

# **Phylogenetic Biology**

## **Week 1**

Biology 1425  
Professor: Casey Dunn  
Brown University

# Front matter...

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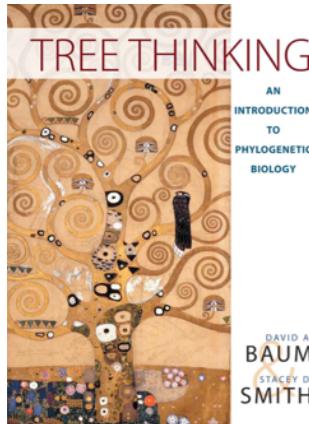
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# Sources

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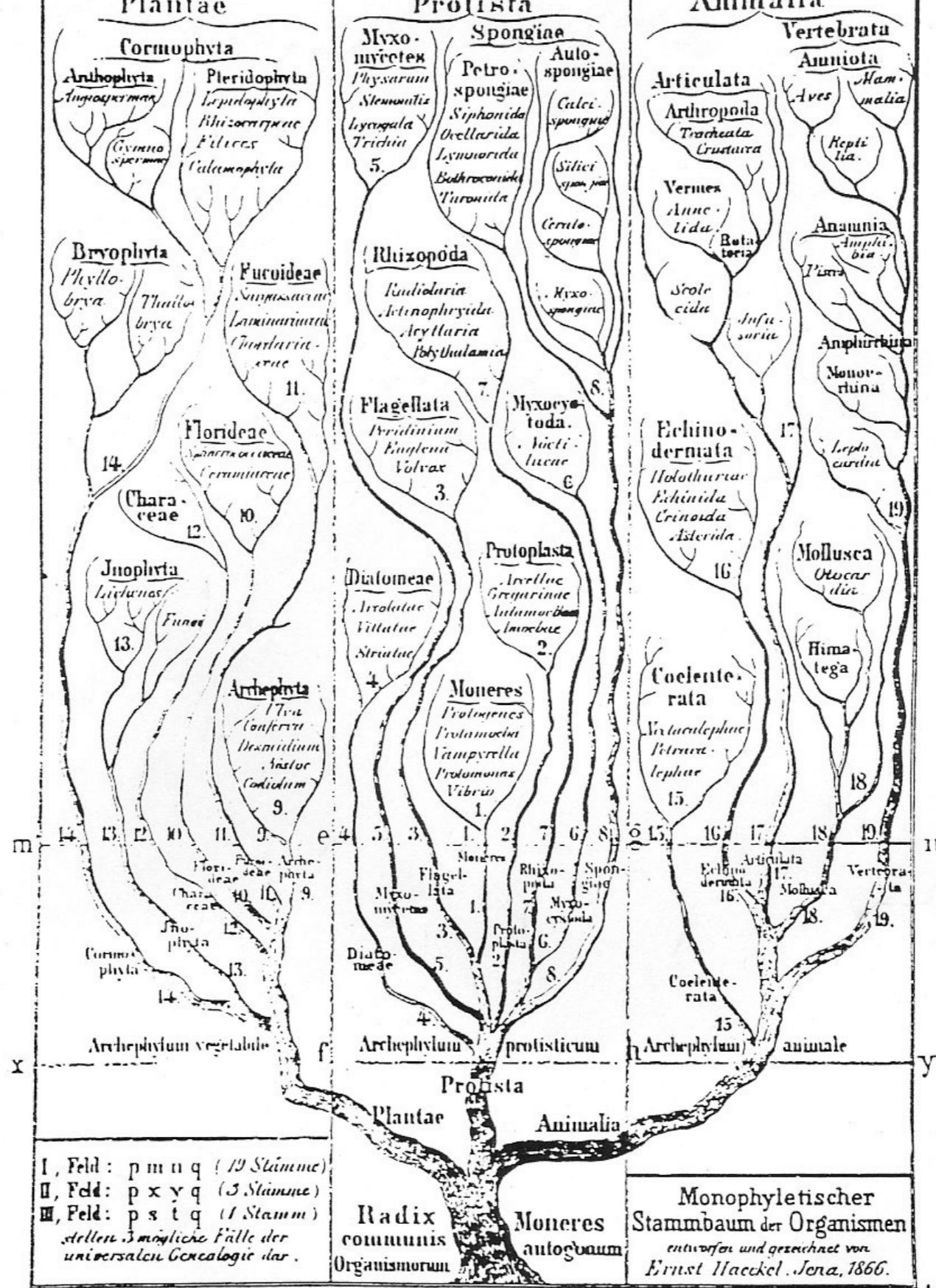
Baum, D and S. Smith (2012) Tree Thinking: and Introduction to Phylogenetic Biology. Roberts and Company Publishers. ISBN 9781936221165

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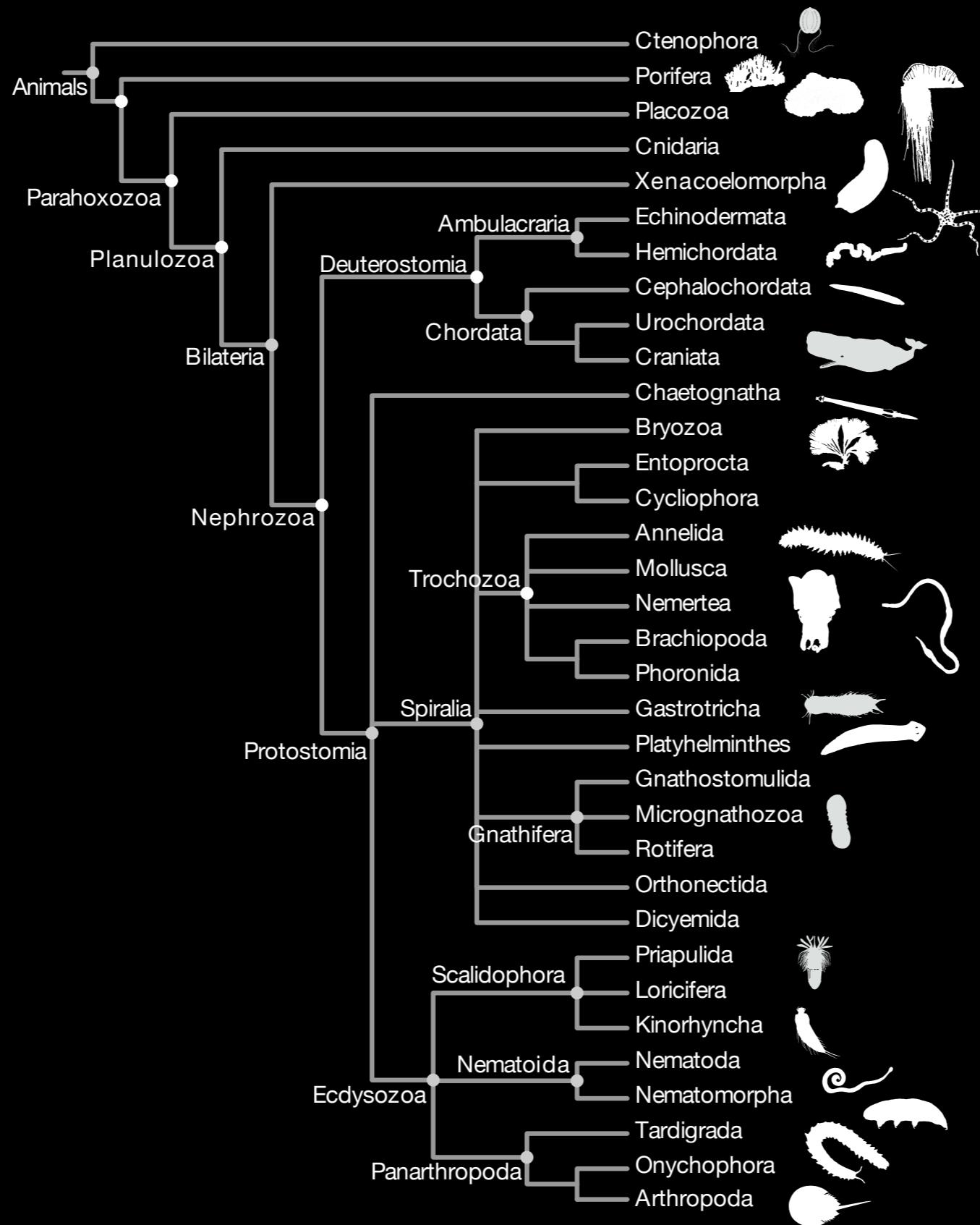
# What is a phylogenetic tree?

A depiction of the relationships between biological entities that descended from a common ancestor

These entities could be anything from genes to populations to species to groups of related species



