Evolution and Biodiversity Laboratory
Systematics and Taxonomy
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Recent estimates of our planet's biological diversity suggest that the species number between 5 and 50 million, or even more. To effectively study the myriad organisms that inhabit the biosphere, we attempt to classify organisms into groups that reflect evolutionary relationships.

I. Taxonomy

Strictly speaking, **taxonomy** is the science of sorting and classifying living organisms into groups called **taxa** (singular = **taxon**). Taxonomy also includes describing and naming the members of those taxa. A scientist who engages in taxonomy is a **taxonomist**.

A taxon is a group of organisms that a taxonomist has judged to represent a cohesive unit. The criteria used to sort specimens into various taxa are not fixed, and the science of taxonomy is not without its internal controversies.

Taxonomists often distinguish between **natural** and **artificial** taxa. A natural taxon is constructed on the basis of evolutionary relationships. While not all taxonomists insist that taxa be natural, most believe that taxonomic groups should consist of evolutionarily related units. The science of determining evolutionary relationships among taxa is known as **systematics**, and its practitioners are **systematists**. Most systematists are also taxonomists, and vice versa.

Since systematists are concerned not only with the ability to sort and identify organisms, but also with determining their evolutionary relationships, taxonomy is used as a tool within systematics.

Biological **nomenclature** is the application of names to organisms recognized to be part of a particular taxon. From most inclusive to least inclusive, the major taxonomic **ranks** are as follows:

**DOMAIN** (e.g., Eukarya)
**KINGDOM** (e.g., Animalia)
**PHYLUM** (e.g., Chordata)
**CLASS** (e.g., Mammalia)
**ORDER** (e.g., Primates)
**FAMILY** (e.g., Pongidae)
**GENUS** (e.g., Homo)
**SPECIES** (e.g., Homo sapiens)

Each **Domain** contains related **Kingdoms**. Each kingdom consists of related **phyla**. Each phylum consists of related **classes**, classes of related **orders**, orders of related **families**, families of related **genera** (singular: **genus**) and genera of related **species**. Within each of the major taxonomic ranks there may be larger and smaller taxa such as subkingdom, superphylum, subclass, subspecies, etc.
Every described, named organism is nested into a complete organizational hierarchy, from species through domain, as shown above for our own species, *Homo sapiens*. Note that the scientific name of an organism (its genus and species) is always written with the genus capitalized and the specific epithet in lower case letters. Because the words are Latinized, they should be *italicized*.

This system of nomenclature was created by Swedish botanist Carl Linne, who published it as *Systema naturae*, in 1735. Linne Latinized his own name to Carolus Linnaeus, and we remember him today as Linnaeus, the father of modern taxonomy.

### A. The Aspects of a Taxon

A taxon is generally considered to have three aspects:

1. **The taxon's name.** The order to which all dogs belong (along with a host of other flesh-eating mammals with specialized cutting teeth called carnassials) is **Carnivora**.

   The scientific name of a group of similar organisms has no more significance than any other convenient label used to describe a group of similar items. An example: the name of the taxon containing all domestic dogs is *Canis familiaris*. Taxonomic names such as "Bacteria," "Felidae" and "Oryctolagus cuniculus" are similar in function to descriptive names of similar objects, such as "shoes" or "machines."

   Don't let names confuse or intimidate you. Once you know the Latin or Greek word roots, seemingly complicated names make perfect sense and become easier to remember. For example, the name of *Eleutherodactylus planirostris*, a frog naturalized in southern Florida gardens, can be broken down into its Greek roots: *eleuthero*, meaning "free," *dactyl*, meaning "toe," *plani*, meaning "flat" and *rostris*, meaning "nose." Our little pal is a flat-nosed frog with unwebbed toes!

2. **The taxon's rank.** Like the taxon's name, the taxon's rank has no true biological significance. It serves only to help the biologist locate the taxon within the hierarchy. An examples: The taxon "Eukarya" is assigned the rank of domain. The taxon "Mammalia" is assigned the taxonomic rank of class.

   You may notice throughout this semester that a given taxon's rank may not always be the same in every source you read. For example, some publications may list "Zygomycota," "Ascomycota" and "Basidiomycota" as subphyla within Phylum Mycota, whereas others assign each of those three taxa the rank of phylum within Kingdom Fungi. Classifications shift as new data become available, but older publications are not changed to reflect the more recent classifications.

   Confusing? We won't deny it. Just remember that as new data come to light, the ranks of familiar taxa may change with authors' attempts to create natural taxa.

   The *relative* rank of a taxon within its larger and smaller groupings is more relevant than the rank itself, which is subject to change. For example, it's important to know that all members of *Felis* are classified within the larger taxon "Carnivora," and that all carnivores are classified within the still larger taxon "Mammalia." It's less important to struggle to recall that "Carnivora" is an order and "Mammalia," is a class.

   Many institutions use a **rankless system**. In this way, a taxon is described only by its name. The rank is left off, but tacitly understood. An author using this system will write "Mammalia" rather than "Class Mammalia" avoiding confusion as names change their rank.
3. The taxon’s content. All the students in your lab are (probably) members of the genus *Homo* and the species *Homo sapiens*. To the systematist, this is perhaps the most relevant aspect of the taxon. By grouping specific individuals within a single species, related species within a single genus, related genera within a single family and so on, the systematist tells us which organisms share common evolutionary ancestry.

Organisms are not classified randomly. The systematist uses morphological characters, DNA sequencing, protein analysis, developmental biology, karyology, ultrastructure and other information to determine evolutionary relationships. It's an ongoing quest—and one in which you might some day participate. Let's start with some simple exercises right now.

