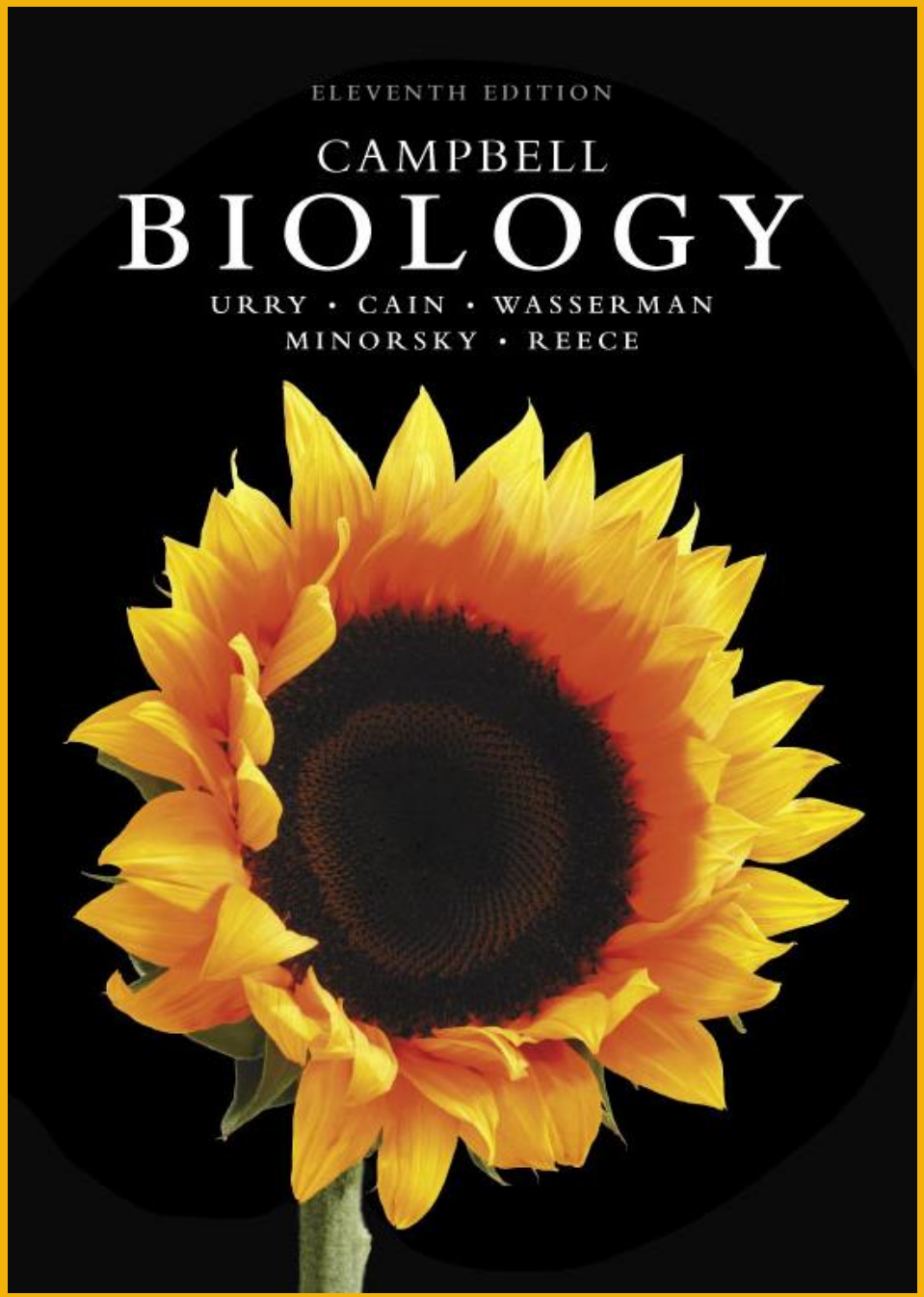


Chapter 26

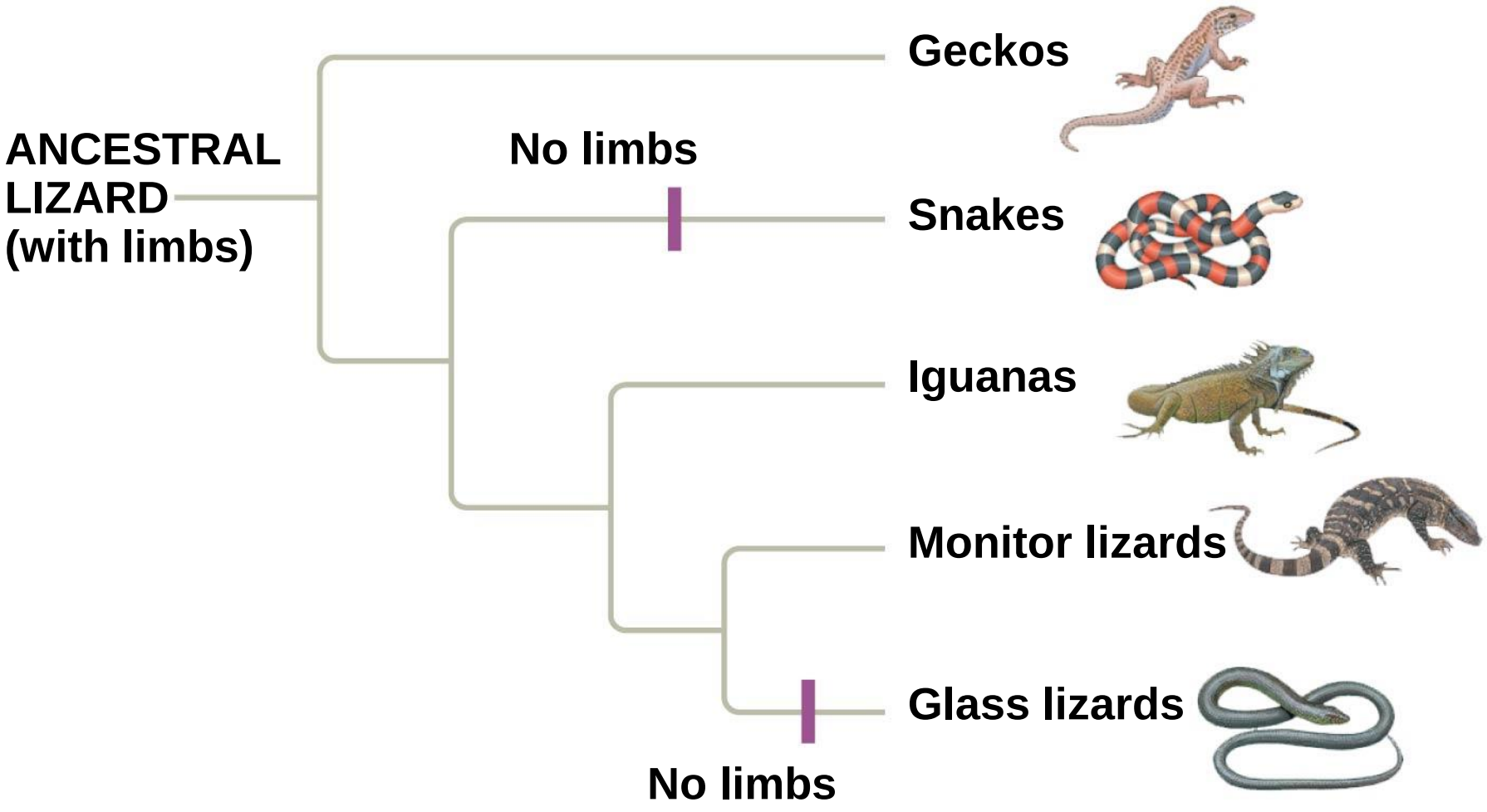
Phylogeny and the Tree of Life

Lecture Presentations by
Nicole Tunbridge and
Kathleen Fitzpatrick

Investigating the Tree of Life

- **Phylogeny** is the evolutionary history of a species or group of related species
  - For example, a phylogeny shows that legless lizards and snakes evolved from different lineages of legged lizards
