

LSU BIOL 1202

General Biology II Lecture



CHAPTER 26

Phylogeny and the Tree of Life

Dr. Adam Hrinkevich

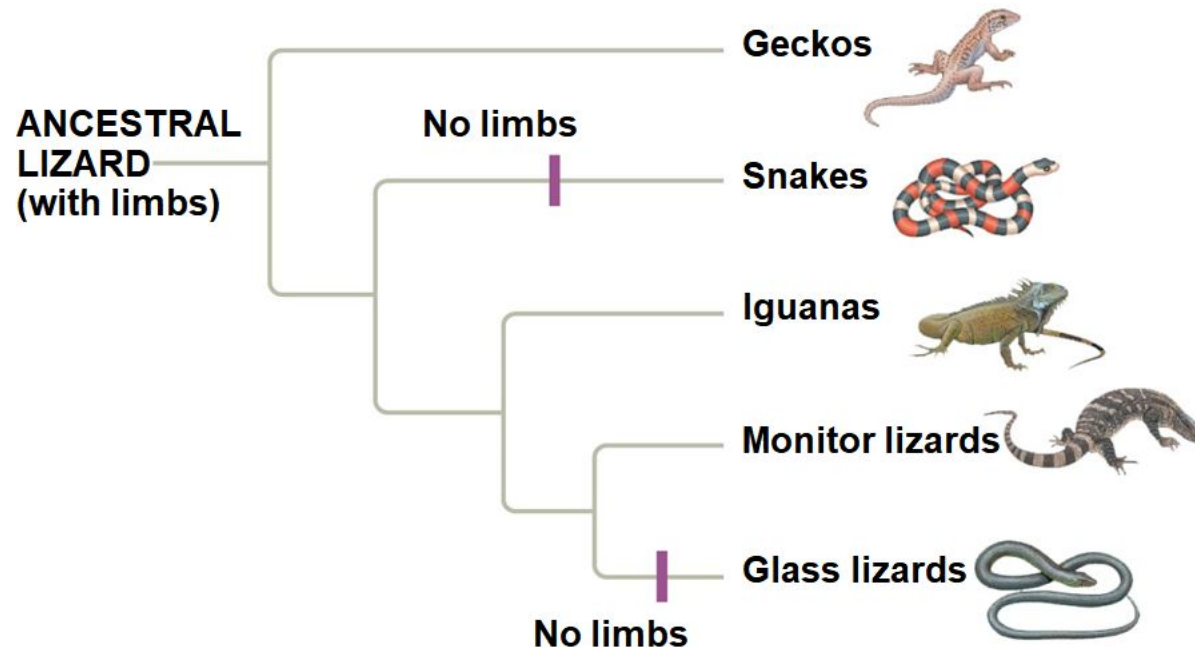
CH 26 Learning Objectives

1. Define phylogeny and explain how phylogenies are used.
2. Explain how phylogenetic trees are inferred from data.
3. Differentiate between derived and ancestral characters and explain how they are used to construct phylogenetic trees.
4. Describe what evidence a genome provides about evolutionary history.
5. Explain what molecular clocks are and how they are used.
6. Describe the possible structure of the tree of all life.
- 7. Complete in-class cladogram construction example.**
- 8. Complete practice exercises posted to MOODLE**

I would suggest completing the crossword puzzle to help you understand the terminology and correlate how the terms relate to topics covered in this chapter.

Investigating the Tree of Life

- **Phylogeny** is the evolutionary history of a species or group of related species
 - EX: 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



Concept 26.1: Phylogenies show evolutionary relationships

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

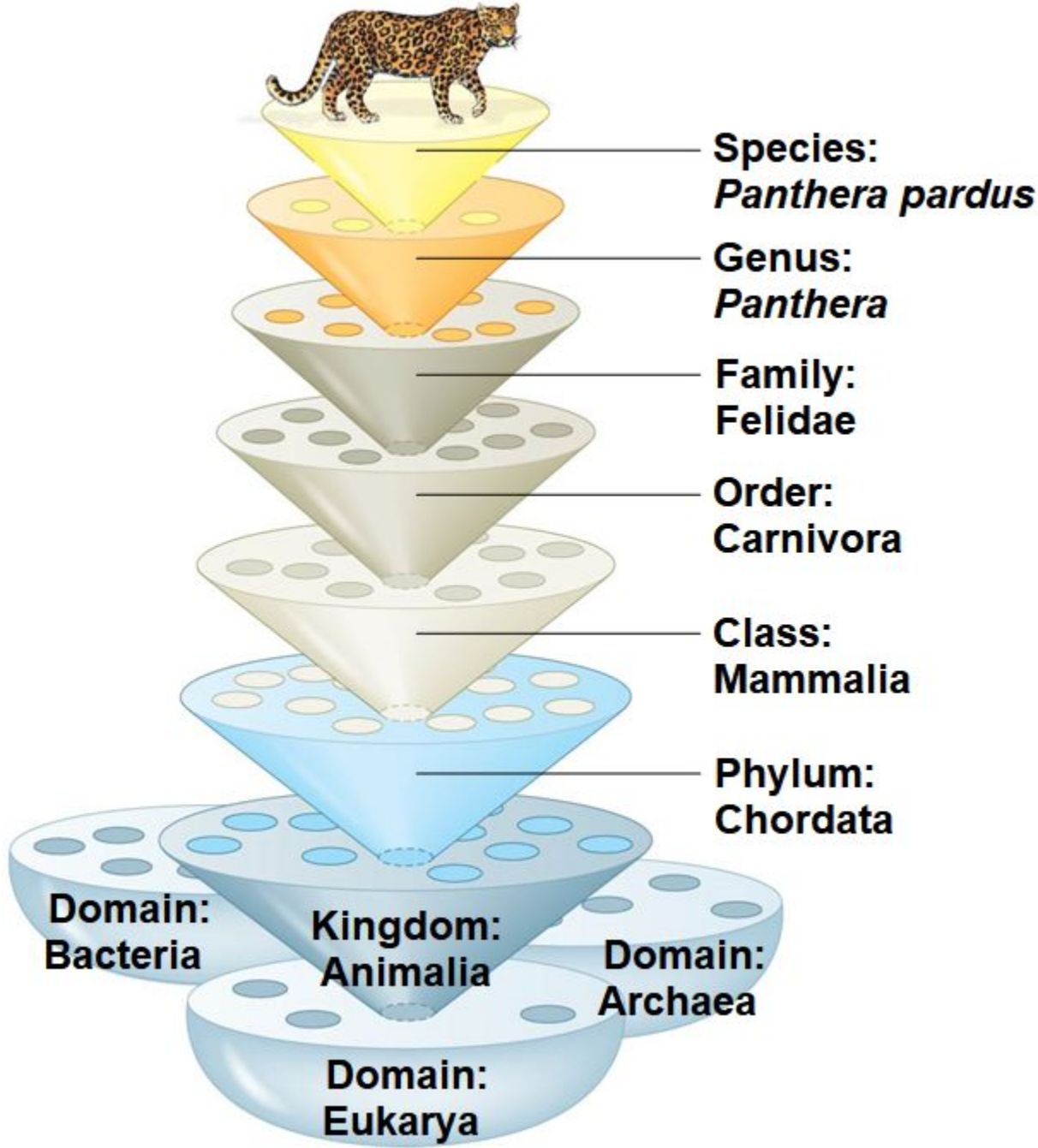


- The two-part scientific name of a species is called a binomial
- The first part of genus
- The second part, called the specific epithet, is unique for each species within the genus
- The first letter of the genus is capitalized, and the entire species name is italicized
- Both parts together describe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

