

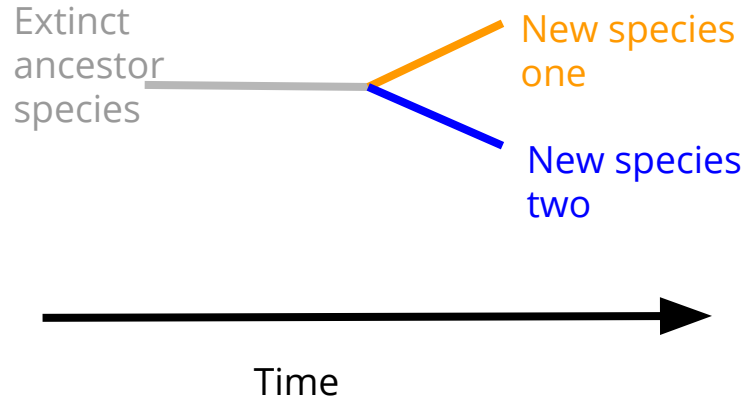
# Phylogenetics: Reading trees

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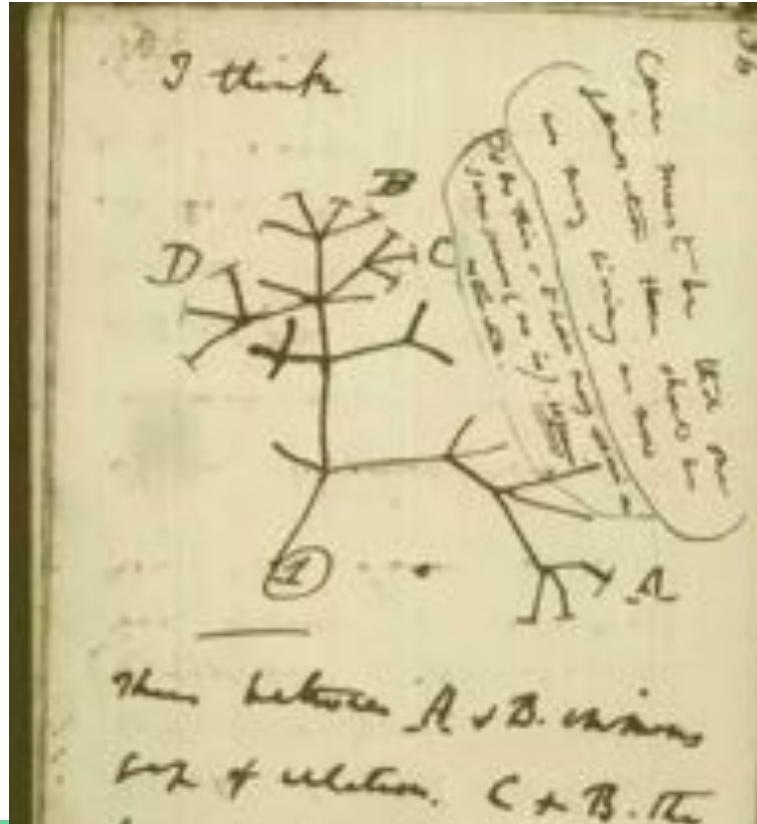
Introduction to Evolution and Scientific Inquiry

Dr. Stephanie J. Spielman; [spielman@rowan.edu](mailto:spielman@rowan.edu)

# Cladogenesis: birth of new clades



# The first ever phylogeny



# Systematics, Cladistics, Phylogenetics

- Systematics: The study of diversity of life and identification of **taxa** (singular: taxon)
- Cladistics: The systematic classification of groups of organisms using *shared characteristics derived from a common ancestor*
- Phylogenetics: The science of creating evolutionary trees that reveal how organisms are related to each other, based on common ancestry

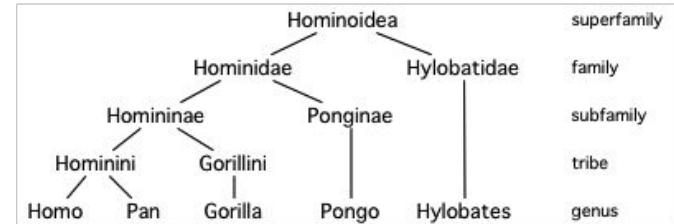
# The Linnaean Hierarchy

Kingdom  
Phylum  
Class  
Order  
Family  
Genus  
Species



Is a “super family” or a “tribe” a real evolutionary entity?

Super family	Family	Sub family	Tribe	Genus	Species
<i>Hominioidea</i>	<i>Hylobatidae</i>			<i>Hylobates</i>	<i>Hylobates sp.</i>
	<i>Hominidae</i>	<i>Ponginae</i>		<i>Pongo</i>	<i>Pongo pygmaeus</i>
		<i>Homininae</i>	<i>Panini</i>	<i>Pan</i>	<i>Pan paniscus</i> <i>Pan troglodytes</i>
				<i>Gorilla</i>	<i>Gorilla gorilla</i>
			<i>Hominini</i>	<i>Homo</i>	<i>Homo sapiens</i>



