Quantifying Stream Biodiversity

Part 1: Background

It is common to hear ecologists talking about ***biodiversity***, particularly in terms of conservation biology. It is one of those terms that is used a lot, and is considered to refer to something important, yet, rarely is it clear exactly what is being discussed. In fact, 'biodiversity' can refer to many things, and has many specific definitions.

The most common definition of biodiversity refers to the number of different species in a given area or ***species diversity***. The greatest biodiversity by this measure would be the number of different species found in tropical rain forests (Fig. 1) which is estimated to be in the millions. Sometimes biologists refer to the diversity within a particular ***taxon***. For example, the southern Appalachians are the world's 'hotspot' for salamander diversity. There are many indices of species diversity that we will explore later.

Biodiversity, in the broad sense, can also refer to variation within species, or among populations. Many species have populations which can be differentiated by morphology or behavior. Typically this occurs within species with large ***ranges***. Consider for example, the extraordinary differences among human populations across the globe. This variation reflects underlying differences in allele proportions among populations and is called ***genetic diversity***. Genetic diversity is of special concern to endangered species because small populations tend to lose genetic diversity through random genetic drift. Without genetic diversity, populations lose their ability to adapt to changing environments, and are more susceptible to be decimated by disease. In populations with normal genetic diversity there will a range of disease resistance among individuals. An extreme example of a species with low genetic diversity is the cheetah (Fig. 2). Cheetah's are so similar genetically that they can accept skin grafts from unrelated individuals without tissue rejection.

On a larger scale, we can consider ***ecosystem diversity*** (Fig. 3). In this case we are not considering individual species, rather a species assemblage in a particular habitat. Ecosystem diversity is a broad concept, encompassing any level of ecological organization above species (e.g. ***habitat***, ***community***, and ***ecosystem***). An example of a major threat to ecosystem diversity in the US is the loss of wetlands to development. It is not easy to quantify ecosystem diversity, as the edges of things like habitat and communities are hard to define. However, it can be argued that the most natural way to preserve all levels of biodiversity is to protect as much and as varied habitat as possible, and then let nature take care of the rest.

Part 2: Measures of biodiversity

Abundance- This is not actually a measure of biodiversity *per se*, rather it is a count (or estimate) of all individuals present. Usually abundance refers to a certain species, but it can refer to all the individuals of all species present.

Species richness- This is the simplest measure of biodiversity being the tally of all the species in the area or community in question. While potentially easy to calculate, this measure is limited in that it lacks information of the relative abundance of the various species.

***Community Dominance Index* (CDI)-** This index reflects how large a proportion of the total species present (in terms of numbers of individuals) is made up of the two most abundant species. It is calculated by the formula:

$$100\frac{y_1 + y_2}{y}$$

Where y_1 and y_2 are the abundances of the two most common species in the sample and y is the total abundance the sample.

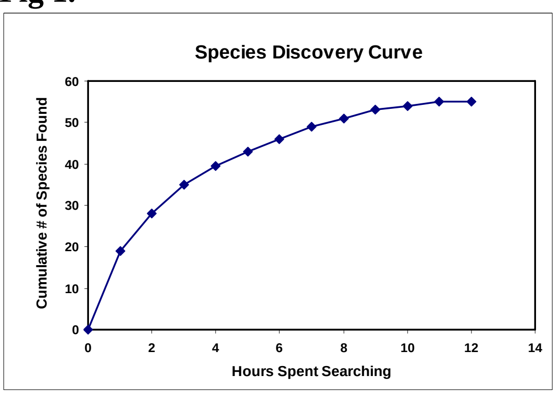
***Shannon-Weiner Index* (SWI)-** This index measures how evenly distributed the numbers of the species present in a sample are. Unlike the CDI, this calculates the value from all the species present, not just the top two. It is calculated by the formula:

$$H' = -\sum_{i=1}^{S} p_i \ln p_i$$

Where p_i is the proportional abundance of the *i*th species (abundance of i / total abundance) and S is the species richness. The higher the index, the more evenly distributed the sample is. The index is maximized if the species are all in equal proportions.

Species Discovery Curve- When sampling for biodiversity, how do you know when you have found all the species? Well, in short, you don't. However, you can get an idea of how many more you *could* find by plotting the cumulative number of species found against some standardized measure of sampling effort (Fig 4).

Fig 1.



The function will be a curve approaching an asymptote of the actual number of species present. The reason it is curved is not (necessarily) because the biologists are getting tired of searching. Rather, it reflects the fact that, as species found accumulate, there is a diminishing probability that the next individual found will be a new species. The curve is also a function of that fact that the most common species are found first, and the rare species are more likely to be missed. From the species discovery curve you can estimate how much more effort it will take to find new species. It allows you to know when you have found most of the species…and decide when it is time to give up.

