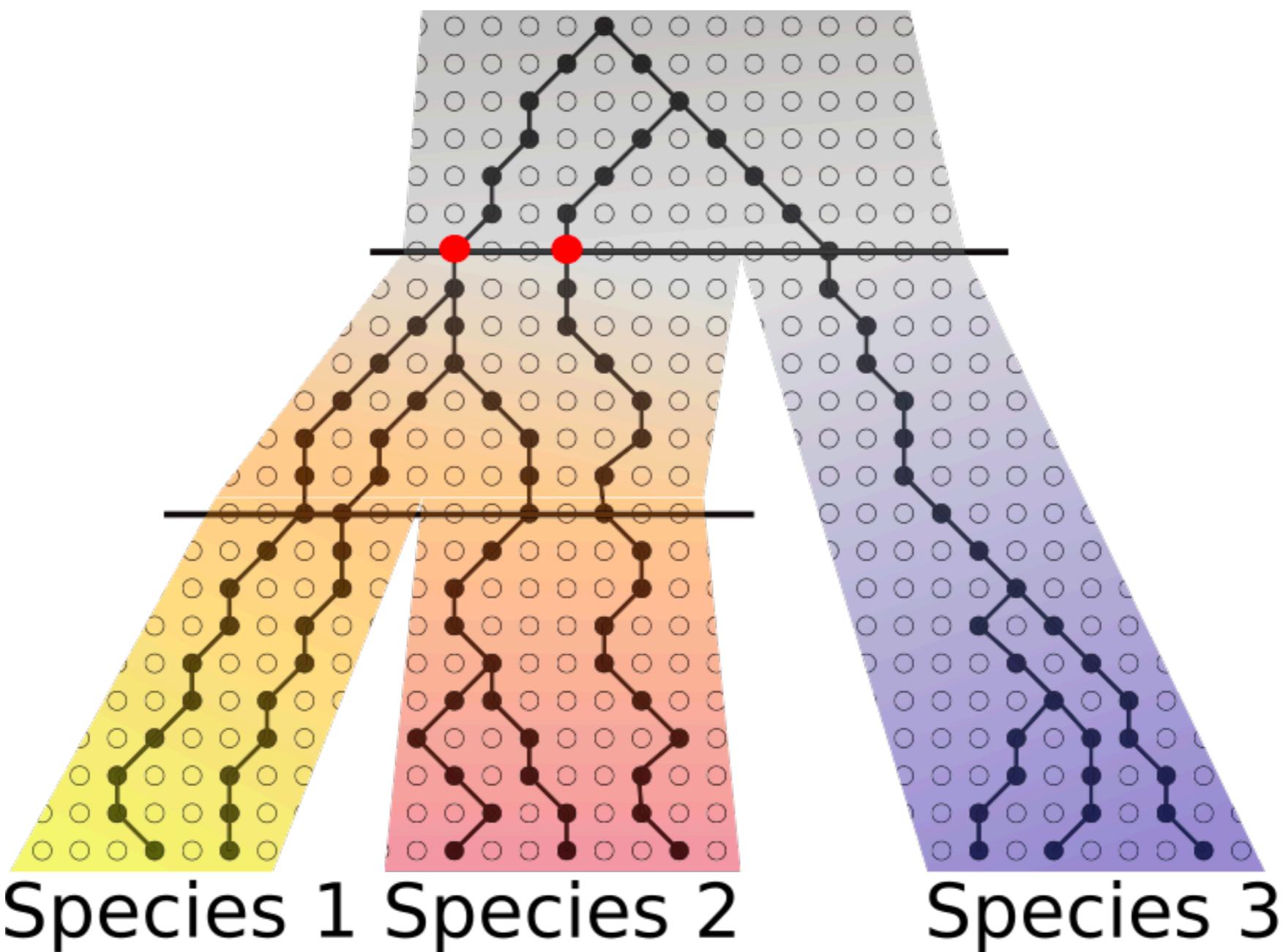
Learning from Trees (BIO 597)

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Think about your project

1. Types of questions you're interested in (or tackling for your thesis)
2. Think about data availability. Especially important for ecological / morphological
3. I'd love to sit down for a coffee and brainstorm
4. But please, touch base with your advisor if you plan on using the project as a thesis chapter

Phylogenies describe evolutionary history



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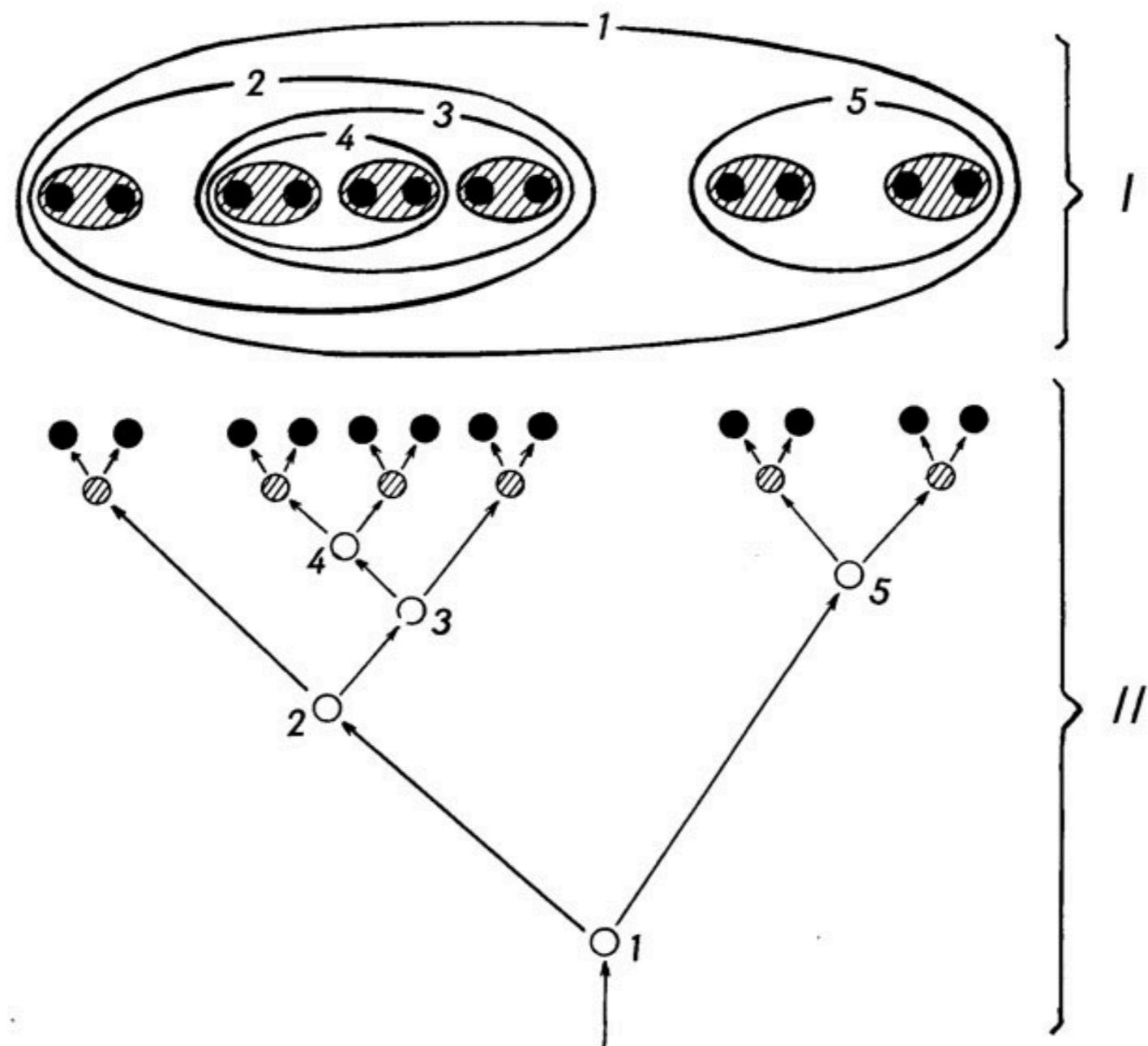


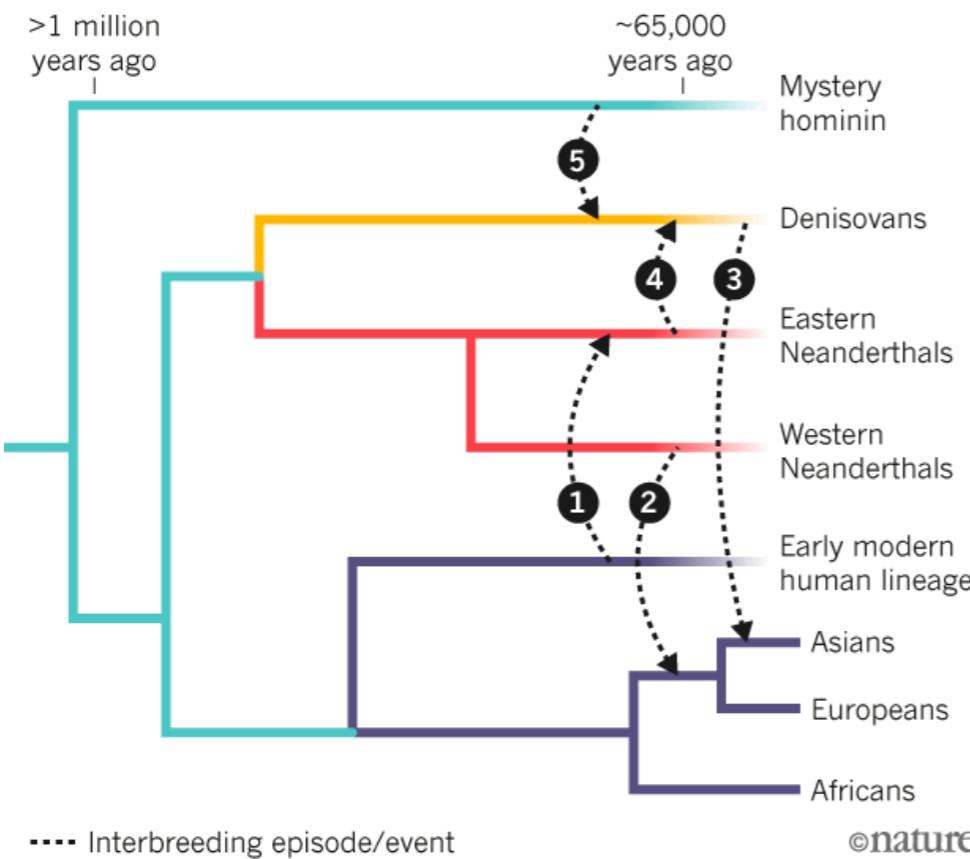
Figure 18. The phylogenetic kinship relations between the species of a monophyletic group, represented in two different ways.

