

LECTURE PRESENTATIONS

For CAMPBELL BIOLOGY, NINTH EDITION

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Chapter 26

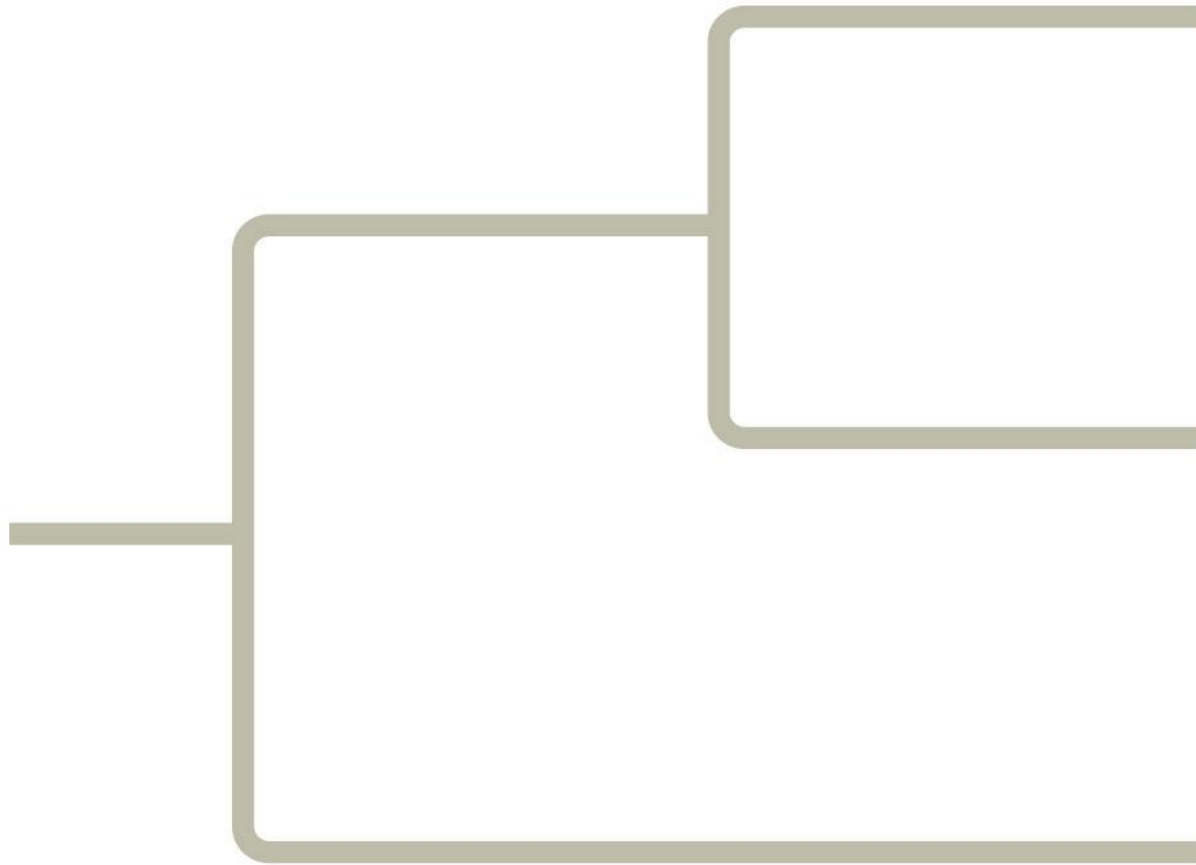
Phylogeny and the Tree of Life



Lectures by
Erin Barley
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- **Phylogeny** is the evolutionary history of a species or group of related species
- The discipline of **systematics** classifies organisms and determines their evolutionary relationships
- Systematists use fossil, molecular, and genetic data to infer evolutionary relationships

Figure 26.2



Concept 26.1: Phylogenies show evolutionary relationships

- **Taxonomy** is the ordered division and naming of organisms

Binomial Nomenclature

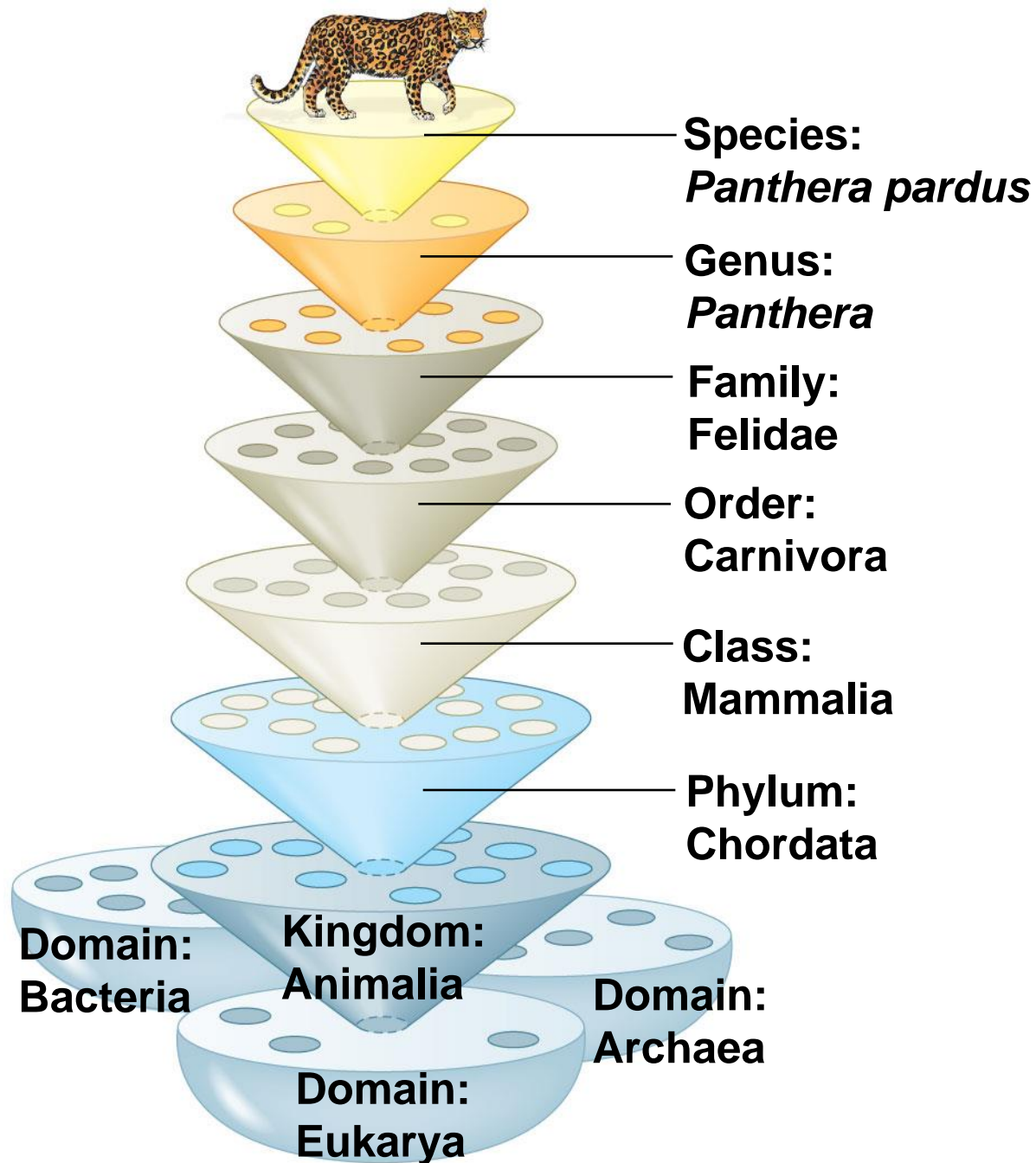
- In the 18th century, Carolus Linnaeus published a system of taxonomy based on resemblances
- Two key features of his system remain useful today: two-part names for species and hierarchical classification