Hierarchical Classification

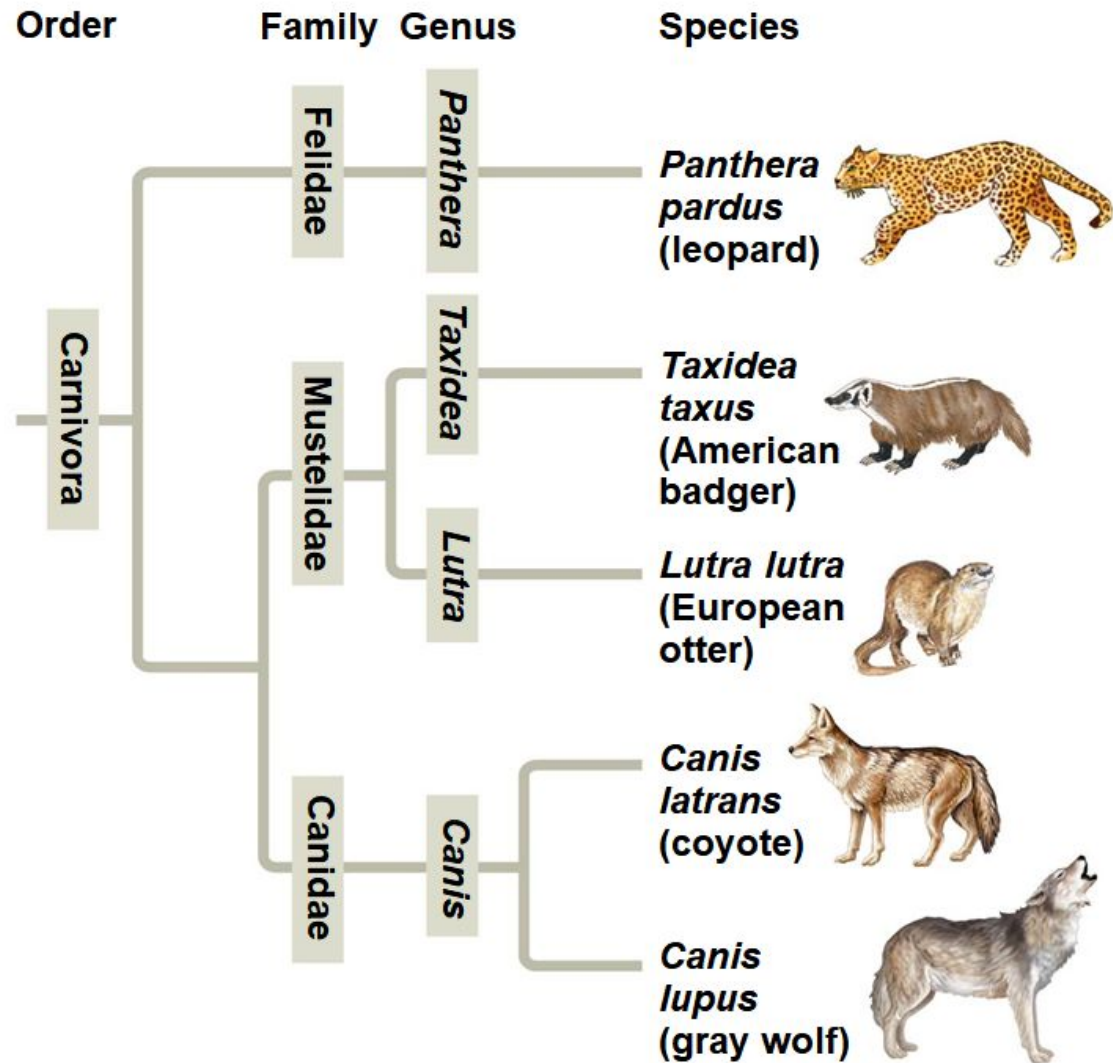
- Linnaeus introduced a system for grouping species in increasingly inclusive categories
- The taxonomic groups from broad to narrow are domain, kingdom, phylum, class, order, family, genus, and species (Dumb Kids Playing Cards On Freeway Get Smashed)
- A taxonomic unit at any level of hierarchy is called a taxon
- The broader taxa are not comparable between groups
 - EX: An order of snails has less genetic diversity than an order of mammals
- Categories become more inclusive and broad going from species to Domain designations

Figure 26.3



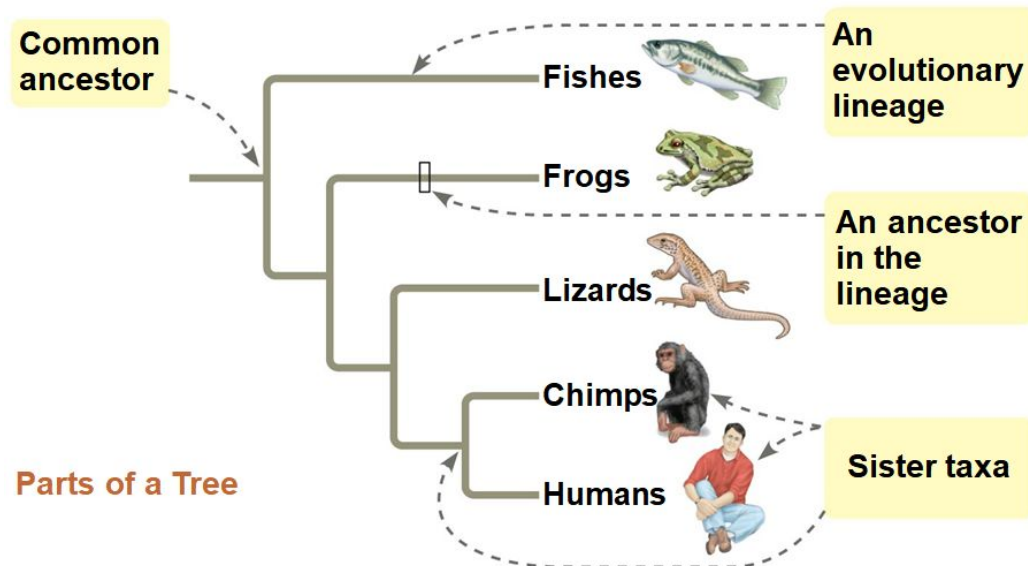
Linking Classification and Phylogeny

- The evolutionary history of a group of organisms can be represented in a branching phylogenetic tree (branching tree)
- The "tips" of the **tree** branches represent the taxa in the study.



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



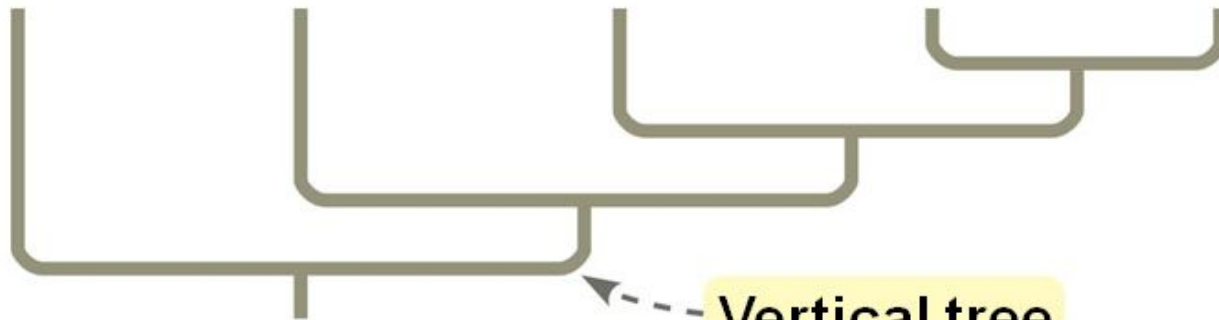
- ## Alternative Forms of Tree Diagrams

Frogs

Lizards

Chimps

Humans



Vertical tree

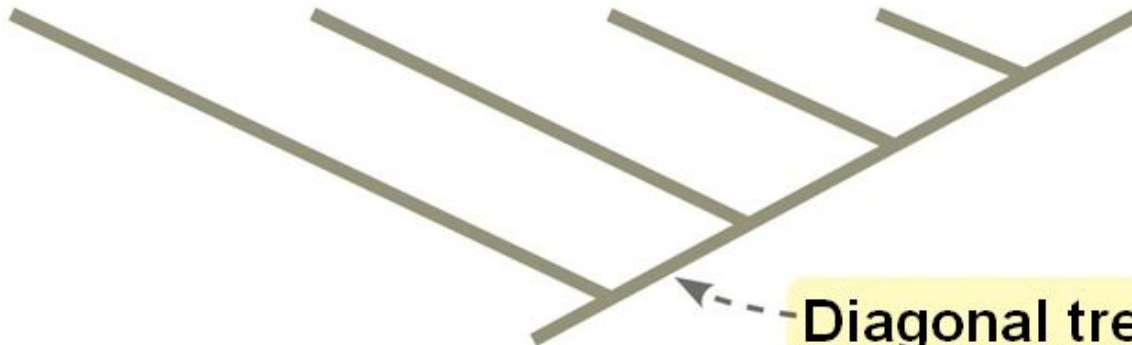
Fishes

Frogs

Lizards

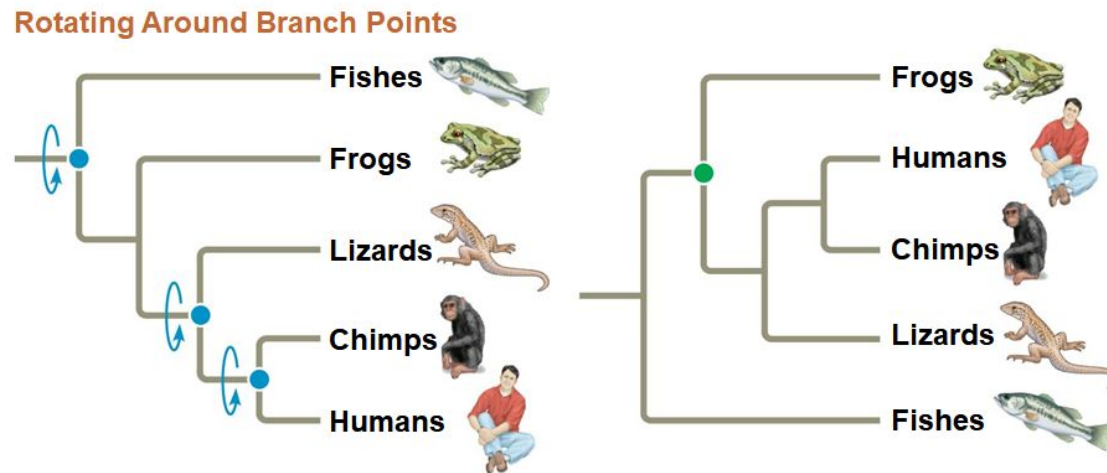
Chimps

Humans



Diagonal tree

- Tree branches can be rotated around a branch point without changing the evolutionary relationships
 - EX: the tree below depicts the SAME information



