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Shift in a life history trade-off linked with change in hormonal cross-talk and behavioral plasticity
Perhaps the most fundamental life history trade-off is that between reproduction and self-maintenance. This trade-off is mediated by the interaction of two major endocrine systems, the hypothalamic-pituitary-gonadal (HPG) axis, which regulates reproduction, and the hypothalamic-pituitary-adrenal (HPA) axis, which regulates response to stressors. We ask whether environmental change that influences this trade-off is reflected in altered hormonal interactions and behavioral plasticity. Recent colonization of an urban environment by the montane Dark-eyed junco has dramatically affected their reproductive and stress ecology, resulting in increased allocation to reproduction and reduced response to stressors. We show that the shift in this trade-off is reflected in lower sensitivity of the HPG to activation of the HPA axis in city birds, and that the impact of stress on reproductive behaviors is lower in city birds. We argue that selection for increased allocation to reproduction has resulted in a rapid shift in endocrine interactions and behavioral plasticity.

W15. Abu Awad, Diala. GEPV, Université Lille 1.
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The numerical load : Understanding the interaction between demography and genetics
New mutations, most of which are deleterious, are constantly introduced into populations. The genetic load, or the effect of segregating deleterious mutations on population fitness, has been considered to be independent of demographic parameters. In literature, the effect of the genetic load and the timing of selection on population size remain ambiguous. We propose a model that explicitly takes into account the interaction between the genetic load and population demography. We consider the evolution of the genetic load at a single bi-allelic locus in a sexually reproducing population. By analyzing the deterministic behaviour of such a model, we find that demography affects and can be affected by selection. The timing of selection has an effect on both the genetic load and population size at equilibrium.

W38. Agashe, Deepa. National Center for Biological Sciences.
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Connecting the ecology, evolution and behavior of natural populations
An ultimate goal of biological research is to connect the genetic, phenotypic, and behavioral features of organisms; however, this remains logistically challenging for most species. I analyze behavioral, ecological, and evolutionary characteristics of over a dozen populations of a generalist insect pest (the red flour beetle *Tribolium castaneum*) collected from different regions of India. Metrics of fitness (performance) and behavioral preference for seven different resources are not consistently correlated across populations, indicating that preference-performance relationships can rapidly evolve to be disjunct. Interestingly, variation in fitness and behavior across populations was sometimes associated with significant reproductive isolation, but was not explained solely by geographical separation. To further understand population divergence, we are now analyzing putatively selected candidate loci that may contribute to the observed variation between populations. Connecting the ecology, evolution and behavior of natural populations of this widespread insect provides deeper and more general understanding of how organisms evolve.

W1. Akcay, Erol. University of Pennsylvania.
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Mechanisms for cooperating under private information
Cooperation underlies almost all living systems. One of the factors that can work against the evolution of cooperation is when interacting individuals possess private information (i.e., can condition their phenotypes on states that other individuals cannot). In these cases, cooperation is hampered, because natural selection favors "dishonest" phenotypes. I will present results from a new theoretical approach adapted from economics, called mechanism design, that deals with how different interaction schemes can maintain cooperation under imperfect information, focusing on bilateral cooperation and public goods games. This approach focuses on how natural selection can act on the structure of the "game" played between individuals, as opposed to only individual strategies in a fixed game. As such, it points the way to a new generation of evolutionary game theory that directly deals with how the natural history of interactions evolves.

M23. Anacker, Brian. University of California, Davis.
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Phylogenetic signal in plant interactions with neighbors and soil biota: Insights from experimental and observational approaches

We placed native plant species from Bodega Bay, CA into competition with neighbors of varying phylogenetic distances in companion field and greenhouse experiments. We also characterized the structure of below-ground soil communities, to assess the importance of soil biota on the strength of plant competition. Preliminary results suggest that both plant survival and competition were highest in home sites, as would be expected given phylogenetic niche conservatism. We also found phylogenetic signal in fungal communities, where closely related plants have more similar fungal communities than expected by chance; this was not the case for bacterial communities. Our study is the first to combine an experimental approach using a large diversity of species with extensive observational data to explore community assembly and coexistence mechanisms in a phylogenetic context.