Stick trees miss a lot of biology!

Hybridization and introgression

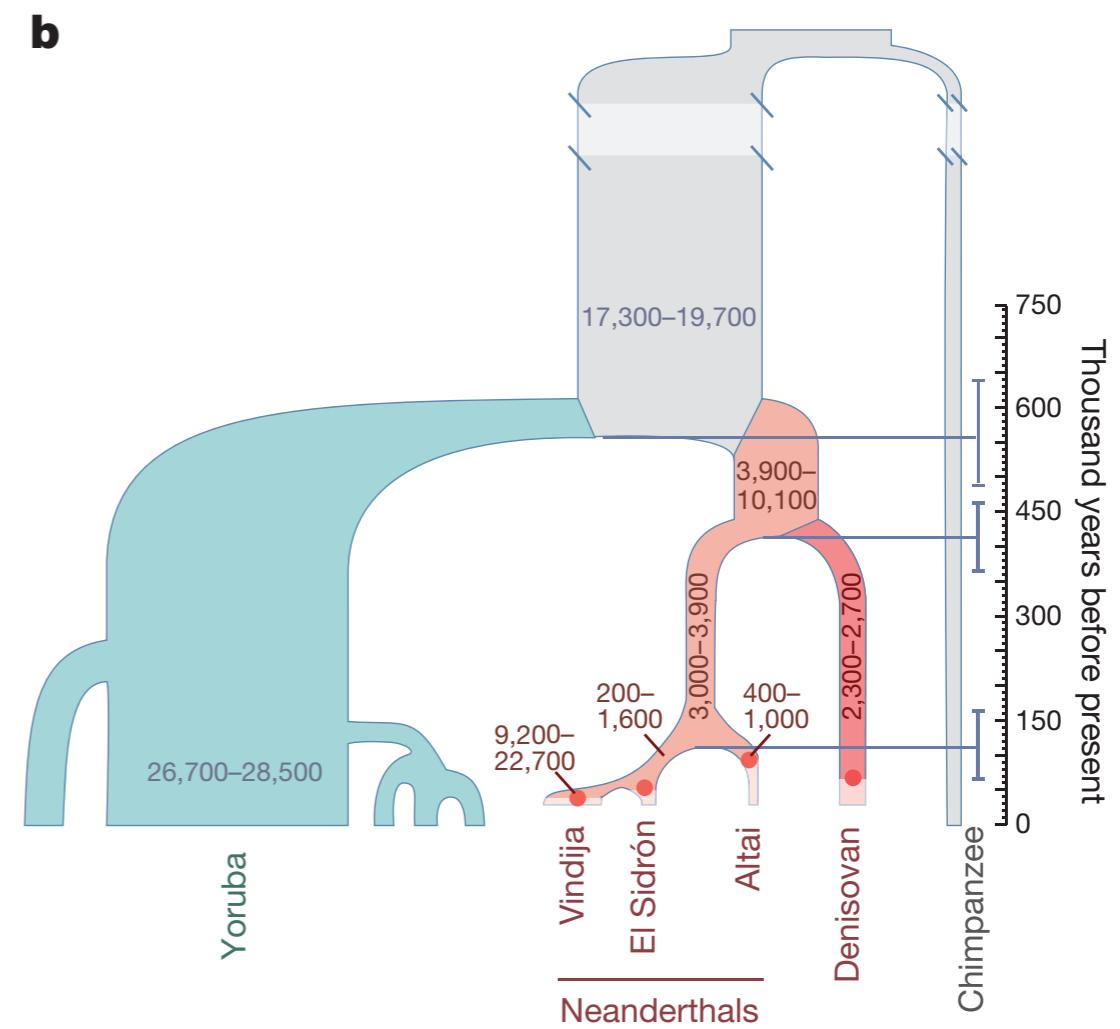
A HISTORY OF INTERBREEDING

Early modern humans, Denisovans, and Neanderthals all interbred with each other on multiple occasions in the past 100,000 years.



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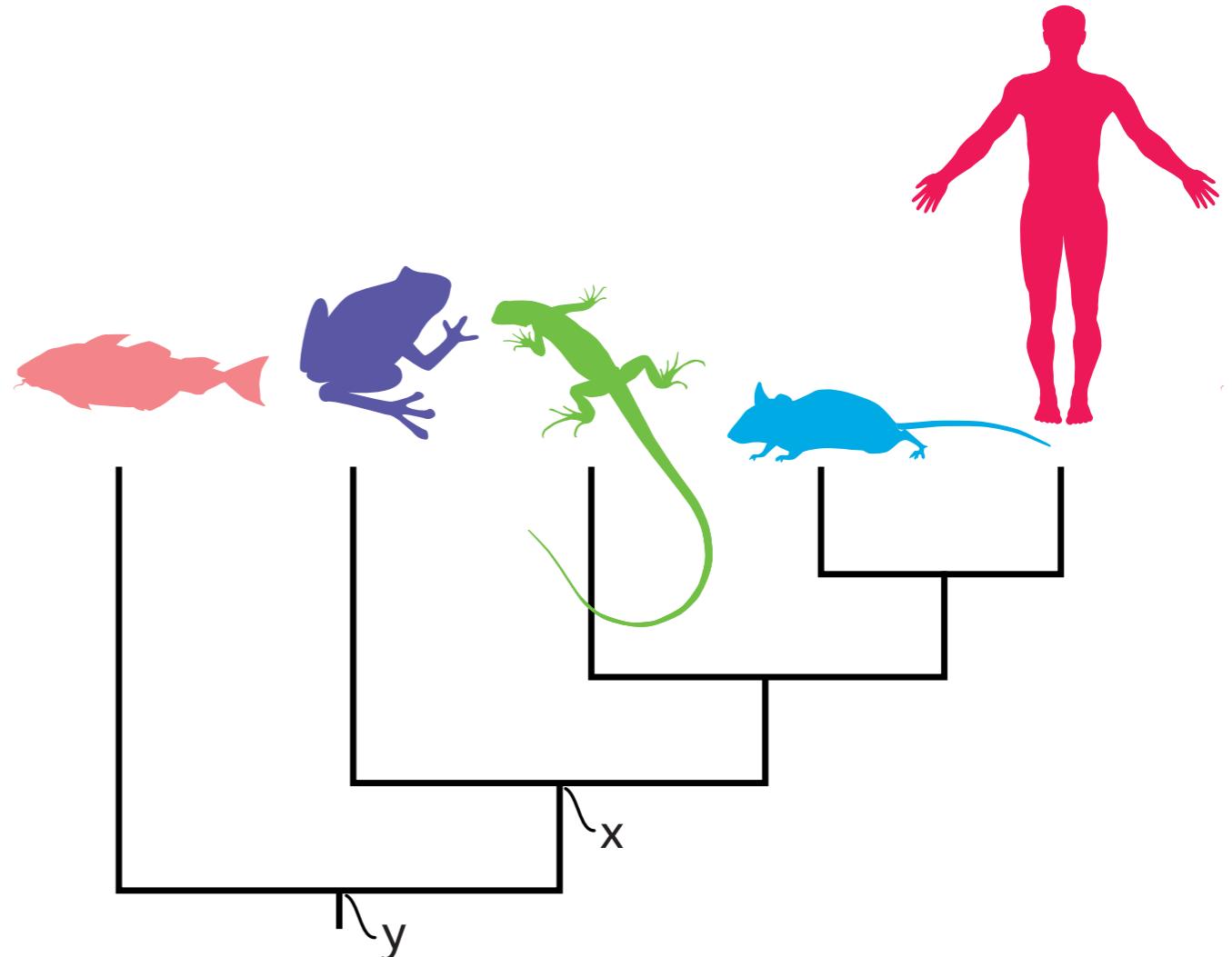
Demography