- The discipline of **systematics** classifies organisms and determines their evolutionary relationships

Figure 26.2



Binomial Nomenclature

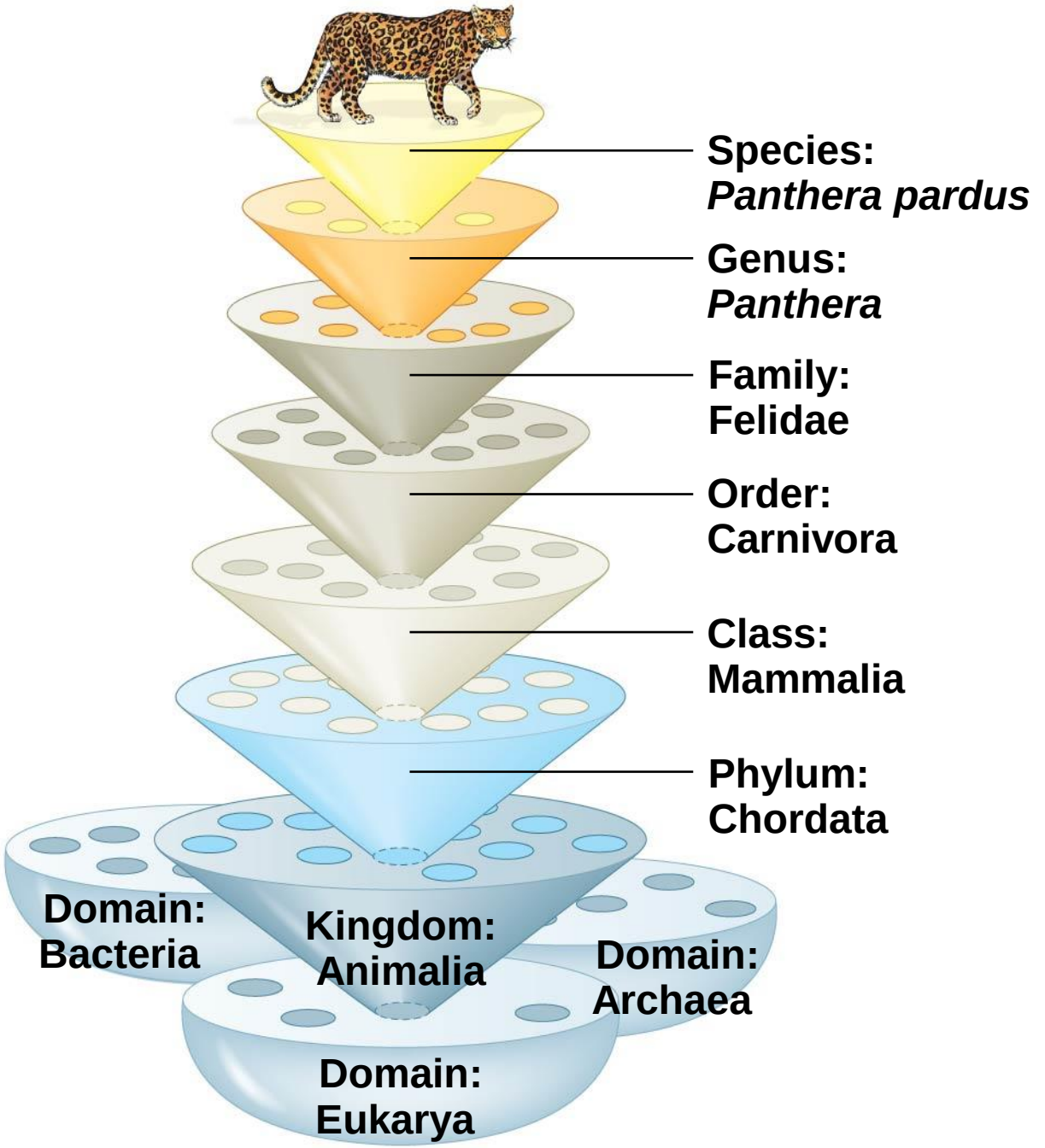
- In the 18th century, Carolus Linnaeus published a system of taxonomy based on resemblances
- Two key features of his system remain useful today: two-part names for species and hierarchical classification

