

PHYLOGENY & THE TREE OF LIFE



PREFACE

- ❖ In this powerpoint we learn how biologists distinguish and categorize the millions of species on earth.
- ❖ Early we looked at the *process* of evolution here we look at the *patterns* of evolution.
- ❖ Specifically we will look at **phylogeny**, or the evolutionary history of a species or group of species.
- ❖ To construct these “histories” we will utilize **systematics**, a discipline focused on classifying organisms and determining evolutionary relationships.

PHYLOGENY

I. Main Idea:

This section explores **taxonomy**, the naming and classifying of organisms and later we explore how their evolutionary relatedness is derived.



Binomial Nomenclature

- ❖ To avoid ambiguity when communicating about organisms scientists use Latin scientific names.

Chrysaora fuscescens



Jellyfish
(cnidarian)

Paranephrops planifrons



Crayfish
(crustacean)

Lepisma saccharina



Silverfish
(insect)

Binomial Nomenclature

- ❖ The two part format is commonly called binomial nomenclature (18th century, C. Linnaeus).
- ❖ The first part is the genus (genera)...capitalized and italicized
- ❖ The second part is the species...italicized

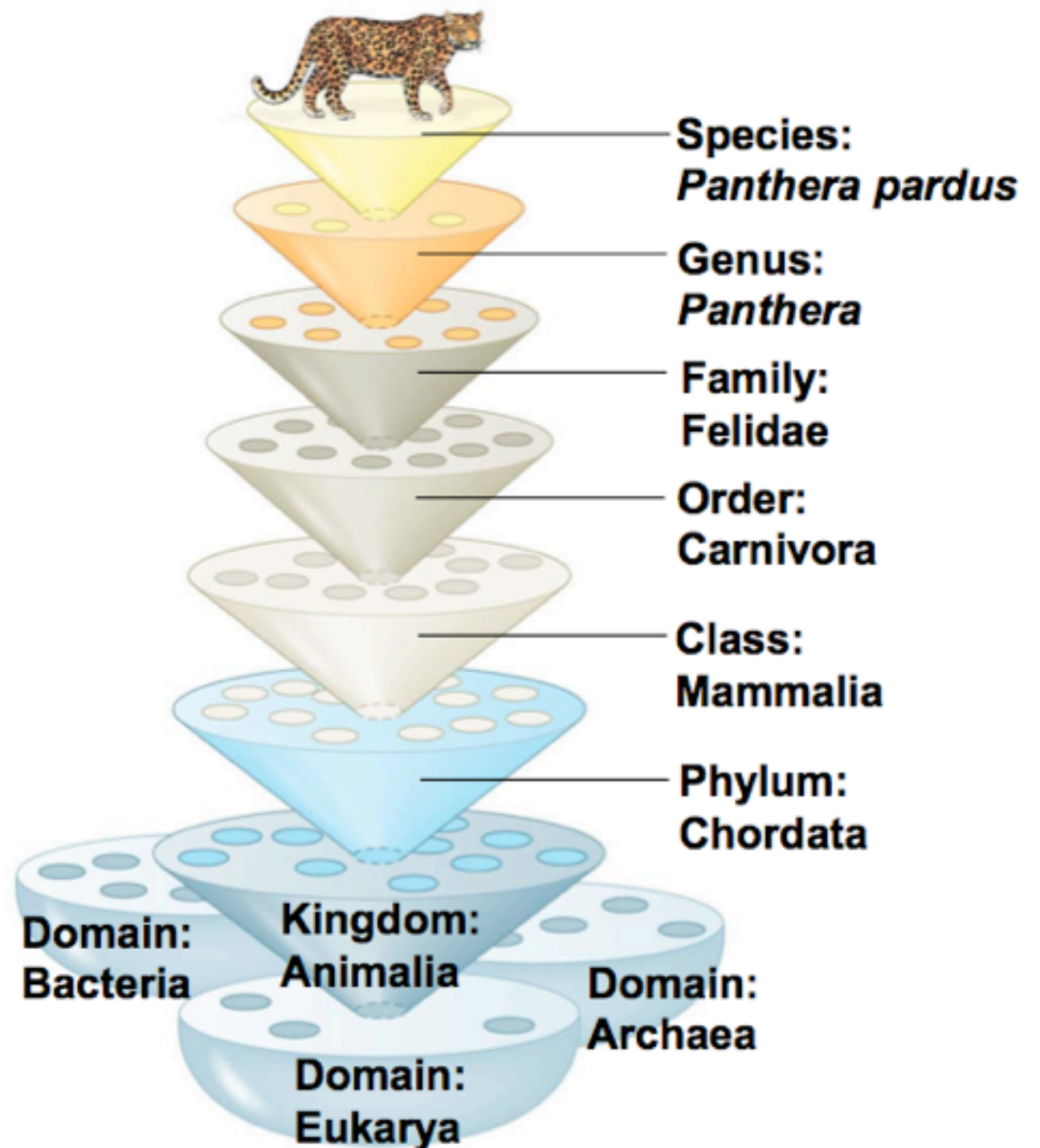
Homo sapiens

“man wise”

Hierarchical Classification

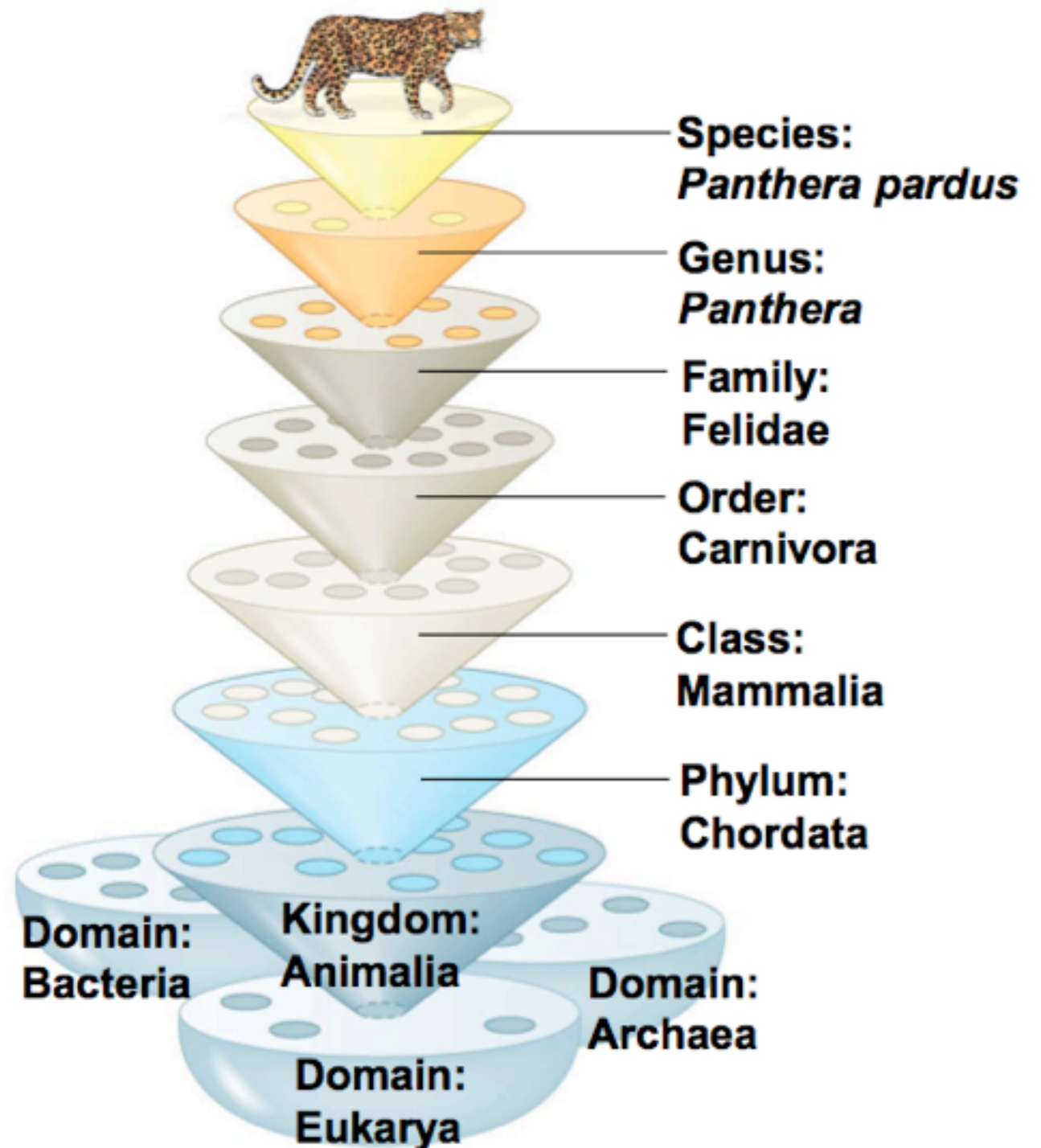
- ❖ In addition to a naming system Carolus Linnaeus also developed a grouping system that relied on a hierarchy of groups of increasing inclusivity.