Reading & Describing Trees

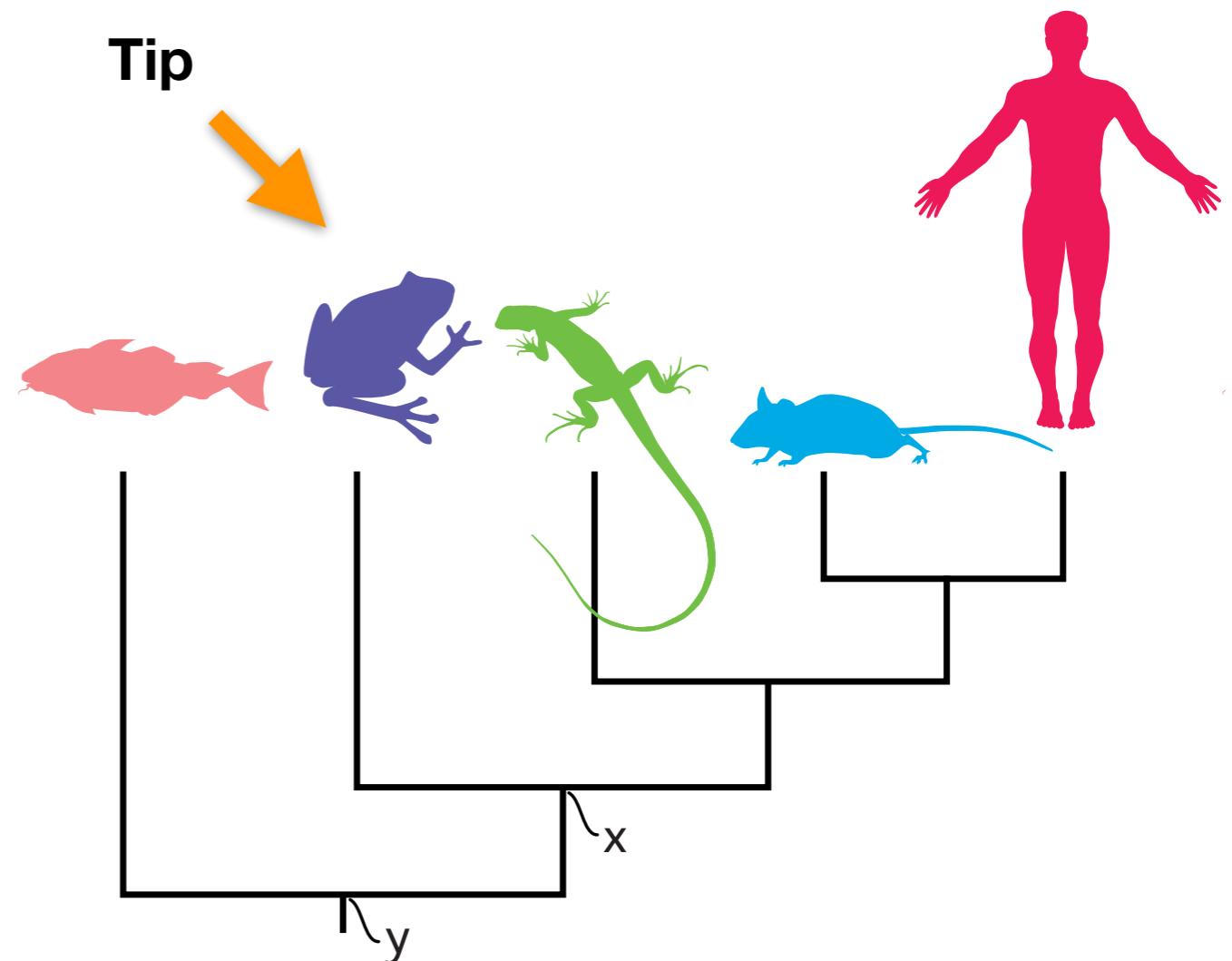
Trees

- Common names
 - Phylogeny
 - Cladogram (meaningless branch lengths)
 - Phylogram (meaningful branch lengths)
- Properties:
 - Topology (structure)
 - Usually have a length (when branch lengths are meaningful)

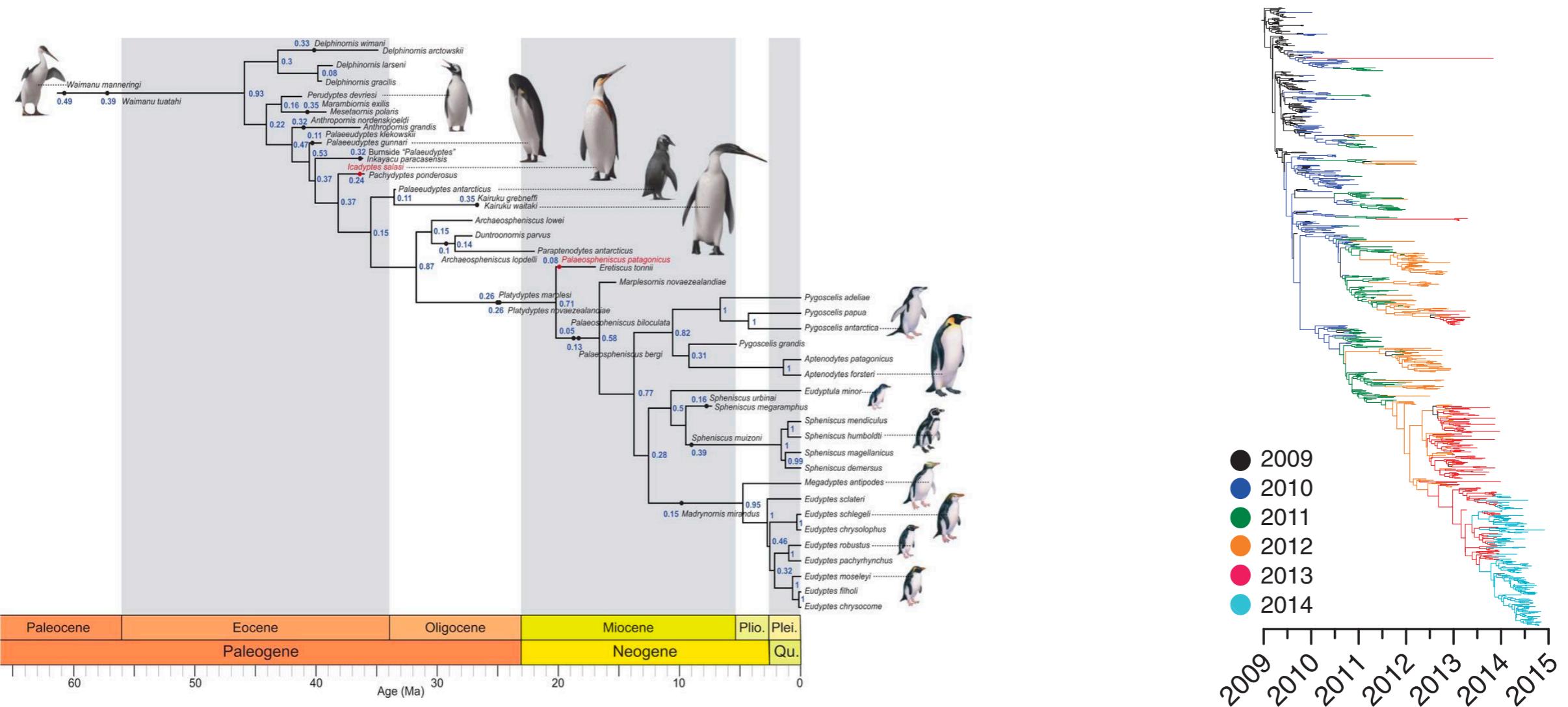


Tips

- Alternative names
 - Terminal
 - Terminal node
 - Leaf
 - Taxon
- Are nodes of *degree 1*
- Do not have to be extant