- The two-part scientific name of a species is called a **binomial**
- The first part of the name is the **genus**
- The second part, called the specific epithet, is unique for each species within the genus
- The first letter of the genus is capitalized, and the entire species name is italicized
- Both parts together name the species (not the specific epithet alone)

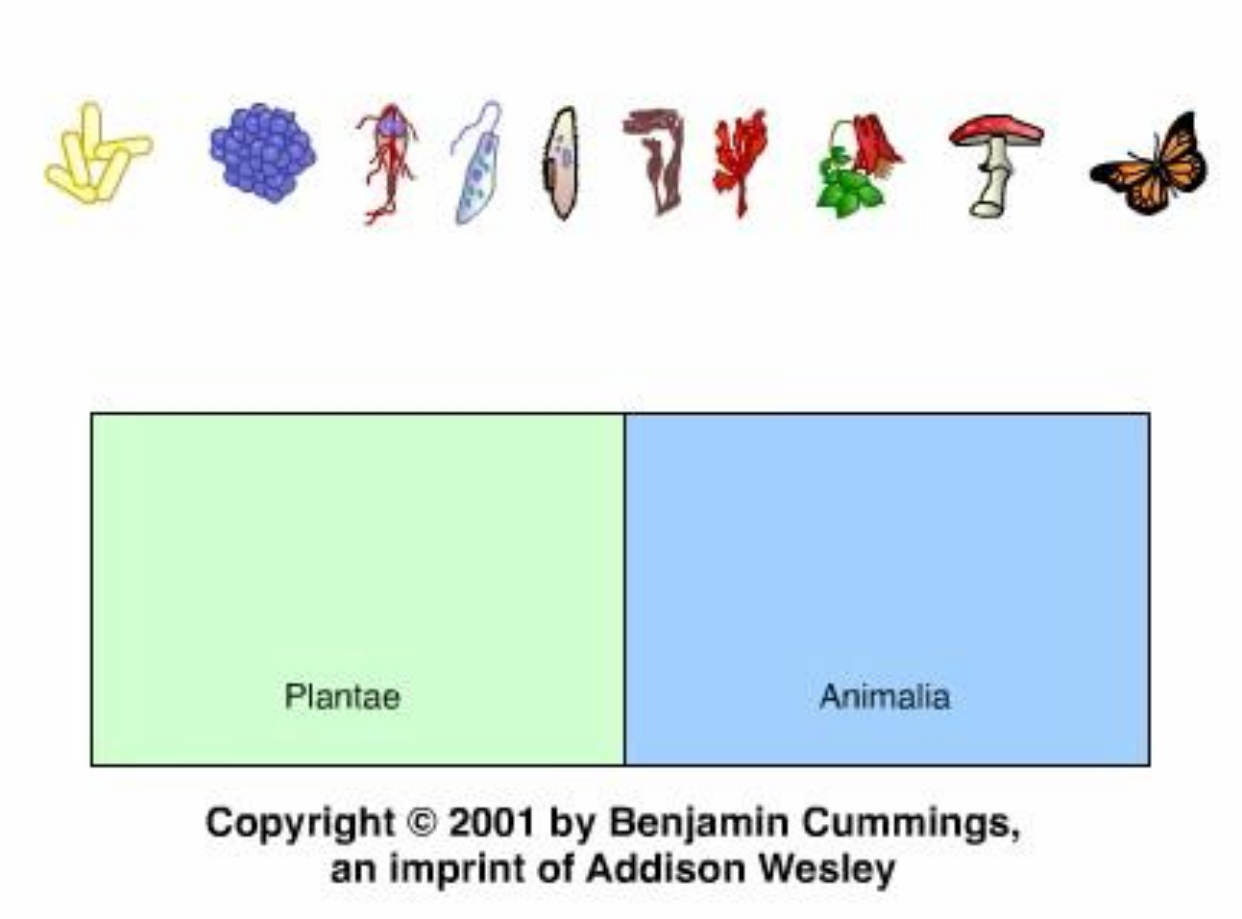
Hierarchical Classification

- Linnaeus introduced a system for grouping species in increasingly inclusive categories
- The taxonomic groups from broad to narrow are **domain**, **kingdom**, **phylum**, **class**, **order**, **family**, genus, and species
- A taxonomic unit at any level of hierarchy is called a **taxon**
- The broader taxa are not comparable between lineages
  - For example, an order of snails has less genetic diversity than an order of mammals