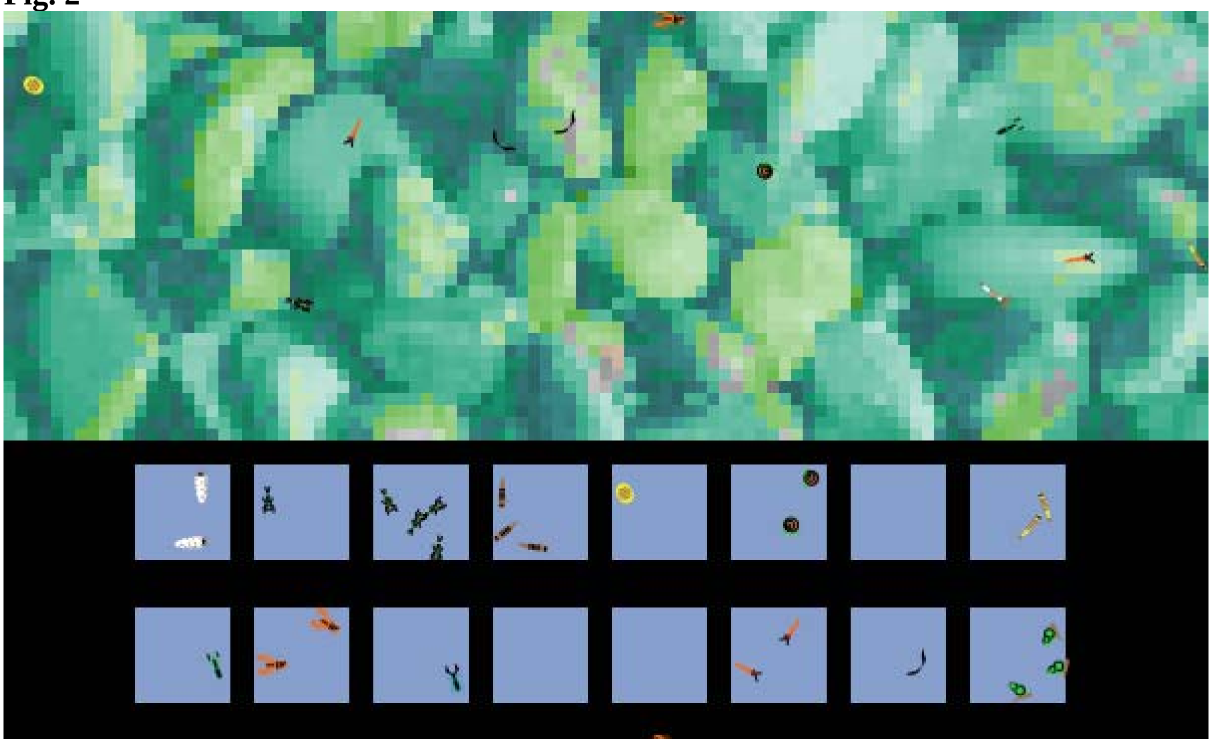
Jaccard Similarity Index- This measure is used to compare the species assemblages of two areas or habitats. It is used to define how similar two samples are in terms of species present. An example of when it would be useful is in deciding which watersheds to focus on protecting those which will preserve the most biodiversity. If you could only protect two of several, you would choose those with the lowest similarity index. The index is calculated as the number of species two samples have in common, divided by the total number of species represented in both samples.

$$J(A,B) = \frac{A \cap B}{A \cup B}$$

General note on sampling- You might imagine that it would take a long time to identify all the individuals in a sample to species, and it certainly would. Most communities have thousands of different species present, many of which appear quite similar. Fortunately, the biodiversity estimates work as long as you can separate individuals into recognizable groups. For example, you do not need to know what two species of snails actually are, you just need to correctly identify them as one or the other. However, the differences between species can be very subtle, and the better the categorizing, the better the estimates.

Part 3: Using the Model

Fig. 2



When this model opens, you will see a section of stream with 16 containers lined up on the bank (Fig. 2). Using the control buttons you can open a seine in the middle of the stream and catch any of the animals that float into it. Captured animals are then sorted into the appropriate containers. The controls and reporters are described below.

Table 1: Controls for Estimating Stream Diversity simulation

Control	Action
Reset	Clears the graph, sets time to 0, removes the seine, releases animals
Go	Sets the stream in motion with animals drifting down
Pollution	Selects stream pollution level (None, Moderate, Severe)
Sampling_Time	The amount of time the seine will be open (simulated seconds)
Open Seine	Places the seine in the middle of the stream, starts sampling & plotting data
Close Seine	Removes the seine, stops plotting data
Release	Dumps captured animals downstream
Clear Plot	Clears lines from the plot, otherwise runs are overlaid
Speed	The slider above the world-view, controls the speed of the simulation

Table 2: Reporters for Estimating Stream Diversity simulation

Reporter	Description
Individual Species Counts	The numbers of each species caught (row below world-view)
Total Catch	Number of all individuals caught
Total Species	Number of different species represented in sample
Sampling Time	The amount of time the seine has been open (simulated seconds)
Line Graph	Cumulative species vs. Sampling time

Procedure

Choose a stream type to sample with the 'Pollution' menu. Then set the 'Sample_Time' slider to how long you want the seine to be open. Click 'Go' to set the stream in motion, then 'Open Seine' to begin sampling. The plot will record the number of species in the sample. If at the end of your sample you release the captured animals, the plot of the next sample will overlay the last on the graph. This can be used to compare samples within parameter set-ups, or to compare different parameters.

Sample questions

1. *What ecological measure does each of the reporters represent?*

    Individual species counts

    Total Catch

    Total Species

2. *Which species appear to be the most sensitive to pollution? Which species are the least sensitive?*

3. *Observe the cumulative species to sampling time plot. Does it behave as predicted by the species discovery curve?*

4. *How does the plot vary from one run to the next?*

5. *The simulation has only ten species, how do you think the variation in the plot would be affected if there were substantially more biodiversity in the stream?*