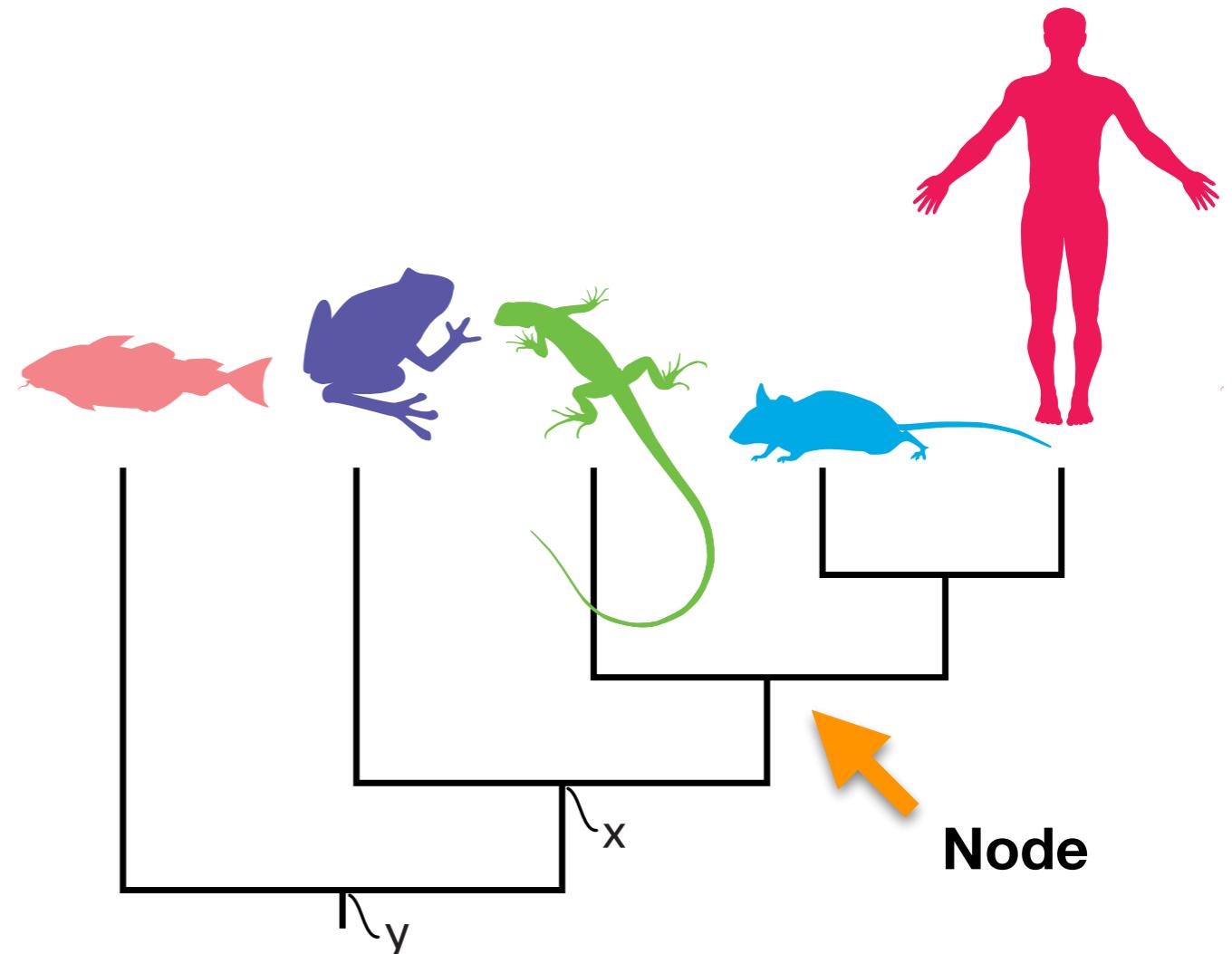


Tips can be fossils or viruses sampled over time



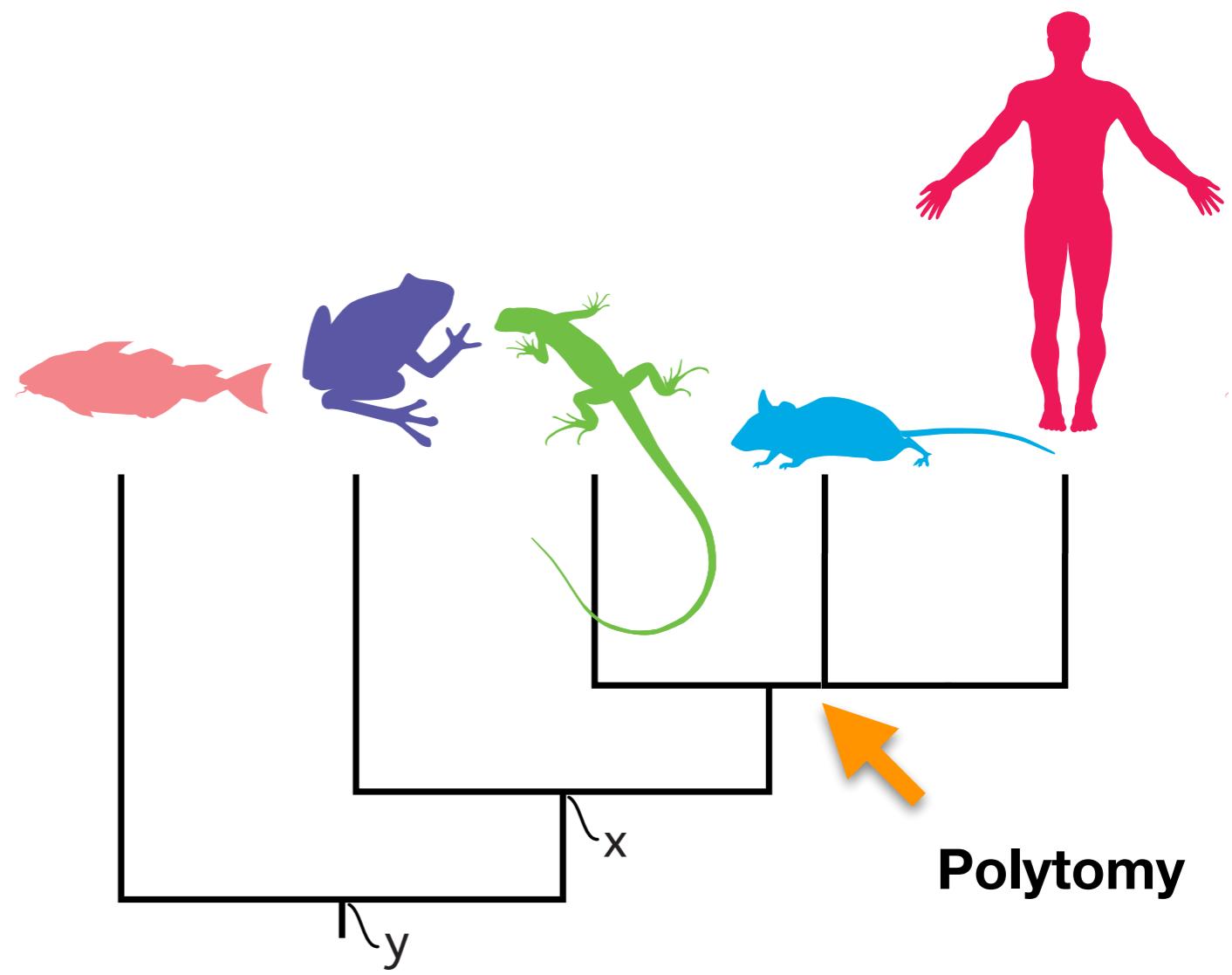
Internal Nodes

- Alternative names
 - Ancestor
 - Node (sloppy shortcut)
- Are vertices of *degree* > 3
- Represent
 - Ancestor species
 - Speciation event
- Have **descendants**, that are either tips or other internal nodes



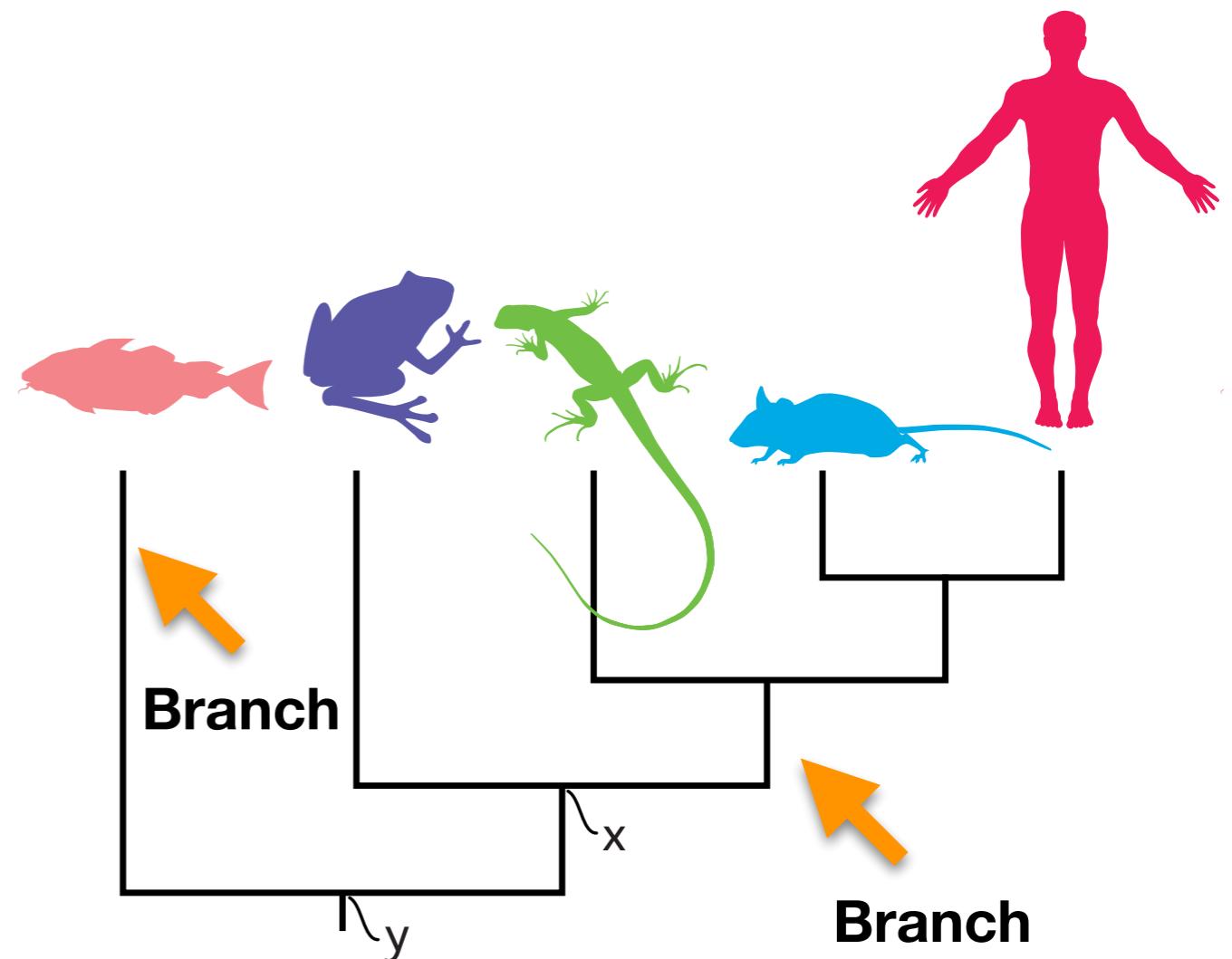
Dichotomy vs Polytomy

- We always assume ancestors only have two descendants. **True tree is dichotomous**
- But we may depict an ancestor having three direct descendants (**polytomy**).
- Polytomy represents **uncertainty** about the relationship



