

### EXERCISE #3: ARTHROPOD SPECIES DIVERSITY

SOME RELATED KEY WORDS: PLANT-INSECT ASSOCIATIONS, SPECIES RICHNESS, TROPHIC RELATIONSHIPS

**OBJECTIVES.** This laboratory is designed to introduce you to the analysis of species diversity patterns. Species diversity refers to the number of species and their relative abundances in a given habitat or community. For example, we know that there are thousands of species of insects in our area, but they are not distributed evenly among all possible habitats. We also know that some species appear to be much more common than others in any given habitat. The various temporal and spatial diversity patterns found in different communities have been a rich source for ecological study for decades. In this exercise, you will use a set of standard measures to compare the species diversity of arthropods in two sampled assemblages occurring on different plant species. Arthropods associated with any particular plant can be quite distinctive, so we anticipate finding differences in species composition, richness, diversity, trophic structure, etc. We typically collect 100-200 different species in 7-8 arthropod orders.

**EXAMPLES OF METHODS.** The simplest measure of species diversity is  $S$ , the number of different species in our community. But how can we be certain that we have representatives of all of the species in any given community? The answer is that we can't, but we can use special methods to approximate what this number is. If we plot the cumulative number of species ( $S$ ) as a dependent variable against the cumulative number of individuals ( $N$ ) in all species encountered on a sample by sample basis, we generate what is called a species accumulation curve (see a recent example in Karlson et al. 2004. *Nature* 429:867-871). In any given sample (call it the first sample), we expect a few species to be common and more than a few to be rare. In our next sample, we expect to find the same common species and some new species. The shape of the curve describing this phenomenon will have a decreasing slope as total numbers of sampled individuals increase. When we get to the point where no new species are being added, the slope of the line will be zero; the curve levels off. In practice we seldom get all of the species in a community (Why?), but stop sampling when we have a nice curvilinear description of the relationship between  $S$  and  $N$ . This relationship can be described by the formula

$$S = N^z, \text{ where } z < 1.$$

(Note that according to this formula the slope never gets to zero, but gets asymptotically smaller as  $N$  increases.)

The nonlinear relationship between  $S$  and  $N$  can be transformed into a straight line by plotting  $S$  as a function of the natural logarithm of  $N$ . The equation

$$S = d \log_e N.$$

describes a straight line with slope =  $d$ . The value of this slope represents a simple relationship between the number of species (= species richness) and the number of individuals in our collection. When we rearrange the equation and solve for the slope, the result is:

$$d = S / \log_e N.$$

Since there can't be any diversity in a community with only one species, we usually express it with the following simple modification and call it Margalef's diversity index:

$$d = (S-1)/\log_e N.$$

Margalef's index permits us to express species diversity as a single value and to make comparisons among communities or over time for the same community. But the blind use of this index (like so many other things in life) can lead to problems. Consider the following example. Suppose there are two communities, A and B, each with five species ( $S = 5$ ) and fifty individuals ( $N = 50$ ), and that the abundance of each species is given in the table below.

Community	A	B
Species #1	10	25
#2	10	10
#3	10	5
#4	10	5
#5	10	5
Total N	50	50

If we calculate Margalef's index (using natural logs) for each community, we get the same value,  $d_A = d_B = 1.02$ . But we can see that there is a difference between these two communities in terms of the apportionment of individuals among species. This component is called "evenness" and is not taken into account by Margalef's index.

Another popular diversity index which does account for both species richness and evenness is Shannon's index:

$$H' = -\sum [P_i \log_e(P_i)]$$

where  $P_i$  = the proportion of individuals in the sample represented by the  $i$ th species;  $P_i = N_i/N$ , where  $N_i$  = the number of individuals in the  $i$ th species and  $N$  = total number of individuals among all species. Therefore, the quantity  $P_1$  is the relative abundance of species #1 (the number of species #1 individuals divided by the total number of individuals in the entire collection). This index of species diversity uses proportions rather than absolute abundances so the total number of individuals in the collection does not affect the index. A species with 10 out of a total of 100 individuals has the same relative abundance as a species with 100 out of 1000 individuals. The negative sign in front of the summation symbol makes the index a positive number ( $H' > 0$ ) since the log of a fraction is negative. Now we can express the differences between the two communities examined above. For A,  $H' = 1.61$  and for B,  $H' = 1.36$ . Check the calculations to make sure you understand the example.

