

Lab 4. Phylogenetic Analysis

*App D due this week (10 pts)

*Lab exam Wed 14 Feb (in lecture – 25 points)

Next week:

*Discussion 2 – (5 pts)

*CSI-HIV homework due – p. 42 (5 pts)

Phylogenetic Analysis 1

Last week we estimated natural selection for latex secretion (an anti-herbivore defensive trait) in a natural weed population. This week we begin a two-week focus on the consequences of evolution, namely phylogenetic patterns of relationships, and more generally, biodiversity. Today's lab has a two-pronged objective. One focus is on introducing trees, mapping traits, and the mechanics of Mesquite phylogenetic software. A second focus is to provide students with the opportunity to examine & handle organisms & identify morphological traits that might be useful in classification & phylogeny. The specimens come from various collections that are managed by the department, and this is a good opportunity to emphasize the important role of collections in biological research. You could let students know that there are different types of collections (e.g., vertebrate & invertebrate animals, living & preserved plants, etc) that are available, and that these are actively used by researchers. Groups of five students will each focus on one group of organisms – we'll have mammals, birds, insects, & plants.

The specimens we have are “working” specimens, meaning they are meant to be used by students in classes like ours. We also have archived specimens of vertebrates, insects, and plants that are not routinely used in classes. Thus, it is fine for students to handle and examine what we have available for them. Having said that, if the specimens are seriously damaged, many of them would be extremely difficult or impossible to replace – even common species – because study skin prep, for example, is not a routine part of departmental or class activities these days. Also it's more difficult to get permits to collect some animals, especially vertebrates, than in the past. It's okay to encourage students to handle the specimens to get their data, but watch them to make sure they do so carefully and properly. They will need to be taught how to hold them so they are less likely to damage them. For example, birds lie dorsally (on their backs) so the bills are less likely to be damaged, whereas mammal skins rest ventrally. Handle insects only by the pins. Generally just keep an eye on things, but don't go overboard and make them terrified to touch anything.

Teaching the lab

The lab has two main components. The first half is meant to introduce them to the process of developing a trait matrix and using Mesquite. This is done in the context of a truncated version of the classic “caminalcules” exercise. I suggest making sure they are finished with this well before the first hour or so is up. The second piece of the lab is meant to have them look at 10-11 real organisms, choose traits that they can see, and score them for all taxa. They should aim for ~10 traits, but if some fall short it's not a big deal. Identifying traits will be challenging for them. It is okay to suggest a few to get them started, but they should be thinking and looking on their own principally. You should remind them that traits need to be scored in binary form (e.g., present or absent), and that traits should help to differentiate groups (i.e., they should be useful synapomorphies). Traits that are unique in all individuals, uniform across the whole group, or present in only one organism are not helpful. Outgroups are identified for each group of organisms, and the same traits need to be scored for the outgroup organism. The outgroup is used to establish character polarity, and thus for each trait scored, the outgroup should have the ancestral condition (i.e., scored as “0”).

Mesquite (and the alignment program, “Muscle”) is available on the laptops. In addition, there is a link to the program website on the class web page, under “lab resources” in the subdirectory labeled “phylogenetics.” Students may download a copy of the program for free from the website if they want to use the program on their own. Also included on the course website are “blank” *.nex files for students to use to construct their trait-species data matrix. Next week I will load the corresponding DNA files.

An important point about this (and all) labs in this class is that the result (ie the topology of the tree) is far less important than the process (ie scoring traits, mapping traits, thinking about phylogenies as hypotheses, etc). We should emphasize and encourage students to examine the specimens, think about characters, and use their data to construct a phylogeny with Mesquite. They will want to know (or may come with ideas about) what is the “real” phylogeny. This will be a good opportunity to remind them that phylogenies are hypotheses about relationships that are built from data, and they are constructing a hypothesis based on their own data, not something they find online or in a book. I think this is a

challenging but important point. Next week they will get a chance to build a phylogeny from their organisms using genetic data, which may provide a different hypothesis. None of us can know what is the “real” or “true” phylogeny until we get a time machine. The phylogenies constructed – by students or professional systematists – are useful primarily as starting points for provoking additional tests about evolutionary history.

Make sure they root their trees with the outgroup, which is indicated in the files with an asterisk (*). This is explained in the lab manual, but it might be worth looking over their shoulders a bit too.

Also, be sure they indicate character trait state changes implied by their tree. We've discussed this in lecture some too – they should include BOTH gain AND loss of traits (or state changes in both directions). This may also require some individual attention to get them on the right track. This seems to be very challenging. Finally, after they've mapped all the traits on their tree they should indicate tree length (# of trait state changes, including gains AND losses). Once they have this in place, they can summarize patterns of trait evolution implied by their tree for each of their traits – this can be done in a separate table, or in a paragraph in their lab manual. I'm mainly interested in getting them thinking about distinguishing homology from homoplasy, at this point. Next week they will continue this, as they map their morphological traits onto the gene tree they build.

There is homework due next week to get them started using genetic data in phylogenies. The file is available online, and they'll have to read NEXT week's lab to learn how to align sequences, etc. Mesquite and Muscle are programs used that are available online for free – they could download them to their own computers. This is supposed to be turned in before class, but in reality they should have plenty of time to do it during class next week.