# Anatomy of a phylogeny

Figure 26.5

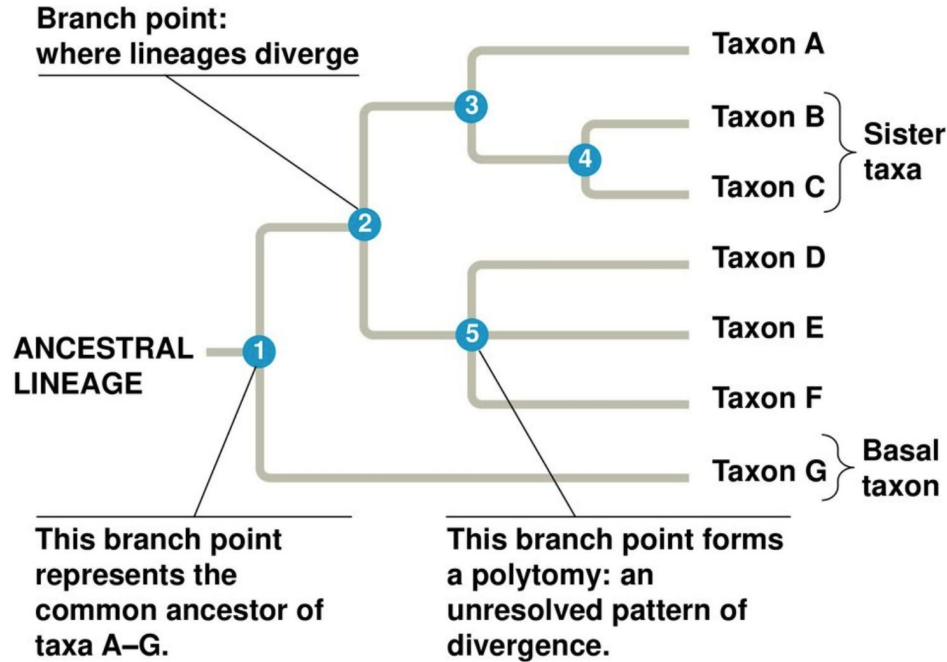
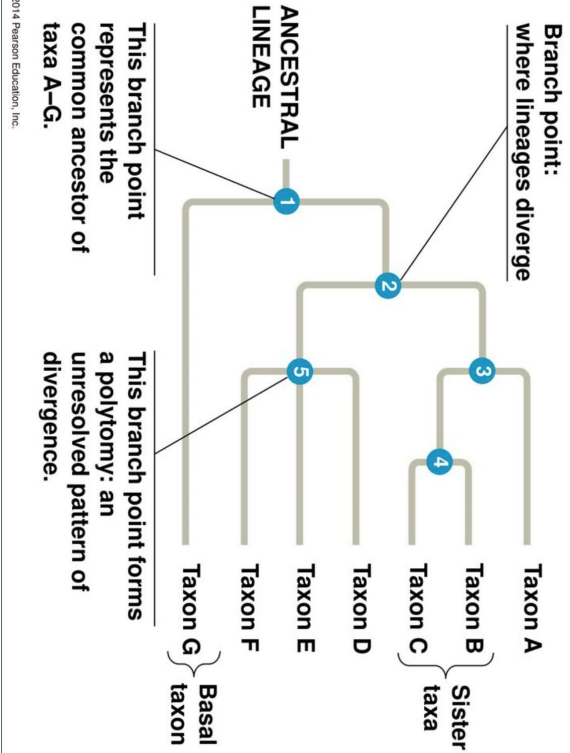
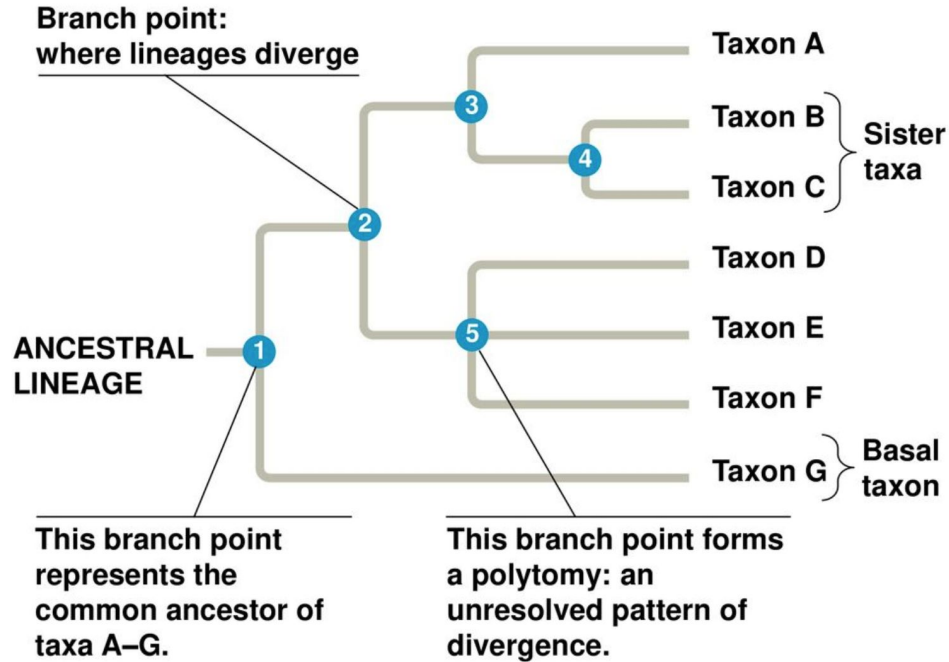


Figure 26.5



# Anatomy of a phylogeny

Figure 26.5

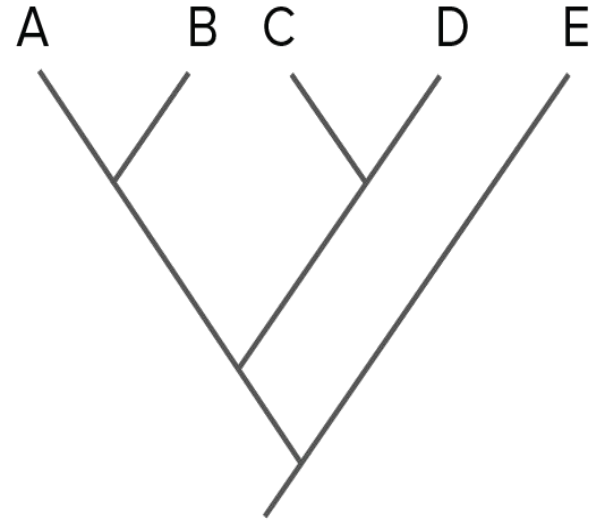


# Sister taxa or clades share a common ancestor

A and B are sister taxa

(A,B) and (C,D) are sister clades

Who is E sister to?

