Cladistics (Phylogenetic Analysis)

Objectives:

- Understand what the basic components of evolutionary trees are: **nodes, branches,** and **branch tips**. An evolutionary family tree is also called a **phylogeny,** and the study of these trees is called **phylogenetics.**
- Understand the difference between **anagenesis** and **cladogenesis** (splitting of lineages by speciation), and how those concepts relate to evolutionary trees.
- Understand the difference between a **derived** trait and an **ancestral** trait, and between a **synapomorphy** and a **symplesiomorphy**; and, which traits are useful for determining evolutionary relationships.
- Understand what a **monophyletic** group is. Quotation marks are often used for groupings that are not monophyletic (**paraphyletic** or **polyphyletic**).
- Be able to build and interpret evolutionary trees.

Introduction
  ▪ **Basic Tree Structure**
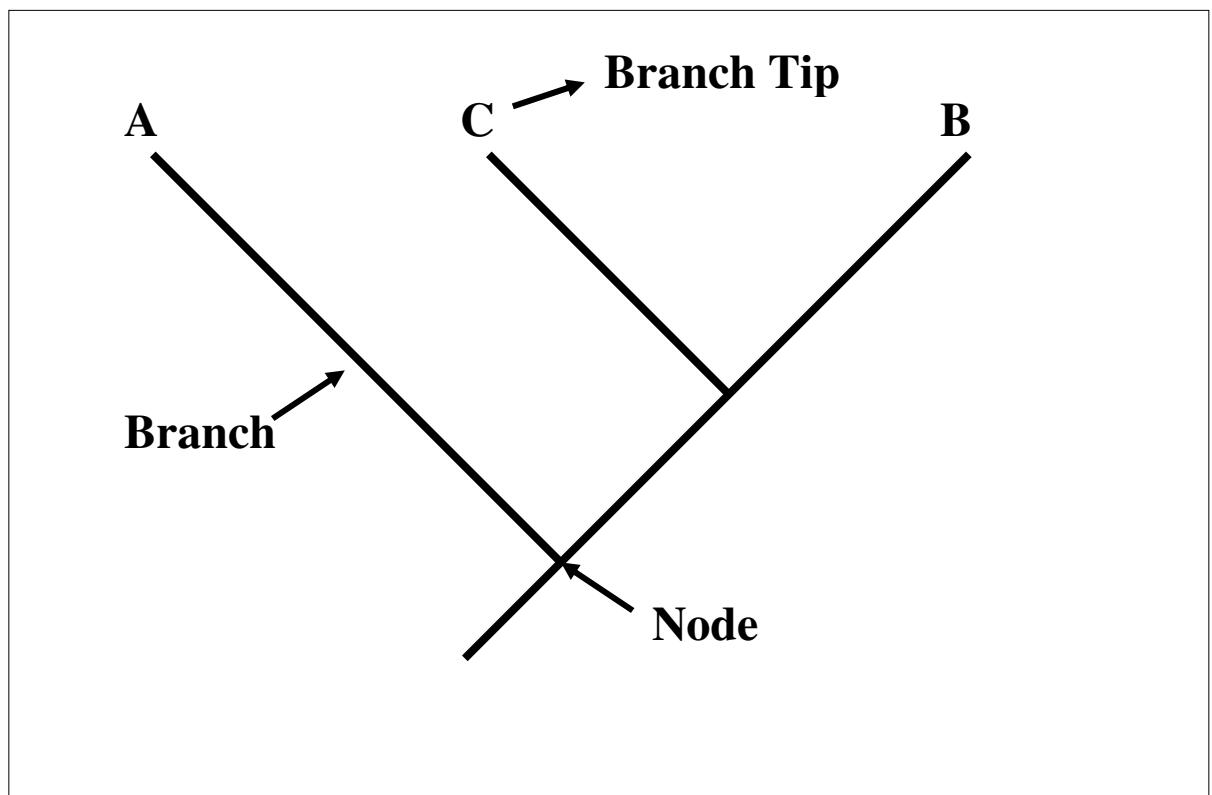
Anagenesis vs. Cladogenesis
- **Anagenesis –** evolution along a single branch within the evolutionary tree.
- **Cladogenesis –** an ancestral population undergoes speciation, splitting into two new groups that evolve independently of one another.
- **Node –** an ancestral population that underwent Cladogenesis.
- **Branch –** one of the two (or more) new distinctly evolving groups (lineages) that emerge from a node.
- **Branch tips –** the groups at the ends of the branches, these are the groups that whose evolutionary relationships are being depicted by the phylogenetic tree.
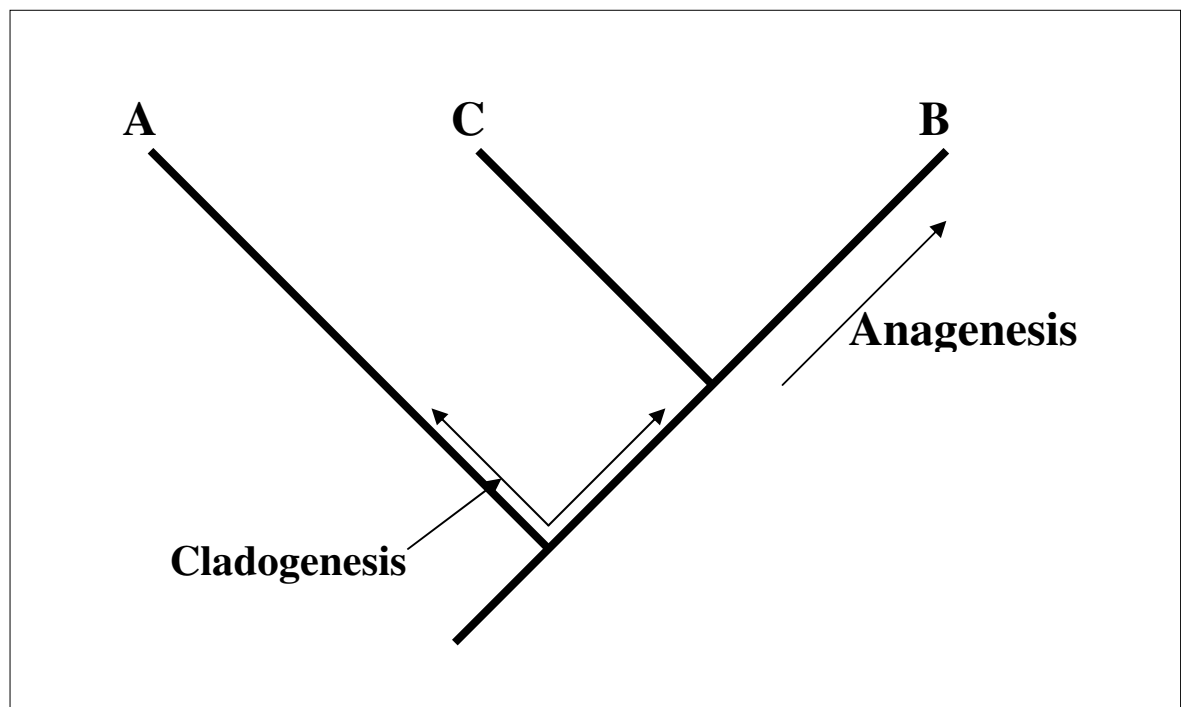

