

Combining Gradients of Space and Time to Understand Biodiversity Dynamics in the Hawaiian Islands

1 Background

Biological diversity is nearing or already past a global tipping point [1]. Beyond this phase transition, the processes regulating biodiversity will change, and the dynamics of their resultant biological systems, from clades to ecosystems, will become non-steady state [1]. Despite the pressing need, our level of understanding of biodiversity dynamics remains rudimentary. We must be able to address how biodiversity has been shaped in the past, what are the expectations as we move into the future, and how will associated ecosystems respond to global change. Phase transitions operate across spatial scales and so we must be able to tackle these questions from plots to biomes in order to detect and understand non-steady state dynamics [2, 3]. The National Ecological Observatory Network (NEON) has laid the foundation for this kind of cross-scale monitoring [2, 4]. What is needed now is a tool that allows us to diagnose and predict which biological assembles, across scales, are being driving out of steady state into alternate dynamics.

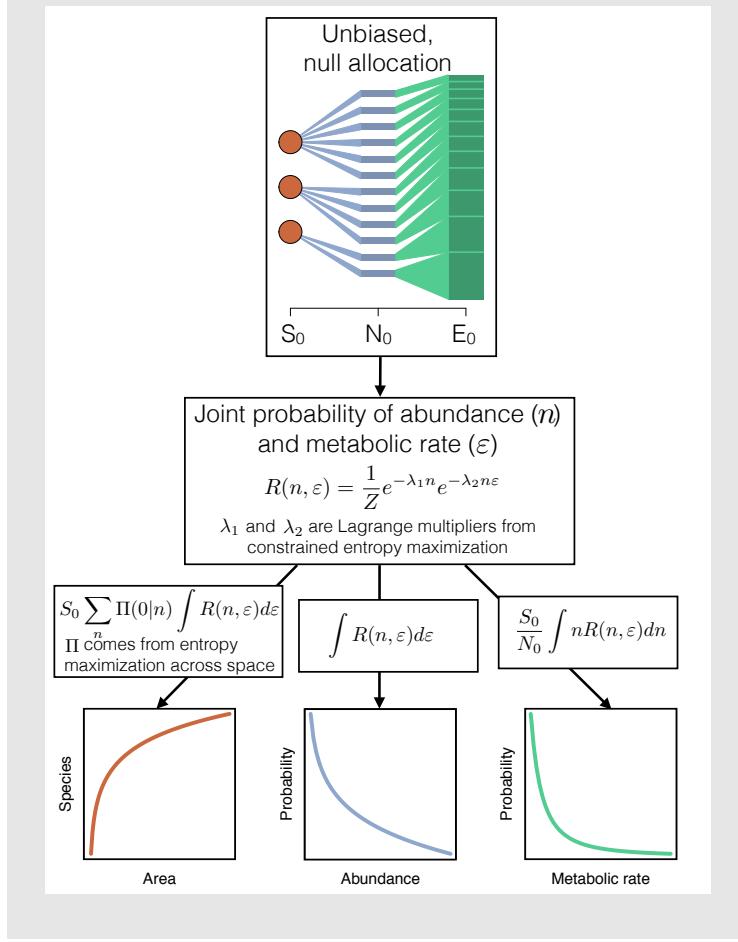
Biodiversity results from both evolutionary and historical processes operating at larger spatiotemporal scales and ecological processes operating at smaller scales [5]. Feedbacks between processes along this evolutionary-ecological continuum drive non-steady state biodiversity dynamics [6–8]. The consequences of non-steady state dynamics, based on state shifts in the geologic past, persist for millions of years [9]. Yet we lack approaches that synthesize across scales of space and evolutionary time to understand the consequences of this eco-evolutionary feedback process. The propensity for systems to transition into non-steady states cannot be assessed given current means of synthesizing ideas from ecology with those from evolution. Additionally, a lack of cross-scale biodiversity data (from plots to landscapes and genes to species) combined with a lack of theoretical framework, limit this synthesis. **We will use the maximum entropy theory of ecology [METE; 10] as a null model to identify communities out of steady state and understand the mechanistic drivers of departures from steady state. We will combine this approach with the intensive data collection efforts of NEON, as well as our complementary advances in bioinformatic approaches to generating large-scale biodiversity data. We will implement our theory-based, quantitative framework in the natural eco-evolutionary experiment of the Hawaiian archipelago.**

1.1 Theory provides a lens on non-steady state processes

Recent theoretical developments have brought mechanistically simplified theory to the forefront of ecological research [10–12]. These simple theories have been critical because they provide robust null models against which to compare real biodiversity patterns in order to rigorously identify which systems deviate from null expectations and what specific biological mechanisms drive those deviations [10, 12, 13]. METE [10] provides one of the most useful null predictive frameworks because it produces multiple falsifiable predictions (making falsifications of the theory more informative [14]). Box 1 details the testable predictions of METE. METE is grounded in the principles of statistical mechanics [10, 15], drawing from the probabilistic properties of large, randomly assembled systems [10]. Thus its predictions constitute a community in statistical steady state. Statistical steady state means specifically that a system is governed by only a few simple state variables, which constitute a state space, and that no additional processes limit the system’s ability to freely explore this state space (see Box 2). Deviations from METE allow us to identify ecological systems out of statistical steady state [8, 10]. Drivers of such non-equilibrium include rapid assembly following disturbance [10] and constraints imposed by evolutionary history and non-neutral adaptive differences between species that violate the statistical assumptions underlying the principle of maximum information entropy [8].

Box 1: Null model predictions from METE

METE uses simple state variables to capture information about a community and develop a null model for it. These state variables are the total number of species (S_0), the total number of individuals (N_0), the total summed metabolic rate of those individuals (E_0), and the total area (A_0) over which the community was sampled. METE mathematically achieves the most parsimonious, probabilistic allocation of those state variables in order to predict the species abundance distribution (SAD), individual metabolic rate distribution (MRD), and the species area relationship (SAR) [10]. This theoretical framework is detailed in the below figure.



sociated arthropod and microbial communities; and 3) Soil communities of arthropods and microbes. In each of these ecosystem domains we will use the maximum entropy theory of ecology to characterize departure from statistical steady state. In order to understand the mechanistic causes of these departures we will also evaluate how deviations from METE can be predicted by the ecology and evolution of the organisms comprising each community, testing the hypotheses outlined below. We will enable this line of research by sampling plants, arthropods and microbes across multiple spatial scales, and across gradients of environment (precipitation and elevation as a surrogate for temperature) and substrate age (as a surrogate for both biogeochemical change and evolutionary development). We will also make use of long term fertilization experiments [see letter of collaboration; 24] to evaluate the roles of evolution-

We propose to use islands of the Hawaiian archipelago to understand how and why ecosystems depart from steady state and the consequences of these departures on biodiversity dynamics and invasibility. Remote island archipelagos provide an opportunity to integrate ecological and evolutionary processes, advancing our understanding of the regulation of biodiversity through the lens of theory. This is particularly true when the component islands are arranged chronologically, as is found in “hotspot” islands that form a geological age gradient representing snapshots of community assembly through evolutionary time. Such islands provide simple and discrete systems, of known age and varying area, allowing them to serve as excellent “natural laboratories” for ecological and evolutionary study in a regional context [16–18]. Our team has a strong foundation of research expertise and experience across the islands on microbes (Brodie, Ceja-Navarro), arthropods (Rominger, Gillespie, Gruner and Krehenwinkel), plants (Chase), ecosystems (Giardina), molecular biology (Brodie, Ceja-Navarro, Krehenwinkel), and theory (Rominger, Chase).

