

# Phylogeny and the history of life

Phylogeny

The history of life

Processes of diversification

# Outline

## Phylogeny

- Constructing phylogenetic trees

- Example: the evolution of whales

## The history of life

- The shape of the tree

- The fossil record

- Putting the timeline together

## Processes of diversification

- Adaptive radiations

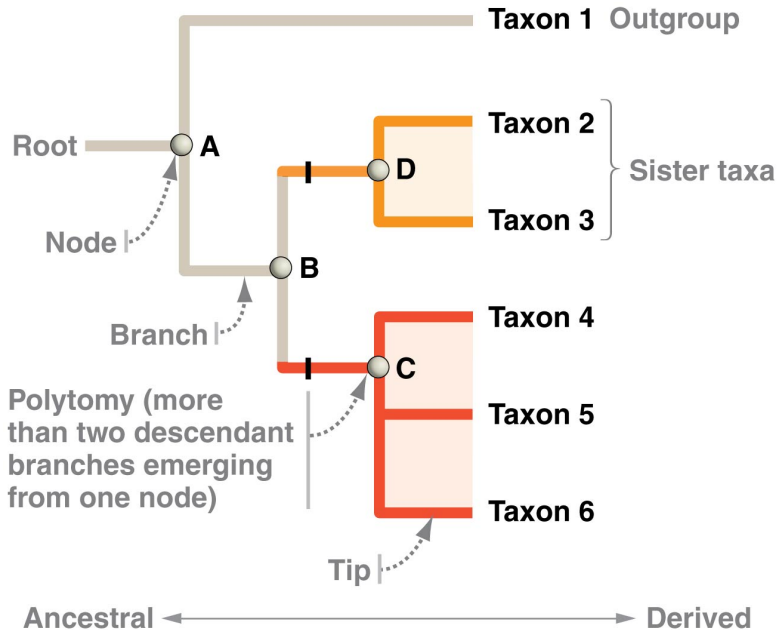
- Mass extinctions

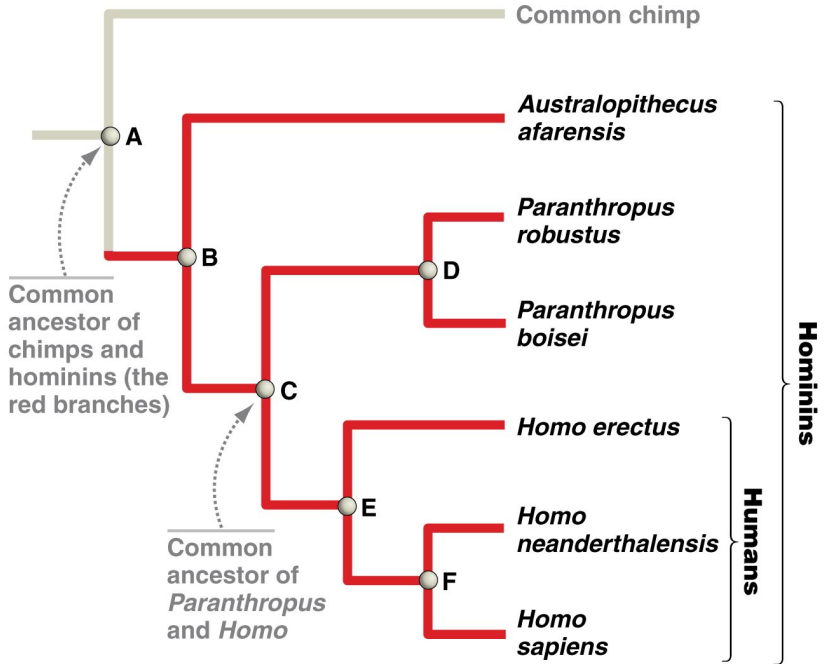
# Phylogeny

- ▶ Phylogeny is the evolutionary history of a group of organisms
- ▶ Based on the idea that organisms are related by evolution
- ▶ Understanding these relationships is critical to our understanding of both evolution, and how biological processes work

# Phylogenetic trees

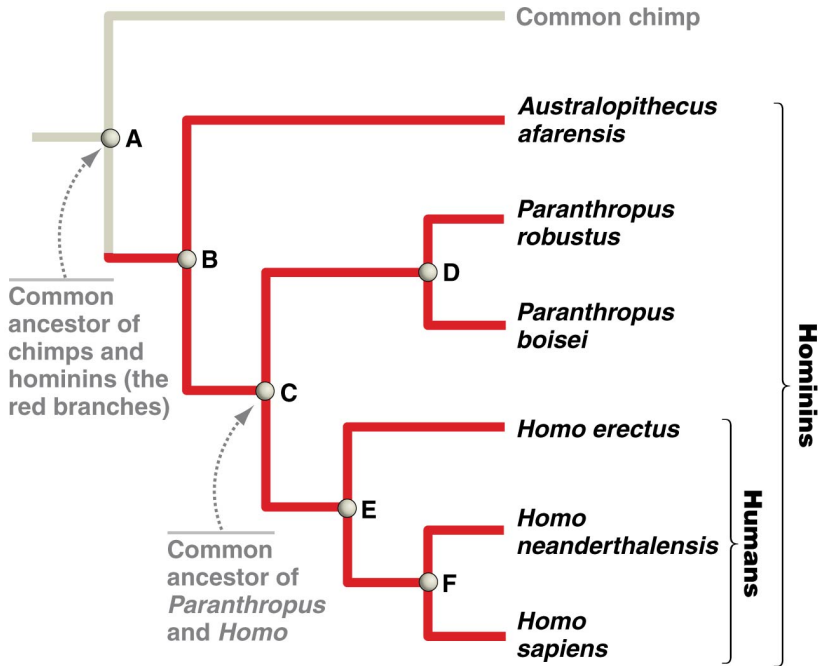
- ▶ A **phylogenetic tree** is a model of how a group of organisms descended from a common ancestor
- ▶ The model consists of **nodes**, where groups split, **branches** where evolution occurs, and **tips** representing observed **taxa** which are the endpoints of the process we are trying to model.
- ▶ A point where more than two branches diverge is called a *polytomy*.
  - ▶ Polytomies mean we don't know which event happened first.