Branches

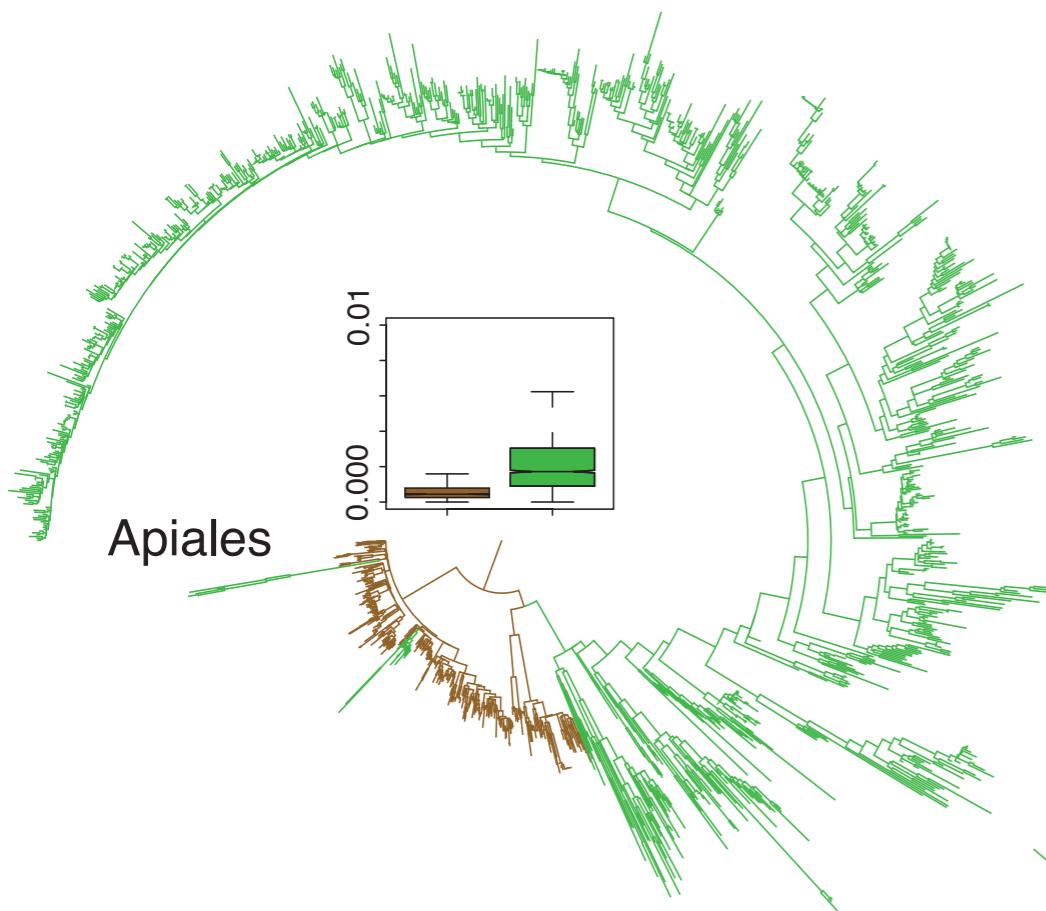
- Alternative names
 - Edges
- Connect nodes
- Define relationships
- Can have lengths depicting
 - Degree of divergence in molecular or morphological characteristics
 - Time, in generations, millions of years, etc.