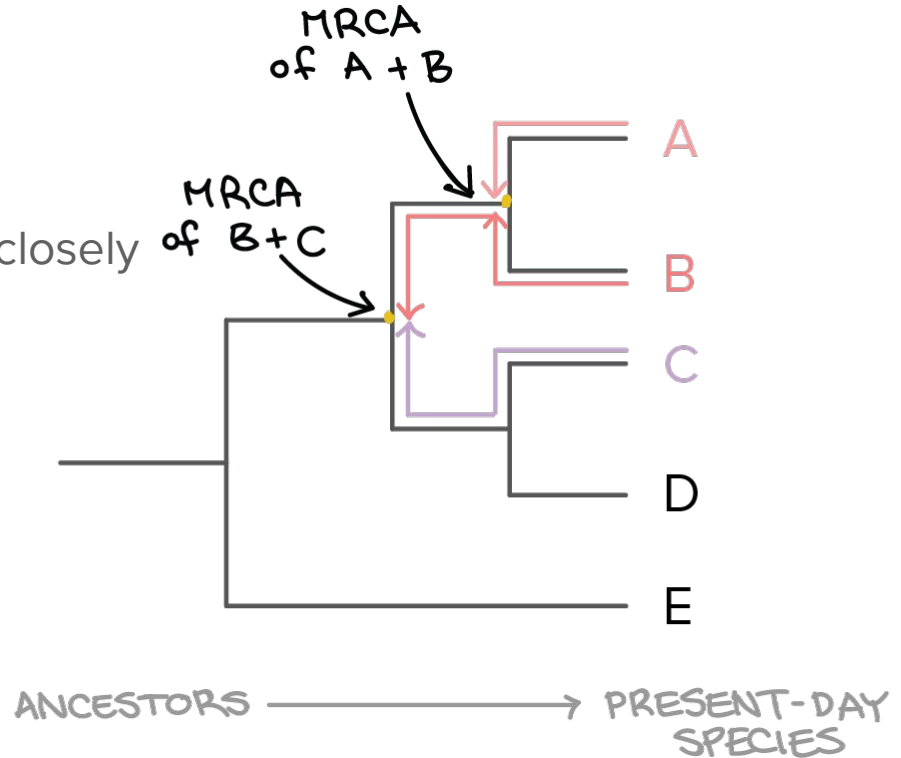




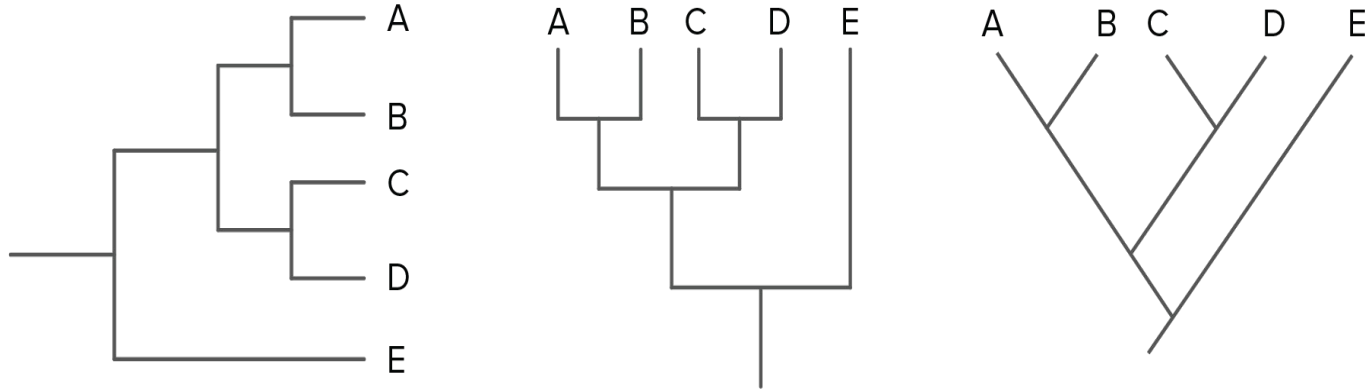
# Read trees by tracing back through branches

