Measures of Diversity

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Shannon-Wiener Index

This diversity measure is based on information theory simply, the measure of order (or disorder) within a particular system. For our uses, this order could be characterized by the number of species and/or the number of individuals in each species, within our sample plot.

By applying these numbers to the Shannon-Wiener equations we can determine what is referred to as the degree of uncertainty. With this number we can then specify our degree of diversity.

In questioning how difficult it would be to predict correctly the species of the next individual collected, we define un-certainty, in turn defining diversity. For example, if our number of uncertainty is low, i.e. we feel confident in naming the next individual's species, our types of species are few. And, of course, vice versa... if our number of un-certainty is high, the number of species is greater and our chances of knowing the next individual's species are low.

Shannon-Wiener index

$$H' = \left| \sum_{i=1}^{C} p_i \log_2 \left(p_i \right) \right|$$

where ***H'*** = Information content of sample, Index of species diversity, or Degree of Uncertainty, ***s*** = Number of species p_i = Proportion of total sample belonging to i^{th} category or species in community ***C***. The vertical bars indicate the absolute value of the sum.

Alternative Form

An alternative form for Shannon-Wiener index:

$$N_1 = 2^{H'}$$

where N_1 is the number of equally common species for the diversity ***H'***.

Measures of Evenness

The maximum Shannon-Wiener index for a given number of species can be calculated as:

$$H'_{\max} = \log_2 (C)$$

The minimum Shannon-Wiener index for a given data set can be calculated as:

$$H'_{\min} = \log_2 (n) \left(\frac{n - C + 1}{n} \right) [\log_2 (n - C + 1)]$$

Where:

C is the number of categories or species
n is the total number of observations.

The evenness of the sample can be calculated by the following two equations:

$$J' = \frac{H'}{H'_{\max}} \qquad Evenness = \frac{N_1}{C}$$

Base conversion with Logarithms

To convert from known log bases to any other log base use:

$$\log_b = \frac{\log_e(x)}{\log_e(b)}$$

where ***b*** is the base value, $\log_e$ is the natural logarithm, and ***x*** is the value to be transformed. For example to take a log base 2 you would use:

$$\log_2 = \frac{\log_e(x)}{\log_e(2)}$$

Other Hints

The theoretical maximum for ***H'*** is $\log_2$(***C***). The minimum value (when ***N≡S***) is $\log_2$[***N / (N-S)***].
This method is best when doing random samples of a large plot in which you know the total number of species.

Also See:

Chapter 10 - Species Diversity Measures pages 361-367 in:

Krebs, C. J. 1998. Ecological Methodology. Harper and Row, Publishers. New York. 620 pp.
or
Chapter 4 - Measures of dispersion and variability pages 32-36 in:
Zar, J. H. 2007. Biostatistical Analysis. Prentice-Hall, Inc. Englewood Cliffs, New Jersey. 718 pp.