1. This is the term given to the evolutionary history of a species or group of related species.

2. Name the discipline that focuses on classifying organisms and their evolutionary relationships using tools such as fossils, morphology, genes, and molecular evidence.

3. Binomial nomenclature uses which two taxa in its naming system?

4. A clade is a group of species that includes an ancestral species and all its descendants. To be a valid clade it must be ________________, signifying that it consists of the ancestor species and all its descendants.
EQ: Why & how do scientists classify & group organisms?

Tracing Evolutionary History

Phylogeny, Taxonomy, & Systematics
Essential Question

Why & how do scientists classify & group organisms?
Classifying by Evolution

Classification of organisms can be done by evolutionary connections.
Phylogeny

- **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** uses evidence from:
  - fossils
  - molecular data
  - genetic data

EQ: Why & how do scientists classify & group organisms?
Can you name the 4 Kingdoms under domain Eukarya

- Protista
- Fungi
- Plantae
- Animalia
EQ: Why & how do scientists classify & group organisms?
Phylogenies show evolutionary relationships

- **Taxonomy** is the ordered division and naming of organisms
- **Taxonomists** are scientists who specialize in the naming of organisms.
Binomial Nomenclature

- 18th century: *Carolus Linnaeus* published a system of taxonomy based on resemblances.
- Two key features system:
  - **two-part names** for species
  - **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).
Ursus maritimus
Figure 26.3

Species: *Panthera pardus*
Genus: *Panthera*
Family: Felidae
Order: Carnivora
Class: Mammalia
Phylum: Chordata
Domain: Eukarya

Domain: Bacteria
Kingdom: Animalia
Domain: Archaea
Did
King
Phillip
Come
Over
For
Great
Spaghetti?

Dumb
Kids
Playing
Catch
On
Freeways
Get
Smashed
Hierarchical Classification

- 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

EQ: Why & how do scientists classify & group organisms?
- **Kingdom**: Animalia
- **Phylum**: Chordata
- **Class**: Mammalia
- **Order**: Carnivora
- **Family**: Ursidae
- **Genus**: Ursus
- **Species**: *U. maritimus*

What is the broadest taxa? The most specific?
Linking Classification and Phylogeny

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

EQ: Why & how do scientists classify & group organisms?
Kingdom: Animalia
Phylum: Chordata
Class: Mammalia
Order: Carnivora
Family: Felidae
Subfamily: Pantherinae
Genus: Panthera
Species: P. pardus

Kingdom: Animalia
Phylum: Chordata
Class: Mammalia
Order: Carnivora
Family: Canidae
Subfamily: Caninae
Tribe: Canini
Genus: Canis
Species: C. lupus
Figure 26.4

<table>
<thead>
<tr>
<th>Order</th>
<th>Family</th>
<th>Genus</th>
<th>Species</th>
</tr>
</thead>
<tbody>
<tr>
<td>Carnivora</td>
<td>Felidae</td>
<td>Panthera</td>
<td><em>Panthera pardus</em> (leopard)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Taxidea</td>
<td><em>Taxidea taxus</em> (American badger)</td>
</tr>
<tr>
<td></td>
<td>Mustelidae</td>
<td>Lutra</td>
<td><em>Lutra lutra</em> (European otter)</td>
</tr>
<tr>
<td></td>
<td>Canidae</td>
<td>Canis</td>
<td><em>Canis latrans</em> (coyote)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td><em>Canis lupus</em> (gray wolf)</td>
</tr>
</tbody>
</table>
• Linnaean classification and phylogeny can differ from each other

• **Systematists** have proposed the **PhyloCode**, which recognizes only groups that include a **common ancestor** and all its **descendants**
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.
Terms in Phylogenetic Trees

- A **rooted tree** includes a branch to represent the **last 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.

- A **polytomy** is a branch from which more than two groups emerge.
Branch point: where lineages diverge

ANCESTRAL LINEAGE

This branch point represents the common ancestor of taxa A–G.

This branch point forms a polytomy: an unresolved pattern of divergence.

Sister taxa

Basal taxon

<table>
<thead>
<tr>
<th>Taxon A</th>
</tr>
</thead>
<tbody>
<tr>
<td>Taxon B</td>
</tr>
<tr>
<td>Taxon C</td>
</tr>
<tr>
<td>Taxon D</td>
</tr>
<tr>
<td>Taxon E</td>
</tr>
<tr>
<td>Taxon F</td>
</tr>
<tr>
<td>Taxon G</td>
</tr>
</tbody>
</table>
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
Phylogenies are inferred from morphological and molecular data

- To infer **phylogenies**, **systematists** gather information about **morphologies, genes**, & **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.
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.

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.