# Animal Phylogeny

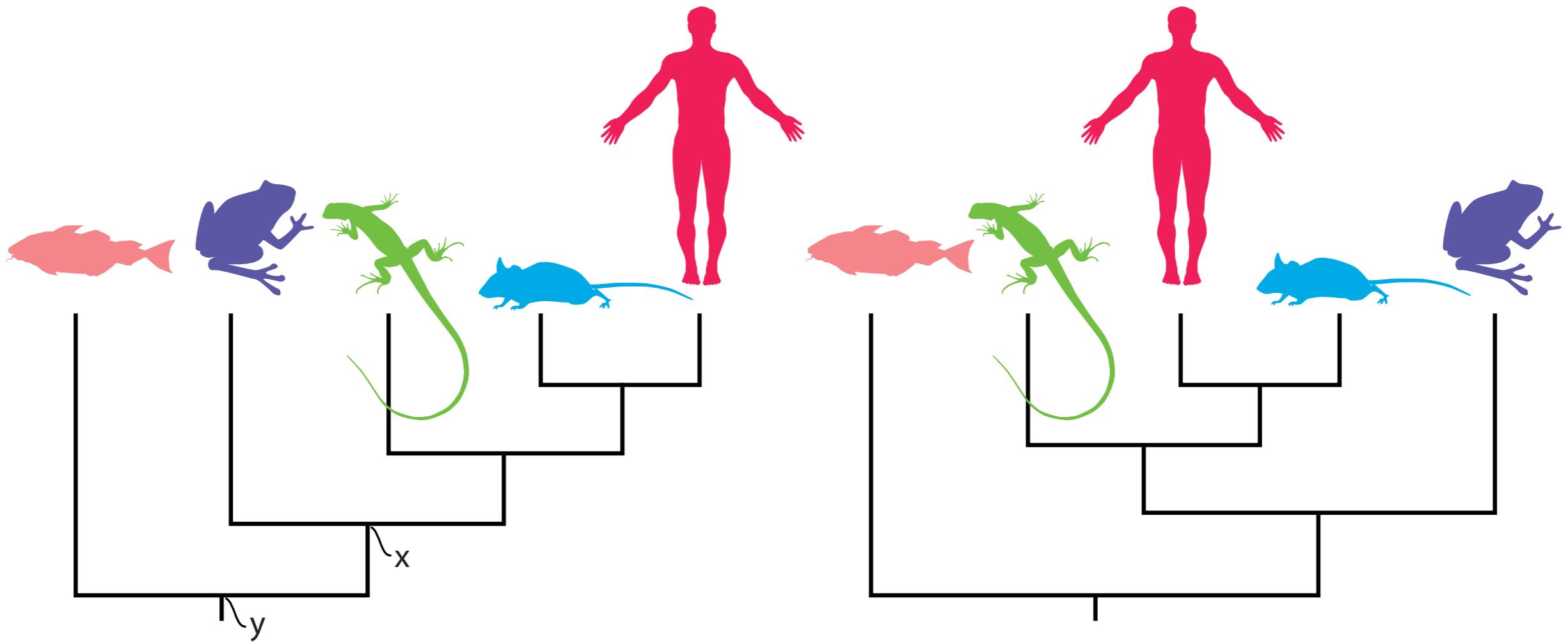


# What a phylogenetic tree is not

A diagrammatic depiction of the similarities between organisms

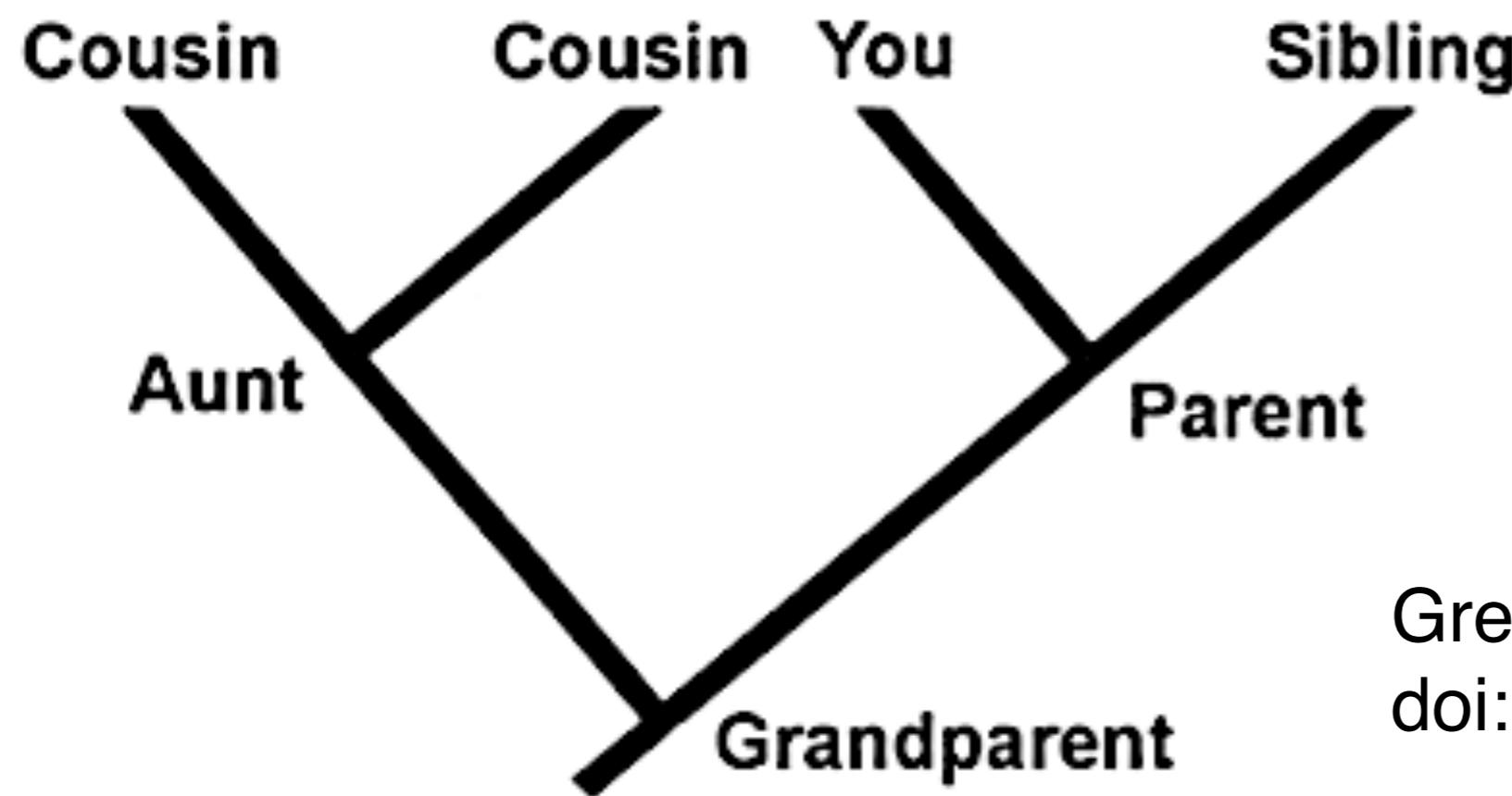
A phylogenetic tree isn't a statement about the specific properties of organisms, it is a statement about their relationships

# Reading a phylogenetic tree



Baum *et al.* 2005, doi:10.1126/science.1117727

Tips are not descended from  
other tips



Gregory 2008,  
doi:10.1007/s12052-008-0035-x

“Contemporary entities are related through common ancestors—they are not themselves ancestors of one another...”

“The reader is not descended from a sibling; rather, both are descended from a shared parent.”

Sponges



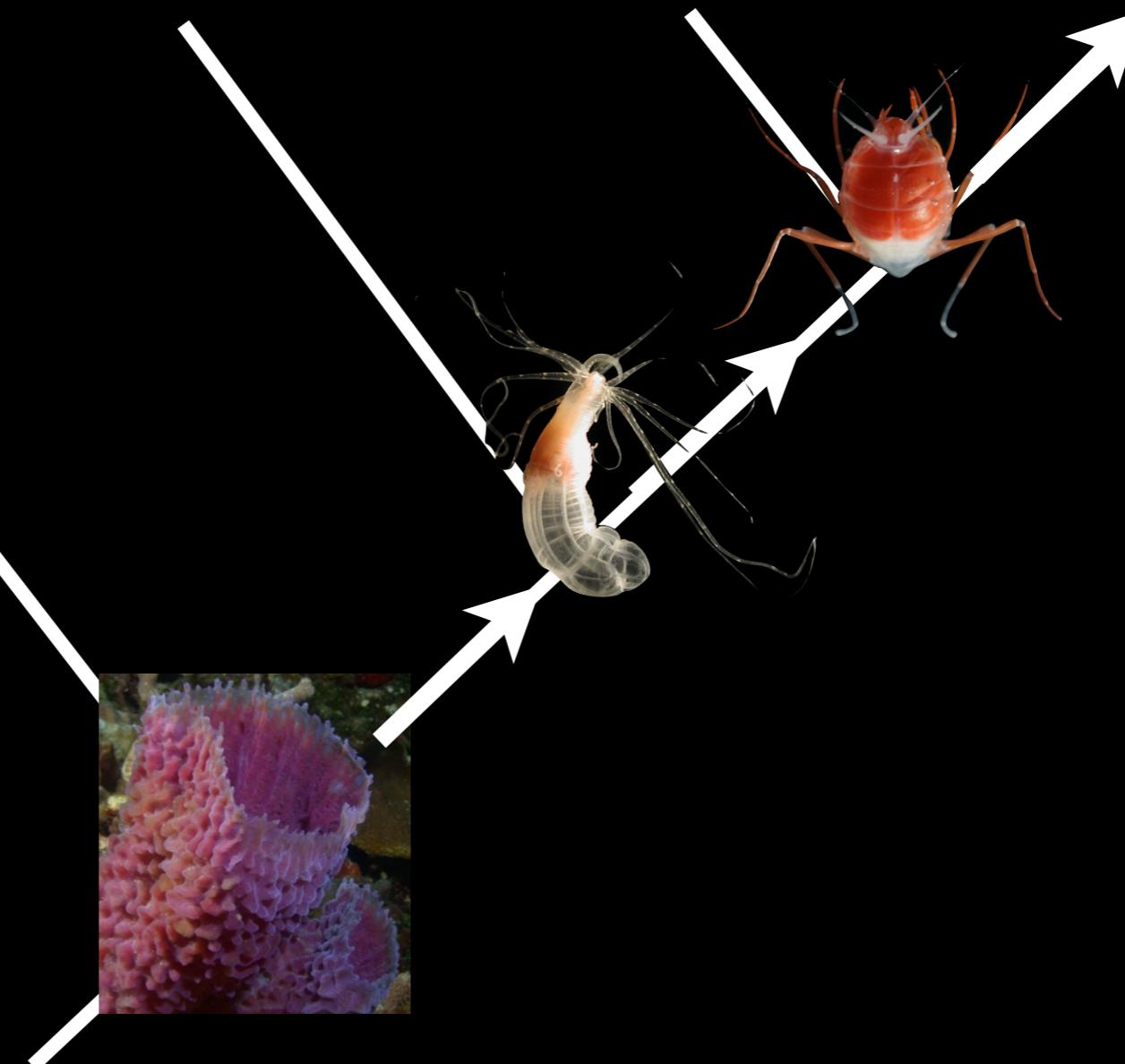
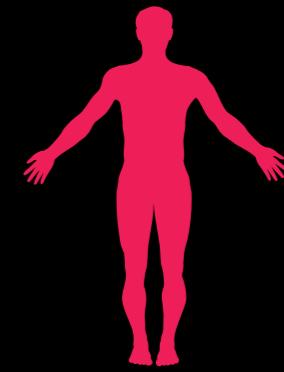
Cnidarians



Arthropods



Humans



Sponges



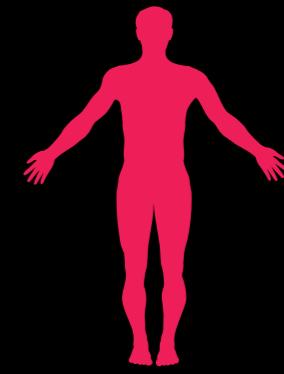
Cnidarians



Arthropods



Humans



You evolve!  
No, you evolve!

Sponges



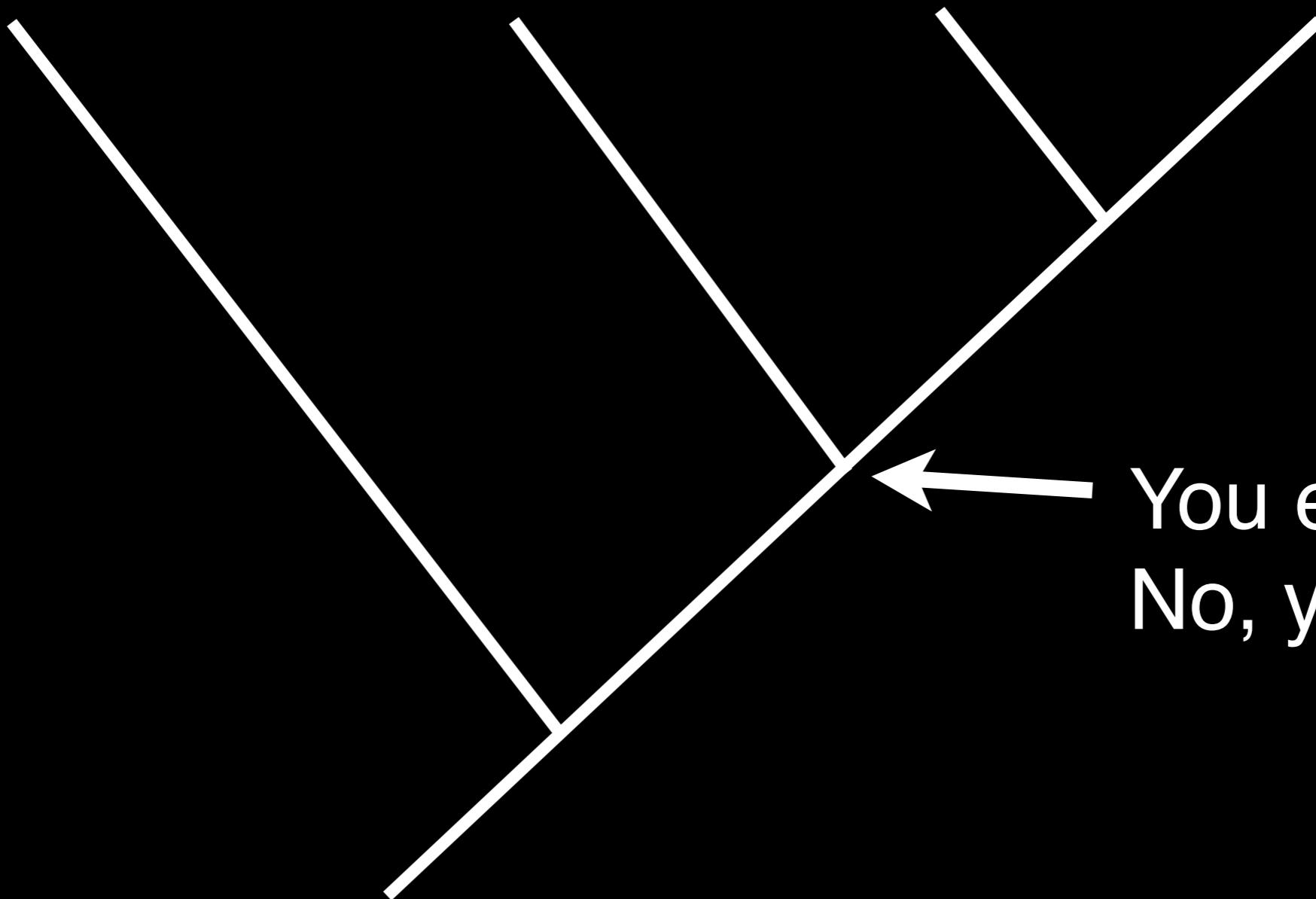
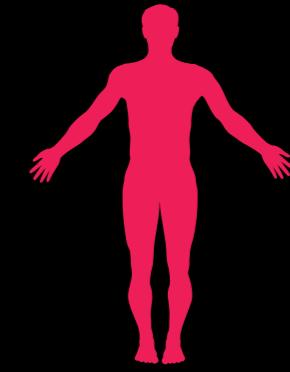
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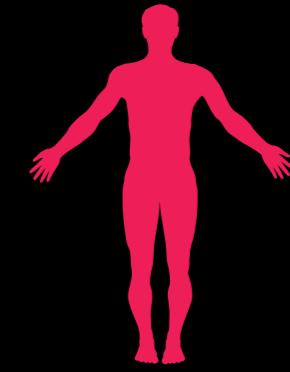
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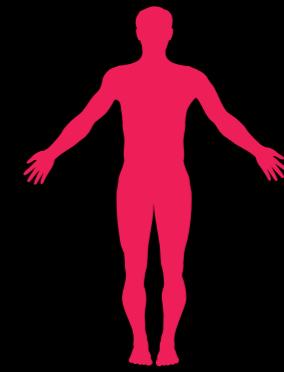
Cnidarians



