

CONCEPTS OF BIOLOGY

Chapter 12 DIVERSITY OF LIFE

PowerPoint Image Slideshow



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FIGURE 12.1 ALL LIVING ORGANISMS ON EARTH ARE RELATED



Although they look different, this bee and flower are distantly related. (credit: modification of work by John Beetham)

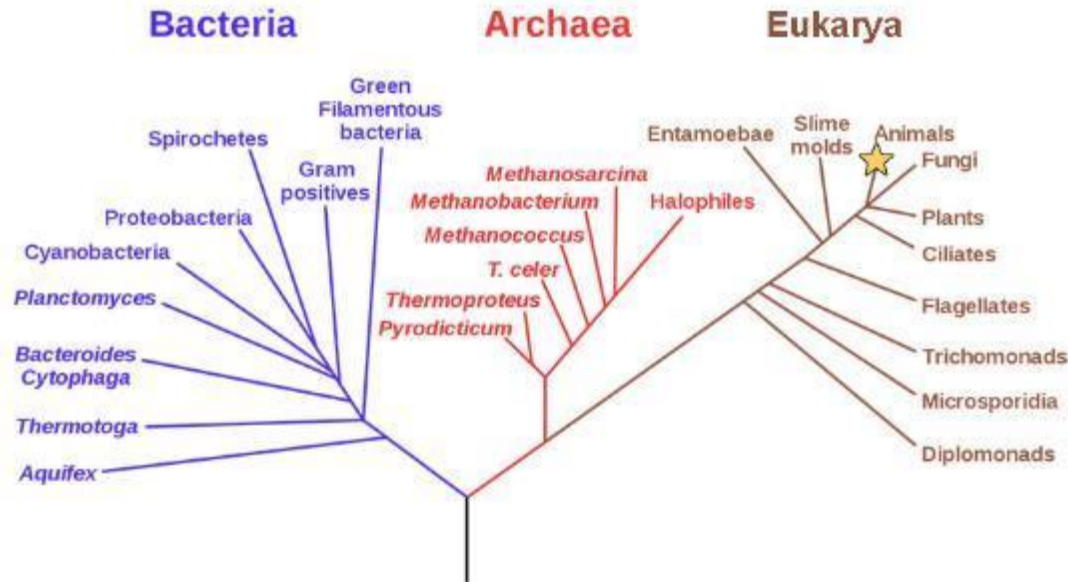
ORGANIZING LIFE ON EARTH 1 OF 2 (12.1)

- All life on earth evolved from a common ancestor.
- Biologists map how organisms are related by constructing **phylogenetic trees**, which show when organisms evolved and shows relationships among different organisms (Figure 12.2).
- The 3 domains of life (Archaea, Bacteria and Eukarya) arise from a single point, diverge and then branch repeatedly.
- In a phylogenetic tree, the pathway can be traced from the origin of life to any individual species.
- Also, by starting at a single species and tracing back to any branch point, the organisms related to it can be identified.

FIGURE 12.2 TREE OF LIFE

Phylogenetic Tree of Life

★ = You are here



In the evolution of life on Earth, the three domains of life—Archaea, Bacteria, and Eukarya—branch from a single point. (credit: modification of work by Eric Gaba)

ORGANIZING LIFE ON EARTH 2 OF 2 (12.1)

- A **phylogeny** is the evolutionary history and the relationships among a species or group of species.
- The study of organisms with the purpose of deriving their relationships is called **systematics**.
- Many disciplines within biology contribute to systematics, including data from:
 - Fossils
 - Studying morphology
 - The structure of body parts
 - Molecular structure (DNA, RNA or amino acids in proteins)
- Trees change as new data arrives, such as the discovery of new species or new character information.

