

# Chapter 26

## Phylogeny and the Tree of Life

PowerPoint® Lecture Presentations for

# Biology

*Eighth Edition*

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Lectures by Chris Romero, updated by Erin Barley with contributions from Joan Sharp

# Overview: Investigating the Tree of Life

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

# Binomial Nomenclature

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- In the 18th century, Carolus **Linnaeus** published a system of taxonomy based on resemblances.
- The **two-part scientific name: *Genus species***.
- The first letter of the genus is capitalized, and the entire species name is italicized
- Both parts together name the species. This is the species **specific epithet**.

# Hierarchical Classification

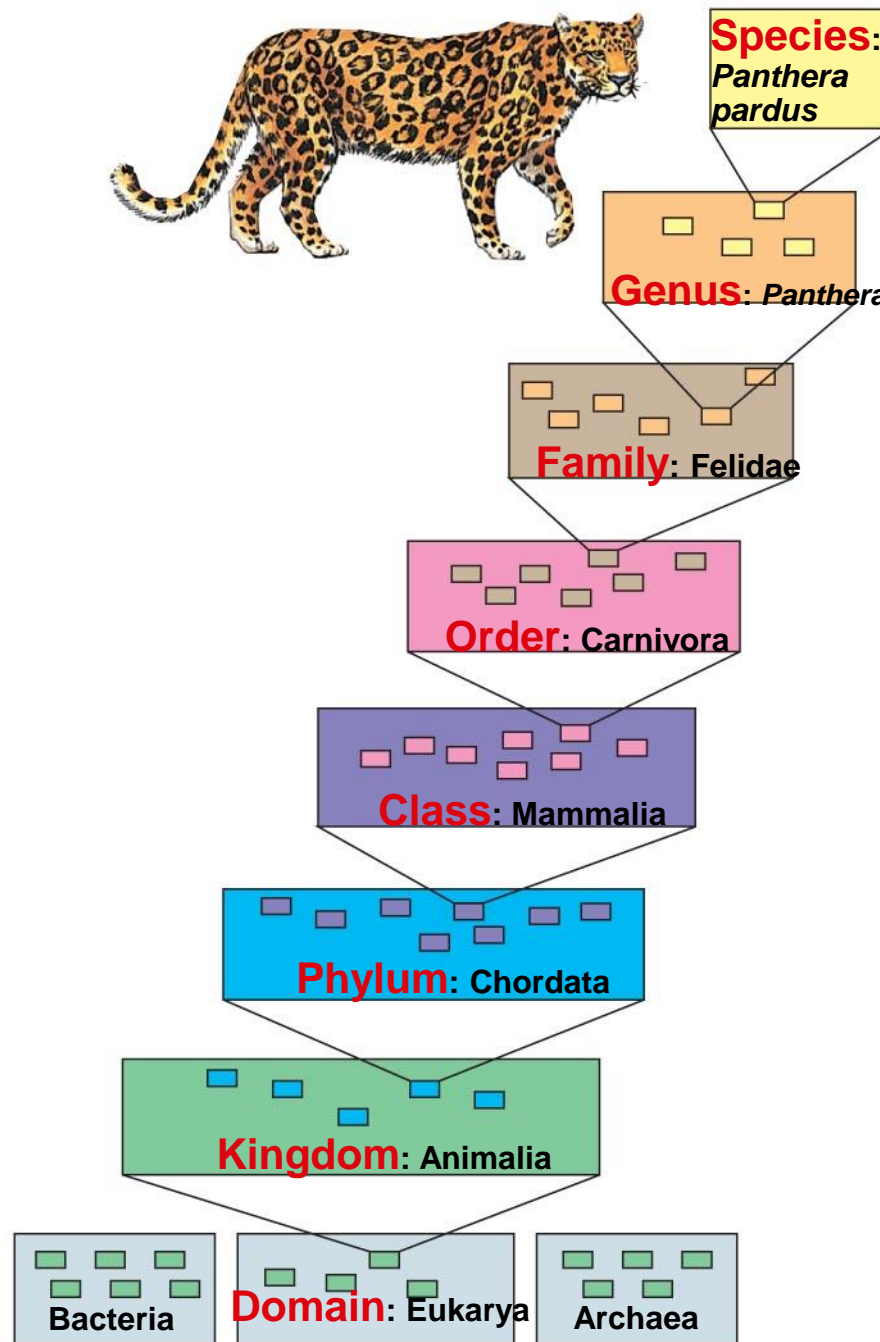
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- Linnaeus introduced a system for grouping species in increasingly broad categories.
- The taxonomic groups from broad to narrow are **domain**, **kingdom**, **phylum**, **class**, **order**, **family**, **genus**, and **species**.
- A **taxonomic unit** at any level of hierarchy is called a **taxon**.

