

Lab 1. The Tree of Life

Notes

- During the first week of classes, lab sections will not meet at the regularly scheduled lab time. Lab 1 is an open lab designed to be completed on your own schedule on Wednesday, Thursday, or Friday afternoons (1:30-4:30pm) of the first week of class.
 - Feel free to complete the lab alone or in small groups.
 - Please complete the activities in this handout in order.
 - For more information on the topics covered in this lab, see the open textbook Biology 2e (<https://openstax.org/details/books/biology-2e>), chapters 20-29. You can either view it online or download a PDF.
 - POST-LAB ASSIGNMENT: Throughout the lab are numbered questions; your responses to those questions, and the completed tree of life handout, constitute your post-lab assignment, due at the start of Lab 2.
 - Bring this handout (all parts) with you to your first regular lab meeting; material in this handout will be used to complete Lab 2.
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Objectives

1. Learn to read and interpret phylogenetic trees.
 2. Gain a stronger sense of the diversity of life and the evolutionary relationships among some of the more common taxonomic groups.
 3. Become more exposed to the major topics that will be covered in BIOL 200.
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KEY WORDS: biodiversity; phylogenetics; speciation; cladogram; phylogeny; node; branch; sister species; root; taxa/taxon; terminal taxa; clade; character; taxonomy; genus/genera; species; morphology

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1 Overview: Biodiversity

Goal: To provide a solid foundation for understanding evolution. A study of college students in introductory biology courses revealed that an early understanding of **phylogenetic trees** (diagrams of evolutionary relationships) is critical to understanding concepts of evolutionary biology. The primary goal

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of this lab is to help you understand how to read and interpret phylogenetic trees. In doing so, you will also benefit in other important ways as indicated in the objectives listed earlier.

Biodiversity refers to the diversity of life on Earth. In one way or another, everything we study in BIOL 200 involves biodiversity. Perhaps you are most familiar with biodiversity as the number of species in a habitat and the relative abundance of each species. However, biodiversity encompasses much more than these measures. Early in the semester we will focus on another element of biodiversity: genetic diversity. In later labs we will shift attention to species diversity and actually measure diversity in a local ecosystem. Towards the end of the course, we will broaden our scope of diversity to include the geographic scale of communities, ecosystems, and biomes.

Today's lab is intended to introduce you to Earth's biodiversity while simultaneously providing a useful framework for talking about biodiversity. In this lab we will learn that it is convenient to talk about biodiversity in a **phylogenetic** context; i.e., based on evolutionary relationships. Thus it is important that in the very first lab of the semester, you become comfortable with reading and interpreting phylogenetic trees.

2 How are organisms related, and how do we depict these relationships?

Currently available evidence suggests that all life on Earth shares a single origin; i.e. every living thing on the planet descends from a single common ancestor that lived around 4 billion years ago. That long-ago ancestor then split into descendant species (a process called **speciation**), which themselves split over and over and over again forming the millions of species on Earth today. Along the way, these species were altered by evolutionary processes such as natural selection and genetic drift, which you will learn about later in the semester. Remember that evolution is nothing more than *the change in genetic structure of populations over time and space*.

How do we depict these genealogical relationships among species, in diagrammatic form? The evolutionary relationships among different species are called phylogenetic relationships, and are typically depicted as a branching diagram referred to as a **cladogram**, a **phylogenetic tree**, or simply a **phylogeny** (all of these words are interchangeable for our purposes). An example phylogeny of different species of oak trees is given on the [Oak Phylogeny Sheet](#) handout. Let's take a few minutes to figure out what is implied by a phylogeny and how to read one.

First of all, how do we read a phylogeny? Go to the Oak Phylogeny Sheet (given at the end of this handout) and look at Tree 1. Find the white oak in Tree 1. If you follow the line leading from the white oak, it intersects with the line leading to the bur oak. The point at which these lines intersect is called a **node** (in this case, it's referred to as node C; all the nodes are assigned a letter in this tree), and this node represents the last shared ancestor of the bur oak and white oak. (The lines themselves are referred to as **branches**; after all, it's a phylogenetic "tree", right?) So, this phylogeny implies that the bur oak and white oak share a common ancestor with each other more recently than with any other group on the tree, and we thus refer to the bur oak and white oak as **sister species**. Another way of thinking about this relationship is that the bur oak and white oak are each other's closest relatives.

