Exercise 6 (Modules 15.11–15.13)

Scientists are beginning to understand the biological mechanisms responsible for large-scale evolutionary changes. Review the biological mechanisms underlying macroevolution by matching each of the descriptions on the left with the best evolutionary example on the right.

- Changes in body form often result from changes in gene regulation, not in the genes themselves.
 Complex structures often evolve step-by-step.
 A structure that evolves in one context and takes on a new role is called an exaptation.
 Slight changes in the relative rates of growth in different body parts can make big changes in the appearance of adults.
 Changes in homeotic genes can radically alter the timing of development and the shape of body parts.
 Selection among different species may result in large-scale evolutionary trends or apparent "trends."
 Paedomorphosis is a change in timing of development, causing juvenile features to be retained by adults.
- A. The horse family
- B. Eyes
- C. Human and chimp skulls
- D. Feathers
- E. Fins to legs
- F. Salamanders with gills
- G. Stickleback spines

Exercise 7 (Modules 15.14-15.19)

Review the principles, methods, and vocabulary of phylogeny and systematics by inserting the correct terms into the following essay.

reflect evolutionary history. Biologists depict these relationships in the form of

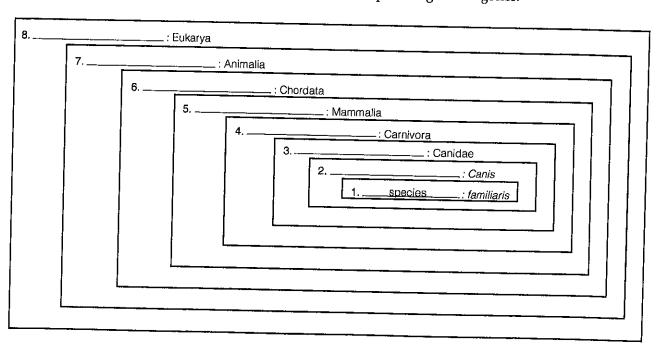
_ (the largest and most inclusive). Ideally, these categories

trees. Species	are the twigs of such a	a tree. The minds of the tree	e are
larger groupings such as orders, cla	_		
The most widely used meth	od in systematics is ca	lled ¹⁴	. It is
a method that that seeks to identify	15	—branches that include ar	n an-
cestral species and all its descendankingdom—is said to be ¹⁶ classification scheme that reflects the	ts. Such an inclusive gr Cladistics r	roup—a genus, family, or makes it possible to constru	
	ū		•• .
Cladistics is based on the ideble trait develops and is passed on to new trait are more ¹⁷	o descendants. Groups related than thos iger, the lion, and the b char and nurses them within reperiod of gestation, no trait, a shared ¹⁹ the Tasmanian tiger. Th of Class Mammalia, re ts with the Tasmanian esents an ²⁰	of organisms that share the that have only ancestral pobcat all have hair and materials. But the Tasmanian to a pouch. The lion and bobourishing them via a structure character, the bobcat and lion are place effecting this evolutionary latiger, the cats constitute articles.	ne tiger cat ture nat ed in his- n in-
guides cladistics, but this has shaken tree. For example, this approach place Several shared ²³ that birds and crocodiles are more clareptiles. Similarly, cladistics separate	es some branches of the ces ²² _ characters, such as a osely related to each of es humans and chimps	"traditional" evolutionary within the reptile clade four-chambered heart, sho ther than crocs are to other from other apes.	w w
Molecular comparisons can cacids, proteins, or other molecules to	determine relatedness se computers to search	is called molecular through and compare nuc	leic
acid ²⁵ sequences	from different species	. In general, the more simil	lar
the base sequences, the more ²⁶	related	the organisms in question.	
Some nucleic acids, such as the DNA			
Thus, mDNA can be used to trace rec			f
various human groups. Other nucleic		_	
over hundreds of millions of years. Be they allow us to calibrate a molecular lutionary branch points. Because a go	ecause some genes app 29od fossil record goes b	that can be used to date evack only about	
numon years,		locks to date divergences	
thought to have occurred before that cats and the Tasmanian tiger, we wou cat would be more alike than homolo cladistics and molecular systematics of	ıld expect that homolog gous genes of a lion an	gous genes of a lion and a l d a Tasmanian tiger. Thus,	oob-
Comparing whole genomes h			
ary relationships. On a molecular leve			
Amazingly ³² of h			
about half our genes are homologous	with genes in 33		ed

eukaryotes! Genomics has revealed that gene ³⁴	has had an important
role in evolution, because it increases the number of genes "raw material" for evolutionary change.	in the genome and provides
Looking at the larger picture, molecular systematic entire tree of life. Back in the day, all life was divided into 35 and 36 But wh photosynthetic organisms that swim? By the 1960s, it look main branches, but soon enough, molecular comparisons of flawed too. More recently, biologists have adopted a three with two groups of prokaryotes, called 38 and one group of eukaryotes, the 40 Plafungi, and protists (like those swimming green guys) are 4 Domain Eukarya.	two kingdoms— ere did this leave bacteria or ed like the tree of life had five showed that that scheme was system, and ³⁹ ,
The most recent discoveries suggest that the tree of During the early history of life, there appear to have been samong the different domains. This took place via 43_process carried out by exchange of plasmids, 44_fusion of whole organisms. Your mitochondria, for example . The tree of life thus becomes a tangly vines, or even a ring.	gene transfer, a infection, or even