# Taxonomy:

## Hierarchical Organization:

Domain  
Kingdom  
Phylum  
Class  
Order  
Family  
Genus  
species

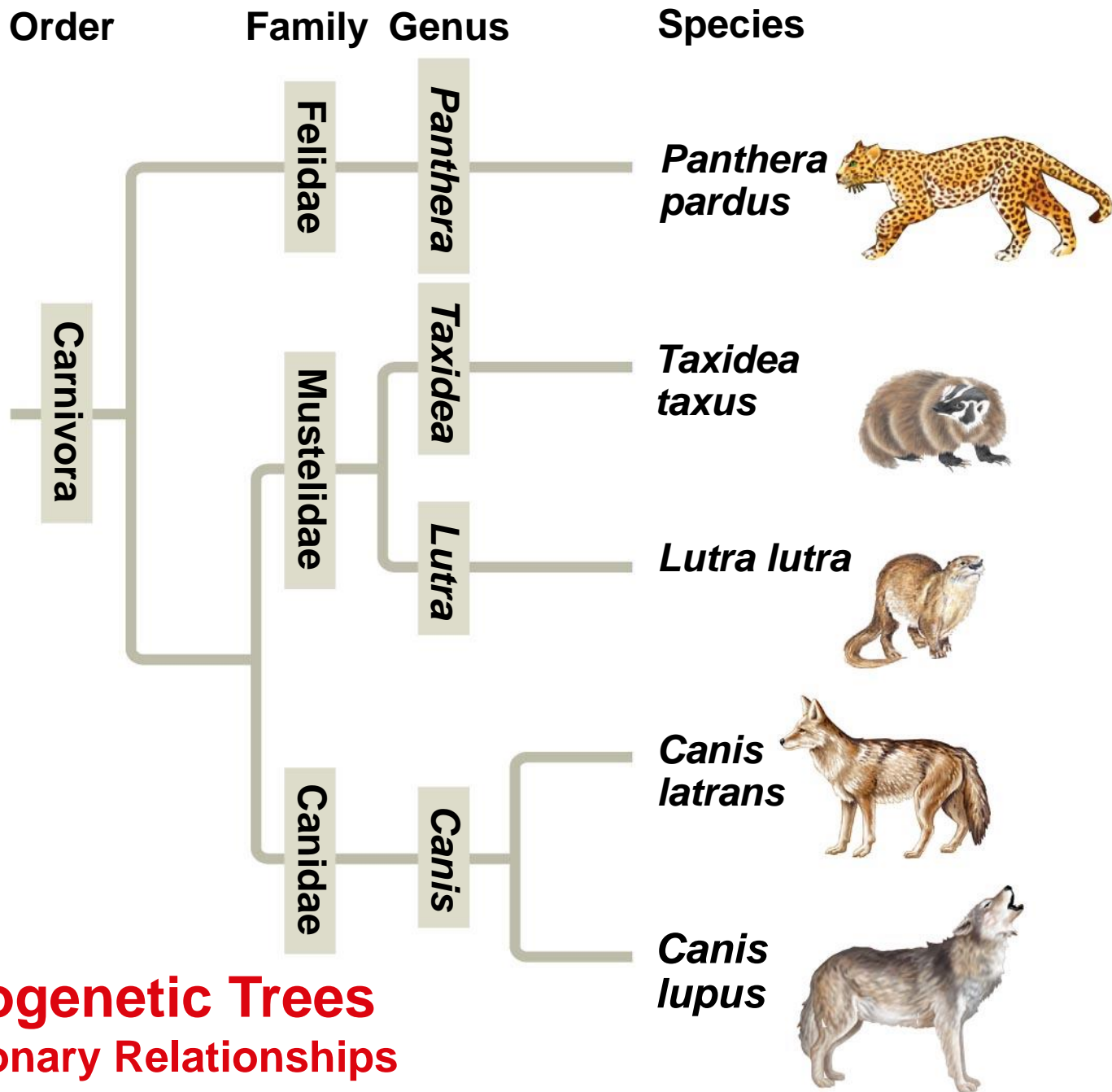


# Linking Classification and Phylogeny

## Evolutionary Relationships

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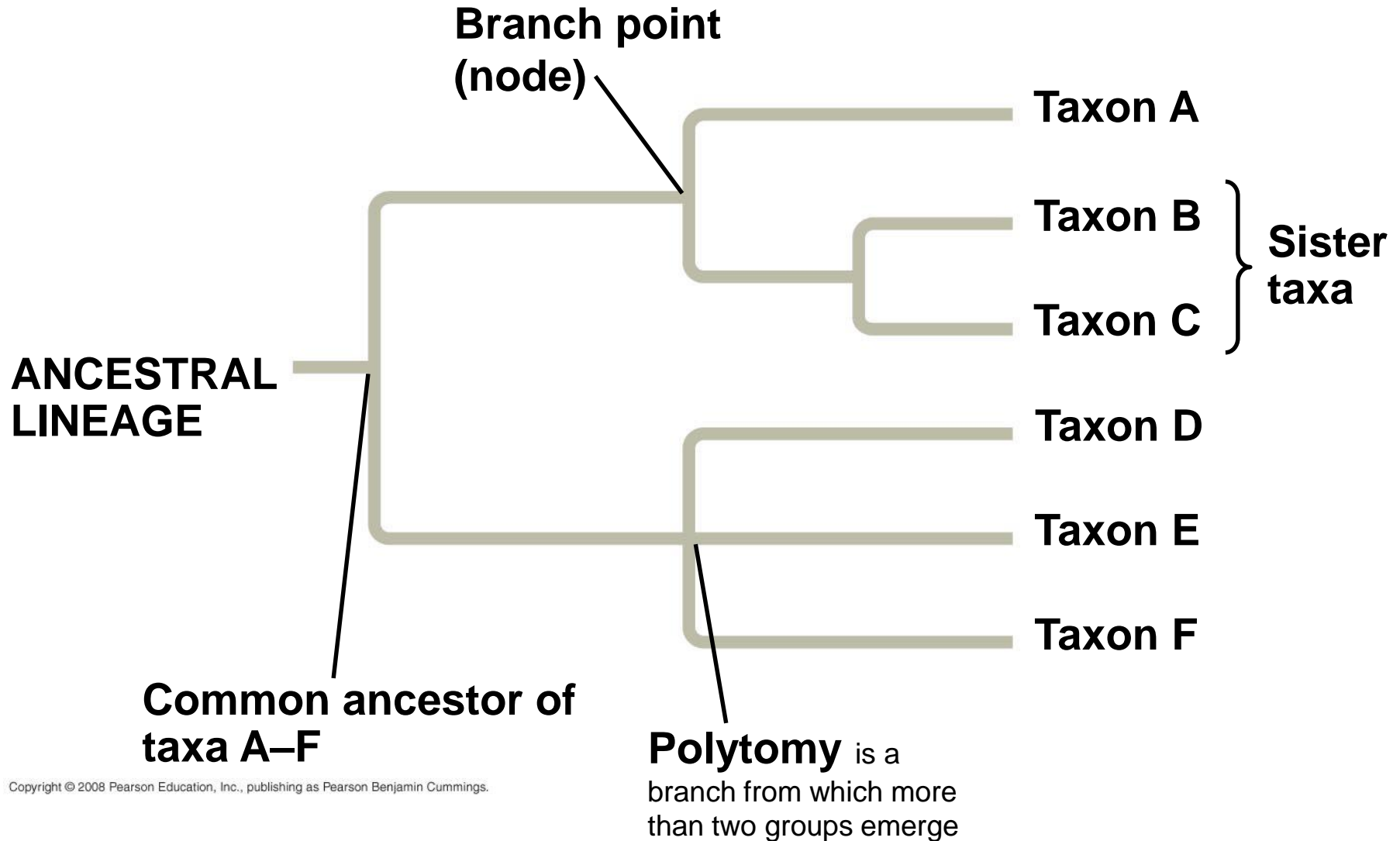
- **Systematists** depict **evolutionary relationships** in branching **phylogenetic trees**.
- Their *PhyloCode* recognizes only groups that include a *common ancestor* and all its *descendents*.
- A phylogenetic tree represents a hypothesis about evolutionary relationships.
- Each **branch point** represents the divergence of two species.
- **Sister taxa** are groups that share an immediate common ancestor.