MRCA = Most Recent Common Ancestor

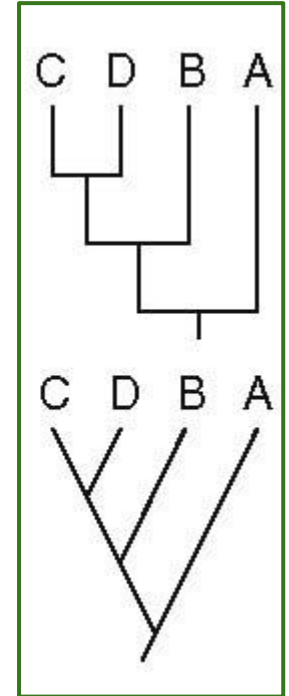
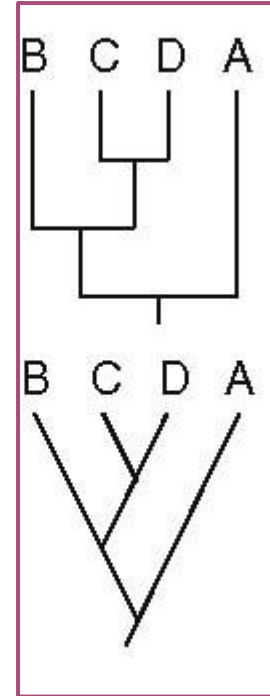
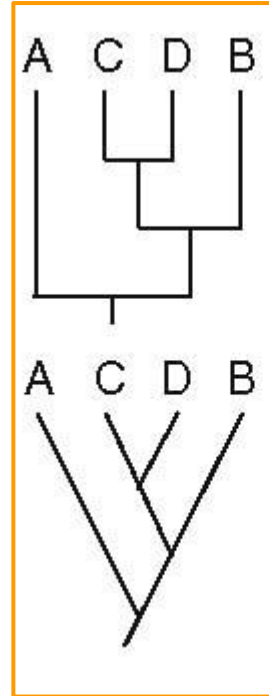
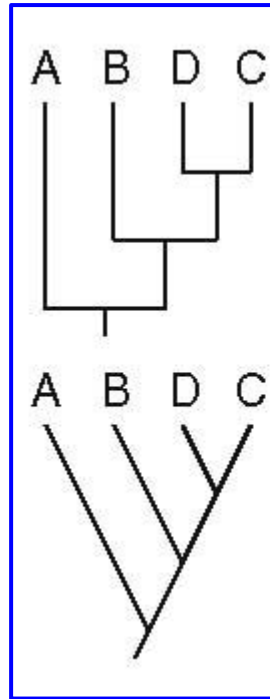
The more recently your MRCA, the more closely you are related.



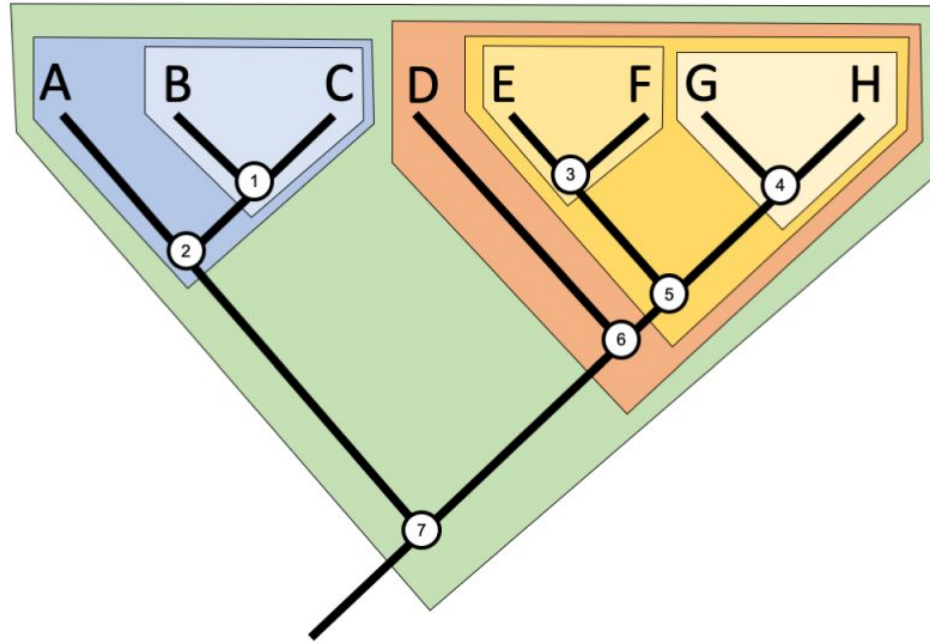
Angled or boxy shapes are still the same. It's all about *tracing through nodes!!*



Each box contains the same tree drawn two different ways



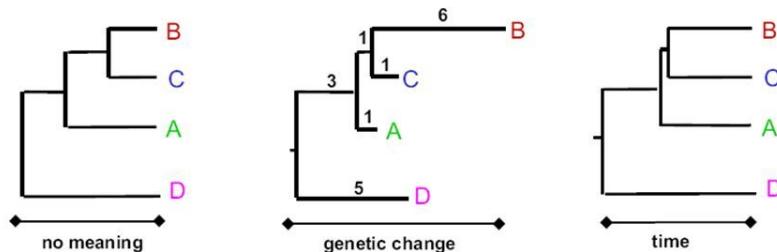
Trees are fundamentally a bunch of nested trees



The tree-thinking challenge!

