Exercise 4A [Pre-Lab]
Measuring Biodiversity

Parts of this lab adapted from *General Ecology Labs*, Dr. Chris Brown, Tennessee Technological University and *Ecology on Campus*, Dr. Robert Kingsolver, Bellarmine University.

In this lab exercise, we will examine several concepts related to **biodiversity**. The term biodiversity describes the number and abundance of species inhabiting a community, habitat or other described area. The most basic measure of biodiversity is **species richness** (S), a total count of species present in the defined area. However, species richness does not give a complete picture of biodiversity. In this exercise, we will examine not only species richness, but also methods to determine **relative abundance** (the proportion of each species present), **species evenness** (how equal in abundance species are) and calculate the **Shannon Index**, a measure of biodiversity.

Introduction

So, how many species are there on the planet? This question is easier to ask than to answer, because we have discovered and described only a fraction of the earth's biota. Most large terrestrial organisms, such as birds and mammals, are so well inventoried that discovery of a new species in these taxonomic groups is a newsworthy event. At the other extreme are soil bacteria, often impossible to culture in standard media, and so poorly studied that there are probably a number of undescribed species thriving beneath your campus grounds. In his influential book *The Diversity of Life,* ecologist E. O. Wilson (1999) reports an estimate of 1.4 million described species, based on interviews with taxonomists specializing in a wide variety of organisms, and comprehensive reviews of databases and museum records. As for the numbers of living species not yet known to science, estimates range from 5 million to 100 million. As ecologists discover new taxonomic categories and new microhabitats, they are constantly revising their estimates. Wilson's argument for more attention to taxonomic questions in biology is compelling, since intelligent management decisions for global species protection begin with some idea of the number of species we have to protect.

How can we improve our appraisal of biodiversity yet to be discovered? One practical approach is based on repeated sampling of a type of organism in a particular place, using the growing database to develop a species accumulation curve. To show how this works, let's visit La Selva, Costa Rica's national rainforest preserve. Here entomologists John T. Longino and Robert Colwell have been collecting ants from the leaf litter of the forest floor in an extended survey of the insect fauna of the park. One of their methods for trapping specimens is the Berlese apparatus. Leaf litter collected from the forest floor is returned to a lab and placed in a funnel lined with screening. A lightbulb placed over the top of the funnel heats up the leaf litter, and all the tiny invertebrates from that sample go down through the screening and into the funnel. The bottom of the funnel leads to a jar of preservative, so the species in this sample can be counted and identified.

Longino and Colwell's Berlese results for La Selva are shown in Figure 4.1. The x-axis shows the number of samples analyzed, and the y-axis shows cumulative numbers of ant species found in all the samples up to that point. The curve rises steeply at first, because new species are discovered in nearly every sample at the beginning of the study. As more and more samples are examined, it becomes harder and harder to find species not already counted, so the slope of the curve gets less and less steep as the sampling effort continues. From a quick examination of the figure, you could predict that biologists could find more ant species if the study was continued, but you could also place an upper limit on the expected number, based on the decreasing slope of the curve. Species accumulation curves have been developed for many kinds of organisms in many kinds of habitats. The shape of the curve varies somewhat, depending on habitat patchiness and the relative frequency of rare species, but declining rates of return on sampling effort are common to all. At some arbitrary stopping point, say less than one new species per 1000 samples, we can conclude for all practical purposes that the fauna in this locale have been adequately described.

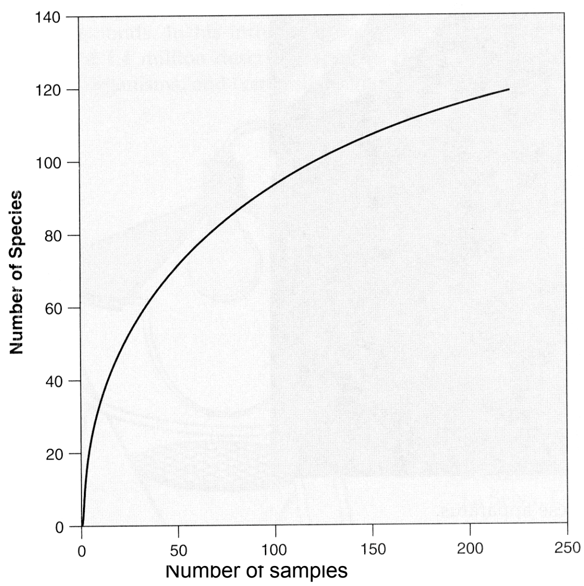


Figure 4.1 Species Accumulation curve for ants collected with Berlese trapping in La Selva Biological Station in Costa Rica.; cumulative species vs. number of samples.