M31. Barney, Bryan. Stanford University - Hopkins Marine Station.

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Searching for selection at highly local scales - evidence for thermal selection in a high dispersal species

Within the rocky intertidal zone, significant differences in temperature can exist across centimeter scales due to variable wave, wind, and solar exposure. This thermal mosaic can be a challenge for the survival of sessile organisms: once settlement occurs, that individual is committed to the long-term thermal regime at that location no matter what its internal intrinsic thermal adaptation. If phenotype-environment mismatches occur, highly localized natural selection may be the result. We investigated the California mussel (*Mytilus californianus*) in mussel beds under different thermal regimes in Pacific Grove, CA. Using transcriptomic techniques to discover single nucleotide polymorphisms (SNPs) within sun-exposed and shaded mussels, we found signals of natural selection for 289 SNPs - many of which lie within genes involved in thermal tolerance. These findings suggest the existence of subtle but recurring localized spatial balancing selection on thermal tolerance phenotypes at the scale of individual mussel beds.

P11. Baskett, Carina. Michigan State University.

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Latitudinal variation in pollination-related traits in *Phytolacca* (pokeweed)

There is evidence that the prevalence and strength of biotic interactions are higher in tropical compared to temperate regions. This has been proposed to cause higher diversification rates in the tropics, and is critical to understand for translating conservation lessons from temperate to tropical regions. More studies of the biotic interaction gradient are needed that span a wide range of latitudes and use phylogenetic control. In a common garden at Kellogg Biological Station (42° N), I planted seeds collected from four North American populations of *Phytolacca americana* (spanning 26-42° N) and one population of *P. rivinoides* from Panama (9° N). I measured pollinator visitation, and floral traits related to pollinator attraction and mating system. I found significant latitudinal variation in several traits (e.g., nectar production and anther dehiscence in the bud), consistent with the hypothesis that higher latitude populations depend less on animal pollination and invest less in attracting pollinators.

T7. Bay, Rachael. Stanford University.

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Genomic differences reflect fitness over a small-scale thermal gradient

Accurate prediction of species response to climate change requires a detailed understanding of potential mechanisms of environmental adaptation. Reef-building corals, the foundation of coral reef ecosystems, are susceptible to high-temperature bleaching, but variance in susceptibility exists even within species. We combine whole-transcriptome sequencing with reciprocal transplantation to examine adaptation to microclimate temperature regimes in the tabletop coral, *Acropora hyacinthus*. We identified single nucleotide polymorphisms (SNPs) associated with temperature regime, even in the presence of gene flow. We found that rare variants representing a broad range of cellular pathways were maintained in more thermally stressful microclimates, evidence for balancing selection in a heterogeneous environment. Survival and growth measurements from transplant experiments mirror genetic data, suggesting some genotypes are more resilient in the face of heat stress than others. These results provide information on possible mechanisms for coral resilience as well as the potential for populations to adapt as ocean temperatures increase.

W30. Behrman, Emliy. University of Pennsylvania.

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Strong seasonal selection results in rapid life history changes in *Drosophila*

Variation in spatial and temporal selection pressures can maintain genetic diversity in natural populations. To investigate if seasonal changes in environmental parameters drive rapid adaptation, life histories and basic population parameters of wild populations of *Drosophila* are examined over seasonal time across replicate years. Patterns of life

history variation are partitioned into effects associated with temporal change in environmental quality (i.e., phenotypic plasticity) and generational change in genetic composition (i.e., evolutionary response). There are distinct trajectories by species: *D. melanogaster* appears a resident population that responds rapidly to environmental selection pressures whereas *D. simulans* does not demonstrate an adaptive response to seasonality. The observed changes in life histories across seasonal time mirror patterns observed across spatial gradients; latitudinal clines may be, in part, driven by the adaptive response to seasonal dynamics and spatial variation in the duration and magnitude of seasons favorable versus unfavorable for insect population growth.