## Phylogenetic Trees

### Evolutionary Relationships

**A rooted tree includes a branch to represent the last common ancestor of all taxa in the tree:**





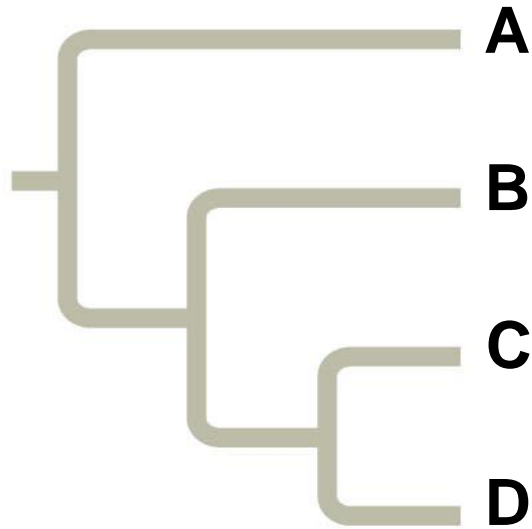
# What We Can and Cannot Learn from Phylogenetic Trees

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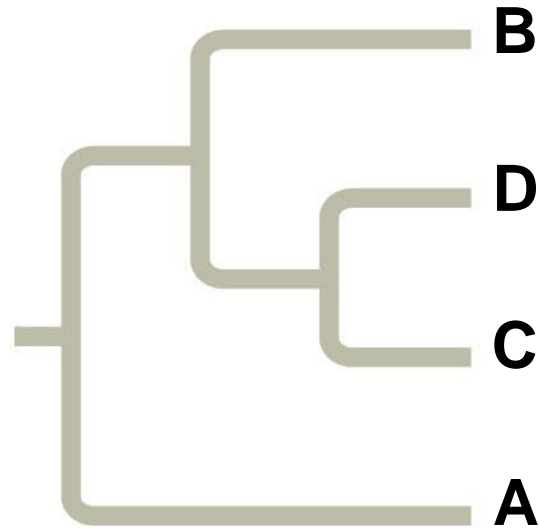
- Phylogenetic trees do **show patterns of descent**.
- Phylogenetic trees do not indicate when species evolved or how much genetic change occurred in a lineage.
- It shouldn't be assumed that a taxon evolved from the taxon next to it.
- *Phylogeny provides important information about similar characteristics in closely related species.*

## ***Possible Phylogenetic Trees:***

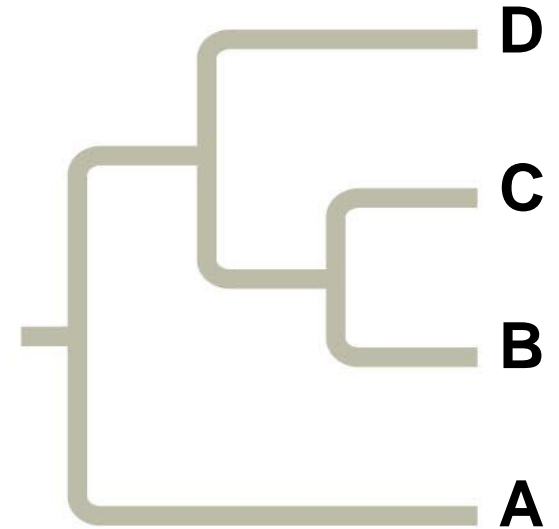
*Provide important information about similar characteristics in closely related species.*



**(a)**



**(b)**



**(c)**

## Concept 26.2: Phylogenies are inferred from morphological and molecular data

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- Organisms with **similar morphologies or DNA sequences** are likely to be **more closely related** than organisms with different structures or sequences.
- 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 - Similar Environmental Selecting Agents

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- Convergent evolution occurs when **similar environmental pressures** and **natural selection produce similar /analogous adaptations in organisms from different evolutionary lineages.**
- Bat and bird wings are homologous as forelimbs, but analogous as functional wings.
- Analogous structures or molecular sequences that evolved independently are also called **homoplasies.**

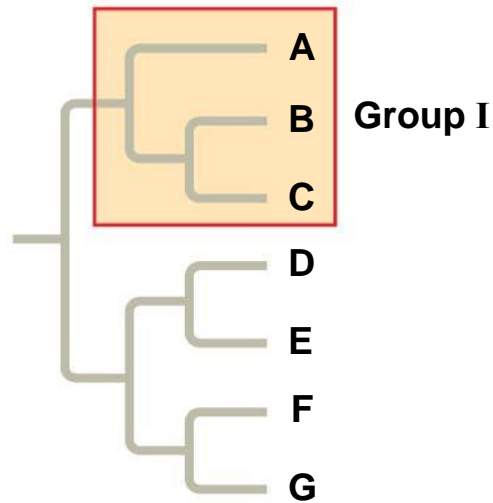
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- Homology can be distinguished from analogy by comparing fossil evidence and the degree of complexity. The more complex two similar structures are, the more likely it is that they are homologous.
  - **Molecular systematics** uses DNA and other molecular data to determine evolutionary relationships.
  - Once homologous characters have been identified, they can be used to infer a phylogeny.

# Cladistics groups organisms by common descent

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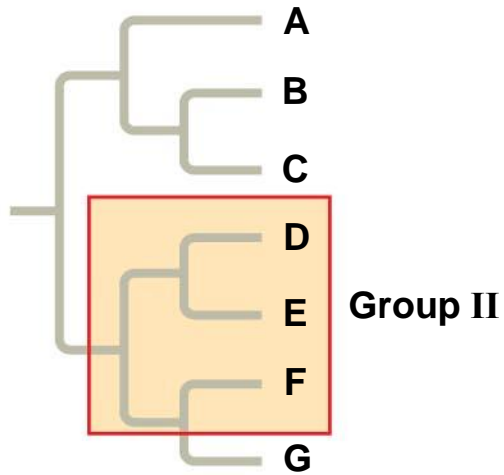
- A **clade** is a group of species that includes an ancestral species and all its descendants.
- Clades can be nested in larger clades, but not all groupings of organisms qualify as clades.
- A valid clade is **monophyletic**, signifying that it consists of the ancestor species and all its descendants.
- A **paraphyletic** grouping consists of an ancestral species and some of the descendants.
- A **polyphyletic** grouping consists of various species that lack a common ancestor.

# Cladistics - Groups Organisms using Evolutionary Relationships

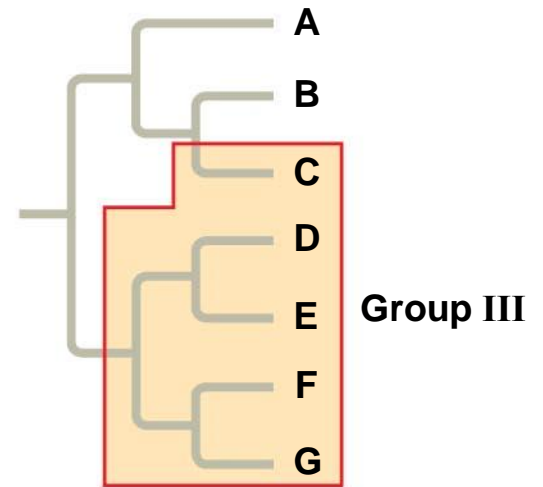


**Monophyletic** group / clade

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**Paraphyletic** group



**Polyphyletic** group

# *Shared Ancestral and Shared Derived Characters*

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- 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.