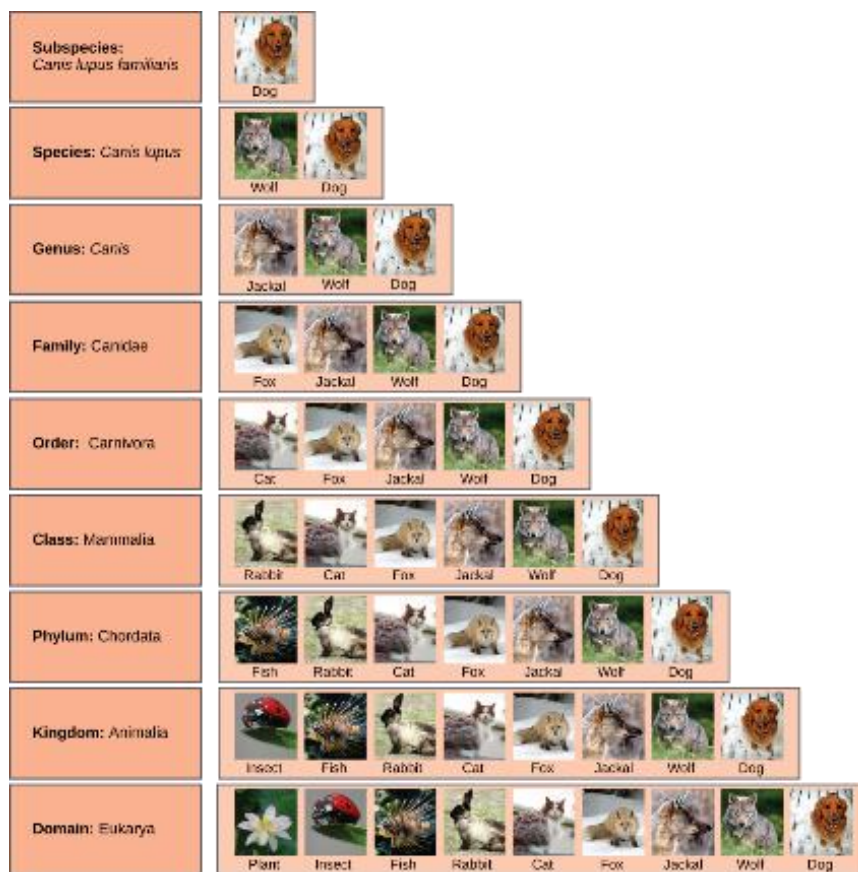
THE LEVELS OF CLASSIFICATION 1 OF 3 (12.1)

- **Taxonomy** is the science of naming and grouping species to construct an internationally shared classification system.
- The classification system is named after **Carolus Linnaeus** (a Swedish naturalist), its inventor.
- The taxonomic system is a hierarchical system in which each group includes all the groups at the next lowest level. The levels are:
 - Domain (the largest group): there are 3 domains (Archaea, Bacteria and Eukarya)
 - Kingdom: there are several kingdoms
 - Phylum
 - Class
 - Order
 - Family
 - Genus
 - Species (the smallest group, a single species)

THE LEVELS OF CLASSIFICATION 2 OF 3 (12.1)

- The classification levels for the domestic dog are shown in Figure 12.3.
- The group at each level is called a **taxon** (plural, taxa).
- Scientists refer to each organism using a two part naming system called **binomial nomenclature**.
 - The two part name is the genus and species (latin or scientific name)
 - The genus name is capitalized and the species name is lowercase
 - The two part name is underlined or italicized
 - For example, the wolf is *Canis lupus*
 - The domestic dog is a subspecies of the wolf, *Canis lupus familiaris*

FIGURE 12.3 CLASSIFICATION OF THE DOMESTIC DOG



At each sublevel in the taxonomic classification system, organisms become more similar. Dogs and wolves are the same species because they can breed and produce viable offspring, but they are different enough to be classified as different subspecies. (credit “plant”: modification of work by "berduchwal"/Flickr; credit “insect”: modification of work by Jon Sullivan; credit “fish”: modification of work by Christian Mehlführer; credit “rabbit”: modification of work by Aidan Wojtas; credit “cat”: modification of work by Jonathan Lidbeck; credit “fox”: modification of work by Kevin Bacher, NPS; credit “jackal”: modification of work by Thomas A. Hermann, NBII, USGS; credit “wolf” modification of work by Robert Dewar; credit “dog”: modification of work by "digital_image_fan"/Flickr)

THE LEVELS OF CLASSIFICATION 3 OF 3 (12.1)

- Taxonomic levels move toward specificity.
- At each sublevel, the organisms become more similar because they are more closely related.
- Since Darwin's theory was published in the 19th century, biologists work to make the classification system reflect evolutionary relationships.
 - All members of a taxon should have a common ancestor and be more closely related to each other than to members of other taxa.
- Changes and updates are made as new discoveries take place.
 - For example, the prokaryotes were recently divided into 2 separate domains (Archaea and Bacteria) because they are so different genetically.