We will characterize the ecological communities, including their abundance, diversity, and network structure, associated with three critical stages in nutrient cycling: 1) Living plants, the arthropods they support and the microbes supported by both; 2) Plant and animal detritus and its as-

ary history versus biogeochemical processes in driving biodiversity patterns. Using plants, arthropods and microbes as discrete test cases, representing a breadth of life history strategies across the tree of life, we will test hypotheses (outlined in section 2.2) about deviations from statistical steady state based on how organisms persist, adapt and speciate in their environments. In order to understand how communities are likely to change in response to non-analog, anthropogenically-driven climate regimes and across spatial scales we will build spatially explicit models that link the mechanistic drivers (e.g. rapid community or population change, and evolutionary novelty) of deviation from statistical steady state to remotely sensed data and detailed ecosystem characterizations taken at the NEON site in Hawaii, and our complementary sampling locations. Our project will contribute theoretical constructs for use across NEON sites and bioinformatic tools to advance the rate and dimensionality of biodiversity data gathered at these sites.

2 Proposed Research

2.1 Research objectives and hypotheses

Our proposed research approach is organized in Figure 1. We have four core research objectives:

- RO1** Describe how deviations from statistical steady state (measured by METE) relate to ecosystem age, environmental variables and invasion.
- RO2** Model niches and interaction networks with respect to age, environment and phylogenetic information.
- RO3** Combine **RO1** and **RO2** to model invasion potential and deviations from statistical steady state across spatial scales and into future climate scenarios.
- RO4** Develop open source lab protocols and software to rapidly advance generation and analysis of multidimensional biodiversity data (taxonomic, genetic and phylogenetic) that can be applied across NEON sites.

We will use maximum entropy theory to identify deviation from statistical steady state across environmental and evolutionary gradients, and long-term experiments. We will place these deviations in the context of ecological and evolutionary information to understand the mechanistic causes for deviations from statistical steady state and its implications for invasion potential. We will produce detailed networks of interactions between arthropods and plants, arthropods and microbes, and microbes and microbes to understand how species interactions evolve and shape conformation to or deviation from statistical steady state. We will also reconstruct the abiotic niches of all taxa (plants, arthropods and microbes) for which sufficient data are available. We will use these reconstructed niches to understand patterns of specialization and generalization, how these ecological states evolve, and their consequences for the steady state of biological assemblages. Finally, we will develop a new bioinformatic approaches to generate massive genetic and phylogenetic data for all communities

Box 2: Statistical Steady State

A statistical steady state exists in an ecological community if changes in biodiversity occur slowly and in sync with environmental changes [10]. This condition is independent of the specific biological mechanisms mediating the interaction of biodiversity with its environment, so long as those mechanisms do not constitute information beyond the state variables (see Box 1) of the system. An example of such additional information would be specialized co-evolution between herbivores and plants that lead to more uniform allocation of primary productivity across consumers than expected by chance. The idea of statistical steady state connects with previously explored ecological theory on stationarity and ergodicity [19], but is not tied to notions of equilibrium as a hypothesized state that ecosystem rate processes may attain or be driven away from [e.g. not: 20–22].

The existence (or non-existence) of such steady states has wide ranging implications. For example, whether conservation should focus on conventional preservationist paradigms or adaptive management [23] depends on whether biodiversity is largely in statistical steady state or not. Whether biodiversity rapidly and consistently tends towards a steady state determines how species and the communities they form will respond to global environmental change [1].

sampled; these data will allow us to analyze networks, niches and deviations from statistical steady state in a phylogenetic framework to evaluate evolutionary signals in observed patterns.

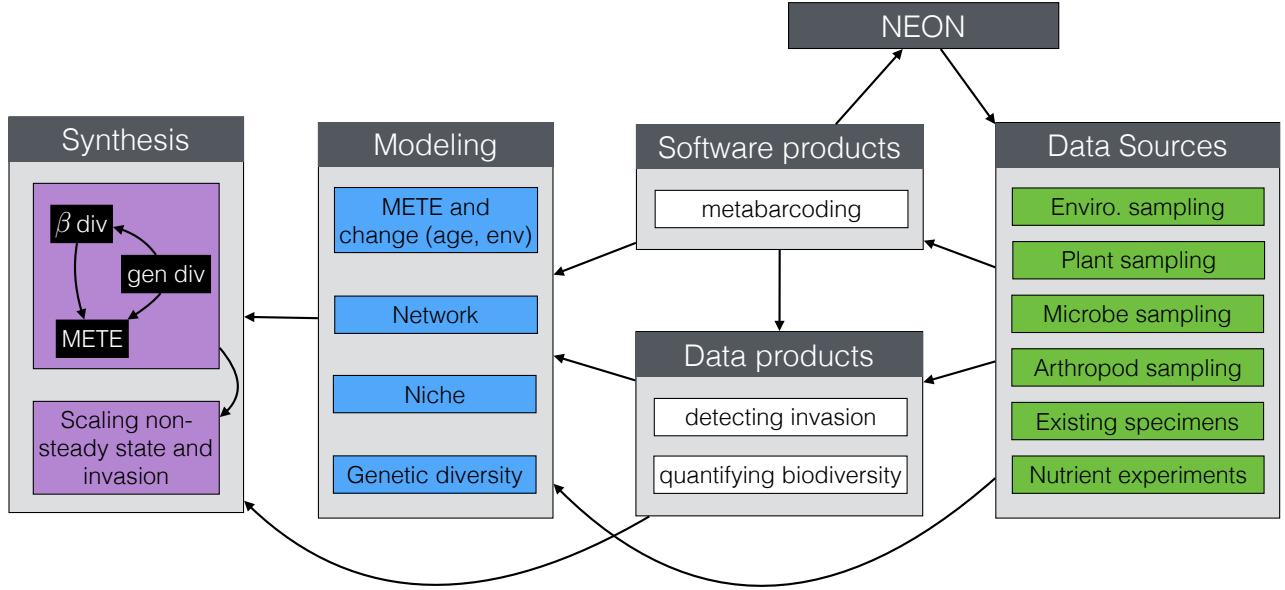


Figure 1: Conceptual network illustrating how we will achieve modeling and synthesis goals using diverse data resources, novel data and software products, and integration with the NEON site in Hawai'i. Synthesis approaches are further detailed in Figure 2.