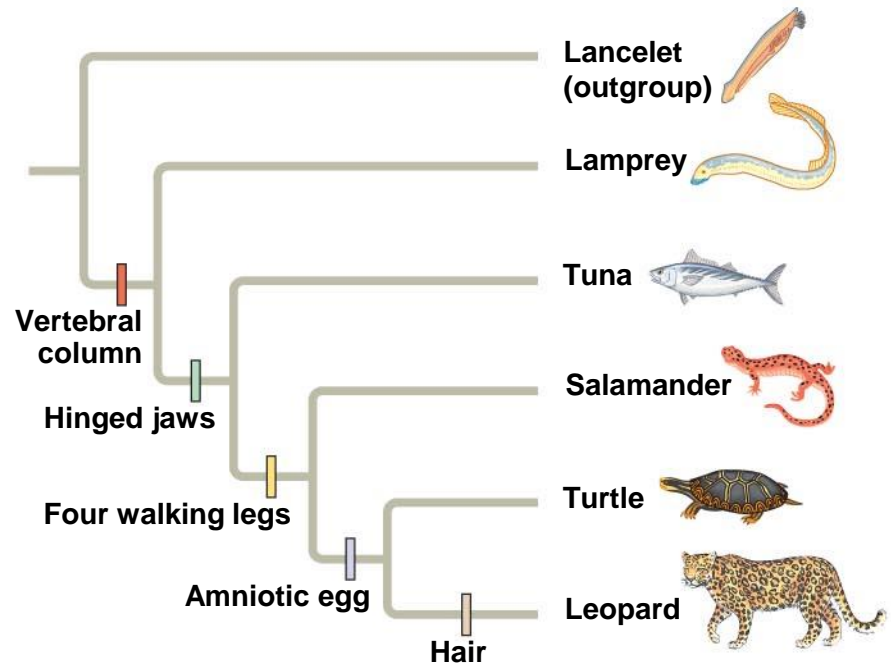


# Inferring Phylogeny from Shared Characters

CHARACTERS	TAXA					
	Lancelet (outgroup)	Lamprey	Tuna	Salamander	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
Amniotic (shelled) egg	0	0	0	0	1	1
Hair	0	0	0	0	0	1

(a) Character table

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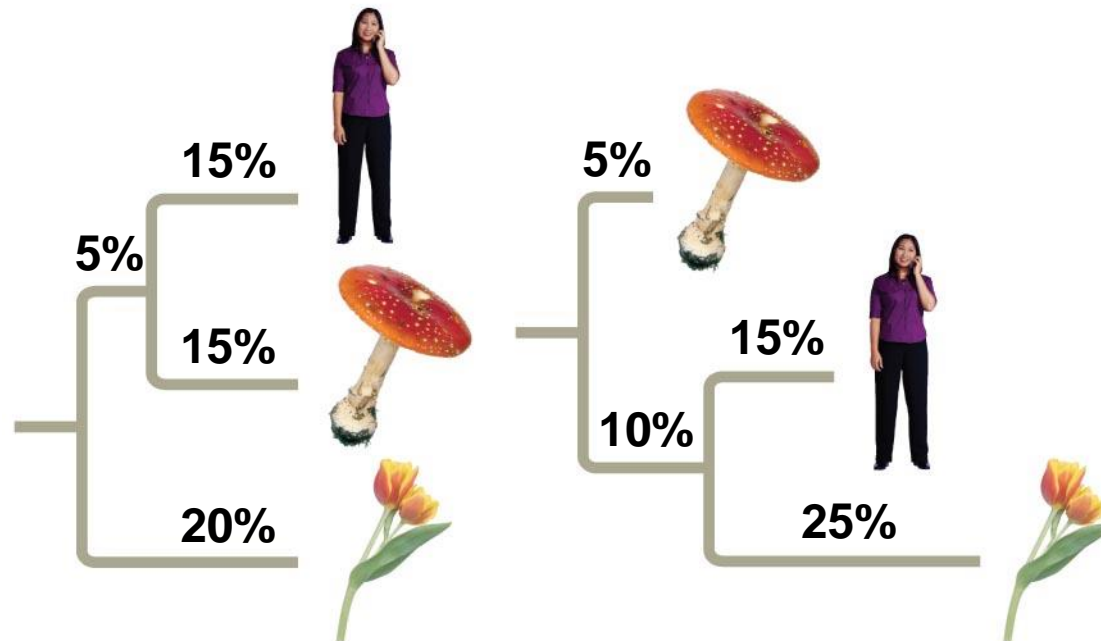
(b) Phylogenetic tree

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- **Maximum parsimony** assumes that the tree that requires the fewest evolutionary events (appearances of shared derived characters) is the most likely.
  - The principle of **maximum likelihood** states that, given certain rules about how DNA changes over time, a tree can be found that reflects the most likely sequence of evolutionary events.
  - The best hypotheses for phylogenetic trees fit the most data: morphological, molecular, and fossil.
  - **Phylogenetic bracketing** predicts features of an ancestor from features of its descendents.

# Maximum Parsimony

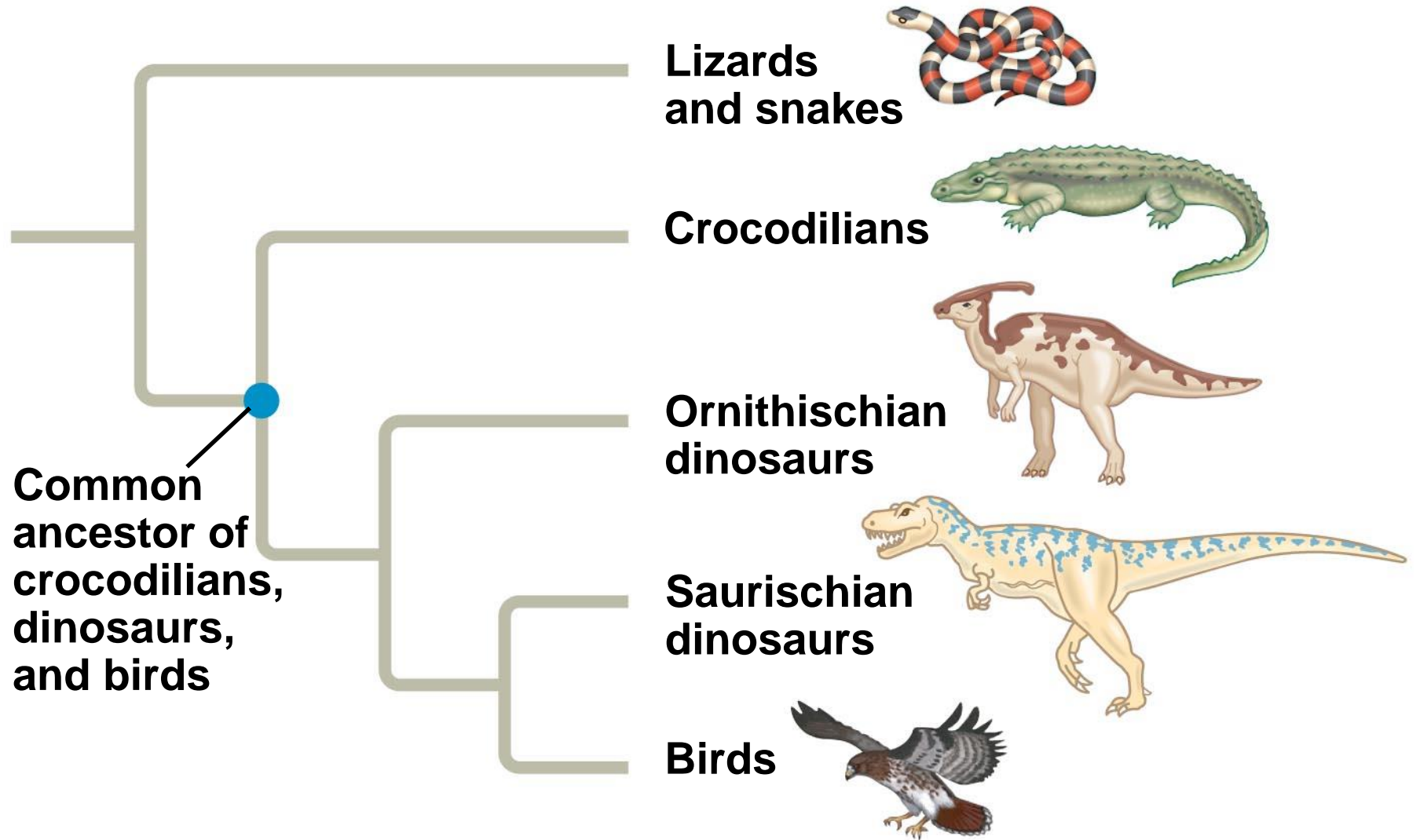
	Human	Mushroom	Tulip
Human	0	30%	40%
Mushroom		0	40%
Tulip			0