Figure 26.3



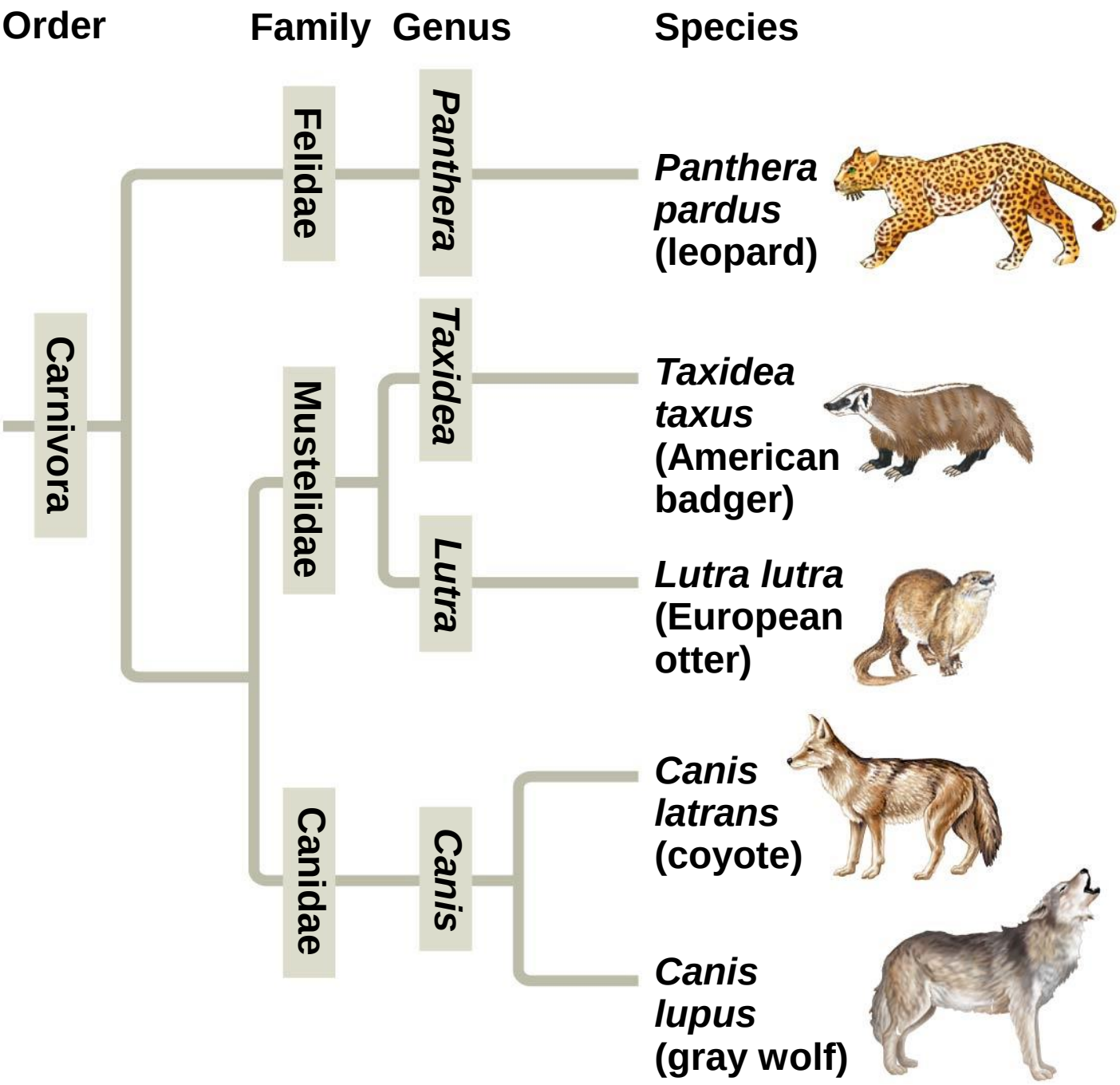
Animation: Classification Schemes



Linking Classification and Phylogeny

- The evolutionary history of a group of organisms can be represented in a branching **phylogenetic tree**