Ancestral vs. Derived Traits and **Synapomorphies**
- Derived traits and synapomorphies help us to determine the evolutionary history of the groups we are interested in.
- **Derived trait –** a trait that is unique to that group (e.g. trait 3 is unique to group B)
- **Ancestral Trait –** e.g. Trait 1 is not unique to group B because it is also found in A and C
- **Synapomorphy –** a shared derived trait (e.g. Trait 2 is a synapomorphy for the group containing B & C)

- **Symplesiomorphy** – shared ancestral traits (these are not useful in working out evolutionary relationships).
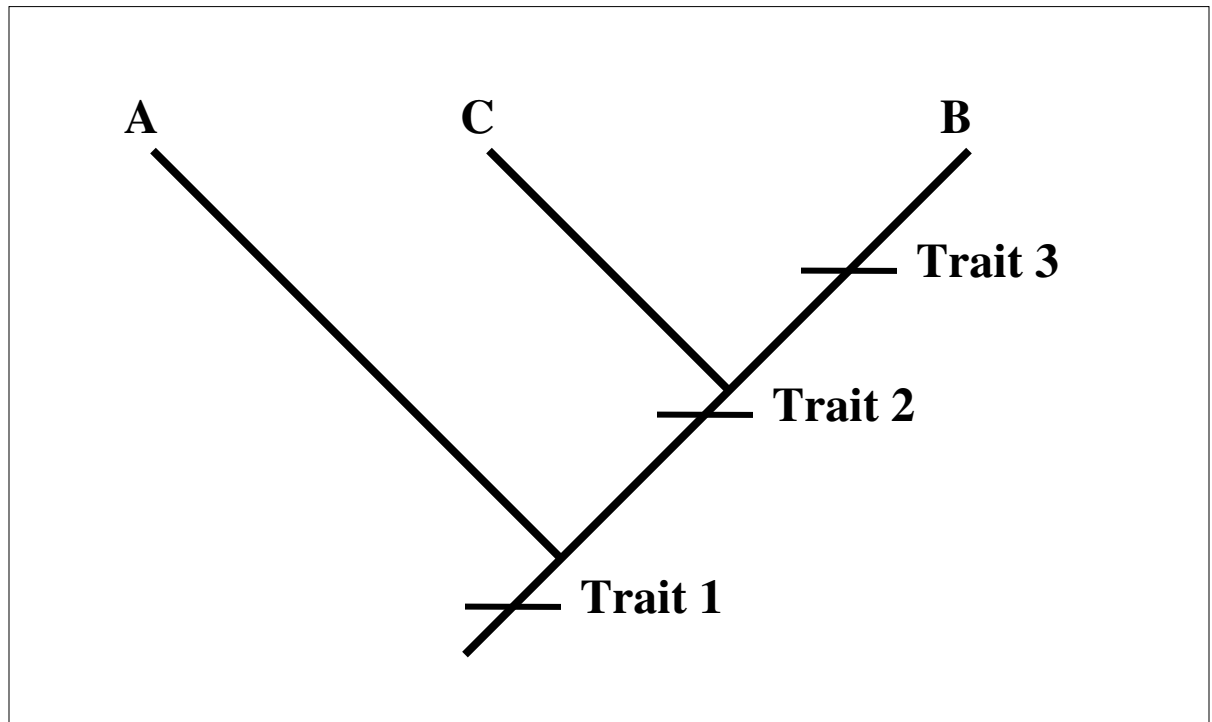
- **It's all relative** – Determining if a trait is derived or ancestral all depends on the groups you are investigating. For example, possessing feathers is a synapomorphy for birds that distinguish them from other reptiles. However if you are looking at the evolutionary relationships among birds, you would not say that possessing feathers is a derived trait for ostriches because feathers are found in all birds. Thus, in this case, the trait would be considered ancestral and would not help us in determining the evolutionary relationships within birds.

