Systematics

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This lab handout contains a few exercises designed to help you become familiar with some important concepts of systematics, the science of classifying organisms evolutionarily.

Keep these definitions in mind as you go through the handout:

Cladistic — A style of systematics in which each characteristic represents a single evolutionary change and no characteristic is considered to be more or less important than others.

Cladogram — A diagram for representing a cladistic phylogeny. Cladograms normally feature only 2-way branching, not multiple branches arising from a single branch point. In a cladogram, each branching point refers to a specific evolutionary change.

Parsimonious — In general use, parsimonious means not wanting to spend money. In scientific terms, we say that an explanation is parsimonious if it's as simple as it can be.

Phylogeny — The evolutionary history or relationships of a group of organisms.

Taxon — (plural: **taxa**) A taxonomic group of organisms – species, family, class, etc.

Taxonomy — The study of naming and classifying organisms. This means basically the same thing as systematics, but the word systematics emphasizes evolutionary relationships.

As you go through the handout, look for the numbered items in bold type:

1. ***This means you're supposed to do something! Answer a question, draw a diagram, or whatever the text says.***

Work together with one partner. Go through the handout, answer all the questions on separate paper, and turn in one set of answers with two names on it.

CLASSIFYING YOUR CLASSMATES

Make your own classification scheme for yourself and your fellow students. This could be tricky, because you already have some preconceived ideas about the genetic relationships among humans. However, to make a scientifically valid classification scheme, you should only use characteristics you can directly observe. So "Asian" wouldn't be a good characteristic to use, because that's based on some observable characteristics and some assumptions. On the other hand, "pierced eyebrow" would be a good characteristic, because you can directly observe it. Your goal should be to create a classification scheme that fits the things you can observe, rather than fitting your preconceived ideas of relatedness. Just look for observable characteristics that allow you to differentiate between one person and another.

1. **Draw a cladogram to classify at least 8 people in the room. Each branching point in the cladogram should represent a characteristic that is present in one branch (people with pierced eyebrows) and not present in the other branch (people without pierced eyebrows). Each branch should be a 2-way split. A stranger should be able to come into the room and use your cladogram to identify the individuals in the group.**

Your classification scheme may not fit into the established taxonomic hierarchy of family, genus, species, et cetera. That's OK; we know we're all the same species anyway. Also, this makes sense in terms of a strictly cladistic approach to systematics. Cladistics sets out to describe evolutionary history, rather than to fit organisms into a predetermined set of taxonomic categories.

Your cladogram should fulfill one of the goals of doing systematics: so you can know what species (or in this case, what individual) you're talking about. But does it also fulfill the other goal of systematics by accurately describing a set of evolutionary relationships? Probably not. The problem is that characteristics shared by two different individuals (pierced eyebrows, for example) may not reflect common ancestry. In other words, they may not be homologous.

CLASSIFYING FAMILIAR ORGANISMS

You already have some idea of how various kinds of organisms should be grouped together. You'd probably guess that you are more closely related to a ferret than you are to asparagus. However, would you say you're more closely related to asparagus or to yeast? Sometimes it's hard to tell.

The fundamental point of modern systematics is that organisms should be grouped together on the basis of shared evolutionary history as inferred from observable characteristics.

2. **Draw a cladogram to classify at least 8 different species that you are familiar with. (Try to come up with species that are not closely related to each other. No more than 4 of the species should be animals.) At each branching point in the cladogram, write in a specific characteristic that is present in the organisms on one branch, and not present in the organisms on the other branch.**

THE PROBLEM OF HOMOLOGY VS. ANALOGY

Homology is a simple concept, but often tricky in practice. **Homologous** means "the same by descent:" a trait found in species A is homologous to a similar trait in species B if both species inherited that trait from the same common ancestor.

The basic question in homology vs. analogy is this: if two different species have some similar characteristics, does that mean they're closely related? For example, if grass is green and grasshoppers are green, does that they both inherited their greenness from a common green ancestor? In this case, the answer is no; the green color of grasshoppers is not homologous to the green color of grass. Characteristics that are similar between two species but are not derived from the same common ancestor are called **analogous**.

If you want to make a cladogram that truly expresses phylogenetic relationships, you somehow have to be able to identify characteristics that are homologous between different groups of organisms, as opposed to characteristics that are analogous. Did this difficulty arise in the cladogram you just did? It should certainly arise in the next one.

MAKING A CLADOGRAM WITH UNFAMILIAR SPECIES

Now it's time to try classifying some organisms when you really don't know how they're related to one another. Remember that in cladistics, you base your classification scheme on specific characteristics that represent evolutionary changes in a lineage; you don't weight one kind of change more than another, and you don't group organisms based on your impression of their overall similarity.