B. The Taxonomic Key: A Tool for Identification

Unfortunately, a biologist does not always receive materials neatly packaged with name and taxonomic information. In many cases, an investigator must identify an unknown specimen. A useful tool for this purpose is the taxonomic key.

A taxonomic key is constructed as a series of paired statements/descriptions based on similarities and differences between taxa in a group being identified. Because the key branches in two at each stage, is called a dichotomous (from the Greek *dicho* meaning "in two" or "split" and *tom*, meaning "cut") key.

The paired statements describe contrasting characteristics found in the organisms being classified. With the specimen at hand, the investigator chooses which of the paired statements best matches the organism. The statement selected may immediately identify the specimen, but more often it will direct the user to the next set of paired, descriptive statements. At the end--if an appropriate key has been used (e.g., you wouldn't use a book called *Key to the Flora of Southern California* to identify an unknown tree you've discovered in Guatemala)--the specimen is identified by name.

Sometimes a key for identification of a specimen you have at hand simply doesn't exist, and you must go to the primary literature to see if any species descriptions match it. Identification of unknown species can be a difficult and challenging enterprise. Fortunately, the specimens you're going to use in today's first exercise are not only easily recognizable, but also included in a ready-made key.

**Exercise I. Using a Taxonomic Key**

Work in pairs for this exercise. At your station you will find a container containing several "species" of pasta native to the United Aisles of Publix. The noodles have an evolutionary relationship to one another: they all are members of the same Order, Semolina, which evolved from a common ancestor resembling a soda cracker. A taxonomic key may or may not reflect these evolutionary relationships. It's simply a tool devised to allow identification of an individual organism to its proper taxonomic group. In this case, the key identifies each to genus and species.

Let’s key out (this is a jargony verb commonly used to describe the process of identifying things with a taxonomic key) some pasta! Select one individual from your container, and use the taxonomic key below to identify its genus and species. Use the key to identify each different "species" of pasta in your container.
A TAXONOMIC KEY TO THE PASTA OF SOUTHERN FLORIDA

1a. Body tubular in shape ................................................................. 2
1b. Body not tubular .................................................................. 4

2a. Skin lined with small, symmetrical ridges .................................. 3
2b. Skin smooth ......................................................................... Ziti edulis

3a. Anterior and posterior ends of organism slanted ...................... Penna rigata
3b. Anterior and posterior ends of organism perpendicular to body axis .................................................. Rigatonii deliciosus

4a. Skin lined with small, symmetrical ridges ............................... Conchus crispus
4b. Skin not lined with ridges .......................................................... 5

5a. Body cylindrical in overall shape ........................................... Rotinii spiralis
5b. Body dorsoventrally flattened in shape .................................... Farfalla aurea

Write the name of each type of pasta underneath its picture below.

There’s no single correct way to create a taxonomic key. The one you used to identify your pasta “species” could have been arranged in many other ways. It is not required that a key reflect evolutionary relationships, though many keys do. Once you have completed the second part of today’s lab (Systematics), you’ll be better prepared to create a key that reflects common ancestry. But for now, it’s not necessary.
Exercise II. Creating a Taxonomic Key

Work in pairs for this exercise. Now that you have seen how simple it is to use a taxonomic key, you should be able to create one. At your station you will find a set of eight cards bearing pictures of imaginary animals. These hypothetical animals, created and "evolved" by J. H. Camin, Professor of Biology at the University of Kansas, are called Caminalcules. (An "animalcule" is a small animal). Caminalcules have served as test material for a number of experiments in systematic theory and practice. Use of imaginary organisms for such studies offers a distinct advantage over using real groups, because preconceived notions and biases about classifications and evolutionary relationships can be eliminated.

Create a dichotomous key of your Caminalcule species. Refer to the pasta key from the previous exercise to guide your organization.

Use your paperback copy of A Guide to Greek and Latin Word Roots by Donald J. Borror to create a Latinized scientific name (consisting of genus and species) for each of your species, and try to be as descriptive as possible with the name. (Some of your individuals might be in the same genus. It's up to you to decide.) Use proper Systema naturae rules in writing the scientific name of your hardware species: Genus capitalized, species lower case, and name italicized.

A Taxonomic Key for Identification of Caminalcules

1a. _____________________________________________
1b. _____________________________________________

2a. _____________________________________________
2b. _____________________________________________

3a. _____________________________________________
3b. _____________________________________________

4a. _____________________________________________
4b. _____________________________________________

5a. _____________________________________________
5b. _____________________________________________

6a. _____________________________________________
6b. _____________________________________________

7a. _____________________________________________
7b. _____________________________________________

Once you have finished your key, including all your Caminalcule species, trade keys with the partners across the table from you. Using each other's keys, try to identify all of each other's species correctly. When you have identified them all, check with your "swap buddies" to see how well you did.
II. Systematics

Because new data constantly change our understanding of evolutionary relationships, classifications are constantly updated and changed. The goal of most modern systematists is to construct monophyletic taxa, which reflect true evolutionary relationships by including all descendants of a single common ancestor. Several different lines of evidence can be used to determine the degree of common ancestry between two taxa, including comparison of morphology (at many levels, including cellular), nucleic acid sequence, protein sequence, embryo development, etc. As new technologies arise, our ability to study evolutionary relationships evolves.

A. Reconstructing Phylogenies

A phylogeny is a history of the evolutionary descent of extant (i.e., presently living) or extinct (i.e., no longer living) taxa from ancestral forms. To date, about 1.4 million species (including 750,000 insects, 250,000 plants and 41,000 vertebrates) of the 5 to 50 million on earth have been scientifically described and classified.