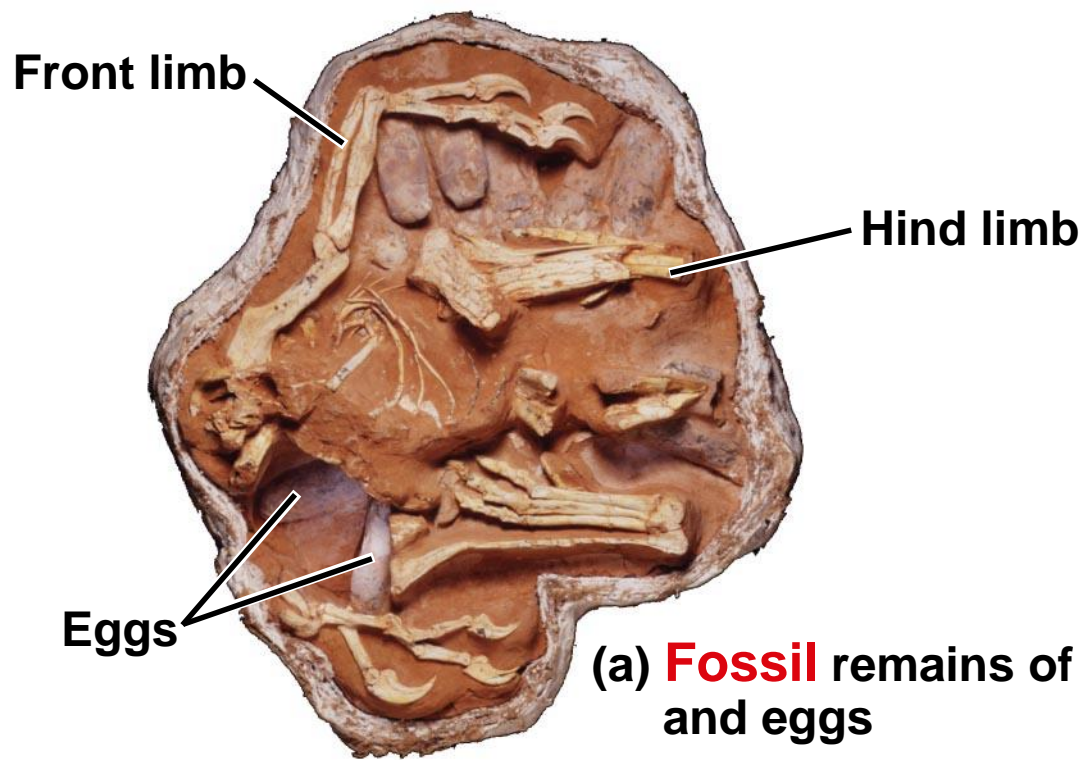
(a) Percentage differences between sequences



(b) Comparison of possible trees

**Phylogenetic bracketing** - predicts features of an ancestor from features of its descendants:





(b) **Artist's reconstruction** of the dinosaur's posture

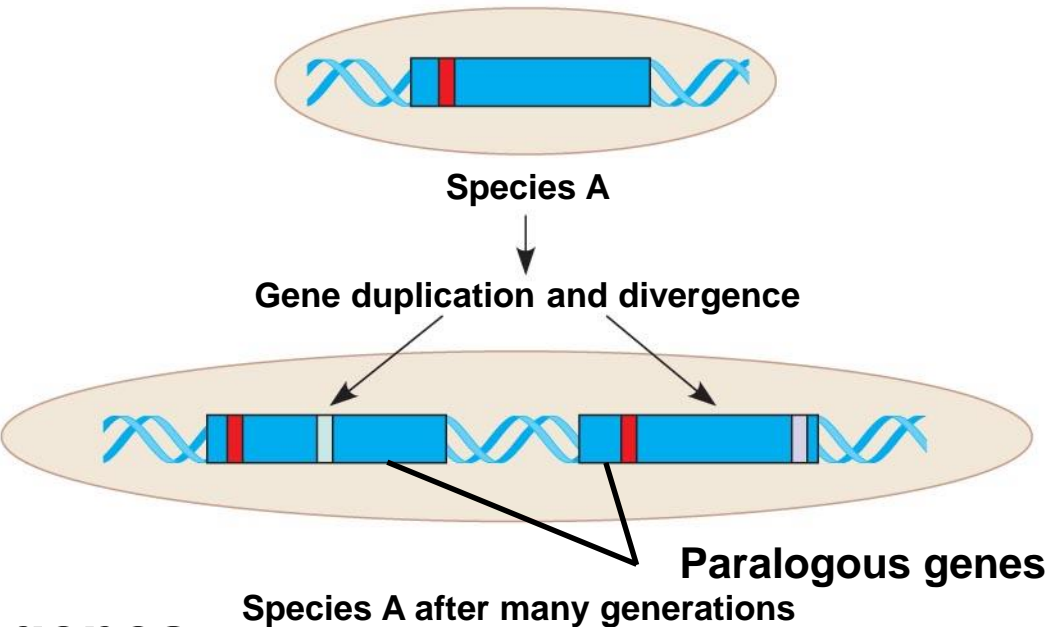
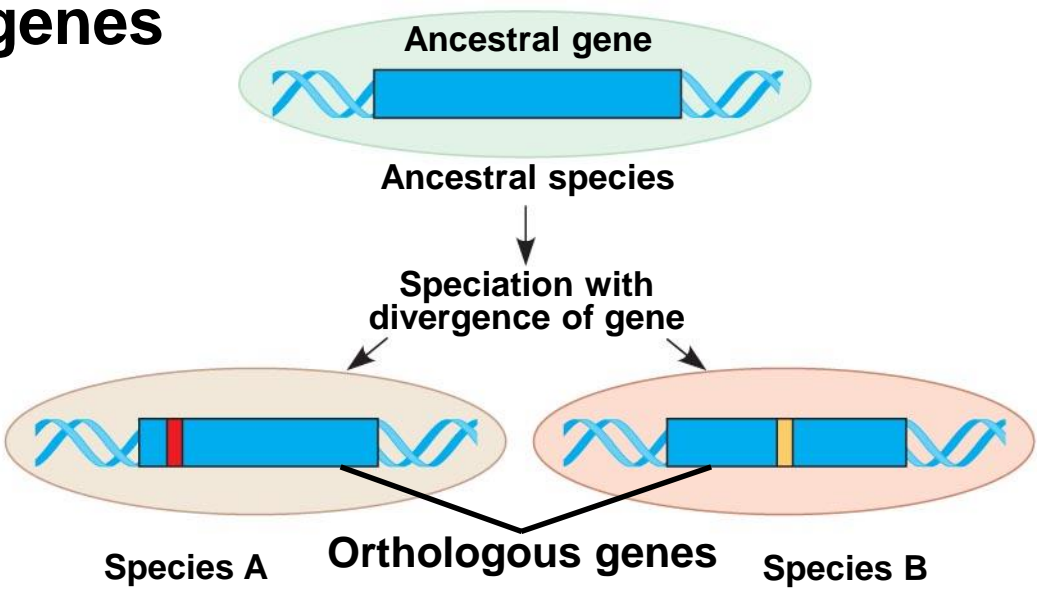
## Concept 26.4: An organism's evolutionary history is documented in its genome