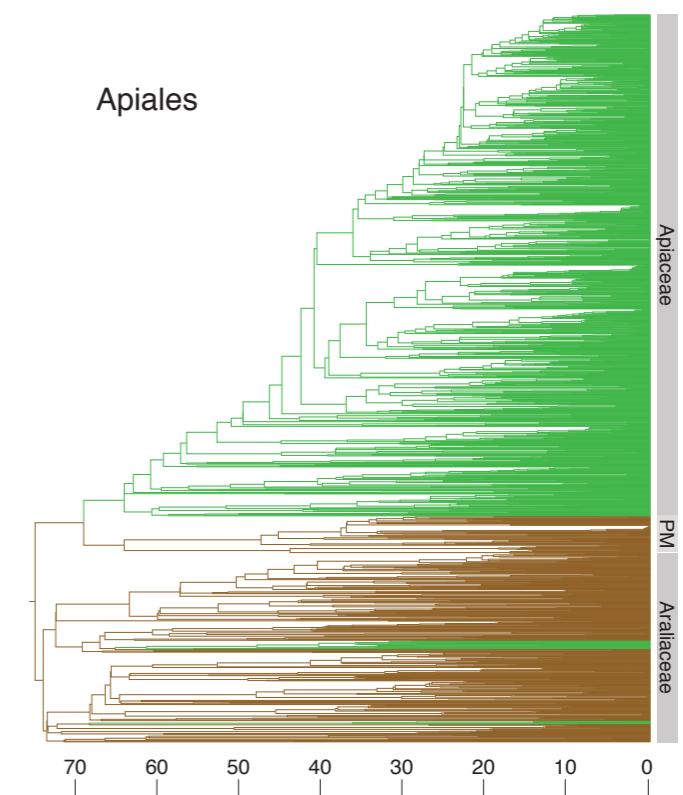
Branch lengths as *mutations per site*

- Estimated from the molecular data and evolutionary model

Molecular divergence tree

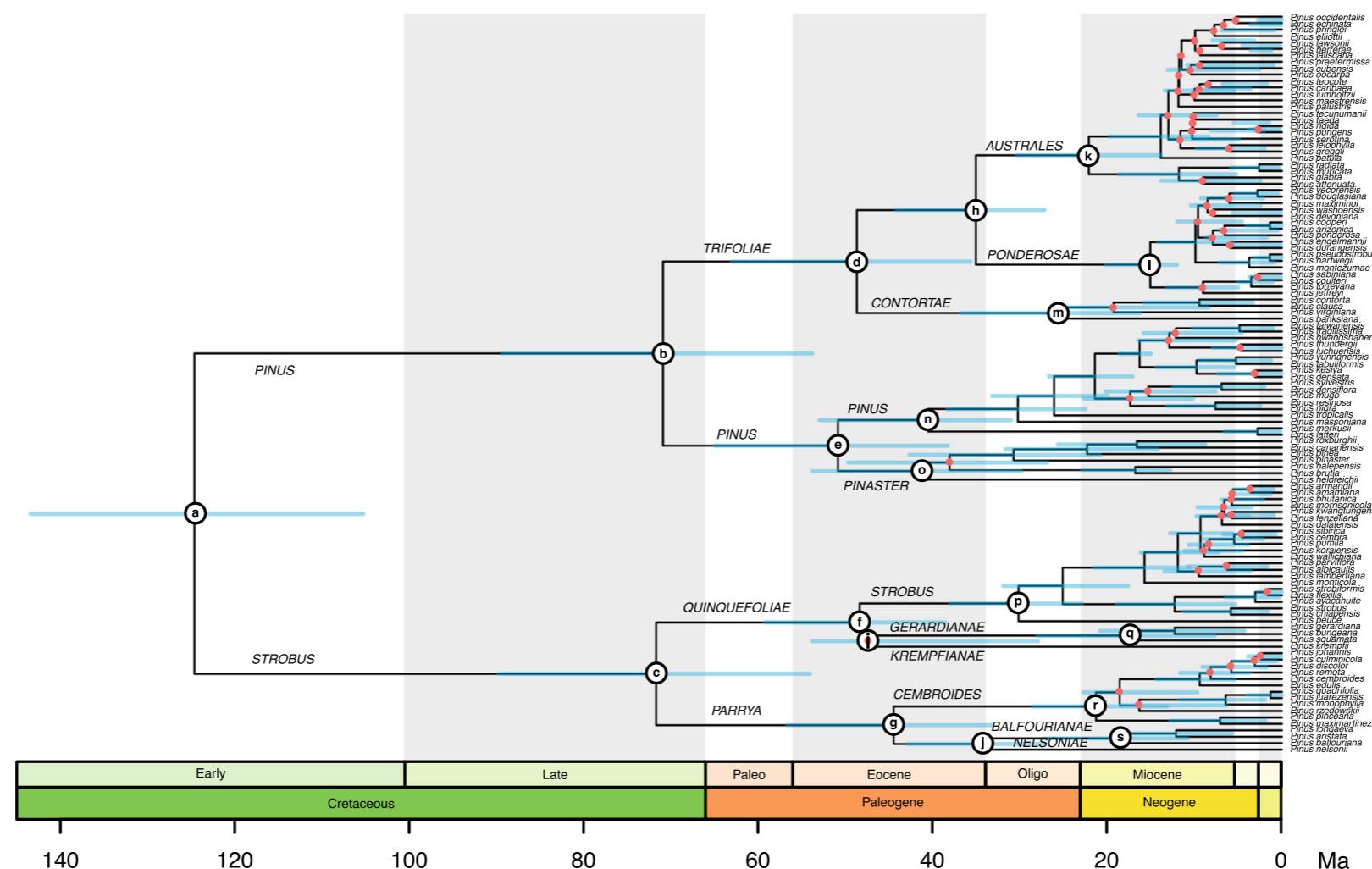


Time tree



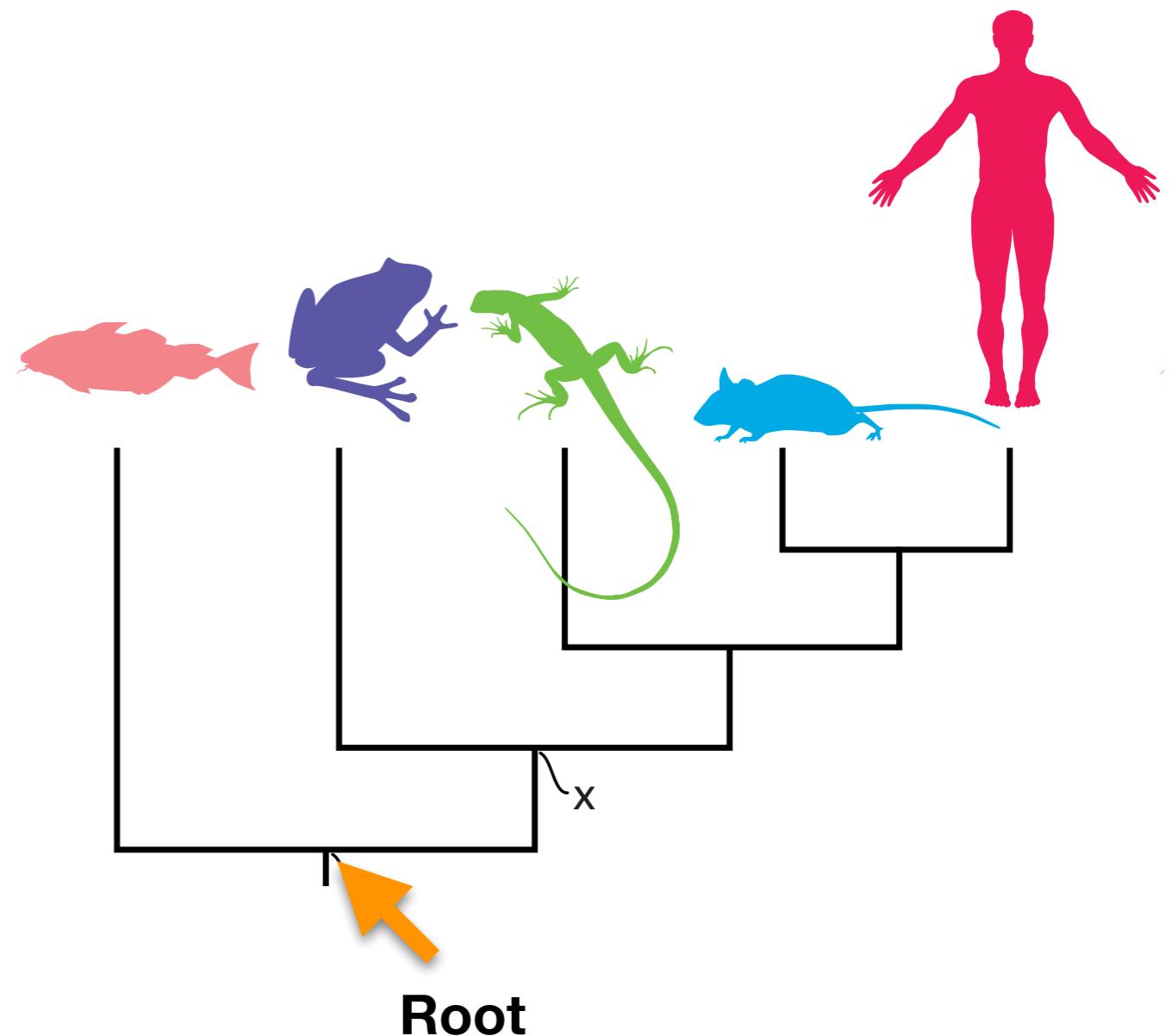
Branch lengths as time

- Calibrated using a molecular clock
 - Node age uncertainty shown as blue bars

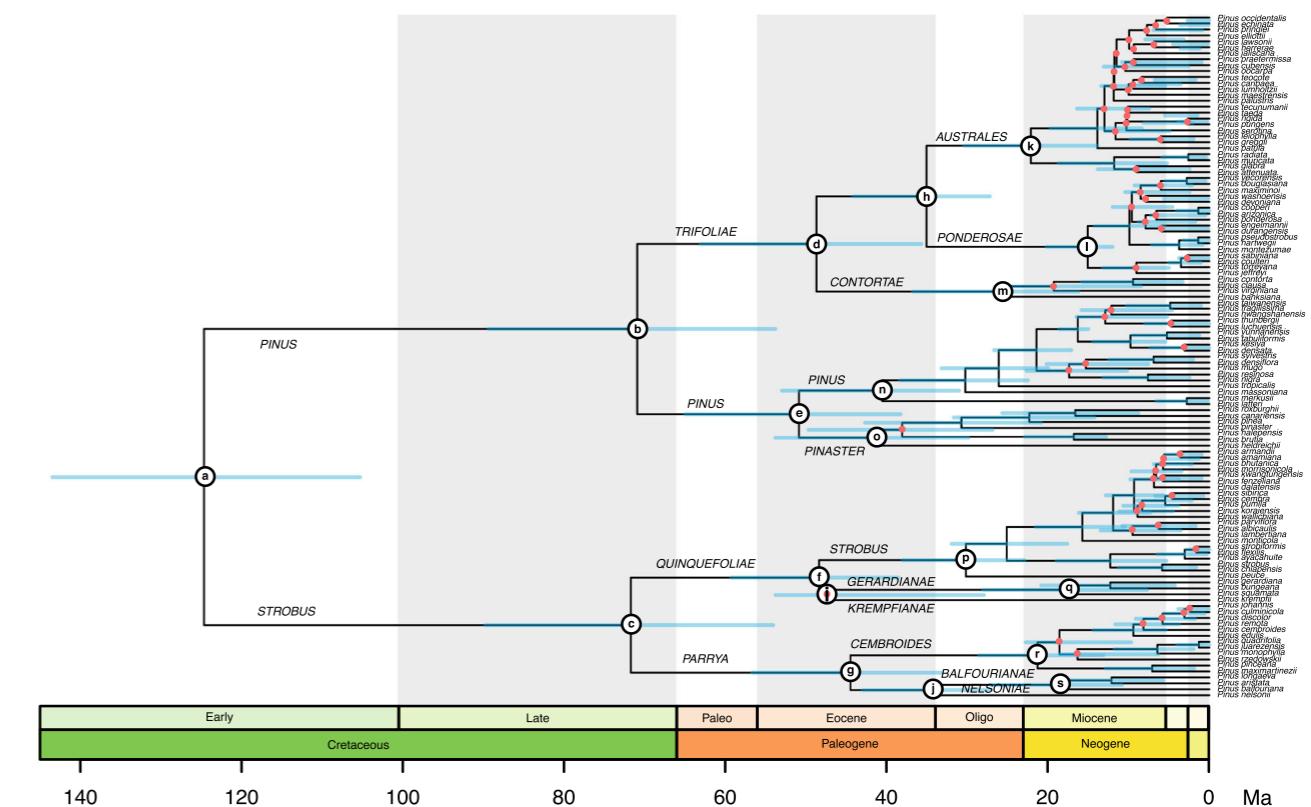
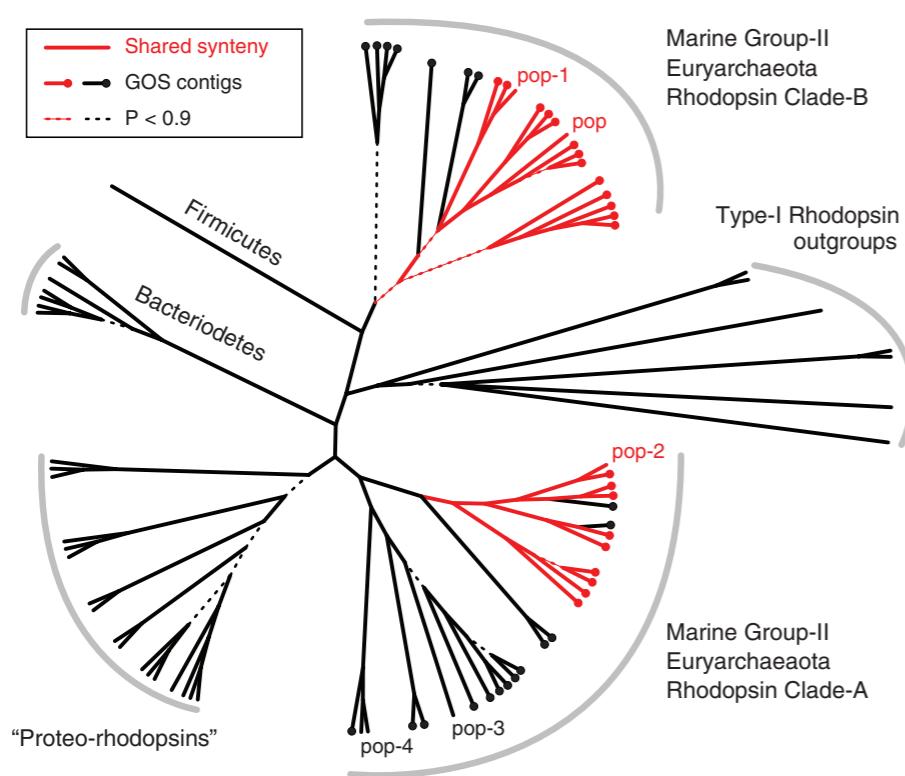


Root

- Alternative names
 - Most recent common ancestor
 - Is a vertex of *degree 2*
 - Represents the ancestor of all taxa at hand
 - The link point between our tree to the rest of the tree of life.