T8. Bergland, Alan. Stanford University.

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Genomic evidence of rapid and stable adaptive oscillations over seasonal time scales in *Drosophila*

In many species, genomic data have revealed pervasive adaptive evolution indicated by the near fixation of beneficial alleles. However, when selection pressures are highly variable along a species' range or through time adaptive alleles may persist at intermediate frequencies for long periods. So called 'balanced polymorphisms' have long been understood to be an important component of standing genetic variation yet direct evidence of balancing selection has remained elusive. We hypothesized that environmental fluctuations between seasons would impose temporally variable selection on *Drosophila melanogaster* and maintain allelic variation at conditionally beneficial polymorphisms. We identified hundreds of polymorphisms whose frequency oscillates among seasons and argue that these polymorphisms are subject to strong, temporally variable selection, respond to acute frost events and have persisted for millions of years. Our results demonstrate that rapid temporal fluctuations in climate over generational scales is a predominant force that maintains adaptive alleles and promotes genetic diversity.

M12. Billiard, Sylvain. GEPV Université Lille 1.

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How ecological processes affect neutral genetic diversity?

Neutral genetic diversity is commonly used by ecologists and evolutionary biologists as markers for making inferences (e.g. phylogenies, demographic history, dispersal patterns, etc.). These inferences are generally possible because of the simplifying assumptions of the population genetics framework, especially that population size is a constant parameter and is always independent of the ecological processes. We will present a model inspired by the Adaptive Dynamics framework, and assume that population size is an emergent property of the underlying ecological and evolutionary processes. We first show that in general the distribution of neutral genetic diversity and the divergence between sequences depend on the ecological processes and their parameters (birth and death rates, competition kernels, etc.). Second, we show that when diversification (or speciation) occurs, then neutral diversity in each population does not evolve independently of each other. Finally, we discuss the implications for the use of neutral markers for inferences.

M9. Boersma, Kate S. Oregon State University.

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Biotic and abiotic disturbances have antagonistic effects on fragmented arid-land aquatic communities

Ecological theory predicts that taxonomic and functional composition in fragmented communities may become more similar (convergent) or more distinct (divergent) through time. Elucidating the biotic and abiotic mechanisms behind these processes is of imminent conservation concern in arid-land stream habitats. Climate change is causing once-contiguous arid-land streams to fragment, resulting in deterioration of abiotic conditions and increased rates of top predator extirpations. We combined data from three independent manipulative and observational studies of aquatic invertebrate community structure in fragmented streams to measure community convergence or divergence resulting from top predator extirpations and drought severity. We found that drought conditions caused functional convergence through time as maladaptive traits were eliminated, however top predator removals caused divergence as the dominant competitor was extirpated. Our results suggest that concurrent biotic and abiotic changes may act antagonistically on taxonomic and functional composition in fragmented arid-land stream communities.

M7. Boettiger, Carl. University of California, Santa Cruz.

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Ecological management for an uncertain world: robust decision theory in face of regime shifts

The effective management of natural resource populations such as fisheries or forests and the ecosystems in which they are embedded is a central goal of much work in both theoretical and applied ecological research. Management

decisions must be made in an uncertain world, coping with errors in data, uncertainty in model parameters and even the choice of models being used. Advances in areas such as risk management, optimization under uncertainty, and adaptive management methods have offered a way forward in spite of such uncertainty. We have only to admit what we don't know, and make the best decision based on the information at hand. The realization that such complex systems can contain tipping points-- thresholds at which the system can transition into a less desirable state rapidly and with little warning -- poses a fundamental challenge to these approaches. Such approaches require that we know what we do not know: we do not use the best guess of a parameter, instead, we have a distribution of possible values it may take. As recent events of the economy have illustrated, estimating the distribution isn't easy; and for complex systems with alternate stable states, a little bit more uncertainty can make a big difference. How then do we make the best decision based on the information available without exposing the system to these sudden crashes? How do we handle that uncertainty we just cannot parameterize -- the unknown unknowns?