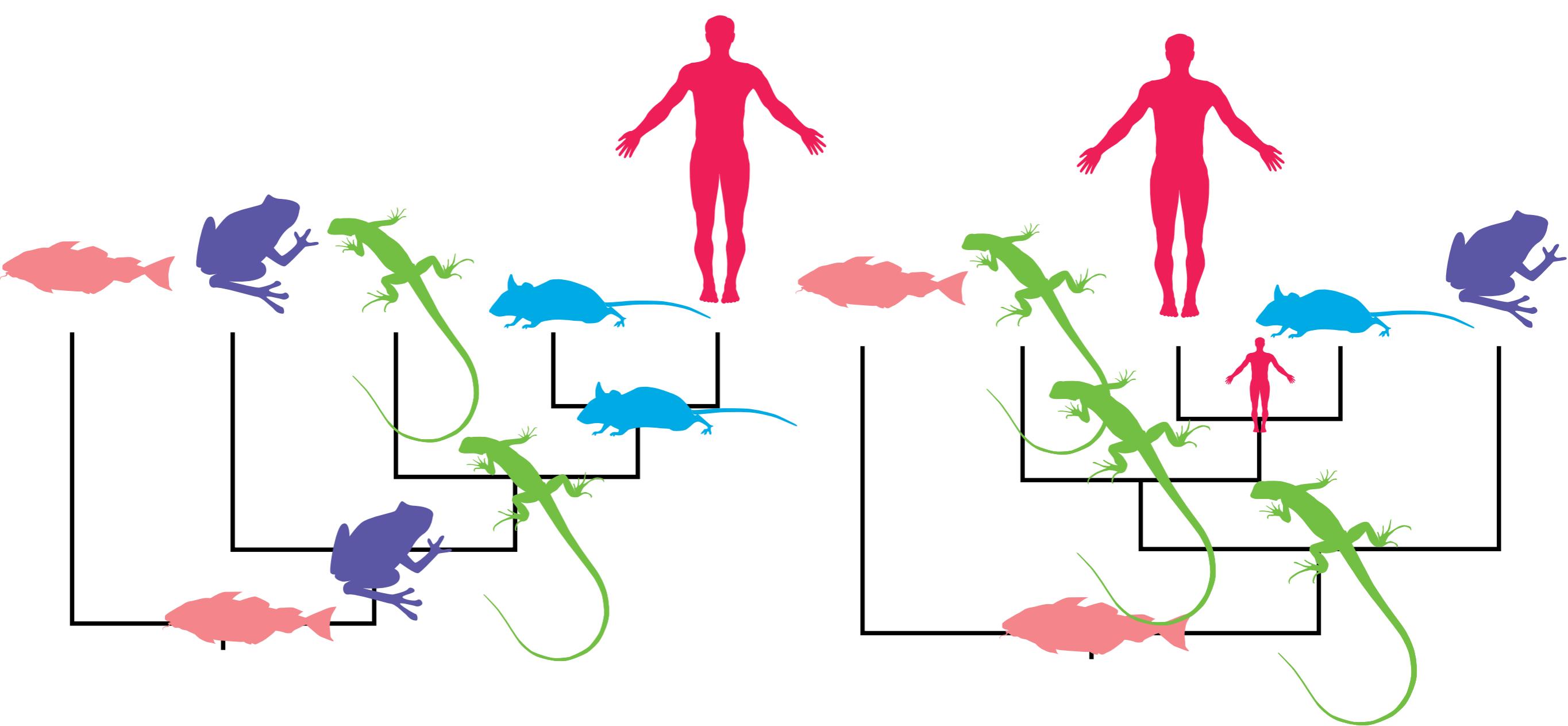
Arthropods



Humans



Which of these organisms  
has evolved for the longest time?



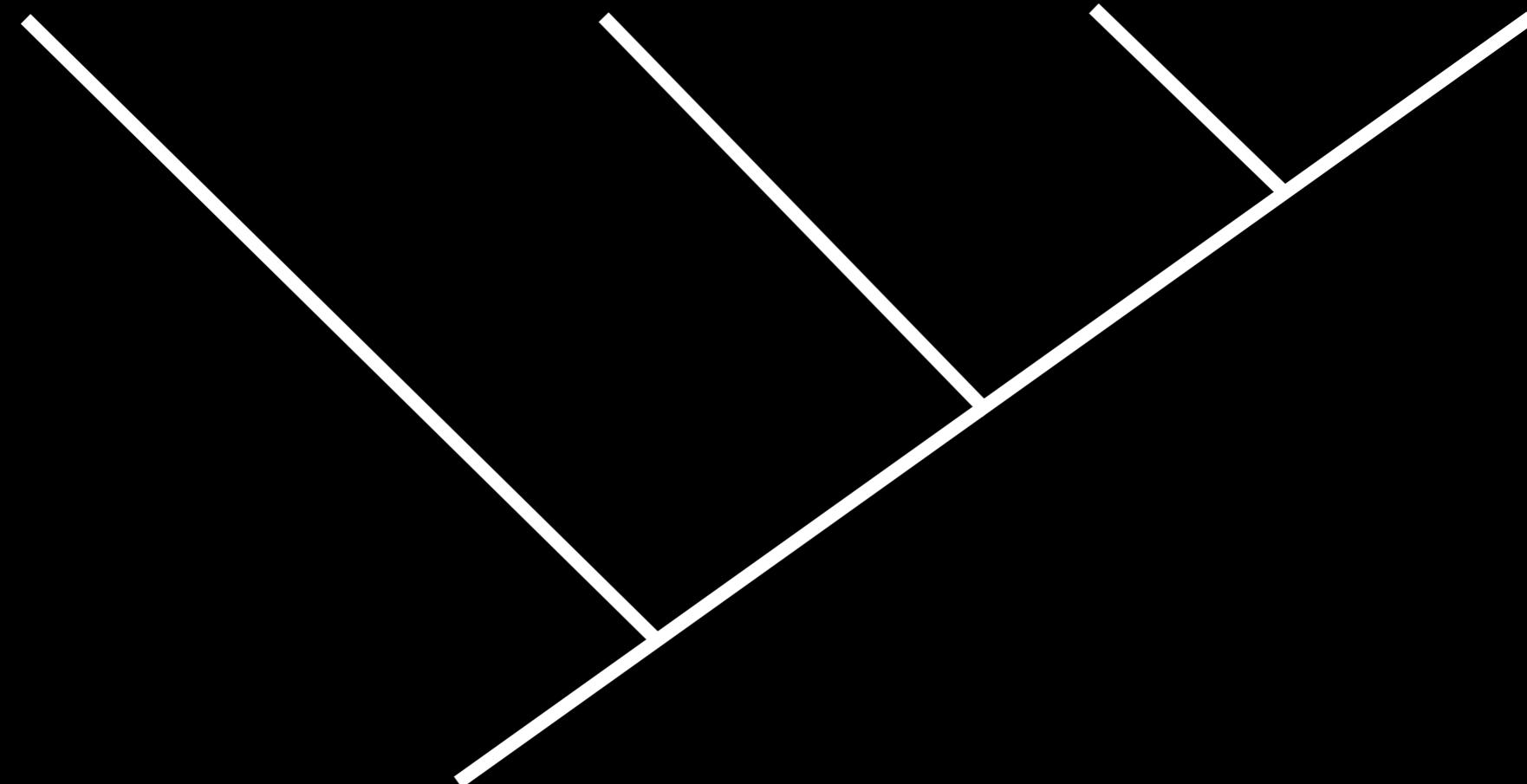
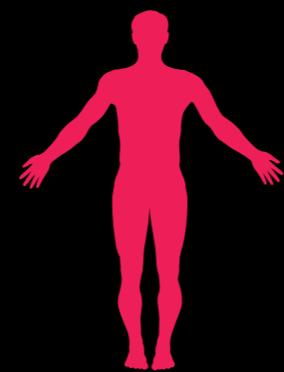
Baum *et al.* 2005, doi:10.1126/science.1117727

# Cnidarians

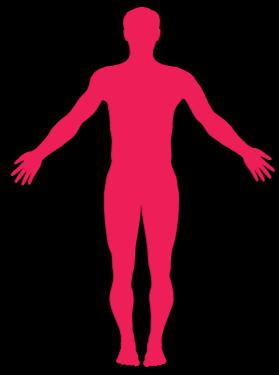


# Bilaterians

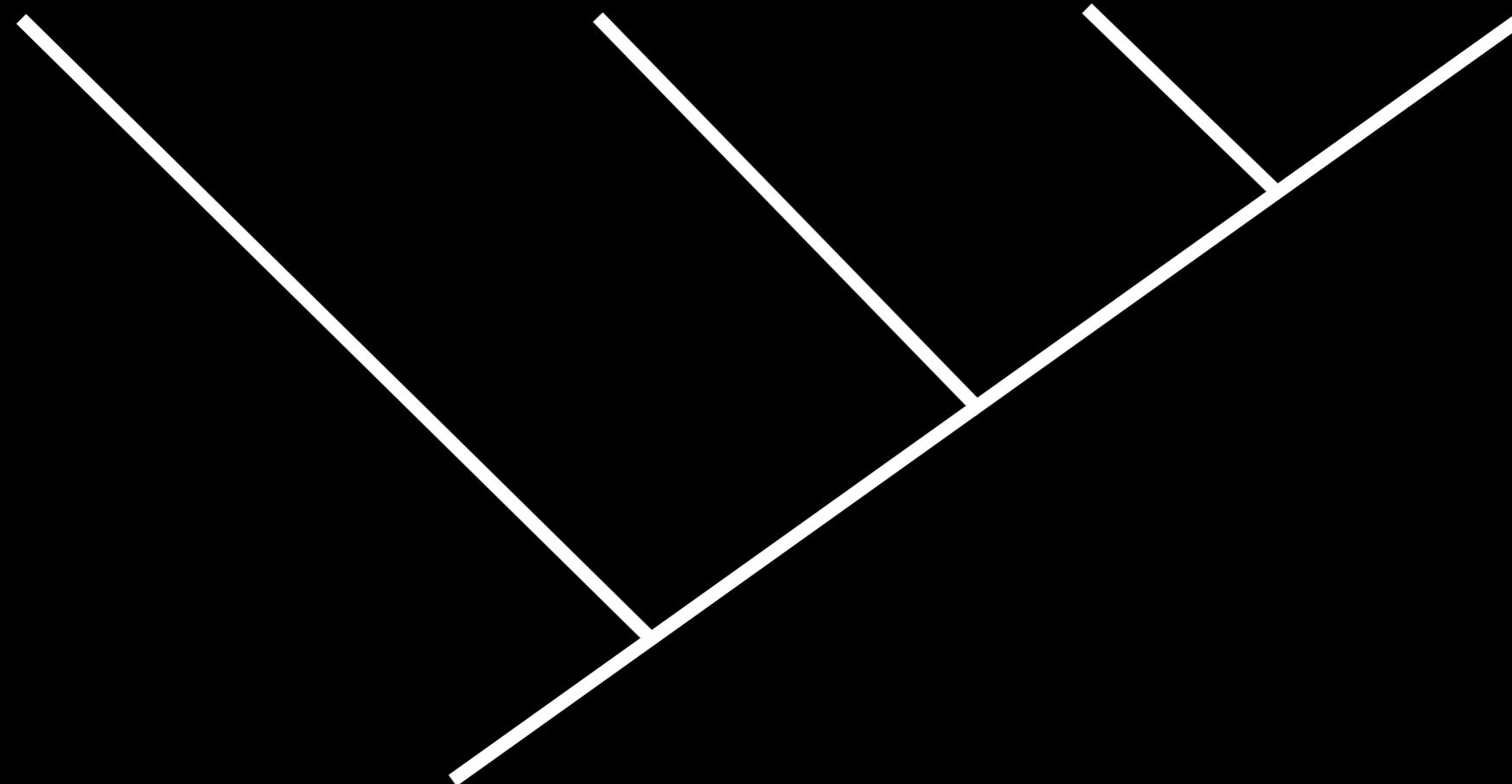
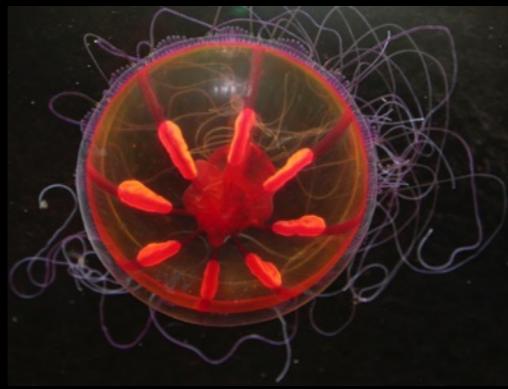
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# Bilaterians