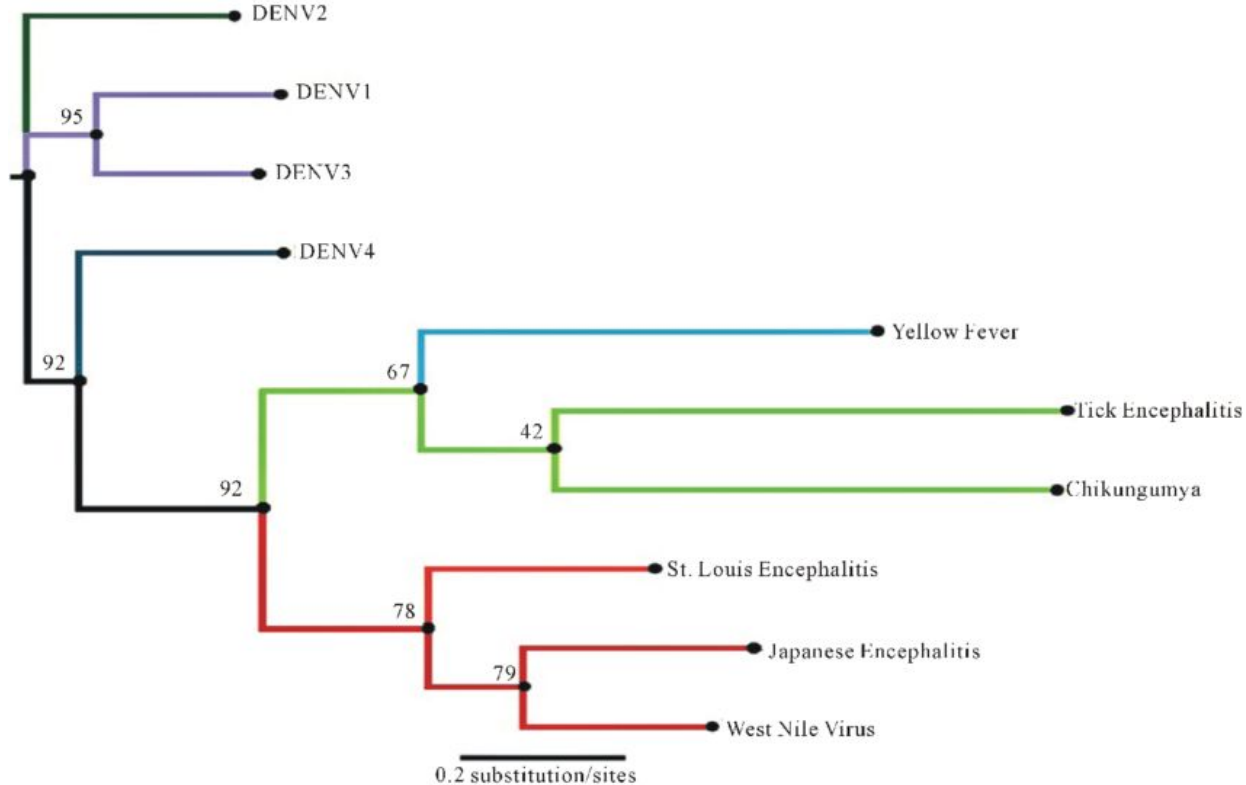
# Components of a phylogeny

- **Topology:** the branching patterns
- **Branch lengths** can represent a variety of things (you'll be told!)
  - Nothing at all ("Cladogram")
  - Evolutionary distance (genetic change)
  - Time since divergence

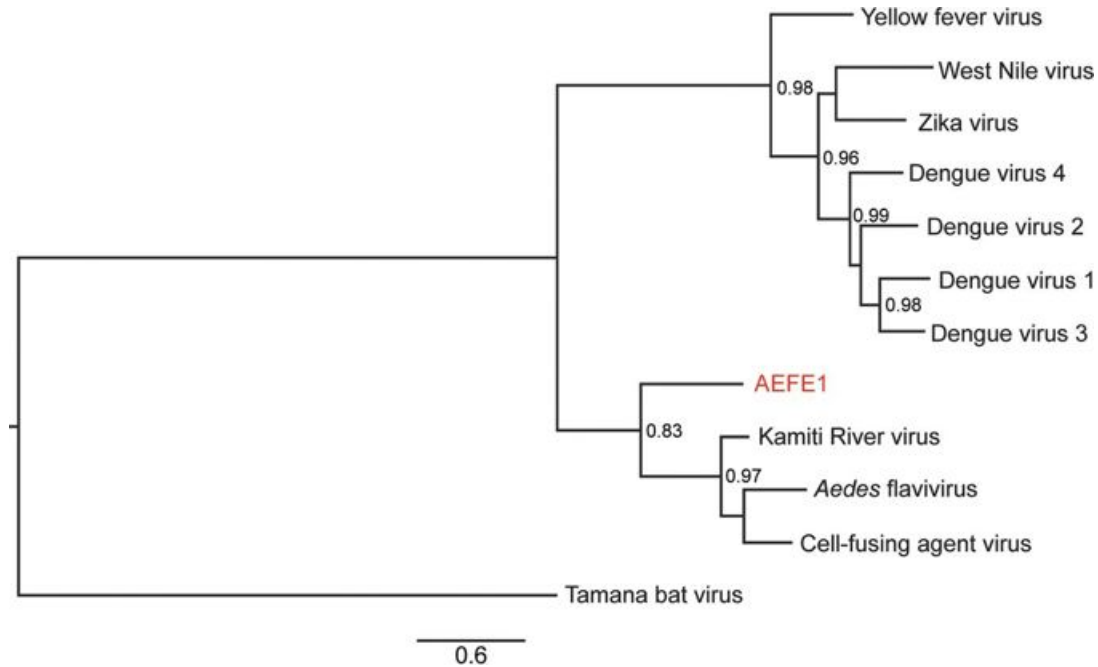


- **Confidence measures at nodes** (usually scaled 0-100)
  - Statistical quantity with complex interpretation. *ROUGHLY means*: How confident are we that this node is correct? Interpreted as, >70 pretty confident.