What is a species? Although biologists still debate the precise definition, we shall use the biological definition of a species as a group of actually or potentially interbreeding natural populations which are reproductively isolated from other such groups. More simply, two organisms can be considered members of the same species if they can breed and produce fertile, viable offspring under natural conditions.

1. Primitive vs. Derived Characters

Ever since Darwin's publication of On the Origin of Species by Means of Natural Selection, the scientific community has labored to understand how different species arise. We know that extant species evolved from previously existing ancestral species, and that this may involve descent with modification of traits (= characters) from one generation to the next. A character that shows little or no change from the same character in an ancestor is said to be primitive, whereas one that has changed in appearance and/or function relative to the ancestral form is derived.

A primitive character is also known as a plesiomorphy; a primitive character shared between two or more taxa is known as a symplesiomorphy (literally "shared primitive character"). A derived character is also known as an apomorphy; a derived character shared between two or more taxa is known as a synapomorphy (literally "shared derived character").

All living things share these most basic symplesiomorphies:

1. Organization of structure (anatomy)
2. Capacity to generate more organisms like themselves (reproduction)
3. Growth and development
4. Ability to utilize energy to do work (metabolism)
5. Response to environmental stimuli (reaction)
6. Regulatory mechanisms to keep the internal environment within tolerable limits (homeostasis)
7. Populations that change in gene composition over time (evolution)

In classifying an unknown organism," the systematist must consider characters that make that organism unique and different from members of other species. To achieve this end, derived characters are the most informative ones to use. The next section explains why.
2. **Symplesiomorphies vs. Synapomorphies**

Because all living things share evolutionary history, however distantly, each taxon shares certain very ancient (i.e., **primitive**, or **plesiomorphic**) characters with other taxa. Shared, primitive characters cannot be used to separate members of different taxa, since everyone has them. However, more recently evolved (i.e., **derived**, or **apomorphic**) characters can set one taxon apart from another. Synapomorphies inherited from a common ancestor can inform the systematist about relative **reency of common descent**. The more synapomorphies two taxa have in common, the more recently they evolved from a common ancestor.

For example, we humans share certain primitive characters with all members of Kingdom Animalia. List six primitive characters all humans share with all other animals, **but not with any other living things** (e.g., plants, fungi):

1. 
2. 
3. 
4. 
5. 
6. 

Note: the characters you have listed above—if they are exhibited only by animals and by no other living organisms—are considered **symplesiomorphies only with respect to Animalia**. But if you are considering all living things, then the very same animal characteristics on your list should be considered **synapomorphies that set animals apart from all other living organisms**. Thus, any given character cannot be "primitive" or "derived" on its own. It can be described as "primitive" or "derived" only when compared to characters in other taxa.

With this in mind, list three derived characters that set mammals (Mammalia, of which you are a member) apart from all other animals:

1. 
2. 
3. 

Do you exhibit all three of the characters listed? (Good! You're a mammal!) Since you share those characters with all your mammalian relatives, the characters are said to be **primitive with respect to all mammals**, though they are **derived with respect to all animals other than mammals**.

See the pattern? Because you share the three characters above with all other mammals, those characters won't help you determine how closely related you are to any other mammal groups. Hence, we must consider synapomorphies at the next level.

List three derived characteristics shared by all primates (Primates, of which you are a member), but not shared by other mammals. (You might have to do some searching.)

1. 
2. 
3. 

What you have listed are three synapomorphies shared by Primates that set them apart from all other mammals. But because all primates share these three characters,
they are symplesiomorphies with respect to primates only. In other words, these three characters will not help you to determine which primates are your closest relatives. To do that, we must find more unique derived characters. Here goes.

List two derived characteristics shared by all great apes (Hominidae, of which you are a member), but not shared by other primates. Again, you might have to do some searching. Notice that it can become more and more difficult to find synapomorphies linking particular taxa as they become smaller/less inclusive.

1. 
2. 

Finally, list as many derived characters as possible that make Homo sapiens different from all other great apes. Be sure to restrict your list to truly BIOLOGICAL characters—not cultural ones. (This is where it gets really challenging, and sometimes there is simply not a clear line to draw, especially where cultural influences ("nurture") interact with a truly genetic and heritable ("nature") character.)

1. 
2. 
3. 
4. 
5. 

As you can see, it is not a simple task to find biological characteristics that truly separate Homo sapiens from other species of great apes. In fact, we share more than 99% of our DNA with our closest ape relatives, the Common Chimpanzees (Pan troglodytes) and Bonobos (Pan paniscus).

Take a look back at the several lists you have made, and note how synapomorphies identified at higher and higher resolutions help us to determine most recent common ancestry among the various taxa. Systematists use this method to construct and revise phylogenies for all living things.

3. Homologous vs. Analogous characters

If the similarity between two characters in two separate taxa can be attributed to their presence in a common ancestor, then those two characters are said to be homologous. For example, the forelimb bones of all tetrapod (four-legged) vertebrates are homologous to one another, because they all evolved from the same bones in a common tetrapod ancestor. Although the bones may have evolved very different sizes, shapes, and functions, they all developed from the same embryonic sources and have evolved from the same ancestral tetrapod limb bones.

List five homologous characters you share with all other vertebrates that perform a similar function in you and all other vertebrates:

1. 
2. 
3. 
4. 
5. 

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Now list five homologous characters you share with other vertebrates that have evolved to serve a different function in you than they serve in some other vertebrates:
1. ________________________________________________________________
2. ________________________________________________________________
3. ________________________________________________________________
4. ________________________________________________________________
5. ________________________________________________________________

Of the five characters you just listed, which are unique to Homo sapiens, and which are shared by at least some other vertebrates? What does this say about the recency of your common ancestry with those other vertebrates?