**Domains have
recently been added**



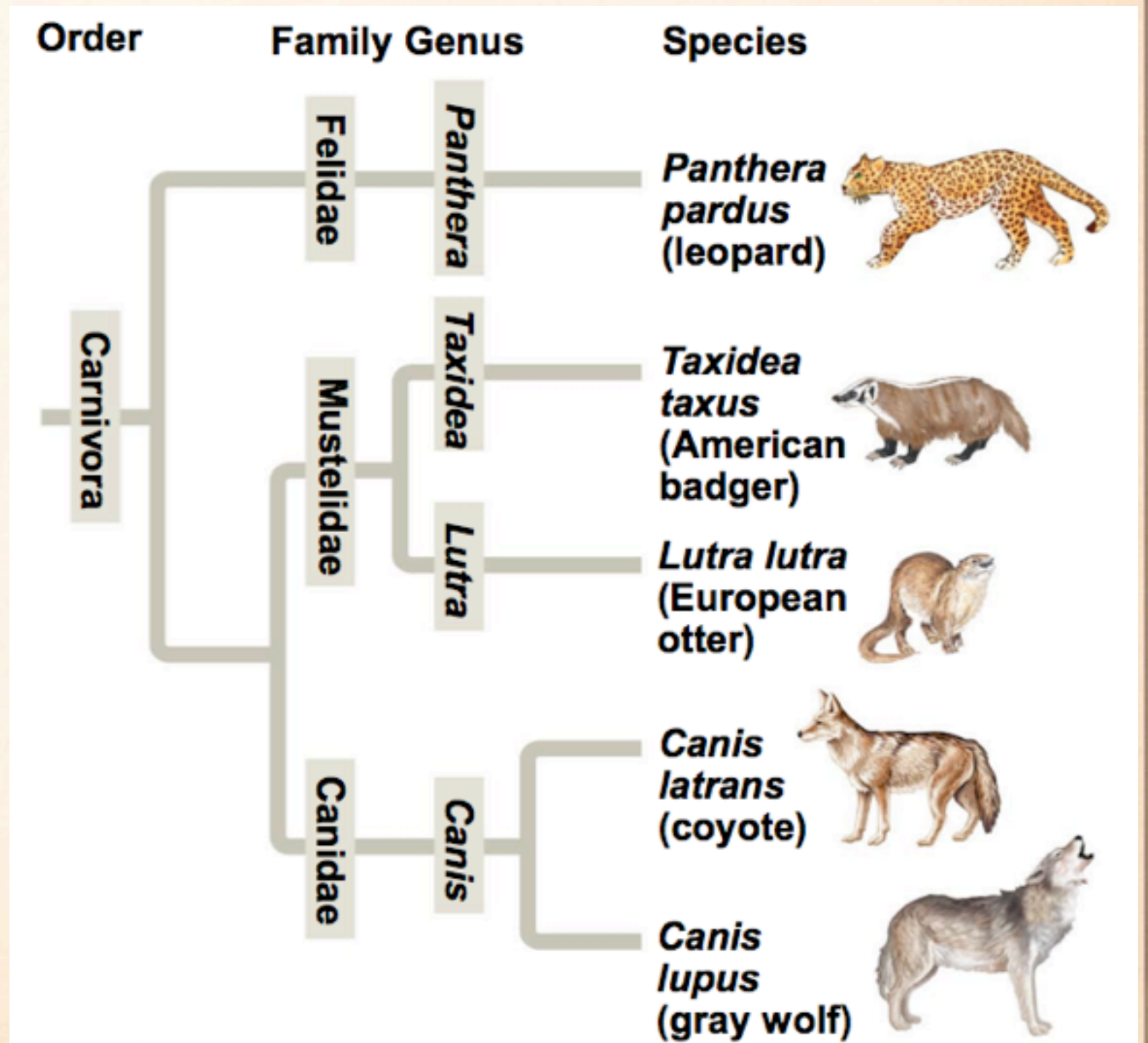
Hierarchical Classification

- ❖ Each level is called a **taxon**, taxons are not italicized, just capitalized.
- ❖ This system, structures life into a human view of the world.
- ❖ This system, does not necessarily reflect evolutionary relationships between groups.

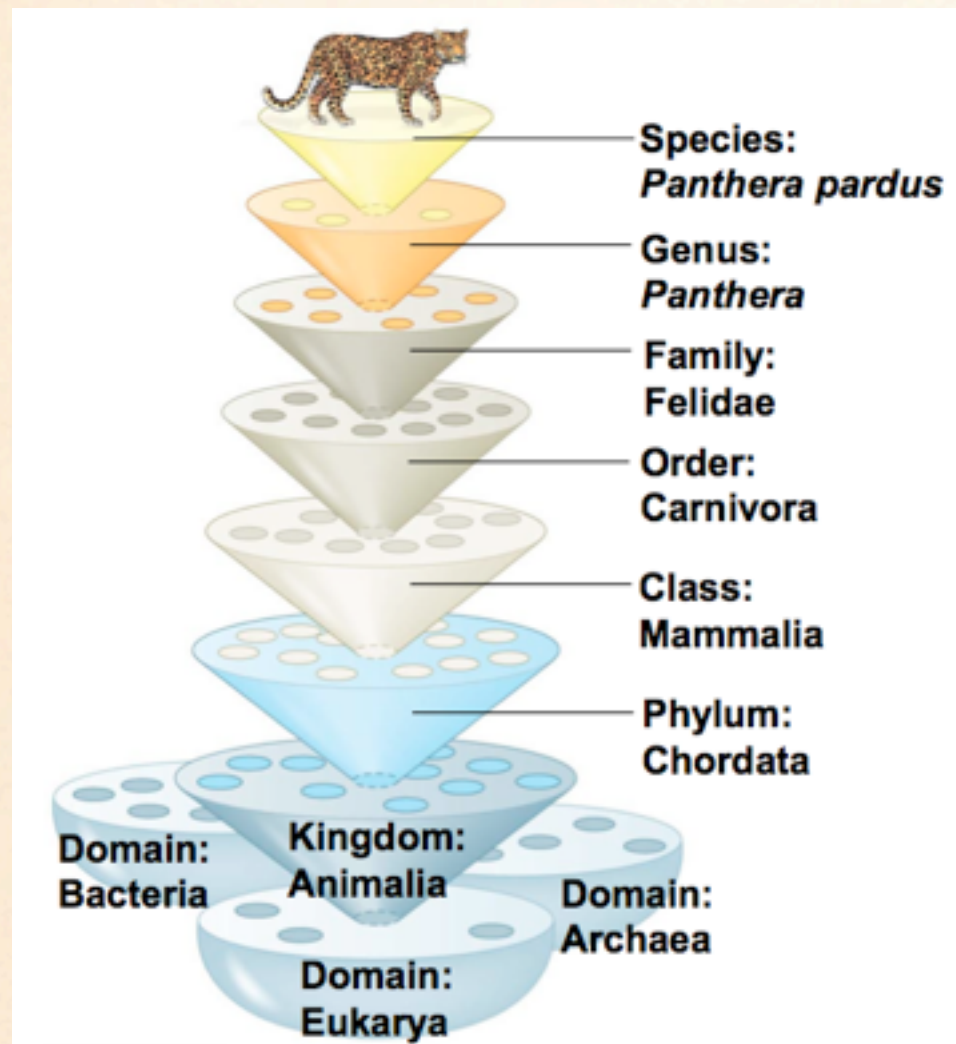


Linking Classification & Phylogeny

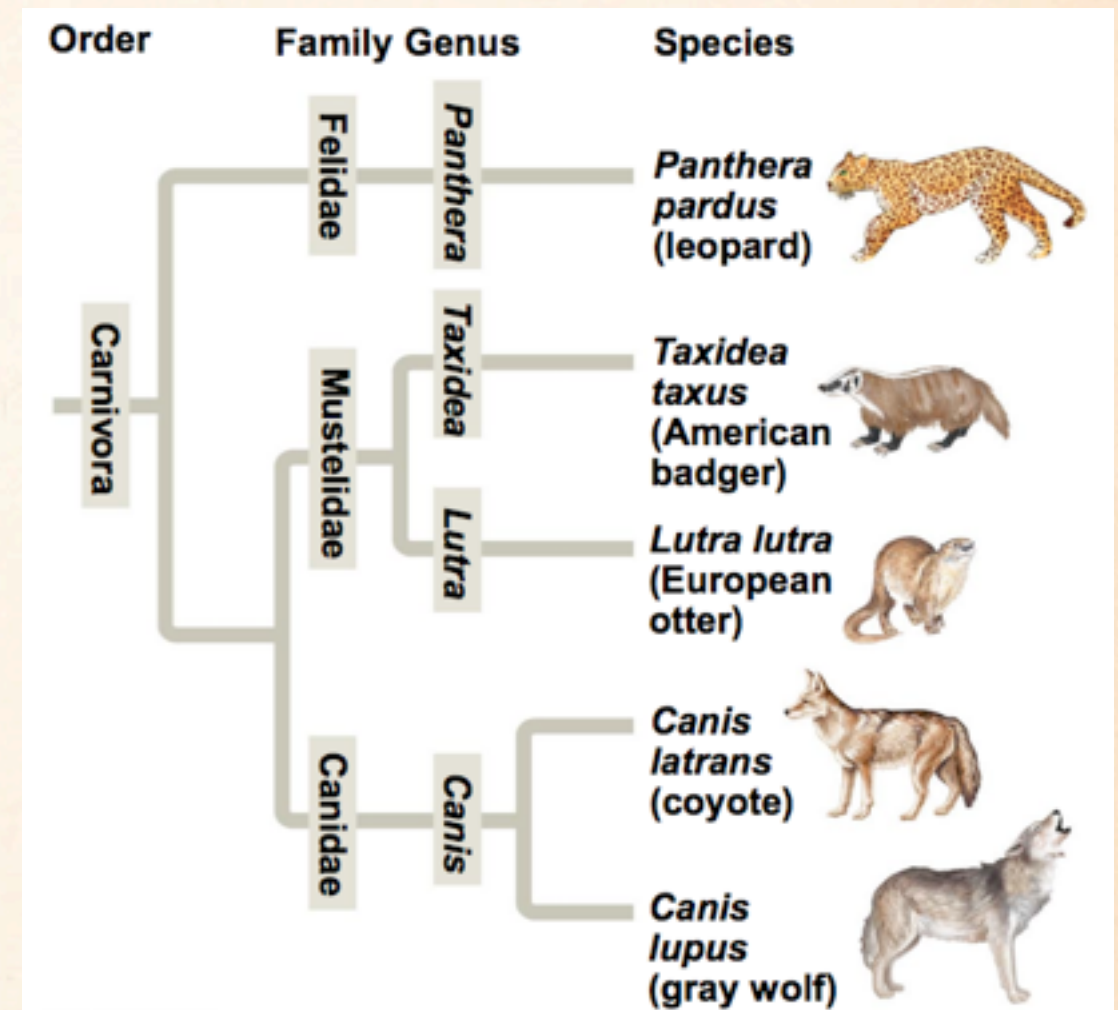
- ❖ The evolutionary history of a group of organisms can be represented in a branching diagram called a **phylogenetic tree**