- 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 broad 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



Linking Classification and Phylogeny

- Systematists depict evolutionary relationships in branching **phylogenetic trees**

Figure 26.4

Order

Family Genus

Species

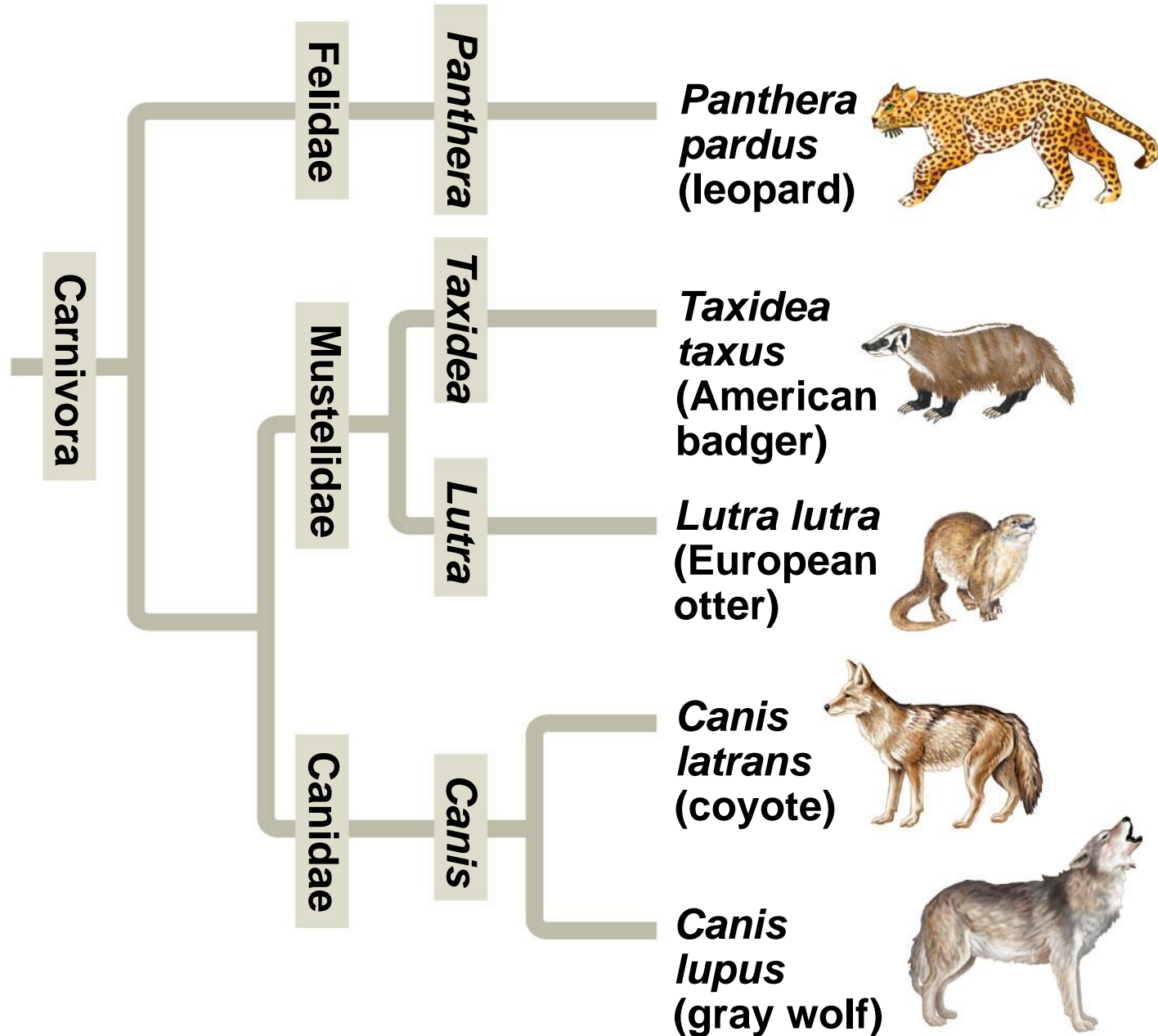
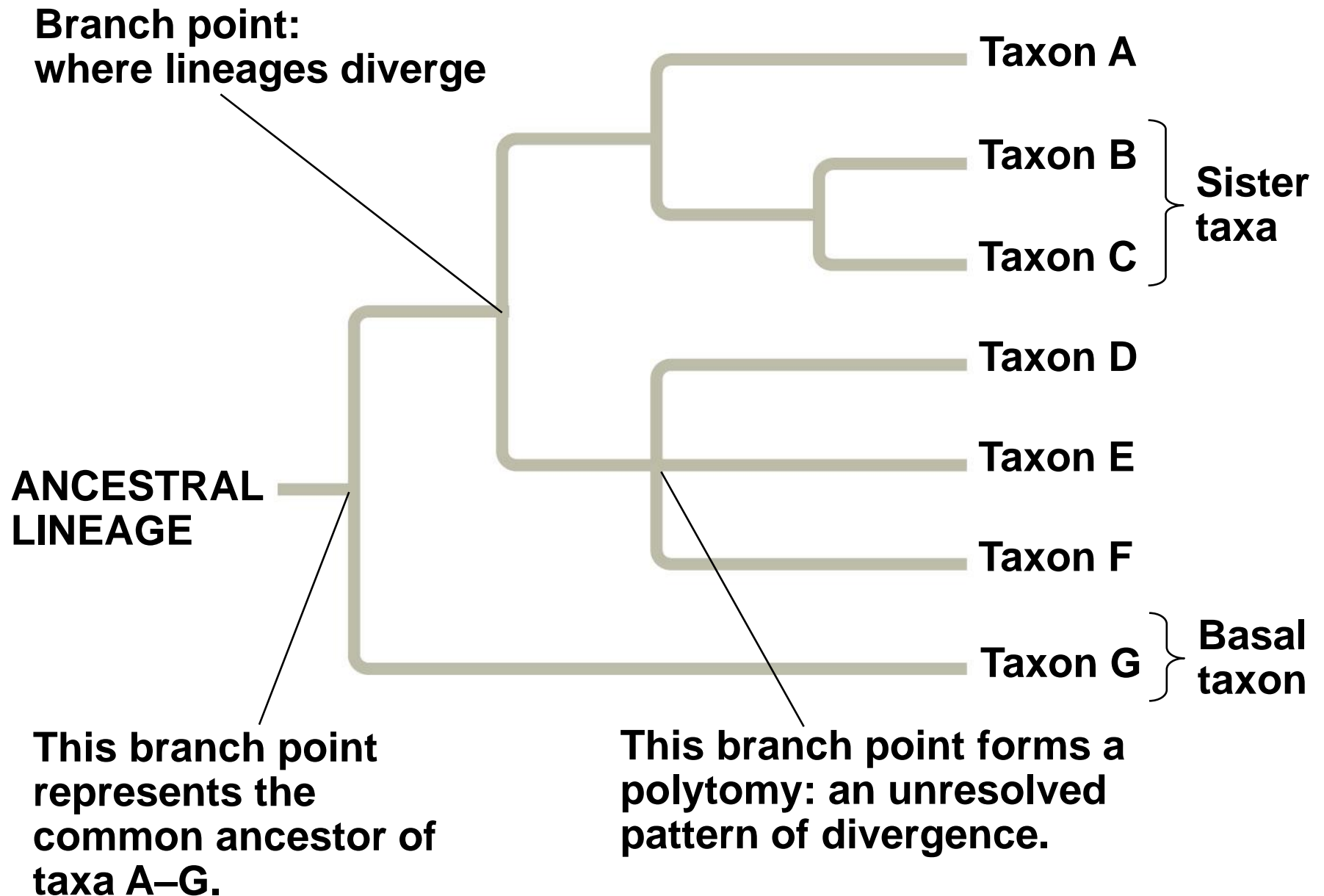