Not all physical similarities are homologous. In many cases, unrelated taxa have evolved superficially similar morphologies in response to similar natural selection pressure. For example, a shark and a dolphin both share a streamlined, fusiform shape well adapted for swift swimming. However, while the shark's body evolved from a fishlike ancestor with a somewhat fusiform shape, the dolphin's fishlike form is secondarily derived from that of a terrestrial, four-legged mammalian ancestor.

The superficial similarity of shark and dolphin is a result of convergent evolution. Specifically, what is meant by the term "convergent" evolution?

Characters that have evolved similar form and function from disparate ancestral sources are said to be analogous. Analogous characters are sometimes called homoplastic characters or homoplasies.

Don't let the similarity of the terms "homoplastic" and "homologous" confuse you! Look up their root derivations in your Dictionary of Word Roots and Combining Forms (Donald Borror). Write their exact, translated meanings here:

- homo (Greek) = _____________________________________________________________
- plas (Greek) = _____________________________________________________________
- analog (Greek) = ___________________________________________________________

List five characters you have that are analogous to characters with the same function but of different ancestral origin in any other species.

1. ________________________________________________________________
2. ________________________________________________________________
3. ________________________________________________________________
4. ________________________________________________________________
5. ________________________________________________________________

B. Modern Systematics: The Cladistic System

The Cladistic System of classification was first published by German zoologist Willi Hennig in 1950. The cladistic system is an objective and quantitative method of modern classification, and it is to its tenets that we—and the vast majority of modern systematists—adhere.
In the Cladistic System, organisms are classified exclusively on the basis of recency of descent from a common ancestor. Taxonomic/phylogenetic relationships are determined strictly on the basis of synapomorphies. The presence of many shared derived characters among taxa is considered strong evidence of their common descent. Differences in the degree or rate of change among branches of organisms are irrelevant to their classification. For example, the cladist recognizes that birds--despite their plumage (modified scales homologous to reptile scales) and "warm-bloodedness"--share a more recent common ancestor with crocodilians than with other vertebrates. Birds and crocodilians (and their extinct relatives) are classified together in Archosauromorpha (literally "ancient lizard form"). In the old system (Classical Evolutionary Systematics), birds were placed in their own class ("Aves"), and crocodilians in a different class ("Reptilia") that did not reflect their common ancestry. Those two old names are now pretty much defunct, except when they are used as common names.

C. Phylogenetic Trees

By considering synapomorphies and symplesiomorphies and by identifying homoplasies, the systematist attempts to construct phylogenies that reflect natural evolutionary relationships. Phylogenies can be represented as treelike diagrams showing how various extant taxa branched from common ancestors and from each other. Such a diagram is called a phylogenetic tree or evolutionary tree (Figure 1).

A phylogenetic tree shows putative evolutionary relationships. Taxa are represented as branches that bifurcate from nodes. A node represents the hypothetical common ancestor of the taxa on the branches above it on the tree, and it also represents the taxonomic unit (order, family, genus, etc.) that contains the taxa represented by the branches. Nodes are considered hypothetical ancestors (also known as hypothetical taxonomic units, or HTUs) because they cannot be directly observed. The base or root of the tree represents the hypothetical common ancestor of all the groups (clades) on the tree.

Phylogenetic trees may be represented in many different ways, some of which are shown in Figure 2. But the different diagrams all provide similar essential information.

A Sample Phylogeny: Primates

Figure 3 shows nine extant lineages of primates. Located beneath (to the left of) them on the tree are their hypothetical ancestors.

The Ancestral Primate gave rise to all primates.

Ancestor A is gave rise to Tarsiers and Anthropoids, but not Lemurs and their kin.

Ancestor E is the most recent common ancestor of all Great Apes, but not Gibbons.

Ancestor G gave only rise to humans, chimpanzees and bonobos.

Note that this phylogenetic tree shows only recency of common descent. It does not indicate which species might be (subjectively) described as "primitive" or "derived" (Those terms are meaningless when applied to an entire species.)
Figure 1. A phylogenetic tree. The taxa included are “human,” “zebra,” and “goldfish.” Each node represents the common ancestor of the taxa to the right of it on the tree. All taxa descended from a common ancestor comprise a clade. (Human and Zebra comprise a single clade; Human/Zebra/Goldfish comprise another, more inclusive clade that will have a higher taxonomic rank than the clade including only Human and Zebra.) Branches diverge from nodes, and represent a genetic unit descended from the ancestor at that node. The root represents the common ancestor of all taxa included on the tree.

Figure 2. Different graphic representations of phylogenies. Whether a tree is upright, on its side, or drawn as an emerging spiral, the information is essentially the same. Nodes represent common ancestors of taxa (branches) above them on the tree, and endpoints represent taxa—whether extinct or extant—in the phylogeny.
Note that two lineages branching from the same ancestor arose at the same geological time. Many people hold the misconception that *Homo sapiens* is the "most highly evolved" species, or even the most recently evolved. Neither is true. Always remember the following rules.

**Rule #1:** The branches at every node can be rotated. The branches do not imply any sort of order; they indicate only recency of common descent. For example, the node at Ancestor F (Figure 3a) could be rotated so that the tree looked like the one shown in Figure 3b, and the information given would be exactly the same. Any node on the tree can be rotated in a similar fashion.

**Rule #2:** Two lineages branching from a single ancestral node are known as sister taxa. Further specialization after a branch point is irrelevant. Therefore, it would be incorrect to say that humans evolved more recently than chimpanzees, or that humans should be placed in their own family simply because they seem so different from chimpanzees. Taxonomic groupings are based on common ancestry only, not subjective perceptions of specialization.