- 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

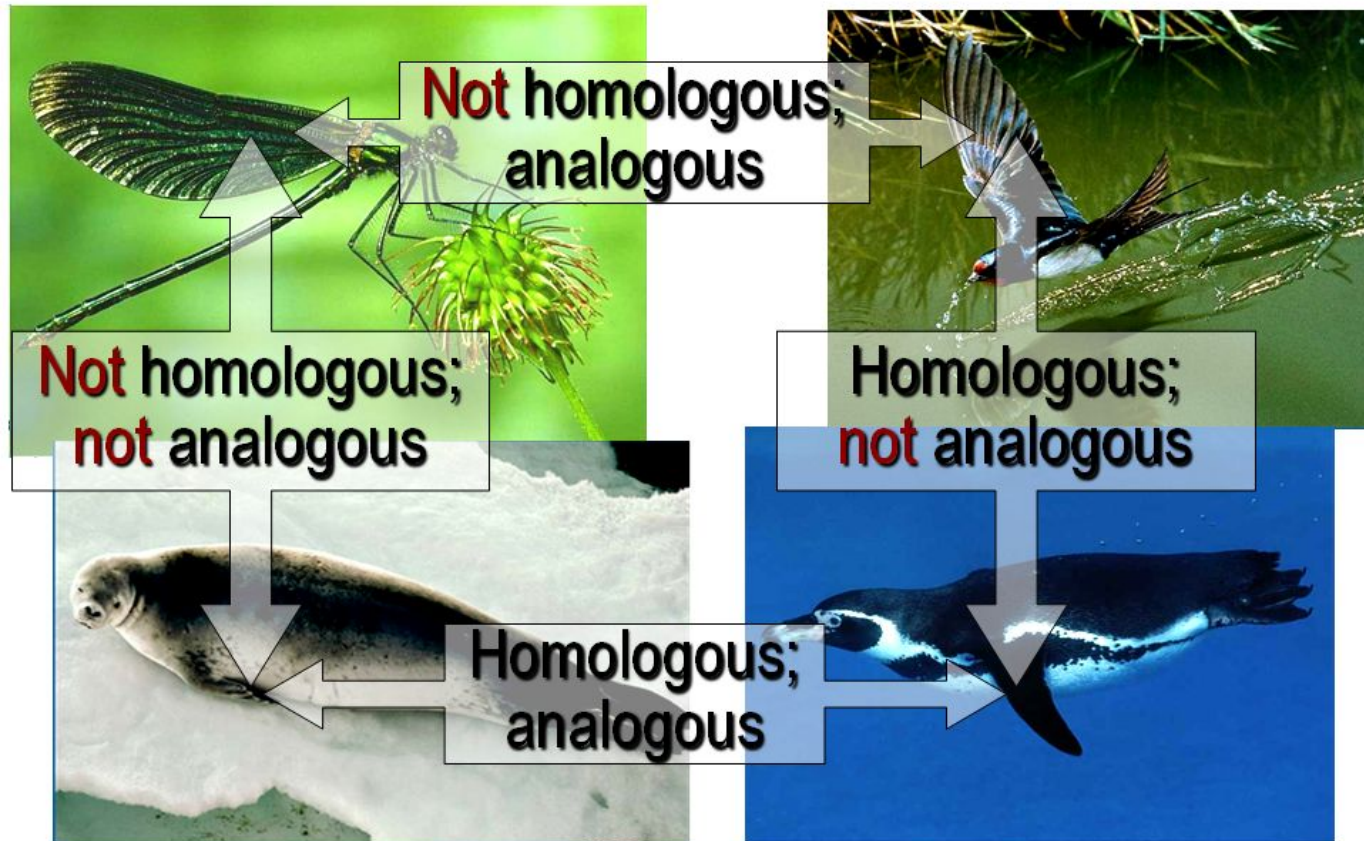
Concept 26.2: Phylogenies are inferred from morphological and molecular data

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

- Systematists need to determine if a similarity is the result of homology or analogy when creating trees
 - Homology is similarity due to *shared* ancestry
 - Analogy is similarity due to *convergent* evolution



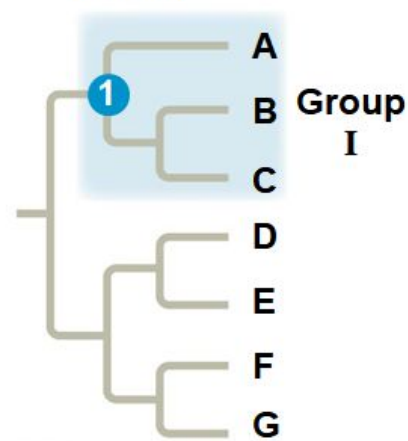
- **Convergent evolution** is when different taxa/species solve a problem in the same way evolutionarily. This examines **ANALOGOUS** structures
 - EX: human legs vs. insect legs
 - **Similar function/use**, but very different structures
 - Both used for locomotion. Humans use muscles/tendons, while insects used pressurized fluids
- **Divergent evolution** is the process by which an ancestral characteristic becomes adapted to new roles. This examines **HOMOLOGOUS** structures
 - EX: human arms vs. front whale flipper
 - **Similar structure or anatomy**, but different function/use
 - Both look like they are “arm” structures. Humans hold/grasp items, while whales use fin to swim

Concept 26.3: Shared characters are used to construct phylogenetic trees

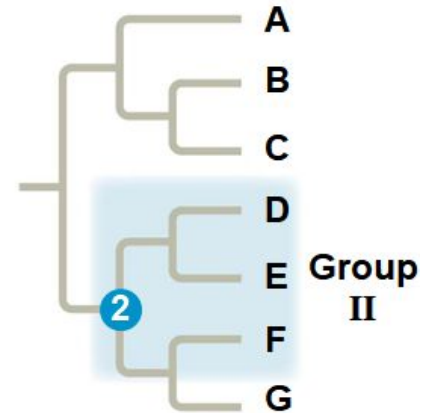
- Once homologous characters have been identified, they can be used to infer a phylogeny
- **Cladistics** groups organisms by common ancestry
- A **clade** is a group of species that includes an ancestral species and all its descendents
- Clades can be nested in larger clades, but not all groupings of organisms qualify as clades

- A valid clade is **monophyletic**, signifying that it consists of the ancestor species and all descendents
- A **paraphyletic** grouping consists of an ancestral species and some, but not all, of the descendents
- A **polyphyletic** grouping includes distantly related species but does not include their most recent common ancestor

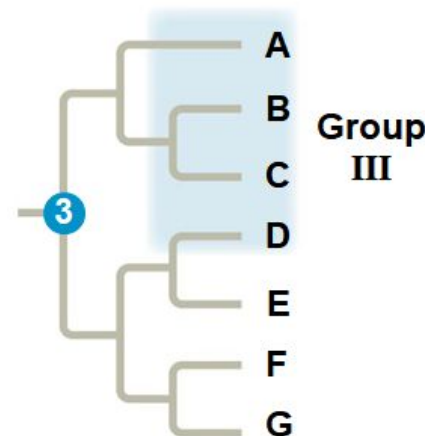
(a) Monophyletic group (clade)