To forecast these mechanistic drivers of departure from statistical steady state into future, non-analog environments we will model networks, niches and community phylogenetics using remotely sensed environmental variables and detailed field measurements from the NEON site and our complementary sampling sites. These models will be spatially explicit and use the framework of Bayesian hierarchical modeling to incorporate diverse data types, including existing biocollections data from previous NSF funded projects in Hawaii (our Hawaii Dimensions in Biodiversity project) and specimen data curated in State and museum databases. To permit theory testing and modeling across large scales we will develop a novel sequencing and bioinformatics approach to generate massive, multidimensional (i.e. taxonomic and genetic) biodiversity data. We will use this combined approach of novel theory testing and novel data generation to test hypotheses outlined below relating departures from statistical steady state to feedbacks between ecological and evolutionary processes.

2.2 Hypotheses

- Departures from statistical steady state (**RO1**):

H1 We predict that deviations from METE will be largely predicted by age along the chronosequence. These deviations will be driven primarily by two processes related to the evolutionary assembly of biotas: (**H1a**) primary succession (both by long distance dispersal and speciation) in newly formed habitats; and (**H1b**) adaptive evolution leading to unique constraints on assembly not consistent with statistical steady state

H1a leads us to predict deviations from METE on young substrates and for generalist taxa, especially those that are dispersal limited (e.g. detritivores in Fig. 3). Additionally, we predict a negative correlation between the breadth of reconstructed abiotic niches and deviation from METE

H1b leads us to predict deviations in communities dominated by specialist taxa in old com-

munities once they have established intricate evolutionary relationships with their co-existing species and environments (e.g. as seen in herbivores in Fig. 3 and our previous published work [8]). Based on this hypothesis we further predict

- a positive correlation between network specialization and deviation from METE
- a negative correlation between phylogenetic diversity and deviation from METE

H1c Because adaptive evolution resulting in niche specialization and dispersal limitation both likely result in strong spatial structuring of communities, measures of spatial turnover and deviations from METE should be positively correlated (e.g. as seen in Fig. 4).

H1d Because rapid population expansion, population contraction, limited dispersal and local adaptation all lead to low allelic diversity within populations [25], genetic diversity should be negatively correlated with deviation from METE.

H2 Given the climatic stability of Hawai'i since the last glacial maximum [26], we predict deviations from METE should not depend on environmental variables after accounting for ecosystem age. This includes the prediction that in long term fertilization experiments, fertilized communities will conform to the same patterns as their unfertilized control communities of the same age regardless of underlying nutrient availability.

H3 However, with rapidly changing climates we do expect environmental variables to predict modeled deviations from statistical steady state. Specifically, with the creation of novel environments and loss of existing environments due to anthropogenic climate change, we expect rapid population changes and exacerbated constraints on movement due to unique evolutionary adaptations to previously stable environments. Thus we predict novel climatic conditions to drive future deviations from METE. Modeling this prediction corresponds to **RO3**.

H4 We predict that in disturbed systems, statistical steady state will be achieved only through rapid assembly of novel ecosystems (i.e. communities dominated by highly vagile invasive taxa). Thus deviations from statistical steady state are expected to promote invasion, while invasion itself will tend to return systems to statistical steady state. This hypothesis leads to further hypotheses:

H4a Community phylogenetic, niche occupancy and network position of invasive species will be similar to generalist taxa that form communities conforming to METE

H4b Models including level of invasion as an explanatory variable will help explain deviations from METE that cannot be otherwise explained by age and environment.

H4c Repeated surveys of communities will show that systems previously deviating from statistical steady state in prior censuses now contain higher proportions of invasives compared to those closer to statistical steady state. This hypothesis cannot yet be tested, but our proposed research lays the groundwork for long term ecological monitoring.

- Evolution of niches and networks (**RO2**)

H5 We predict that niches will become more constrained across evolutionary time, leading to the further predictions that:

H5a reconstructed niches will be smaller for taxa endemic to older islands

H5b spatial turnover will be stronger across gradients on older islands

H5c networks will become more specialized across evolutionary time [supported by our previous work on network evolution 8]

H6 We predict that closely related taxa will overlap in niche space if they occupy broad distributions across abiotic environments and generalist network positions, whereas specialist taxa will show phylogenetic signals of over-dispersion owing to adaptive differentiation.

Tests of the first four hypotheses (**H1–H4; RO1**) will be used to understand how deviations from statistical steady state result from the evolutionary and ecological characteristics of a community. Tests

of hypotheses **H5** and **H6 (RO2)** will be used to illuminate how those eco-evolutionary drivers themselves respond to environmental constraints across space and through evolutionary time. Quantifying these eco-evolutionary patterns and mechanisms is permitted by **RO4**. Combining the insights of both sets of hypotheses will allow us to model deviations from statistical steady state and resultant changes in invasion potential across space and into future climate scenarios (**RO3**).

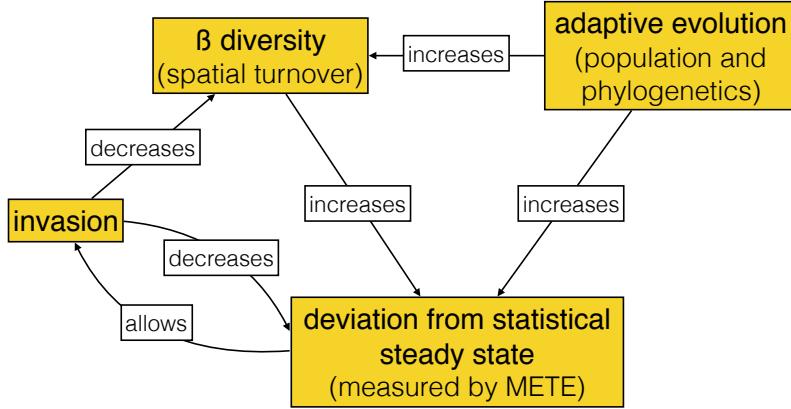


Figure 2: Network illustrating hypotheses as connections between core components of the proposed research. In order to scale deviations from statistical steady state and invasion potential across space we will model the drivers of changes in spatial turnover and phylogenetic signal—evolution of niches and networks.

2.3 Significance and Rationale

Understanding how environmental change will alter the feedback between ecology and evolution and drive biodiversity out of statistical steady state is at the core of our proposal. Using METE to capture statistical steady state and understand deviations from it promises to be a powerful diagnostic tool in evaluating ecosystems nearing tipping points. Hawaii is an ideal study system to realize this potential due to its varying chronology (allowing tests of theory in communities of different stages of evolutionary development) and due to its replicated environmental gradients across this chronology (see Fig. 5. The NEON site at Pu'u Maka'ala Natural Area Reserve on Hawai'i Island will provide the core measures needed to quantify the abiotic environment. We will replicate these measurements across gradients of elevation and precipitation, using ground-truthed remotely sensed measurements to provide both fine grain and broad-scale environmental data products. These combined sampling sites lay the groundwork for significant long-term ecological monitoring.