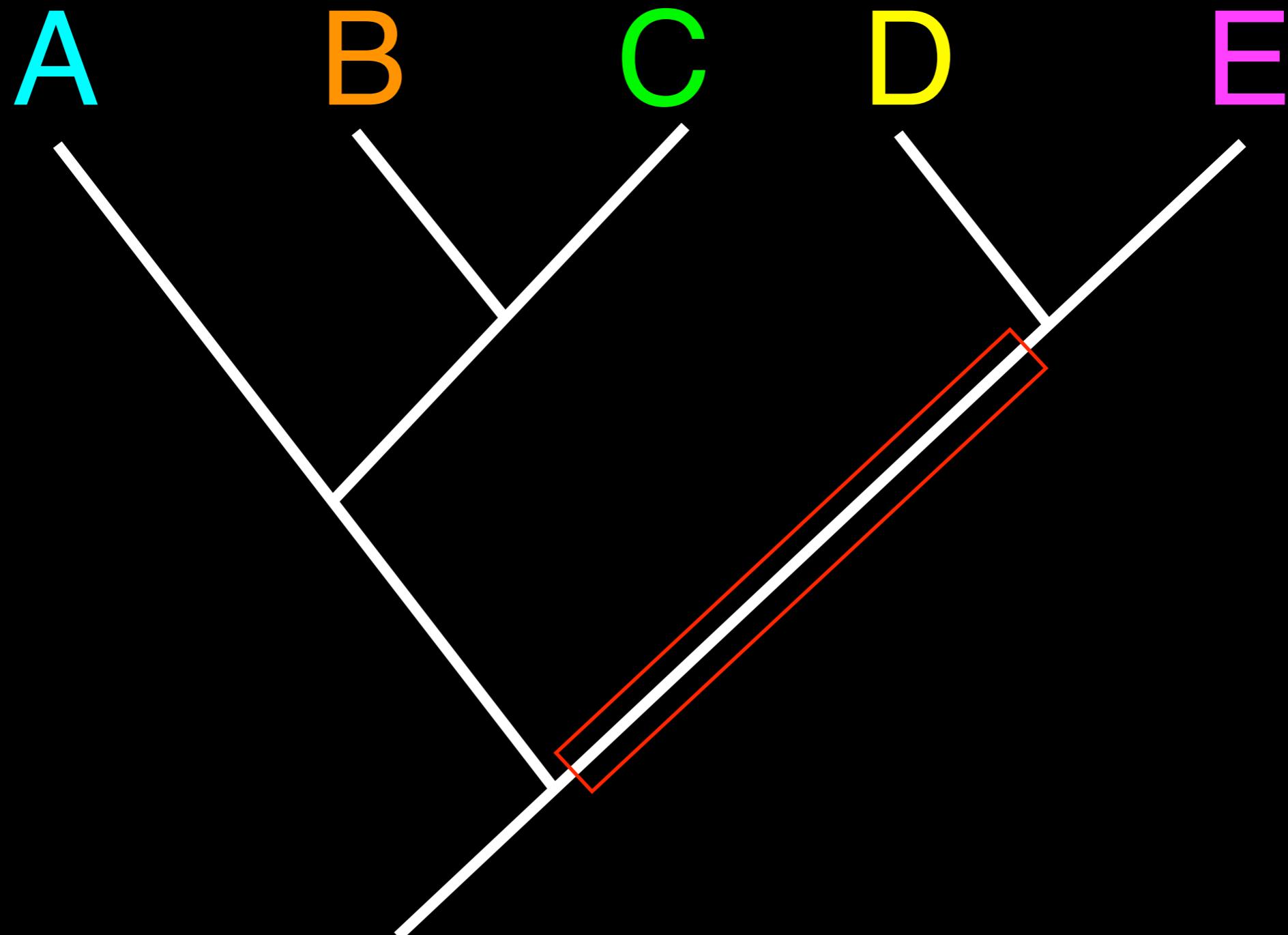


# Cnidarians

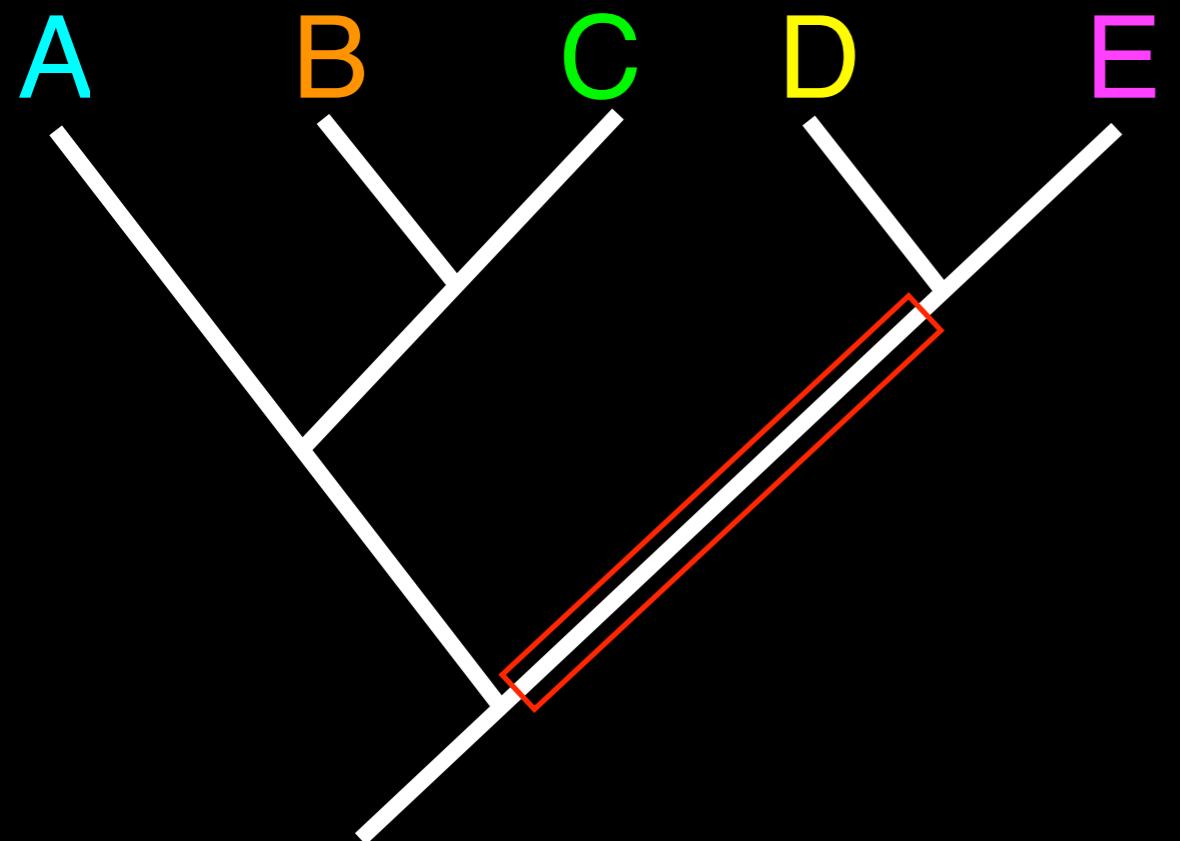


# Reading branch lengths

“BRANCHES” of a phylogeny: historical lineages



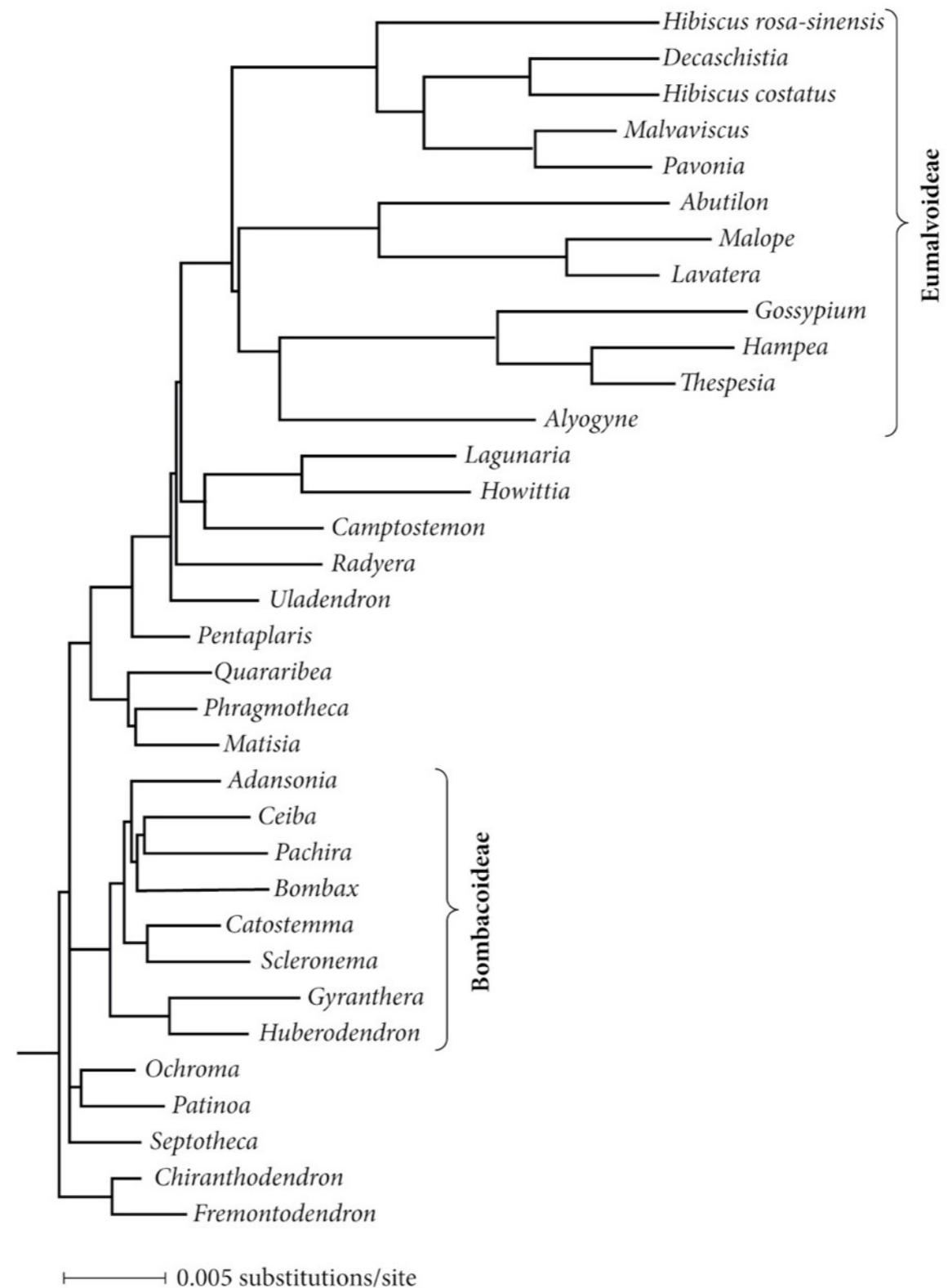
branch lengths often, but not always, mean something