- **Monophyly** – a monophyletic group is a group comprised of an ancestor and <u>all</u> of its descendants.
    - A group containing B & C is monophyletic. It includes Ancestor 2 and all of its descendants.
    - A group containing A & C is not monophyletic. Its most recent common ancestor is Ancestor 1, and B is also a descendent of this ancestor.
    - When discussing groups that are not monophyletic, quotation marks are used. For example the group "reptiles". The common use of this term includes turtles, crocodiles, squamata (lizards and snakes), and extinct lineages such as dinosaurs, but birds have been traditionally excluded. If we are to consider reptiles a monophyletic group, birds must be included because they are derived from within the therapod dinosaurs.
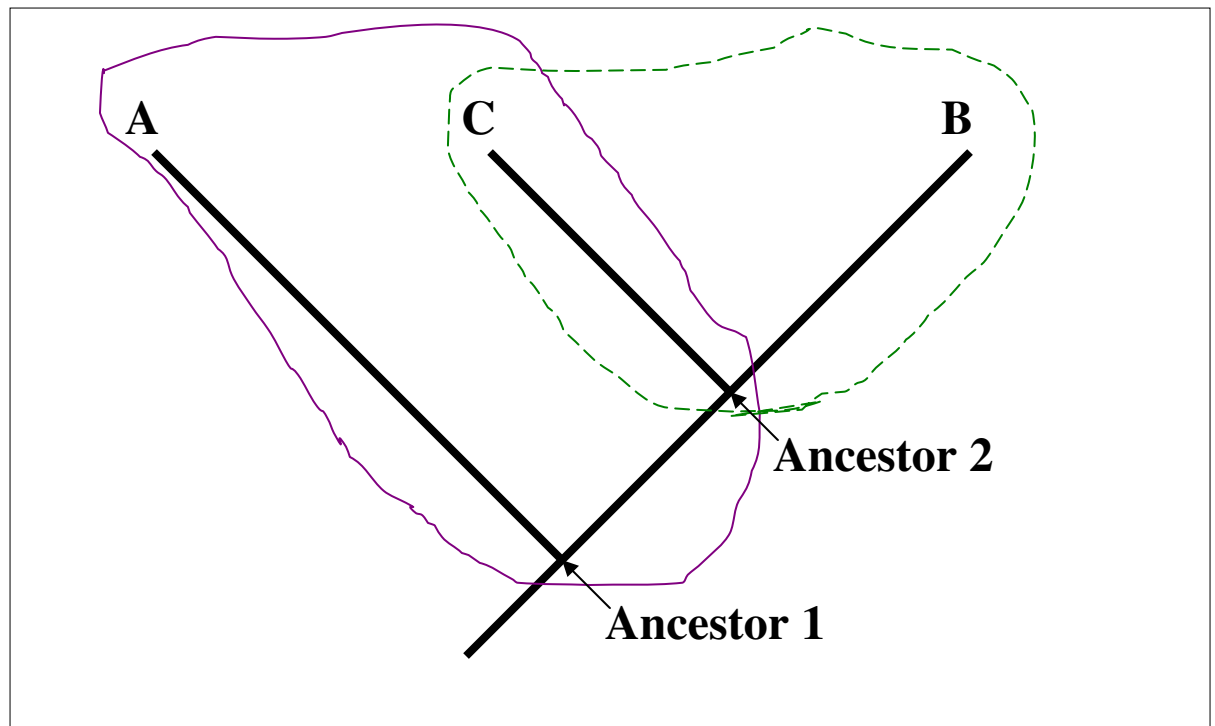
Exercise 1 – Tree Thinking Challenge

On your desk you will find a recreation of the phylogenetic tree depicted in Baum et al. (2005) made out of K'nex. Use this tree to answer to do the following activities and answer the associated questions.

On your K'nex tree, identify the nodes, branches, and branch tips.

Based on this tree is a frog more closely related to a fish or a human? WHY?


Phylogenetic Tree from Baum et al. (2005):
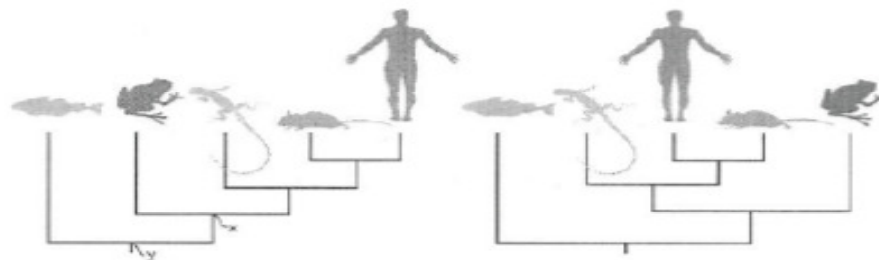
Which phylogenetic tree is accurate? On the basis of the tree on the left, is the frog more closely related to the fish or the human? Does the tree on the right change your mind? See the text for how the common ancestors (x and y) indicate relatedness.

Identify the node that represents the most recent common ancestor of a frog and a fish, and identify the node that represents the most recent common ancestor between a frog and a human. Does this clarify your answer above?