- ❖ Often the branching pattern match the nesting relationships of the taxons, sometimes however taxonomists classify a species into a group to which it is not closely related.



VS.

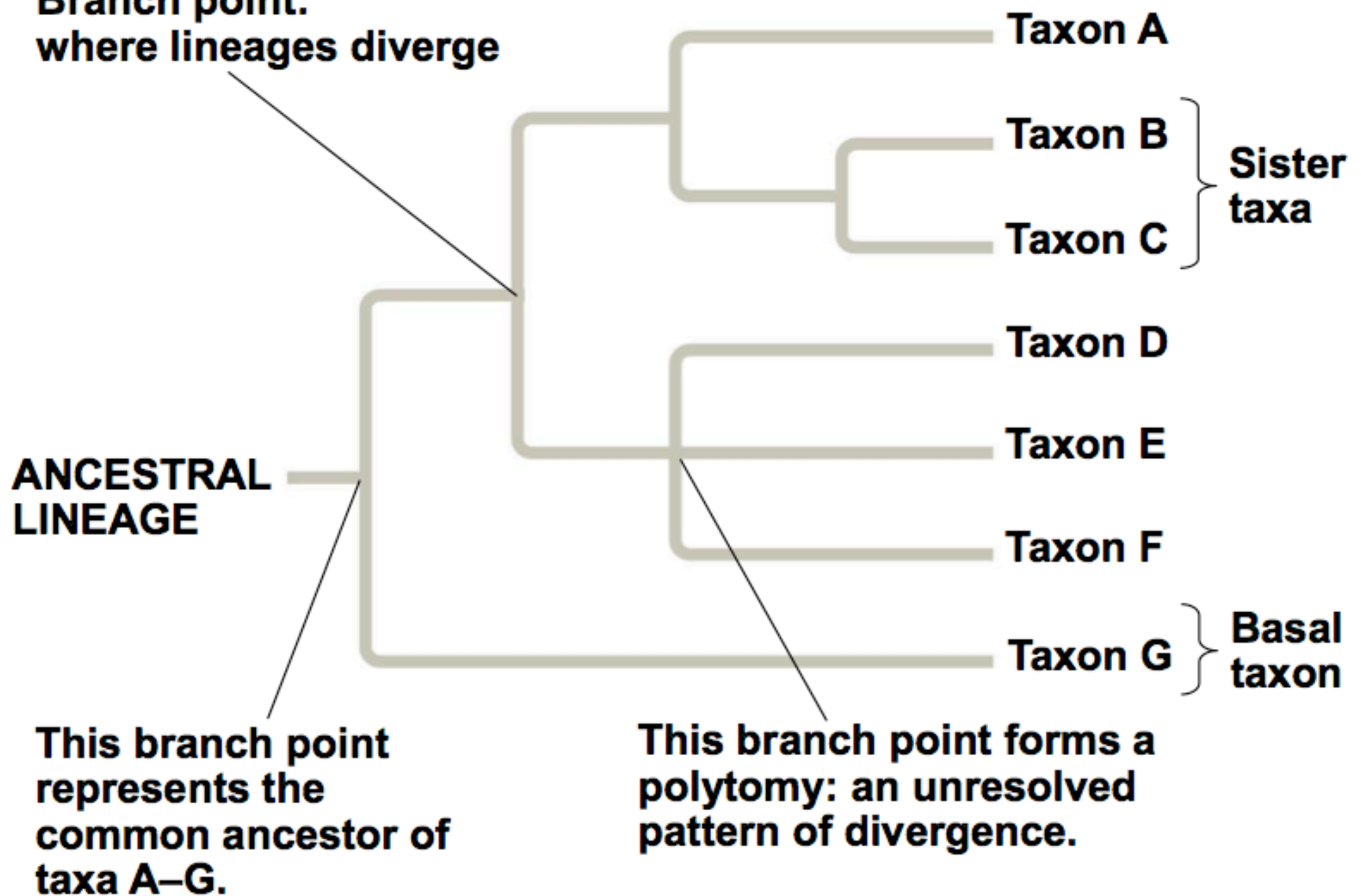


- ❖ One reason for this disagreement may lie in the fact a species lost a key feature shared by its close relatives, if DNA or other evidence supports this the species will be reclassified.

- ❖ In fact to avoid these disagreements some systematists have suggested a classification based entirely on evolutionary relationships a system called the...
- ❖ **PhyloCode** where groups would include a common ancestor and all its descendants.
- ❖ it would change how taxa are defined and recognized
- ❖ groups would no longer have ranks assigned to them
- ❖ their names would remain the same

- ❖ **Regardless of which one is used, 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
- ❖ A **rooted** tree includes a branch to represent the last common ancestor of all taxa in the tree

**Branch point:
where lineages diverge**



What can we can learn, what we cannot learn from Phylogenetic trees

- ❖ **First, phylogenetic trees are intended to show patterns of decent NOT phenotypic similarity.**
- ❖ **Second, the sequence of branching shows only the pattern of descent** they do NOT necessarily indicate the actual or absolute ages of a particular species
- ❖ **Third, the common ancestors in a tree are extinct and they were distinct from todays extant species,** it should NOT be assumed that a taxon evolved from the taxon next to it.

Applying Phylogenies

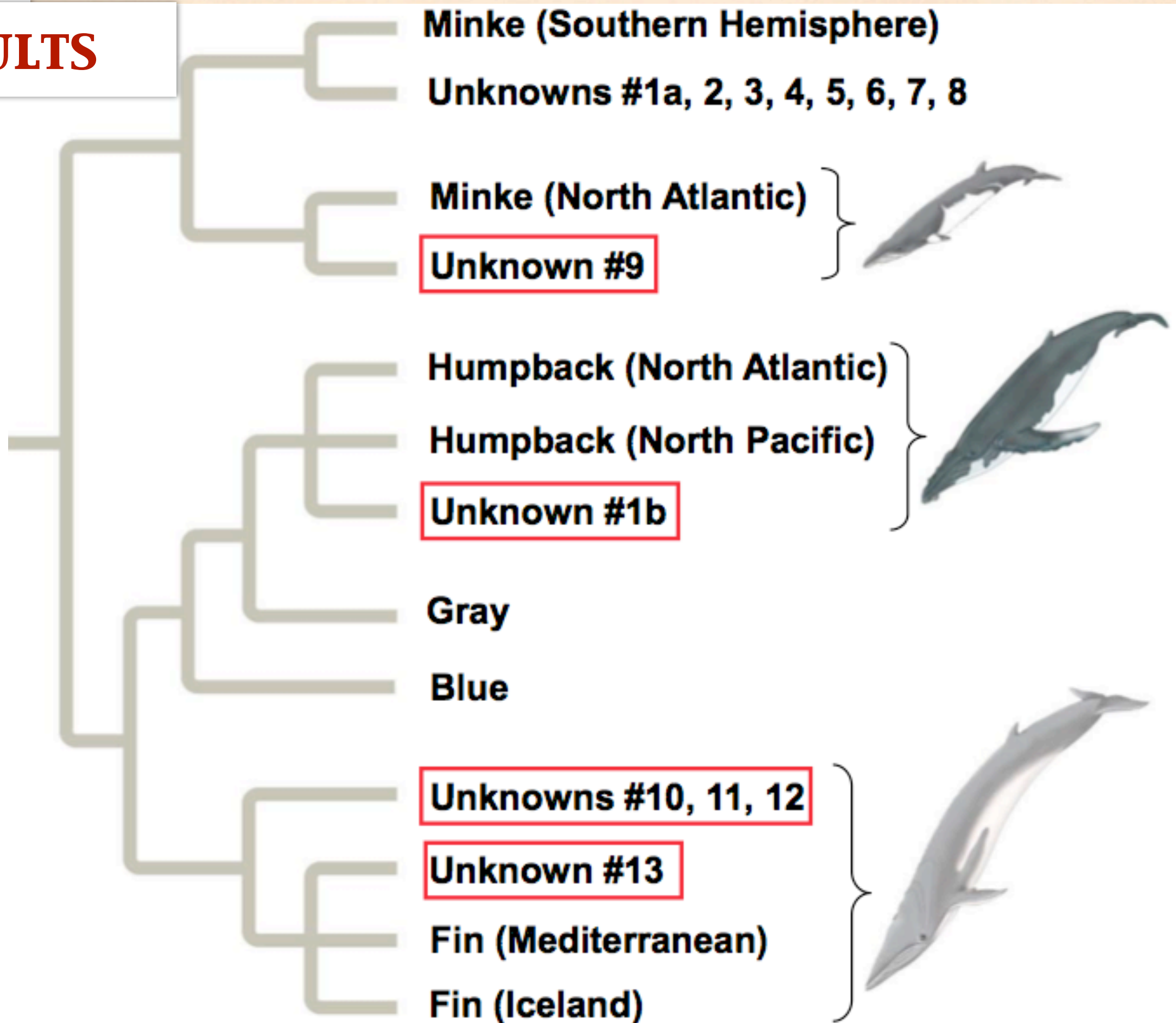
- ❖ Phylogeny provides important information about similar characteristics in closely related species
- ❖ Because phylogenies use DNA data to help create them we can use phylogenetic trees to identify closely related species
- ❖ Understanding phylogeny can have practical applications.