The same ability to generate massive amount of environmental data via remote sensing does not exist for organismal ecology and evolution. As part of our Dimensions in Biodiversity grant, Rominger and Krehenwinkel are developing laboratory and bioinformatic methods to obtain sequence data, and estimates of abundance and biomass for thousands to millions of arthropods collected via ecological sampling. As part of the current proposal this promising new approach will be developed into an open source lab protocol and software package that can be distributed across all NEON sites.

Our use of METE as a diagnostic tool has been corroborated in the Hawaiian system with previous and current work. Rominger, with Gillespie, Gruner, and Harte as collaborators and co-authors, has shown that deviations from METE show consistent patterns across the chronosequence for different arthropod guilds with different life history characteristics (Fig. 3). Additionally, these patterns can be predicted by the amount of spatial turnover in species composition between sites, and by the proportion of the community dominated by invasive species (Fig. 4). This work confirms our hypotheses that deviations from statistical steady state can be predicted by limited dispersal and niche

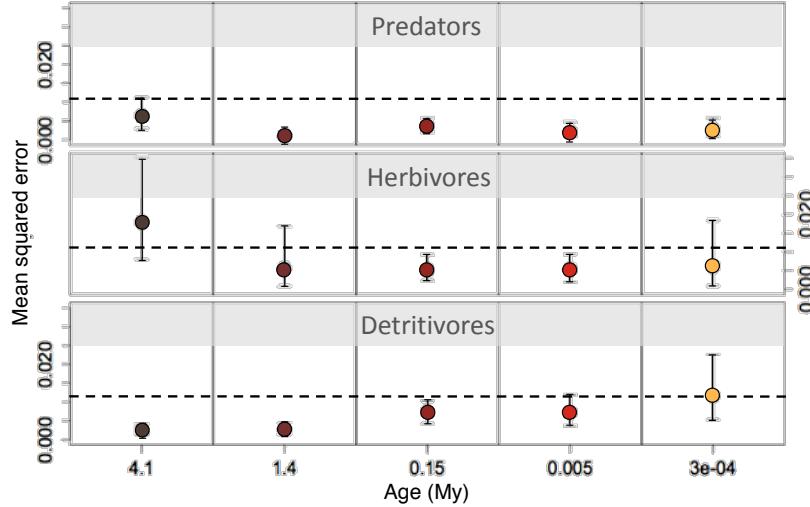


Figure 3: Deviations from METE (measured as mean squared error) across the Hawaiian chronosequence (colors correspond to ages in Fig. 5) for three different arthropod guilds [data from 27]. Dashed line represents statistical grounds for rejecting METE. Note that predatory arthropods have high dispersal ability and low population genetic structure compared to detritivorous arthropods [8], which explains greater deviations from statistical steady state in detritivores, especially in younger aged ecosystems. The poor fit of herbivores in older ecosystems is likely due to their unique evolution with host plants, corroborated in our study of network structure across the chronosequence [8].

partitioning (leading to increased spatial turnover) and that deviation from statistical steady state is related to invisibility of ecosystems. Our proposed work will extend this approach by explicitly testing more nuanced hypotheses about the role of evolutionary processes in driving these non-steady state observations and extending these predictions across space and into future environments with hierarchical models.

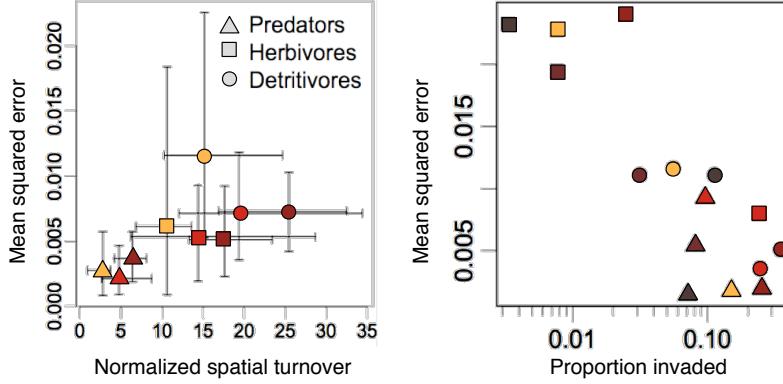


Figure 4: Across arthropod guilds and substrate ages (colors correspond to age in Fig. 5) deviations from METE (measured as mean squared error of METE predictions) are predicted by spatial turnover or species composition (left panel). More heavily invaded systems conform best to METE (right panel) suggesting that invasion acts to bring non steady state systems back into steady state by an influx of highly vagile, generalist invasive species. Data from [27].

2.4 Methods

2.5 Integration with NEON and sampling design across environmental and age gradients

NEON site. The goal of NEON is to provide ecological data at multiple spatial and temporal scales. Our plan is anchored with the Pu'u Maka'ala Natural Area Reserve on the Mauna Loa volcano on the Big Island of Hawaii (19.553° , -155.317° ; Fig. 5), a Core Terrestrial site with the launch date planned for 2017. The site represents montane wet forest with mostly native vegetation dominated by the endemic tree, *Metrosideros polymorpha* (Myrtaceae). However, 95% of the world's terrestrial climates are represented in the greater region of the Hawaiian archipelago [28], and a single site will fail to characterize this tremendous diversity in climate, habitats and species composition. By replicating core NEON protocols at carefully selected sites with orthogonal variation in temperature and precipitation, along a geological chronosequence representing evolutionary time, the Hawaiian macrosystem will yield the precision of NEON measurements to test ecological theory and to predict consequences of future changes in climate. We aim to combine data to be collected by NEON with data from sites across the Hawaiian Islands, in order to understand regional-scale ecological processes and how these respond to change over space and time.

Complementary sites. We will collect data in an explicit, nested design that allows integration with the NEON-generated data, while using data from the entire terrestrial region of the Hawaiian Islands to provide information on processes of several groups of organisms across multiple scales. Data will be gathered across elevation and precipitation gradients from evolutionarily old, middle aged and young islands (Kaua'i: 4–5 my; Maui: 1–1.5 my; and Hawai'i: 0.001–0.5 my). On each island we will establish 6 sites (1 ha in size): 3 along a windward (i.e. high precipitation) elevation gradient and 3 along a leeward (i.e. low precipitation) elevation gradient (Fig. 5). Windward sites will be constrained to be within 4000–5000 mm annual precipitation, while leeward sites will be constrained to be within 1500–2500 mm annual precipitation. We will consider an elevation gradient from 900 – 2500 m elevation. On Hawai'i Island we will use the area adjacent to the Pu'u Maka'ala NEON site as one of these 6 sites. Each site will consist of 3 replicate plots to insure thorough coverage of local variation. The sampling locations and design are given in Figure 5.

