Lab 9  
Calculating Species Diversity

**Diversity.** The health of a community is reflected by the number of species found in it, and the relative abundance of individuals within each species. This is often referred to as diversity. We often hear of the word diversity, and how the more there is of it the better. But how do scientists measure it? The simplest measure of a diversity is to count the number of species. This is known as species richness. Each species, however, is not likely to have the same number of individuals in that community. One species might be represented by 1000 individuals, and another by 200, and a third by a single individual. The distribution of individuals among species is called **species evenness,** or **species equitability.** Evenness is maximized when all species have the same number of individuals. **Species diversity** is a combination of richness and evenness; it is species richness weighted by species evenness, and there are formulae that permit the diversity of a community to be expressed in a single number.

There are 3 types of species diversity: Alpha, Beta and Gamma.  
**Alpha diversity** ($\alpha$) – Also ‘local diversity’ - refers to the diversity within a particular area, or habitat  
**Beta diversity** ($\beta$) - refers to the difference in diversity between habitats.  
**Gamma diversity** ($\gamma$) – Also ‘regional diversity’ – this refers to the diversity of species observed in all habitats within a region, or ecosystem.

Today you will calculate the diversity of animals in a box – animal crackers.

**Species Richness**  
A simple index of diversity concerned exclusively with the number of species (S) in one location, sample, or region. This is also known as alpha diversity. The greater the number of species in the sample, the more diverse the community.

\[
S = \text{the number of species in the sample}
\]

Calculate the species richness of your sample below:

\[
S =
\]
**Berger-Parker Index (d)**

Think of this index as a measure of the dominance of a community or sample. The formula just involves the most abundant species in the sample. The reciprocal form (1/d) is often used so that an increase in the value of the index is associated with an increase in diversity and a reduction in the dominance.

\[
d = \frac{N_{\text{max}}}{N}
\]

where \(N_{\text{max}}\) = the number of individuals in the most abundant species

\(N\) = the total number of individuals in the sample

Calculate 1/d for your sample below:

\[
1/d =
\]

**Shannon Evenness (J)**

This index measures the evenness of a community, which is the degree to which species are equally abundant. Maximum diversity occurs when all species are equally abundant. \(J\) is constrained between 0.0 and 1.0, with 1.0 representing a situation in which all species are equally represented in the population.

\[
J = \frac{H}{\ln S}
\]

where \(H\) = observed diversity

\(\ln\) = natural log

\(S\) = species richness

\[
H = -\sum \pi_i \log_{10} \pi_i \quad \text{[Note – \(H\) is a traditional measure of species diversity.]}\]

where \(\pi_i\) = a ratio between the number of individuals in species \(i\) and the total number of individuals found in the sample

\[
\pi_i = \frac{n_i}{N}
\]

To calculate \(J\), you need to first calculate \(H\). The easy way to calculate \(H\) is to use the equation:

\[
H' = (N \log N) - \sum [n_i \log n_i] / N
\]

Where \(N\) = to total number of plants in the sample
And \(n_i\) = the number of species \(i\)

This is made easier by using the \(n \log n\) table that has the values for all of the \((N \log N)\) and \((n_i \log n_i)\) combinations up \(N\) or \(n_i = 490\).
For example, the diversity of a habitat with 12 squirrels, 2 chipmunks, 5 mice can be calculated as:

1) \((N \log N) = 24.296\) \hspace{1cm} N = 19
2) \([n_1 \log n_1]\) for squirrels = 12.950 \hspace{1cm} n_1 = 12
3) \([n_2 \log n_2]\) for chipmunks = 0.602 \hspace{1cm} n_2 = 2
4) \([n_3 \log n_3]\) for mice = 3.495 \hspace{1cm} n_3 = 5

\[
H' = (24.296) - \frac{[(12.95) + (0.602) + (3.495)]}{19}
\]

\[
H' = 0.8972
\]