TAXONOMY CONCEPT IN ACTION

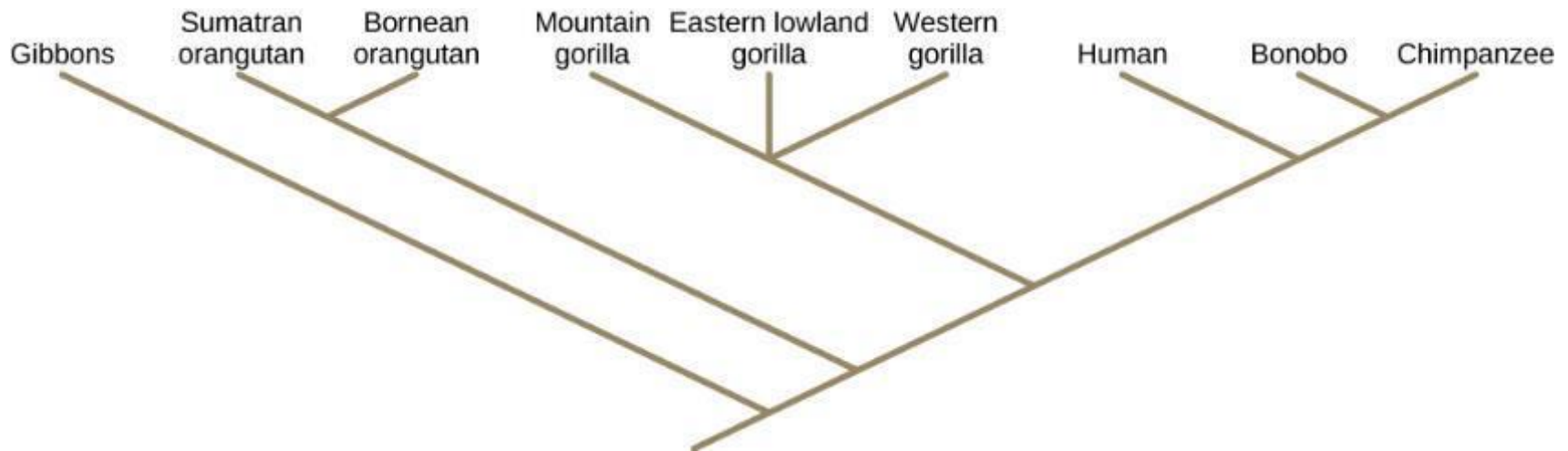
Visit this PBS site to learn more about taxonomy. Under Classifying Life, click Launch Interactive.

[Launch Interactive](#)

CLASSIFICATION AND PHYLOGENY 1 OF 2 (12.1)

- A **phylogenetic tree** is a diagram used to reflect evolutionary relationships among organisms or groups of organisms.
 - Scientists consider phylogenetic trees to be a hypothesis of the evolutionary past because one cannot go back in time to confirm the proposed relationships
- A phylogenetic tree is constructed using shared characteristics and can be read like a map of evolutionary history (Figure 12.4).
- **Branch point** → the point where a split occurs in a tree
 - Represents where a single lineage evolved into distinct new ones
- **Rooted** → a tree with a single ancestral lineage to which all organisms represented in the diagram relate
- **Sister taxa** → two lineages that diverged from the same branch point
 - For example, the 2 groups of orangutans are sister taxa