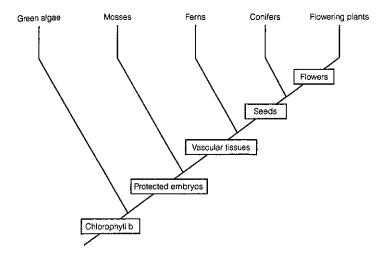
Exercise 8 (Module 15.15)

The system of taxonomic categories used by biologists is like a set of boxes into which organisms are sorted. A cocker spaniel—Canis familiaris—for example, is first placed in a small box, the specific name familiaris that separates it from all other species. This is placed in a slightly larger box, the genus Canis, which also holds Canis lupus (the wolf) and Canis latrans (the coyote). This genus box is placed in a larger box, along with other genera of doglike animals, and so on, all the way up to the last box that separates eukaryotes from prokaryotes. Imagine that the nested boxes below represent the taxonomic categories, starting with species (omitting subphylum). Label the boxes to show the relationships among the categories.



Exercise 9 (Module 15.16)

Cladistics, the most widely used method of systematics, seeks to clarify evolutionary and taxonomic relationships by grouping organisms into clades. A clade is a group of organisms made up of an ancestor and all its descendants. This simplified phylogenetic tree uses cladistics (based on anatomy, but backed up by molecular data) to reconstruct the relationships among four groups of plants and their closest relatives, the green algae. Read Module 15.16, examine the trees in the module and below, and then answer the following questions. This exercise is rather difficult, so take your time.

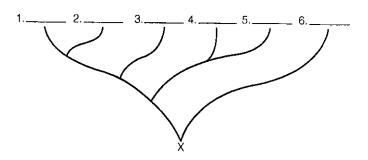


- 1. Which four groups of organisms above make up the in-group?
- 2. Which organisms constitute the out-group?
- 3. Which is more useful in cladistics, analogies or homologies?
- 4. Which characters are unique to a lineage of organisms, shared derived characters or shared ancestral characters? Which are more useful in differentiating among (separating out) distinct lineages?
- 5. What is a shared ancestral character common to all plants?
- 6. What is a shared derived character common to all plants?
- 7. What is a shared ancestral character common to all plants with seeds?
- 8. What is a shared derived character common to all plants with seeds?
- 9. Which characters are most useful in deciding whether an organism is in the out-group or the in-group, shared ancestral characters or shared derived characters?
- 10. If we are interested in focusing on all plants that have vascular tissues, which groups on the phylogenetic tree constitute the out-group? The in-group?
- 11. What is the name of a taxonomic group consisting of an ancestor and all its descendants?
- 12. What other organisms are in the clade that includes the first plants with seeds?
- 13. Name or describe nine different clades shown on the phylogenetic tree above.

Exercise 10 (Module 15.17)

Homologous structures—similar structures derived from the same structure in a common ancestor—tell us about phylogenetic relationships among organisms. But convergent evolution can make unrelated organisms look alike; their similarities may be analogous, not homologous. Fortunately, we can dig beneath surface similarities and compare biological molecules to measure relatedness between species. For example we can compare protein amino acid sequences, RNA base sequences, or DNA base sequences—even whole genomes. Imagine that you have sequenced mitochondrial DNA (mDNA) for six species of rodents, A through F. All the rodents are thought to have evolved from a common ancestor, X. The number of differences in mDNA sequence are compiled in the table below, which reads like a road map mileage chart. For example, there are four differences between A and C, and nine differences between A and D. Use the differences in sequence to place species A through F on the phylogenetic tree. (Hint: Don't get too mathematical; just "eyeball" overall numbers.)

Α						
В	10					
C	4	11				
D	9	5	10			
Ε	14	16	15	15		
F	10	2	10	6	16	
	Α	В	C	D	Ε	F



Test Your Knowledge

Multiple Choice

- 1. The science of naming and classifying organisms is called
 - a. biology.
 - b. polyploidy.
 - c. genetics.
 - d. taxonomy.
 - e. parsimony.
- 2. Large-scale changes in the history of life, such as mass extinctions, the development of walking legs from fins, and the appearance of new groups of organisms such as birds, are termed:
 - a. macroevolution.
 - b. adaptation.

- c. exaptation.
- d. microevolution.
- e. paedomorphosis.
- 3. Which of the following is thought to have been the first step in the origin of life?
 - a. cooperation among molecules
 - **b.** formation of protobionts
 - c. formation of organic monomers
 - d. replication of primitive "genes"
 - e. formation of organic polymers
- 4. Systematics is concerned with
 - a. naming organisms.
 - **b.** studying biological diversity.
 - c. taxonomy.
 - d. tracing phylogeny.
 - e. all of the above.