- Why do you think this is?
Systematists use computer programs and mathematical tools when analyzing comparable DNA segments from different organisms.
<table>
<thead>
<tr>
<th></th>
<th>CCATCAGAGTC</th>
<th>CCAATCAGAGTC</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td></td>
<td>CCAATCAGAGTC</td>
</tr>
<tr>
<td>2</td>
<td></td>
<td>CCAATCAGAGTC</td>
</tr>
</tbody>
</table>
Figure 26.8-2

Deletion

Insertion

1  C  C  A  T  C  A  G  A  G  T  C  C
2  C  C  A  T  C  A  G  A  G  T  C  C

↓

Deletion

1  C  C  A  T  C  A  G  A  G  T  C  C
2  C  C  A  T  C  A  G  A  G  T  C  C

G  T  A  Insertion
Figure 26.8-3

1. Deletion

1. $\text{CATCAGAGTCC}$
2. $\text{CATCAGAGTCC}$

2. Insertion

1. $\text{CATCAGAGTCC}$
2. $\text{CATCAGAGTCC}$

3. $\text{CATGTAACAGAGTCC}$
Figure 26.8-4

1. Deletion

2. Insertion

3. Deletion

4. Insertion
• Important to distinguish homology from analogy in molecular similarities
  • Mathematical tools help to identify molecular homoplasies, or coincidences
• Molecular systematics uses DNA and other molecular data to determine evolutionary relationships
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 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.
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.
Figure 26.10

(a) Monophyletic group (clade)

(b) Paraphyletic group

(c) Polyphyletic group

Group I

Group II

Group III
Shared Ancestral and Shared Derived Characters

- If an organism has evolved from an ancestor, it makes sense that organism will have some characteristics in common, and others different with those of its ancestor.
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.
### (a) Character table

<table>
<thead>
<tr>
<th>CHARACTERS</th>
<th>Lancelet (outgroup)</th>
<th>Lamprey</th>
<th>Bass</th>
<th>Frog</th>
<th>Turtle</th>
<th>Leopard</th>
</tr>
</thead>
<tbody>
<tr>
<td>Vertebral column</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>(backbone)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Hinged jaws</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Four walking legs</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Amnion</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Hair</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
</tr>
</tbody>
</table>
(b) Phylogenetic tree

- Lancelet (outgroup)
- Lamprey
- Bass
- Frog
- Turtle
- Leopard

- Vertebral column
- Hinged jaws
- Four walking legs
- Amnion
- Hair

© 2011 Pearson Education, Inc.
(a) Character table

<table>
<thead>
<tr>
<th>CHARACTERS</th>
<th>Lancelet (outgroup)</th>
<th>Lamprey</th>
<th>Bass</th>
<th>Frog</th>
<th>Turtle</th>
<th>Leopard</th>
</tr>
</thead>
<tbody>
<tr>
<td>Vertebral column (backbone)</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Hinged jaws</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Four walking legs</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Amnion</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Hair</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
</tr>
</tbody>
</table>

(b) Phylogenetic tree

- Lancelet (outgroup)
- Lamprey
- Bass
- Frog
- Turtle
- Leopard

- Vertebral column
- Hinged jaws
- Four walking legs
- Amnion
- Hair
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.
- Comparisons of ingroup species with the outgroup help 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 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.

EQ: Why & how do scientists classify & group organisms?
In other trees, branch length can represent **chronological time**, and branching points can be determined from the fossil record.
Reading Quiz: What type of DNA has been used most commonly in determining phylogenetic relationships? Why?

The genes for the small subunit ribosomal RNA molecule tend to change relatively slowly. As a result, they are used to determine relationships among groups of organisms that are not closely related.

Mitochondrial DNA mutates at a faster rate and is therefore more likely to provide evidence of more recent divergences that occur among closely related species.
The phylogenies developed using DNA sequence analysis may differ from those constructed using morphology and physiology. How do scientists know which method is more correct?

If the mechanisms used to develop competing phylogenies are both valid, there is no easy way to determine which is correct. Scientists will often fuse the different results to produce a reconciled phylogeny until more data becomes available.
<table>
<thead>
<tr>
<th><strong>a.) Definition or purpose:</strong></th>
<th><strong>Taxonomy</strong></th>
<th><strong>Phylogeny</strong></th>
</tr>
</thead>
<tbody>
<tr>
<td>A system for <strong>naming</strong> and <strong>classifying</strong> organisms</td>
<td><strong>Categorizes organisms based on their evolutionary relatedness.</strong></td>
<td></td>
</tr>
</tbody>
</table>

| **b. Types of characters used to develop:** | **Mostly based on **visible** characteristics** | **Based on historical information – fossil record, DNA sequence...** |

| **c. Similarities between the taxonomy of a given group and its phylogeny:** | **Phylogenetically related organisms often share similarities in morphology. As a result, many taxonomies reflect phylogenetic relationships as well.** |

| **d. Key differences between the taxonomy of a given group and its phylogeny:** | **By definition, taxonomies are developed to categorize and name organisms. There is no specific intent to determine phylogenetic relationships in the development of taxonomy.** |
On the phylogenetic tree shown above, the group containing humans, whales, crocodiles, and birds would be considered **monophyletic**. Why?
2.) On the phylogenetic tree shown earlier, the group containing humans, whales, crocodiles, and birds:

would be considered **polyphyletic** because no common ancestor is included.