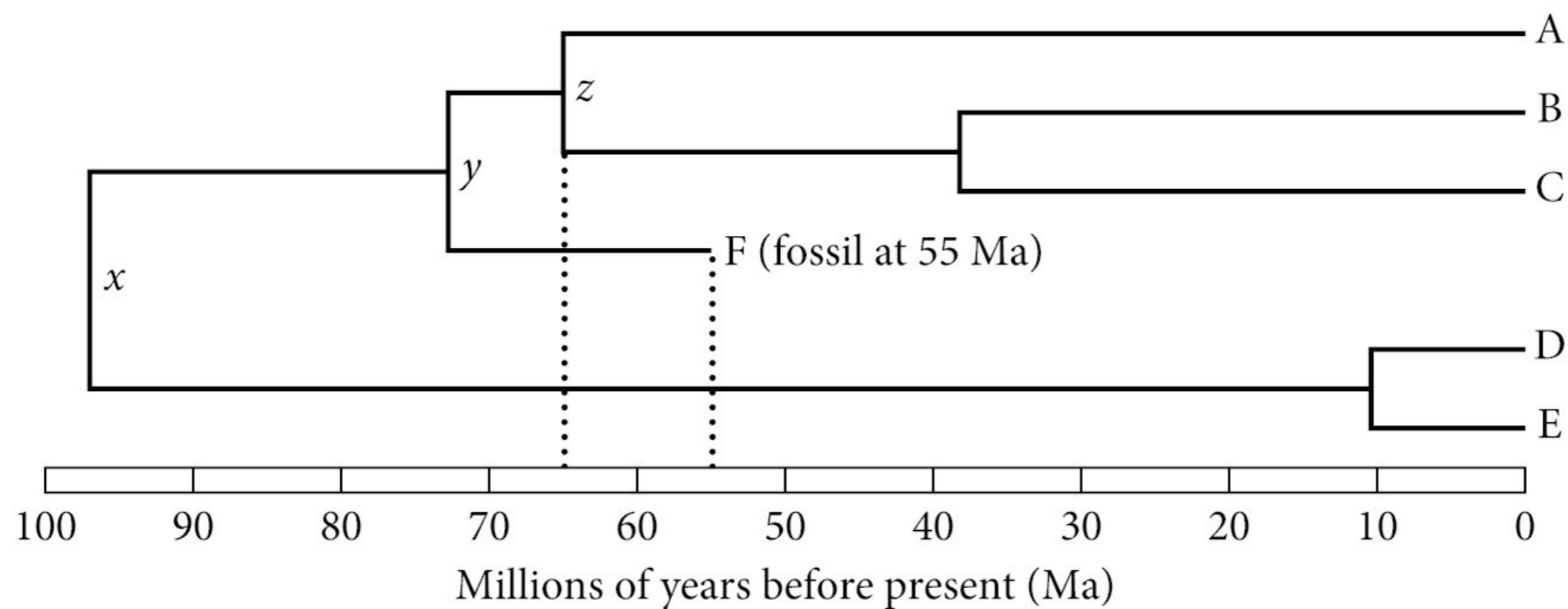


‘cladogram’ - branch lengths meaningless

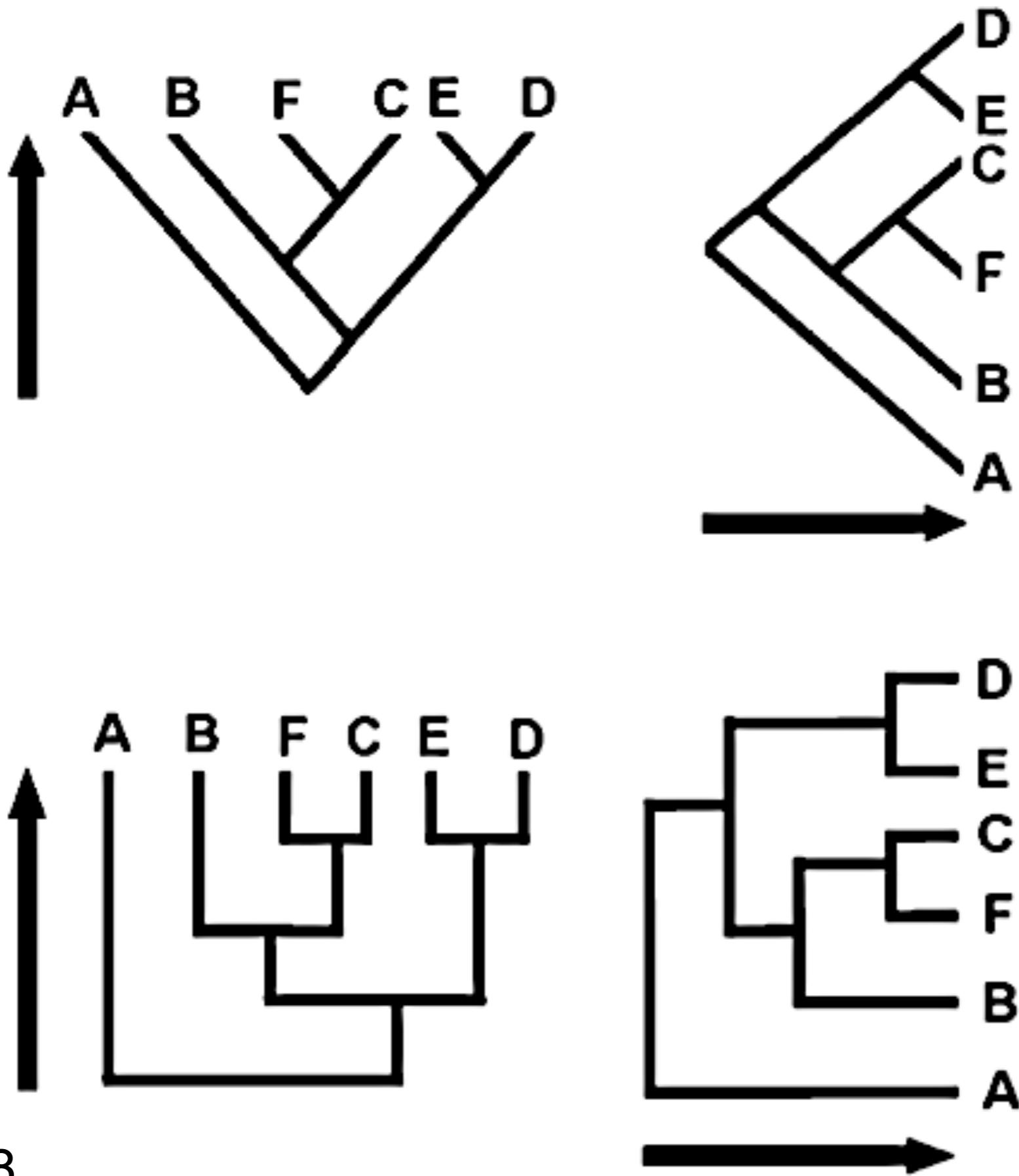
‘phylogram’ - branch lengths proportional to amount of change separating two nodes

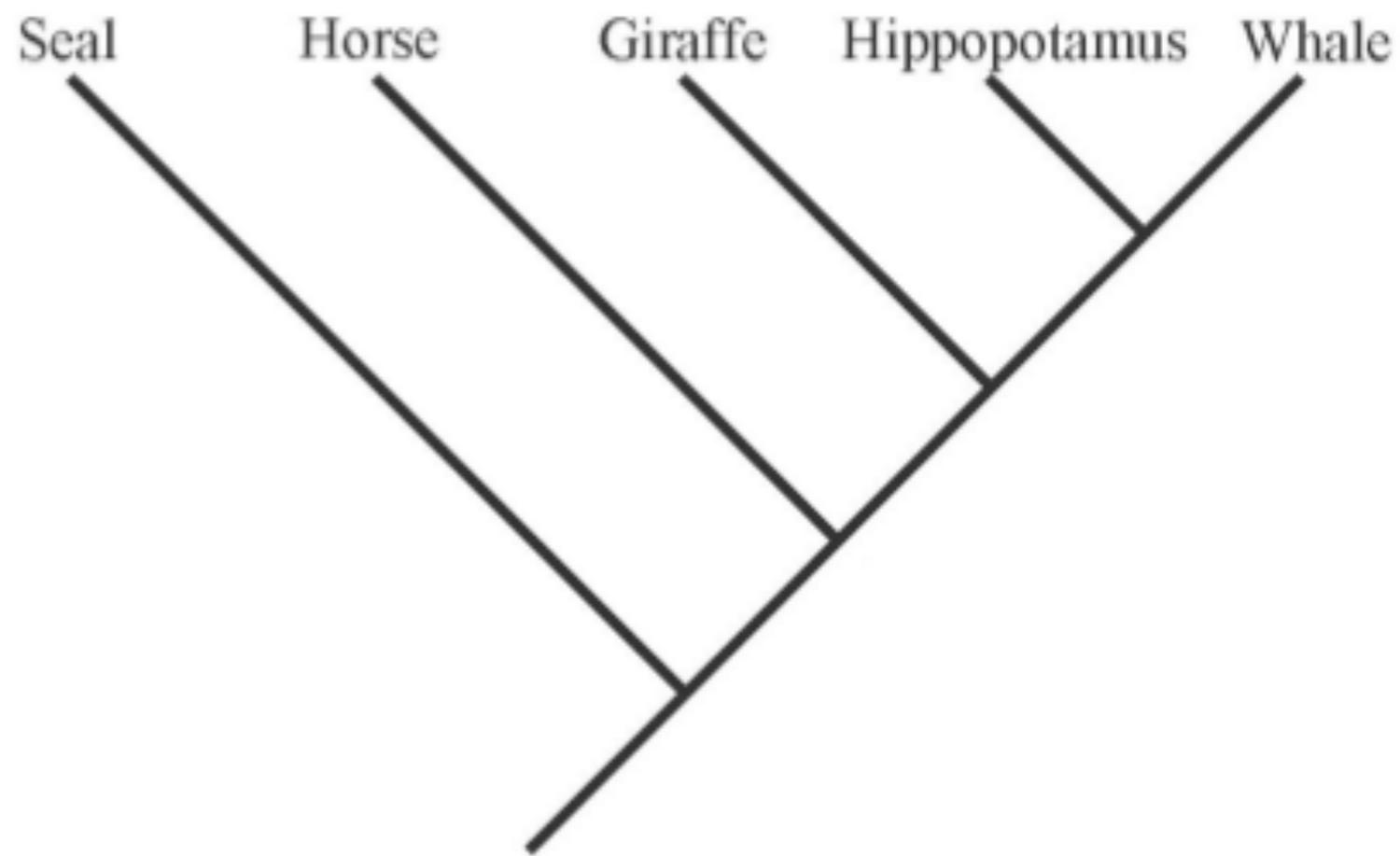
‘chronogram’ - a phylogram scaled to time, relative or real





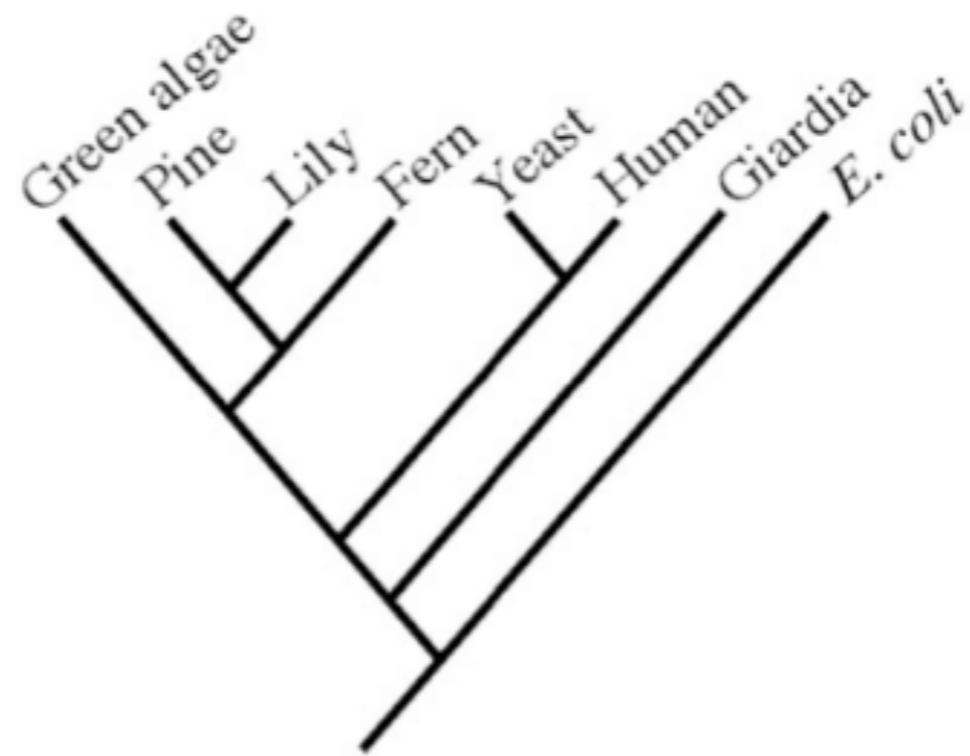
The same tree can be drawn  
in many ways



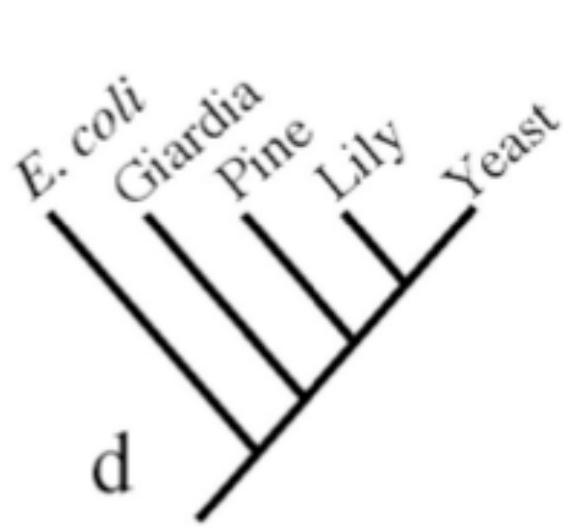
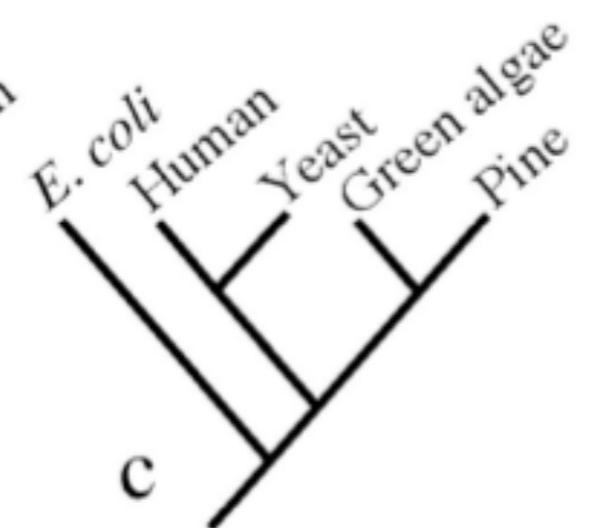
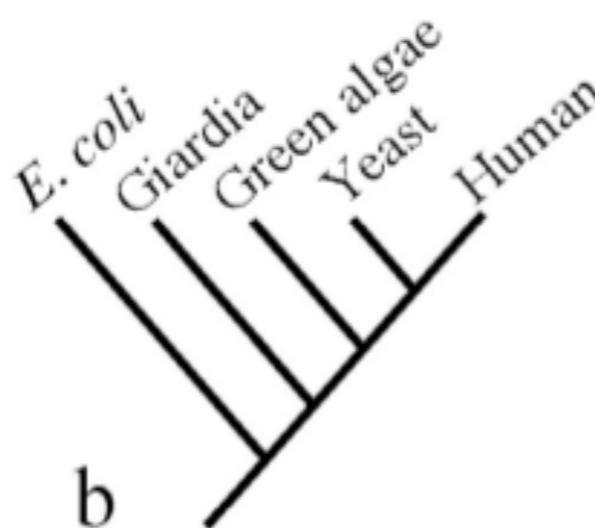
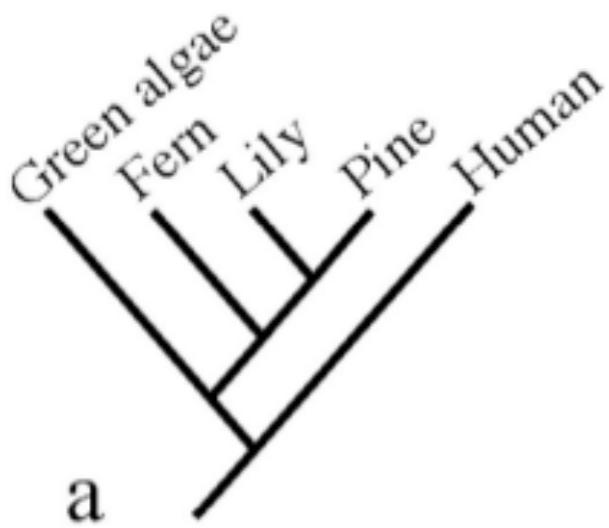