It is extremely important to realize that phylogenies imply time in addition to relationships. In other words, the groups you are actually examining or discussing (the **terminal taxa**) are placed at the tips of the branches, and as you follow the branches all the way to the **root** of the tree (the root represents the

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common ancestor of all the species in the tree), you are traveling backwards in time. How much time has elapsed between nodes, you might ask? Well, in a simple cladogram such as the one you see above, the absolute amount of time is not specified; only relative time is implied (i.e., the ancestor at node B must have lived before the ancestor at node C, but how much earlier is impossible to say using this tree alone). There are ways of inferring the absolute amount of time that has elapsed between nodes, but they are beyond the scope of today's lab.

Now let's take some time to practice reading trees. Look at Tree 1 on the Oak Phylogeny Sheet and use it to answer the following questions. Remember to turn in your Oak Phylogeny Sheet along with the completed handout!

1. List the terminal taxon or taxa (in this case, species) identified by their most recent common ancestor, that are sister to each oak below.
 - A. northern red oak is sister to...
 - B. post oak is sister to...
 - C. black oak is sister to...
 - D. swamp white oak is sister to...
2. TRUE / FALSE Swamp white oak is most closely related to bur oak. Briefly explain your answer below.
3. What is the most recent common ancestor of each of the pairs of species listed below? In other words, which node unites the following pairs of species? Write the correct letter for each node in the space next to each pair of species.
 - A. pin oak & shumard oak
 - B. post oak & southern red oak
 - C. bur oak & chestnut oak
4. Rank the following nodes in Tree 1 in order of *increasing* age (i.e. youngest to oldest): A, D, K

3 Rearranging branches on trees

When reading trees, keep in mind that what matters is how the branches connect to the nodes. It is possible to rearrange the order of the branches on a tree **WITHOUT** changing the way the branches attach to each other. These rearranged trees may at first glance look much different than the original, but in fact they depict identical relationships.

5. Refer back to the Oak Phylogeny Sheet, and find Trees A, B, and C. Each of these three trees has the same species as in Tree 1, but the relationships among them are different; i.e. at least some of the relationships differ in each of these three trees. However, **ONE** of the three shows the **exact same** relationships as in Tree 1. Which one?

Now let's add one more wrinkle to reading trees. There are many ways that phylogenies can be drawn, but they all depict the same thing—the evolutionary relationships among taxa. Two frequently encountered alternative ways of drawing cladograms are provided as Trees D and E at the bottom of the Oak

Phylogeny Sheet. **Don't be fooled by the different shapes or by what seem to be extra branches in these depictions**—they still show relationships among species. For example, look at node C in Trees D and E. Node C shows the same sister relationship between white oak and bur oak that is depicted in Tree 1 (convince yourself of this fact). In Trees D and E, there is still just one branch leading from node C to white oak; the branch simply makes a 90° turn along the way!

6. Trees D and E depict identical relationships; they also depict identical relationships with respect to EITHER Tree A, B, or C. Which one of these three trees are Trees D and E identical to?

4 Taxa and clades

Now, let's move on to a couple other items. First, an important note: trees don't have to have species as the organisms at the tips. We can depict the relationships among larger taxonomic groups in exactly the same way as we do individual species. For example, we could show the phylogenetic relationships among the orders of mammals (i.e. branch tips would be labeled "Rodents", "Primates", "Carnivorans", etc. instead of individual species names). For this reason, we can use the catch-all term **taxon** (plural is **taxa**) to refer to any organisms at the tips of a phylogeny. Taxon can refer to any named taxonomic group; e.g. a species is a taxon, a genus is a taxon, an order is a taxon, etc.

Second, another important term to become familiar with is **clade** (which, in fact, is the root word for cladogram). A clade is entirely composed of an ancestor (i.e. a node) and all of its descendants (even those descendants not labelled on the tree). For example, in Tree 1, the group containing node C, its descendant taxa white oak and bur oak, and the branches leading from C to the terminal taxa forms a clade, as does the group containing node B and all its descendants. The latter clade happens to contain the clade defined by node C; in other words, one clade can contain within it many other clades (another way to say this is that clades are nested). Keep in mind that a clade is defined by common ancestry, but, as we will see next week, we identify (or diagnose) clades by traits the organisms share. Definition and diagnosis are different processes, so be sure that you do not confuse them.

NOTE: Now that you've read sections 3 and 4, you might want to review your answers to earlier questions, especially question 1!