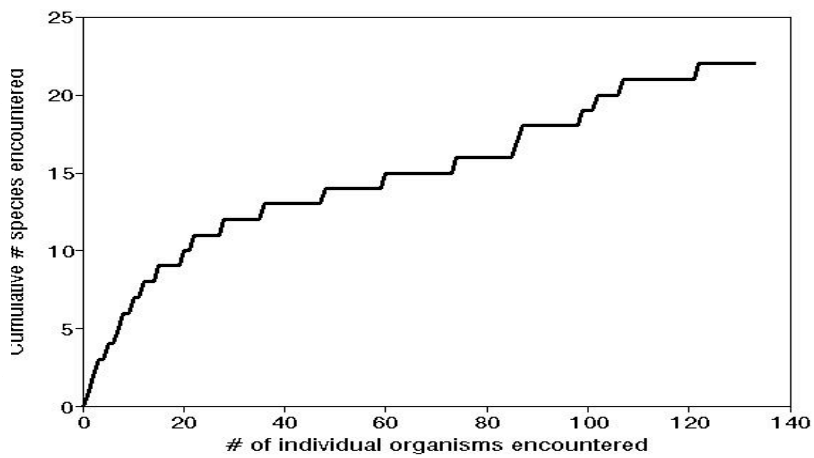


Figure 4.2 Example of Species Accumulation curve with cumulative species vs. total number of organisms observed.

In another example of a species abundance curve (Figure 4.2), the cumulative number of species is plotted against the total number of organisms observed (instead of the number of samples). You should note two things about these graphs. First, the *y*-axis counts <u>cumulative</u> number of species; that is, for each new sample you add <u>only</u> <u>new</u> <u>species</u> to the already existing total. Second, the curve flattens out as you increase the number of samples taken. In Figure 4.2, for example, you only have to look at about 22 organisms to reach 10 distinct species. However, to add *another* 10 distinct species you have to look at an additional 80 or so individuals (that is, you don't get to 20 total species until you've gone through about 105 individuals). This indicates that, initially, you find a lot of new species, but as you go along the chances of finding something new gradually decreases, since in later samples most of the organisms you collect have previously been collected.

A second way to illustrate our results is to construct a graph of proportional abundance versus rank (with rank = 1 being the most abundant, rank =2 being second most abundant, and so on), which we call a **rank-abundance curve**.

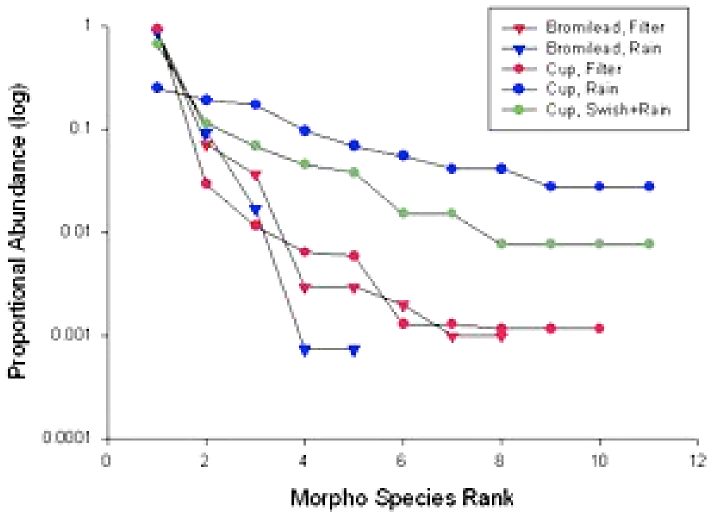


Figure 4.3 Rank-Abundance Curve

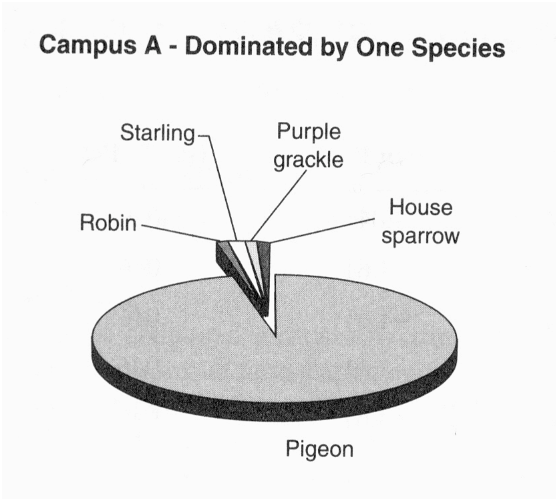
You'll note that all rank-abundance curves decline as the rank increases, but some do so more steeply than others. For example, the curve labeled "Bromilead, Rain" goes down much more rapidly than does, for instance, the curve "Cup, Rain." This tells you that the "Bromilead, Rain" community is less even than the "Cup, Rain" community; in other words, the bromeliad community is dominated by a few common species, while the cup community has a number of equally common species.

An Example of Evaluating Biodiversity

Suppose ecology students at two hypothetical colleges held a contest to see which had the most biologically diverse bird community (or avifauna) on their campus. College A students spent a Saturday morning walking the campus, counting numbers of each species they encountered. Students at College B engaged in a similar sampling routine. Assume that both colleges had the same species richness (five species) and the same sample size of 100 birds, but that numbers of each kind of bird were distributed differently. (For a visual representation of the two campus data sets, see Figure 4.4.)