Sampling approach and collection of organismal data. We will select sites in clearly defined ohia/koa montane, wet and mesic forest communities. The rationale here is that (i) Ohia (*Metrosideros polymorpha*) is the dominant canopy tree in these forests, forming a nearly continuous layer, with patches of sub-dominant koa (*Acacia koa*) and numerous associated understory trees, shrubs, herbs, and ferns. This forest type (and the presence of *Metrosideros* in particular) has been used as an important landscape feature in our ongoing work through the Hawaii Dimensions of Biodiversity, as it has for a generation of studies on long-term ecosystem development. This constrains sampling to vegetation and soils of similar physiognomy and evolutionary history, while allowing major climatic state factors to vary. (ii) The proposed NEON site is characterized by this forest type. Finally, (iii) *Metrosideros* growth rate, growth form and chemical composition (all detectable by various satellite and airborne spectroscopic techniques [29–31] reflects the coupled but nonlinear effects of ecosystem age and fertility, which in turn affects the community of organisms in a given forest stand [27, 32]. Differences in plant traits can affect the structure of an entire food web through a series of direct and indirect effects [33, 34].

Figure 5 details the proposed layout of our sampling plots. Within each 1-ha site, we will establish three 20 m by 20 m plots to be selected as representative of forest height mean, maximum, heterogeneity found in that 1-ha site. Each plot will be further gridded into 4 m quadrats (100 in total). Within each quadrant we will record all tree species ≥ 1 cm at breast height. Within three randomly selected quadrats we will also sample all herbaceous species. We will sample all arthropods within each quadrant using timed beating (24 seconds per quadrant). Within the same three randomly selected quadrats used for herbaceous plant surveys we will also extract arthropods using Berlese funnels from litter and

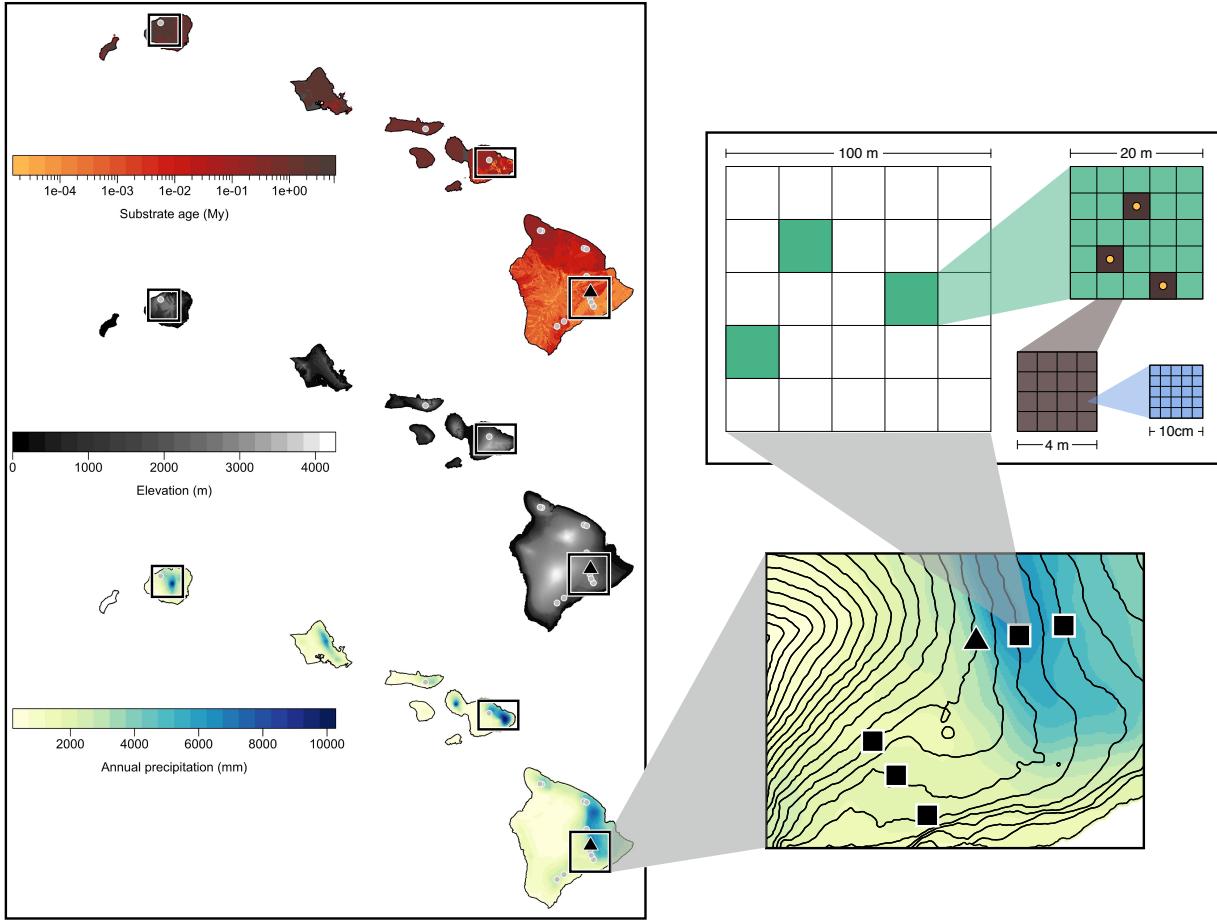


Figure 5: Map of Hawai'i showing chronological age, elevation, and precipitation. Gray dots represent sampling locations with existing data from our Dimensions in Biodiversity project. Triangle corresponds to the NEON site at Pu'u Maka'ala. Regions delineated with rectangles represent proposed areas where sampling sites will be established (6 per island). Black squares in the detail map represent potential sampling sites complementing the NEON site. In the detail map, precipitation is color coded as before, but elevation is shown as 200 m contours. Sites will be organized in a nested fashion. Green plots represent our stratified sampling plots within a site, brown quadrats correspond to litter and soil sampling quadrats, and the blue 10 cm x 10 cm sub quadrat corresponds to our microbial samples. Orange dots represent locations of temperature and humidity data loggers, in addition to litterfall collection locations.

soil samples, gridded to 1 m² cells (in keeping with the ground beetles collected at the NEON site). Arthropods will be collected into RNAlater to preserve their DNA and RNA as well as the DNA and RNA of their associated microbes and gut contents. While NEON protocols focus on ground beetles (Carabidae), mosquitoes (Diptera: Culicidae), and ticks (order Ixodida), our study will include all arthropods because ground beetles constitute an eclectic group of lineages, most often arboreal and unevenly distributed across the main islands [35], and there are no native mosquitoes or ticks [36].

Microbial richness and abundance will also be sampled in a gridded design (Fig. 5). Within the three randomly selected quadrats used for herbaceous plants, litter and soil sampling, we will take a soil sample 100 cm in surface area (10 cm by 10 cm) and 10 cm deep. In the lab this will be divided into a regular 2 cm grid and each will be sequenced.