Application

EXPERIMENT

C.S. Baker (Univ. of Auckland) and S.R. Palumbi (Univ. of Hawaii) purchased 13 samples of “whale meat” from Japanese fish markets. They sequenced a specific part of the mitochondrial DNA from each sample and compared their results with comparable DNA sequence from known whale species. To infer identity of each sample, they constructed a gene tree, a phylogenetic tree that shows patterns of relatedness among DNA sequences rather than among taxa.

RESULTS



Application

CONCLUSION

This analysis indicated that DNA sequences of six of the unknown samples (in red) were most closely related to DNA sequences of whales that are NOT LEGAL to harvest.

PHYLOGENY

II. Main Idea:

The generate phylogenetic trees systematists gather information about morphology, biochemistry and of course genes.



Morphological & Molecular Homologies

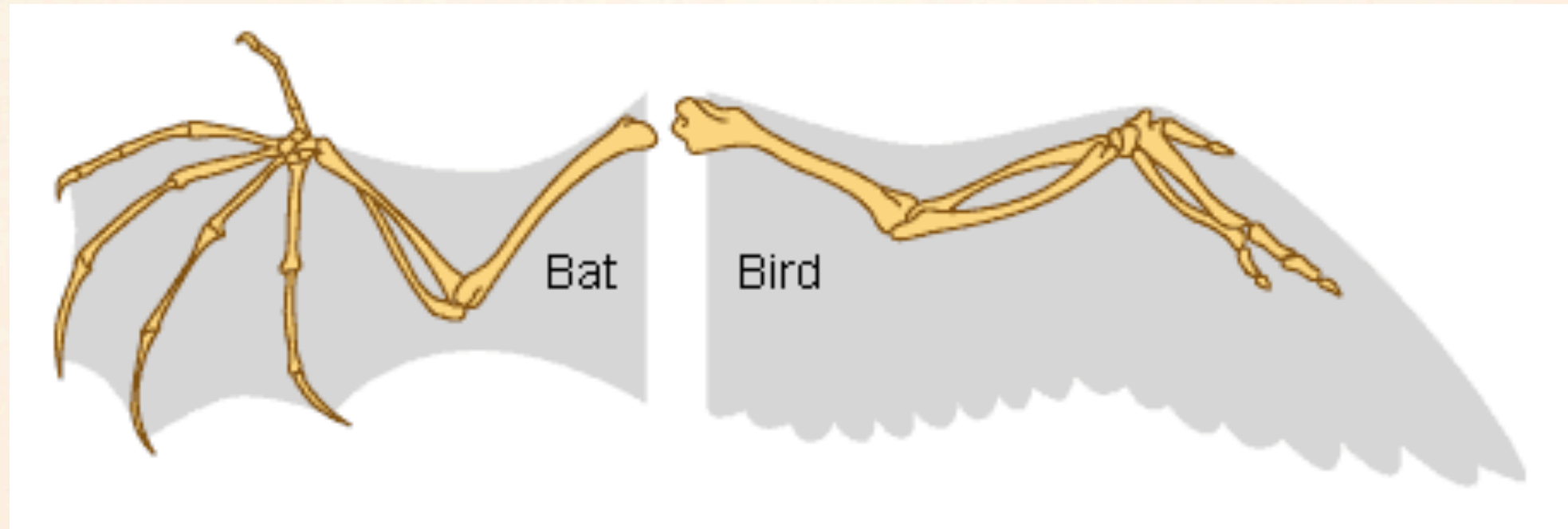
- ❖ Recall **Homologies**- phenotypic and genotypic similarities due to shared ancestry.
- ❖ In general organisms that share similar morphology or DNA are likely to be more closely related than others that do not share these similarities.
- ❖ Sometimes strikingly different looking organisms share much the same DNA sequences or vice versa and provides challenge to those trying to construct accurate phylogenetic trees.

Sorting Homology from Analogy

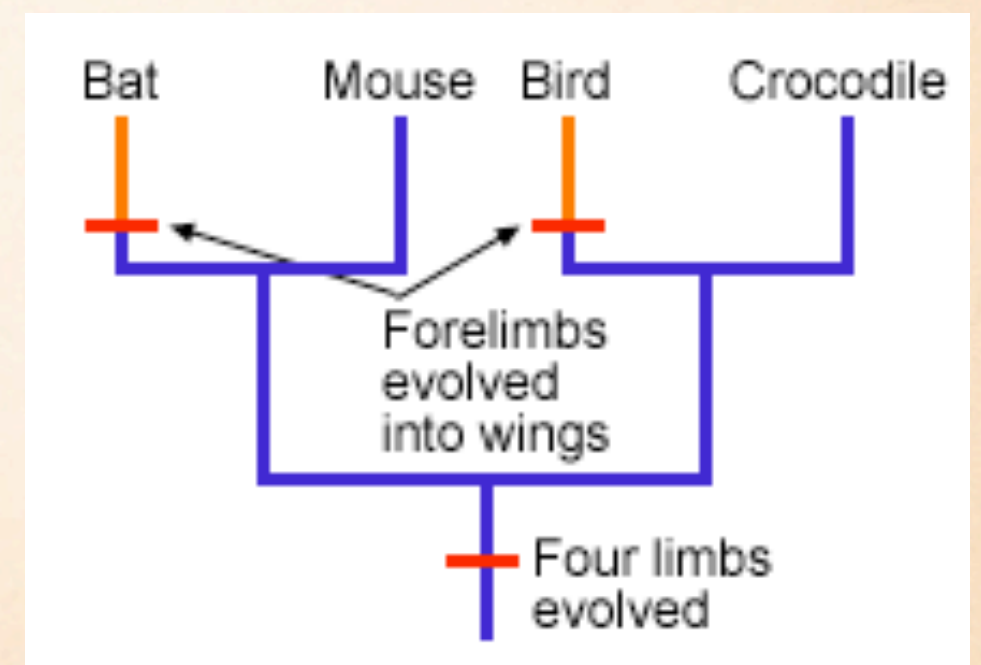
- ❖ One major obstacle in generating phylogenetic trees is distinguishing between homology and analogy.
- ❖ Recall Analogy results when organisms are similar due to convergent evolution not because of recent shared ancestry.
- ❖ Recall Convergent Evolution occurs when similar environmental pressures and natural selection produce similar adaptations in organisms from different lineages.



- ❖ Analogous structures that arose independently are also called **homoplasies**.



- ❖ The bat wing consists of stretched skin while the bird uses feathers for flight.
- ❖ Ironically birds are more related to crocodiles than bats.



Sorting Homology from Analogy

- ❖ Another clue in distinguishing between homology and analogy lies in the complexity of the characters being compared.
- ❖ The more elements that are similar in a two complex structures the more likely share a recent common ancestor
- ❖ The same argument can be made at the level of the gene.

Evaluating Molecular Homologies

- ❖ Comparing DNA sequences between organisms is likely the best way to establish relatedness but it also poses the greatest technological challenges as well.
- ❖ To start with DNA in each organism has to be sequenced (challenging by itself but science is better at sequencing everyday and to date has sequenced over 100 billion bases from 1000's of species).
- ❖ Next these sequences must be compared (perhaps even more challenging)
- ❖ In general, the more the sequences align the more similar they are

Species 1

Species 2

..**A**TACGGATACGG..

..**T**TACGGATACGG..

..**T**ACGGATACGG**G**..

..**T**TACGGATACGG..