MS7. Bolnick, Daniel. University of Texas at Austin.

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Deep matters: microgeographic clines with depth within lake populations of stickleback

Adaptive variation across a landscape is expected when the spatial grain of environmental variation is coarser than individuals' lifetime dispersal capacity. In such cases, gene flow between environments is low and divergent natural selection is capable of generating genetic differentiation. This well-supported view can, however, create blinders for researchers if it dissuades them from testing for adaptive divergence at still finer spatial scale. At such fine spatial scales, where individuals readily and often disperse across habitat boundaries, adaptive divergence should be swamped by gene flow. In my talk I present a counter-example, drawing from studies of morphology, diet, color, and behavioral variation in threespine stickleback. Much to our own surprise, we have repeatedly found genetic and phenotypic divergence over spatial scales of mere meters, in highly mobile threespine stickleback. I will present evidence for this divergence and describe experiments intended to test alternative explanations for this divergence, including assortative mating, phenotypic plasticity, and habitat choice.

M16. Boughman, Janette. Michigan State University.

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Speciation by divergent sexual selection

Whether sexual selection leads to speciation is controversial. Several elegant case studies offer support while comparative studies are equivocal, casting doubt on the general importance of sexual selection to speciation. We show the discrepancy exists because comparative studies ignore the very reason sexual selection causes speciation -- because it causes divergence in the traits used to select mates, thereby preventing mating between species. We test whether the strength of mate preferences or how much they differ between species predicts the amount of diversification in male display using quantitative measures from case studies across diverse taxa. We find that diversification in male display is explained by preference divergence, not preference strength. Without such divergence, even when sexual selection is strong, little reproductive isolation results. Thus, the distinction between how strong sexual selection and how much it differs between populations is crucial to understanding the role sexual selection plays in speciation.

W12. Brassil, Chad. University of Nebraska.

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The complications of temporal fluctuations on population dynamics: elevation, depression, and time-lags

The dependence of population growth on temperature has been described for a large number of species. We asked to what degree can these profiles be used to understand a population growing in fluctuating abiotic conditions. Standard temperature-growth profiles are generated by growing the population in constant conditions; can fluctuating conditions be predicted by simply integrating under the constant temperature-growth curve? We tested this in duckweed populations of *Lemna minor*. For simple sine-wave fluctuations, we found the constant temperature-growth curve successfully makes predictions about elevating and depressing effects of temporal fluctuations depending on the concavity of the temperature-growth curve. However, the consequences of stochastic population fluctuations were not predictable. In part this is because the current growth rate of the population depends on past temperature conditions, reducing the utility of the constant temperature-growth profile as a predictive tool for understanding the consequences of abiotic fluctuations in populations.

W3. Briggs, Heather. University of California, Santa Cruz.

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Pollinator traits and community composition interact to shape dynamic responses to single pollinator species losses

Interspecific interactions (e.g. competition) can dynamically shape individual and species-level resource use within communities. We have shown that interactions between native pollinators shape species' functional roles via changes in short-term foraging specialization ("floral fidelity"), and that loss of single pollinator species reduces floral fidelity in the remaining pollinators. In contrast to predictions from network studies that suggest plant communities will be resilient to losing many or most of the pollinator species in an ecosystem, we show that single pollinator losses reduce plant reproductive function, even while effective pollinators remain in the system. This study unpacks the community-wide response to pollinator losses and explores how traits—specifically pollinator tongue length, known to dictate pollinator resource partitioning—influence phenotypic plasticity and drive dynamic interspecific interactions. Understanding how traits drive these community and ecosystem functional relationships will help us to predict the impacts of biodiversity loss.

T5. Brown, Simon. University of California, Santa Cruz.

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Predicting future life histories of ectotherms under climate change

We present a framework based on the metabolic theory of ecology for predicting the effects of climate warming on the life history traits and demographic parameters of ectothermic species. We assembled a database of intraspecific variation in trait values among geographically separated populations. From this we construct a phylogenetically hierarchical model for predicting the slope of traits values versus temperature. Using this model allows us to project change in the life histories of ectotherms under different scenarios of climate change.