# Monophyletic group

- ▶ A **monophyletic group** is a group *defined by* a single common ancestor
  - ▶ All descendants of the ancestor must be in the group
- ▶ Monophyletic groups can also be called **clades** or **taxa**.
- ▶ As biologists, we should try to think in terms of clades
  - ▶ Are flying vertebrates a clade?
  - ▶ What are some prominent groups that are not clades?
    - ▶ \* **apes, reptiles, trees**



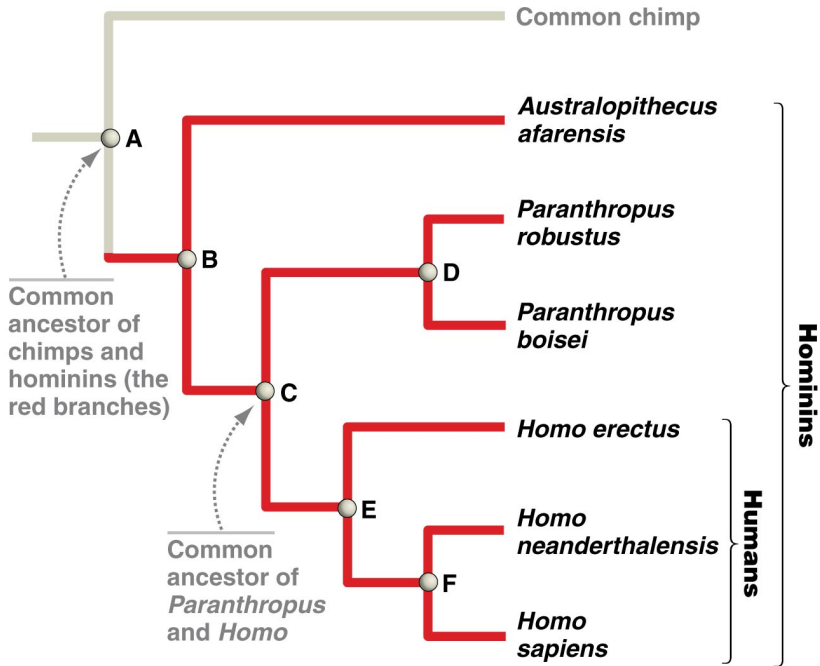


# Sister taxa

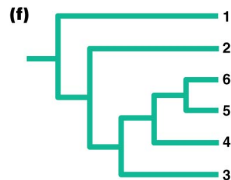
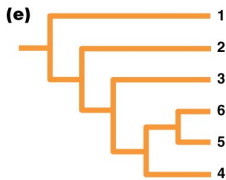
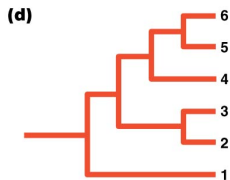
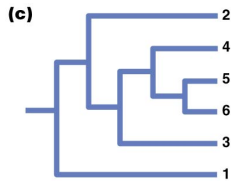
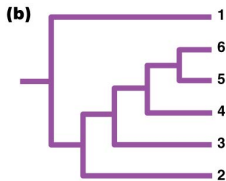
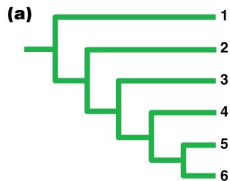
- ▶ Sister taxa can be a useful way of thinking about trees
  - ▶ two taxa that share a common node
  - ▶ You need to take the whole taxon
- ▶ E.g., sisters of: *Homo sapiens*; *Homo erectus*; humans?
  - ▶ \* *Homo neanderthalensis*; *Hn* and *Hs*; *Paranthropus*

# Reading phylogenetic trees

- ▶ The tree indicates the pattern of branching of **lineages** (evolving lines)
- ▶ Tips are *assumed* by the model to be monophyletic
- ▶ A tree is a model of how evolution occurred
  - ▶ Trees that correspond to the same model are considered equivalent