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- **Comparing nucleic acids** or other molecules to infer relatedness is a valuable tool for tracing organisms' evolutionary history.
- **DNA** that codes for **rRNA** changes relatively slowly and is useful for investigating branching points hundreds of millions of years ago.
- **mtDNA** evolves rapidly and can be used to explore recent evolutionary events.
- Gene duplication increases the number of genes in the genome, providing more opportunities for evolutionary changes.

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- Like homologous genes, 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 only after speciation occurs.
  - **Paralogous genes** result from gene duplication, so are found in **more than one copy** in the genome.
  - They can diverge within the clade that carries them and **often evolve new functions**.

# Orthologous genes



# Paralogous genes

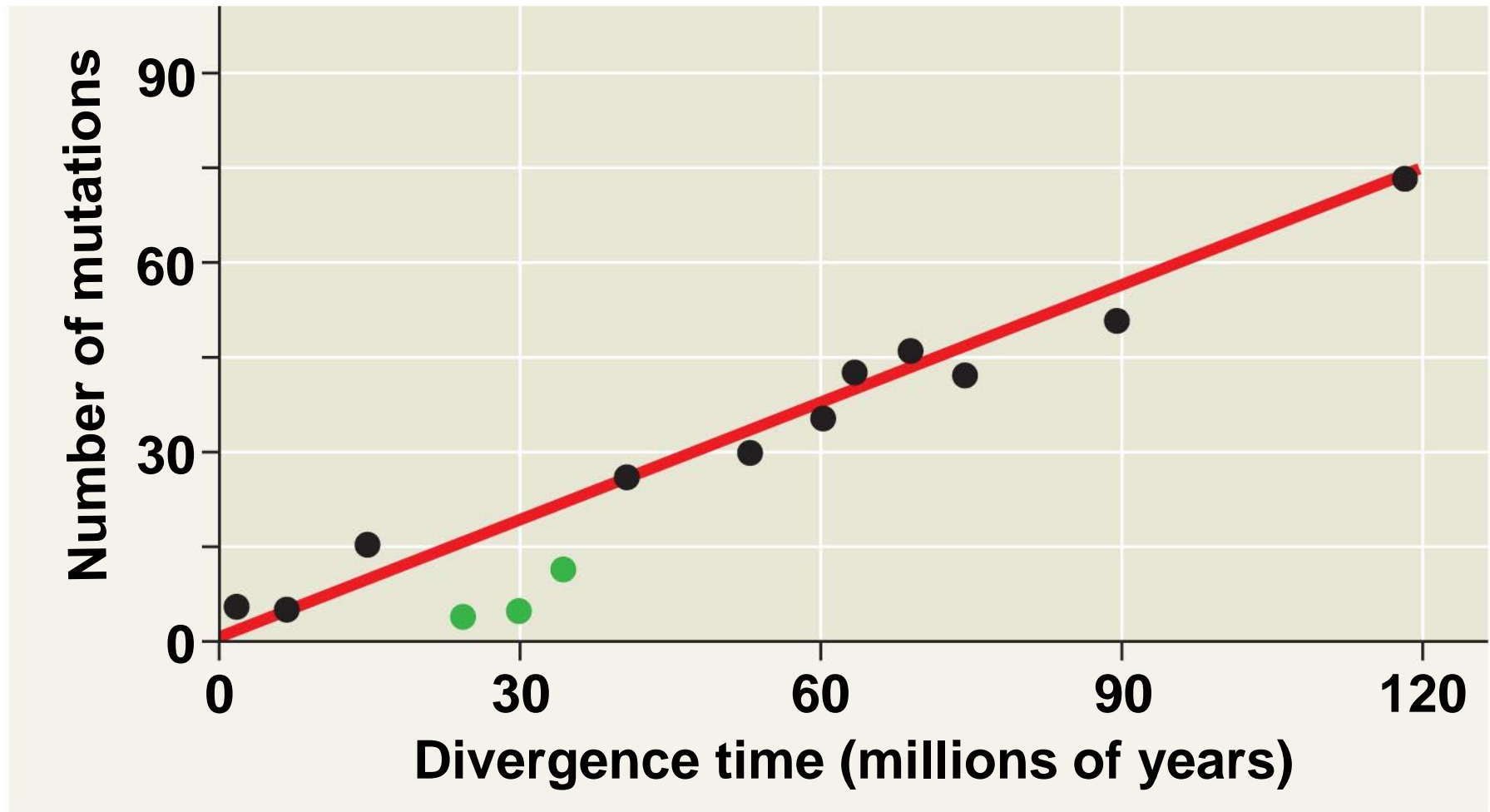


# Molecular Clocks

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- A **molecular clock** uses **constant rates of evolution** in some genes **to estimate** the absolute **time of evolutionary change**.
- Molecular clocks are calibrated against branches whose dates are known from the fossil record.
- **Neutral theory** states that **much evolutionary change** in genes and proteins has **no effect on fitness** and therefore is not influenced by Darwinian selection.
- It states that the **rate of molecular change** in these genes and proteins should be **regular** like a clock.