**Rule #3:** There is no such thing as a “most highly evolved species”. All extant species are descended from successful ancestors, and are evolved to survive and reproduce in the context of their specific environment. Evolution is a process. It has neither a goal nor a subjective value system.

**Rule #4.** No extant nor extinct taxon is considered ancestral to any other extant or extinct taxon. Nodes represent hypothetical ancestors, not taxonomic units. When an ancestral lineage diverges to become two separate taxa, the ancestral lineage (hypothetical ancestor) is considered extinct, even if one of the descendant taxa is (or might be) virtually the same as that hypothetical ancestor. This should be remembered when one hears the oft-repeated, but incorrect statement “humans evolved from monkeys”. They did not. Humans and monkeys share a common ancestor. That’s not the same thing.

**Rooted and Unrooted Trees**

The trees in Figure 3a and 3b show the evolutionary relationships of Primates as they branched into their respective taxa from a hypothetical ancestor at the root of the tree. Sometimes, however, the hypothetical ancestor is not known, and not included on the tree.

In a rooted tree (Figure 4), each node represents the most recent common ancestor of the taxa branching from it. Rooted trees are directional, with all taxa evolving or radiating from that single common ancestor at the root. In rooted trees, each ancestor is united to each node by a unique (evolutionary) path.

In an unrooted tree (Figure 4) there is no hypothetical ancestor, and no directionality to the tree. The tree shows only the putative evolutionary relationships of the taxa on the tree, without the evolutionary directionality implied by an ancestor.

In order to root a tree, one must consider a taxonomic unit that is closely related to but phylogenetically outside the group of taxa being studied. This closely related group is known as the outgroup.
**Figure 3a.** Phylogeny of Primates. The nodes from which branches emerge represent the hypothetical common ancestor of all taxa above that node on the tree. The endpoints of the branches represent the descendants of that ancestor. Some phylogenetic trees include both extinct and extant (still living) taxa. In modern systematics, extinct taxa (represented by fossils) are treated the same way as extant taxa, and are not considered ancestral to extant taxa.

**Figure 3b.** Phylogeny of Primates demonstrating a rotation of the node at Ancestor G, relative to the original drawing shown in Figure 3a. Rotating the node in this manner does not change the phylogenetic information.
Homologous characters are used to group taxonomic units together on the basis of synapomorphy. The character state of the appropriate outgroup is considered to represent the primitive, ancestral condition of that character.

In some phylogenetic analyses, the degree of change in a particular branch (taxon) as compared to others can be represented. Longer branches indicate more change, and shorter branches, less change. A tree with branches calibrated to show degree of change is called a **scaled tree**. Sometimes, but not always, a time scale is included with a tree to indicate how long ago divergence from an ancestor occurred. (Figure 4).

![Figure 4.](http://www.ncbi.nlm.nih.gov/About/primer/phylo.html)

**Monophyly, Polyphyly, Paraphyly**

A phylogenetic tree is not constructed randomly. The systematist uses data on morphology, homology of nucleic acids, congruence of similar proteins, etc. to determine recency of common descent.

A **clade** is a group of species that includes an ancestral species and all of its descendants. Such a group is said to be **monophyletic**. The systematist uses cladistic techniques to construct monophyletic phylogenies that reflect true common ancestries. However, this is not always easy. When new data become available, it is sometimes discovered that a taxon under study is not monophyletic.

A **paraphyletic** taxon fails to include all descendants of a particular common ancestor. A **polyphyletic taxon** includes members that have descended from more than one different ancestor, but the common ancestor of those has not been included. These are illustrated in Figure 5.
Figure 5. Representative vertebrate taxa are grouped in monophyletic (a), paraphyletic (b) and polyphyletic (c) assemblages, shown by blue shading. Note that the paraphyletic tree (b) shows the traditional, evolutionary system for classifying Reptilia (turtles, crocodilians, snakes, and lizards), which does not reflect actual evolutionary relationships. Reptilia can be made monophyletic by including Aves (birds). The polyphyletic tree (c) illustrates what can happen when organisms are classified on the basis of superficial similarity, such as “warm bloodedness” or “four-chambered heart”. These characters most likely evolved independently in mammals and in birds.

Figure 6. A hypothetical phylogeny of the pasta of the United States. The hash-marks along the tree indicate the appearance of synapomorphies found only in the taxa above that character on the tree. A flat noodle serves as the outgroup, indicating the primitive condition of the characters used to group the taxa.
Using some of the characteristics of the pasta you met earlier in this exercise, we have constructed a hypothetical phylogenetic tree showing their possible evolutionary relationships. (Figure 6) This may not be the only possible tree. The more data used, the more likely the tree will reflect actual evolutionary relationships.

Exercise III. Constructing a Phylogenetic Tree

Classifications should be "natural," meaning that they reflect evolutionary relationships as closely as possible. We do not, for example, place slime molds and whales in the same family. Biosystematics, then, is a two-part endeavor. First, one must erect an hypothesis of evolutionary relationship among the organisms under study. Second, one must devise a classification scheme that faithfully reflects the hypothesized relationship. We will use our Caminalcules to create a phylogenetic tree.

Examine the Caminalcules in Figure 7. These will be your Operational Taxonomic Units (OTUs)—a name we use to avoid assigning them to any particular taxonomic rank (such as species). Think of them as biological species, and refer to them by number.

Figure 7. A variety of Caminalcules, arranged in no particular order.

Using Synapomorphies to Construct a Phylogeny

In the Cladistic System, the investigator groups OTUs together on the basis of synapomorphies. The presence or absence of a synapomorphy in two or more OTUs is inferred to be the result of inheritance (or lack thereof) from their common ancestor.