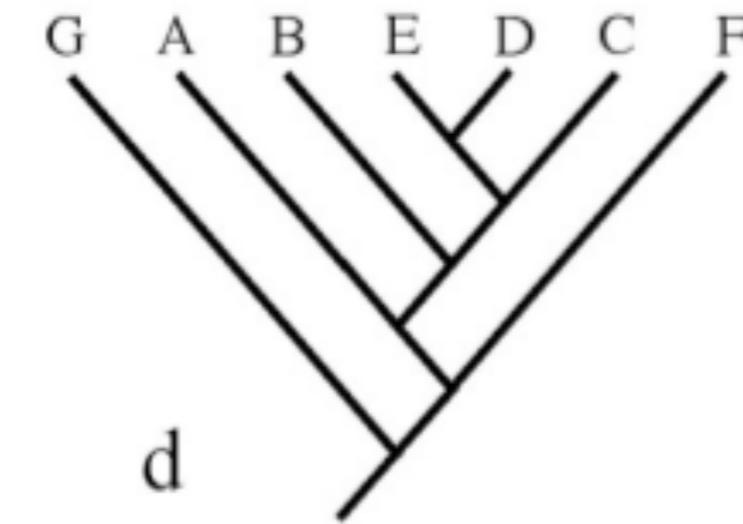
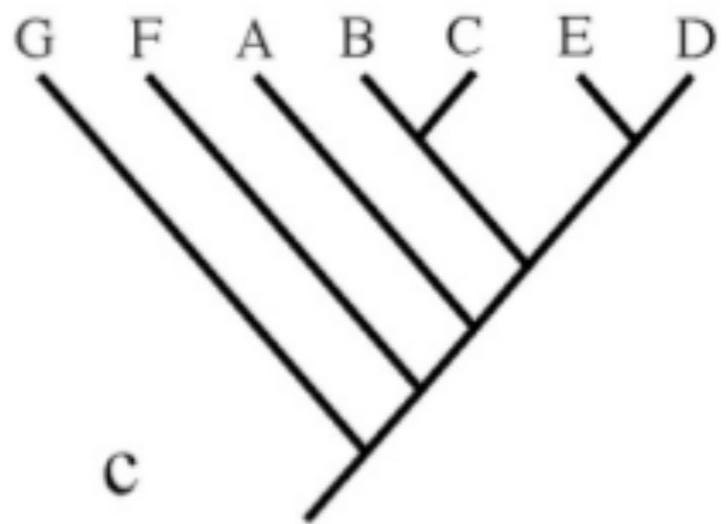
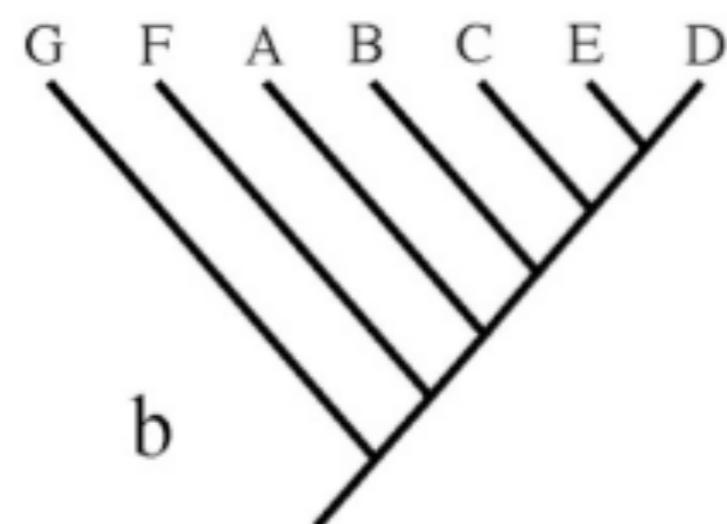
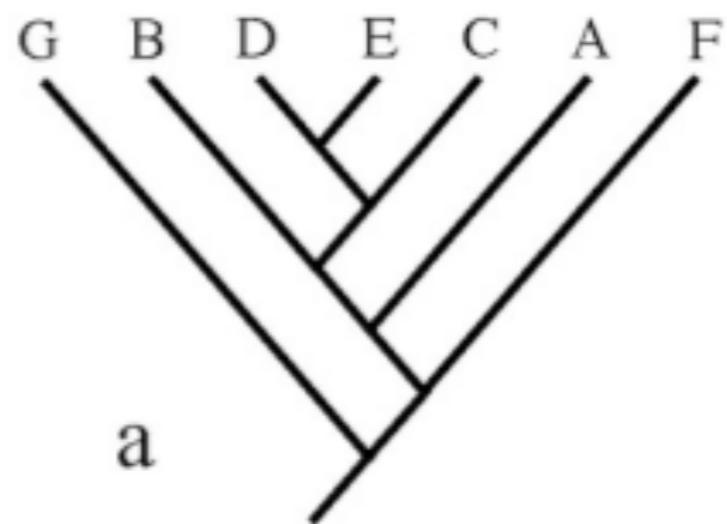
3) By reference to the tree above, which of the following is an accurate statement of relationships?

- a) A seal is more closely related to a horse than to a whale
- b) A seal is more closely related to a whale than to a horse
- c) A seal is equally related to a horse and a whale
- d) A seal is related to a whale, but is not related to a horse

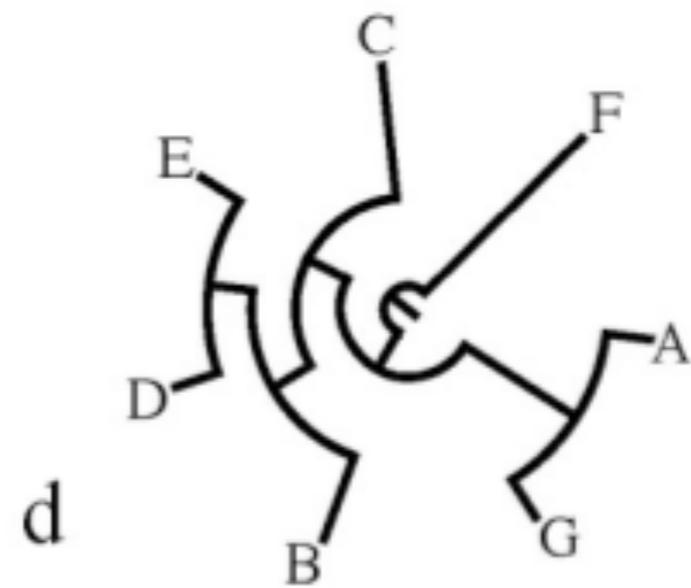
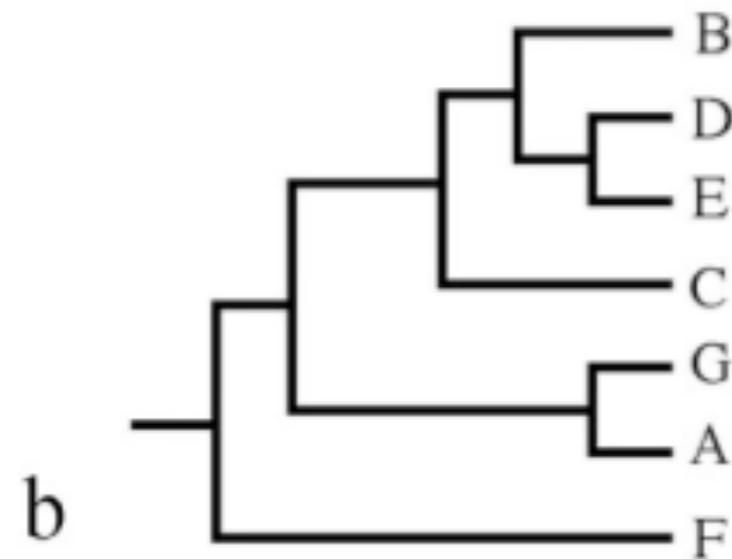
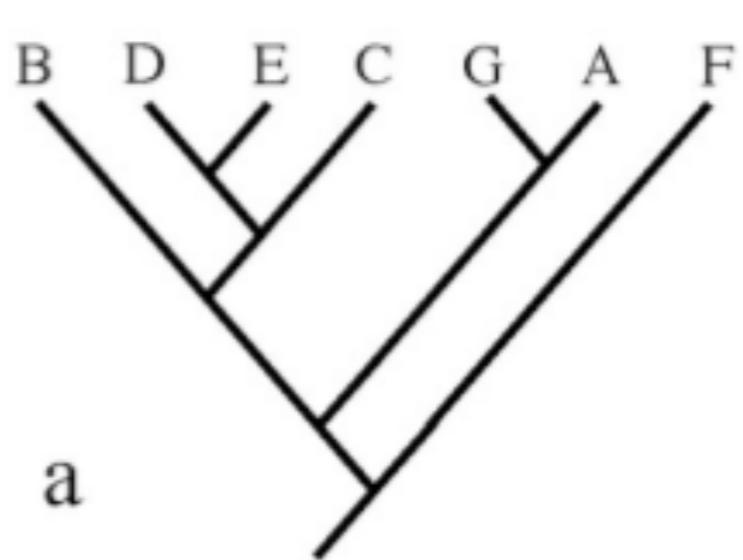


6) Which of trees below is false given the larger phylogeny above?





7) Which of the four trees above depicts a different pattern of relationships than the others?



8) Which of the four trees above depicts a different pattern of relationships than the others?

# Building phylogenies

These methods aren't just placing more similar taxa together!

Similarity can be due to a **pleisiomorphies**-shared ancestral characters

Trees are built with **synapomorphies**-shared derived characters

Tree inference methods identify synapomorphies and use these to infer relationships

- 1- Collect character data, and identify homologous characters across organisms
- 2- Look for the phylogeny that best explains the character data according to an evolutionary process and an optimality criterion
- 3- Assess how strong the support is for particular relationships

# Optimality criteria

**Parsimony** - Find the tree that minimizes the number of changes needed to explain the character data

**Maximum likelihood** - Find the tree that maximizes the likelihood of the observed character data given a sequence evolution model

# Maximum likelihood cont...

Likelihood is the probability of the data (D) given a hypothesis (H).

In our case, the data is our character information and the hypothesis is a particular tree and model of character evolution