FIGURE 12.4 PHYLOGENETIC TREE

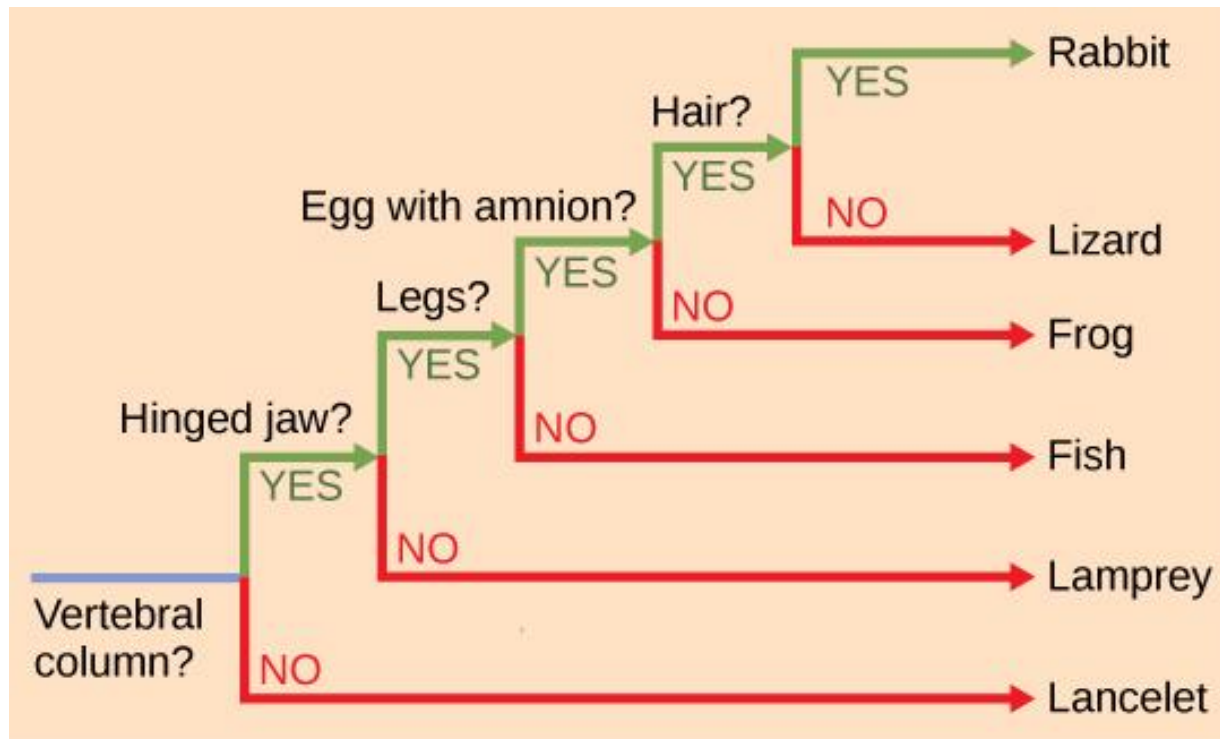


A phylogenetic tree is rooted and shows how different organisms, in this case the species and subspecies of living apes, evolved from a common ancestor.

CLASSIFICATION AND PHYLOGENY 2 OF 2 (12.1)

- The branch points in a phylogenetic tree also imply evolutionary change.
- Sometimes the significant character changes are identified on a branch or branch point (Figure 12.5)
- For example, the branch point that gives rise to the mammal and reptile lineages from the frog lineages shows the origin of the amniotic egg character

FIGURE 12.5 PHYLOGENETIC TREE



This phylogenetic tree is rooted by an organism that lacked a vertebral column. At each branch point, organisms with different characters are placed in different groups.

SPECIES CONCEPT IN ACTION

This interactive exercise allows you to explore the evolutionary relationships among species.

[Launch Interactive](#)

LIMITATIONS OF PHYLOGENETIC TREES (12.1)

- It is easy to assume that more closely related organisms look alike, but this is not always true (Figure 12.5).
 - Two closely related lineages could evolve under different surroundings or a major adaptation could evolve
 - Then closely related lineages could look quite different from each other
 - For example, rabbits and lizards are more closely related (by the presence of an amniotic egg) than lizards and salamanders (even though they look more alike)
- Also, unless otherwise noted, the branch points do not indicate length of time (only the order in time of evolutionary events)
 - For example, the tree does not indicate how much time has passed between the evolution of amniotic eggs and hair, just the order in which things took place.