In all systems, microbial diversity will focus primarily on the Domain Bacteria due to its phylo-

genetic breadth, and metabolic and respiratory plasticity. Bacterial diversity will be estimated using molecular tools to sequence 16S rRNA gene biomarkers in multiplex using a barcoding approach. DNA extraction and 16S rRNA gene amplification and Illumina sequencing will be carried out according to Earth Microbiome Project standards (www.earthmicrobiome.org/emp-standard-protocols). Ancillary and meta data collection standards will follow the NEON the soil microbial data collection and metadata tracking worksheet (goo.gl/nE9zPk). Microbial 16S rRNA gene data will be analyzed according to Shi et al. [37]. Richness will be estimated using both taxonomic (OTUs) and phylogenetic (Faith's phylogenetic distance) metrics. Absolute bacterial abundances will be determined using quantitative PCR as described in [37] while relative abundances of bacterial taxa will be determined based on the fractions of sequence reads assigned to each taxon using adjustments for rRNA gene copy number [38]. In order to relate bacterial taxa to metabolic rate we will use observed relationships between rRNA copy number, genome size and metabolic rate [39].

Environmental and biogeochemical data. In order to characterize the environment experienced by our focal organisms and model deviations from statistical steady state, achieving research objectives **RO1–RO3**, and testing hypotheses **H1–H6**, we will replicate select NEON measurements and instrumentation, and make use of remotely sensed data products.

1. Plot-level measurements: In each microbial sampling quadrant we will deploy data loggers to record air temperature and moisture content. We will similarly deploy data loggers to record soil temperature and moisture. We will also measure soil physical characteristics, pH, total carbon, nitrogen, phosphorous and sulfur. We will measure monthly litterfall using litter traps as a surrogate for nutrient cycling [40, 41] in addition to litter chemistry (pH, total carbon, nitrogen, phosphorous and sulfur) in keeping with protocols at the core NEON sites [4].
2. Remote Sensing and Airborne Observation Platform: We will make use of both existing [e.g., 29, 42] and planned airborne remote sensing data which can provide information on vegetation composition and land cover and will be used in particular to examine the complex mosaic of forest structure and composition. The NEON Airborne Observation Platform (AOP) measures vegetation biochemical and biophysical properties with spectroscopy, vegetation structure and biomass with LiDAR, and produces high resolution imagery that can be subject to analyses of land use and relative cover [4]. The combination of detailed field measurements at the NEON site (several of which we will replicate) and broad coverage remote sensing will allow use to develop spatially highly resolved surrogates for biogeochemical processes and abiotic environmental variables across the Hawaiian islands, following known approaches with which Giardina is integrally involved [e.g., 42, 43]. These spatial products, both derived by NEON and adapted by our interdisciplinary group, will be used to achieve **RO1** and **RO2**—modeling statistical steady state and its eco-evolutionary drivers across space.

2.6 Modeling evolutionary and environmental drivers of assembly

Maximum entropy theory of ecology across gradients of environment and age To test our hypotheses relating age, environment and organism/community traits to deviations from METE (**RO1** and **H1–H4**) we will use the R package `meteR` [developed by Rominger 13] to evaluate the goodness of fit of METE for soil microbes, arthropods, plants, and microbial associates of arthropods and plants at our sampling sites across gradients of precipitation, elevation and age. Goodness of fit will be measured as the normalized log likelihood squared [described in 13]. Using generalized linear models we will evaluate how the goodness of fit varies between major groups (microbes, arthropods and plants) and as a function of the underlying age and environment of each site.

To further explore the relative importance of age as a proxy for evolution versus biogeochemical environment (hypothesis **H2**) we will use Vitousek's long term fertilization experiments [see letter of collaboration; 24] to test whether alleviating nutrient limitations in old and young plots changes the way in which arthropod and microbial communities deviate or conform to METE.

Modeling niches, networks and community phylogenetics across space and evolutionary time We will develop a Bayesian hierarchical modeling framework to understand how ecological and evolutionary drivers of deviations from statistical steady state depend on local and regional environments (**RO2** and hypotheses **H5–H6**). In all models we will incorporate explanatory environmental variables as spatial averages with an exponentially decaying distance weighted function. Each variable will receive maximum weight at the point location of the specimen and exponentially less weight as distance from the point location increases. The exponential rate of decay will be fit as a free parameter in our Bayesian hierarchical model.

We will use island age as an explanatory variable interacting with environment to evaluate how the niche occupancy and network position of each species changes with evolutionary age (hypothesis **H5**). Because we will have phylogenetic data from metabarcoding for all species we will evaluate patterns of niche occupancy and network position in a phylogenetic framework, testing hypotheses of whether closely related taxa overlap or diverge in niche occupancy, and whether more recently diverged species tend to be generalists or specialists (hypothesis **H6**).

To test whether the niche spaces of taxa change across the chronosequence we will build probabilistic niche models for all species of plants and arthropods with sufficient data ($n \geq 15$ points per island). We will use data sources from our gradient plots, plots from our Hawaii Dimensions in Biodiversity project, digitized museum specimens and species occurrence data made available reporting by the Hawaii Division of Land and Natural Resources. Because the nature of these data is variable (abundance and presence-only) we will use Bayesian hierarchical models to combine them into one analysis [44]. We jointly model the niches of all species in this hierarchical approach.

To test how networks evolve across the chronosequence we will quantify network structure using four complementary approaches: 1) deviation from the maximum entropy predictions; 2) classic ecological network metrics of nestedness and modularity; 3) network dissimilarity; and 4) network specialization. We will again take a phylogenetic approach to evaluate how changes in network position of taxa and changes in overall structure of networks relates to the phylogenetic distance between component taxa.

2.7 Projecting deviations from statistical steady state into the future

Once we understand the connections between network structure, niche occupancy, population size change, evolutionary diversification and deviation from statistical steady state, we can use our models for niches, networks, and their phylogenetic context to project these drivers into the future, predicting where (at a regional scale) statistical steady state will be violated (**RO3**). Using our understanding of how statistical steady state contributes to invasibility of a community (**RO1** and hypothesis **H4**) we will also be able to model invasion risk across scales and into future climate scenarios.