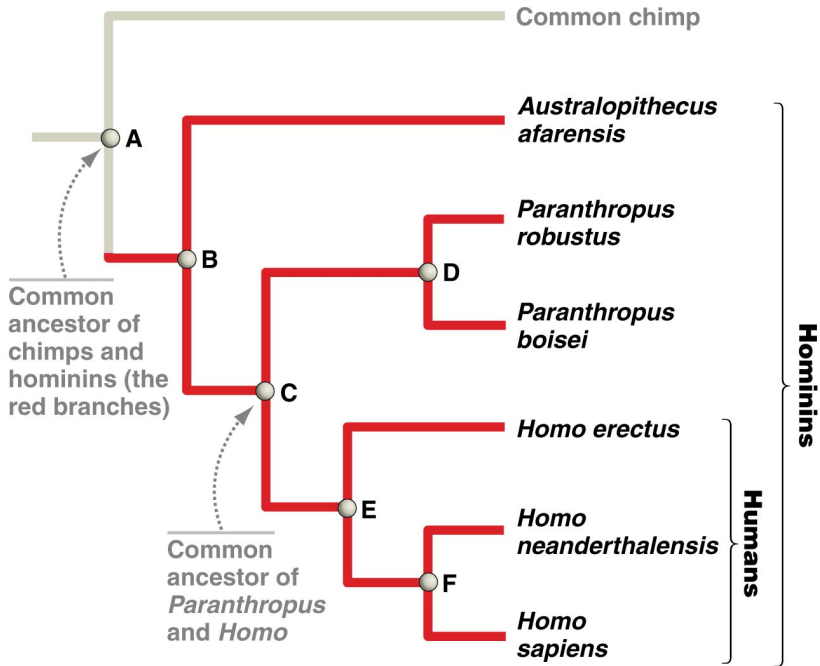
*Activity: which of these things is not like the others?  
(present)*



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# Order of species

- ▶ Except for the branching pattern, we don't interpret anything about the order of a tree
  - ▶ No species are higher or lower than others, according to the tree
  - ▶ We've all been evolving for the same amount of time
- ▶ How do we judge how closely related two organisms are, according to a tree?
  - ▶ \* By looking for their common ancestor



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- Adaptive radiations

- Mass extinctions

# Constructing phylogenetic trees

- ▶ First, measure **characteristics** (or **characters**) of the taxa of interest – i.e., anything that seems useful to measure
  - ▶ Can be **morphological** (i.e., physical) or genetic
- ▶ Then infer (make an educated guess about) the phylogenetic relationships.
  - ▶ **Phenetic** approaches use measures of distance between organisms
  - ▶ **Cladistic** approaches are based on modeling how evolution occurs on the tree



# Morphological vs. genetic characteristics

- ▶ Should we use morphological or genetic characteristics to infer phylogenies?
  - ▶ We usually have more information from genetic characteristics, and this information is easier to measure precisely
- ▶ When should we use morphological characteristics?
  - ▶ \* When genetic information is not available
    - ▶ \* Most fossil organisms
  - ▶ *Some viruses evolve so fast that morphological characteristics can be more stable than genetic characteristics*

# Phenetic vs. cladistic analysis

- ▶ Cladistic analysis makes use of the phylogenetic model of organisms evolving from each other to infer phylogenies
- ▶ Phenetic analysis ignores the phylogenetic model of organisms evolving from each other while inferring phylogenies
- ▶ Which is better?
  - ▶ \* Cladistic analysis
- ▶ When should we use the other one?
  - ▶ \* When our data are only distances, with no characters available – e.g., certain molecular techniques
  - ▶ \* When we don't have enough baseline information

# Synapomorphies

- ▶ Classical cladistic analysis is based on **synapomorphies** – shared, **derived** characters – as evidence that two taxa are related
- ▶ Why do we focus on derived characters?
  - ▶ \* These are things that evolved in the relevant context
  - ▶ \* So they are the things our model (the phylogenies) must explain

# Flight as evidence

- ▶ Oaks and fish don't fly, but birds do
  - ▶ \* We're pretty sure that the common ancestor didn't fly
  - ▶ \* No evidence (any model will have flight evolve once)
  - ▶ \* Flight evolved once in either case
- ▶ Mosquitoes and birds fly, but fish don't
  - ▶ \* Evidence (flight might have evolved once or twice on this tree)
  - ▶ \* But this evidence points in the wrong direction
    - ▶ \* This is why we combine evidence from different sources

# What characters are derived?

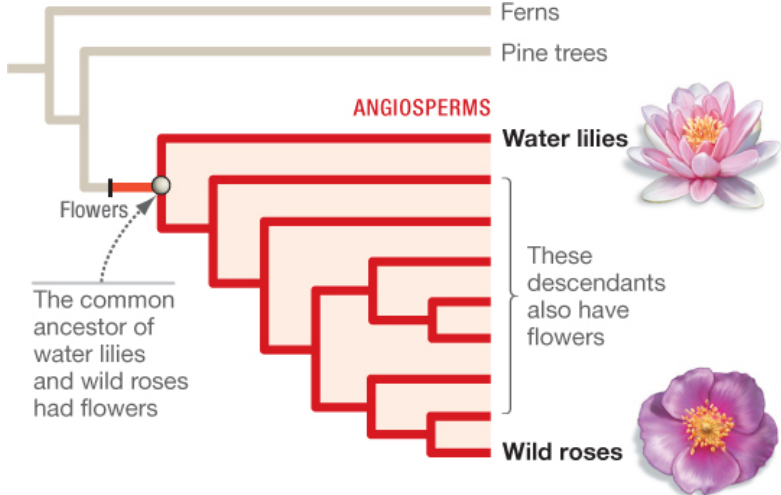
- ▶ Derived compared to what?
  - ▶ The common ancestor (characteristics of the common ancestor are called **basal** or **ancestral** characters).
    - ▶ What if our flight example was ostriches, hawks, and sparrows?
      - ▶ \* No evidence for similarity between hawks and sparrows
      - ▶ \* We believe the common ancestor could fly, so there is no shared, derived characteristic
  - ▶ A **derived** character is a character not shared by the common ancestor of the group that we are currently thinking about
  - ▶ One way to think about cladistic vs. phenetic analysis is that phenetic analysis treats derived and basal characters equally