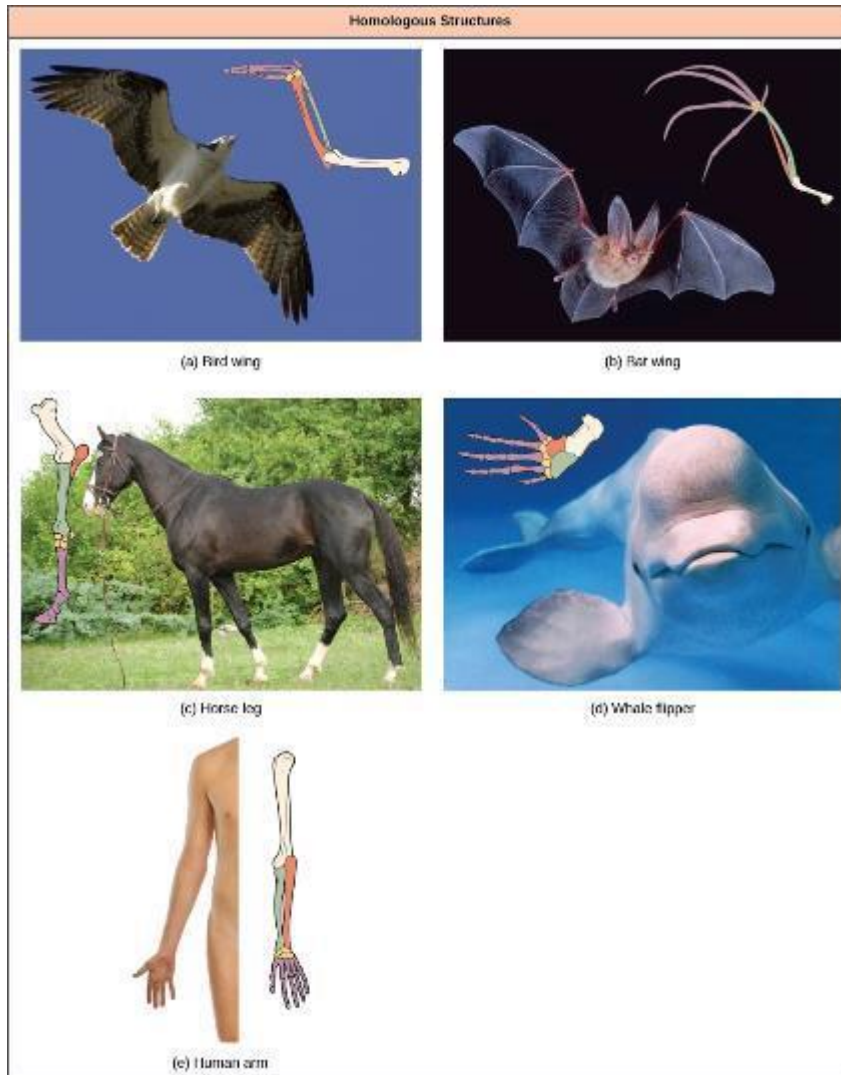
DETERMINING EVOLUTIONARY RELATIONSHIPS (12.2)

- In the case of phylogeny, evolutionary investigations focus on 2 types of evidence:
 - Morphologic (form and function)
 - Genetic

TWO MEASURES OF SIMILARITY (12.2)

- Organisms that share similar physical features AND genetic sequences tend to be more closely related than those that do not
 - Features that overlap both in morphology and genetics are called **homologous structures**
 - For example, the bones in the forelimbs of vertebrates (Figure 12.6) are homologous and indicate that these organisms share a common evolutionary past
- Some organisms may be closely related even though they look quite different due to a minor genetic change causing a major morphological difference. This can be misleading.
 - For example, the chimpanzee skull and human skull look quite different even though these organisms are closely related (Figure 12.7)

FIGURE 12.6 HOMOLOGOUS STRUCTURES



Bat and bird wings, the foreleg of a horse, the flipper of a whale, and the arm of a human are homologous structures, indicating that bats, birds, horses, whales, and humans share a common evolutionary past. (credit a photo: modification of work by Steve Hillebrand, USFWS; credit b photo: modification of work by U.S. BLM; credit c photo: modification of work by Virendra Kankariya; credit d photo: modification of work by Russian Gov./Wikimedia Commons)

FIGURE 12.7 CHIMPANZEE VS HUMAN JAW



(a)



(b)

(a) The chimpanzee jaw protrudes to a much greater degree than (b) the human jaw.