A monophyletic group would require all the other members of a group to share a common ancestor.

(a) Monophyletic group (clade)  (b) Paraphyletic group  (c) Polyphyletic group
3.) Considering only individual representative organisms in the phylogenetic tree (bird, whale, frog), which can be used as good examples of analogy or convergent evolution? As good examples of homology? Explain.
3.) Considering only individual representative organisms in the phylogenetic tree (bird, whale, frog), which can be used as good examples of analogy or convergent evolution? As good examples of homology? Explain.

- **Convergent:** Fish & Whale
  - Fish evolved in aquatic habitat. Whale evolved from mammalian terrestrial ancestor that took up an aquatic habitat.
  - Large animals must be able to move efficiently through water, over time, both evolved torpedo-like forms, fins, and tails. Body forms not suited to an aquatic habitat were eliminated.

- **Homology:** Crocodile, bird, human, & whale
  - are all **homologous** with regard to their pentadactyl limb structures.
  - Function varies from species to species, each has one upper limb bone, two lower limbs bones, & 5 digits.
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 (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.
<table>
<thead>
<tr>
<th></th>
<th>Human</th>
<th>Mushroom</th>
<th>Tulip</th>
</tr>
</thead>
<tbody>
<tr>
<td>Human</td>
<td>0</td>
<td>30%</td>
<td>40%</td>
</tr>
<tr>
<td>Mushroom</td>
<td>0</td>
<td>40%</td>
<td></td>
</tr>
<tr>
<td>Tulip</td>
<td></td>
<td></td>
<td>0</td>
</tr>
</tbody>
</table>

(a) Percentage differences between sequences
(b) Comparison of possible trees

Tree 1: More likely

Tree 2: Less likely
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 descendents.
  - For example, phylogenetic bracketing allows us to infer characteristics of dinosaurs.
Common ancestor of crocodilians, dinosaurs, and birds

- Lizards and snakes
- Crocodilians
- Ornithischian dinosaurs
- Saurischian dinosaurs
- Birds
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 descendents, 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 26.6: 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.
Animation: Classification Schemes
Right-click slide / select “Play”
Figure 26.21

**Eukarya**
- Land plants
- Green algae
- Forams
- Ciliates
- Diatoms
- Amoebas
- Animals
- Fungi
- Euglena
- Trypanosomes
- Leishmania

**Archaea**
- Sulfolobus
- Thermophiles
- Halophiles
- Methanobacterium

**Bacteria**
- Green nonsulfur bacteria
- (Mitochondrion)
- Spirochetes
- Chlamydia
- Green sulfur bacteria
- Cyanobacteria
- (Plastids, including chloroplasts)
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

Billions of years ago

Bacteria

Eukarya

Archaea

© 2011 Pearson Education, Inc.
Some researchers suggest that eukaryotes arose as an 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.
<table>
<thead>
<tr>
<th>Major Domains of Life</th>
<th>Key Characteristics</th>
</tr>
</thead>
</table>
| **Bacteria**          | Prokaryotic cell structure  
Circular chromosomes  
**Cell walls contain peptidoglycan**  
Use *formyl methionine* as their initiator amino acid to start protein synthesis |
| **Archaea**           | Prokaryotic cell structure  
Circular chromosomes  
**Cell walls DO NOT contain peptidoglycan**  
Several types of RNA polymerase can be found among different archaeal species  
Use *Methionine* as their initiator amino acid to start translation |
| **Eukarya**           | *Eukaryotic Cell Structure* (double membrane-bound nucleus and membrane bound organelles)  
Linear chromosomes  
Eukaryotic cell walls (no peptidoglycan)  
Use *Methionine* as their initiator amino acid to start translation |
Branch point

Most recent common ancestor

Polytomy

Taxon A

Taxon B

Taxon C

Sister taxa

Taxon D

Taxon E

Taxon F

Basal taxon

Taxon G

© 2011 Pearson Education, Inc.
<table>
<thead>
<tr>
<th>Character</th>
<th>Lancelet (outgroup)</th>
<th>Lamprey</th>
<th>Tuna</th>
<th>Salamander</th>
<th>Turtle</th>
<th>Leopard</th>
<th>Dolphin</th>
</tr>
</thead>
<tbody>
<tr>
<td>Backbone</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Hinged jaw</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Four limbs</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1*</td>
</tr>
<tr>
<td>Amnion</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Milk</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Dorsal fin</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
</tr>
</tbody>
</table>

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

Archaea

Eukarya
Lizards and snakes

Crocodilians

Ornithischian dinosaurs

Saurischian dinosaurs

Birds

Dimetrodon

Cynodonts

Mammals
Figure 26: UN10

The diagram represents the evolutionary relationships among different domains of life. The domains listed are:

- **Archaea**
- **Bacteria**
- **Eukarya**

The diagram shows the branching order as follows:

1. **Archaea**
   - **Bacteria**
   - **Eukarya**
2. **Bacteria**
   - **Archaea**
   - **Eukarya**
3. **Eukarya**
   - **Bacteria**
   - **Archaea**