T28. Burghardt, Karin. Yale University.

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Can plasticity in plant defensive traits mediate nutrient cycling?

How plants respond (tolerance vs. defense) to herbivory may depend on the environmental context in which herbivory occurs. To test this idea we grew 8 genotypes of field-collected *Solidago altissima* in 4 nutrient contexts. These plants were then exposed to variable herbivory from a dominant grasshopper, *Melanoplus femurrubrum*. In general, *S. altissima* exhibited highest induced resistance to herbivores at the highest nutrient level. In contrast, plants in low nutrient environments exhibited the highest tolerance of herbivory. Resistant and tolerant plants tended to associate with different suites of plant functional traits. Because these traits are a major determinant of decomposition dynamics in ecosystems, divergent or plastic trait responses to herbivory may feedback to create heterogeneity in environmental (nutrient) context and thus impact future plant/herbivore interactions. Preliminary results from a multi-year mesocosm experiment that explicitly tests how induced defense and tolerance traits impact nutrient cycling and plant fitness will also be presented.

M43. Burghardt, Liana. Duke University.

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Predicting how genetic and environmental factors influence the environment experienced by plants during reproduction

Organisms transition through multiple life stages that differ in environmental tolerances and responses. Therefore, predicting the seasonal timing of life stage transitions is critical for understanding how organisms will respond to environmental change. In particular, the environment experienced during reproduction can have trans-generational effects and can limit reproductive output. We have developed a model to predict the timing of life-stage transitions and life-cycle expression. This model, parameterized for *A. thaliana*, generates predictions of whole life-cycle phenology of different genotypes in complex environments. Here we use this framework to explore across the European range how allelic variation in the timing of germination and flowering alters the environment experienced by developing seeds and the length of the period favorable for reproduction. We find that both location and genotype alter the environment during seed maturation and lead to variable seasonal windows for reproduction.

W8. Burls, Kevin. University of Nevada Reno.

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Parasitism and mutualism in a lycaenid butterfly: Temporal and geographic variation in parasitoid attack with no evidence for ant protection

Interactions between caterpillars, ants and parasitoids inform much of what is known about tri-trophic ecological dynamics, though detailed studies that encompass all three trophic levels are limited to relatively few natural systems.

Our study investigated interactions between the Melissa blue butterfly (*Lycaeides melissa*: Lycaenidae), mutualistic ants, and parasitoids on both native and introduced host plants over two years to quantify the diversity and abundance of these interactions and to ask how host plants and ant tending influenced parasitism rates. The abundance and diversity of parasitoids reared from caterpillars varied considerably across sites and years. Ant tending did not appear to reduce parasitism, in contrast to a study of *L. melissa* that found evidence for ant protection against predators. This study also revealed novel ant-caterpillar and caterpillar-parasitoid interactions. These findings highlight the importance of investigating ecological interactions, including interactions with other trophic levels, when studying ecological diversification in herbivorous insects.

T39. Callahan, Benjamin. Stanford University.

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Niche Construction Evolves Quickly and Repeatably in Experimental Microbial Populations

We used experimental evolution to explore the contribution of niche construction to adaptation in populations of the bacterium *Pseudomonas fluorescens*. Several replicate lineages of an initially identical ancestor adapted to a novel environment for hundreds of generations. We then isolated the environments modified by the evolved strains from the bacteria themselves via filtration, and performed competition experiments in those constructed environments. We found that adaptive niche construction accompanies adaptation. That is, evolved strains are more competitively fit in the environment they modified than in the environment modified by their ancestor. Adaptive niche constructing variants were detectable within one hundred generations, and after four hundred generations adaptive niche construction was ubiquitous. Fast evolution of adaptive niche construction has a number of potential ecological consequences, such as amplifying the process of adaptive radiation and causing priority effects between related species, which will influence the generation and maintenance of biodiversity.