Results of a cladistic analysis are summarized in a phylogenetic tree called a cladogram (from the Greek clad meaning "branch"), an explicit hypothesis of evolutionary relationships. You already have seen an example of a cladogram in Figures 3a and 3b, and know that monophyletic taxa are constructed on the basis of synapomorphies unique to each group. Now you'll get to do one yourself! Oo!
**Step One.** Select a series of characters that can be expressed as binary (i.e., two-state). For example:

Character a: "eyes present" (+) versus "eyes absent" (-)
Character b: "body mantle present" (+) versus "body mantle absent" (-)
Character c: "paired, anterior non-jointed appendages present" (+) versus "paired, anterior non-jointed appendages not present" (-)
Character d: "anterior appendages flipperlike" (+) versus "anterior appendages not flipperlike" (-)
Character e: "eyes stalked" (+) versus "eyes not stalked" (-)
Character f: "body mantle posterior bulbous" (+) versus "body mantle posterior not bulbous" (-)
Character g: "eyes fused into one" (+) versus "eyes separate" (-)
Character h: "forelimbs with digits" (+) versus "forelimbs without digits" (-)

**Step Two.** Examine all your organisms and determine which character state it exhibits. Enter the data in a matrix like the one shown in Table 1.

- Note that in this example, character a (presence or absence of eyes) and character b (presence or absence of a body mantle) is the same in all eight OTUs. Hence, this (primitive) character is not useful to us in finding differences between the OTUs.
- Note also that only OTUs 2 and 7 share character e (stalked eyes), which is absent from all other OTUs. This suggests that OTUs 2 and 7 both inherited this character from a common ancestor. Likewise, OTUs 1, 4, and 6 share character f (bulbous mantle posterior), which is absent from all others. This supports the hypothesis of common ancestry among OTUs 1, 4, and 6. The same reasoning argues for common ancestry between OTUs 3 and 5 (character h), and so on.

A cladogram consistent with the distribution of these eight characters among the eight OTUs is shown in Figure 8.

This is not the only possible phylogeny consistent with the character distribution among the OTUs. In practice, there are often several—or even many—cladograms consistent with the data. In such cases, systematist generally applies a parsimony criterion for selecting the "best" cladogram. The rule of parsimony states that when two or more competing hypotheses are equally consistent with the data, we provisionally accept the simplest hypothesis. This is not to say that evolution is always parsimonious, only that our hypotheses should be.

In the case of competing cladograms, the rule of parsimony would require that we accept the simplest cladogram, the one with the fewest "steps" to each of the taxa on
the tree. In our example, we could hypothesize that OTU 6 is actually more closely related to OTU 1 than to OTU 4. However, this would require that character g (fused eyes) had evolved once, and then secondarily lost in both OTUs 4 and 6. This is less parsimonious than stating fused eyes evolved only once, in OTU 1 only.

![Cladogram Diagram](image)

**Figure 8.** A cladogram based on synapomorphies in Caminalcules 1 - 8.

**Cladistics and Linnaean Classification**

Given an hypothesis of evolutionary relationships, the second step in biosystematic endeavor is to erect a classification that faithfully reflects those relationships. Because the results of a cladistic analysis (i.e., the cladogram) are hierarchical, they can easily be incorporated into the Linnaean hierarchy, as shown in Figure 9. (Remember Linnaeus? If not, go back to page one.)

In cladistic analysis, all taxa must be **monophyletic**, meaning that they must include the common ancestor (almost always hypothetical) and all descendants of that common ancestor. Thus, in the cladogram above, OTUs 2 and 7 together with their common ancestor (at the branch point just below them) constitute a monophyletic genus, as do OTUs 1, 4, 6 and 8 and their common ancestor (at the branch point just above the appearance of character d).

A Family consisting of only OTUs 2 and 7 would not be monophyletic, because it does not include all the descendants of the common ancestor (at the branch point just below character d). Such a group would be considered **paraphyletic** (containing some, but not all, of a particular ancestor's descendants).

A Family consisting of OTUs 2 and 7 plus OTUs 3 and 5 would be considered **polyphyletic** (consisting of species derived from more than one most recent common ancestor). This is because such a taxon would be made up of groups descended from both the ancestor just below the appearance of character h, and the one just below the appearance of characters c and e.
Figure 9. Incorporated results of a cladistic analysis showing Linnaean relationships among the OTUs.

**Exercise: Constructing a Cladogram Based on Synapomorphies**

Using the Caminalcules in the packet at your lab station, go through the steps of sample cladistic analysis we did for the Caminalcules in Figure 7. Use the Tables 5 and 6 to list shared, derived characters that help you group the OTUs into taxa that reflect their (hypothetical) evolutionary relationships. Finally, in the space provided, draw a cladogram of your Caminalcules, showing the appearance of each character, as in Figure 9. Is it rooted or unrooted? Be careful!

**Outgroup Analysis: Rooting the Tree**

As you may already realize, your phylogenetic tree of Caminalcules should be **unrooted** because you have no way to know which character states are derived. One is tempted to automatically assume that a more complex form is the more derived state. However, there is always the chance that a taxon has **lost** an ancestral character (or character state). (Can you think of any examples in our own species?)

To root your tree, you will need to consider the character states in an **outgroup**. But how? Fortunately, we have some for you right here in the lab.

Once you have completed your initial analysis and your cladogram has been examined and approved by your laboratory instructor, select a member of your team to go to the front desk and randomly select a card from the envelope labeled “outgroups.”

Each card has an illustration representing one individual of a species of Caminalcules related to yours, but not in the same taxa. Use this outgroup to root your tree. Note that the rooted tree may be quite different from your unrooted one.
Table 5. Character states in Caminalcule Packet.