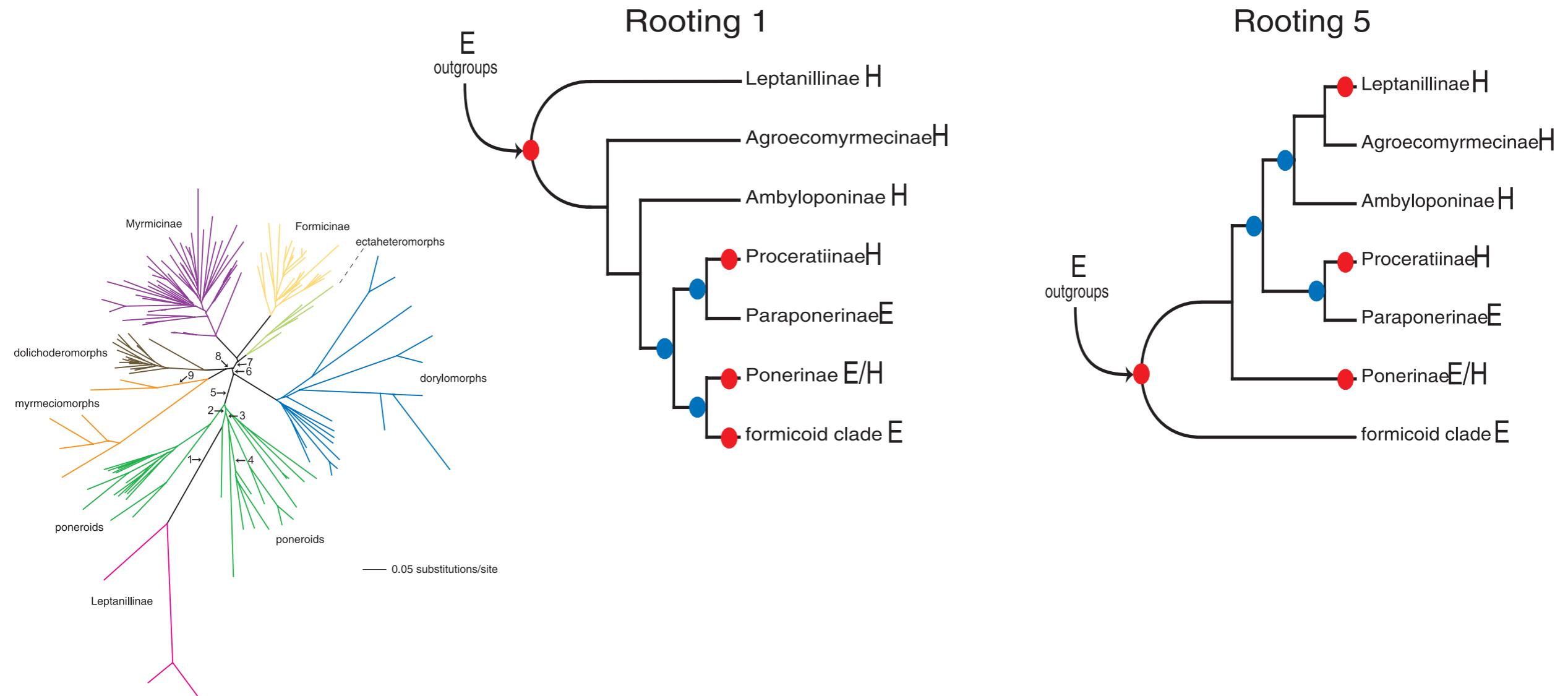


Rooted vs Unrooted Tree



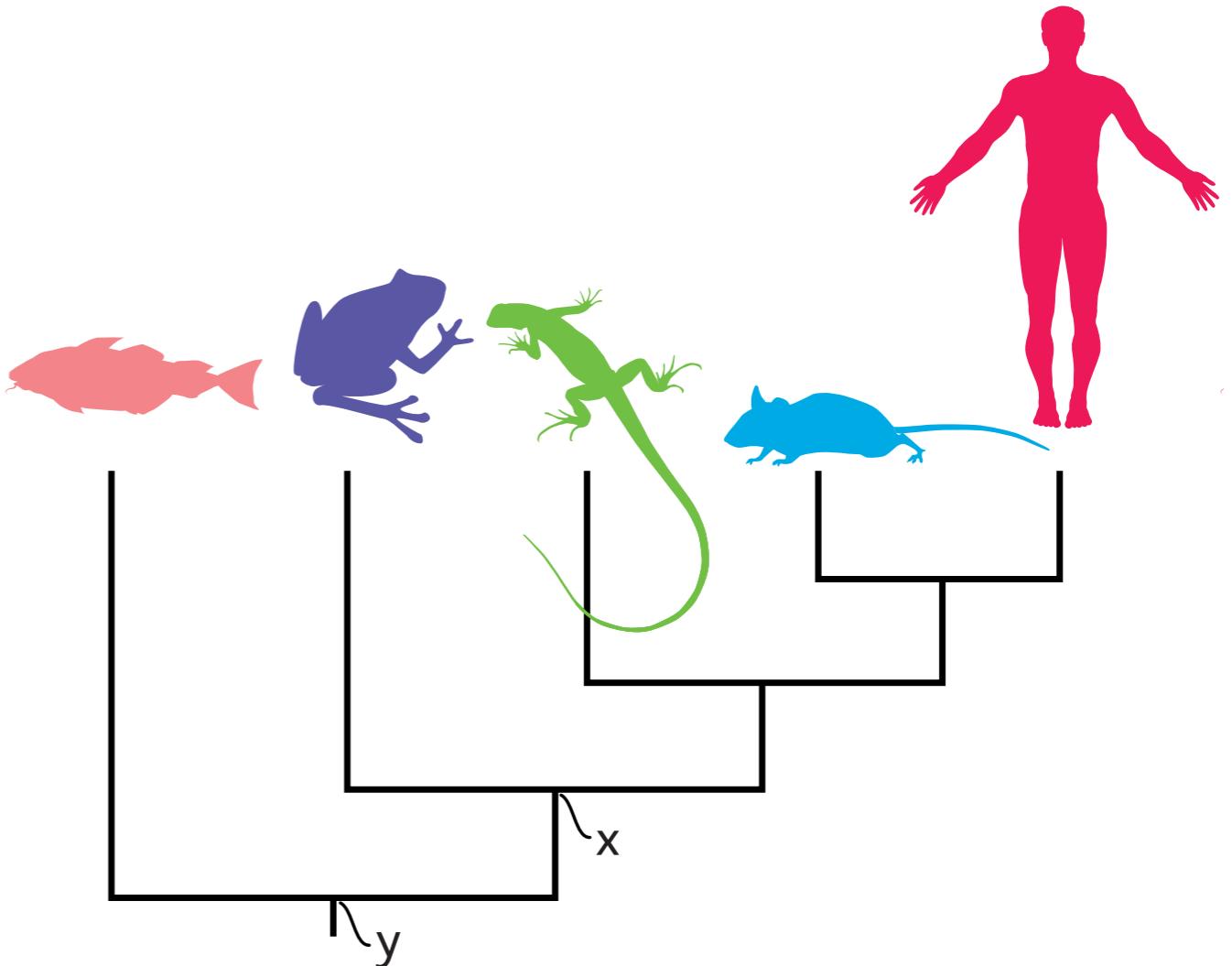
Rooting matters for inference

H = small colony
E = large colony



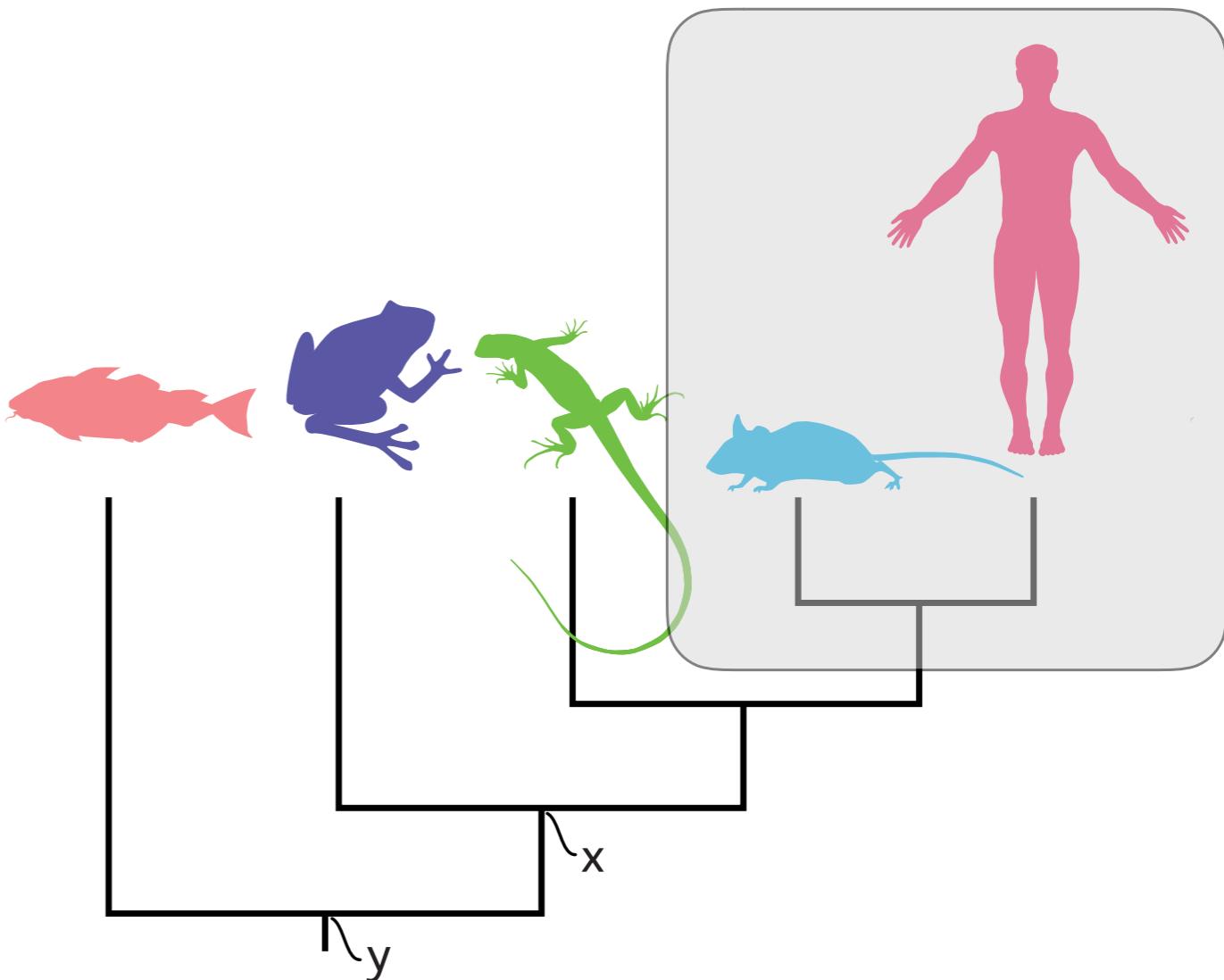
Describing trees: Sister groups

- The two descendants form the same ancestor:
 - ***Amphibians and tetrapods are sister***
 - ***Humans are sister to mice***



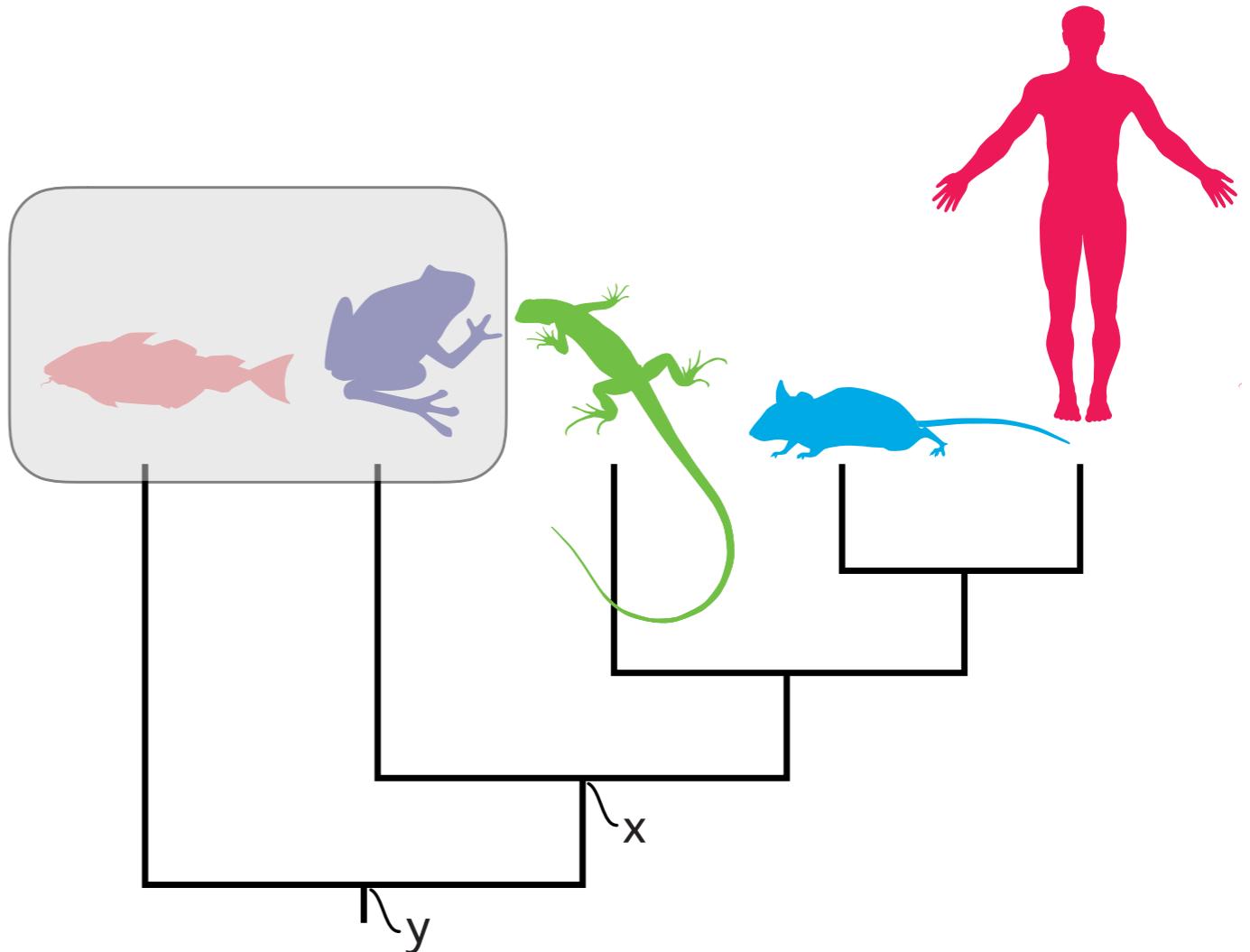
