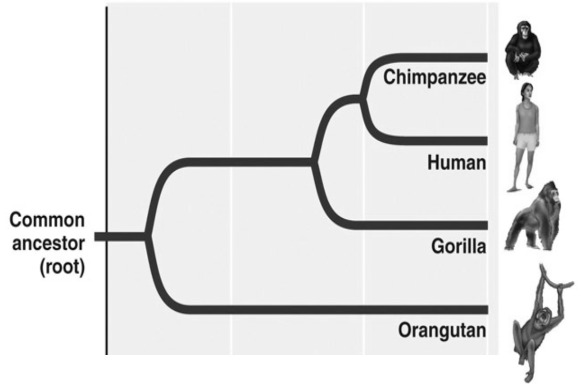
Chapter 16: Reconstructing and Using Phylogenies

Chapter Review

1. Use the phylogenetic tree shown at the right to complete the following.



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a. Explain how many clades are indicated:

Three: (1) chimpanzee/human, (2) chimpanzee/human/gorilla, and (3)chimpanzee/human/gorilla/orangutan

b. Explain which branch point occurred most recently:

Chimpanzee/human, because the node where the phylogenetic tree splits into chimpanzees and humans is the farthest from the common ancestor.

c. Discuss the reasons why one of the organisms on the tree is interested in its evolutionary relationships to the other three organisms.

Humans are the only group of the four that developed adequate brain function to consider evolutionary relationships. The groups share a common ancestor, with the nodes indicating that the groups diverged evolutionarily three times in response to some speciation event. The relationship between the four organisms is of interest because of their shared ancestry. Phylogenies such as this can be used to make comparisons and predictions about shared traits and evolutionary history, and this information may be used to discover changes in the genome of that affect health. For example, the association of a particular genetic change in response to a specific medical treatment can provide a hypothesis that can be tested experimentally using species that are closely related genetically.

2. Homologous structures are of great use in determining evolutionary relationships. Explain the homology that is present in each pair of items below.

a. The spinal cord of a shark and that of a chimpanzee.

All living vertebrates have a vertebral column, as did the ancestral vertebrates from which they evolved. Thus, the vertebral column is a trait that evolved from a single condition, the ancestral trait, to another condition, the derived trait. Derived traits that are shared among a group of organisms, like vertebrates, are viewed as evidence of the common ancestry and are called synapomorphies.

b. The wing of a bird and that of a bat.

The wings of birds and bats are not homologous. Although they serve similar functions, they evolved independently along different lineages, a phenomenon called convergent evolution.

c. A vision-related gene that is identical in fruit flies and mice.

The vision-related gene present in both fruit flies (insects) and mice (mammals) is an example of a homologous trait. Since most scientists believe that this gene, which produces visual sensitivity in animals, was derived from a common ancestor, it would be considered an ancestral trait as well as another example of synapomorphy.

3. Use the data presented in the table below to label the small circles with the derived trait shown in the diagram below.

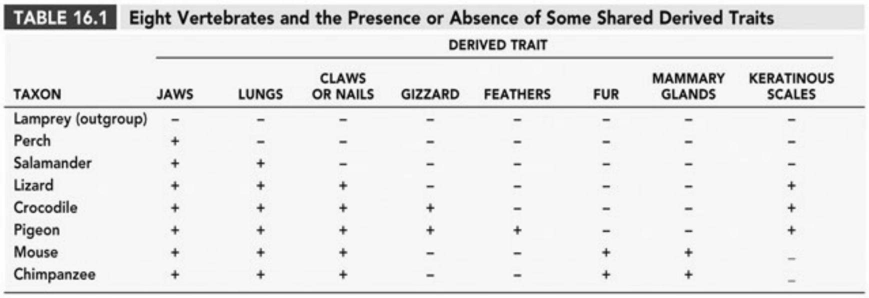

TABLE 16.1 Eight Vertebrates and the Presence or Absence of Some Shared Derived Traits

	DERIVED TRAIT							
TAXON	JAWS	LUNGS	CLAWS OR NAILS	GIZZARD	FEATHERS	FUR	MAMMARY GLANDS	KERATINOUS SCALES
Lamprey (outgroup)	–	–	–	–	–	–	–	–
Perch	+	–	–	–	–	–	–	–
Salamander	+	+	–	–	–	–	–	–
Lizard	+	+	+	–	–	–	–	+
Crocodile	+	+	+	+	–	–	–	+
Pigeon	+	+	+	+	+	–	–	+
Mouse	+	+	+	–	–	+	+	–
Chimpanzee	+	+	+	–	–	+	+	–