Figure 26.4

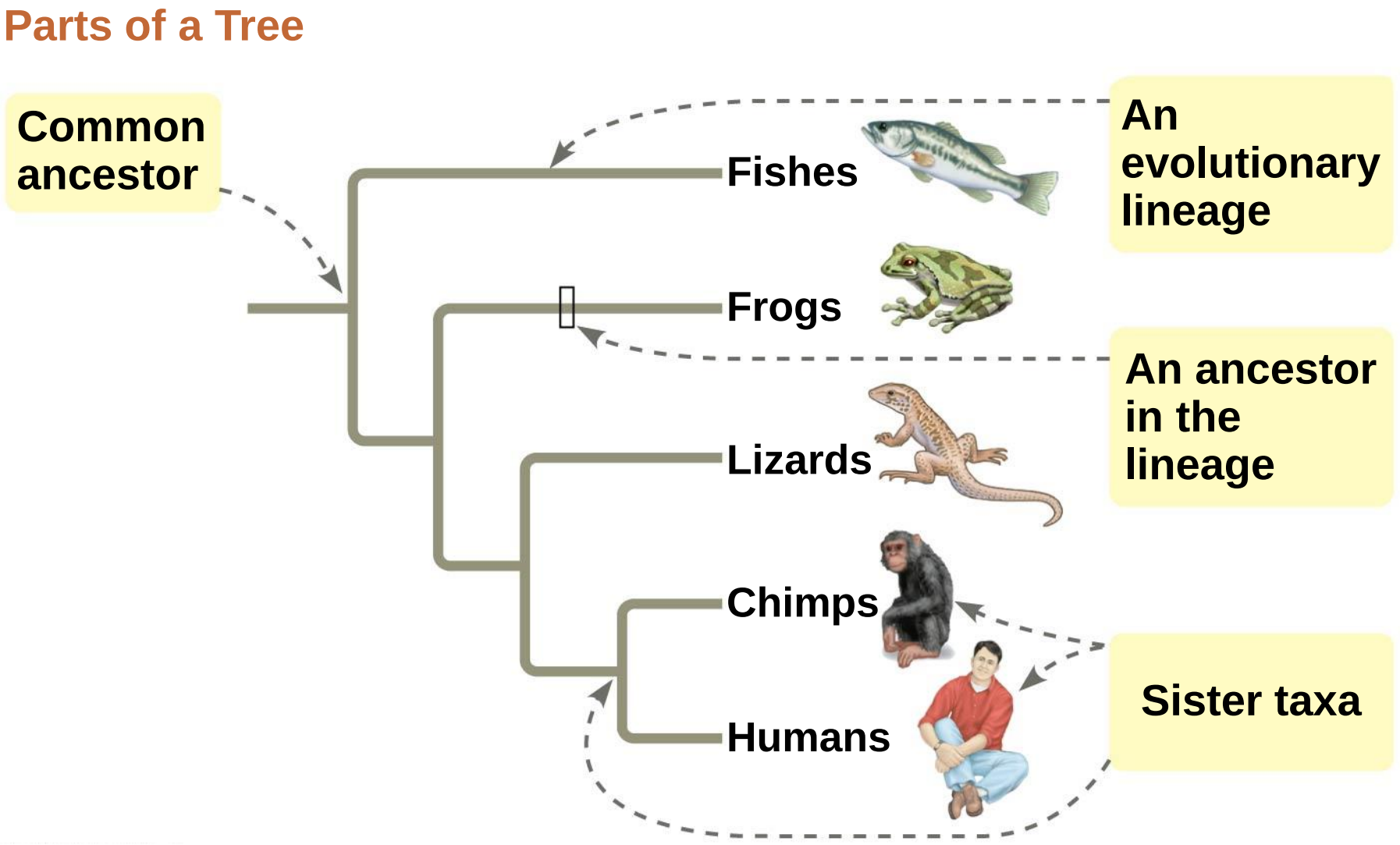


- Linnaean classification and phylogeny can differ from each other
- Systematists have proposed a classification system that would recognize only groups that include a common ancestor and all its descendants

What We Can and Cannot Learn from Phylogenetic Trees

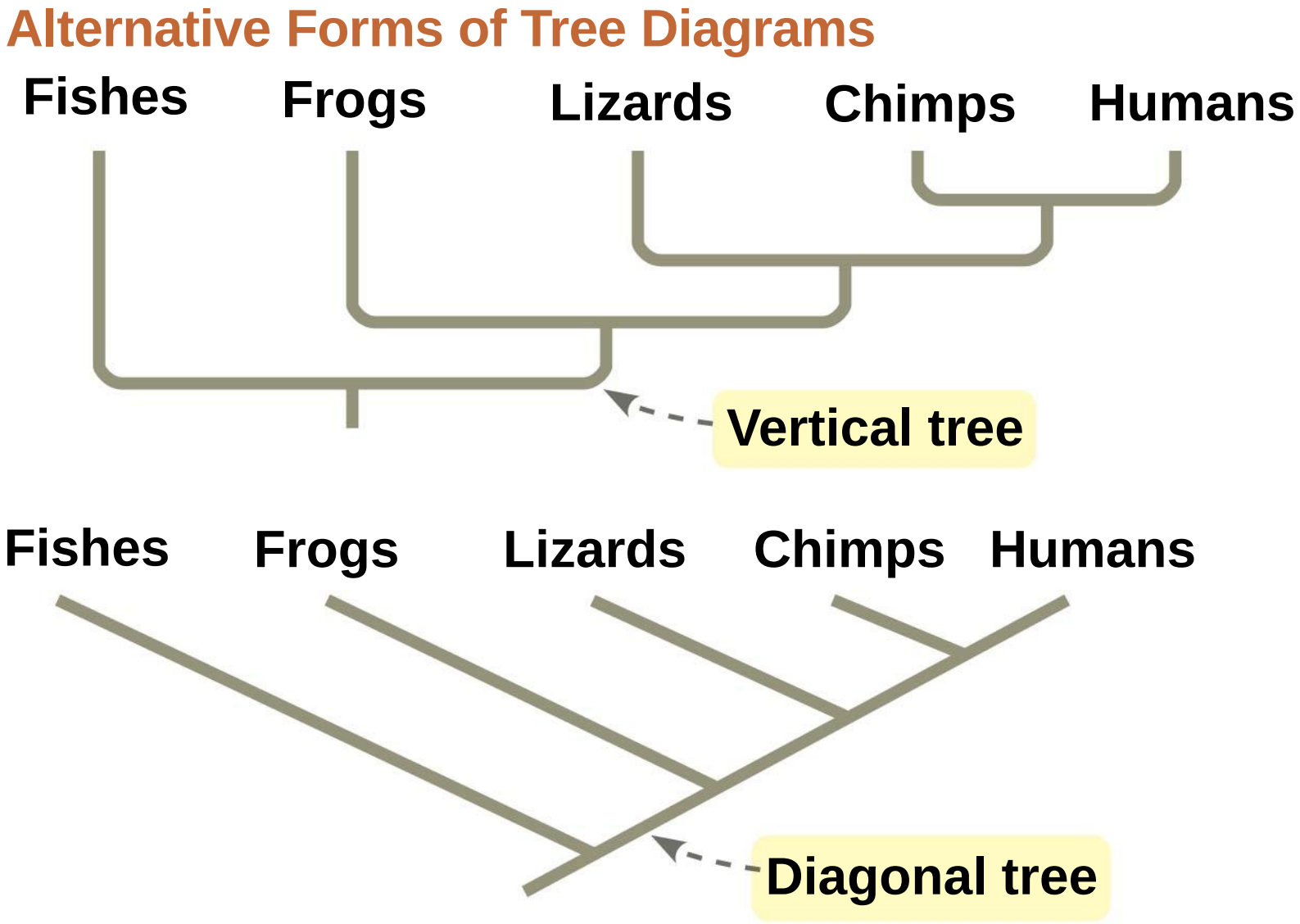
- A phylogenetic tree represents a hypothesis about evolutionary relationships
- Each **branch point** represents the divergence of two evolutionary lineages from a common ancestor
- **Sister taxa** are groups that share an immediate common ancestor that is not shared by any other group