2.8 Quantifying evolutionary and macroecological patterns using metabarcoding

Next generation sequencing technology has ushered in a revolution in evolutionary biology and ecology. The large scale recovery of species richness, food web structure, cryptic species, identification of juveniles and hidden diversity, e.g. internal parasitoids, promise unprecedented new insights into ecosystem function and assembly [45–48]. While species richness can be routinely identified by sequencing bulk samples, estimating species abundance remains challenging [49] and severely limits the application of metabarcoding to many studies. We are developing wet lab and bioinformatic methods to overcome this issue and revolutionize the generation of ecological and genetic data (**RO4**). We will apply this approach primarily to bulk arthropod collections, while complementary approaches will be used to reconstruct microbial diversity, and networks between plants, arthropods and microbes. Our novel pipeline consists of three steps (Fig. 2.8):

1. Extraction and sequencing of pooled community samples
2. Matching the resulting sequences to a reference phylogeny for identification
3. Using Bayesian hierarchical models to reconstruct unbiased estimates of abundance

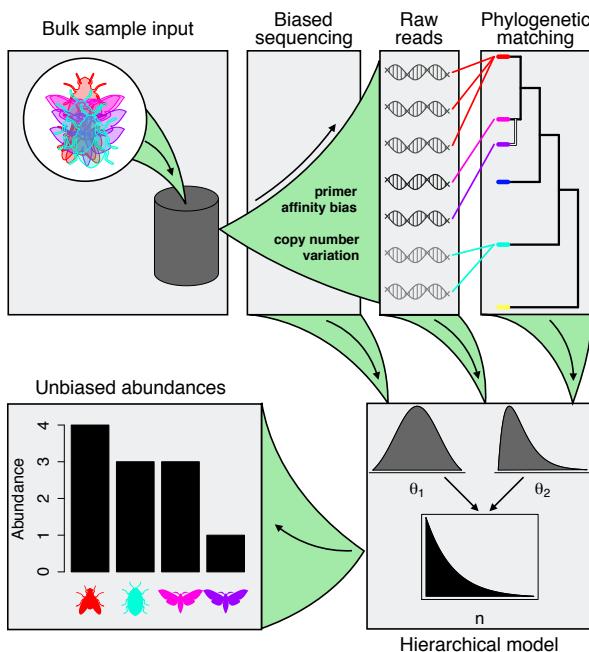


Figure 6: Pipeline for generating and analyzing metabarcoding samples.

will use amplicon sequencing of the COI barcoding region [48] which has shown the greatest reliability in preliminary trials.

(2) *Matching the resulting sequences to a reference phylogeny for identification.* In order to resolve the taxonomy of sequences derived from mixed samples we are developing a library of the barcoding region for species across the Hawaiian archipelago, such that unknown sequences can be phylogenetically matched to the reference library. Sequences not found in the tree of all reference sequences will be grafted and their status as a unique operational taxonomic unit assessed using a cutoff of 3% divergence (Fig. 2.8). These bioinformatic steps will be included in the R package.

In collaboration with taxonomist and ecologist on Hawaii, we are currently working on generating the barcode reference library for a diverse range of several hundred Hawaiian arthropod taxa. These taxa were sampled across the chronosequence of the Hawaiian Archipelago (Fig. 5). DNA is extracted from each taxon and reference sequence generated for the mitochondrial COI barcoding region. To achieve a comprehensive sampling of the Hawaiian arthropod diversity, samples from environmental gradients (e.g. precipitation) will be included in this reference collection. Such gradients have been shown to have a profound influence on community composition on Hawaii [50].

In order to build a robust phylogenetic backbone for our reference library, the genomic DNA extracts for all species will be sequenced using the Illumina HiSeq2500. An assembly of the resulting reads promises to generate near complete mitochondrial genomes and nuclear ribosomal clusters of each taxon. To support the Illumina short read assemblies, we will generate long read information by PacBio sequencing. The resulting sequence information will allow us to reconstruct a well resolved community-phylogenetic framework for ecological hypothesis testing. These same specimens will also be used to quantify the microbiomes and feeding habits of hundreds of arthropod species across our sites (discussed further in section “Quantifying networks of microbes, arthropods and plants”).

Step (1) is already well developed [45–48]; steps (2-3) will be developed into an open source R package that allows users to implement these methods in their study systems. We propose that our open source pipeline can be implemented across NEON sites to generate both taxonomic and phylogenetic data for focal taxa.

Preliminary results from controlled experiments show there is a strong correlation between amount of arthropod tissue sequenced and total number of reads; however, this relationship is variable across taxa. A Bayesian model is able to capture this variability across taxa and thus indicates the success of more general applications of the modeling approach to field collections.

(1) *Extraction and sequencing of pooled community samples.* We will generate sequence information for mixed arthropod community samples, collected across precipitation gradients on the Hawaiian Archipelago. The samples will be roughly pre-sorted taxonomically and grouped into different body size classes to minimize the confounding factors of abundance and body size in determining amount of DNA per taxon. We

(3) *Using Bayesian hierarchical models to reconstruct unbiased estimates of abundance* Bayesian hierarchical models permit inference of key quantities (e.g. abundance) while accounting for multiple sources of error and leveraging heterogeneous data types to facilitate inference [51]. The goal of hierarchically modeling metabarcoding data is to estimate the abundances of species while correcting for known biases inherent in amplicon-based sequencing. We will account for bias from copy number variation and primer affinity [49] by directly modeling it, while also using data on the total number of individuals being sequenced, their body sizes, and the phylogenetic relationship between their sequences to constrain the estimates to be more accurate. Furthermore, information from controlled experiments (for example making mock communities of known composition and sequencing those) can be used to constrain prior distributions and obtain even more accurate abundance estimates.

2.9 Quantifying networks of microbes, arthropods and plants

Using the specimens reserved from metabarcoding (i.e. those used to build the reference library and phylogenetic backbone) we will sequence the microbial associates of each species and their gut contents, for herbivorous arthropods. These sequences will allow us to reconstruct the networks between arthropods and their microbial associates as well as herbivorous arthropods and their plant hosts. We will additionally reconstruct microbial networks based on covariance between prevalence of microbial taxa in samples using established approaches [52].

3 Broader Impacts

The research will train 3 postdocs, including one who will serve as PI for the proposal and gain experience in leading the effort. It will also train 2 graduate students, and 12 or more undergraduates, at the intersection between macroecology and evolution, and across microbes to macroorganisms.

We will use the rich natural and dynamic landscape of Hawaii, and the acute environmental issues affecting the environment, to build a program of education and outreach. The PIs are already well positioned for such activities. The primary areas we plan to develop are:

1. Experiences for undergraduates and Masters students. We will build research experiences for undergraduates and Masters students from both the University of Hawaii Hilo (minority-serving, 24% Hawaiian) and the University of Hawaii Maui College (also minority-serving, 37% Hawaiian). At the University of Hawaii Hilo, we will connect with the Ecology, Evolution and Conservation Biology (EECB) and Tropical Conservation Biology and Environmental Science program (TCBES, tcbes.uhh.hawaii.edu); Gillespie is already an Affiliate Faculty member of TCBES. The ECB and TCBES Programs give high priority to the recruitment and training of students from groups under-represented in sciences with an emphasis on Native Hawaiian and Pacific Islanders. These efforts will be facilitated through the Pacific Internship Programs for Exploring Science (PIPES) program (www.uhh.hawaii.edu/uhintern), a UH Hilo program designed to connect underrepresented undergraduate students, especially Native Pacific Islanders, to research internship opportunities relating to environmental issues in Hawaii; we will recruit undergraduates through this program (see letter attached). The research will involve each of the undergraduates coming out into the field with researchers involved in the project. We have already established close ties with Cathy Davenport, a faculty member at the University of Hawaii Maui College (see letter attached). The students will assist in field sampling at specific locations associated with the main sampling locations for the overall grant program. Specific projects that the students could conduct are as follows (i) comparison of species diversity of key groups of arthropods on young versus old lava flows; (ii) relationship between substrate age and diversity of targeted arthropod species; and (iii) analysis of the effects of forest fragmentation (natural and human) on species diversity of targeted arthropod species.
2. Experiences for High school and Middle School students. The USDA Forest Service co-leads, with the University of Hawaii at Manoa, a “Teaching Change Program.” This program features over-

