

## **ECOLOGICAL APPROACHES TO ANALYZING COMPLEX COMMUNITY DATASETS**

The study of fungi has developed largely outside the realm of mainstream ecology, so many of the more commonly used statistical analyses are not well-known to the mycological community. The artificial division between these two fields, however, is quickly disappearing and mycologists are increasingly eager to apply rigorous statistical approaches to the data they are collecting. The goal of this workshop is to introduce mycologists to a diverse array of statistical tools available for analyzing the composition and structure of fungal communities. The emphasis of the workshop is to provide researchers with the opportunity to learn about as well as actually begin using various freely available web-based statistical packages. The workshop will consist of a small group of experts giving relatively brief presentations on their package of expertise followed by a "lab" period where researchers can begin to analyze data (their own or data provided) with the help of speakers. In the labs, attendees will work individually or in small groups and come back together at the end to discuss successes/challenges.

### **Workshop Format**

We have confirmed speakers for four analysis programs, **EstimateS**, **Vegan in R**, **PhyloCom**, and **UniFrac**. The workshop will be held over a two day period on July 25-26, the Saturday and Sunday before the main MSA/BSA meeting. The introductions and labs for each type of analysis will be held back-to-back, with each lasting around 3 hours total. Each day will begin at 8:30 am and last until 5 pm.

### **Session 1: Biodiversity Estimation & Community Structure (Saturday July 25)**

The first day of the FESIN workshop will focus on statistical tools for analyzing ecological communities. The two primary topics covered will be *Estimation of Biodiversity* and *Analysis of Community Structure*. Because the observed number of species in a sample or plot can be biased by factors such as sampling effort and species abundance distributions, ecologists have turned to statistical tools such as rarefaction and non-parametric richness estimators to allow more accurate comparison of diversity between study units. In the first part of the session we will introduce participants to the program **EstimatesS**, one of the most popular tools for implementing these types of biodiversity analysis. Multivariate statistical techniques have also revolutionized the analysis and visualization of ecological community structure. However, techniques such as non-metric multidimensional scaling (NMDS), principle components analysis (PCA) and analysis of similarity (ANOSIM) are complex to calculate or require expensive software. One free option, the R computing language, is challenging to learn but has become increasingly popular among ecologists. This is particularly due to the easy implementation of a wide variety of multivariate analyses through a community ecology package known as **Vegan**. The second half of the Session 1 will be dedicated to teaching participants

the basics of the R language and learning how to implement the community ecology statistics implemented in Vegan.

On Saturday evening (5-7 PM) there will be an informal social event that will allow everyone attending the workshop to meet and talk over food and drink.

## **Session 2: Community Phylogenetics (Sunday July 26)**

The second day will focus on the emerging field of *community phylogenetics*. Because closely related species are often more similar in their ecology than distantly related species, the phylogenetic structure of local communities can yield novel insights into the processes underlying community assembly. For example, communities in which species are more closely related than expected by chance may be produced when habitat filtering is working on functional traits that are evolutionarily conserved. The two programs that will be introduced on Sunday – **UniFrac** and **PhyloCom** – have become the most widely used in studies of bacterial and plant phylogenetic community ecology. Given that most fungal community studies involve the collection of phylogenetically useful DNA sequence data, these programs can be easily adapted to the needs of fungal ecologists. The session will be aimed at helping users learn to format their data, navigate the interface and interpret phylogenetic community statistics such as Net Relatedness Index (NRI) and the P-test generated by these packages.

On Sunday afternoon (3:30-5:00 pm), speakers will participate in a closing panel discussion on about what types of sampling design considerations are important in collecting the community data used for these analysis packages. This will give workshop attendees a chance to ask questions about their own projects and also allow each of the speakers to discuss ways to collect datasets in a robust way.