<table>
<thead>
<tr>
<th>character</th>
<th>state of character if (+)</th>
<th>state of character if (-)</th>
</tr>
</thead>
<tbody>
<tr>
<td>a</td>
<td></td>
<td></td>
</tr>
<tr>
<td>b</td>
<td></td>
<td></td>
</tr>
<tr>
<td>c</td>
<td></td>
<td></td>
</tr>
<tr>
<td>d</td>
<td></td>
<td></td>
</tr>
<tr>
<td>e</td>
<td></td>
<td></td>
</tr>
<tr>
<td>f</td>
<td></td>
<td></td>
</tr>
<tr>
<td>g</td>
<td></td>
<td></td>
</tr>
<tr>
<td>h</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Table 6. Synapomorphies in Caminalcule Packet.

<table>
<thead>
<tr>
<th>character</th>
<th>OTUs</th>
</tr>
</thead>
<tbody>
<tr>
<td>a</td>
<td></td>
</tr>
<tr>
<td>b</td>
<td></td>
</tr>
<tr>
<td>c</td>
<td></td>
</tr>
<tr>
<td>d</td>
<td></td>
</tr>
<tr>
<td>e</td>
<td></td>
</tr>
<tr>
<td>f</td>
<td></td>
</tr>
<tr>
<td>g</td>
<td></td>
</tr>
<tr>
<td>h</td>
<td></td>
</tr>
</tbody>
</table>

A Cladogram of Caminalcules:
II. Systematics and Taxonomy: Getting a Handle on Biodiversity

You may be wondering what all this classification has to do with your biodiversity project. In short: everything. The ecologist who cannot identify organisms from a field study will be unable to draw conclusions about specific findings in a study of biodiversity. Unless you know what you are looking at, you will not be able to do further research into the basic characteristics of organisms that can determine where they live, what their environmental tolerances are, and other basic information that will help you make sense of this project.

Exercise IV. Constructing an Identification Key for a Field Sample.

Before you came to lab today, you were instructed to bring a sample of sediment from a local body of water in a plastic cup, using the techniques described in section A (Collecting Data) below. This is where you get to meet who’s who in your sample and to practice identifying organisms you will commonly find in our local bodies of water (and in your actual project samples).

Before you begin, your lab instructor will guide you through a series of live, known samples we have available for you in the lab, and show you the proper technique for viewing them under the microscope. There are also prepared slides showing preserved, stained specimens so that you can observe them to get an idea of their general characteristics.
A. Collecting Data
Each student should collect a known volume of water (or sediment, as the case may be) from your choice of aquatic ecosystem/microhabitat on campus or near your home. Place your sample in a covered, plastic container and label it with:
   a. your name
   b. your lab section
   c. the type of ecosystem (freshwater? Brackish canal? Lake Osceola? Be as specific as possible)
   d. type of sample (water column? Water surface? Sediment?)
   e. Date and time of day the sample was collected.
To observe your organisms, draw up one cc (= one milliliter (mL)) of sample. (Again: be sure everything is properly labeled so that your samples won’t be misidentified.) To count organisms in your sample:
1. Place two drops of your sample on a convex microscope slide
2. Drop a coverslip onto the liquid
3. Place one drop of methyl cellulose at the edge of the coverslip, and allow to diffuse under the coverslip. (This will slow down any rapidly swimming microorganisms)
4. STARTING ON LOW POWER, observe your sample under the microscope.
5. Begin at one corner of the coverslip, and gradually work your way across and down, in a zig-zag pattern, until you have observed the entire coverslip field.
6. Whenever you find a motile organism (protist or animal), stop and identify it as completely as you can by using the Identification Guide following this section.
   Online sources and the Photo Atlases in lab can also be useful.
7. Record your results on the appropriate tally sheets provided.
8. Write down the characteristics that allowed you to identify your organism in each case.

B. Organism Identification Guide
Since this is your first introduction to some of the vast diversity of Life, we don’t expect you to be able to identify with any great precision the many organisms we hope you will see. However, this guide should help you narrow down the identification of the living organisms in your sample.
   Feel free to use online resources for identification. Once you have identified an organism as a diatom, for example, a Google image search might well yield a possible identity for your organism. (Be careful, though. When it comes to protists, it sometimes takes a real expert to tell them apart. We’ll be happy if you learn to tell a flagellate from a ciliate at this stage of the game.)
   A broad overview of the types of organisms you might encounter can be found at these handy sites:

   http://tinyurl.com/tmhz

   http://www.microscopyu.com/moviegallery/pondscum/

If you find something you can't identify, ask your instructor for help.
1. Protists
These are the simplest of the eukaryotic organisms, and they are a very diverse assemblage now assigned to several different candidate kingdoms once subsumed under the now-defunct taxon "Protista." The types you are likely to see today will be very small and usually highly motile. To see them well, you'll probably have to use methyl cellulose to slow them down. Most common in daytime samples will be diatoms and small flagellates. But the occasional ciliate or amoeba will show up.

