**Dimensions – Introductory Framework**

I. *Other studies* -- The challenge in understanding biodiversity is to “disentangle the influence of evolutionary and historical processes operating at larger spatiotemporal scales from ecological processes operating at smaller scales” (Lessard et al). What makes this difficult is that ecological and evolutionary processes form a continuum: While we can observe and test local ecological phenomena, we must infer evolutionary processes, often at larger spatial and temporal scales, based on current information. Efforts to reconcile the effects of ecological and evolutionary processes have largely adopted one of two approaches. The first has been to synthesize extensive data sets typically in broad comparative studies (Belmaker & Jetz, Chase & Myers). These studies have used sophisticated approaches, including network analysis, dispersion (Carstensen et al). Because of their sweeping scope these studies have added tremendously to our understanding of how regional large-scale processes contribute to diversity at the local scale. A second approach uses detailed phylogenetic hypotheses across entire lineages, coupled with data on current ecological traits and patterns of richness (Wiens, Anacker & Harrison). Here, sophisticated tools and the increasing availability of data across broad taxonomic and spatial scales, can provide test of how the interplay between evolutionary and ecological processes have shaped present-day biodiversity.

II. *What is missing* – Despite the massive data and innovative analyses, the approaches to date are limited in inferring past processes from current observations. What’s missing is observations of small scale ecological processes, including colonization, ecological fitting, etc, that together give rise to larger and longer term processes of diversification and adaptation. The importance of understanding how the gradual change from “ecological” to “evolutionary” processes plays out is the black box of biodiversity that has been found to be so critical for other processes. Because biological processes vary unpredictably over time, the details along the way are critical to understanding biodiversity.

III. *Our project goals* – Our goal is to understand the relative importance of ecological factors and evolutionary factors in the assembly of communities, and ultimately the origins of biodiversity. Here, we introduce a system that holds promise for disentangling large scale evolutionary processes from smaller scale ecological processes—habitat islands in a chronosequence. Because of its closed nature and defined geological setting we can not only observe the processes in real time, but also look at snapshots of assembly over time. The power of this approach is that it can provide insights into how interactions vary across the ecological-evolutionary continuum, and how specific differences between taxa affect the nature of the dynamic. To this end, we focus on the youngest island of the Hawaiian chain. Our objectives are to understand:

1. The extent to which taxa in communities are connected ecologically in space and time. Here, we use genetic tools to infer gene flow and connectivity between communities.
   1. What is the rate and pattern of connectivity of different taxa as they diversify from populations to form new species? And, are differences among taxa predictable, especially taxa in different trophic levels?
   2. Do communities and their resulting networks become more independent with time with relatively more species added to the community through evolutionary processes as community assembly becomes more complex?
2. The processes underlying macroecological metrics of community structure..
   1. Using predictions from Network Theory, ask how do network structures and component interactions change over ecological and evolutionary time?
   2. Using predictions from the Maximum Entropy Theory of Ecology, ask why do species abundance distributions differ between taxonomic groups and over ecological and evolutionary time?
3. The processes involved in diversification as taxa species form and accumulate
   1. Role of genetic fusion and fission and how this differs across taxonomic groups, potentially leading to genetic enrichment and/or divergence, and at different rates.
   2. Role of adaptation and divergent selection versus drift during the process of population divergence.
   3. Relative rates of speciation and extinction, and how these change over time to give rise to temporal diversity characteristics of a lineage.

IV. *What we will do in this paper*–The current paper provides preliminary data to show how we will address (1) and (2). We are currently generating detailed molecular data using Next Generation sequencing technologies in order to test (3)