Figure 26.5



What We Can and Cannot Learn from Phylogenetic Trees

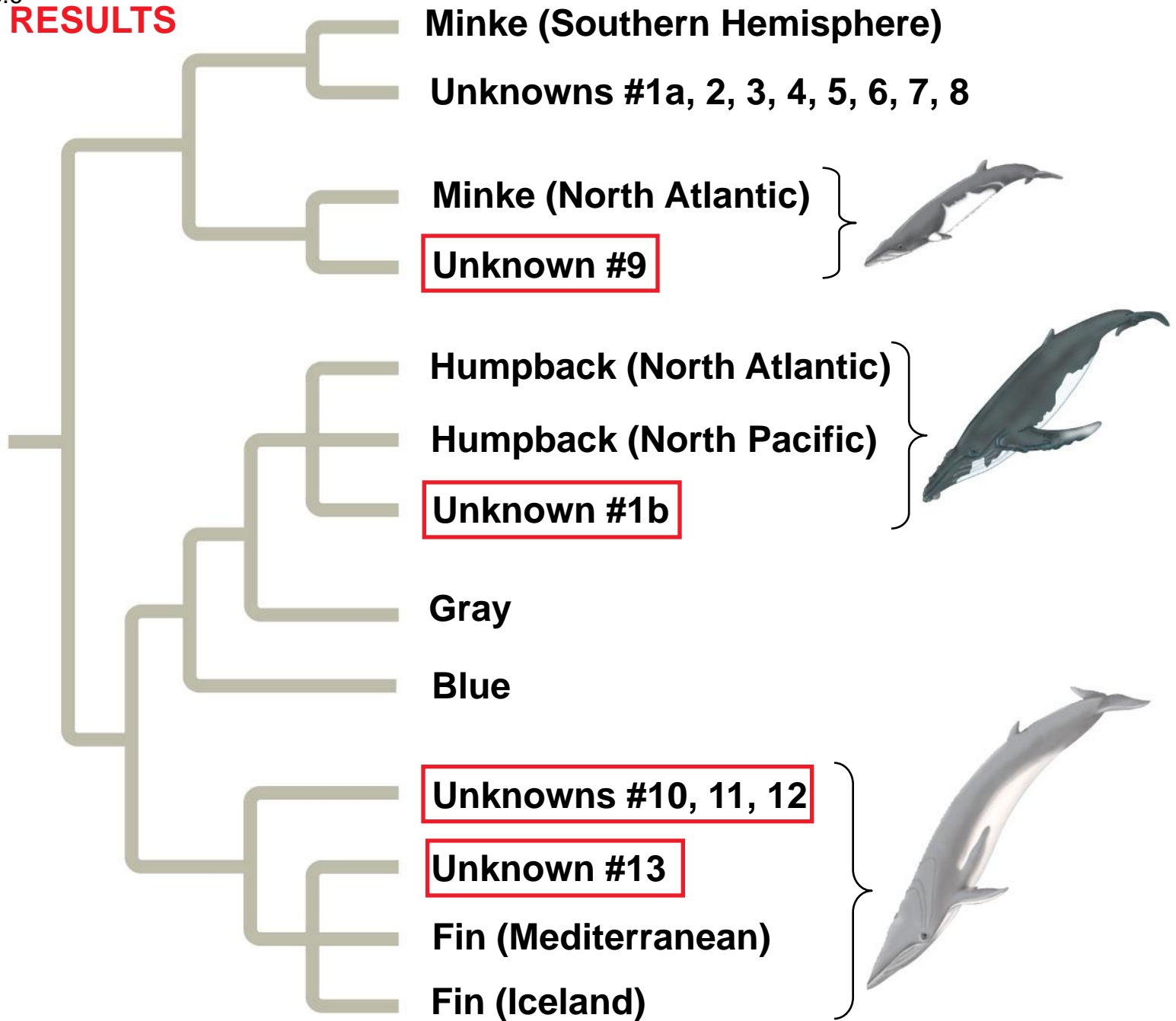
- Phylogenetic trees show patterns of descent, not phenotypic similarity
- Phylogenetic trees do not indicate when species evolved or how much change occurred in a lineage
- It should not be assumed that a taxon evolved from the taxon next to it