Table 4.1 Number of Birds Species Identified on Two Campuses

Type of Bird	Campus A	Campus B
Pigeon	96	20
Robin	1	20
Starling	2	20
Purple Grackle	1	20
House Sparrow	1	20



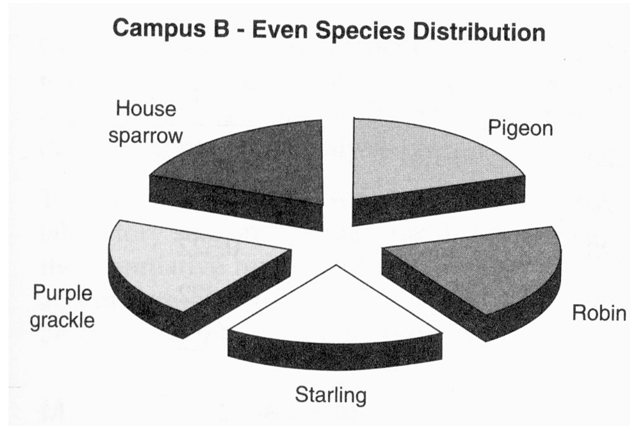


Figure 4.4 Species distribution contributes to biodiversity. Campus A, dominated by one bird species, is less biologically diverse than Campus B, even though both sites have 5 species.

Which school has the more diverse avifauna? Clearly, four of the birds on Campus A's species list make little contribution to the bird community. Campus B's sample, illustrating maximum evenness, demonstrates greater biodiversity. On Campus B, interactions between different species are much more frequent because the community has no single dominant type. Another way of thinking about this as an observer is to ask, what is the probability of encountering the same species twice in a row? On Campus A, the probability is very high, but on Campus B it is much lower.

This probability of change in encounters was used along with species richness to design a way to measure biodiversity that takes both numbers of species and their proportions into account. Called a Shannon diversity index, this methodology measures the likelihood of repetition in adjoining samples.

The diversity index is calculated as follows:

Shannon Diversity Index:

$$\mathbf{H} = \sum_{i=1}^{S} -(\mathbf{P}_i \cdot \mathit{ln}\, \mathbf{P}_i)$$

where:

H = the Shannon diversity index
$\mathbf{P}_i$ = fraction of entire population made up of species i
S = numbers of species encountered
Σ indicates the sum from species 1 to species S

To calculate the index, first divide the number of individuals of species #1 you found in your sample by the total number of individuals of all species. This is P_1, which should be expressed as a decimal value between 0 and 1. Then multiply this fraction times its own natural logarithm. This gives you the quantity ($P_1 * \mathit{ln}\, P_1$). Since the natural log of a fraction yields a negative number, a minus sign is placed in front of the parentheses in the equation to convert the negative product back to a positive number. Next, plug in species # 2 numbers to calculate – ($P_2 * \mathit{ln}\, P_2$). Repeat for all species through the last on your species list, which is species number 5. Finally, sum the - ($P_i * \mathit{ln}\, P_i$) products for all species to get the value of the index, H.

The following table demonstrates calculations of the diversity indices for the bird data on Campus A and Campus B.

Table 4.2 Calculation of Shannon Index for Campus A and Campus B

CAMPUS A BIRDS	**N_i**	**P_i**	***ln* P_i**	**– ($P_i \cdot$ *ln* P_i)**
Pigeon	96	.96	-.041	.039
Robin	1	.01	-4.61	.046
Starling	1	.01	-4.61	.046
Purple grackle	1	.01	-4.61	.046
House sparrow	1	.01	-4.61	.046
TOTAL	100			H = 0.223

CAMPUS B BIRDS	**N_i**	**P_i**	***ln* P_i**	**– ($P_i \cdot$ *ln* P_i)**
Pigeon	20	.20	-1.61	0.322
Robin	20	.20	-1.61	0.322
Starling	20	.20	-1.61	0.322
Purple grackle	20	.20	-1.61	0.322
House sparrow	20	.20	-1.61	0.322
TOTAL	100			H = 1.610

High values of H represent more diverse communities. A community of only one species would have an H value of 0, since P_i would equal 1.0, and it would be multiplied by *ln* (1.0) = O. Campus A's H value is small, because its community is dominated by one species. If all species are equal in numbers, the equation yields a maximum H value equal to the natural logarithm of the number of species in the sample. For example, Campus B has five species. The H value of 1.61 = *ln* (5), so Campus B is as diverse as a five-species community can possibly be.

✍ Check your progress

What added information about biodiversity does the Shannon index convey that could not be derived from a simple species count?

In addition to species richness and the Shannon Index, there is a measure called **species evenness**, which attempts to measure the equality of the abundances for each species. The formula for evenness is given below:

Shannon evenness index: $J = H / \ln(S)$

Where:
- J = Shannon Evenness Index
- H = Shannon Index
- S = species richness (# of species)
- *ln* = natural log

Using our values calculated above, we get J = 0.139 for Campus A, and J = 1 for Campus B (try it and see!). J has a maximum value of 1, which occurs when all species have equal abundances. Thus, we can conclude that Campus B has greater evenness than Campus A.