# Inferring the common ancestor

- ▶ We want to know what the common ancestor was like, so we can tell which characters are derived (as opposed to basal)
- ▶ This can be done sometimes by common sense
- ▶ Inferring the common ancestor statistically is difficult, for technical reasons
  - ▶ We can make use of an **outgroup** to study a group. An outgroup is an organism closely related to, but outside, the group being studied.
  - ▶ We assume that the the **root**, or beginning, of the tree is where the outgroup branches from the group

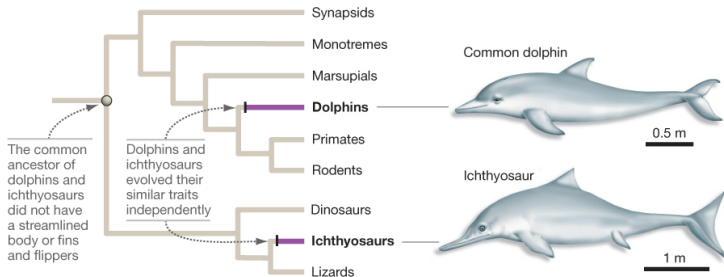
# Confusing the phylogeny

- ▶ Two species may have the same trait because the trait evolved twice independently – **convergent evolution**
  - ▶ \* Flight, trees, dolphins and ichthyosaurs
- ▶ An organism may lack a character that its ancestors had – **secondary loss**
  - ▶ This can be even more confusing
- ▶ Similarities that are not homologies (ie., not due to common ancestry) are called **homoplasies**



**Figure 25.2 Homology: Similarities Are Inherited from a Common Ancestor.** Flowers in diverse plants, such as water lilies and roses, are homologous.





**Figure 25.3 Homoplasy: Traits Are Similar but Not Inherited from a Common Ancestor.** Dolphins and ichthyosaurs look similar but are not closely related.

# Parsimony

- ▶ Classical cladistic analysis is based on searching for the tree that can explain the observed data most **parsimoniously** – with the fewest number of changes necessary.
- ▶ How do we address the problem of convergent evolution and homoplasy?
  - ▶ \* Make use of many different characteristics, when possible
  - ▶ \* It may also help to use many different taxa
- ▶ *Modern approaches that use genetic data may use more sophisticated approaches, rather than simple parsimony*

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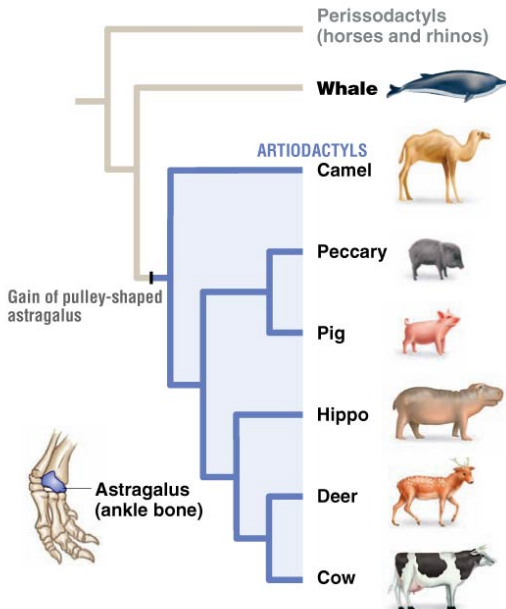
## Example: the evolution of whales

- ▶ Whales seem, on the surface, to be pretty different from other mammals, including the closest group, the artiodactyls
- ▶ Early phenetic analyses showed whales in their own group (sisters to artiodactyls)
  - ▶ Whales lack the distinctive artiodactyl ankle structure (surprise!)
- ▶ What about cladistic analysis?

## *Biology is crazy! (Extra)*

- ▶ Which of these doesn't belong?
  - ▶ Whale
  - ▶ Rhinoceros
  - ▶ Hippopotamus
  - ▶ Elephant
- ▶ Add FUNSLIDE needs an annotation on complete notes

**(a) Data set 1 (morphological traits):**  
**Whales diverged before the origin of artiodactyls.**



## Activity: Tree-construction analysis

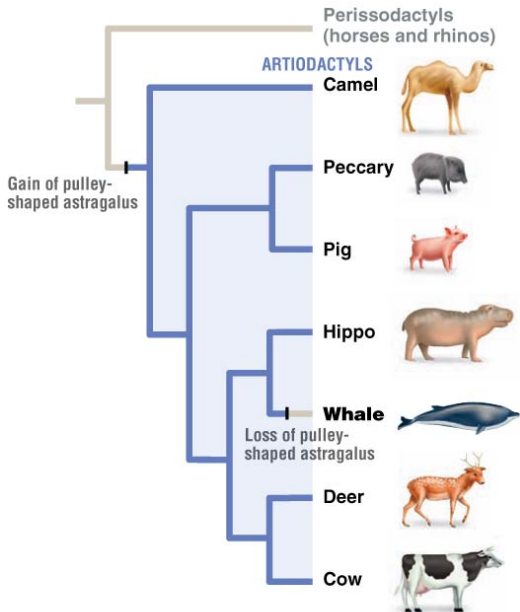
- ▶ Hippos have derived characters A, B, C, D, Z
- ▶ Cows have derived character A, Z
- ▶ Whales have derived characters B, C, D, E, F, G, H, I, Z
- ▶ Calculate distances, and make a phenetic tree
- ▶ List synapomorphies, and make a cladistic tree