Now manipulate your tree so that it looks like the tree depicted on the right in the above diagram from Baum et al. (2005), and identify the node that represents the most recent common ancestor between a frog and a human. Did this change from your previous answer? Why or why not?

Answer the following questions:
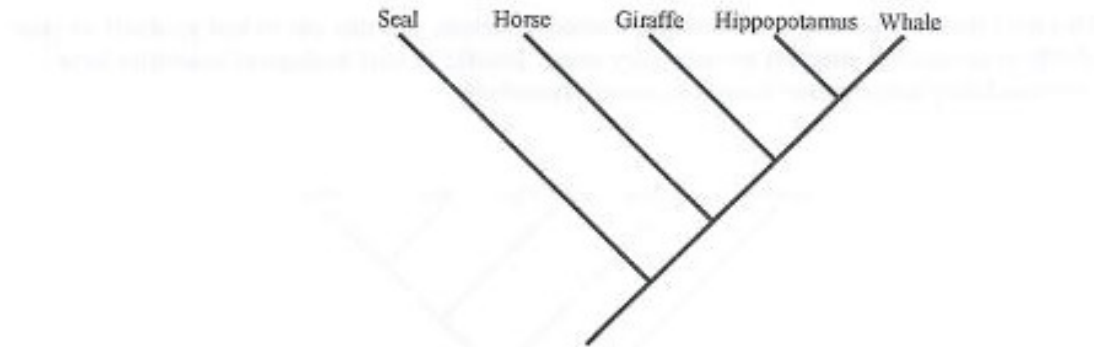

Amoeba   Red Alga   Green Alga   Moss   Pine
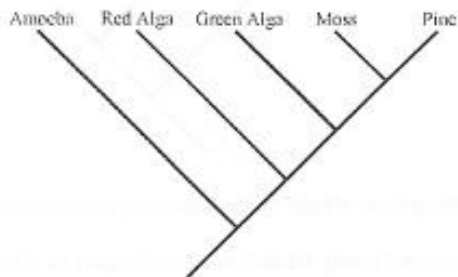
1) By reference to the tree above, which of the following is an accurate statement of relationships?
   a) A green alga is more closely related to a red alga than to a moss
   b) A green alga is more closely related to a moss than to a red alga
   c) A green alga is equally related to a red alga and a moss
   d) A green alga is related to a red alga, but is not related to a moss

Lizard   Crocodile   Dinosaur   Bird
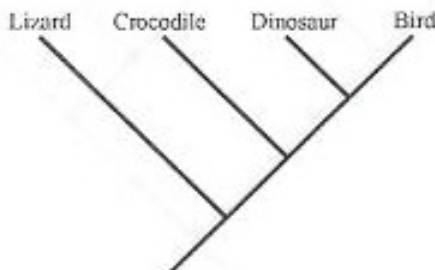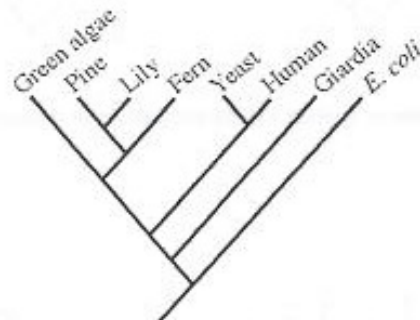
2) By reference to the tree above, which of the following is an accurate statement of relationships?
   a) A crocodile is more closely related to a lizard than to a bird
   b) A crocodile is more closely related to a bird than to a lizard
   c) A crocodile is equally related to a lizard and a bird
   d) A crocodile is related to a lizard, but is not related to a bird
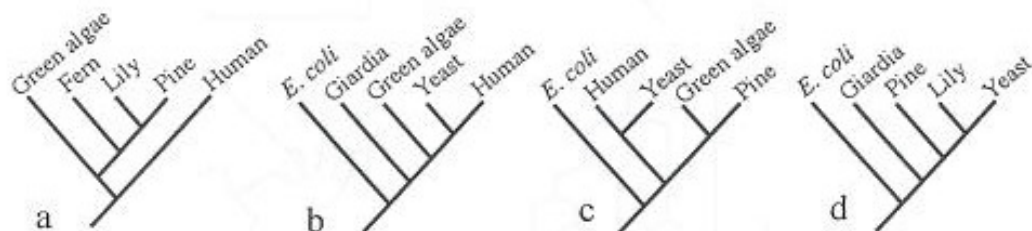
Seal   Horse   Giraffe Hippopotamus Whale