Now let's practice taxa and clades—look at Tree 1 on the Oak Phylogeny Sheet and answer the following questions.

7. Which terminal taxa are in the clade that is defined by node E?
8. Now find all of the clades in Tree 1. On Tree F (an exact replica of Tree 1), circle all of the clades you can identify. (Remember, when circling, that the clade is defined by an ancestor and all of its descendants, so all should be contained in the circle.)
9. Below are several groups of taxa, some of which form clades in Tree 1 and others of which do not. Place an X next to each group of taxa below that collectively form a clade in Tree 1.
- A. ___ white oak, bur oak, swamp white oak, Node B, and all of its descendants
 - B. ___ southern red oak, post oak, overcup oak, Node K, and all of its descendants
 - C. ___ black oak, northern red oak, shumard oak and all of Node I's descendants

- D. — northern red oak, pin oak, southern red oak, and Node H
- E. — post oak, overcup oak

Now that we have some practice reading phylogenetic trees, let's try adding taxa to a tree while learning about how to "map" traits onto a phylogeny.

5 Understanding trait evolution on phylogenetic trees

Find the [Tree of Life Sheet](#) (see the last page of this handout), which depicts a phylogeny of some of the major groups of organisms on Earth. However, the taxa are blank! You will be adding in these taxon names using specimens representing these taxa, as well as information gleaned from the suggested textbook.

But first, let's get familiarized with placing trait values on trees. You will notice that superimposed on top of many branches in the Tree of Life are hatch marks labeled with lowercase letters, which correspond to the names of traits found in the character key. These hatch marks indicate the branches on which certain traits evolved, either appearing (the trait has newly evolved) or disappearing (the trait has been lost). These marks are an example of **character mapping**, or "mapping" the branch of origin of certain "characters", which is just another word for trait. Let's look at an example close to home—find the letter that corresponds to the presence of mammary glands (that's "O"). Of course, you can guess which taxon is attached to this branch—none other than mammals. This hatch mark means that the mammary glands evolved at some point along the branch leading to mammals, but **AFTER** the split with its nearest relatives. It also implies that all mammals have mammary glands since this trait evolved **BEFORE** the earliest evolutionary splits between mammal groups (these splits aren't shown because all mammals are treated as a single group in this tree).

Now let's practice interpreting trait evolution on phylogenetic trees—use the Tree of Life sheet to answer the following questions (you don't need to know the taxon names to answer these questions). **ANSWER THESE QUESTIONS BEFORE FILLING IN THE TAXON NAMES.** These questions will help familiarize you with the tree prior to filling in the names.

10. How many taxa on this tree possess vertebrae?
11. Find the branch where "segmentation" evolved. Is this trait present in all of the descendants of this ancestor?
12. On the Tree of Life sheet, place an X next to the following taxa:
 - A. the taxon that has alternation of generations but lacks vascular tissue
 - B. all taxa that are segmented but lack a collagen cuticle

6 Inferring trait evolution

On the Tree of Life Worksheet, we furnished you with the information about where certain traits evolved. But—**and this is extremely important**—it is also possible to *infer* where traits evolved if given a tree and information about the traits possessed by the taxa at the tips of the branches. So, if we can determine the phylogenetic relationships among taxa (a subject we will return to in lab throughout the semester), then we will be able to make inferences about trait evolution.

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Let's look at a straightforward example of this process in our original oak example. Go to Tree 1 on the Oak Phylogeny Sheet and answer the following questions:

13. Did you notice how some of the oak species have leaves whose tips are pointy (e.g., blackjack oak, northern red oak, pin oak), while other species have smooth lobes instead (e.g., chestnut oak, white oak, post oak, overcup oak)?
 - A. Mark the terminal taxa that have pointed tips with a 'P'.
 - B. How many times did pointed tips evolve in oaks, given the leaves and relationships you see in this tree?
 - C. Place a hatch mark labeled "pointed tips" on the branch or branches where pointed tips evolved.
 - D. Did the ancestor of all oaks have pointy or smooth lobes? In other words, which of these traits was ancestral?