# Tree discussion

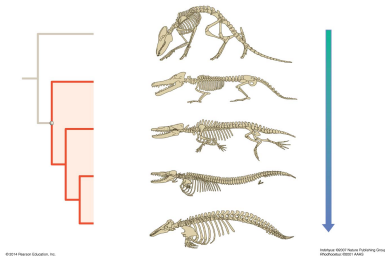
- ▶ What is the effect of universal characteristics (like Z, above)?
  - ▶ \* None
- ▶ What is the effect of unique characteristics (like E, F, G, H, I)
  - ▶ \* They affect phenetic trees, but not cladistic trees
  - ▶ \* As long as we are sure that they are derived!
- ▶ Why might whales have more derived characters than the other species?
  - ▶ \* Because they have had to adapt more since moving to the water



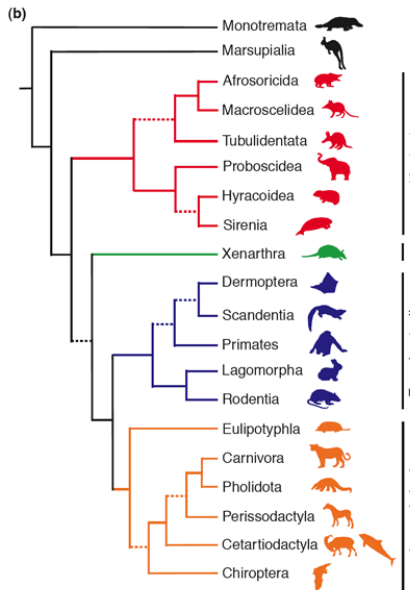
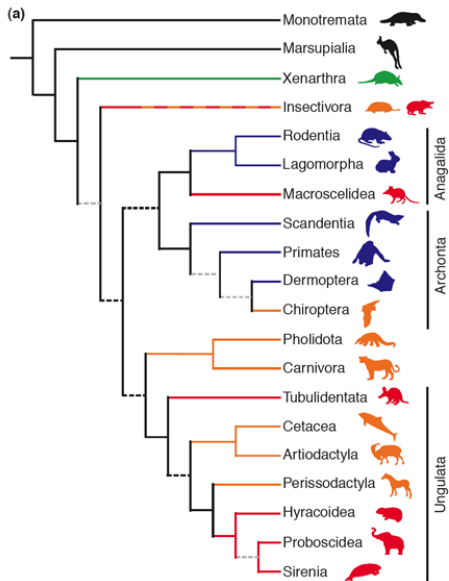
**(b) Data set 2 (DNA sequences):**  
Whales and hippos share a common ancestor.



## Confirmation



- ▶ Intermediate forms between hippo-like animals and whales
- ▶ Discovered *after* they were predicted from DNA evidence!



# How to make a phenetic tree

- ▶ 1. Join the two open nodes that are closest to each other
  - ▶ Shortest distance
- ▶ 2. They are no longer active. Make a new node halfway between them
  - ▶ Average the traits
  - ▶ This step is conceptually simple and practically tricky
  - ▶ *This is why we have computers*
- ▶ 3. Go back to step 1

# How to make a phenetic tree in this course

- ▶ 1. Join the two open nodes that are closest to each other
  - ▶ Shortest distance
- ▶ \* 2. *Stop! You're done.*
  - ▶ \* I will only give you three species
  - ▶ \* Seriously.
- ▶ *I'm here to teach you concepts, not to teach you how to be a really bad computer.*

# Lessons

- ▶ Phenetic analysis uses less information
- ▶ To do a cladistic analysis, inferences about the common ancestor can be crucial
  - ▶ What if we thought the artiodactyl ancestor was aquatic?
    - ▶ E, F, G, H and I could all be basal characters
    - ▶ \* We would conclude that cows are closely related to hippos

# Genetic vs. morphological

- ▶ Why was the genetic analysis more effective than the morphological?
  - ▶ \* It can be hard to tell which traits are derived
    - ▶ \* This can also be a problem with the genetic analysis
  - ▶ \* Genetic analyses typically allow us to analyze more traits

# Phylogenetic trees are approximations!

- ▶ Phylogenetic trees are tremendously useful and powerful tools for organizing, understanding and analyzing biological data
- ▶ But they have limitations:
  - ▶ The true history of life cannot really be summarized by a tree
    - ▶ Sex, other forms of combination or gene transfer
  - ▶ Trees constructed by humans are not necessarily even the best approximations to the true history of life
  - ▶ Our guesses often change over time