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

Figure 26.6

RESULTS



Concept 26.3: Shared characters are used to construct phylogenetic trees

- Once homologous characters have been identified, they can be used to infer a phylogeny

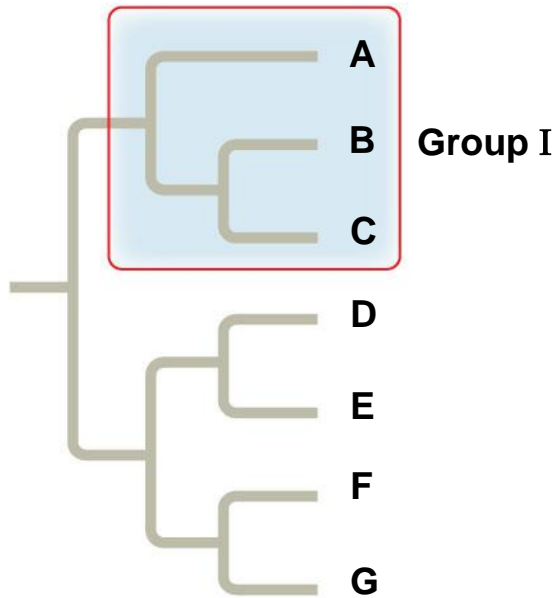
Cladistics

- **Cladistics** groups organisms by common descent
- A **clade** is a group of species that includes an ancestral species and all its descendants
- Clades can be nested in larger clades, but not all groupings of organisms qualify as clades

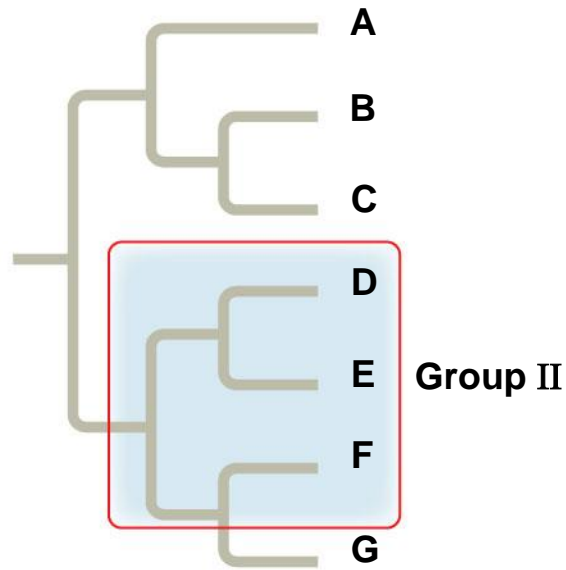
- A valid clade is **monophyletic**, signifying that it consists of the ancestor species and all its descendants

Figure 26.10

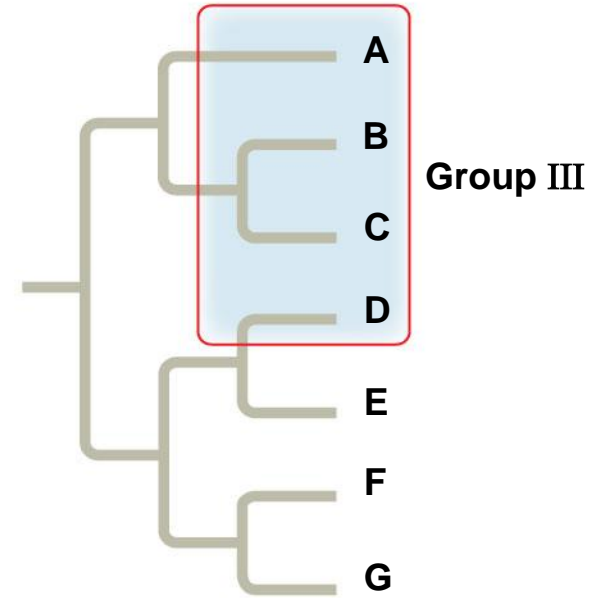
(a) Monophyletic group (clade)



(b) Paraphyletic group



(c) Polyphyletic group



- A **paraphyletic** grouping consists of an ancestral species and some, but not all, of the descendants

- A **polyphyletic** grouping consists of various species with different ancestors

Shared Ancestral and Shared Derived Characters

- In comparison with its ancestor, an organism has both shared and different characteristics

- A **shared ancestral character** is a character that originated in an ancestor of the taxon
- A **shared derived character** is an evolutionary novelty unique to a particular clade
- A character can be both ancestral and derived, depending on the context

Inferring Phylogenies Using Derived Characters

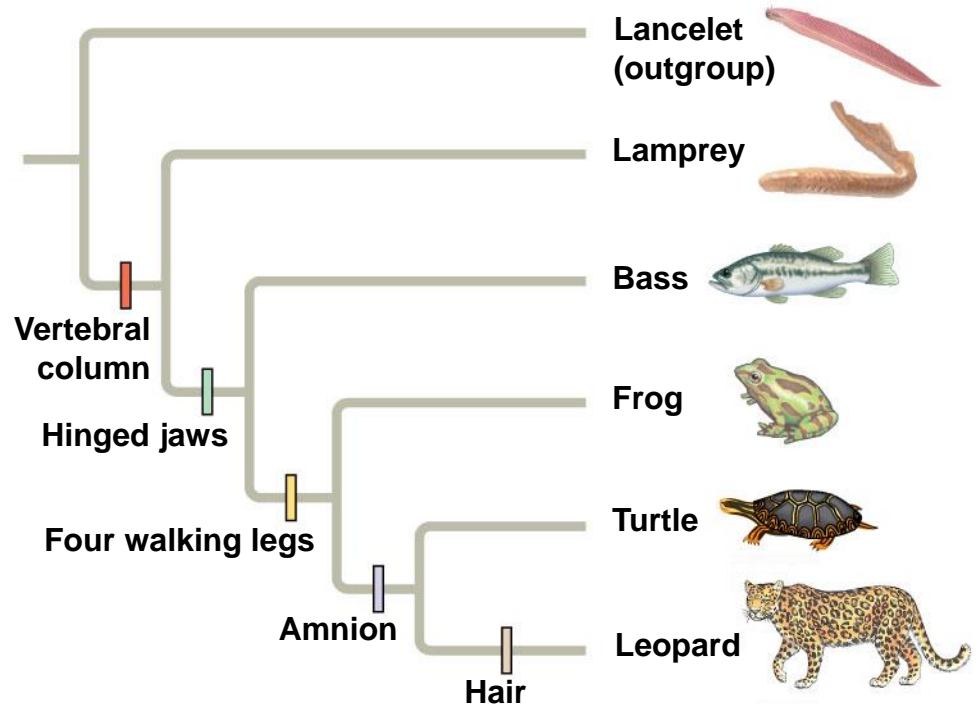
- When inferring evolutionary relationships, it is useful to know in which clade a shared derived character first appeared