2. Animalia, Porifera - The Sponges
The sponges are the simplest of animals, and they are found in both freshwater and marine habitats. They are characterized by an amorphous body shape with no distinguishable head or tail end. Lacking true tissues, these animals have an array of diversified cell types, each of which performs a specific function. But you will not likely to be able to see individual cells in a sponge under the microscope. It will just look like an amorphous blob with slightly greater degree of organization than pond sludge. You can find a variety of freshwater sponge images as [http://tinyurl.com/porif](http://tinyurl.com/porif)

3. Animalia, Cnidaria - Radially Symmetrical Diploblasts
Found in both freshwater and marine habitats, these animals are radially symmetrical (i.e., the body is divisible into identical "pie shaped" wedges) and have two true tissue layers (endoderm and ectoderm). The most common ones in freshwater will be hydras, and in marine habitats you may find small medusae, the free-swimming "jellyfish" form cnidarians sometimes take. Check out some images here: [http://tinyurl.com/pondhydra](http://tinyurl.com/pondhydra) [http://tinyurl.com/fwmedusa](http://tinyurl.com/fwmedusa)

4. Animalia, Platyhelminthes - The Flatworms
If the body is dorsoventrally flattened (i.e., flattened from "top" to "bottom") and there is a distinct head end that guides the animal's movements, there's a good chance you're looking at a flatworm. (If you're not sure, call the instructor for a positive I.D.) These animals have three true tissue layers (endoderm, ectoderm and mesodermal mesenchyme) and simple organ systems. View a flatworm in action at [http://www.youtube.com/watch?v=_jjzQrR5PLQ](http://www.youtube.com/watch?v=_jjzQrR5PLQ)

5. Animalia, Rotifera - The Wheel Animalcules
These tiny animals are no bigger than a large protist, yet they have three true tissue layers and complex organ systems. They feed by means of a cephalic (head end) corona of cilia which beats food particles from the water into the mouth. They also use the corona for swimming; it pulls the animal through the water like a little propeller when it decides to weigh anchor (pull up its sticky pedal disk) and move.
Check out the dramatic video of rotifers at [http://www.youtube.com/watch?v=YF8OJt_pujc](http://www.youtube.com/watch?v=YF8OJt_pujc) And yes, that's the rotifers singing.

6. Animalia, Nematoda - The Roundworms
These worms are very thin, symmetrical, and tapered at both ends. There is no evidence of body segmentation, and they move with a characteristic sinusoidal wave motion unique to this phylum. This is because the body wall has only longitudinal muscles, another characteristic unique to this phylum. Nothing else moves quite like a nematode, and you can see them swimming at [http://www.youtube.com/watch?v=SpgjnXEfadg](http://www.youtube.com/watch?v=SpgjnXEfadg)
7. Animalia, Annelida - The Segmented Worms

The familiar earthworm is a member of this large, diverse phylum. You can identify a segmented worm by the ringlike markings on its body, which delineate the body segments. Internally and externally segmented, the body design and function is based on this characteristic metamerism, which is found in many other more derived (i.e., not primitive) animal taxa. Paired bristles are a dead giveaway that you’re looking at a segmented worm (either a polychaete or an oligochaete). Check them out at: http://www.youtube.com/watch?v=X7O7UFOmRuk (annelid at 00:38)

8. Animalia, Mollusca - The Mollusks

Closely related to the Annelids, the mollusks have secondarily lost their body segmentation, though it is present in the larval forms which you might see in your sample today. Mollusks can usually be identified by the presence of a distinct head and a muscular foot, though if you happen to find a bivalve, these features will be hidden inside the two shells.


Closely allied to the arthropods, the tardigrades are microscopic, segmented, cuticle-covered cuties. They can survive in the most extreme environments known, which makes them of great interest to the folks at NASA. Check them out here: http://www.youtube.com/watch?v=6H0E77TdYnY

Watch the water bear meet a Paramecium at: http://www.youtube.com/watch?v=iLj4tBp00wo

10. Animalia, Arthropoda - The Arthropods

This is the most diverse of all animal phyla, with hundreds of thousands of species (The beetles alone comprise more than 350,000 described species!). Arthropoda includes the familiar insects, crustaceans, and spiders, as well as other less familiar forms. Like the annelids to which they are closely related, the arthropods show distinct body segmentation. And if it has distinctly jointed appendages, it's an arthropod.

11. Animalia, Echinodermata - The Spiny-Skinned Animals

Our closest invertebrate relatives that you might see today are the starfish and their relatives, though you'll probably see only ciliated larval forms. Adults are pentaradially symmetrical. These animals are strictly marine, and may not be present in either of your samples. Their lack of an excretory system makes osmoregulation in freshwater or brackish water impossible for them, so you will find them only in oceanic ecosystems.

12. Animalia, Chordata - The Chordates

This familiar group includes the sea squirts (Urochordata), the lancelets (Cephalochordata) and the vertebrates (Vertebrata). All are united by the presence of a cartilaginous skeletal support rod (the notochord) present at some time during development, a muscular, post-anal tail, segmentally arranged muscle bundles (at least in development) and pharyngeal gill slits. The only kinds you're likely to see today are fish or amphibians, if any. We just thought you'd like to know they're there.

Using the general identification guide above along with your Photo Atlas, try to locate and differentiate as many different species within the listed taxonomic groups as you can. Simply use hashmarks to keep count of the number in each category, and enter these on the tally sheets provided for each of the two habitats sampled.
Now consider the list of organisms you have found, and the characteristics you used to identify them. Construct a simple identification key to these organisms in the space below.

**A Taxonomic Key for Identification of Aquatic Organisms**

1a. _____________________________________________
1b. _____________________________________________

2a. _____________________________________________
2b. _____________________________________________

3a. _____________________________________________
3b. _____________________________________________

4a. _____________________________________________
4b. _____________________________________________

5a. _____________________________________________
5b. _____________________________________________

6a. _____________________________________________
6b. _____________________________________________

7a. _____________________________________________
7b. _____________________________________________

8a. _____________________________________________
8b. _____________________________________________

9a. _____________________________________________
9b. _____________________________________________

10a. _____________________________________________
10b. _____________________________________________

11a. _____________________________________________
11b. _____________________________________________

Wasn’t that fun? Just a little?