7 Placing taxa on the tree of life sheet

To learn more about the major groups of organisms on Earth, let's practice placing taxon names on the phylogeny depicted on the Tree of Life sheet. Scattered around the Biology 200 lab room (K119) are several numbered stations with specimens. Take a few minutes to examine each specimen (there is no particular order you must follow), and **find the taxon represented by that specimen in a reference text (either a Biology textbook physically available in lab, or the e-book)**. Then, using both the information provided for that taxon in your textbook and the traits on the tree, determine where on the tree that organism belongs and write its name and number in that box on the tree. As an example, the taxon Amoebozoa has already been placed on the tree. Should you need assistance, ask your instructor or a TA!

A HELPFUL HINT: Find a clue that leads you to an organism or taxonomic group with which you are already somewhat familiar, then use it as your starting point.

8 Travels in the great tree of life

It is extremely important to keep in mind that the branches on a cladogram may represent up to tens or even hundreds of millions of years of time. For example, on the Tree of Life sheet, the branch separating plants with alternation of generations from its nearest relative represents 300-500 million years of evolution. Of course, there is no way to tell that just by looking at this tree; it's just a cladogram, after all—it only depicts relationships, not the amount of time that has elapsed. The point here is that a huge amount of evolutionary change could have occurred on any of the branches of this tree. We are simply showing where some key, diagnostic traits appeared relative to when lineages split.

9 A note about taxonomy and phylogeny

Taxonomy is simply another word for classification system. Biologists have long endeavored to produce reasonable and useful classification schemes for the world's biodiversity. Traditional taxonomic systems are based on the concept of **hierarchical ranks**; that is, they consist of nested groups. In other words, each rank may be composed of numerous taxa of the next lowest rank: an order may consist of several families, a family may consist of several genera (the plural of genus), and a genus may consist of several species. The major ranks of the modified **Linnaean system** of taxonomy we use today are, in descending order:

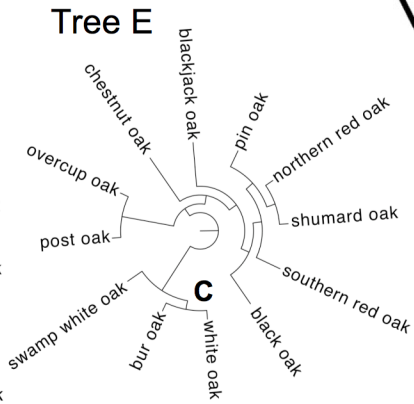
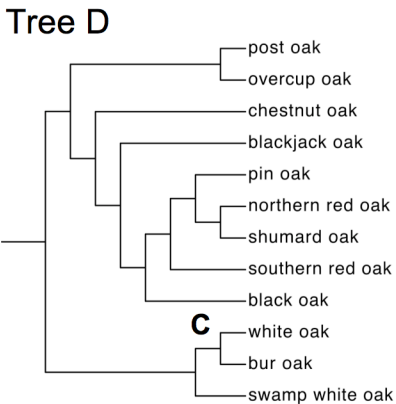
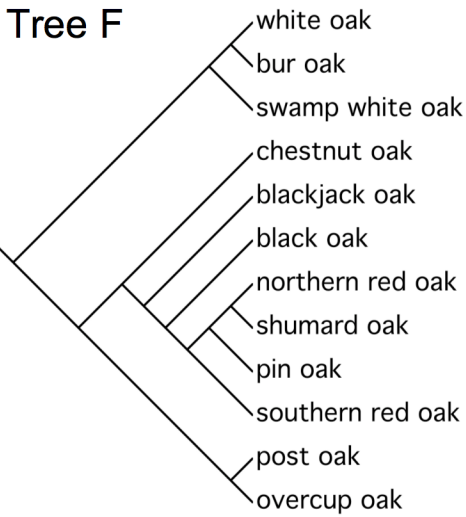
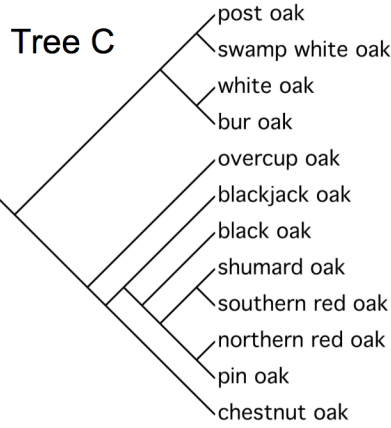
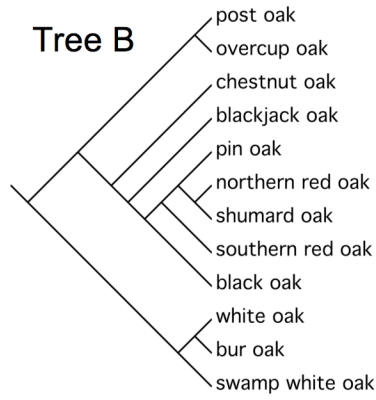
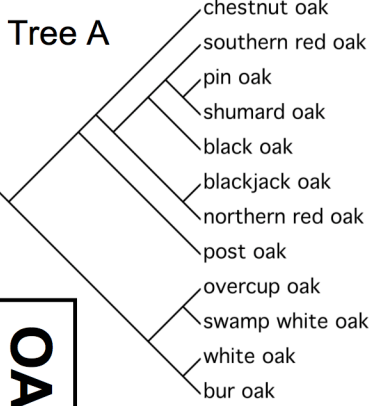
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Kingdom, Phylum, Class, Order, Family, Genus, Species. Linnaeus used visible characteristics to classify organisms and described only two kingdoms: plants and animals. However, today we classify organisms in a Three Domain System, which is based on anatomical, life-history, and genetic traits.

