Lab 1-Discovering Diversity

The famous evolutionary biologist Niles Eldridge split biologists into two basic camps: those who study processes and those who study patterns. BIS2 will introduce you to both of these schools of thought. BIS 2B focuses on biological process, specifically evolution and ecology, while patterns (or the products of evolution) will be the focus of BIS2C. In BIS2B we are interested in the questions of "How come there is so much diversity and where did it all come from?" Before one can begin any study of diversity, we must begin with the question "What is diversity?" Lab 1 in BIS2B is designed to help you start answering this most basic question.

Lab 1 in Five Words

The intent of Lab 1was to get you thinking about diversity, what are the basic components of diversity, and how can we measure it in a meaningful way. We can easily summarize the lab with this five word question: How diverse was my habitat? The task of the lab was to answer that very question.

What is Diversity?

In the pre-lab you were asked to calculate the Shannon-Wiener index (H') (there are many more indices and this is just one). This index asked you to consider two basic parameters of diversity: 1) how many species occur, and 2) how many individuals of each species are there. So diversity is not just the total number of species, but how many individuals of each species are present. Keep in mind that there are other forms of diversity mentioned in class which we do not address in lab (e.g., genetic diversity, ecological diversity). In lab you sampled a habitat, calculated its H', and then compared your results with another group who studied the same habitat. The higher the H' value, essentially the higher the diversity. Prove to yourself that this is true. Try the calculation with just one species and 10 individuals. Then use 100 individuals of only one species, then 10000 individuals all of one species. What is your H' value? How does this compare to what you saw in lab?

Sampling

One of your first tasks was to figure out how to sample your habitat. Usually there are so many organisms that one does not have the time nor the resources to count each individual. Think about why sub-sampling is a more practical means of estimating diversity then counting every individual (what would it be like to do this same project in a 100 acre wood? Can you see the benefit of sub-sampling?) So we subsample and use that as our estimate of the true diversity. We gave you a choice of two commonly used sub-sampling techniques—the transect or quadrat. You used only one method but you want to be sure you have a basic understanding of the other. The other choice you had to

make was how to define your species. Lecture may or may not address different definitions of what a species is, but for lab we asked you to just use an operational definition (basically, does it look different than the other plants or animals). This was our Operational Taxonomic Unit (OTU). Some questions you might ask yourself now in hindsight might be: did you take into account age or other possible morphological variation? Would time of year influence your ability to identify species? You will learn in BIS2C that the presence of flowers on flowering plants can be critical in identifying groups correctly, and frequently flowers are only present at specific times of the year. These are hard questions, and ones with which biologist always struggle.

Are You Done?

Now you have collected a lot of individuals and calculated your H' values, how do you know you pretty much sampled all organisms in your habitat— put another way: how do you know you have a good estimate of true diversity of that habitat? This is where the rarefaction plot comes into play. As you collect more and more individuals, you should be finding fewer and fewer species that you had not collected previously. You know in your first sample that all your species were previously uncollected (because you hadn't done any previous collection and so everything is new). Your second sample yields more total individuals, but you probably have fewer previously uncollected species. And the same holds true for the rest of your samples. You know you have a good estimate when no matter how many more individuals you collect, you are not finding anymore previously uncollected species. Your curve levels off to a horizontal line. If your line continues to climb, you probably have more work to do.

Look at the objectives in your lab manual for lab 1, as these will form the basis for questions on the lab practical.

Study Questions:

1. What is meant by diversity? In this lab two components of diversity were considered. In your own words explain each component.

2. How can one measure diversity?

3. In lab you used the Shannon-Wiener Diversity Index, which was

$$H' = -\sum_{i=1}^{s} p_i(\log_2 p_i)$$

A. In your own words, explain what is p_i. Why are you adding up multiple values of p_i?

B. What does the H' value tell you?

C. If H' of habitat 1 is greater than H' of habitat 2, what can you conclude about these two habitats?

D. If you calculated H' = 0, what does this tell you about the habitat? What must be true in order to calculate H' = 0 (plug numbers in and you will see)?

4A. In lab rather than using an exact species name for each organism, we asked you to identify Operational Taxonomic Units (or OTU's). What is the value of using OTU's initially rather than formal scientific names?

4B. What would be the value of ultimately assigning formal scientific names to your OTU's?

5. When choosing areas to sample, why was it important to randomize? How did you randomize your sampling?

6. Describe the difference between a transect and a quadrat?

Answers (Don't look at these until you tried the questions yourself)

1. There are several different ways to look at diversity. The simplest is the total number of different types; however, in biology we are also interested in the relative number of individuals of each species, not just total species number. Other types of diversity include genetic diversity or ecological diversity.

2. Think about what you did in lab one. If you are looking at genetic diversity, obviously you might need to do things differently.

3A. p_i = the number of individuals of a species divided by the total number of individuals of all species. We are adding up multiple values of p_i because there are multiple species present.

B. How diverse our habitat is.

C. Habitat 1 is more diverse than habitat 2.

D. There is only one species present.

4A. For example, you are not a plant expert so the OTU helped you document the different types of organisms present.

4B. So someone else can do the same study and have results that can be compared or confirmed (science should be repeatable).

5. Randomizing eliminates our own biases as we might choose a sample with the most or fewest individuals (depending how motivated we are). You can randomize in a number of ways using random number tables, rolling dice etc.

6. A transect is a line you draw through the habitat where you sample at regular or random intervals. A quadrat is a known area (we gave you $1m^2$ quadrat sampler) that you sample—it is not linear.