3) By reference to the tree above, which of the following is an accurate statement of relationships?

        a) A seal is more closely related to a horse than to a whale
        b) A seal is more closely related to a whale than to a horse
        c) A seal is equally related to a horse and a whale
        d) A seal is related to a whale, but is not related to a horse

Green algae Pine Lily Fern Yeast Human Giardia E. coli

6) Which of trees below is false given the larger phylogeny above?

a) Green algae Fern Lily Pine Human

b) E. coli Giardia Green algae Yeast Human

c) E. coli Human Yeast Green algae Pine

d) E. coli Giardia Pine Lily Yeast

G B D E C A F   G F A B C E D

a   b

G F A B C E D   G A B E D C F

c   d
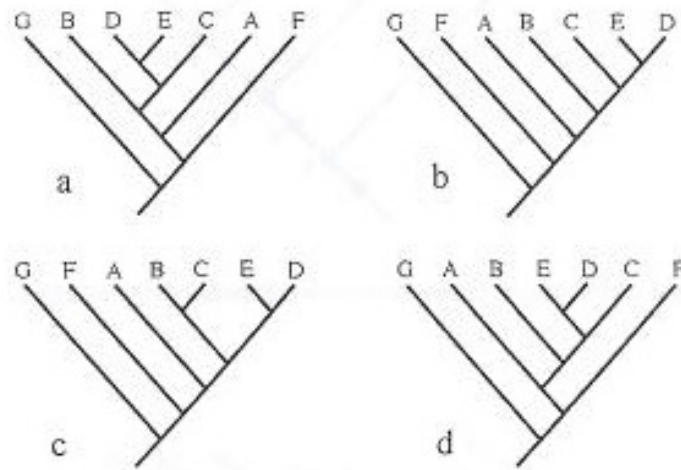
7) Which of the four trees above depicts a different pattern of relationships than the others?
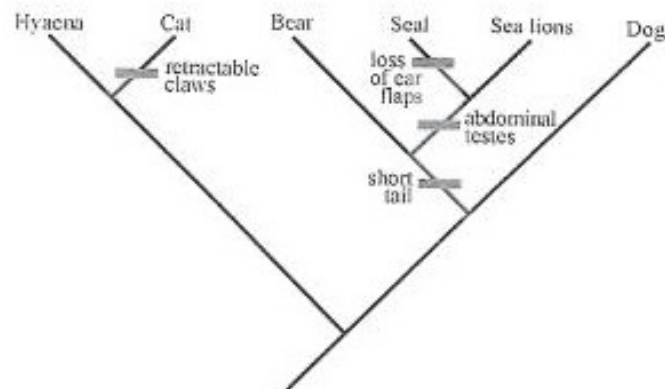
9) In the above tree, assume that the ancestor had a long tail, ear flaps, external testes, and fixed claws. Based on the tree and assuming that all evolutionary changes in these traits are shown, what traits does a sea lion have?

    a) long tail, ear flaps, external testes, and fixed claws
    b) short tail, no ear flaps, external testes, and fixed claws
    c) short tail, no ear flaps, abdominal testes, and fixed claws
    d) short tail, ear flaps, abdominal testes, and fixed claws
    e) long tail, ear flaps, abdominal testes, and retractable claws

Exercise 2 – Building a Tree, part 2A: four initial species

You and your crew of exobiologists (biologists studying life outside Earth) are on a mission to study life in the galaxy. At each planet you landed on, your job was to gather data for your supercomputer to analyze. The computer is then able to give the evolutionary relationship for all the life forms in each planet.

