Biodiversity Lab: Characterizing a Forest and Associated Leaflitter Community of McCormick Ravine

Ecology and Evolution Biol 220

Journal Reading: Linking forest structure and composition: avian diversity in successional forests of Chiloé Island, Chile

Introduction:

Species diversity is a central theme in ecology. The patterns of variation and diversity noticed by Darwin and other early naturalists still hold significant interest for ecologists today. Measures of diversity are often seen as indicators of the status of an ecosystem. Different, often adjacent, ecosystems can differ dramatically in both number and identity of species.

There are many ways to measure species diversity. The simplest is **species richness**, that is, a simple count of the number of species present in a community. However, it can also be useful to take into account additional information. **Species composition** adds the dimension of species' identity. Understanding of species composition is one of the foundations of community ecology. For example, if you are running a nature preserve, the number of species may not be nearly as important as the presence of certain native, rare, and/or endangered species. An additional level of detail is added by examining the relative abundances of species in a community. **Abundance** refers to the number of individuals within a species. **Species diversity** combines both **species richness** and **species composition** by measuring the **relative abundance** of each species, i.e. how common or rare each a species is compared to other species in the community. Relative abundance information allows a communities, such as which species are most dominant, which species are rare, etc. The Shannon-Weiner Diversity Index (H) is one calculation ecologists use to estimate diversity that includes both species richness and relative abundance.

In most natural communities, like prairies, it would be impossible, or highly impractical to measure the species richness, composition, and relative abundance of all organisms in the entire area (especially if you were to integrate seasonal changes!). Sub-sampling techniques, like the quadrats and plots we will be using in this lab, are shortcuts that allow ecologists to estimate species richness, composition, and relative abundance for a community by taking measurements in small spatial subsets of that community. However, shortcuts have their costs. Small subsets may, or may not accurately represent the attributes of a larger area, depending on how the subset of areas to be directly sampled is selected. A simple plot of number of species encountered vs. area of sample, or number of new species encountered with each new sample can help reveal how effective our sampling has been at capturing the attributes of the entire community.

For this lab, we will characterize the tree community and associated leaf-litter invertebrates in McCormick Ravine. We will do this by measuring and calculating some of the most fundamental descriptors of ecological communities: species richness and species diversity (where both species composition and abundance attributes are integrated in an index, e.g. the Shannon-Weiner Diversity Index). This lab is part of a national effort by Ecology Professors at Liberal Arts Colleges to collect long term datasets on Forest Biology for teaching and research (erenweb.org). Today, you will be establishing the first permanent forest plots to be used by Bio220 and Lake Forest College and these plots will be integrated into all future Bio220 classes and will be used as a resource for other classes at Lake Forest College and other schools across the country. The data you collect on tree size and identity will be uploaded to a national database. This is a very exciting opportunity to establish baseline data for future students.

Part 1: Basic Methods for sampling tree plots

- 1. When you arrive at the site, you will see a plot 20m x 20m marked with flags at each corner. As a class, you will then mark the plot every 5 meters with flags. Then each group will be assigned to one quarter of the plot.
- 2. For this lab, we will be using different spatial scales for our analysis. Leaf-litter sampling will be at 1-m², and tree sampling will take place in 5x5 m quadrats. This will allow us to analyze the 20x20m plot at multiple scales to examine the differences in sampling scale. We will perform our sampling on the first day of this lab and on the subsequent lab day, we will identify the leaf-litter samples and perform our analyses.
- 3. Our goal is to uniquely identify and mark every tree in the plot. In order to do that, first we will assign each 5x5m quadrat an individual quadrat-color combination for easy marking. See figure 1 below.

NW			NE
1	2	5	6
Blue	White	Blue	White
3	4	7	8
Yellow	Red	Yellow	Red
9	10	13	14
Blue	White	Blue	White
11	12	15	16
Yellow	Red	Yellow	Red
SW			SE

Figure 1: 20x20m plot layout, including quadrat color assignments.