# Branch lengths show evolutionary distance

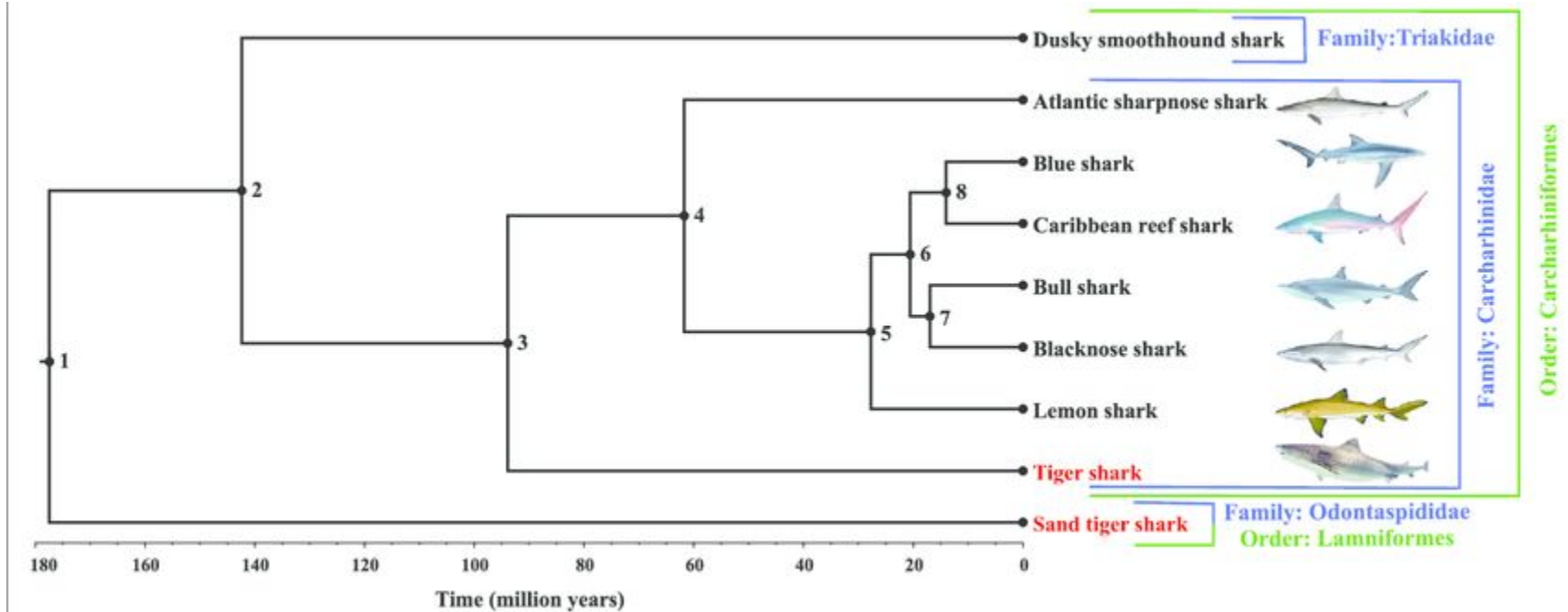


# More flaviviruses

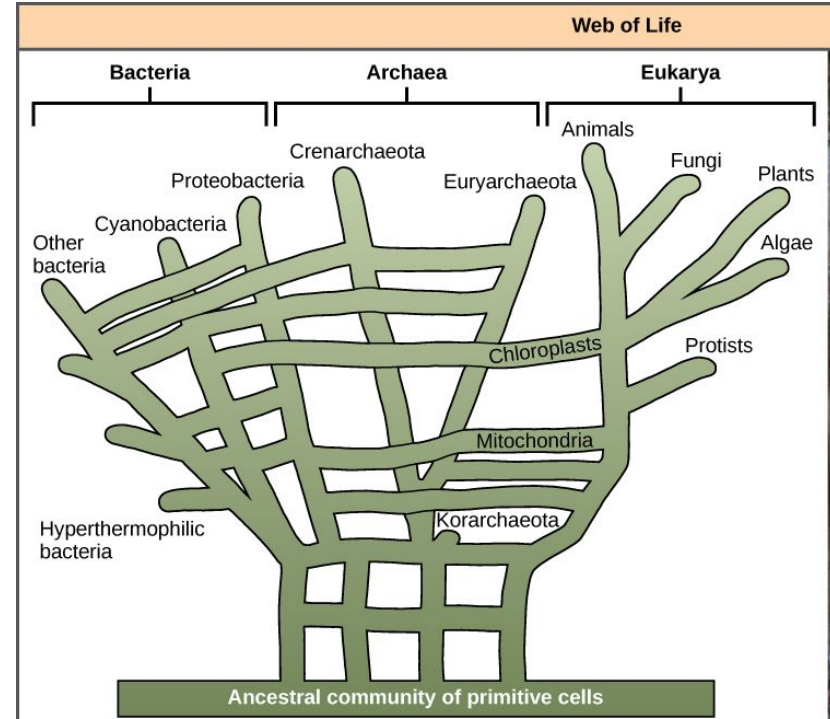
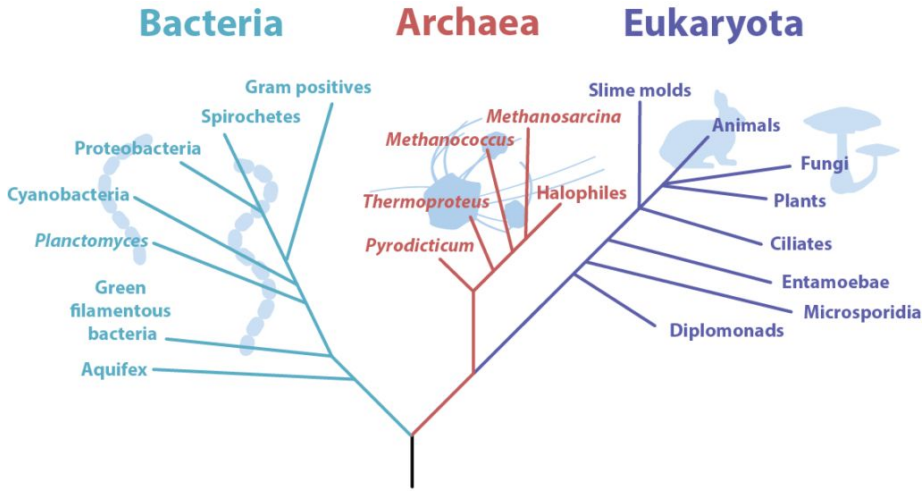