Now the sequence looks very different, when in fact only a single base deletion represents the difference

To address such problems researchers have developed computer programs and statistical tools that estimate the best way to align comparable DNA segments of differing lengths and differentiate among molecular homoplasies.

PHYLOGENY

III. Main Idea:

The method used to infer phylogeny is called cladistics, an approach that uses common ancestry as its primary criterion for classifying organisms.

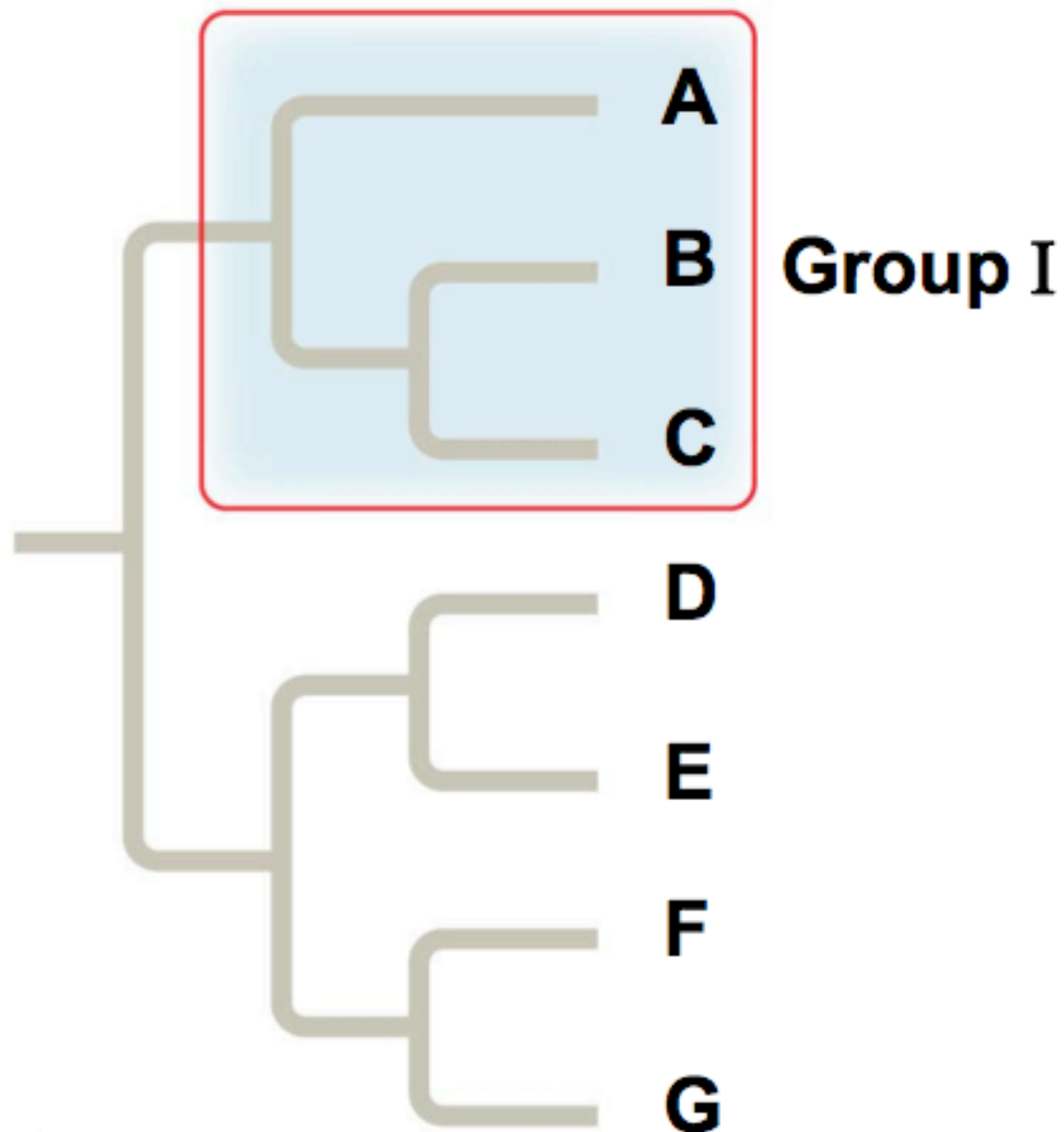


Cladistics

- ❖ One approach to classify organisms relies on a system called **cladistics** where organisms are primarily classified together by common ancestry.
- ❖ In this approach systematists attempt to place species into groups called **clades**, each clade includes the common ancestor and all its descendants.
- ❖ Like taxonomic groups clades are nested within larger clades
- ❖ There are 3 types of clades.
 - ❖ **monophyletic, paraphyletic, polyphyletic**

Types of Clades

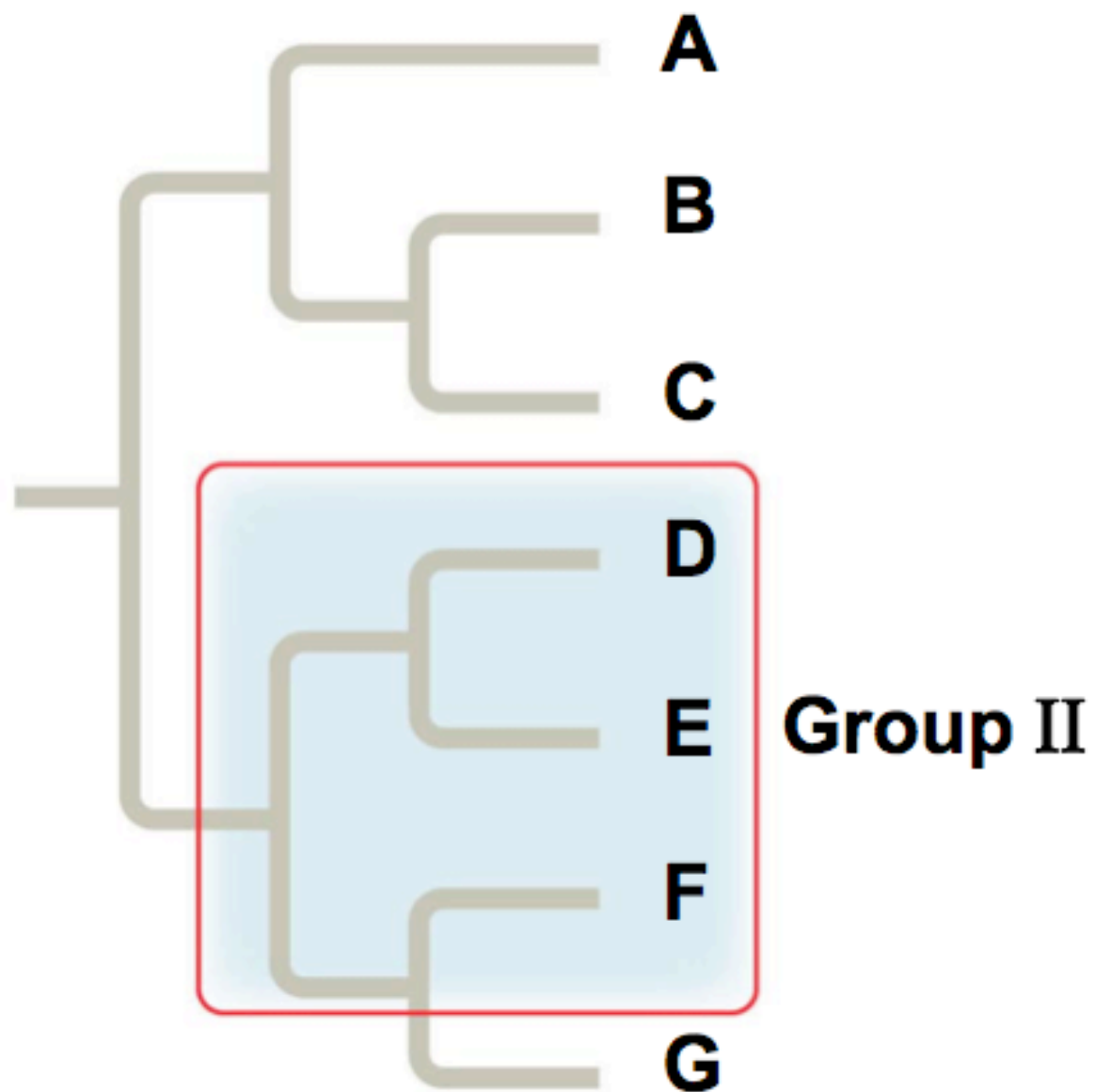
(a) Monophyletic group (clade)