You don't always know if a characteristic that is shared by two groups is homologous or analogous. Did the trait evolve just once or more than once? You have to look for the most parsimonious cladogram, which is the one that assumes the smallest number of evolutionary changes. An evolutionary change could mean a new characteristic appearing or an old one disappearing.

3. **Make a cladogram based on the table below.** The table lists 13 species, along with some of their traits. You may not be familiar with all (or any!) of the species listed, but the information in the table should be enough for you to make a cladogram. Your cladogram won't necessarily be right in terms of evolutionary relationships (because there are many other traits to consider), but it should be consistent with the data in the table.

Species	Chloroplasts	Mitochondria	Notochord	Nucleus	Mammae	Flowers	Amniotic eggs	Chitin Exoskeleton	Focusing Eyes	Collagen	Histones	Cell Wall
Circus cyaneus	0	1	1	1	0	0	1	0	1	1	1	0
Culex tarsalus	0	1	0	1	0	0	0	1	0	1	1	0
Eschscholzia californica	1	1	0	1	0	1	0	0	0	0	1	1
Giardia lamblia	0	0	0	1	0	0	0	0	0	0	1	0
Halalkalicoccus tibetensis	0	0	0	0	0	0	0	0	0	0	1	1
Helix aspersa	0	1	0	1	0	0	0	0	0	1	1	0
Hyla regilla	0	1	1	1	0	0	0	0	1	1	1	0
Loligo opalescens	0	1	0	1	0	0	0	0	1	1	1	0
Procyon lotor	0	1	1	1	1	0	1	0	1	1	1	0
Serratia marcescens	0	0	0	0	0	0	0	0	0	0	0	1
Ulva lactuca	1	1	0	1	0	0	0	0	0	0	1	1

You don't need to know the details of all the listed characteristics in order to make a cladogram. Many of these characteristics will be discussed in detail later in Bio 6A or in 6B. For now, here are some brief explanations:

Chloroplasts mitochondria, nucleus and *cell wall* are specialized structures found in some types of cells.

Amniotic egg refers to a type of egg with a specific set of surrounding membranes that protect the egg.

Histones are a specific type of protein that is bound to DNA in some organisms.

Collagen is a type of protein that binds the cells together in some groups of organisms.

Note that the species and the traits are not listed in any particular order. You can start by trying to draw a cladogram or by reorganizing the table and grouping together species with similar characteristics. Please don't look up the species to see what they look like – that would give you a preconceived idea of how the organisms should be grouped, and that's exactly what cladistics is supposed to avoid.

4. Give two examples of homology from your cladogram.

5. Give two examples of analogy from your cladogram.

MAKING A CLADOGRAM WITH PROTEIN SEQUENCES

One big problem with the cladogram you just made is that you don't necessarily know which characteristic to put in the cladogram first. A cladogram that truly reflects evolutionary history would have the characteristics that evolved earliest near the root (bottom) of the cladogram – but how would you know if it's right?

There's another way of figuring out relationships that avoids this problem by using DNA or protein sequence data. As you may know, both DNA and proteins are huge molecules that are made up of strings of smaller subunits. A DNA molecule is a chain of nucleotides, and a protein molecule is a chain of amino acids. (Don't worry – we'll cover this in great detail in Bio 6B.) Just as all words in the English language use the same set of 26 letters, all proteins in an organism use the same set of 20 or so amino acids. However, the number of possible combinations of letters or amino acids is infinite. Therefore, you can compare one protein to another by comparing the sequence of amino acids.

Take a look at the short sequences listed below. Each letter represents one kind of amino acid (V for valine, A for alanine, etc.). Each 17-letter sequence represents a short piece of a protein (a whole protein could have hundreds of amino acids).

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#1  V N F K L L S H C L L V T L A A H
#2  V N F K L L S H C L L V T L A C H
#3  E N F R L L G N V L V C V L A H H
#4  E N F K L L G N V L V C V L A H H
#5  K Y L E F I S E C I I Q V L Q S K
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Your task is to use a cladogram to group the sequences by similarity. Note that sequences 1 and 2 are nearly identical, differing only at the second-to-last amino acid position, while sequences 1 and 5 have many differences.

6. **First, fill in the table below to show how many differences there are between each pair of sequences.** For example, if you compare sequence 1 to sequence 2, you should see 1 difference. Write a 1 in the first column across from the 2. Half of the table is grayed in because you only need to use half.

	1	2	3	4
1				
2				
3				
4				
5				

7. **Now draw a cladogram based on the table you filled in.** If two sequences are similar, they will be close together, separated only by a short branch. If two sequences are very different, they will be separated by a branch closer to the bottom of the cladogram.