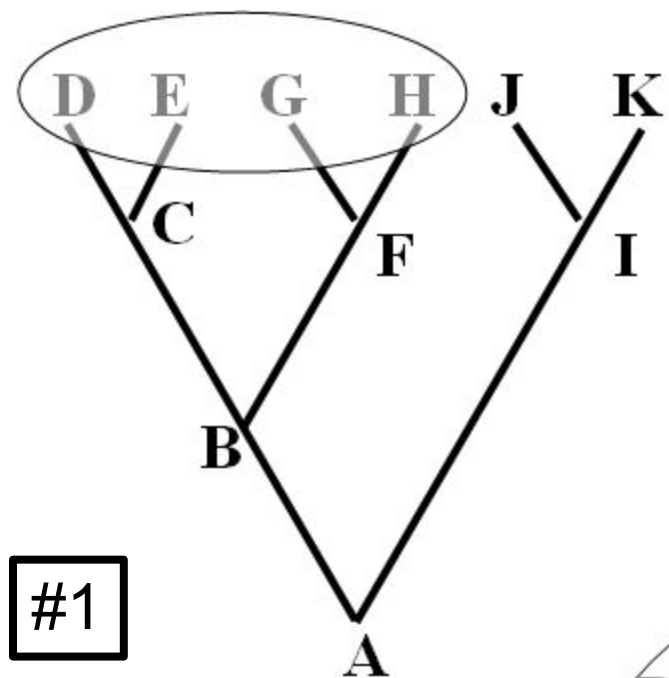
(b) Paraphyletic group



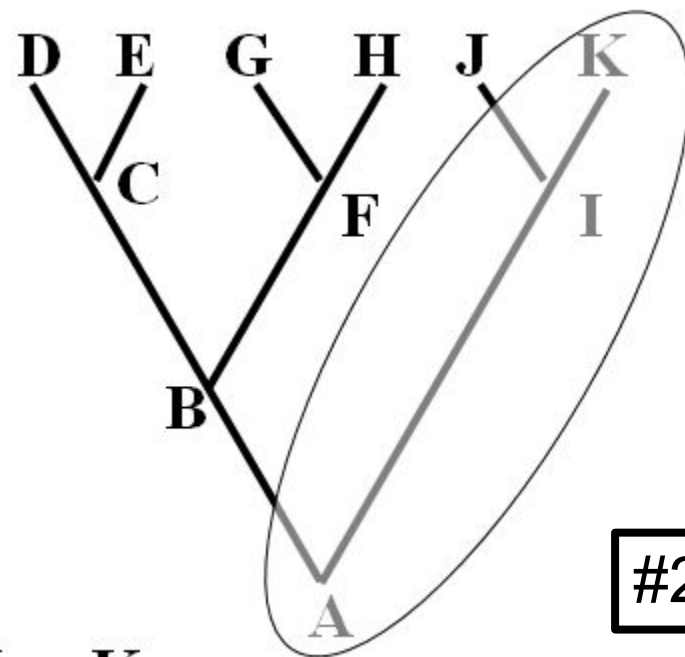
(c) Polyphyletic group



?



?



?

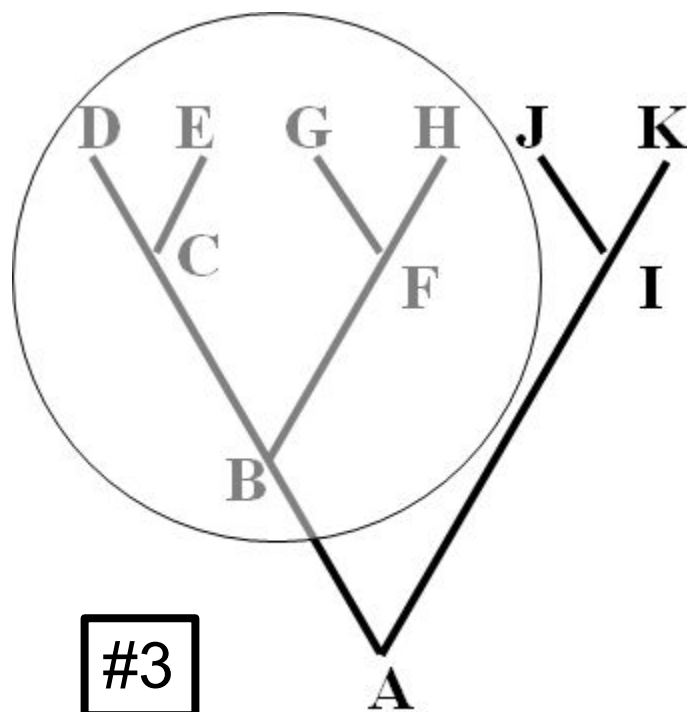
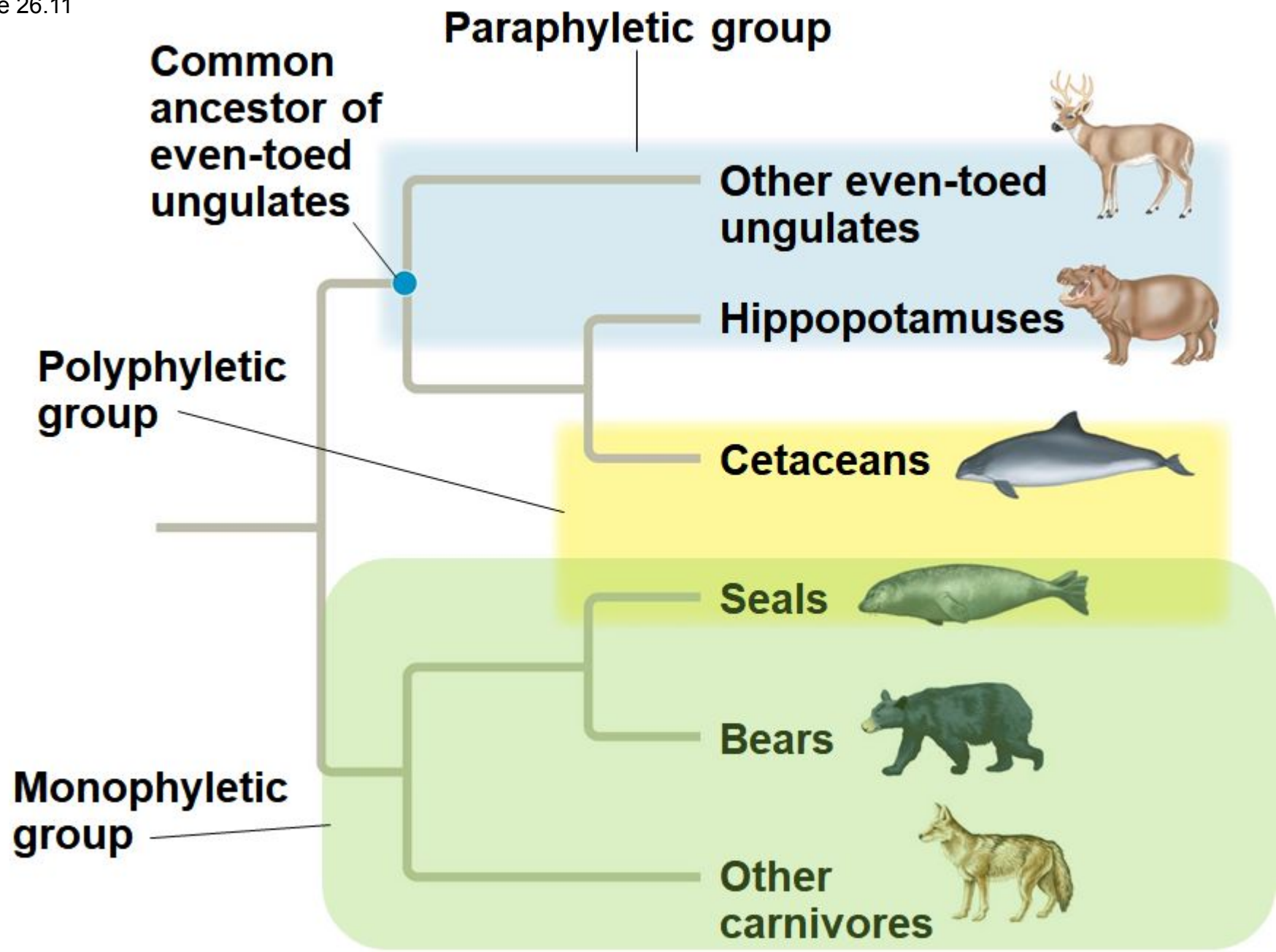


Figure 26.11



You should be able to identify the different types of groups

Shared Ancestral and Shared Derived Characters

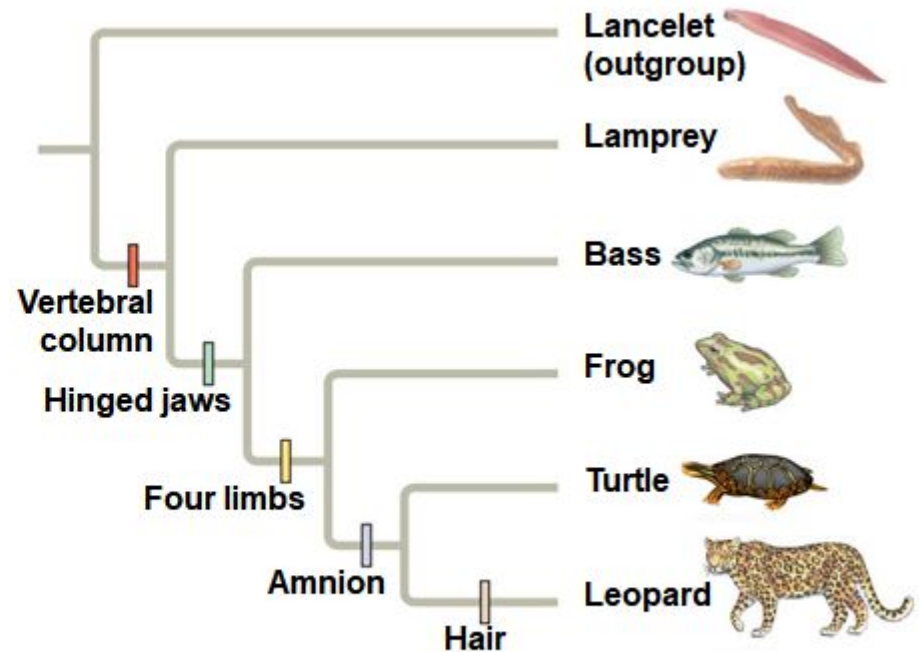
- In comparison with its ancestor, an organism has both shared and different characters
- A **shared ancestral character** is a character that *originated* in an ancestor of the taxon
- A **shared derived character** is an evolutionary novelty *unique* to a particular clade
- A character can be both 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