# Molecular Clocks



# *Difficulties with Molecular Clocks*

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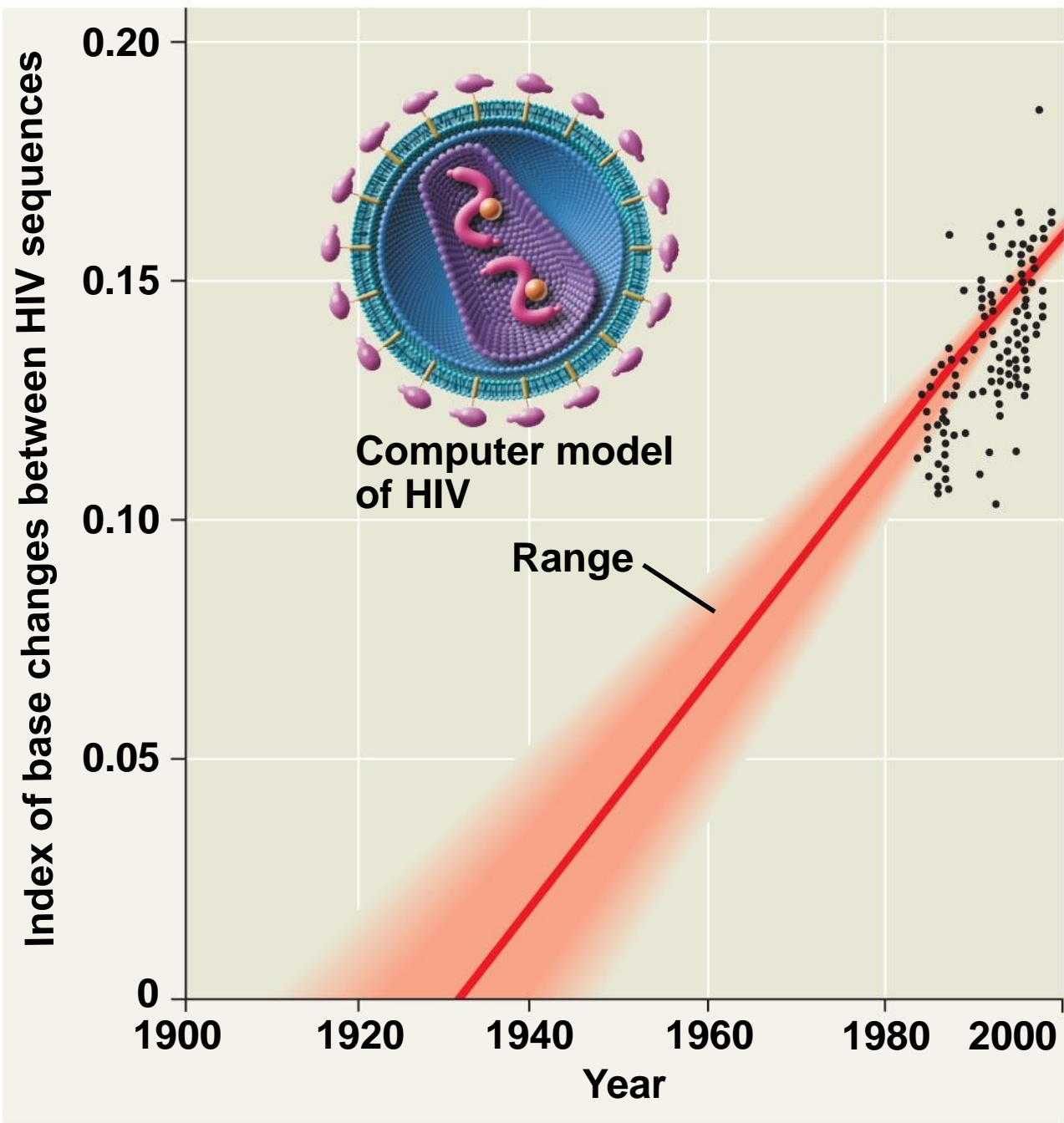
- Irregularities result from **natural selection** in which **some DNA changes are favored over others**.
- Estimates of evolutionary divergences older than the fossil record have a high degree of uncertainty.
- The use of multiple genes may improve estimates.

# Applying a Molecular Clock: The Origin of HIV

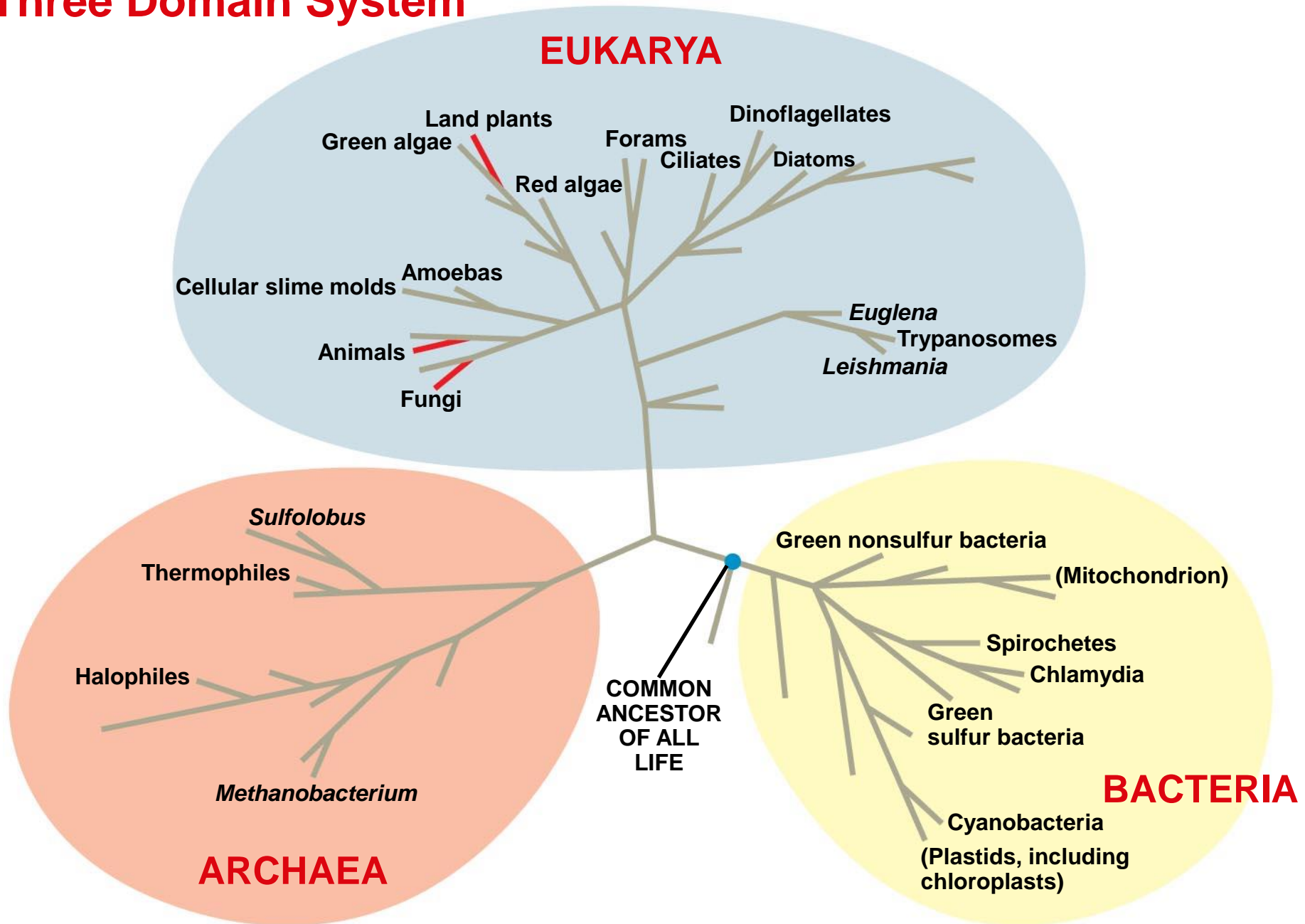
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- Phylogenetic analysis shows that HIV is descended from viruses that infect chimpanzees and other primates.
- Comparison of HIV samples throughout the epidemic shows that the virus evolved in a very clocklike way.
- Application of a molecular clock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