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

Types of Clades

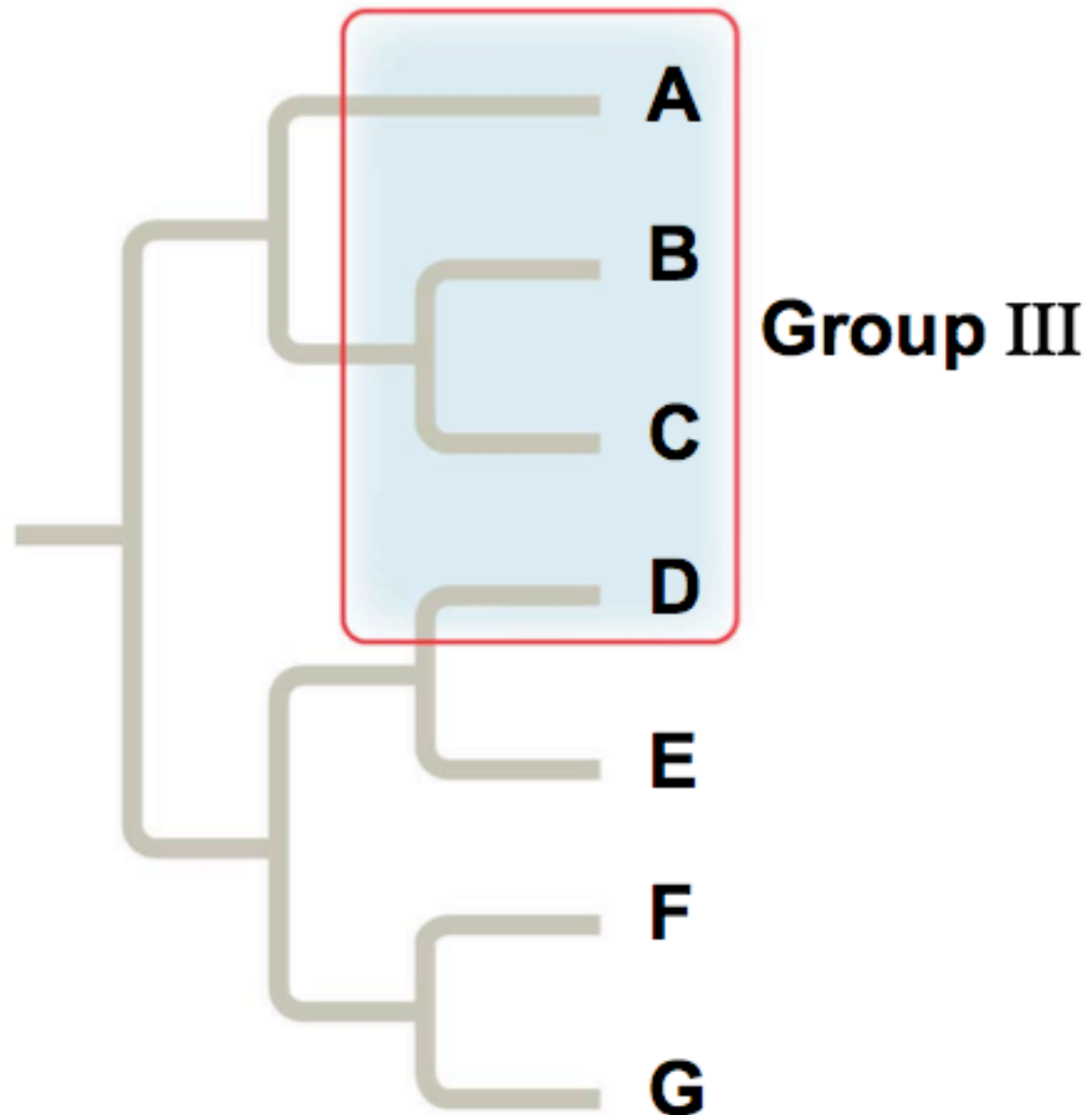
(b) Paraphyletic group



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

Types of Clades

(c) Polyphyletic group



A polyphyletic
grouping consists of
various species with
different ancestors

Ancestral & Derived Characters

- ❖ As a result of evolution, organisms both share traits and have their own unique traits compared to their ancestors.
- ❖ **Shared Ancestral Character**, one that originates in the ancestor of the group, taxon or clade
 - ❖ Backbone in mammals, shared by all mammals including its common ancestor
 - ❖ thus backbones predate the branching of mammals from other vertebrates

Ancestral & Derived Characters

- ❖ As a result of evolution, organisms both share traits and have their own unique traits compared to their ancestors.
- ❖ **Shared Derived Character**, a novel trait is unique to a group, taxon or clade
- ❖ Hair in mammals, shared by all mammals but not found in the common ancestor of mammals
- ❖ *Ancestral & Derived traits are relative...remember the backbone example... if you go back to a deeper branch point you could find this trait separating vertebrates from other animals thus it now becomes derived*

Inferring Phylogenies using Derived Characters

- ❖ Shared derived characters are unique to particular clades.
- ❖ All characters arose at some point in the history of life,
- ❖ It should be possible to determine the clade in which a derived character first appeared
- ❖ Then using information about shared derived characters one can begin to infer evolutionary relationships, or construct a phylogeny

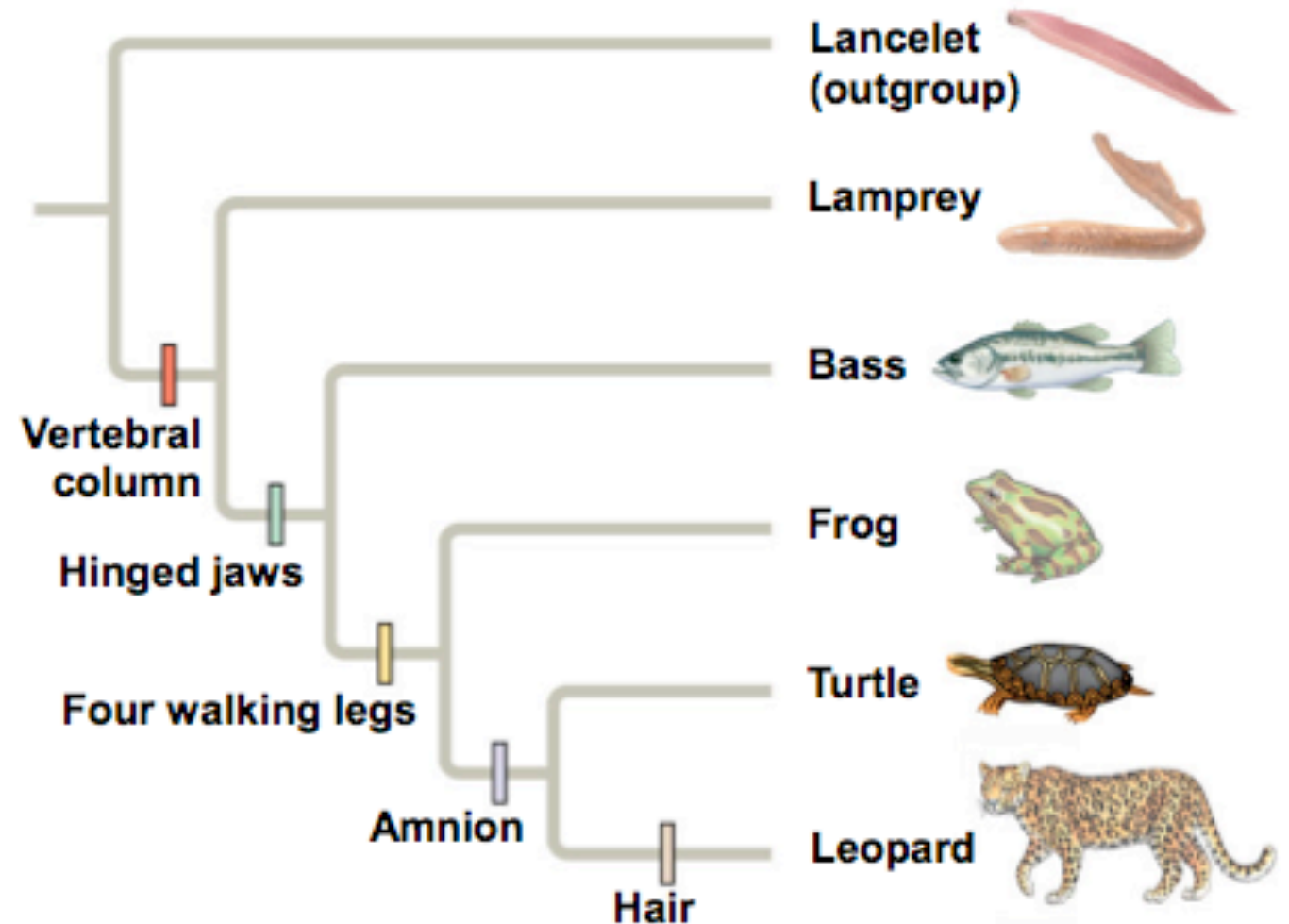
Inferring Phylogenies using Derived Characters

- ❖ Start by selecting an outgroup as a basis of comparison.
- ❖ **Outgroup** is a species or group of species from lineage that is known to have diverged before the **Ingroup**, the species that are being studied.
- ❖ A suitable outgroup can be determined by morphology, paleontology, embryology or gene sequences.
- ❖ Comparing members of the ingroup with each other and the outgroup, we can deduce which characters were derived at various branch points