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

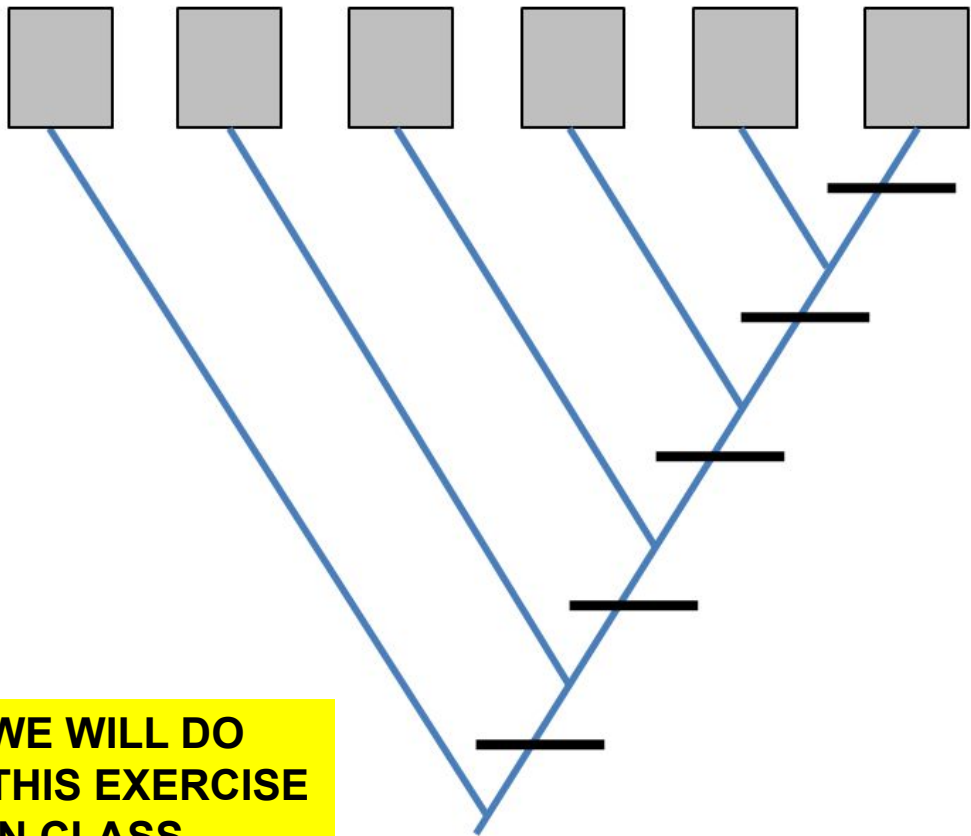
(a) Character table



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

Tree Building Activity



	Thick Hooves (1)	Big Teeth (2)	Soft Fur (3)	Squeaky Voice (4)	Red Nose (5)
Dasher (D)	Y	N	Y	N	N
Prancer (P)	N	Y	N	Y	N
Vixen (V)	N	Y	N	N	N
Comet (C)	Y	N	N	N	N
Rudolph (R)	Y	N	Y	N	Y
Blitzen (B)	Y	Y	N	N	N

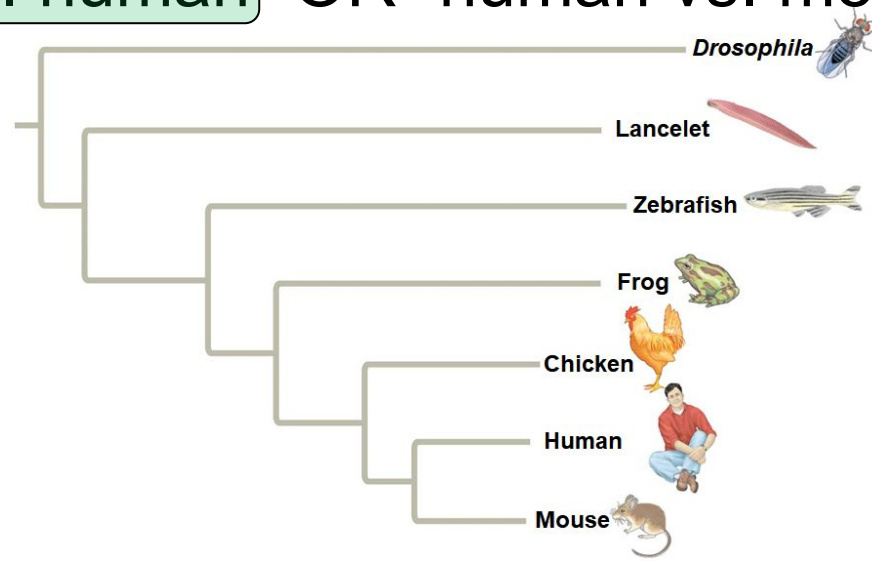
*** For cladistic purposes, Rudolph will be considered the OUTGROUP since he is the OLDEST

WE WILL DO THIS EXERCISE IN CLASS

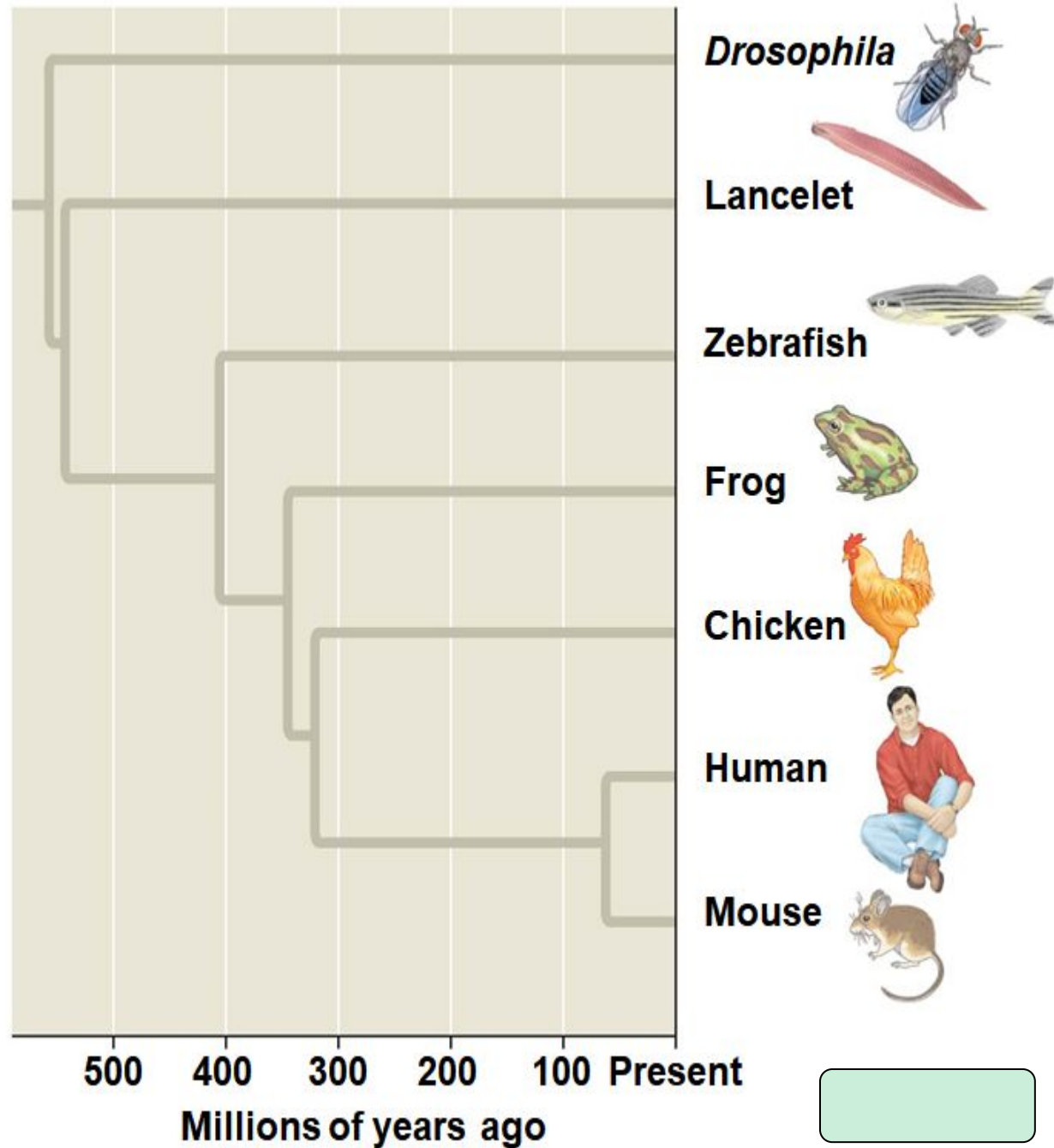
Based on the information in the table below, construct a cladogram (or family tree) that depicts the relatedness of Christmas reindeer based on ancestral or derived characters. **Place each of the reindeer "D, P, V, C and B" in the boxes on the terminal branches of the tree.** Also, **place the character state using the character numbers (1-5) on the dashes which intersect the tree.** Be sure to indicate whether these characters APPEARED or DISAPPEARED at that intersection on the tree.