(credit a: modification of work by "Pastorius"/Wikimedia Commons)

DETERMINING EVOLUTIONARY RELATIONSHIPS 1 OF 3 (12.2)

- In contrast, unrelated organisms may appear very much alike even though they are only distantly related. This is also misleading.
- This usually occurs because common adaptations to similar environmental conditions evolved in both
- When organisms evolve similar characteristics because they are adapting to similar environments (convergent evolution), the structures are called **analogous structures**
 - For example, the wings of insects, appear similar to the wings of bats and birds. However, insects are not closely related to bats and birds and the embryonic origin of the wings are different (Figure 12.8)
- Similar traits can be either homologous or analogous.

FIGURE 12.8 ANALOGOUS STRUCTURES



(a) Bat wing



(b) Bird wing



(c) Insect wing

The wing of a honey bee is similar in shape to a bird wing and a bat wing and serves the same function (flight). The bird and bat wings are homologous structures. However, the honey bee wing has a different structure (it is made of a chitinous exoskeleton, not a boney endoskeleton) and embryonic origin. The bee and bird or bat wing types illustrate an analogy—similar structures that do not share an evolutionary history. (credit a photo: modification of work by U.S. BLM; credit b: modification of work by Steve Hillebrand, USFWS; credit c: modification of work by Jon Sullivan)

PHYLOGENETIC CONCEPT IN ACTION

This website has several examples to show how appearances can be misleading in understanding the phylogenetic relationships of organisms.

[Link to Website](#)

DETERMINING EVOLUTIONARY RELATIONSHIPS 2 OF 3 (12.2)

- **Molecular systematics** is using molecular evidence to identify phylogenetic relationships
 - Involves the use of DNA sequencing, amino acid sequences of proteins and other molecular measures
 - Confirms many earlier classifications and also uncovers previously made errors
- Phylogenies assume that the more similar the sequences are in two organisms, the more closely related they are
- Different genes evolve at different rates and this affects the level at which they are useful at identifying relationships
 - Rapidly evolving sequences are useful for determining relationships among closely related species
 - More slowly evolving sequences are useful for determining relationships between distantly related species

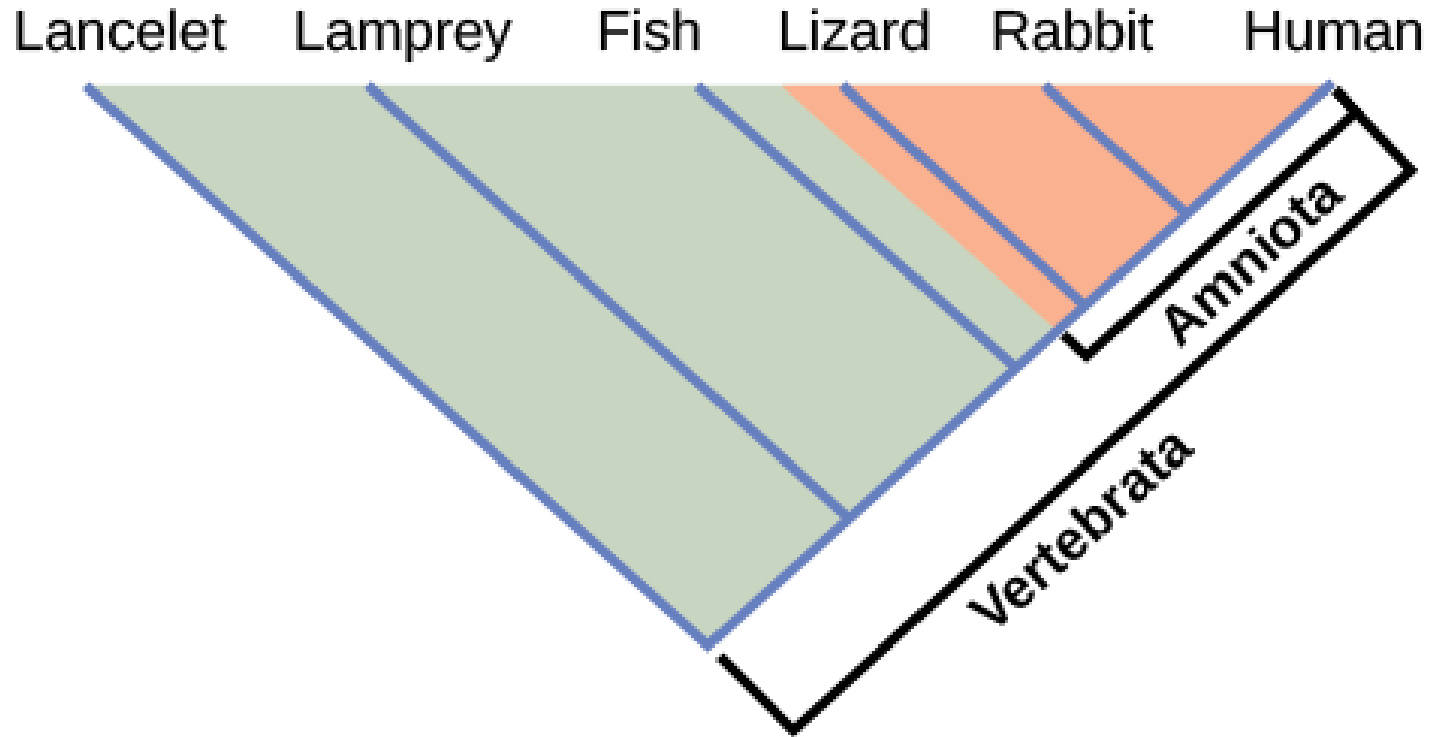
DETERMINING EVOLUTIONARY RELATIONSHIPS 3 OF 3 (12.2)