Shannon's index is derived from information theory. It measures the degree of "uncertainty" of predicting to which species an individual will belong when it is drawn at random from a collection. The greater the uncertainty, the greater the diversity. It takes into account both species richness and evenness. But since richness and evenness can vary independently, it is sometimes

desirable to look at each separately. Species richness is measured simply as the total number of species ( $S$ ). Evenness is a bit more complicated, but still quite simple if  $H'$  already has been calculated. A biologist named Hill devised an index called  $J'$  where

$$J' = H'/H'_{\max}.$$

For any given collection of species there is a maximum value of  $H'$  which is reached when evenness is greatest (when all species have equal abundances) and

$$H'_{\max} = \log_e S.$$

Therefore,

$$J' = H'/\log_e S.$$

For community A in the above example  $H' = H'_{\max} = \log_e S = 1.61$  and  $J' = 1.00$ , which is as even as you can get. For community B, which clearly is not as "even" as A,  $J' = 1.36/1.61 = 0.84$ . As with Margalef's "d", each of these indices permit us to make comparisons among different communities using single values.

Lastly, we can approximate the total number of species occurring in a habitat (let's call it  $S_{\text{habitat}}$ ) based on the frequency of rare species in our samples. Let  $a$  = the number of species for which only a single individual occurs in our samples from a particular habitat, and  $b$  = the number of species for which only two individuals occur in these samples. This extrapolation allows us to estimate the total species richness for the habitat as follows:

$$S_{\text{habitat}} = S + a^2/(2b).$$

In the example above, there are no really rare species even in community B. Thus  $S_{\text{habitat}} = S$ . However, past experience with our samples of real arthropod assemblages indicates that rare species can be quite common and  $S_{\text{habitat}}$  can be substantially higher than  $S$ .

**EXERCISE.** We are going to generate two data sets and compare them using actual species composition, the various indices described above ( $S$ , Margalef's "d",  $H'$ ,  $J'$ , and  $S_{\text{habitat}}$ ), and plots of the cumulative number of arthropod species vs. the cumulative number of individuals sampled. These plots begin at the origin and rise to reach the maximum value for  $S$ . Typically we must infer relative richness patterns based on comparable number of individuals sampled or on estimates of total species richness per habitat. Arthropod samples associated with particular types of vegetation (e.g., goldenrod in the genus Solidago, hops in the genus Humulus, hay, etc.) will be collected in the field using sweep nets. While sweep net methods are not ideal for estimating absolute field densities, they do represent a standard method for studies of terrestrial arthropod communities. We will take a number of samples from at least two areas. The arthropods from each sample will be killed and stored in individual sample containers. This sample-taking phase represents the easy part of any community study. The next step will be to bring the samples into the laboratory and sort and count the species in each sample. This phase represents the hard part of insect community work. None of us is skilled enough to sort our insects to species, but with a little effort we should be able to sort them into reasonable taxonomic categories which will permit us to carry out our community analyses. Your ultimate goal will be to make a quantitative comparison of species diversity patterns in the sampled areas based on the sweep net collections. The key on the following page should help you discriminate among the very common insects. Use the following headings for columns on your

data sheets to be filled in during the second week: SITE DESIGNATION, SAMPLE #, INSECT ORDER DESIGNATION, TYPE A-ZZ (=this is our species category), & NUMBER OF INDIVIDUALS.

Here's an example of a **dichotomous key** to the adults of very common orders of insects. Notice how it focuses one's attention on mouthparts (feeding adaptations) and wings.

1. Mouthparts fitted for chewing (jaws and palpi prominent)-----2  
     Mouthparts fitted for sucking (beak of some type present)-----5
2. Front and hind wings unlike in texture-----3  
     Front and hind wings alike in texture, membranous-----4
3. Front wings leatherlike, usually narrower than hind wings which are delicate and fold in repose in the manner of a fan (crickets, grasshoppers, katydids, mantids,etc.)-----ORTHOPTERA  
     Front wings hard, shell-like, meeting in a straight line down the back, concealing the folded membranous hind wings (beetles)-----COLEOPTERA
4. Wings with few veins and cross-veins, not forming a close network. Mouthparts mandibulate but some with lapping and sucking structures also present (ants, bees, wasps)-----HYMENOPTERA  
     Wings with many veins and cross-veins, forming a network. Front and hind wings of similar shape. Thorax cylindrical (lacewings, ant lions, etc.)-----  
     NEUROPTERA
5. One pair of wings present; second pair forming halteres (flies)-----DIPTERA  
     Two pairs of wings present-----6
6. Wings covered with scales. Proboscis, when at rest like a coiled watch spring (butterflies and moths)-----LEPIDOPTERA  
     Wings not covered with scales. Proboscis not coiled-----7
7. Proboscis triangular, unjointed. Tiny, slender insects with fringed wings (thrips)---  
     THYSANOPTERA  
     Proboscis segmented. Wings not fringed-----8
8. Front wings of uniform texture, either entirely leathery or entirely membranous; hind wings membranous (cicadas, leafhoppers, aphids, scales, etc.)-----

HOMOPTERA

Front wings with basal portion leathery, apical portion membranous (true bugs)-----  
HEMIPTERA