Phylogenetic Trees with Proportional Branch Lengths

- In some trees, the length of a branch can reflect the number of genetic changes that have taken place in a particular DNA sequence in that lineage
- EX: the longer the branch lengths connecting two organisms, more genetic changes have taken place
- Which would have more genetic changes: comparing **chicken vs. human** -OR- human vs. mouse?



- In other trees, branch length can be proportional to time, and branching points can be determined from the fossil record
- Which organism is the most ancient here?

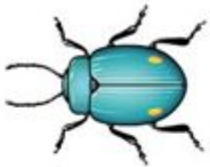


Maximum Parsimony and Maximum Likelihood

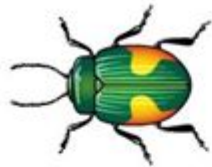
- Systematists can never be sure of finding the best tree in a large data set
- They narrow possibilities by applying the principles of maximum parsimony and maximum likelihood
- **Maximum parsimony** assumes that the tree that requires the fewest evolutionary events is the most likely
- **Maximum likelihood** is based on probability rules about how DNA changes over time (i.e. mutations) and assumes a tree can be found that reflects the most likely sequence of evolutionary events

Applying parsimony to a problem in molecular systematics

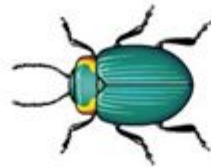
Technique



Species I



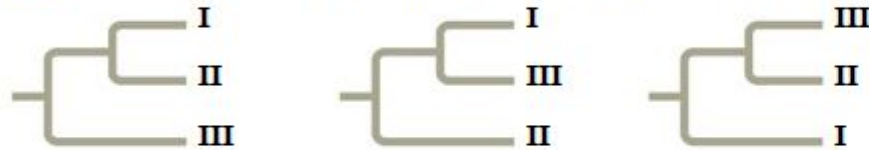
Species II



Species III

1

Three phylogenetic hypotheses:



2

Site

1 2 3 4

Species I

C T A T

Species II

C T T C

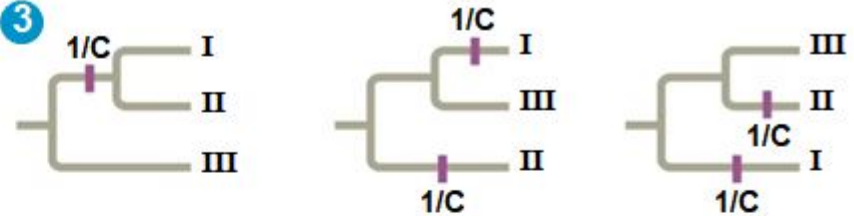
Species III

A G A C

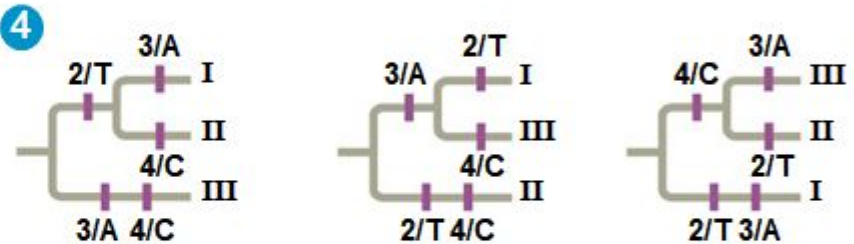
Ancestral sequence

A G T T

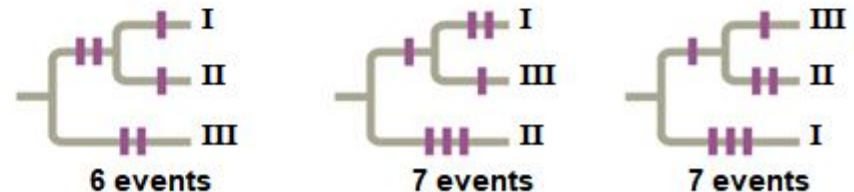
3



4



Results

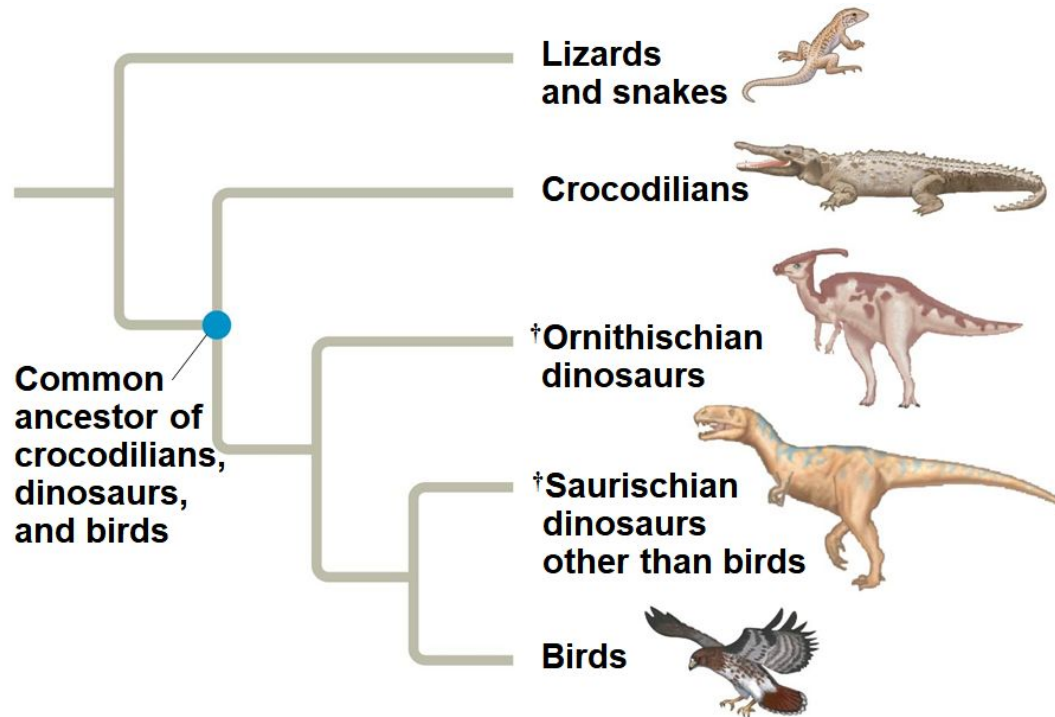


So which two species would be more closely related using this approach?

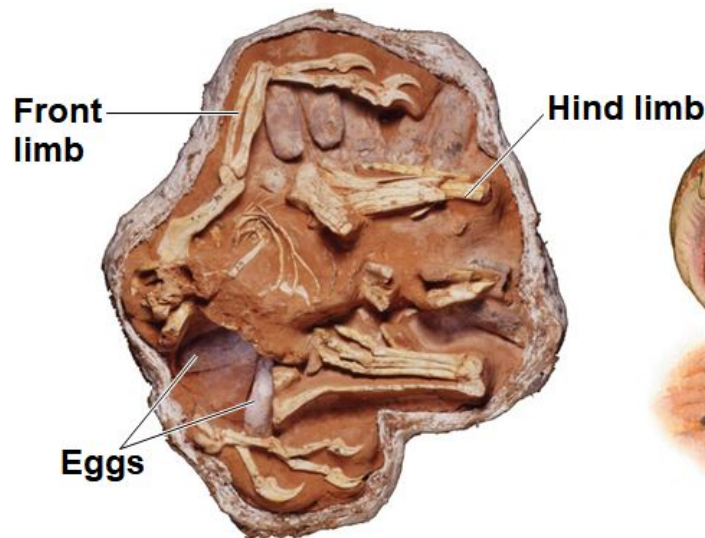
ANSWER: Species I and II

Phylogenetic Trees as Hypotheses

- The best hypothesis for a phylogenetic tree fits the most data: morphological, molecular, and fossil
- Phylogenetic bracketing allows us to predict features of an ancestor from features of its descendants
 - EX: phylogenetic bracketing allows us to infer characteristics of dinosaurs