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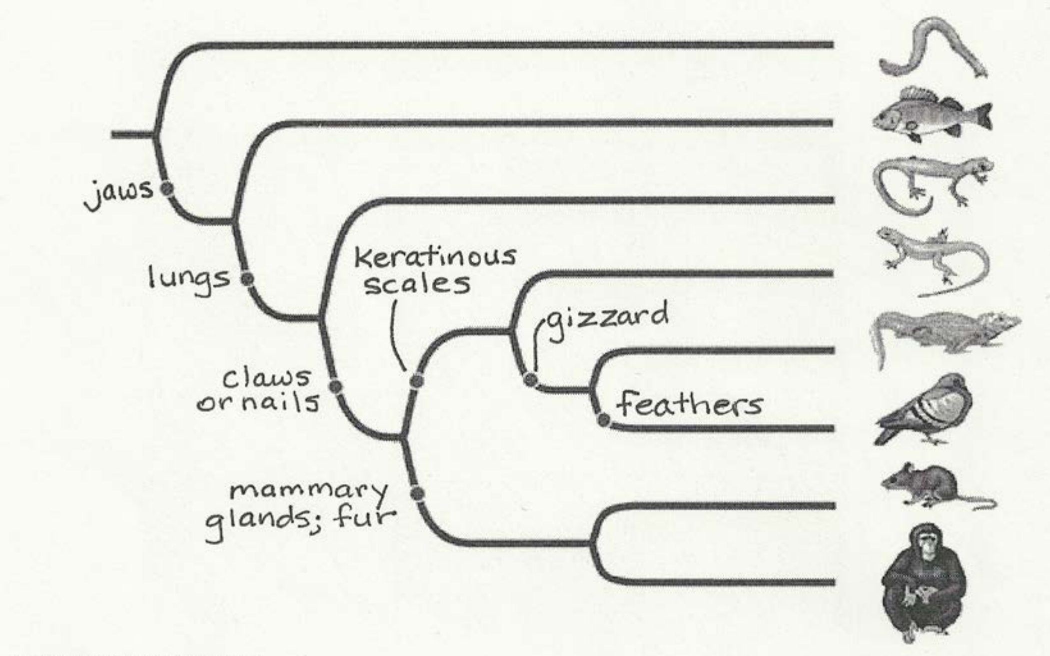

PRINCIPLES OF LIFE, Figure 16.3
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4. “Parsimony” is a term used to describe how the analysis completed in the above question would resolve the complications of adding more traits and more organisms to phylogenetic analysis. Describe what “parsimony” means in this context.

The principle of parsimony applies to the reconstruction of phylogenies using the minimal number of evolutionary changes that need to be assumed over all characters in all groups in the tree. Specifically, the best hypothesis under the parsimony principle is one that requires the fewest homoplasies, or as in Occam’s razor, the best explanation is the one that best fits the data while making the fewest assumptions. Phylogenetic trees represent our best estimates about evolutionary relationships, given the evidence available. Modifications can be made as new information becomes available.

5. Though their body shapes are similar, snakes and worms have substantially different evolutionary histories. Discuss how this convergence might have occurred and suggest additional data that could be sought in determining the differences in evolutionary heritage.

Although snakes and worms are not closely related species, they share a common morphology, i.e. they both possess tubular shaped, limbless bodies. This convergence may have occurred in response to external or environmental conditions where tubular shape and lack of limbs favored produced higher rates of reproduction and survival. The streamlined, tubular shape shared by snakes and worms enables them to burrow in the soil underground more easily. More angular, less continuous shapes, especially those with limbs, would make burrowing much more difficult. The morphology of these very different species enabled them to survive and reproduce in a specific niche. Additional data to determine differences in evolutionary heritage could be obtained by observing developmental patterns, behavior, and molecular data encoded in the DNA sequences of the genomes of each species.

6. Explain why phylogenetic trees based on gene sequences are more accurate in showing evolutionary relationships than are phylogenetic trees based on morphology.

As biologists began to utilize DNA sequences to infer phylogenies, they developed explicit mathematical models describing how these sequences change over time. These models account for multiple changes at any given position in DNA sequence. They also take into account the differing rates of change at different positions in a gene, at different position in a codon, and among different nucleotides. This provides a level of detail and accuracy not possible relying solely on comparison of morphological traits. And as we have seen, morphological similarities may be misleading since they could be based on convergent evolution and rather than a close genetic relationship. Comparisons made on the basis of base changes in DNA demonstrate explicit relationships, rather than inferred.

7. Explain how protein analyses can help to meet the challenge of determining the approximate time that an evolutionary change took place; i.e., describe and discuss the “molecular clock” of protein change.