night immersive learning experiences to students by bringing students to natural areas of Hawaii Island. The current two-day curriculum focuses on linking phenology, conservation biology, and climate change on the island of Hawaii. Each month students visit a site to: (i) learn about native forest ecosystem ecology, including disturbance regimes and the general concept of change; (ii) learn about human-induced climate change and its potential impact on native ecosystems; (iii) measure plant phenology and publish these data with the USA National Phenology Network; and (iv) participate in native forest bird research. With monthly trips, this program is generating a unique tropical montane forest dataset on plant phenology and exposes students to: (i) native ecosystems that they would never otherwise have the opportunity to visit; (ii) the concept of plant and avian phenology and its utility for monitoring native ecosystems; and (iii) the concept of change, including anthropogenic climate change. Over the past four years the program has served 400+ students. The program has a particular focus on underprivileged and underrepresented youth from Hawai'i. It also provides Teacher Training Workshops for local teachers and offers annual Conservation Career Days for students and their families to learn about professional and educational opportunities in Hawai'i in conservation biology and natural resource management to inspire and empower the next generation of land managers in Hawai'i.

3. Land Management Professionals. Fieldwork in Hawaii will be timed to coincide with the annual Hawaii Conservation Conference, the largest gathering of people ($\gg 1000$ participants) actively involved in the protection and management of Hawaii's environment (see hawaiiconservation.org). The goal of the conference is to foster interaction between natural resource managers and the scientific community. In addition to holding a workshop to present and discuss our results at the conference, we plan to have one afternoon of round table discussion for the local community on the island of Hawaii, allowing a smaller group from university, state (DLNR), private (The Nature Conservancy of Hawaii), and federal (USGS, USFS, USDA, USFWS) agencies, and others, to discuss the work, its results and significance.

Besides working with local communities in Hawaii, we also plan to make use of avenues for outreach and education at UC Berkeley. We plan to develop a diverse, high-performing, and interdisciplinary [53, 54] community of researchers as we have done in the past, that includes postdocs, graduate, and undergraduate students. In addition, we plan to:

1. Work with staff at the UC Berkeley Natural History Museums in the development of material for the Understanding Evolution (evolution.berkeley.edu) web site, designed for science teachers of all grade- and experience-levels. The system, which couples elements of evolution and ecology, field and laboratory, theoretical and empirical, provides an opportunity to convey some essential yet complex concepts in a relatively straightforward manner.
2. Use the forum provided by LBNL's Open House for connecting to the local community (www2.lbl.gov/openhouse) and especially the Science at the Theater (uctv.tv/scienceattheater) events.

4 Results from prior funding

Chase: DEB 0949984 Mechanisms of species-area relationships in Ozark glades. 2010-2015, \$748,046.00 (co-PI; Tiffany Knight, PI). Intellectual merit. The observation that larger areas typically support more species is the basis for the species-area relationship, one of the oldest and best known relationships in ecology. Nevertheless, the mechanisms underlying this relationship remain poorly understood. Specifically, the lower diversity found in small habitats is often a consequence of there being fewer rare species in those habitats than would be expected based on sampling. This grant funded a long-term, large-scale experiment in experimentally restored Ozark Glade communities. Population and community-level patterns were monitored, providing important implications for understanding, and trying to mitigate, biodiversity loss from small habitats, especially loss of rare species. **Broader Impacts:** The primary impact of this research outside of basic understanding of restoration ecology principles was to engage

cohorts of undergraduate and high school students (many from underrepresented groups) in genuine research experiences at the field station. More than 50 such students participated in research in these glades over the course of the experiment, as well as 5 PhD students and 3 postdoctoral fellows. Papers to date: [55–58], with 6 others currently submitted or in revision.

Gillespie: DEB 1241253 Dimensions: A community level approach to understanding speciation in Hawaiian lineages. 2013-2018 (PI; co-PIs John Harte, Rasmus Nielsen, Patrick OâŽGrady), \$1,181,407 to UC Berkeley (collaborators in Cornell, University of Hawaii Hilo, U Maryland, Pacific Ecoinformatics, for a total award of \$1,999,910). Intellectual Merit. This project aims to transform understanding of the impact of the dynamic community on biodiversity by integrating (1) evolutionary models, and (2) macro-ecological theory. The synergy between the two approaches is made possible through the use of a habitat chronosequence, and corresponding space-for-time substitution, provided by the dynamic geomorphology of the young islands of the Hawaiian archipelago. We selected 6 plots in each of 15+ sites and are sorting thousands of arthropod specimens while creating an mtDNA barcode library and testing metabarcoding approaches. From these data we are estimating macroecological metrics and conducting food web analysis. For focal lineages, genomic data is providing information on population differentiation over the island chronology for different trophic groups. **Broader Impacts:** New species are being discovered and research is integrated into education; trained 7 postdocs, 10 graduate students, 14 undergraduates, and one high school student in the last year and gave > 11 presentations at scientific meetings. To date this work has produced 10 papers [8, 13, 45, 59–65].

Gruner: DEB-1020007 Collaborative Research: Interactive effects of predation and ecosystem size on arthropod food webs in Hawaiian forests fragmented by lava flows. 2010-2015 (collaborative PIs Tad Fukami, David Flaspohler, Christian Giardina), \$329,949 to U Maryland (collaborators at Stanford, Michigan Tech, and US Forest Service, for a total award of \$1,213,843). Intellectual Merit. This project examined forest food webs in naturally fragmented landscapes on Hawaii Island over a 100-fold ecosystem size gradient. Our overarching objective was to test the contingent effects of an invasive omnivore, the black rat *Rattus rattus*, on bird population dynamics, arthropod food webs, and ecosystem processes. By eliminating rats from fragments up to 12 ha in size in a 4-yr press experiment, and independently excluding birds from tree canopies, we provided evidence for non-consumptive effects of rats in altering bird foraging behavior and their impacts on arthropods. This work has produced 10 peer-reviewed papers [66–72], with three more in review or in revision. **Broader Impacts:** More than 25 undergraduate students participated as interns and paid assistants in this research. Two students were mentored through the Pacific Internship Programs for Exploring Science (PIPES) program, which is committed to recruiting and retaining local Hawaiian students in research. Three students completed MS degrees at University of Hawaii Hilo (Phifer, 2012; Mueller et al. In review; Wilson Rankin et al. In review), one PhD project is ongoing at Stanford University, and three postdocs were mentored and placed in subsequent positions. The project was featured in volume 16 (2012) of the *Natural Inquirer*, a middle school science education journal produced by the US Forest Service.