Inferring Phylogenies using Derived Characters

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

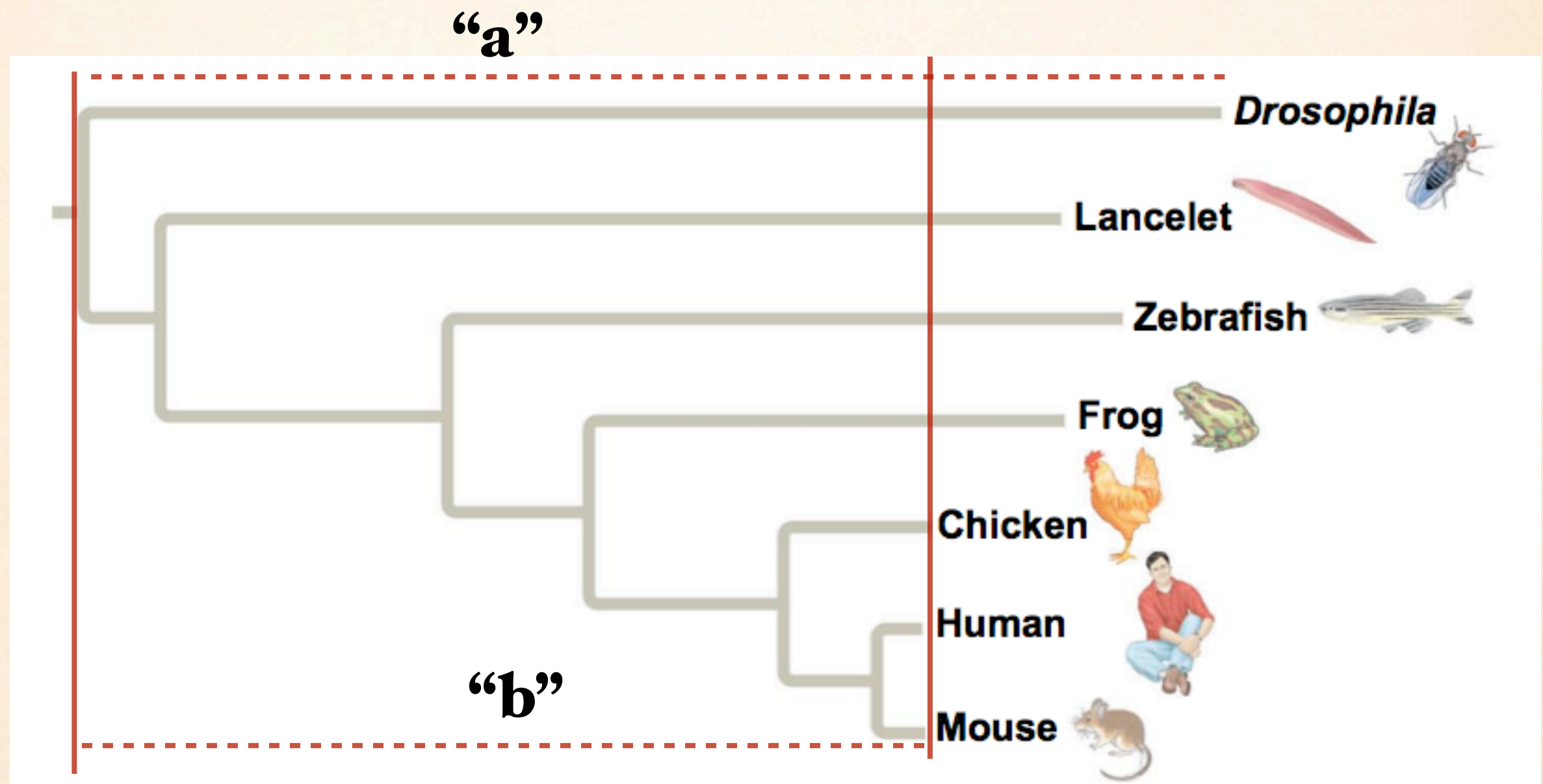


(b) Phylogenetic tree

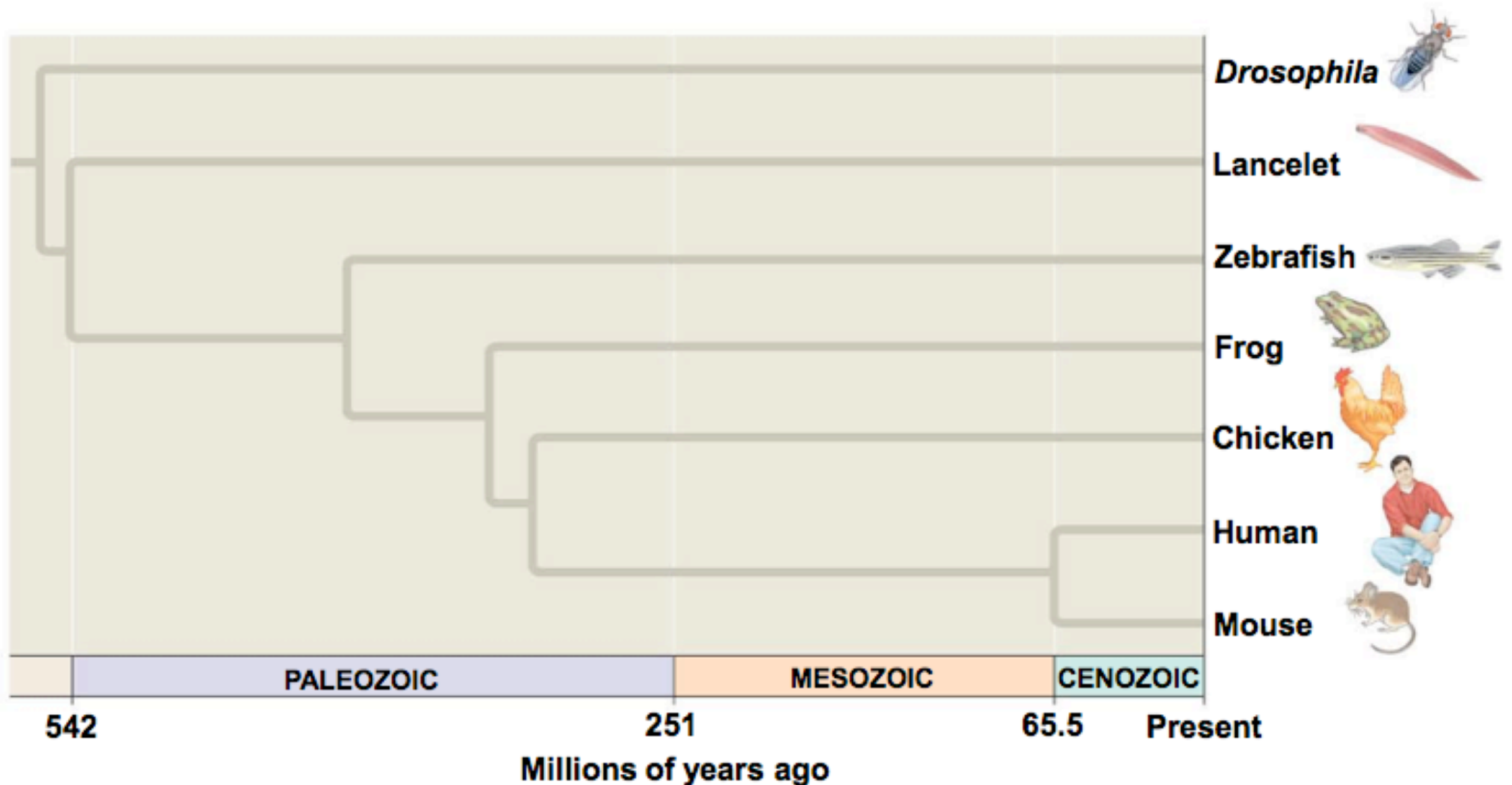
Phylogenetic Trees with Proportional Branch Lengths

- ❖ The phylogenetic trees presented thus far and most that you will likely encounter are “relative”, the branches do NOT indicate degrees of change.
- ❖ They are also “relative” in time, the branching pattern does NOT reflect absolute time but rather relative time in the sense that one event happened earlier than another.
- ❖ However, some phylogenetic trees are built to show degrees of change, absolute time or both.

- ❖ Line “**a**” is longer than line “**b**” this implies that more genetic changes occurred in the fruit fly lineage than in the mouse lineage from the time they diverged from a common ancestor to present.



- ❖ This tree was developed using fossil data, its branch lengths are proportional to absolute time, all lineages have diverged from the common ancestor for equal amounts of time.



Maximum Parsimony & Maximum Likelihood

- ❖ A growing database of gene sequences allows systematists to better develop phylogenies however the wealth of data are also makes it more difficult.
- ❖ In studying just 50 species there are 3×10^{76} different ways to arrange the trees, Which of these trees is the correct one?
- ❖ Science can never know for certain, but they can get close by narrowing the possibilities by applying the principles of maximum parsimony and maximum likelihood.

Maximum Parsimony

- ❖ The principle of **maximum parsimony**, states that one should first investigate the simplest explanation that is consistent with the facts, also called “Occam’s Razor”
- ❖ William Occam was a 14th century English philosopher who advocated this minimalist problem solving technique
- ❖ If you build a tree use morphological data, the most parsimonious tree requires the fewest evolutionary events.
- ❖ If you build a tree use genetic data, the most parsimonious tree requires the fewest base changes.