Although different genes evolve at different rates, depending upon many biological and physical factors, a given gene typically evolves at a reasonably constant rate among closely related species. Therefore, the protein encoded by the gene accumulates amino acid replacements at a relatively constant rate. A “molecular clock” uses the average rate at which a given gene or protein accumulates changes to gauge the time of divergence for a particular split in the phylogeny. These molecular clocks must be calibrated using independent data, such as the fossil record, known times of divergence, or biogeographic dates. Using calibrations such as these, the times of divergence have been estimated for many groups of species that have diverged over millions of years.

8. Female swordtail fish (*Xiphophorus*) show a mating preference for males with long swordtails, suggesting that sexual selection for longer tails over evolutionary time has occurred. Even though the males of a related species of platyfish do not have long tails, females of that species demonstrate a preference to mate with male platyfish that have been fitted with artificial long tails. Discuss what the females’ mating preference suggests about the phylogenetic background of both groups of fish.

Experimental observations that female platyfishes prefer males with artificial sword tails support the idea that this appendage evolved as a result of a preexisting preference in the females. This preference remains encoded in their genes today, even though today’s short-tailed species of male platyfishes do not have sword tails.

9. Discuss how studies of the “molecular clock” allowed an estimate of the specific year of origin for the human immunodeficiency virus.

The earliest HIV-1 samples date to the 1950s. Scientists can use the observed changes in HIV-1 to project back to the common ancestor of all HIV-1 isolates, and thus can estimate when HIV-1 first entered human populations from chimpanzees. The clock is calibrated with the samples from the 1980s and 1990s, and then can be compared to the samples from the 1950s to observe the temporal pattern of changes.

10. Describe the Linnean binomial nomenclature of your own species.

The binomial nomenclature for humans was proposed by the Swedish biologist Carolus Linnaeus who created the phylogenetic classification system for all organisms in the 1700s. It includes the genus name *"Homo,"* which is from the Latin *humanus*, meaning "man." The species name *"sapiens"* is derived from the Latin for "wise." Humans are the only living members of the genus *Homo*, which includes mammals of the primate order that originated in Africa.

11. Place these taxonomic terms in correct sequence, from most inclusive to most specific.

order, genus, family, species, classes, phyla, kingdoms

kingdoms, phyla, classes, order, family, genus, species

12. Explain why it is essential that each group of organisms included in gene bank databases has an accurate and specific taxonomic identity.

While there may be dozens of common names in many different languages for an organism, biologists around the world follow the rules of biological nomenclature to facilitate communication and dialogue. The rules of biological nomenclature are designed so that there is only one correct scientific name for any single recognized taxon, i.e. each scientific name is specific, unique, and universal. This system helps prevent confusion and ambiguity in the literature and throughout the worldwide scientific community. When gene bank data are used to construct phylogeny, the accurate identification of the source sequence is critical for accurate deductions.

13. In a recent newspaper, an article about humans described humans as the genus *sapiens*. Explain why this is inaccurate and why *sapiens* cannot be used by itself.

The rules of biological nomenclature are designed so that there is only one correct scientific name for any single recognized species. There are typically several species with the same genus name, and there may be other organisms from different genera with the same species name, but the rules prevent any organism from having the same combination of genus and species names. For example, the genus *Drosophila* refers to both the common fruit fly and genus of fungi. Not using both parts of the scientific nomenclature for either of these organisms would lead to confusion. Referring to humans as simply *"Sapiens"* could cause the same type of uncertainty. Of course, our genus is *Homo.*

Science Practices & Inquiry

14. Living in water would seem to suggest shared evolutionary heritage. We will survey traits of four animals with aquatic lifestyles: sponges, fish, newts and whales. Sponges do not have a circulatory system, fish have a two-chambered heart, aquatic newts have a three-chambered heart, and whales have a four-chambered heart. Sponges, fish and newts are poikilothermic (cold-blooded) and whales are homeothermic (warm-blooded). Sponges reproduce both asexually and sexually; when reproducing sexually, sponges shed gametes externally. The fish and newt shed their gametes externally; internal fertilization, internal development (gestation, or pregnancy), and nursing of offspring are the reproductive pattern of whales. Sponges do not have true tissues, while fish, newts, and whales all have true tissues. Produce a table showing the presence of these traits in a table and then draw a phylogenetic tree.

	Homeothermic	True tissues	Circulatory system/# of heart chambers	Exclusively sexual reproduction	Gametes fertilized internally/nursing of young
sponges	-	-	-	-	-
fish	-	+	+ / 2	+	-
newts	-	+	+ / 3	+	-
whales	+	+	+ / 4	+	+