Figure 26.5a



- Phylogenetic trees can be drawn horizontally, vertically, or diagonally without changing the relationships between groups

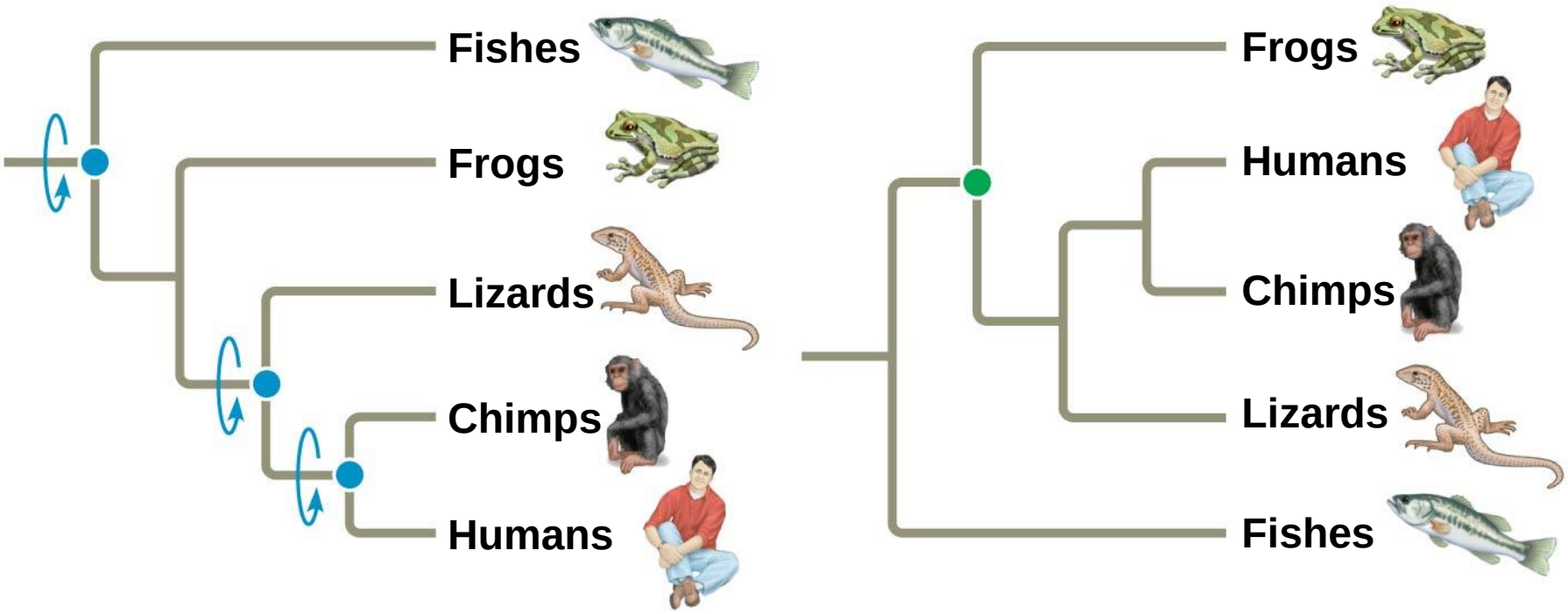
Figure 26.5b



- Tree branches can be rotated around a branch point without changing the evolutionary relationships