- Birds and crocodiles share several features: four-chambered hearts, song, nest building, and brooding
- These features 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



(a) Fossil remains of *Oviraptor* and eggs



(b) Artist's reconstruction of the dinosaur's posture based on the fossil findings

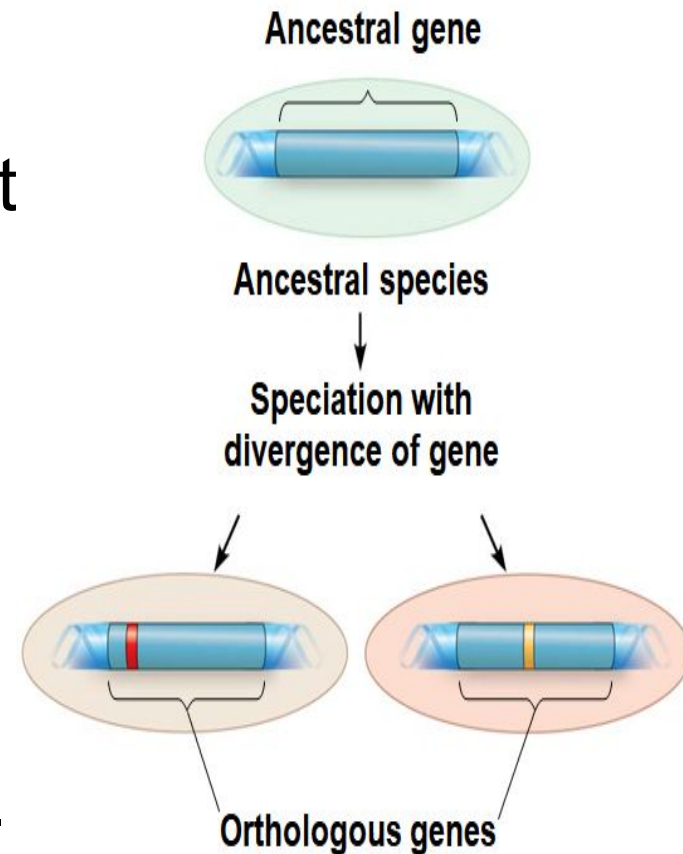
Concept 26.4: An organism's evolutionary history is documented in its genome maternal

- Comparing nucleic acids or other molecules to infer relatedness is a valuable approach for tracing organisms' evolutionary history
- DNA that codes for rRNA changes relatively slowly and is useful for investigating branching points that diverged hundreds of millions of years ago
- mtDNA evolves rapidly and can be used to explore recent evolutionary events
 - mutation rate is 10x higher than in nuclear DNA
 - subject to damage from reactive oxygen molecules
 - lacks the DNA repair mechanisms found in the nucleus

Gene Duplications and Gene Families

- Gene duplication increases the number of genes in the genome, providing more opportunities for evolutionary changes
- Repeated gene duplications result in gene families
- Duplicated genes can be traced to a common ancestor
- **Orthologous genes** are found in a single copy in the genome and are homologous between species
- They can diverge after speciation occurs

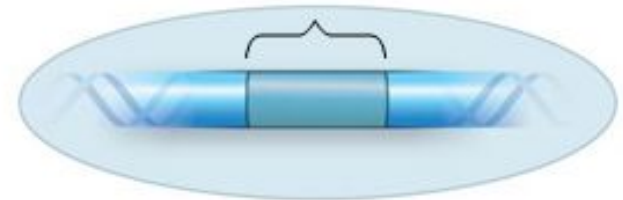
(a) Formation of orthologous genes:
a product of speciation



- **Paralogous genes** result from gene duplication so are found in **more than one copy** in the genome
- They can diverge within the species that carries them and often evolve new functions

(b) Formation of paralogous genes: within a species

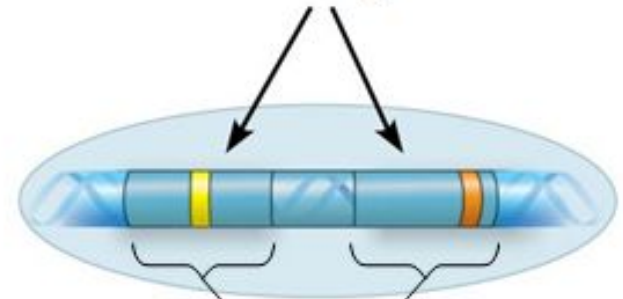
Ancestral gene



Species C



Gene duplication and divergence



Paralogous genes

Species C after many generations

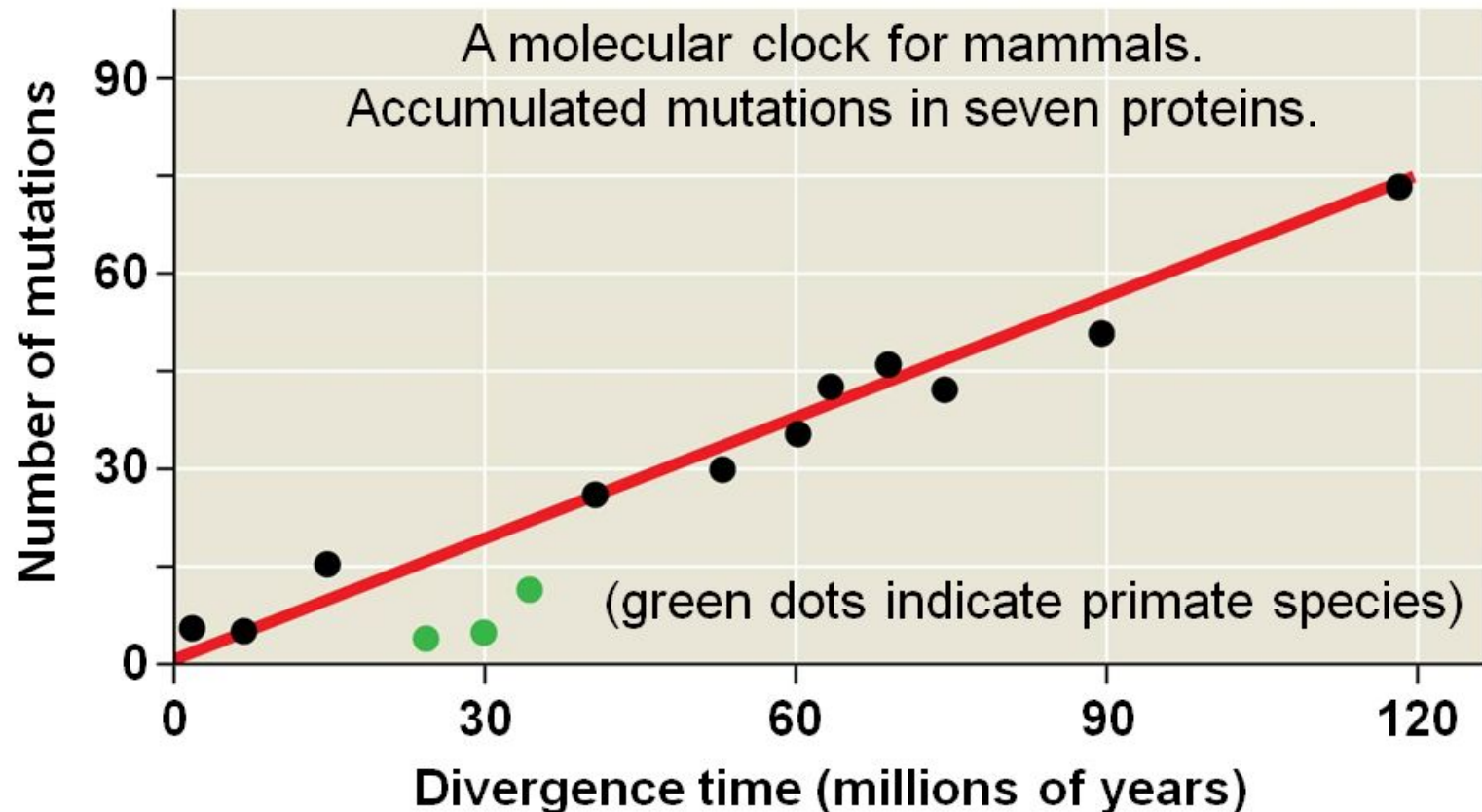
Genome Evolution

- Orthologous genes are widespread and extend across many widely varied species
 - EX: humans and mice diverged about 65 million years ago, and 99% of our genes are orthologous
- Gene number and the complexity of an organism are not strongly linked
 - EX: humans have only four times as many genes as yeast, a single-celled eukaryote
- Genes in complex organisms appear to be very versatile, and each gene can encode multiple proteins that perform many different functions

Concept 26.5: Molecular clocks help track evolutionary time

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

- Molecular clocks are calibrated against branches whose dates are known from the fossil record
- Individual genes vary in how clocklike they are
- Primate proteins appear to have evolved more slowly than other mammals