Figure 26.11

CHARACTERS	TAXA					
	Lancelet (outgroup)	Lamprey	Bass	Frog	Turtle	Leopard
Vertebral column (backbone)	0	1	1	1	1	1
Hinged jaws	0	0	1	1	1	1
Four walking legs	0	0	0	1	1	1
Amnion	0	0	0	0	1	1
Hair	0	0	0	0	0	1

(a) Character table

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(b) Phylogenetic tree

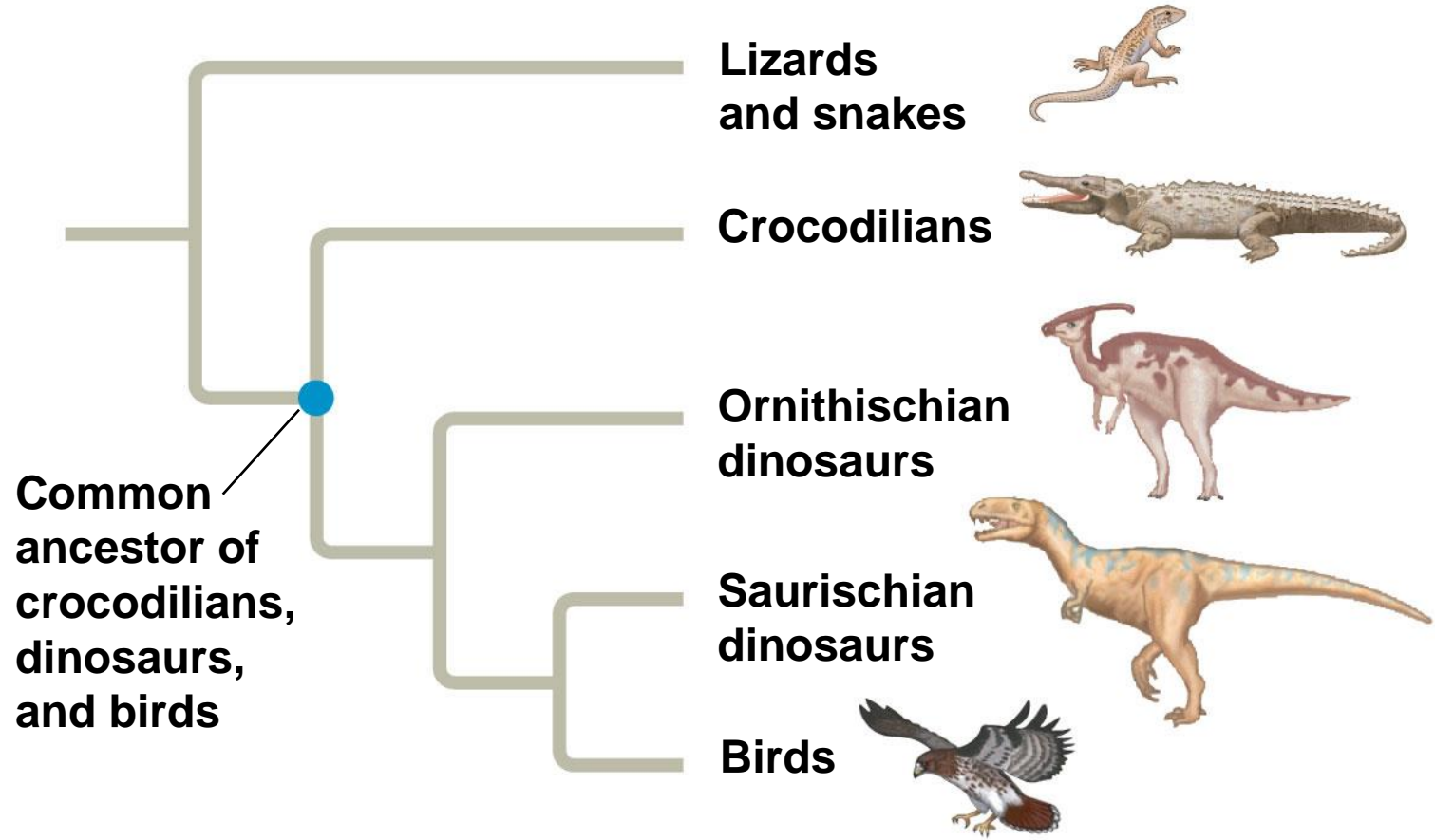
- An **outgroup** is a species or group of species that is closely related to the **ingroup**, the various species being studied
- The outgroup is a group that has diverged before the ingroup
- Systematists compare each ingroup species with the outgroup to differentiate between shared derived and shared ancestral characteristics

- Characters shared by the outgroup and ingroup are ancestral characters that predate the divergence of both groups from a common ancestor