W13. Clark, Adam. University of Minnesota.

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Defining ecosystems by their interactions: Using process to demystify pattern

Much of contemporary community ecology focuses on intense study of pattern: Observed distributions of species and environmental variables are used to predict how communities and environments interact. This has resulted in a rich field of multivariate analysis techniques. Much less development has focused on using observations of changes to gain insight about ecosystem interactions. This alternative process-based view uses observational time series to estimate rates of change among species populations (e.g. mortality and birth), and environmental properties (e.g. resource supply and consumption). These “demographic traits” can then be used to describe ecosystems using mechanistically informative and quantifiable variables, and may be useful for predicting future ecosystem behavior in response to management or perturbation. Using data describing almost a century of grassland succession at Cedar Creek Ecosystem Science Reserve, I present an example of this process-based approach for estimating demographic traits in ecosystems, and show how these parameters can be analyzed."

P3. Clark, Robert. Wesleyan University.

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A keystone mutualism between a community of ants and sap-feeders indirectly benefits plants

The effectiveness of plant anti-herbivore defenses is often contingent on herbivore-predator interactions. Tri-trophic interactions resulting in plant defense often utilize predator recruitment as a mechanism. One means of attracting predators may occur when plants are hosts to sap-feeding herbivores. Sap-feeding herbivores engage in food-for-protection mutualisms with ants. This strong direct interaction is considered a “keystone mutualism,” an extension of the keystone species concept. Because keystone species are often powerful examples of niche construction theory, we are interested in looking at keystone mutualisms through the same lens. Traits that make plants susceptible to sap-feeding insects, instead of being deleterious, may benefit plants by increasing the chance they will be host to a keystone mutualism. Here we present a study in which ant and sap-feeder mutualisms fundamentally alter interactions across three trophic levels. As a result, sap-feeders generate defense for plants by increasing caterpillar mortality and decreasing leaf area lost to herbivory.

TS6. Davies, Jonathan. McGill University.

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Identifying the evolutionary transitions linking phylogenetic diversity and ecosystem function

Recent studies have suggested a link between phylogenetic diversity and ecosystem function. However, such studies typically assume that phylogenetic branches of equivalent length are more or less interchangeable. Here I suggest that

there is a need to consider not only branch lengths but also their placement on the phylogeny. If phylogenetic diversity captures important functional diversity, biodiversity theory would predict a correlation between evolutionary distinctiveness and functional contribution. In contrast, if one or a few evolutionary innovations play key roles in ecosystem function, the relationship between evolutionary distinctiveness and functional contribution may be weak or absent. I show how phylogenetic elements associated with high functional contribution can be identified from regressions between phylogenetic diversity and productivity; however, using an empirical dataset on plants, I find no evidence for an association between evolutionary distinctiveness and ecosystem functioning.

T14. De Lisle, Stephen. University of Toronto.

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Independent evolution of the sexes drives amphibian diversification

Sexual dimorphism is a large and ubiquitous component of organismal diversity. Yet classic ecological theory predicts that the evolution of sexual dimorphism constrains net diversification, by limiting the morphospace available for ecological speciation. These predictions rest on the assumption that the sexes share a common adaptive landscape; which, by definition, will be violated in any lineage with separate sexes because the sexes themselves are defined by their divergent life history strategies. Thus sexual dimorphism may in fact represent a key innovation, driving rather than constraining diversification, if the ability of the sexes to evolve independently allows the exploration of morphospace that would be maladaptive for a sexually monomorphic lineage. We test predictions of this verbal model by examining the relationship between sexual dimorphism and diversification across the amphibians. Consistent with predictions, female-larger sexual size dimorphism is associated with increased species richness, diversification rate, and reduced species IUCN extinction threat status. Our work reconciles conflicting predictions from ecological and evolutionary genetic theory and illustrates that the ability of the sexes to evolve independently has been a key driver of some of the most spectacular recent vertebrate radiations.

MS3. de Meester, Luc. University of Leuven.