# HIV Virus



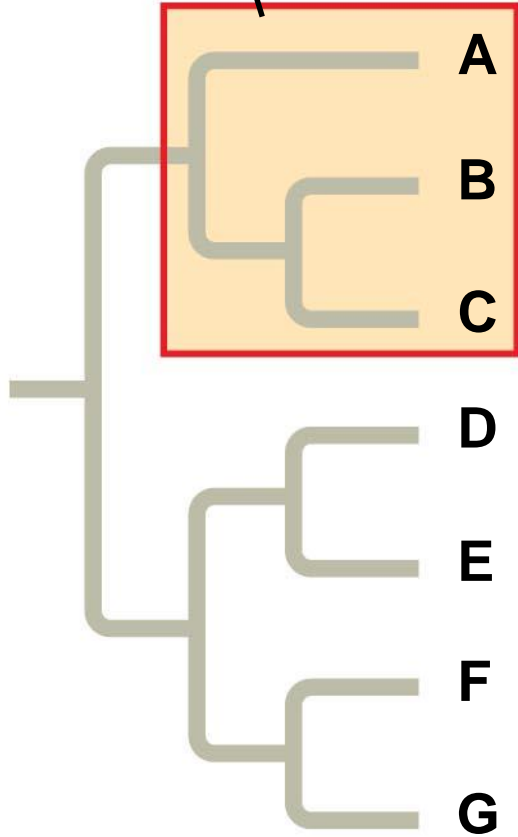
# Three Domain System



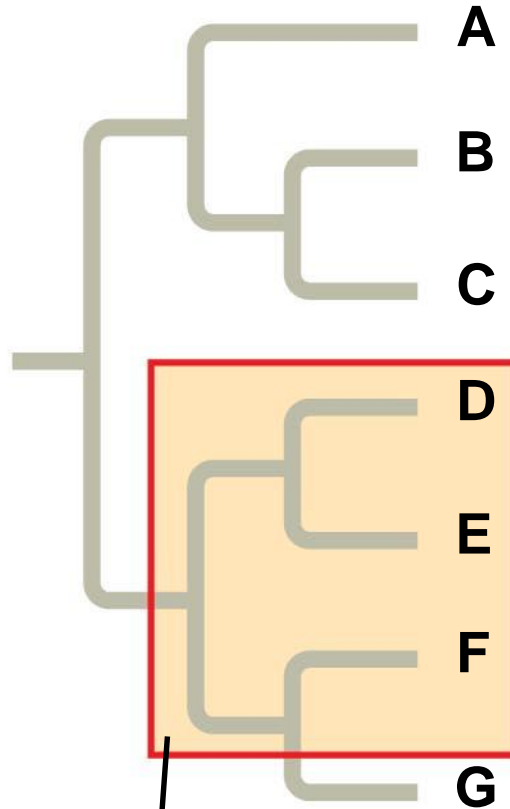
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- There have been substantial interchanges of genes between organisms in different domains.
  - **Horizontal gene transfer** is the movement of genes from one genome to another.
  - Horizontal gene transfer **complicates efforts to build a tree of life.**
  - Some researchers suggest that eukaryotes arose as an endosymbiosis between a bacterium and archaean.

# Review

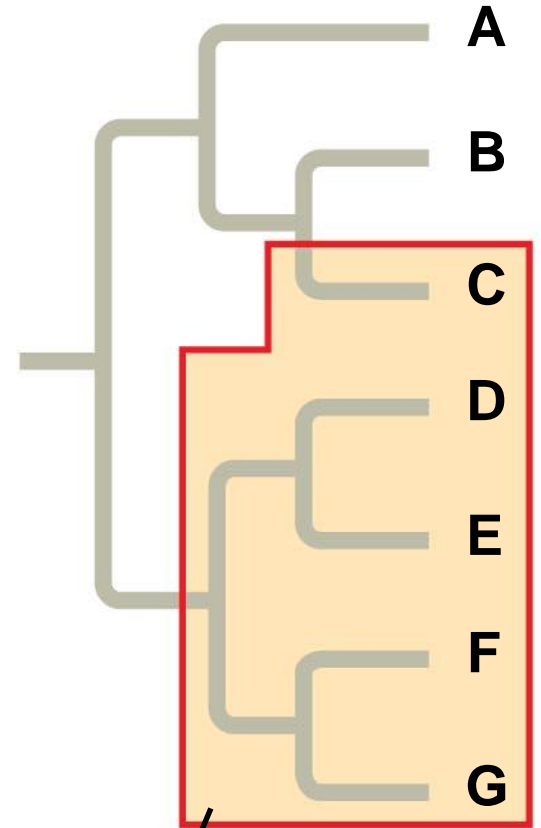
**Monophyletic group**



**Paraphyletic group**



**Polyphyletic group**





# Clades - Characters

Character	SPECIES						
	<i>Lancelet (outgroup)</i>	<i>Lamprey</i>	<i>Tuna</i>	<i>Salamander</i>	<i>Turtle</i>	<i>Leopard</i>	<i>Dolphin</i>
Backbone	0	1	1	1	1	1	1
Hinged jaw	0	0	1	1	1	1	1
Four limbs	0	0	0	1	1	1	1*
Amniotic egg	0	0	0	0	1	1	1
Milk	0	0	0	0	0	1	1
Dorsal fin	0	0	1	0	0	0	1

\*Although adult dolphins have only two obvious limbs (their flippers), as embryos they have two hind-limb buds, for a total of four limbs.

# You should now be able to:

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1. Explain the justification for taxonomy based on a PhyloCode.
2. Explain the importance of distinguishing between homology and analogy.
3. Distinguish between the following terms: monophyletic, paraphyletic, and polyphyletic groups; shared ancestral and shared derived characters; orthologous and paralogous genes.
4. Define horizontal gene transfer and explain how it complicates phylogenetic trees.
5. Explain molecular clocks and discuss their limitations.