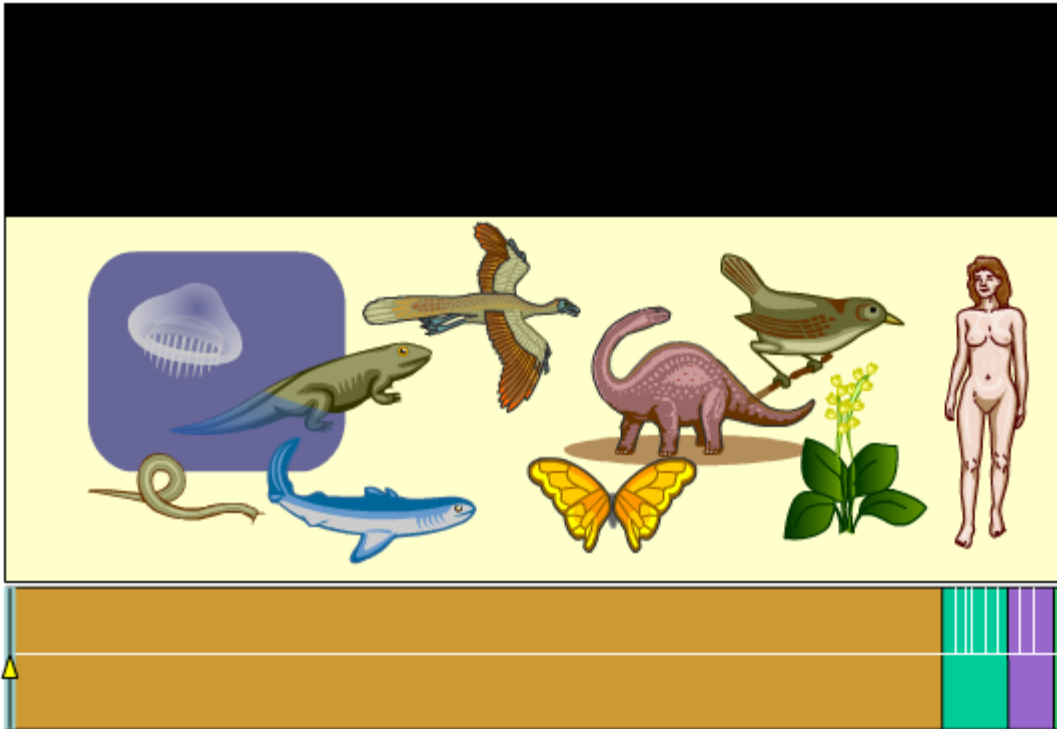
Phylogenetic Trees as Hypotheses

- The best hypotheses for phylogenetic trees fit the most data: morphological, molecular, and fossil
- Phylogenetic bracketing allows us to predict features of an ancestor from features of its descendants
 - For example, phylogenetic bracketing allows us to infer characteristics of dinosaurs

Figure 26.16

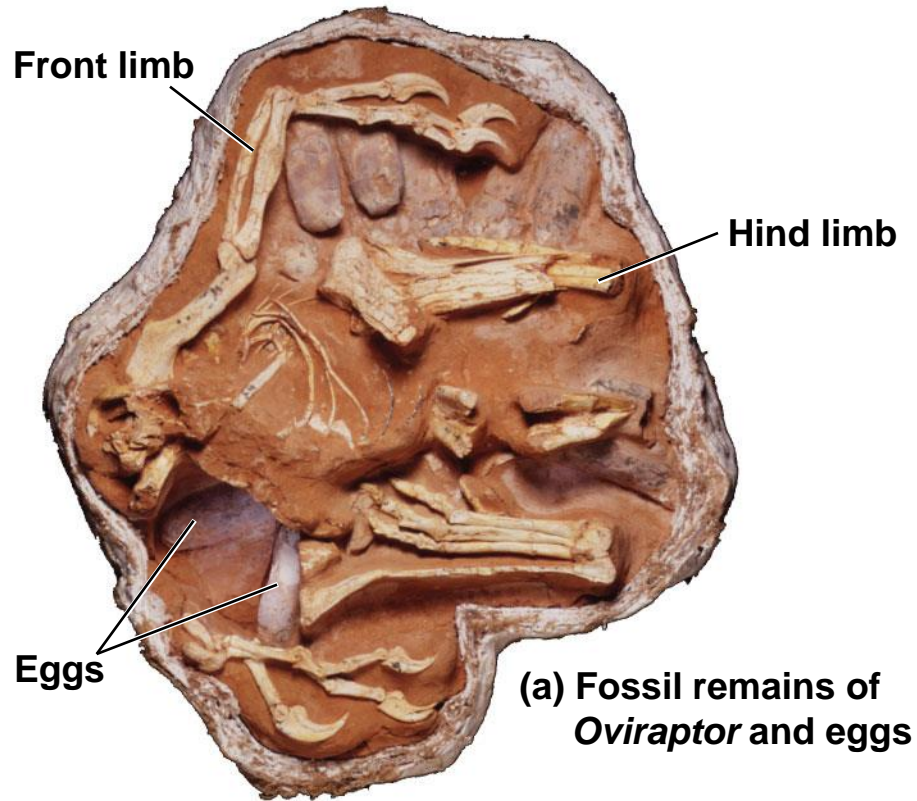


- Birds and crocodiles share several features: four-chambered hearts, song, nest building, and brooding
- These characteristics likely evolved in a common ancestor and were shared by all of its descendants, including dinosaurs
- The fossil record supports nest building and brooding in dinosaurs



Geologic record

Animation: The Geologic Record
Right-click slide / select "Play"



Concept 26.5: Molecular clocks help track evolutionary time

- To extend molecular phylogenies beyond the fossil record, we must make an assumption about how change occurs over time

Molecular Clocks

- A **molecular clock** uses constant rates of evolution in some genes to estimate the absolute time of evolutionary change
- In orthologous genes, nucleotide substitutions are proportional to the time since they last shared a common ancestor
- In paralogous genes, nucleotide substitutions are proportional to the time since the genes became duplicated