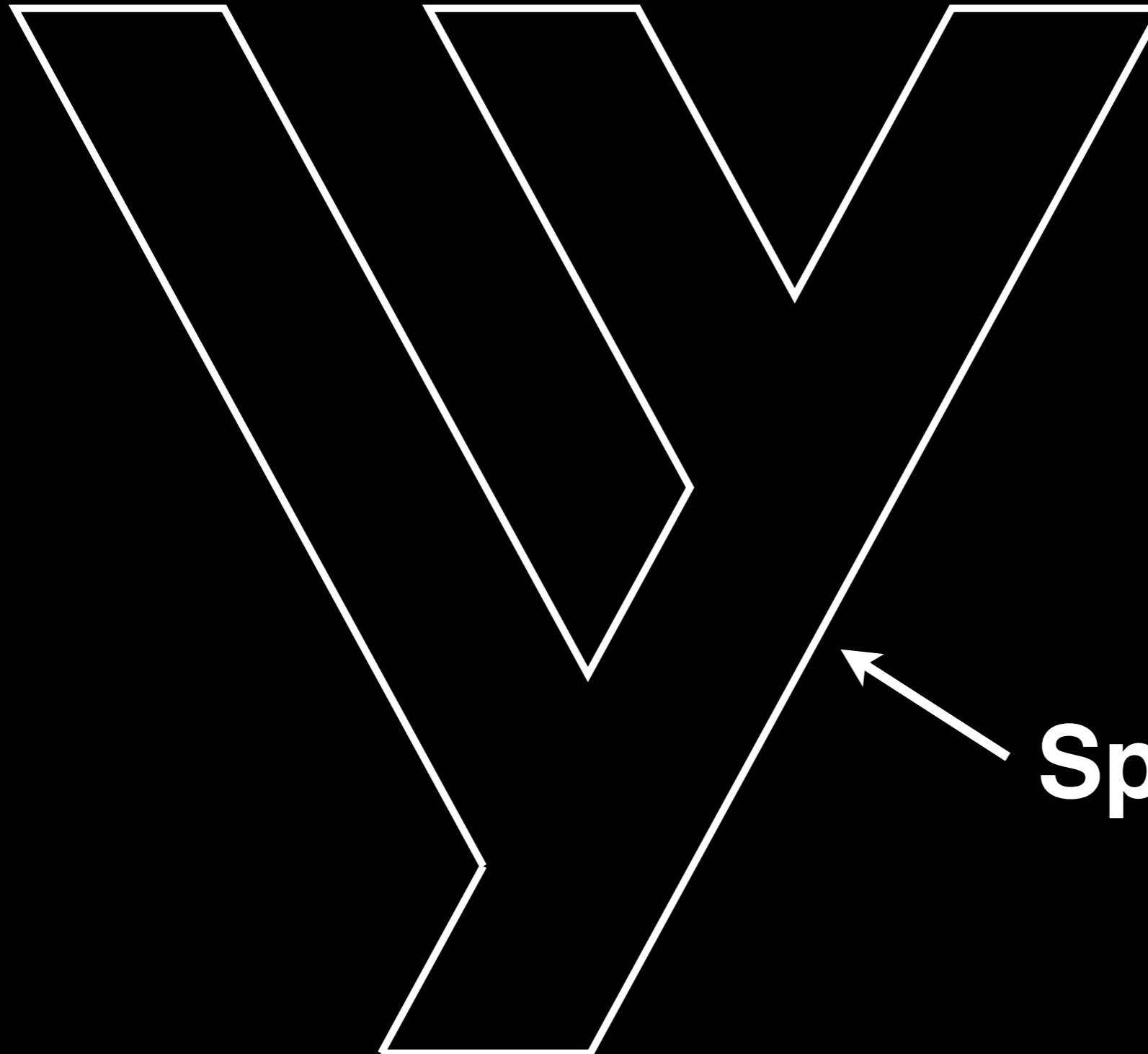
**Species A**



**Species B**



**Species C**



**Species tree**

**Species A**



**Species B**



**Species C**



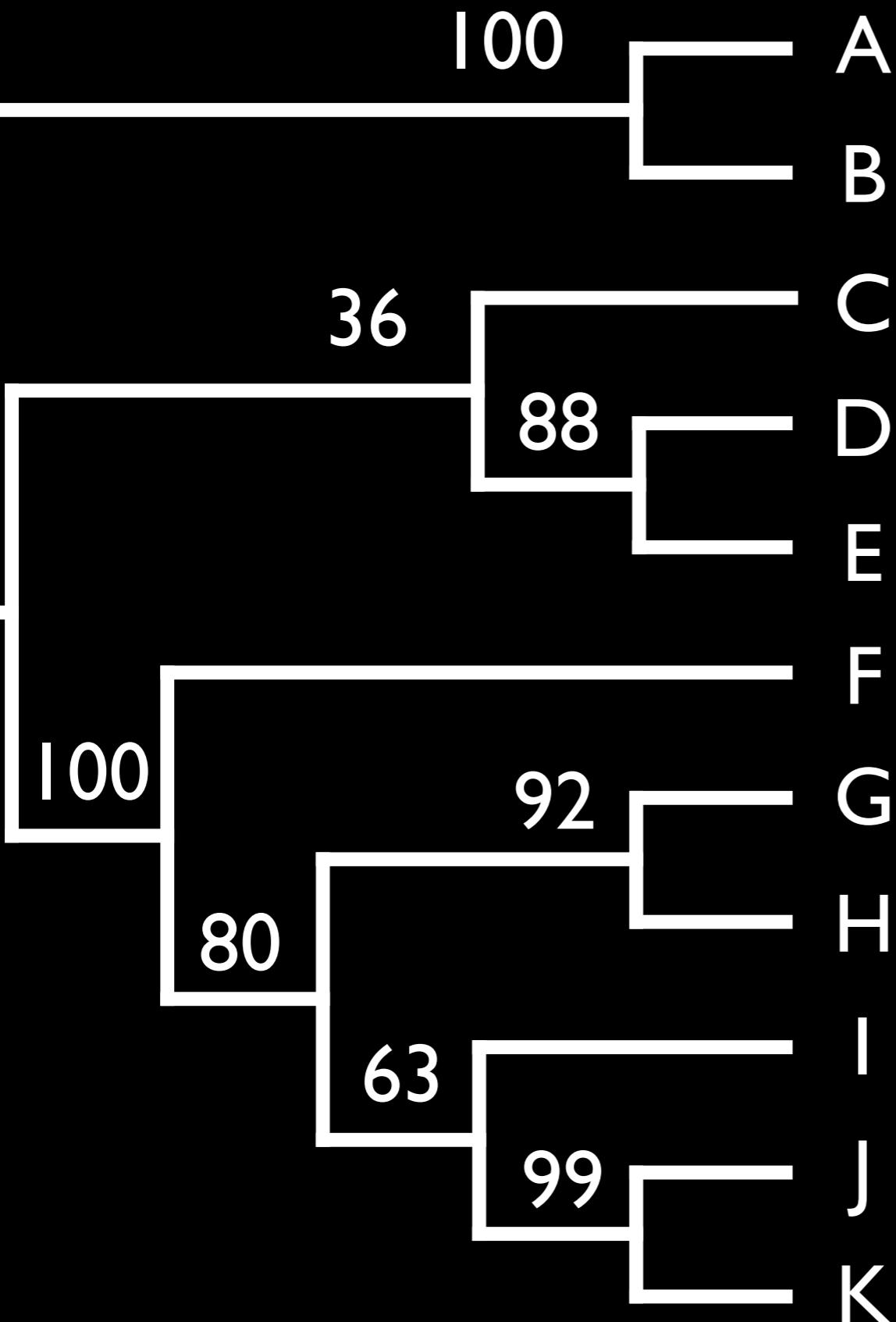
**Gene tree**

**“Orthologs”**

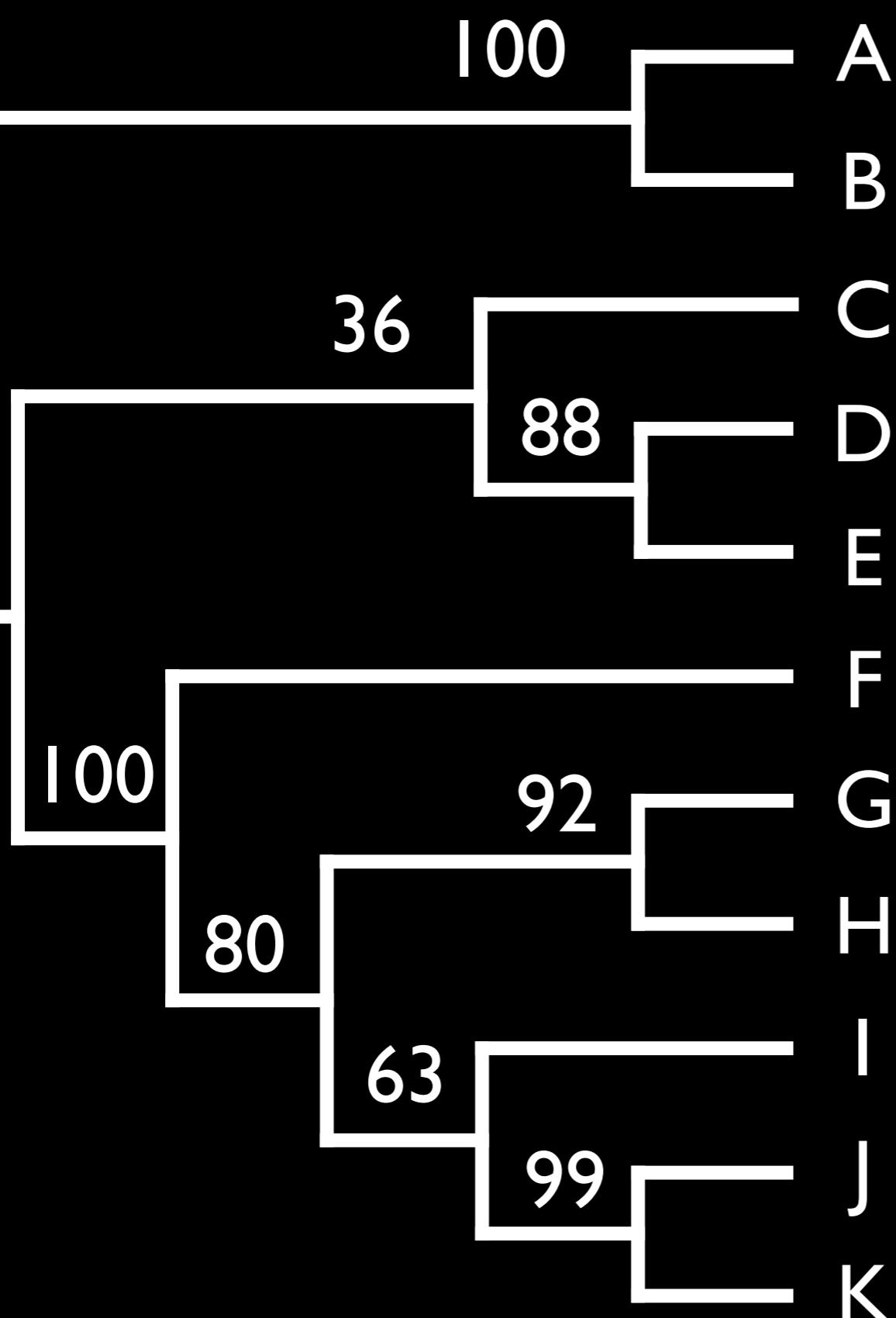
Gene divergence  
due to speciation

# Interpreting support

# Confidence values

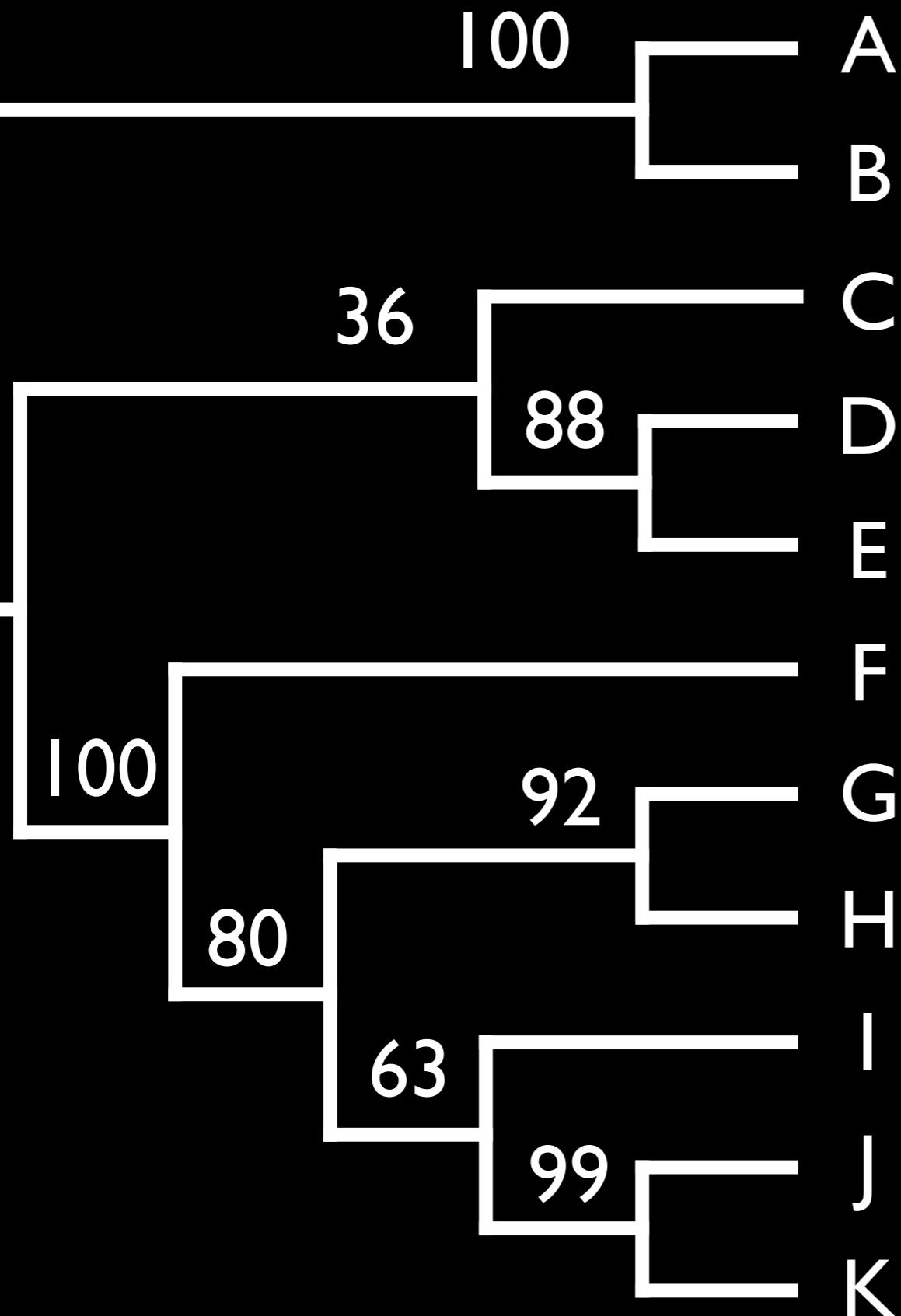


# Confidence values - Bootstraps



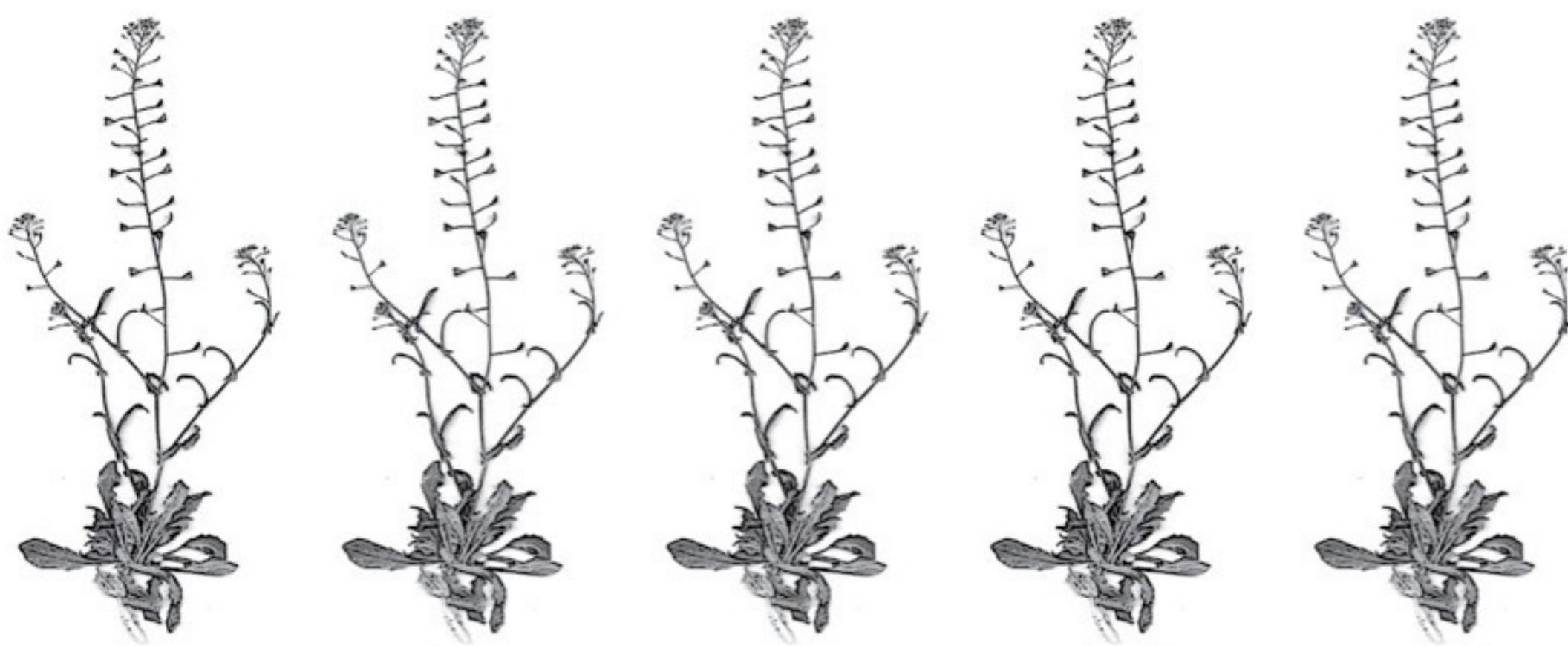
- A relative index of how well supported clades are across characters
- B
- C
- D
  - 1. Resample from the real data to generate many pseudoreplicate datasets
- E
- F
- G
  - 2. Look for the best tree supported by each dataset
- H
- I
- J
  - 3. Measure how often each relationship is recovered when the resampled data are analyzed
- K