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Local genetic adaptation of *Daphnia* to ecological gradients at the landscape level, and its link to population genetic as well as metacommunity structure

There is much evidence that populations of the water flea *Daphnia* can adapt to fine-scale microgeographic settings. I will here provide examples of local genetic adaptation in the water flea *D. magna* to the complex mosaic of environmental gradients found in natural landscapes, including anthropogenic disturbance. I will highlight a number of key attributes of microgeographic adaptation in this model system: (1) genetic tracking of environmental change can occur within a short time span, (2) it is largely fueled by standing genetic variation, (3) selection and microgeographic adaptation impact the landscape genetic structure of this species, and (4) there is scope for interactions of microgeographic adaptation and metacommunity dynamics. The latter relationship may be complex, and needs to be studied in more detail both experimentally and through landscape-wide analyses.

W29. Des Roches, Simone. University of Idaho.

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Ongoing natural selection of two rapidly evolving lizard species in White Sands

Studying colonization of new environments can tell us about how selection and adaptation shape biodiversity. White Sands, New Mexico, is an ideal system to study evolution after colonization. White Sands formed in the last 6,000 years and supports an ecosystem biologically distinctive from the surrounding desert. Since its formation, White Sands has been colonized independently by three lizard species that have evolved in parallel. Rapid convergent evolution of the three species indicates presence of strong divergent selection. In our ongoing project, we measure the direction and magnitude of ongoing selection on ecologically important traits in White Sands lizards. We document differential survival of *Holbrookia maculata*, and *Sceloporus undulatus*, two of the three White Sands species. We hypothesize that selection, in terms of differential survival of White Sands *Holbrookia maculata* and *Sceloporus undulatus*, acts on a suite of phenotypic traits including dorsal color and body shape. Survival data and morphology measurements combined with regression analysis allows us to evaluate selection's direction and magnitude via correlation. By using mark-recapture we measure selection by incorporating survival as a proxy for fitness. Results from three field seasons suggest varying direction and magnitude of selection from year to year.

P1. Diepeveen, Eveline. University of California, Berkeley.

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The genetic basis of convergent thick-lipped phenotypes in distantly related cichlid fishes

Cases of convergent phenotypes, due to adaptation to similar ecological niches, are particularly illuminating of the genetic mechanisms underlying adaptive evolution. A remarkable case of independent convergence involves the thick-lipped phenotype found in cichlid species in both the East African Great Lakes and in several Central American lakes. The 'fleshy' lips are associated with hard-shelled prey, such as mollusks and other invertebrates. With a comparative Illumina RNA sequencing approach we identified 141 candidate genes that appear to be involved in the morphogenesis of the thick-lipped phenotype in the African *Lobochilotes labiatus*. Six of these candidate loci were tested with comparative quantitative real-time PCR analyses in both an African and a Nicaraguan thick-lipped and thin-lipped species pair. Similar trends in gene expression between African and Central American thick-lipped species appear to indicate that an overlapping set of genes was independently recruited to build this particular phenotype in both lineages.

P13. Dittmar, Emily. Michigan State University.

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Adaptation to Serpentine Soil in *Leptosiphon parviflorus*

Local adaptation is a driving force underlying biodiversity, but the mechanisms that contribute to fitness trade-offs between environments are not well understood. To address this, I investigate adaptive divergence between two populations of *Leptosiphon parviflorus*. This native California wildflower sometimes grows on serpentine soil, which is characterized by harsh conditions and strong selective pressures. At Jasper Ridge Biological Preserve, populations of *L. parviflorus* grow on and off serpentine soil in close proximity. Despite ongoing gene flow, these populations are locally adapted to their soil types as demonstrated by two years of reciprocal transplant studies in the field. Flower color and flowering time contribute to local adaptation and F5 hybrids were grown on both soil types in the field and greenhouse to measure selection on these traits. Ongoing work aims to understand the factors that contribute to fitness trade-offs between soil types and to investigate the genetic basis of serpentine adaptation.

M13. DiVittorio, Christopher. University of California, Berkeley.