Describing trees: Clades

- Alternative names
 - Lineage
 - ***Monophyletic*** group
- An ancestor and all of its descendants
 - ***Mice and humans form a clade***

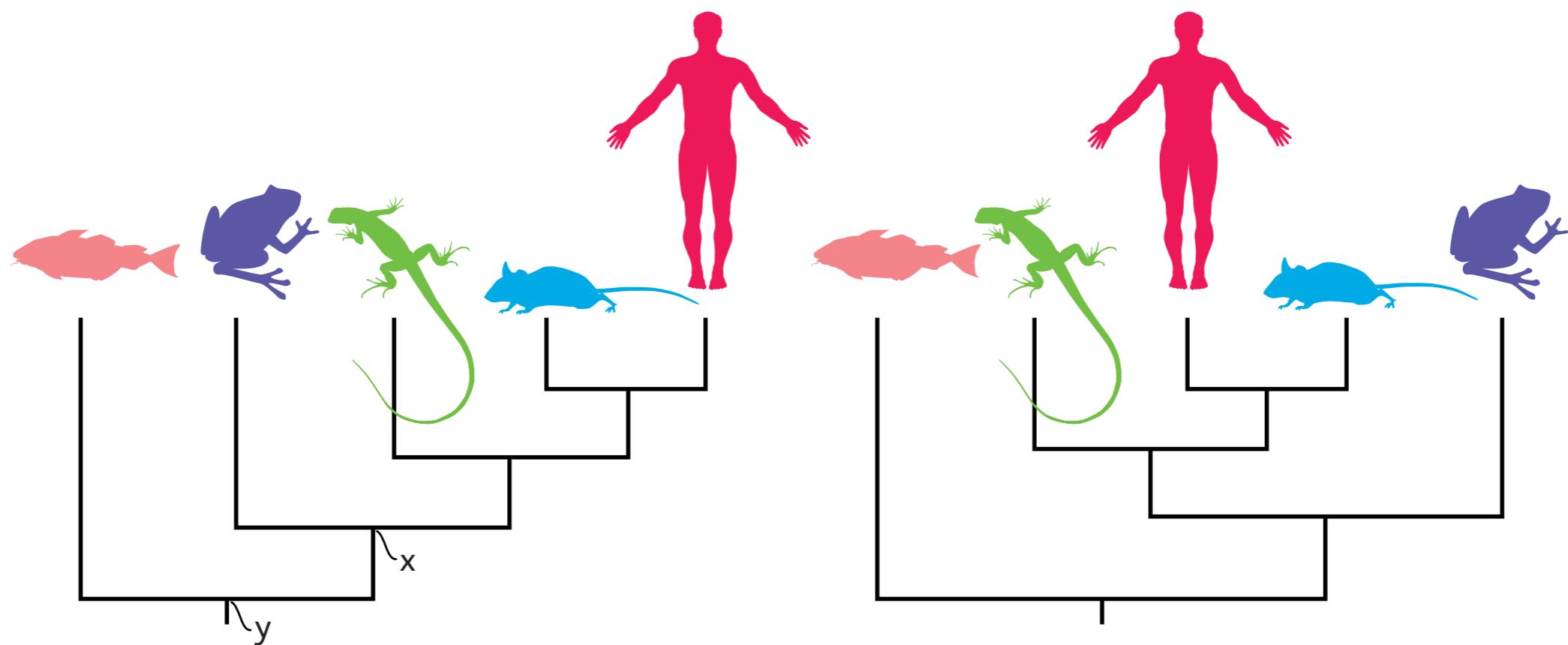


Describing trees: Paraphyletic

- An ancestor and **some** but **not all** of its descendants
 - *Slimy skinned animals are a paraphyletic group*



Reading a tree



Next time:
**Importing, manipulating,
and visualizing trees in R**