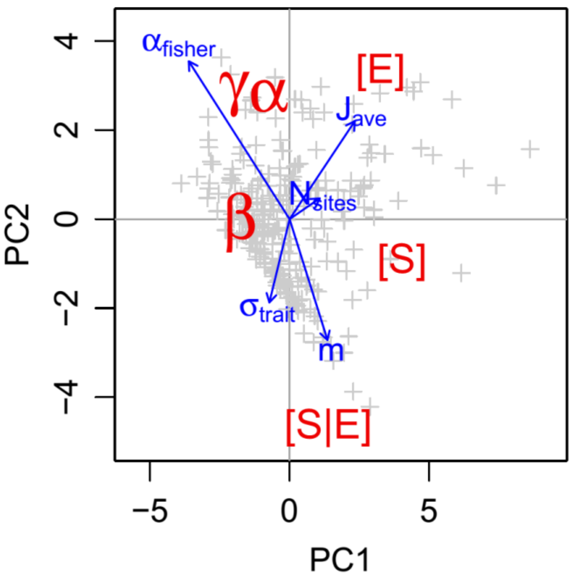
Metacommunity Dynamics in the McMurdo Dry Valleys and Beyond… - Jeb Barrett

The metacommunity concept is a major advance in ecology because it provides a theoretical framework to link ecological processes with biodiversity patterns at multiple scales. Metacommunities consist of assemblages of interacting species, typically linked over broad spatial scales by ecological processes influenced by spatial dynamics, environmental factors, and species traits. Diversity patterns in a metacommunity are thus influenced by niche-based species-sorting and dispersal dynamics. In recent analyses of soil microbial diversity in the MDV and across the Transantarctic Mountains, we found that distinct components of the microbial community respond to environmental gradients at different spatial scales and environmental contexts (Sokol et al. 2013, Van Horne et al. 2013).

We (Sokol and Barrett) have been supported by the LTER Network Office to develop a metacommunity simulation model (MCSim, Sokol 2013, https://sites.google.com/site/metacommunitysimulation/) to understand how metacommunity dynamics influence observed diversity patterns in Antarctic soils, and across the LTER network. We are developing a model of metacommunities simulating biodiversity patterns at local and regional spatial scales, and estimating the sensitivity of biodiversity to different types of shifts in metacommunity dynamics. This simulation-based approach not only provides insight into the dynamics that organize microbial metacommunities in the MDV, but also provides a framework to understand similarities and differences in biodiversity patterns for a wide range of taxa and ecosystems.



Principal Component Analysis of diversity outcomes for 260 metacommunity simulations. Each “+” represents a simulated metacommunity. Simulations were ordinated by alpha-, beta-, and gamma-diversity (Jost 2007), and the environmental [E] and spatial [S] components of beta-diversity calculated using variation partitioning (Borcard et al. 2004, Peres-Neto et al. 2006). Simulation parameters that most influenced diversity outcomes are plotted as vectors. In the model, niche breadth (σ_{trait}) is a parameter that determines the neutrality of the simulations.

Selected Parameters:

- The legacy of the initial regional species richness and evenness (α_{Fisher}, Fisher et al. 1943)
- Rate of introduction of novel species into the metacommunity (v, Hubbell et al. 2001)
- Dispersal limitation modeled as the slope of a dispersal kernel (w)
- Connectivity to the regional pool (m) as determined by immigration
- Niche breadth (σ_{trait}), increased niche breadth results in greater functional equivalence among species in the regional pool, decreasing the influence of niche-based species sorting and increasing the neutrality of the simulation (Gravel et al. 2006)
- Assemblage size (J, Hubbell 2001)