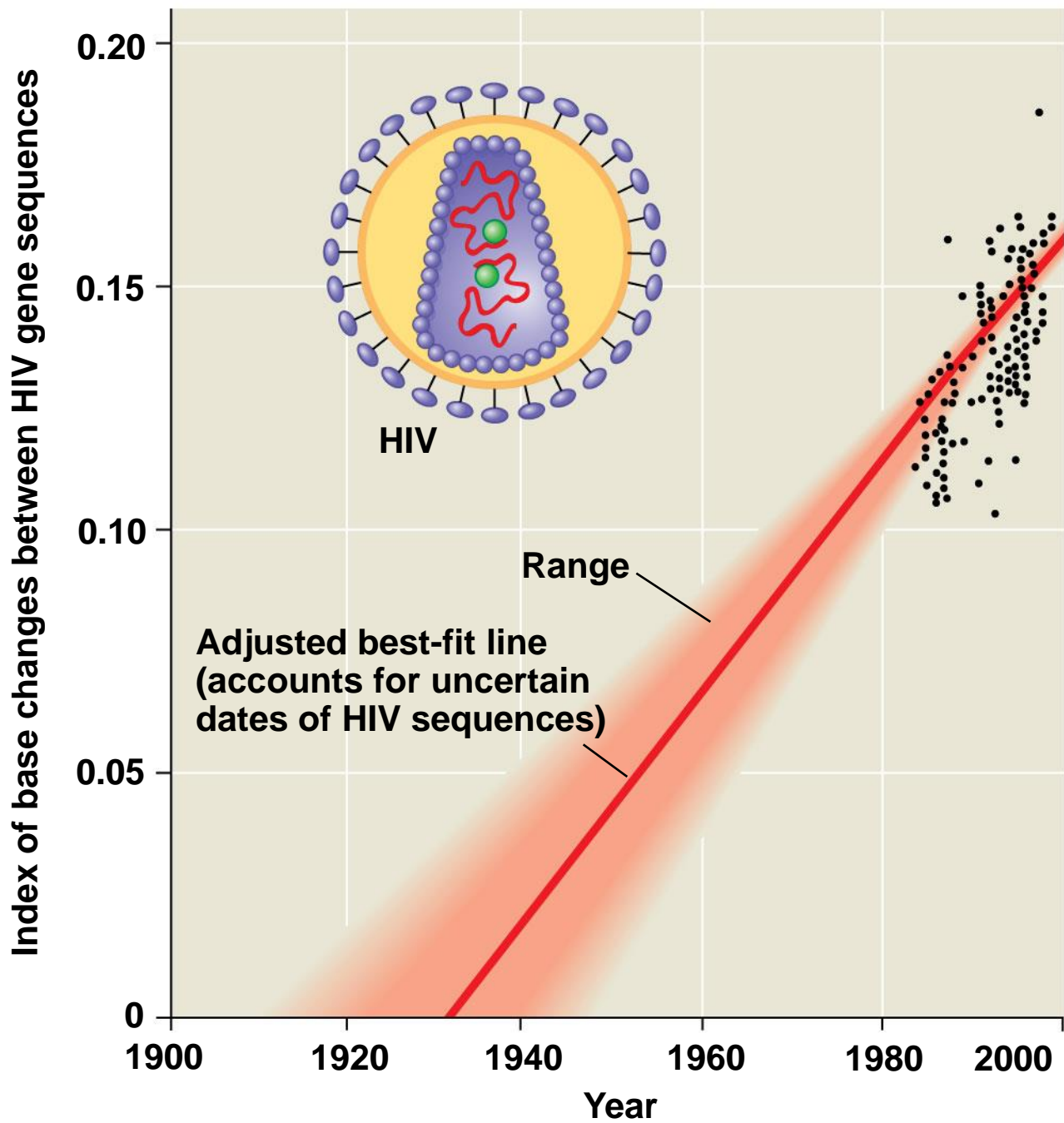
Problems with Molecular Clocks

- The molecular clock does not run as smoothly as neutral theory predicts
- Irregularities result from natural selection in which some DNA changes are favored over others
- Estimates of evolutionary divergences older than the fossil record have a high degree of uncertainty
- The use of multiple genes may improve estimates

Applying a Molecular Clock: The Origin of HIV

- Phylogenetic analysis shows that HIV is descended from viruses that infect chimpanzees and other primates
- HIV spread to humans more than once
- Comparison of HIV samples shows that the virus evolved in a very clocklike way
- Application of a molecular clock to one strain of HIV suggests that that strain spread to humans during the 1930s

Figure 26.20

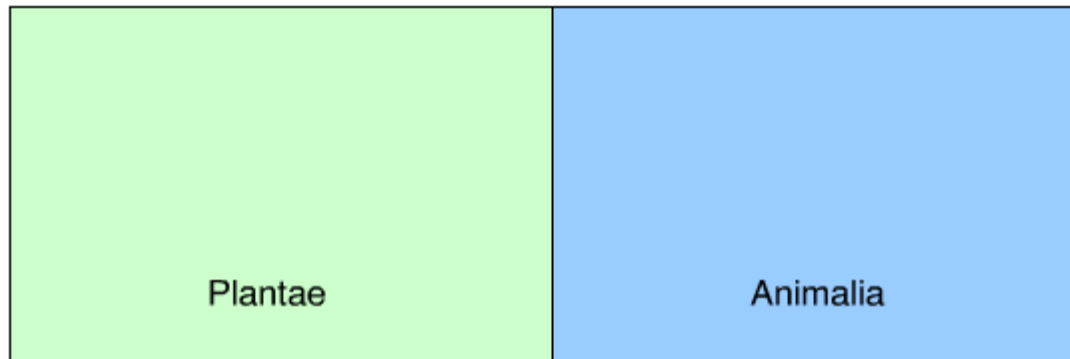


Concept 26.6: New information continues to revise our understanding of the tree of life

- Recently, we have gained insight into the very deepest branches of the tree of life through molecular systematics

From Two Kingdoms to Three Domains

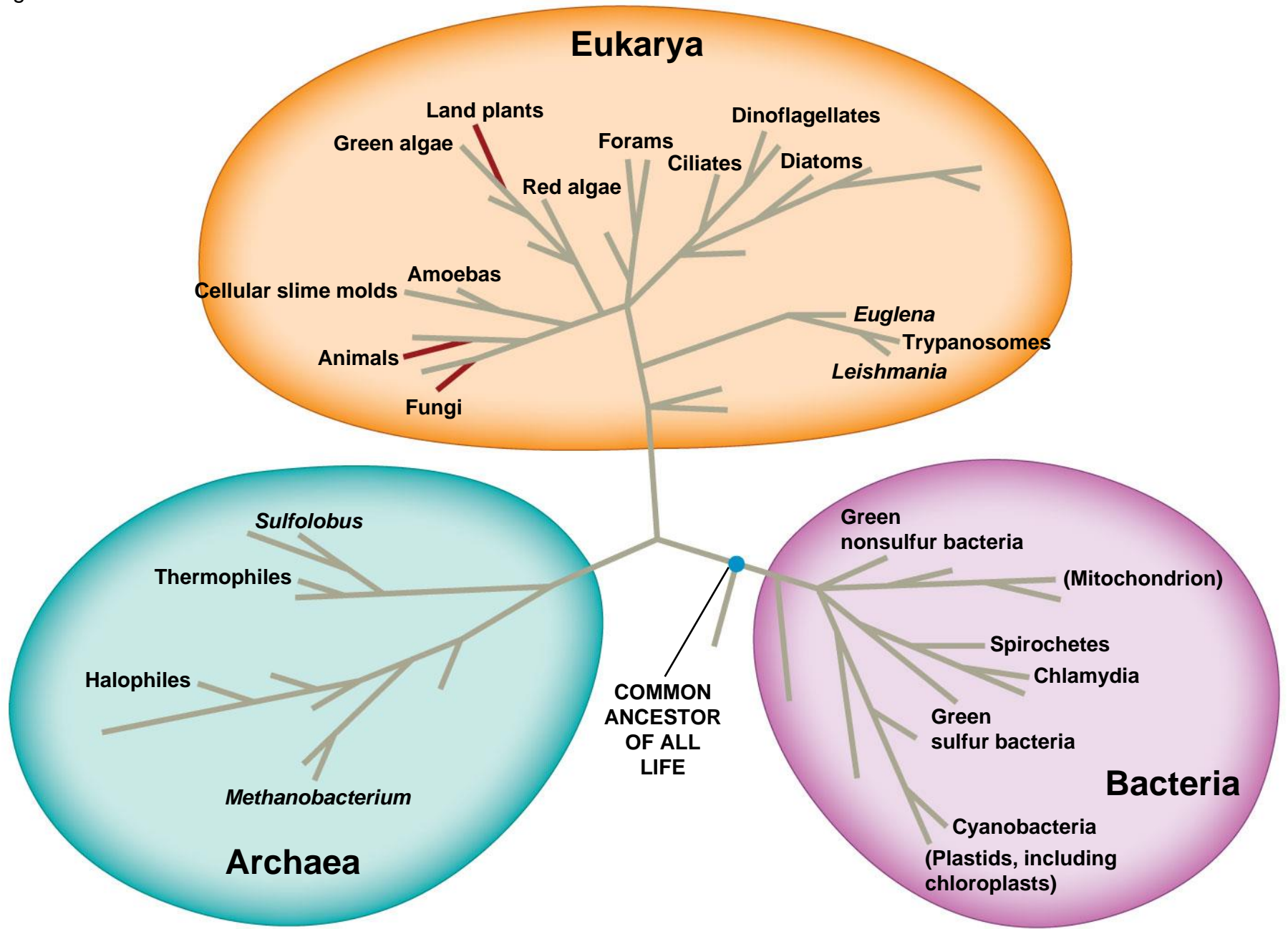
- Early taxonomists classified all species as either plants or animals
- Later, five kingdoms were recognized: Monera (prokaryotes), Protista, Plantae, Fungi, and Animalia
- More recently, the three-domain system has been adopted: Bacteria, Archaea, and Eukarya
- The three-domain system is supported by data from many sequenced Classification Schemes genomes