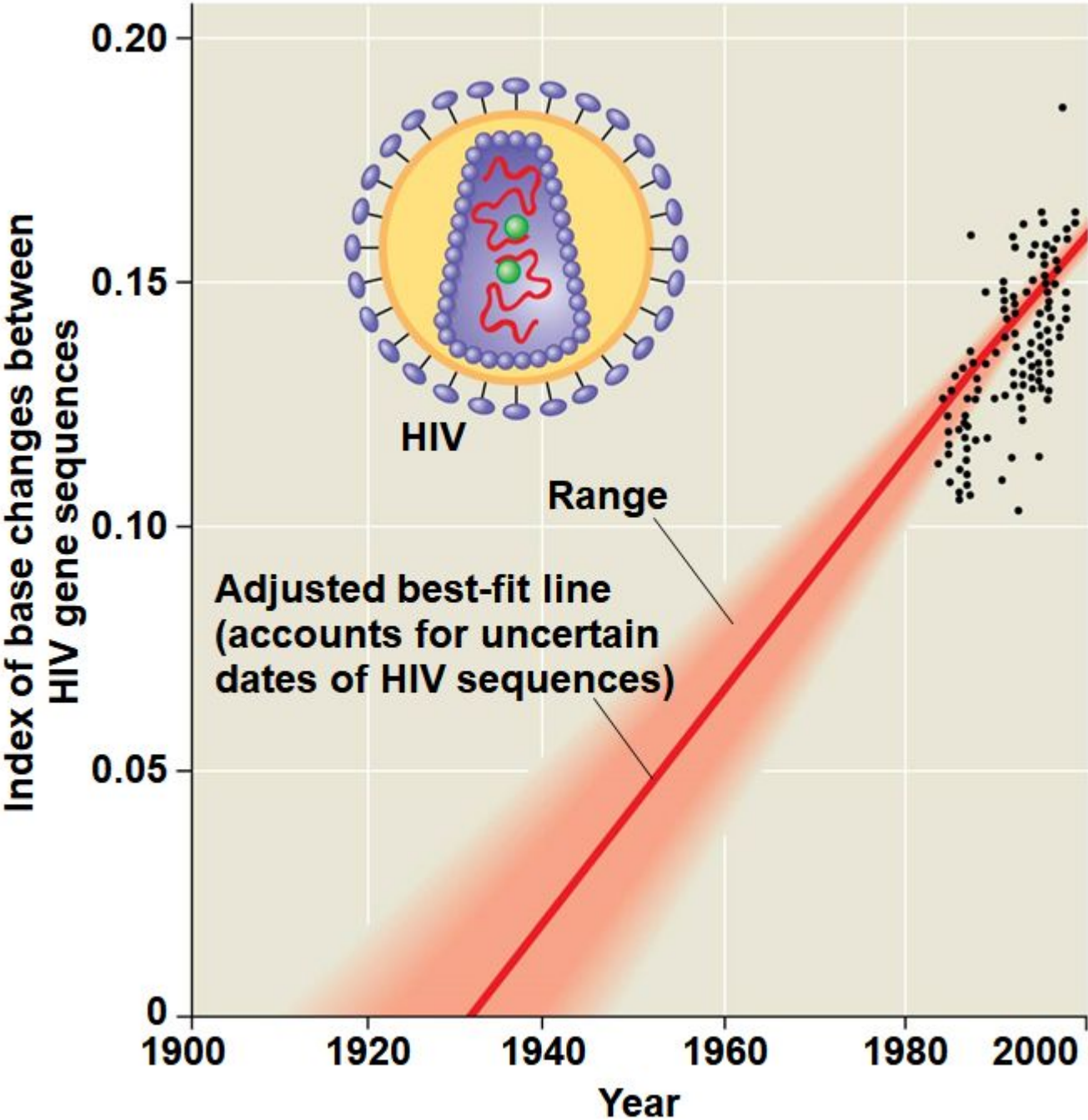
Differences and Problems in Clock Speed

- If most of the evolutionary change has no effect on fitness, then molecular change rate should be even
- Differences in clock rate for different genes are a function of the importance of the gene and how critical the specific amino acid is to protein function
- The molecular clock does not run as smoothly as expected if mutations were neutral
- Irregularities result from natural selection
- Estimates of evolutionary divergences older than the fossil record have a high degree of uncertainty
- The use of multiple genes or genes that evolved in different taxa may improve estimates

Applying a Molecular Clock: Dating 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 the strain spread to humans during the 1930s
- A more advanced molecular clock approach estimated the first spread to humans around 1910

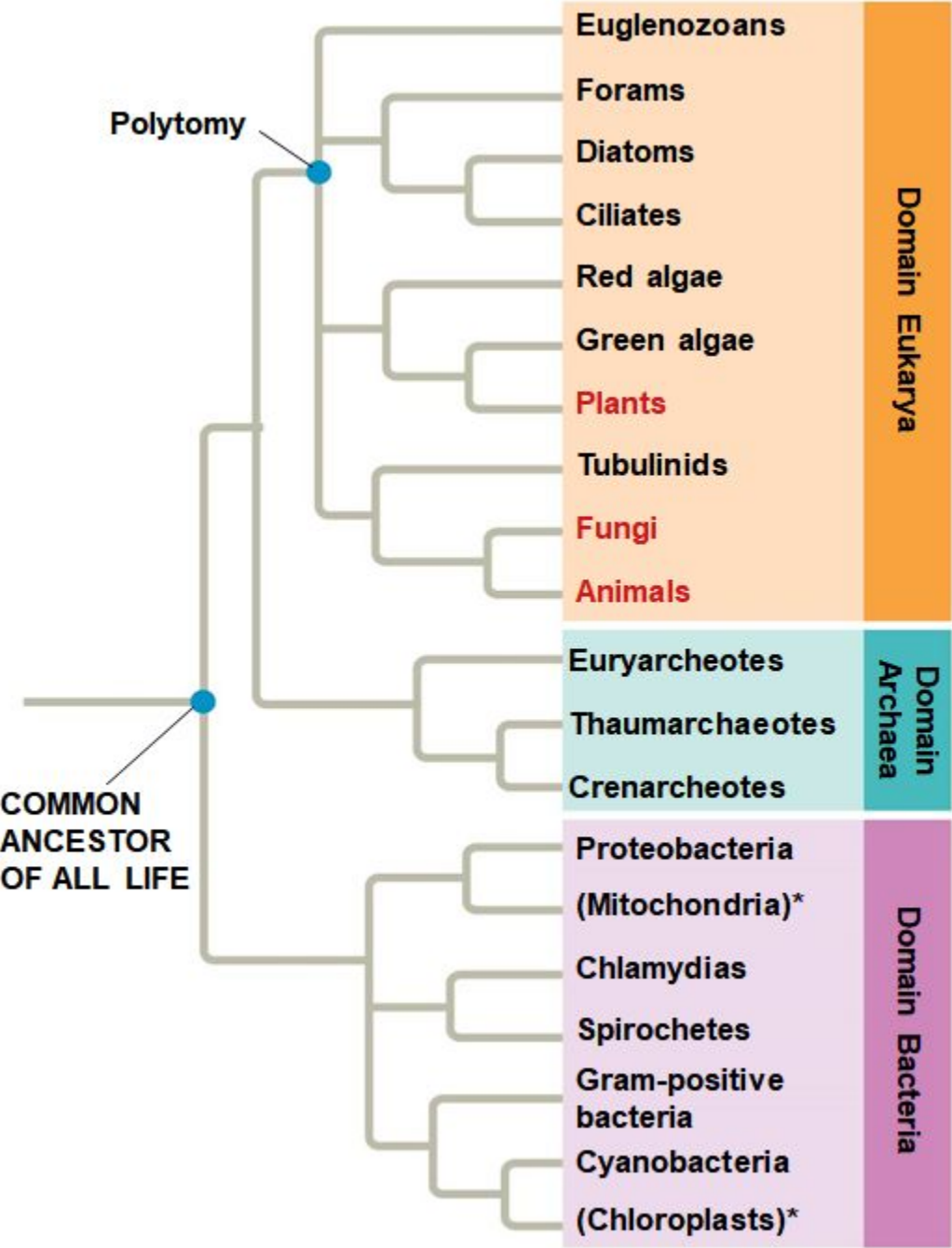
Figure 26.20



Concept 26.6: Our understanding of the tree of life continues to change based on new data

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

Figure 26.21



The Important Role of Horizontal Gene Transfer

- 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; but, some other genes reveal different relationship
- 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 possibly fusion of organisms

- Disparities between gene trees can be explained by the occurrence of horizontal gene transfer
- Horizontal gene transfer has played a key role in the evolution of both prokaryotes and eukaryotes
- Eukaryotes can acquire nuclear genes from bacteria and archaea
 - EX: the alga *Galdieria sulphuraria* acquired about 5% of its genes from bacterial and archaeal species
- Some biologists argue that horizontal gene transfer was so common, early life history should be shown as a complex network of connected branches
- Bottom Line: Determining precise relatedness among organisms can be very difficult to fully understand

Figure 26.23