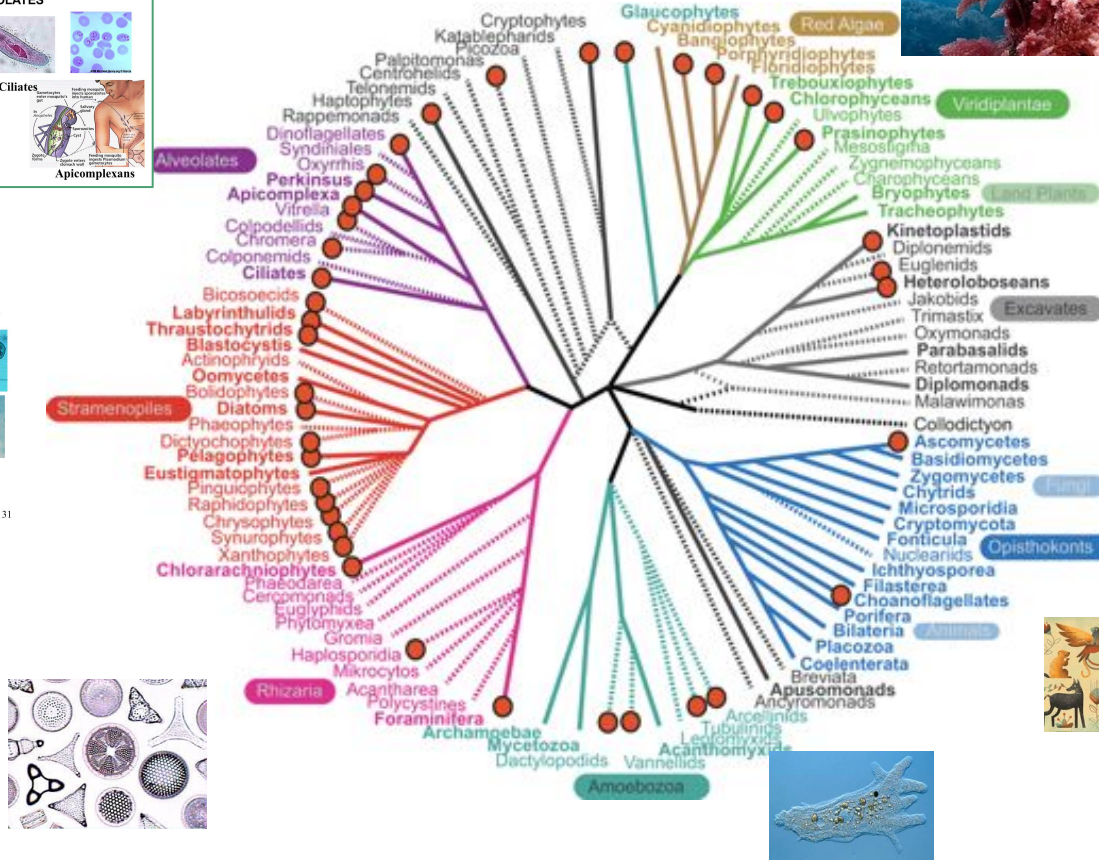
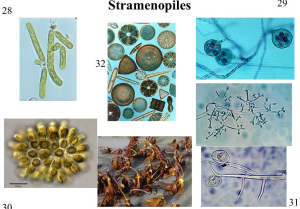
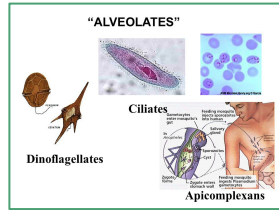
# Time-scaled branch lengths, for example