# Confidence values - Bayesian analyses

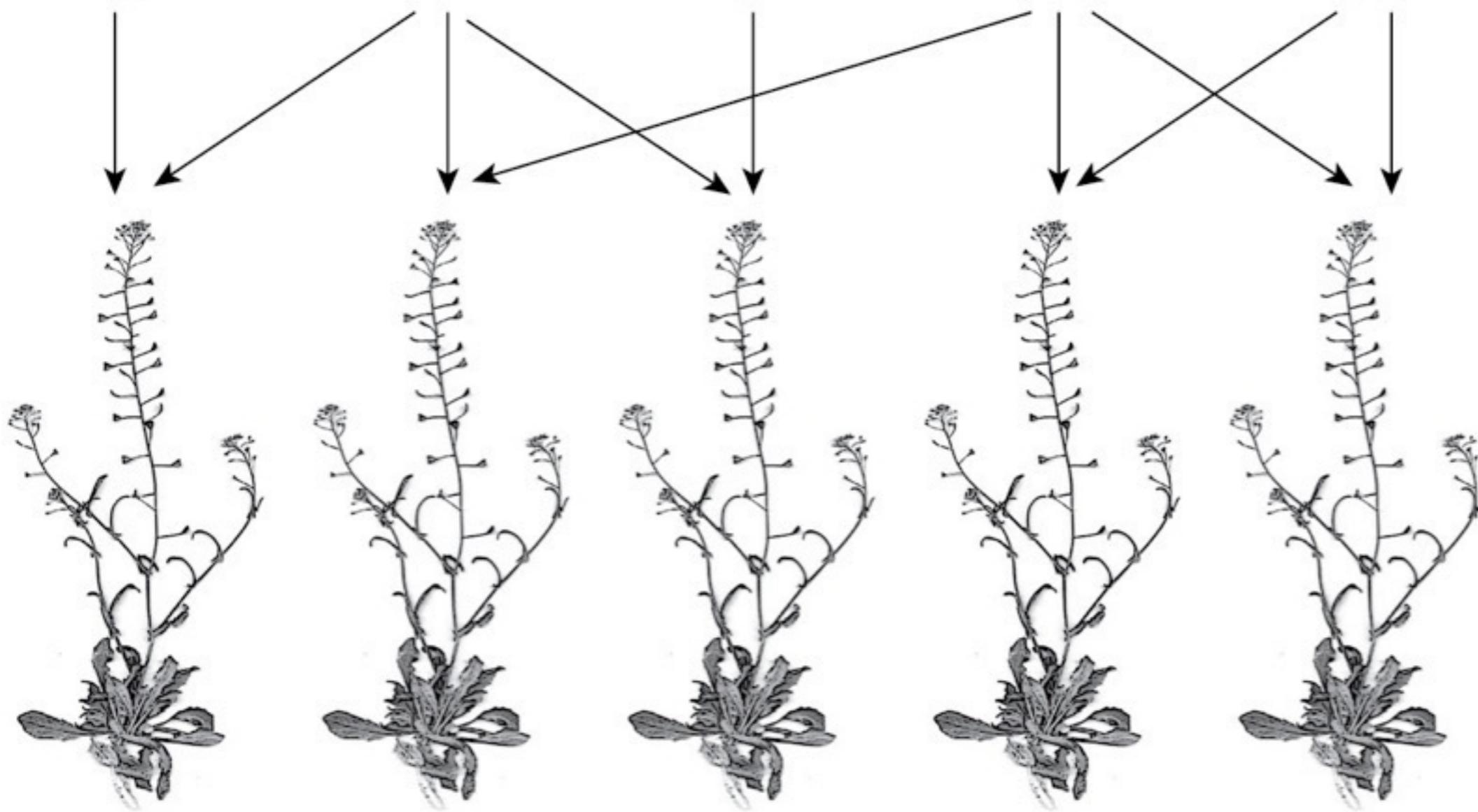


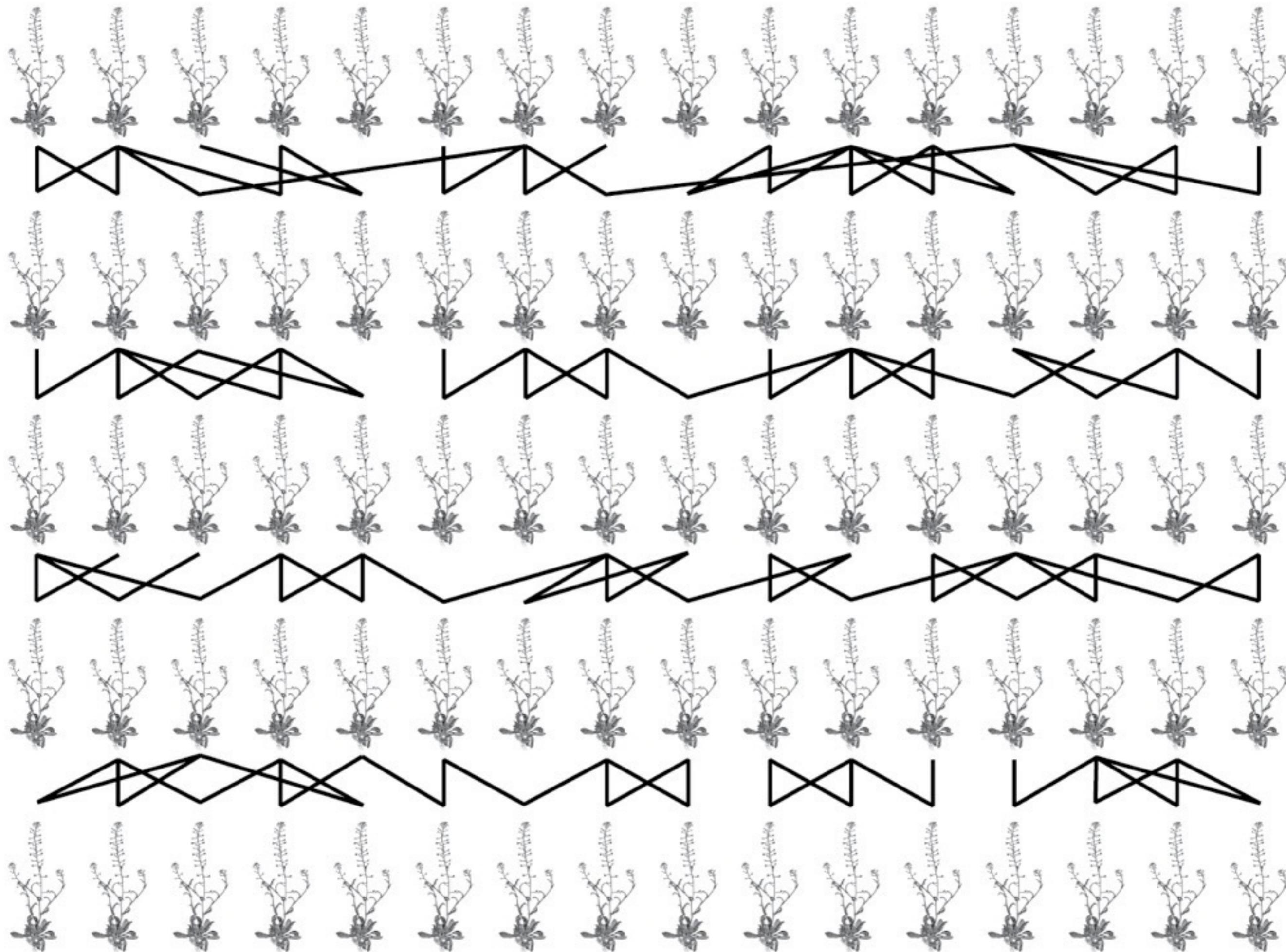
Phylogenies summarize  
population  
demographics

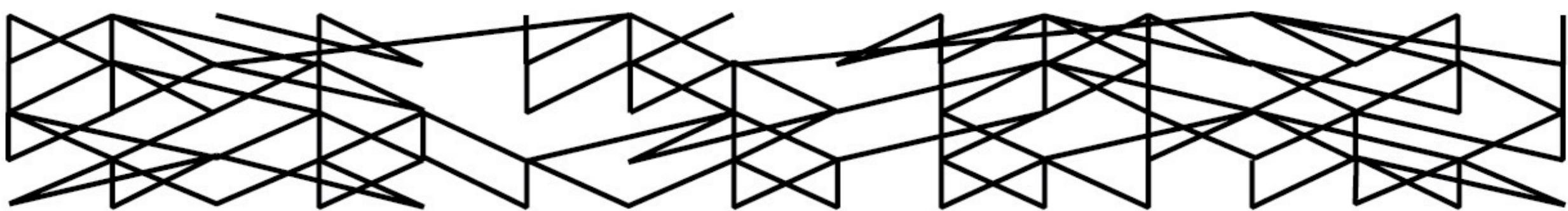
Parents—  
Generation 1

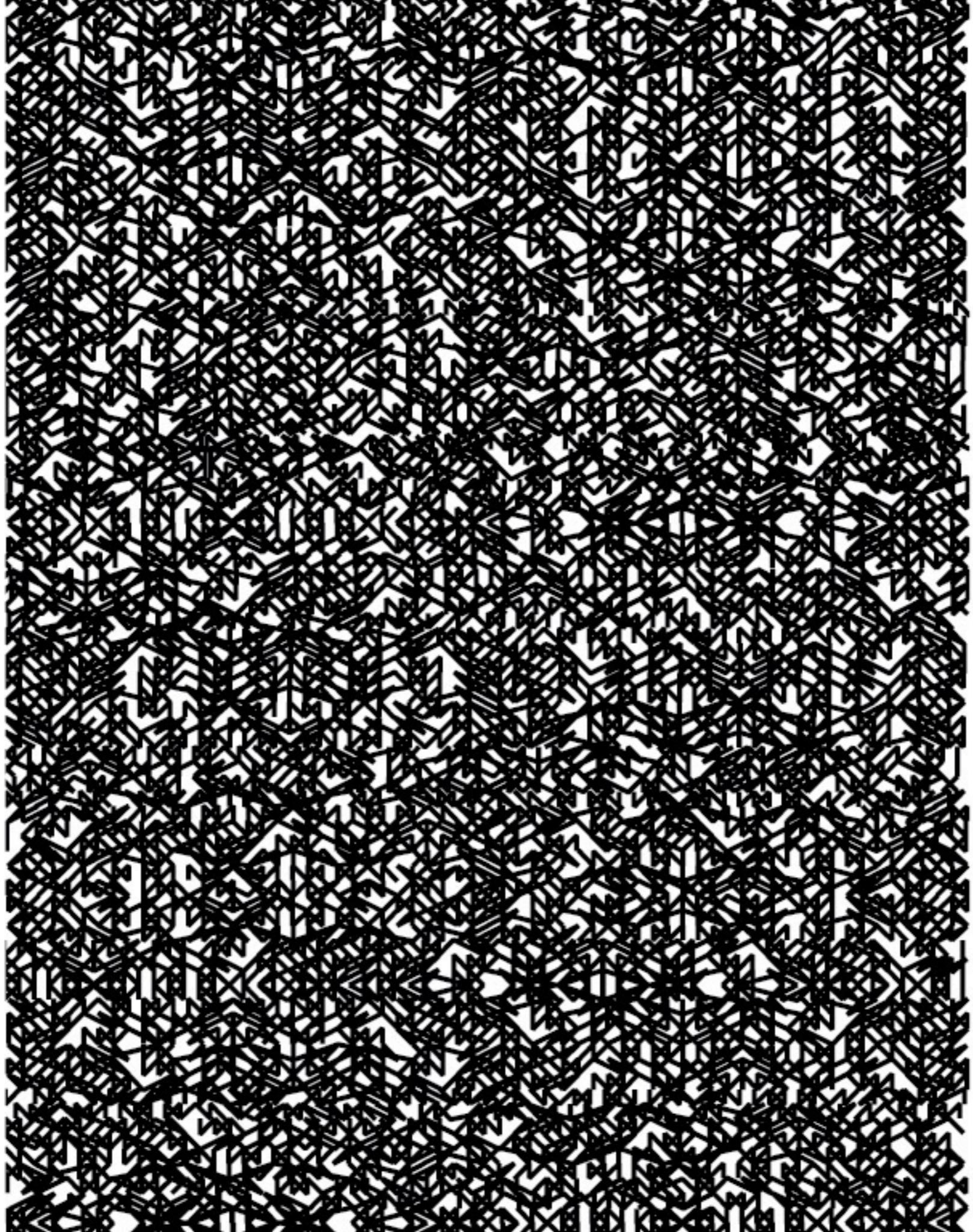


Offspring—  
Generation 2











Past



Present