- 4. Sampling trees
 - a) Place a flag of the correct color at the base of each living or dead tree/vine that is ≥2.5 cm in diameter at 1.37m diameter breast height (DBH) in each quadrat assigned to your group.
 - b) Count the number of flags in each quadrat (NW = ; NE = ; SW = ; SE =)
 - c) Once you have marked each tree/vine in all your plots, ask the instructor for the list of numbers you will use for each tree.
 - d) Fill out the **Plot Maps hand-out**, mapping out each tree using the numbers provided by your instructor. Your instructor will use the map to permanently label each tree with the help of one group member.
 - e) Measure the DBH and identify each tree/vine filling in the Tree Data Form hand-out.
 - If a tree has multiple stems ≥2.5cm DBH, each stem is measured and labeled with a decimal point after the tree number (2.1, 2.2, 2.3)

5. Our second goal is to assess invertebrate species diversity in our plots by removing leaf litter and taking it to the lab for further treatment and analysis. Sampling leaf litter

- a) Each group will randomly select two quadrats.
- b) Collect and sift all the leaf litter in randomly placed 1m² within each selected quadrat.
- c) Save leaf litter in bag, **WITH a label stating the quadrat**.
- d) Put leaf litter into Winkler sifter upon returning to lab.
- e) Attach an alcohol vial with label inside to the bottom of the Winkler sifter.
- 6. Give the Plot Map hand-out and Tree Data Form hand-out to your instructor for photo-copying.
- 7. Your lab group is responsible for copying the material from the **Tree Data Form hand-out** onto the excel file sent to your lab group. You will email this excel file back to your instructor the following day (24 hrs).

Part 2: Processing data in the lab

1. Count the individuals of each different species of tree you identified in each quadrat. This will allow you to determine relative abundance. Your excel file should look as below, where the numbers inside each cell are your tallies of the numbers of individual trees of each species for each quadrat.

Species	Quadrat 1	Quadrat 2	Quadrat 3	Quadrat 4	Quadrat 5	Quadrat 6	Quadrat 7	Quadrat 8
Sp. #1								
Sp #2								
Sp. #3								
Etc ↓								

- 2. You need to identify to morpho-species all the organisms you captured in your Winkler sifters and count the number of individuals of each morpho-species.
 - a) Look at every other groups' samples and identify and count the number of individuals in each morphospecies from their samples.
 - b) Enter the data just like you did above for the tree abundances.

Part 3: Calculations

- 1. Calculate species richness (the total number of species) for each quadrat of the forest plot.
- 2. Construct the species accumulation curves for your individual data *and* the combined data of the whole class.
- 3. Tabulate the number of individuals of each species per quadrat and the total number of individuals (all species combined) in each quadrat. Now calculate the same for your <u>combined</u> samples in each community. Use the above data to calculate the Shannon-Weiner diversity index (H):

H=- $\sum P_i \ln P_i$

where P_i is the *fraction of all individuals* in the community contained in species i. For example, if there are 10 individuals of red oaks out of a total of 100 individuals in the quadrat, then $P_i=0.10$. Multiply that by the LN of 0.10. Then calculate $P_i ln P_i$ for each of your species, add them all together and take the negative. This is H. In order to compare trees and invertebrates based on your replicate samples, you will need to calculate H for each quadrat.

4. Carry out an appropriate statistical analysis on the data you collected.

Hints for biodiversity calculations

To calculate the Shannon-Weiner Diversity Index, set up a data sheet in Excel that looks like this:

	N _i =No. of	$P_i =$	ln P _i	P _i *lnP _i
	individuals	N _i /Total		
Species				
	TOTAL:			TOTAL:

 \mathbf{H} = -(TOTAL of this column)

Remember to type a formula in excel, start with =. And to repeat the same formula in the whole column, drag the lower-right corner of the highlighted cell down (or across).

Use this kind of data sheet to calculate H for each quadrat within the plot.

Part 4: Design your own comparison

Now that you've measured diversity, what other characteristics of the quadrats or communities (trees vs. invertebrates) could you compare? How would you go about quantifying possible differences?

Complete the calculations, graphs and statistical analyses indicated below and include them with your lab report. Your lab report should present a comparison between

- A) The plot level data (20x20m) collected by all lab sections to document forest diversity and the quadrat level data (5x5m) to determine tree diversity.
- B) Compare the patterns of tree diversity in the quadrats to the patterns of invertebrate diversity in the quadrats.

Your report should include *four graphs*:

- 1) Species accumulation curves comparing the 20x20m plots for the whole class to your 5x5m quadrats.
- 2) Species accumulation curves comparing your 5x5m tree quadrats with your 1m² invertebrate quadrats.
- 3) A linear regression of invertebrate species richness compared to tree species richness.
- 4) A linear regression of invertebrate species diversity compared to three species diversity.

Journal Club Readings

- 1) Direct and indirect effects of white-tailed deer in forest ecosystems
- 2) Spatiotemporal changes of beetle communities across a tree diversity gradient
- 3) Sapling herbivory, invertebrate herbivores and predators across a natural tree diversity gradient in Germany's largest connected deciduous forest
- 4) Effects of stand tree species composition and diversity on abundance of predatory arthropods
- 5) Recruitment of three non-native invasive plants into a fragmented forest in southern Illinois