- **Why does phylogeny matter?**
- Phylogeny enhances our understanding of the evolutionary history of species
- It also has numerous practical applications like helping us understand the evolution and transmission of disease and helping us make decisions about conservation efforts

BUILDING PHYLOGENETIC TREES 1 OF 3 (12.2)

- The most accepted method currently for constructing phylogenetic trees is called **cladistics**.
- Cladistics sorts organisms into **clades**, which are groups of organisms that are most closely related to each other and the ancestor from which they are descended.
 - A clade is also called a **monophyletic group** and must include the ancestral species and all of the descendants from a branch point.
 - For example, in Figure 12.9, all the organisms in the shaded region evolved from a single ancestor that had amniotic eggs.

FIGURE 12.9 A PHYLOGENY BASED ON CLADISTICS



Lizards, rabbits, and humans all descend from a common ancestor in which the amniotic egg evolved. Thus, lizards, rabbits, and humans all belong to the clade Amniota. Vertebrata is a larger clade that also includes fish and lamprey.

BUILDING PHYLOGENETIC TREES 2 OF 3 (12.2)

- Cladistics relies on 3 assumptions:
 - Living things are related by descent from a common ancestor
 - Speciation occurs by splits of one species into two
 - Traits change enough over time to be considered to be in a different state and one can identify the direction of change for a state
- If a characteristic is found in all members of a group, it is called a **shared ancestral character**. These are not useful in cladistics.
- If a characteristic is shared only by a certain group of organisms (only some of the organisms), it is called a **shared derived character**.
 - Shared derived characters have changed some during descent
 - Only shared derived characters should be used in cladistics
 - For example, the amniotic egg in Figure 12.9 is derived because only the lizard, rabbit and human have it, and are thus more closely related.

BUILDING PHYLOGENETIC TREES 3 OF 3 (12.2)

- Usually computers generate phylogenetic trees using cladistics.
- If there is more than one way to construct the tree based on the data, the principle of maximum parsimony is used.
- **Maximum parsimony** means that the simplest, most obvious way with the least number of steps is used to construct the tree.

Concept in Action

Go to the website below to learn how maximum parsimony is used to create phylogenetic trees.

[Link to Website](#)

VOCABULARY

- Analogous structure
- Binomial nomenclature
- Branch point
- Clade
- Cladistics
- Domain
- Kingdom
- Maximum parsimony
- Molecular systematics
- Monophyletic group
- Phylogenetic tree
- Phylogeny
- Rooted
- Shared ancestral character
- Shared derived character
- Sister taxa
- Species
- Systematics
- Taxon
- Taxonomy