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Mass extinctions

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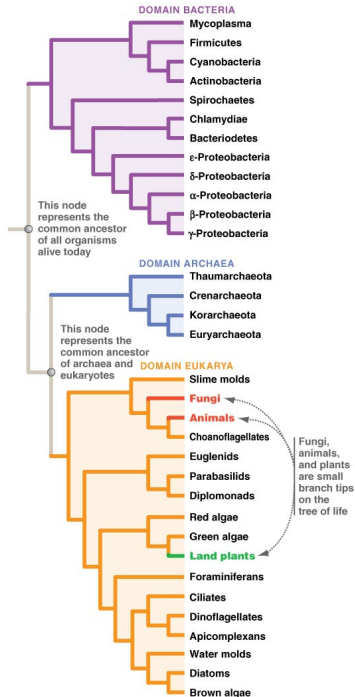
- Mass extinctions

# The shape of the tree

- ▶ Big recent innovations have told us a lot about the history of life
  - ▶ Detailed genetic information
  - ▶ Sophisticated analysis techniques
  - ▶ Electronic computers

# Three domains

- ▶ Bacteria
  - ▶ no nuclei; mostly small
  - ▶ most of the micro-organisms you see
- ▶ Archaea
  - ▶ no nuclei; mostly small
  - ▶ rarer, or live in more extreme environments
- ▶ Eukarya
  - ▶ large, nucleated cells

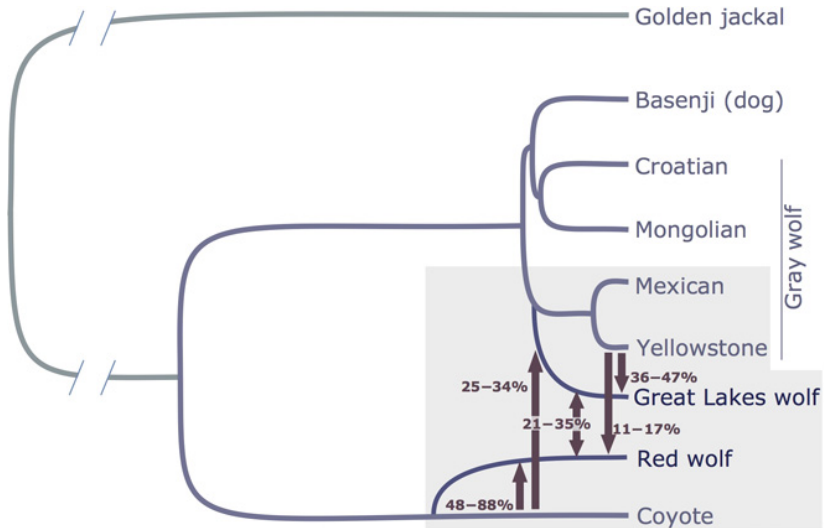


# Eukaryotes

- ▶ Seem to be sisters with archaea, according to most of our key genes
- ▶ Characterized by **nuclei** and **mitochondria**
- ▶ Mitochondria came later, and are captured bacteria!
- ▶ Where did the nucleus come from?
  - ▶ Nobody knows

# The web of life

- ▶ The tree is only part of the story!
  - ▶ If genes (or even whole bacteria) can be transferred, life is not really a tree
- ▶ Reuniting can create new species
  - ▶ Hybridization
  - ▶ Allopolyploidy
    - ▶ \* Polyploids arising from different (allo-) species
- ▶ Wolf-coyote example





## *Five kingdoms (Extra)*

- ▶ Animals
- ▶ Plants
- ▶ Fungi
- ▶ Protists
- ▶ Bacteria

# Five kingdoms

- ▶ Not really a good way to describe the evolution of life
- ▶ So why has this idea persisted for so long?
  - ▶ \* It matches the way the world *looks* – animals, plants and fungi dominate *visible* life
    - ▶ \* Some branches are have organisms that are much smaller, or just have much fewer organisms
  - ▶ \* Archaea and bacteria are difficult to tell apart even with a microscope

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# The fossil record

- ▶ A **fossil** is a physical trace of an organism from the past
  - ▶ Intact fossils retain their form and substance
  - ▶ Compression fossils are squashed into a thin film
  - ▶ Cast fossils occur when the decomposing piece is replaced by minerals different from the surrounding ones
  - ▶ Permineralized fossils occur if minerals infiltrate cells as they are decomposing
- ▶ *Does any of this seem likely?*