Figure 26.5c

Rotating Around Branch Points



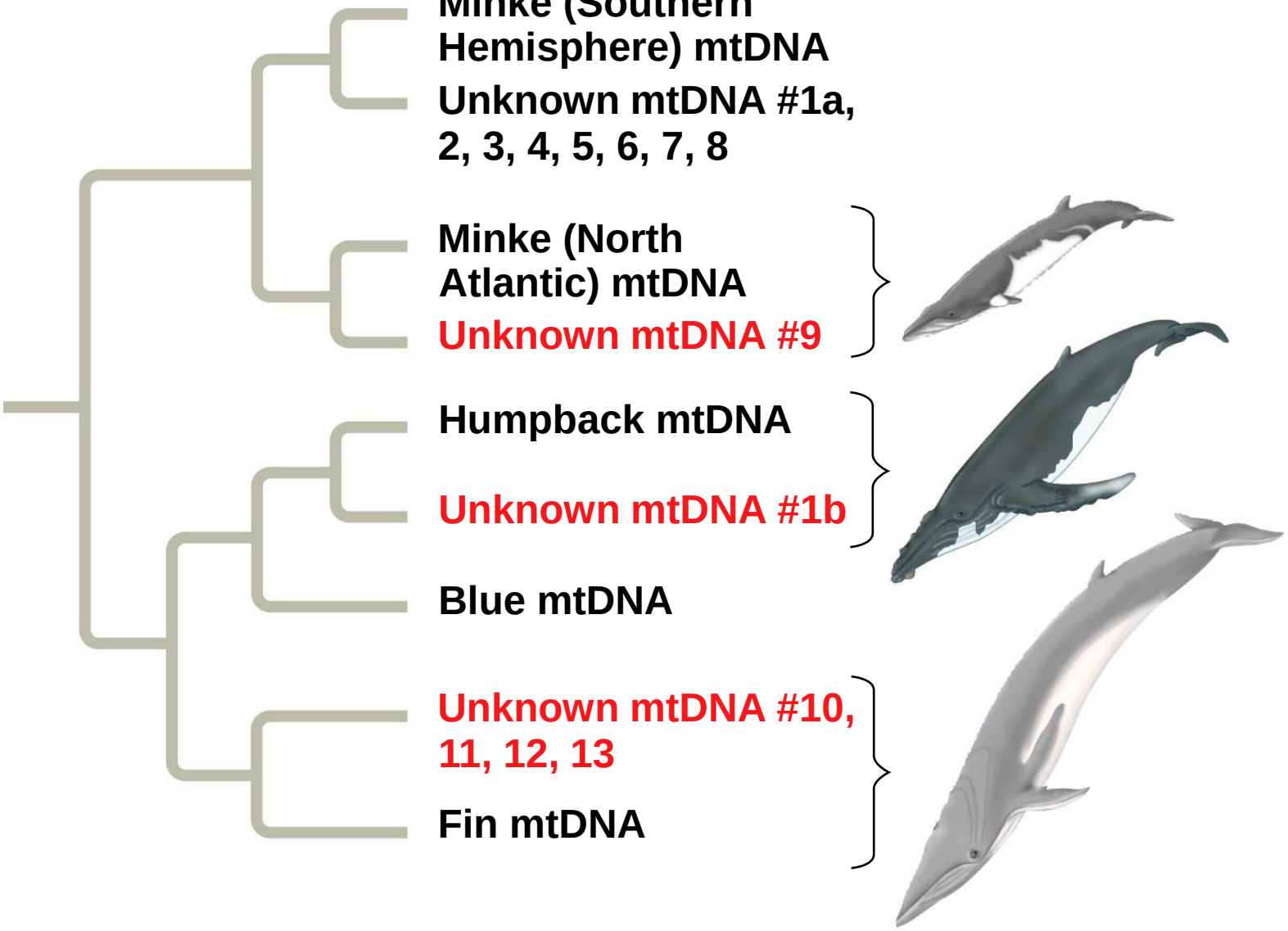
- A **rooted** tree includes a branch to represent the most recent common ancestor of all taxa in the tree
- A **basal taxon** diverges early in the history of a group and originates near the common ancestor of the group

- Phylogenetic trees show patterns of descent, not phenotypic similarity
- Phylogenetic trees do not indicate when species evolved or how much change occurred in a lineage
- It should not be assumed that a taxon evolved from the taxon next to it

Applying Phylogenies

- Phylogeny provides important information about similar characteristics in closely related species
- A phylogeny was used to identify the species of whale from which “whale meat” originated to discover if the whale was harvested illegally

Figure 26.6 **Results**



Data from C. S. Baker and S. R. Palumbi, Which whales are hunted? A molecular genetic approach to monitoring whaling, *Science* 265:1538–1539 (1994). Reprinted with permission from AAAS.