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Animation: Classification Schemes
Right-click slide / select "Play"

Figure 26.21

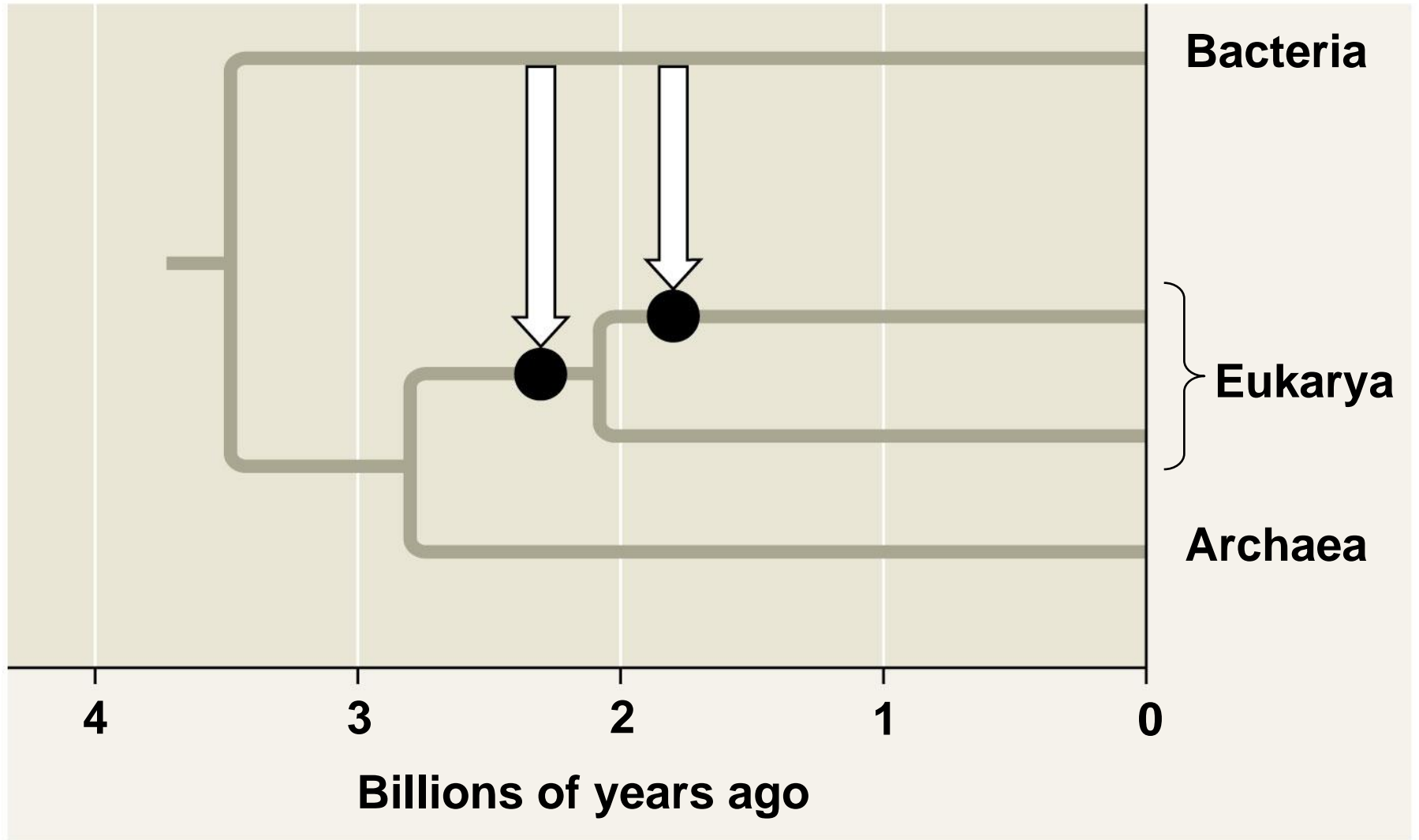


A Simple Tree of All Life

- The tree of life suggests that eukaryotes and archaea are more closely related to each other than to bacteria
- The tree of life is based largely on rRNA genes, as these have evolved slowly

- There have been substantial interchanges of genes between organisms in different domains
- **Horizontal gene transfer** is the movement of genes from one genome to another
- Horizontal gene transfer occurs by exchange of transposable elements and plasmids, viral infection, and fusion of organisms
- Horizontal gene transfer complicates efforts to build a tree of life

Figure 26.22



Is the Tree of Life Really a Ring?

- Some researchers suggest that eukaryotes arose as a fusion between a bacterium and archaean
- If so, early evolutionary relationships might be better depicted by a ring of life instead of a tree of life

Figure 26.23