**(a) Intact fossil (pollen)**



**(b) Compression fossil (leaf)**



**(c) Cast fossil (bark)**



**(d) Permineralized fossil (tree trunk)**

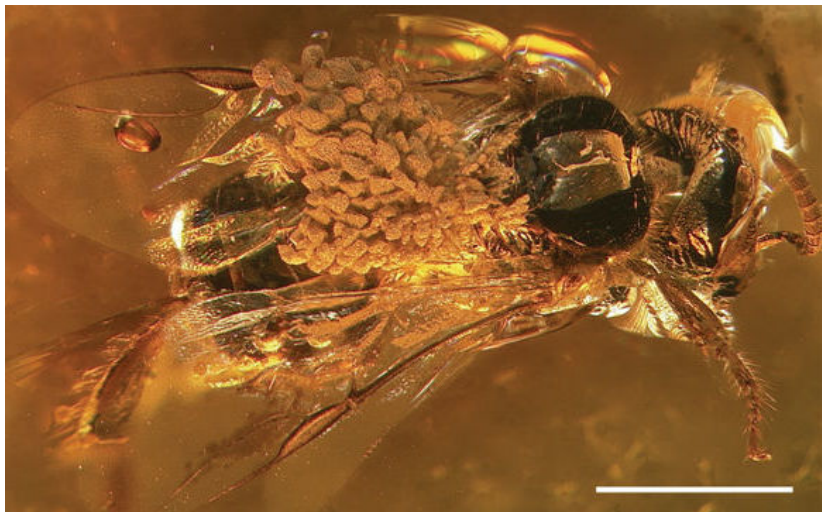


# Biases in the fossil record

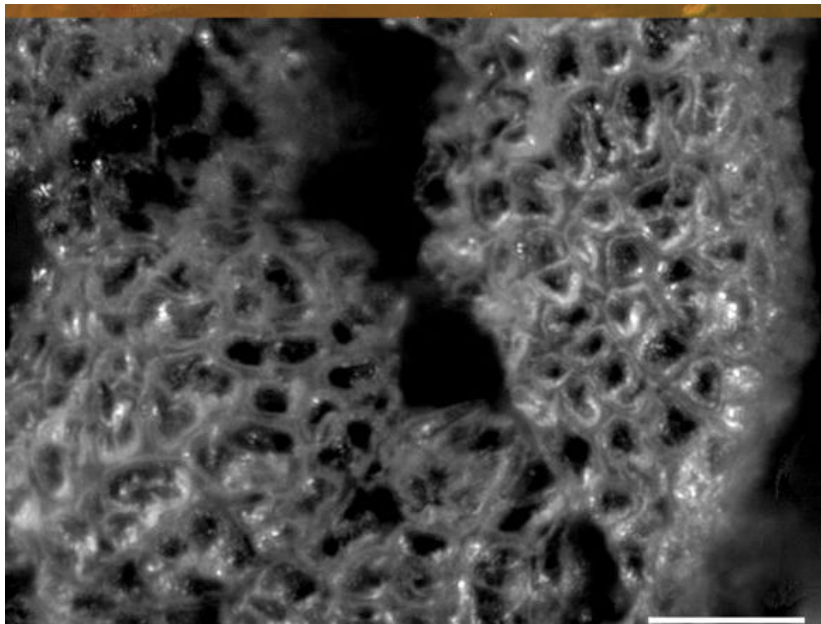
- ▶ Scientists have learned a lot from studying fossils, but care is needed. Very few things fossilize, and some things are much more likely to fossilize than others, for example:
  - ▶ Things that live in swampy areas, or underground (**Habitat bias**)
  - ▶ Hard things, or hard parts of things (**Taxonomic bias**)
  - ▶ Things that lived more recently have had less time to be destroyed, or to be buried too deep for recovery (**Temporal bias**)
  - ▶ Things that are more abundant have more chances to be preserved (**Abundance bias**)

# Accounting for biases

- ▶ Because the fossil record is biased, scientists must be very careful about making inferences from what they see
  - ▶ Just because you don't see it, doesn't mean that it wasn't there
  - ▶ Just because you see a lot, doesn't mean that there were a lot (relatively speaking)
- ▶ Trying to figure out what happened based on what kind of fossils we happen to find is tricky
- ▶ Orchid phylogeny







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# Putting the timeline together

- ▶ Dates of specimens can be inferred using radioactive isotopes (harder than it sounds)
- ▶ Geologic inferences can be made about the relative age of different things (for example, if one was deposited on top of another).
- ▶ Molecular clocks are based on inferences about how fast things are evolving
- ▶ These techniques are complicated, and making the timeline is a difficult and exciting puzzle

## Guessing game (*Extra*)

- ▶ For most of Earth's history, there has been:
  - ▶ No life
  - ▶ Life, but no multi-cellular organisms
  - ▶ Multi-cellular organisms, but no plants, animals or fungi
  - ▶ Plants, animals, and fungi, but no flowering plants, birds or mammals
  - ▶ Flowering plants, birds and mammals, but no good espresso

## Guessing game (Extra)

- ▶ For most of Earth's history, there has been:
  - ▶ No life
  - ▶ **Life, but no multi-cellular organisms**
    - ▶ Probably
  - ▶ Multi-cellular organisms, but no plants, animals or fungi
    - ▶ Probably not – may depend on definitions
  - ▶ Plants, animals, and fungi, but no flowering plants, birds or mammals
  - ▶ Flowering plants, birds and mammals, but no good espresso

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# Processes of diversification

- ▶ Diversity sometimes arises gradually, and sometimes dramatically (**radiation** events)
- ▶ Species (and families, and bigger groups) sometimes disappear gradually, and sometimes dramatically (**mass extinction** events)

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# Adaptive radiations

- ▶ An **adaptive radiation** occurs when a single lineage produces many descendant species, in a short period of time, that make their living in a variety of different ways
- ▶ Triggered by opportunity, either in the environment, or because of the evolution of the organisms themselves