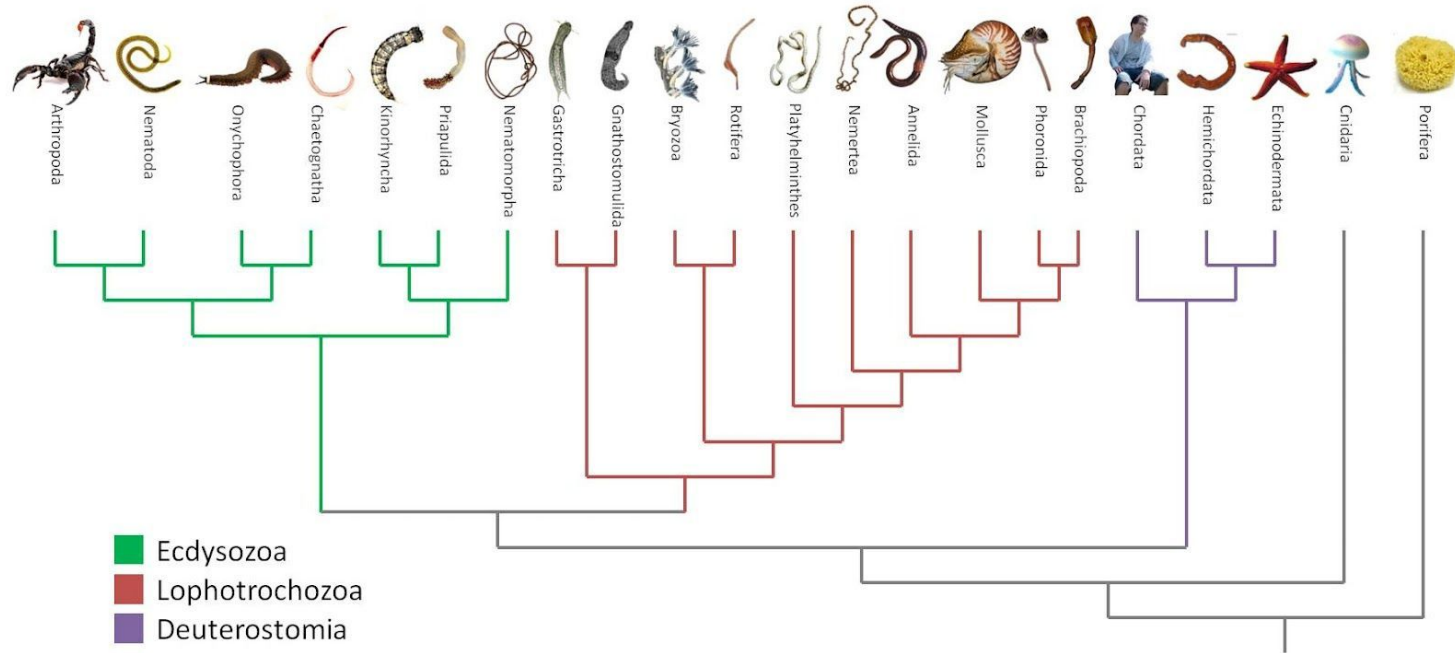
# Our place in the tree of life



# The eukaryotic tree of life

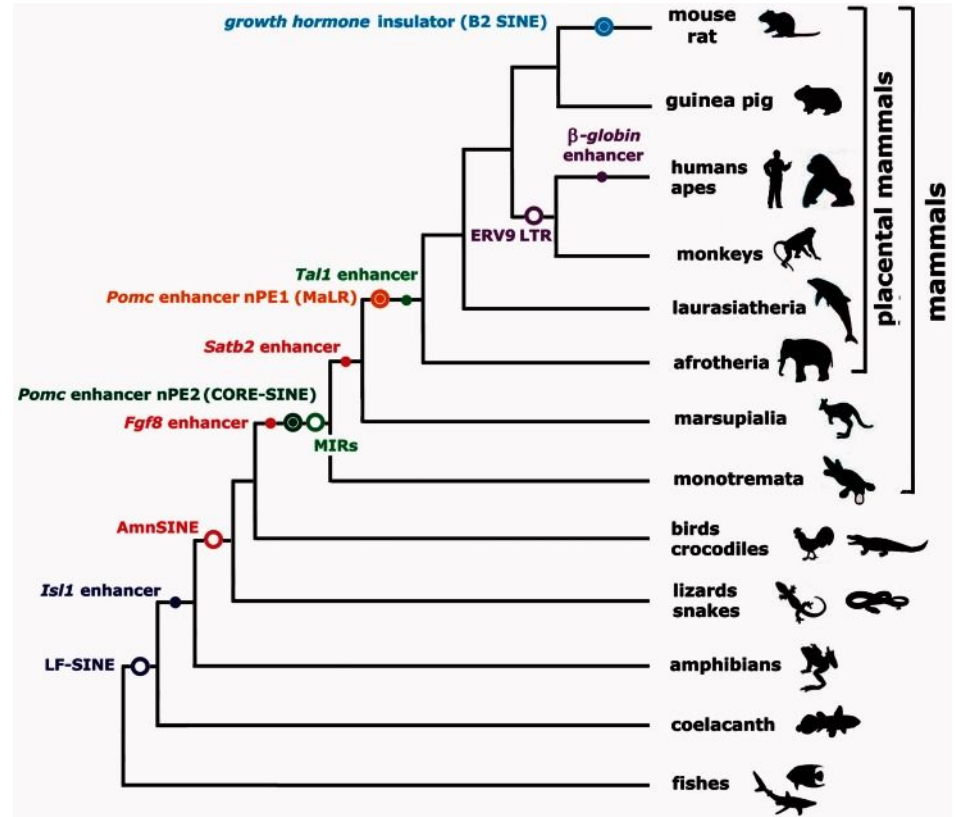


# The Metazoan tree of life (animals!)

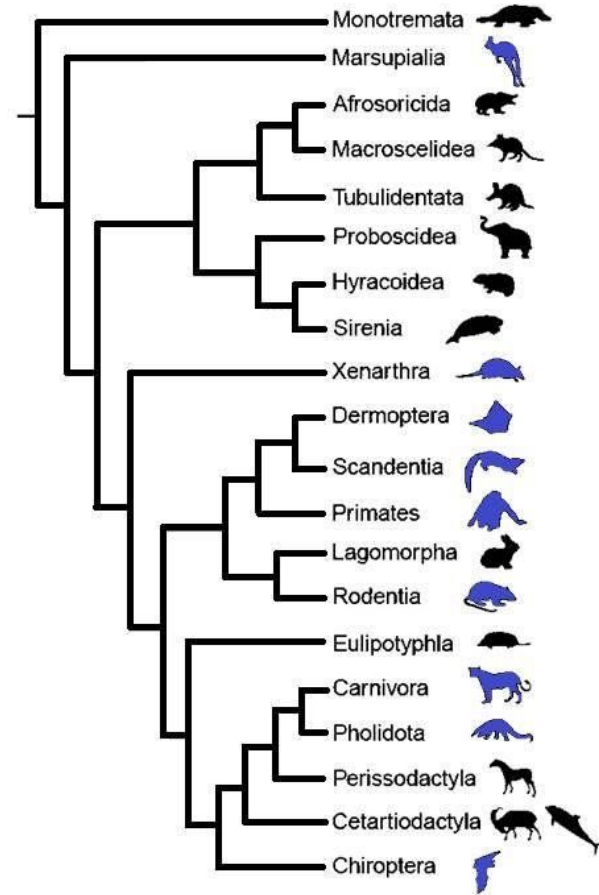


# Vertebrate tree of life

(ignore marker dots at nodes)



# Mammalian tree of life



# The primate tree of life

(ignore branch colors)

