Community Assembly on Isolated Islands: Macroecology Meets Evolution

Islands are bedrock model systems in the development of ecological and evolutionary theory. The Hawaiian Islands in particular have expanded our understanding of island biogeography, with phylogeographic studies of rapid diversification and the dynamics of adaptive radiation overlaid upon a detailed understanding of ecosystem development and senescence. These studies demonstrate the overriding importance of *in situ* speciation in biodiversity patterns of highly isolated archipelagoes, beyond the reach of equilibrium colonization dynamics.

We synthesize ecological and evolutionary perspectives to analyze processes driving emergent patterns of island biodiversity. We apply this approach to a simple and relatively isolated system that occurs across a 1 million-year space-for-time chronosequence on the Big Island of Hawaii. We use this natural experiment to develop a novel analytical pipeline that combines both macroecological (interaction networks and maximum entropy inference) and evolutionary (population genetics and phylogenetics) approaches.

We construct food webs based on arthropod taxa found at a given site with substrates ranging from very young (50 years) to old (> 500,000 years). Linkages among these networks' nodes are then compared to those predicted by a theory of maximum entropy and a model of food-web dynamics. These theories lack mechanisms for diversification. Deviations of data from theory may thus illuminate mechanisms of differentiation, such as population structure, incipient speciation, ecological function, and site age in the evolutionary assembly trophic interaction networks. We aim to use this system to build a predictive understanding of the interplay between ecology and evolution in dynamically shaping the macroecology of complex ecosystems.