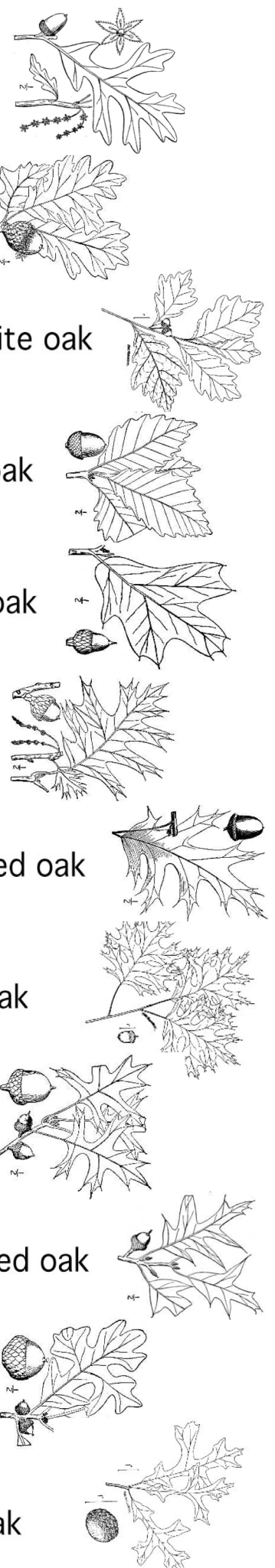
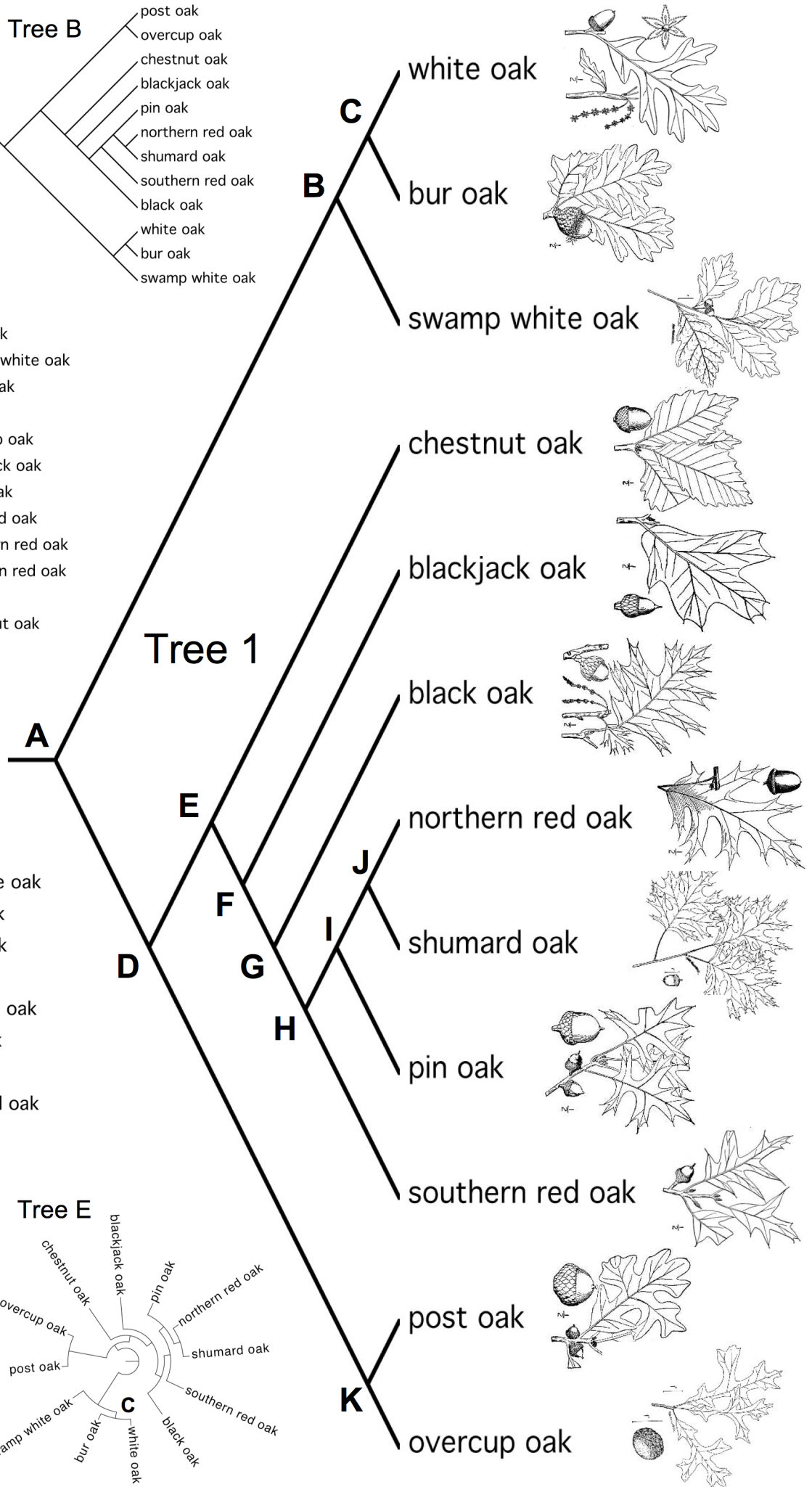
Note that, when used formally, each rank in the hierarchy is capitalized, except for the **specific epithet**, which is in lowercase. Scientific names are **binomials**, having two parts. For example, *Ulmus americana*, is the **species** name for American elm. The first name – *Ulmus* – is the **genus** for elms and the second name – *americana*, meaning “of America”, is the **specific epithet**. The scientific name can be abbreviated as *U. americana*, but one cannot use *americana* alone, as that epithet is used for other taxa, such as the white ash, whose species name is *Fraxinus americana*. The genus is always capitalized, but the epithet usually is not. Note that **standard scientific nomenclature** requires that formal scientific names are written either in italics or are underlined. **YOU ARE EXPECTED TO USE THE STANDARD FORMAT IN ALL WRITTEN WORK FOR THIS COURSE.**

