6. Diversity Sampling

Z620: Quantitative Biodiversity, Indiana University

OVERVIEW

Instead of generating biodiversity data from nature, we are going to use Jelly Belly jelly beans to reinforce principles of biodiversity. In the process, you will construct a site-by-species matrix and quantify diversity. Last, you will test hypotheses about how the random, stochastic process of sampling can influence estimates of diversity.

1) SOURCE COMMUNITY

We created a source community containing *XXXX-725* jellybeans. In the field of ecology, this is sometimes referred to as total abundance (N). We are going to treat different flavors of jellybeans as though they are different species. Actually, we classified the jellybeans based on their morphotype, specifically colors, spots, and clarity. Based on this, there are *XXX-26* "species" of jellybeans.

2) VICARIANCE EVENT

In nature, events can arise (e.g., new rivers, mountain ranges, new highways) that physically seaprate species from moving across the landscape. Such events can have important implications for the ecology and evolution of populations. We are going to simulate this type of vicariance event (although we will not allow for subsequent growth and reproduction) and test whether this affects patterns of biodiversity. Split the source community into two subcommunities and label.

3) SAMPLING AND SITE-BY-SPECIES MATRIX

Half the students are then randomly assigned to sample one of the subcommunities. Sample **30** individuals (i.e., jellybeans) from the beaker. Classify the species and abundances of jelly beans in your sample. Using Excel, make a spreadsheet that will serve as a site-by-species matrix. Make sure you include a sample identifier (student name) as well as what subcommmunity you sampled from. One person should add this to their student repository and make a pull request.