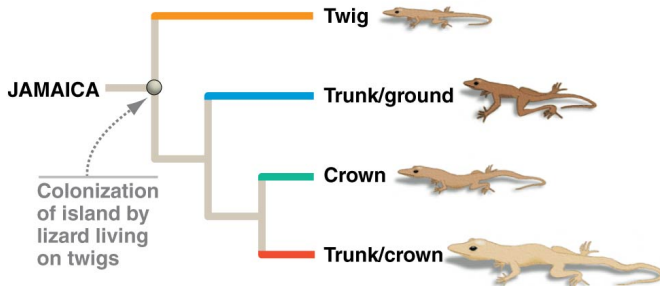
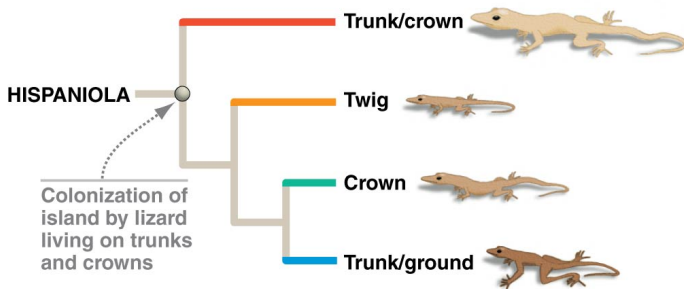
# Triggers for adaptive radiation

- ▶ Ecological opportunity
  - ▶ An organism arrives in an area with no similar organisms
  - ▶ A group of competing species is driven extinct (or nearly extinct) by some other cause
- ▶ Morphological innovation: an organism comes up with a good, new idea
  - ▶ Legs in tetrapods
  - ▶ New body plans in the Cambrian explosion
  - ▶ Multi-cellularity
- ▶ Co-evolution: the evolution of one group creates new niches for another group, and vice versa
  - ▶ The insects and the flowering plants

# Colonization

- ▶ In many different cases, a new kind of organism has colonized an area, and diversified rapidly
- ▶ This is an opportunity for studying how evolution can go:
  - ▶ What is the same, and what is different, between similar cases?
  - ▶ Finches
  - ▶ Silverswords in Hawaii
  - ▶ Anolis lizards

**(c)** The same adaptive radiation of *Anolis* has occurred on different islands, starting from different types of colonists.



# Competition

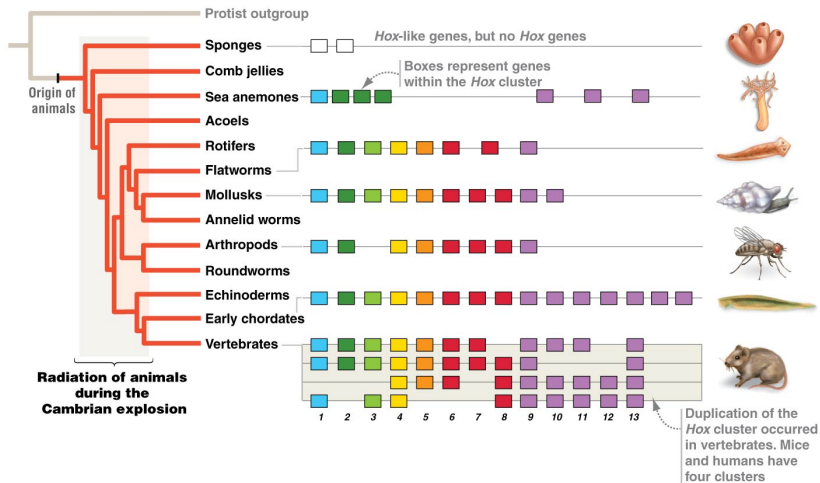
- ▶ Mammals did very well after the dinosaurs went extinct
- ▶ We have seen major tree extinctions due to introduced diseases in the last century
  - ▶ \* It remains to be seen whether new evolution will fill this opportunity

# Morphological innovation

- ▶ A new adaptive mutation can open up further possibilities for adaptation
  - ▶ **Hox gene** mutations allowed early animals to develop complex body plans
  - ▶ The arthropod body plan
    - ▶ insects, arachnids, crustaceans ...
  - ▶ The tetrapod body plan
    - ▶ reptiles, mammals ...
  - ▶ Flowering plants
    - ▶ This opened many new opportunities for *everyone* (insects, mammals, birds), not just the innovators
    - ▶ \* Co-evolution

# Hox genes

- ▶ **Hox genes** are involved in determining the identity of different body parts
- ▶ Taxa with simpler body structures tend to have fewer hox genes
  - ▶ Phylogenetic comparisons provide important evidence that hox genes were involved in evolution of complex body plans
- ▶ Evidence that new hox genes were largely created by **gene duplication** events
  - ▶ A rare but important type of mutation
  - ▶ Natural selection must have played a role in the development of this much complexity





# Gene duplication

- ▶ One or more genes may be accidentally duplicated so that the genome has two copies of each gene
- ▶ This may make the organism less efficient, and thus be selected against
- ▶ It may also allow for innovation. Why?
  - ▶ \* Because one copy can continue to do the old function, while the other evolves a new function

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# Mass extinctions

- ▶ Five major mass extinctions so far
- ▶ The last one (and maybe others) was caused by a cosmic impact
  - ▶ It could happen again
- ▶ Are we in the middle of a mass extinction now?
  - ▶ Extinction rate very high over the last 400 years
  - ▶ Time will tell, but we should be worried

# Conclusion

- ▶ The best way to reconstruct evolution is with a *model* of how it occurred
  - ▶ Molecular information, and computer modeling has changed our view of the tree of life
  - ▶ life is not really a tree
    - ▶ genetic information can be transferred
    - ▶ sexual mixing occurs at different scales
- ▶ Scientists use many clues to figure out the history of life on earth
  - ▶ Fossils, geology, phylogeny
- ▶ Life has diversified both gradually, and with dramatic episodes
  - ▶ Adaptive radiations, mass extinctions