Prior to the advent of technology for DNA sequencing, taxonomists primarily used assessments of anatomical similarity as the basis for defining taxonomic groups. However, as we will see later in the semester, **morphology** (which is another word for anatomy) is occasionally misleading. There is now broad agreement among taxonomists that classification systems should reflect shared ancestry, even when morphology contradicts phylogeny. In other words, taxonomic groups should always correspond to clades. Consequently, understanding phylogeny is now a critical prerequisite to defining taxonomic groups.

The rise of DNA sequencing over the past 30 years has revolutionized our understanding of organismal relationships — as we will see, DNA provides an excellent source of phylogenetic information. This much-improved view of the Tree of Life has resulted in major changes to the taxonomy of many groups. This alteration may seem frustrating, but our better understanding of organismal phylogeny will act to stabilize taxonomic systems once and for all.



OAK PHYLOGENY SHEET



BIOLOGY 200: Tree of Life

CHARACTER KEY

- a alternation of generations
- b calcareous shell
- c cell compartmentalization
- d cell wall composed of chitin
- e chlorophyll a/b
- f cilia
- g collagen cuticle
- h deuterostome development
- i feathers
- j flagella
- k flowers and fruit
- l great flexibility in shape
- m jointed appendages
- n kinetic skull
- o mammary glands
- p multicellularity
- q organ systems
- r pentaradial symmetry
- s protective cuticle
- t seeds
- u segmentation
- v segmentation lost
- w spicules
- x tissue level organization
- y vascular tissue
- z vertebrae