Assume that your ship had reached a new destination, planet BI-140 in the WSU system. As you ready your expedition on the planet, the super-highly-intelligent computer decided to take a vacation, shutting down all the non-essential systems and leaving only the life support system for the crew. In its last message, the computer promised to return once the crew had finished creating a cladogram for life on this planet. To aid in creating a cladogram, the computer left you this list of instructions before it took off:
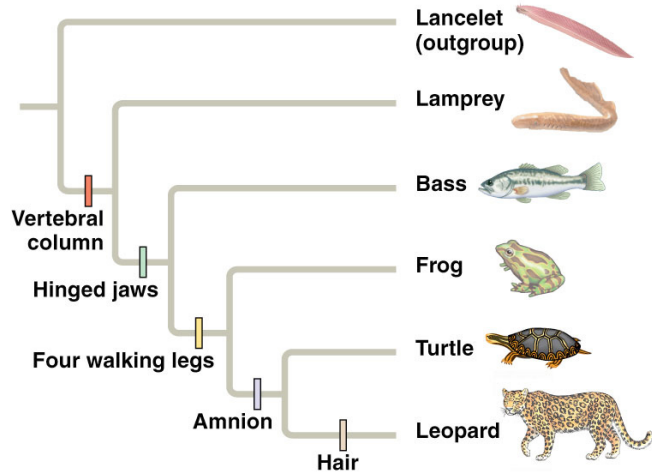
- Gather the data you have on the life forms found on this planet.
- List all the characteristics of each creature. The characteristics you can use are anything you can observe - texture, number of digits, color, appendages (limb, horn, wing, antenna, etc...), relative size. The characteristics that you **cannot** use are absolute size (these holographic reconstructions lack any information about absolute size), the inside of the creature (you do not have the equipment to dissect these creature), and any reference to any animal on Earth. <u>Remember this is not Earth, these animals might look superficially similar to Earth creatures, but they are not Earth creatures</u>. (For this reason, if it looks like a duck, call it a duckoid or neo-duck or quacker or Donald instead of the Earth-name "duck".)
- Consider whether the characteristics you listed are defining characters for any group. Determine if these characters are derived or ancestral.
- Between the nodes on your tree, you must have a character state change.
- Use the principle of parsimony (=simplicity) to create the best possible cladogram (i.e. the one that requires the fewest number of trait changes).

Here is a helpful example of generating a tree by using a character matrix:

TAXA

CHARACTERS	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
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(b) Phylogenetic tree

Other good examples are shown at these addresses online:

http://abacus.bates.edu/acad/depts/biobook/Clado1.pdf

http://abacus.bates.edu/acad/depts/biobook/Clado2.pdf

Create your <u>Character Matrix</u> on a separate sheet of paper. Discuss this matrix, and share it with the other students in your group. In particular, identify which traits are <u>ancestral</u> for your family tree. A species possessing only ancestral traits may be called an "outgroup" relative to the rest of the tree.

Now, draw a <u>Phylogenetic Tree (Cladogram)</u> based on your character matrix. Make sure to show <u>changes in traits</u> on your tree, in the manner shown above! Ask for help if you need it.

Exercise 2, part 2B: three more species

You and your crew have conducted a second exploration of planet BI-140 and have discovered three additional species. (This is not so far-fetched: imagine Spanish and Portuguese explorers encountering American species for the first time in the 1500s, or Captain Cook and his crew finding Australian species in the late 1700s.)

Create a new, enlarged character matrix that includes all seven species. (Did you need to reassess what traits were ancestral and which were derived?)

Draw a new, enlarged phylogenetic tree including all seven species. (Could you easily fit the new species into your original cladogram? Did you need to re-assess the branching sequences, or the direction of evolutionary change?)

Instructions for write-ups:

Each lab group should submit a single joint report, consisting of a Results section and a Discussion. (See Knisely's Handbook, listed on the Syllabus, for an explanation of what these sections mean.)

- The Results should include a four-species character matrix, a four-species cladogram, an enlarged 7-species character matrix, & a 7-species cladogram.
- The Discussion should explain, among other things, how you decided which traits were ancestral, which were derived, which were synapomorphies, and which were potentially misleading.
- See also the general directions for lab assignments posted online at http://abacus.bates.edu/acad/depts/biobook/LabInfo.htm