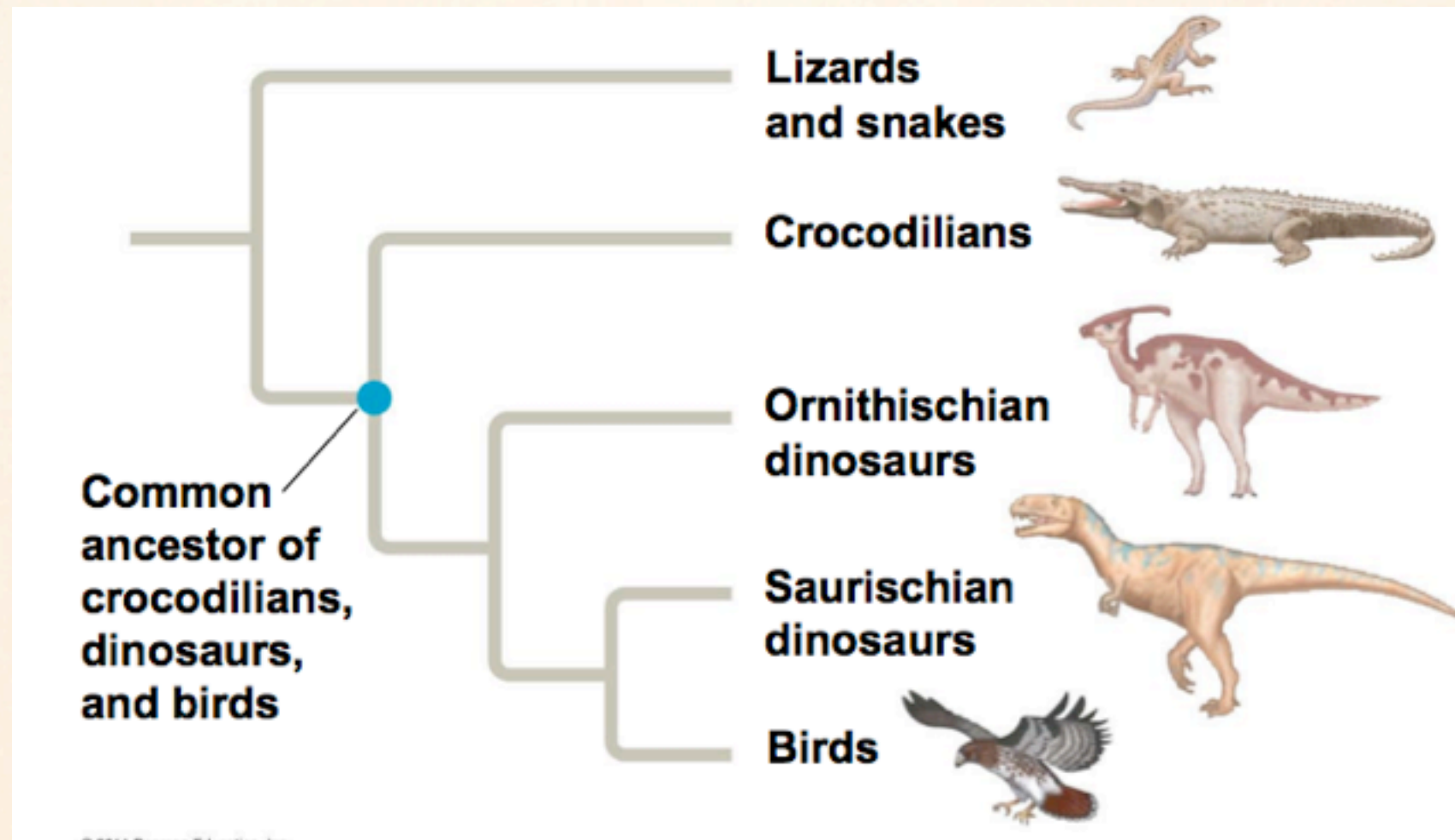
Maximum Likelihood

- ❖ The principle of **maximum likelihood**, states that given certain probability rules about how DNA sequences change over time, a tree can be found that reflects the most likely sequence of evolutionary events.
- ❖ Maximum likelihood methods can get complex, not suprisingly computers can help crunch data in the most likely and parsimonious ways.

Phylogenetic Trees as Hypotheses

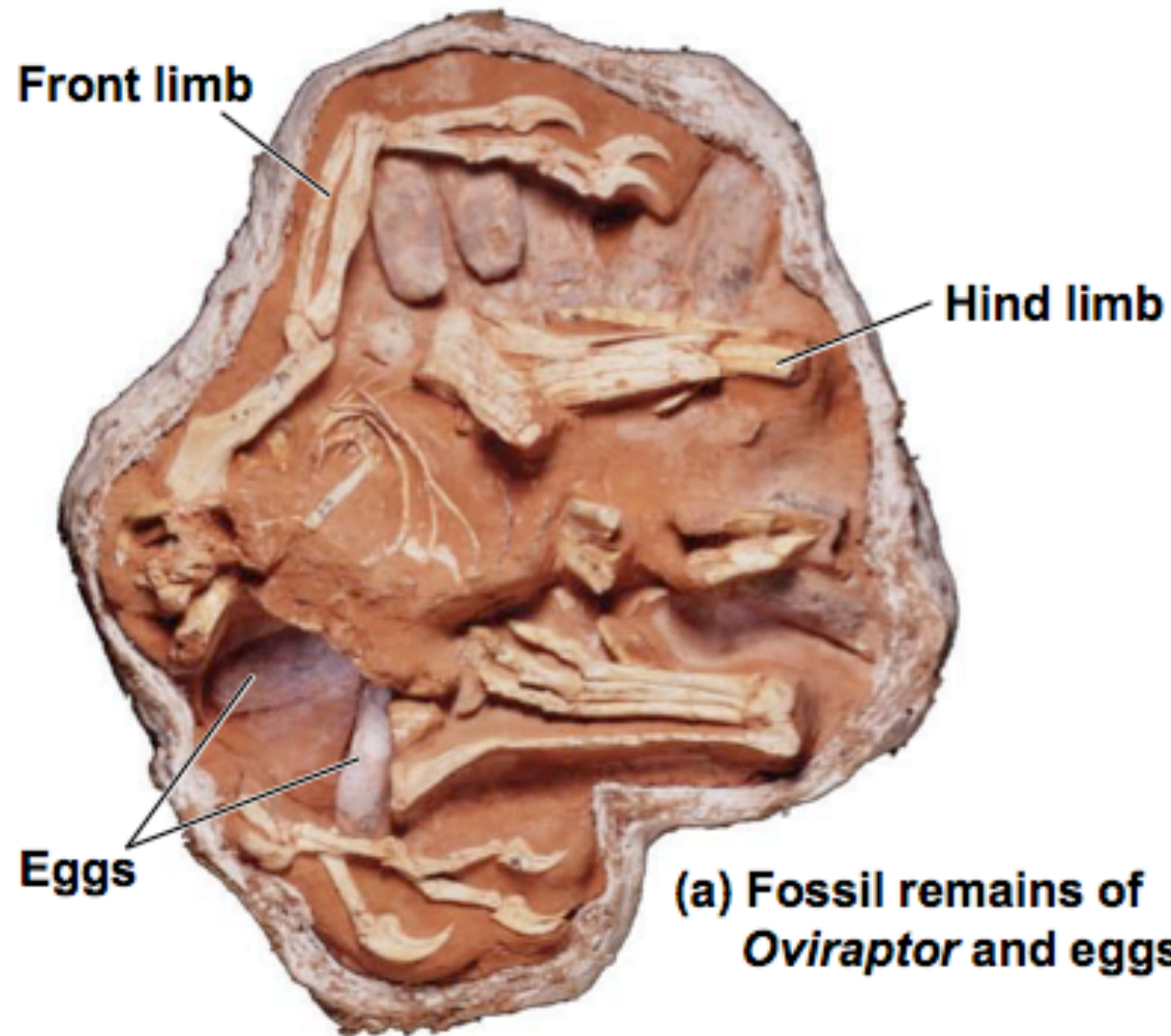
- ❖ Remember phylogenies are possible explanations, they may change or be modified with new and compelling evidence.
- ❖ Scientists can make and test predictions by using and assuming that a phylogeny is correct
- ❖ For example we can compare extant crocodiles and birds, any similarities in structure or behavior is assumed present in their common ancestor, in this same way we might make certain predictions about the structure and behavior of dinosaurs

- 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



PHYLOGENY

IV. Main Idea:

New information continues to revise our understanding of the tree of life.



From Two Kingdoms to Three Domains

- ❖ Early taxonomists placed all life into one of two kingdoms: plants and animals!
- ❖ In the 1960's, with growing and gained acceptance, the five kingdom taxonomic scheme took hold.
- ❖ Monera, Protista, Fungi, Plants and Animals
- ❖ The scheme was highlighted by two fundamentally different cell types prokaryotic and eukaryotic cells

From Two Kingdoms to Three Domains

- ❖ However, phylogenies based on genetic data soon revealed problem, some prokaryotes differed from each other as much as they differed from eukaryotic cells.
- ❖ Biologists responded by adopting three domains-
Bacteria, Archaea and Eukarya
- ❖ ...a taxonomic level above kingdoms
- ❖ 4 kingdoms are still recognized, but Monera is now obsolete because it has members in two different domains (“protista is also now crumbling apart”)

Three Domains