Concept 26.2: Phylogenies are inferred from morphological and molecular data

- To infer phylogenies, systematists gather information about the morphologies, genes, and biochemistry of living organisms

Morphological and Molecular Homologies

- Phenotypic and genetic similarities due to shared ancestry are called **homologies**
- Organisms with similar morphologies or DNA sequences are likely to be more closely related than organisms with different structures or sequences

Sorting Homology from Analogy

- When constructing a phylogeny, systematists need to distinguish whether a similarity is the result of homology or **analogy**
- Homology is similarity due to shared ancestry
- Analogy is similarity due to convergent evolution

- Convergent evolution occurs when similar environmental pressures and natural selection produce similar (analogous) adaptations in organisms from different evolutionary lineages

Figure 26.7

Australian “mole”

African golden mole

- Homology can be distinguished from analogy by comparing fossil evidence and the degree of complexity
- The more elements that are similar in two complex structures, the more likely it is that they are homologous
- If the genes in two organisms share many portions of nucleotide sequence, it is likely they are homologous

Evaluating Molecular Homologies

- Systematists use computer programs and mathematical tools when analyzing comparable DNA segments from different organisms

Figure 26.8_1

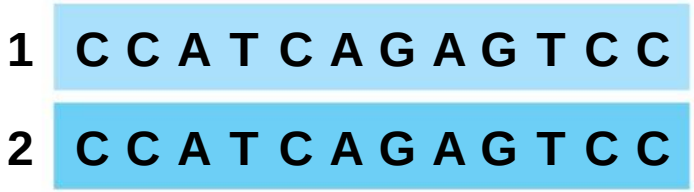


Figure 26.8_2

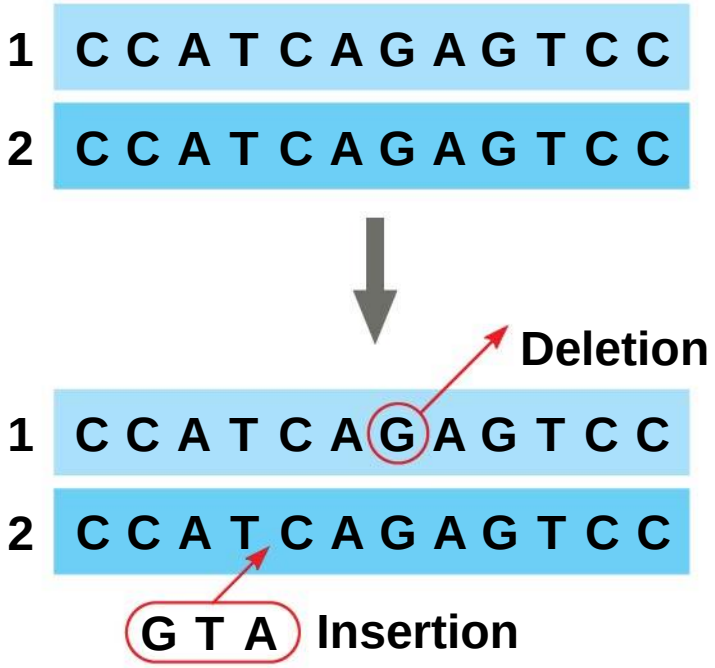


Figure 26.8_3

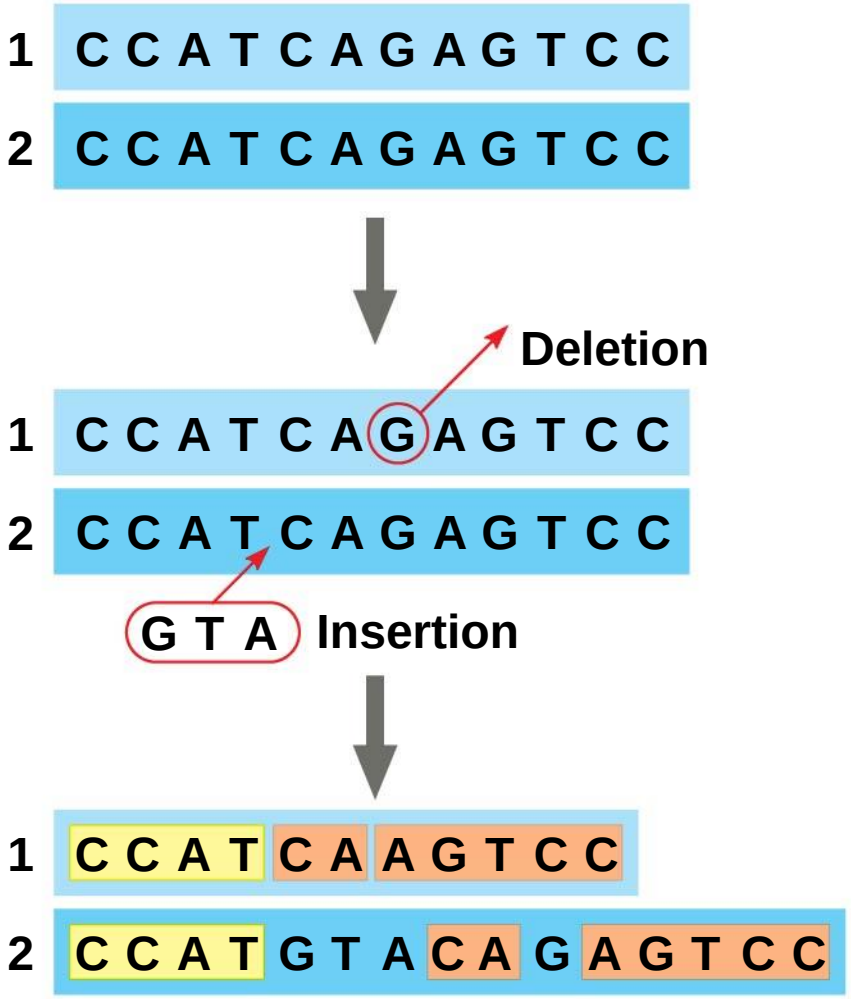


Figure 26.8_4