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Extremely strong natural selection across a wild sunflower hybrid zone

Ecologically based divergent natural selection is presumed to be involved in most speciation events. However, the levels of natural selection required in many models of parapatric or sympatric speciation may be unrealistically high. Using reciprocal transplant and resource manipulation field experiments at a hybrid zone between fully interfertile dune and desert shrubs I measured selection coefficients of 0.98-0.76 against parental migrants and 0.10-0.69 against hybrids, values that are theoretically sufficient to maintain divergence despite observed hybridization rates of up to 25%. The mechanism of selection is further shown to be dependent on gradients of water availability, herbivory and disturbance. Classic biosystematic work showed no evidence of any intrinsic incompatibilities in hundreds of experimental crosses, thus the lack of species fusion at this site appears to represent divergence maintained almost entirely by extrinsic natural selection.

T6. Donihue, Colin. Yale School of Forestry and Environmental Studies.

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Anthropogenic impacts on lizard adaptability and ecological dynamics in the Greek Archipelago

Humans are modifying landscapes globally, driving species to adapt to their changing context or die. Understanding the impacts of humans on the ecological dynamics of a system is critical, but those dynamics are mediated by species traits that can change in response to context, making predictions difficult. The Aegean Wall Lizard, *Podarcis erhardii*, is common in the Greek Cyclades and, on populated islands, is most often found living in and around stonewalls. My research investigated the context dependence of a suite of morphological traits in the lizard along with two ecologically relevant performance traits: bite force and sprint speed. I found that lizards living on walls were significantly different in morphology and performance to conspecifics living in "pristine" areas within the same island. A large-scale, full-island manipulation experiment is planned to further examine these differences and explore their import for the dynamics of the ecosystem as a whole.

WS5. Donohue, Kathleen. Duke University.

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Niche construction through phenological cuing

Genetically based phenological traits, such as flowering and germination time, are highly sensitive to seasonal cues, such that development to the next life stage occurs only under specific combinations of seasonal conditions. Therefore, the phenological responses of prior life stages determines the seasonal environment experienced by

subsequent life stages. As such, phenological cuing can be a precise form of habitat selection or niche construction. Such habitat selection/niche construction influences life-cycle expression in demographically important ways. It also influences allelic effects of genes involved in life-history variation; allelic effects of genes that regulate one life stage can ramify across subsequent life stages, or they can be masked because of niche construction. Niche construction through phenological cuing can also influence natural selection on life-history alleles, even altering the direction of selection and imposing balancing selection on them. Examples of these dynamics are given in the annual plant, *Arabidopsis thaliana*.

T33. Duckworth, Renee. University of Arizona.

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Eco-evolutionary dynamics: What are the causal links between population density, natural selection and phenotypic change?

Recent examples of rapid evolutionary change indicate that eco-evolutionary feedback loops may be an important, albeit neglected, factor in driving ecological interactions. Isolating the mechanistic links in eco-evolutionary feedback loops, both in terms of identifying sources of variation in traits and in terms of determining how and why natural selection varies with population density, is crucial for understanding the ecological consequences of phenotypic change. Here I use colonization cycles of western bluebirds (*Sialia mexicana*), a species that depends on successional habitat and must continually colonize new areas to survive, to show that cyclical changes in aggression, population density and natural selection are due to a combination of selection on genetic variation, maternal effects and colonization dynamics. Because the majority of cases of rapid evolutionary change have been in species invading new environments, these results suggest that colonization dynamics may be an important, yet understudied, driver of eco-evolutionary feedback loops.

W18. Dwyer, John. The University of Queensland.

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Climate regulates release from nutrient limitation in diverse annual plant communities

Niche differences are theorized to permit inferior competitors to coexist with superior competitors via tradeoffs, but only if there are opportunities for tradeoffs to operate. In systems limited by multiple resources, tradeoffs can occur along resource axes, but when limiting resources are supplied, trade-off opportunities are lost. In the extreme, light becomes the major limiting resource and competitive exclusion ensues. The impact of local-scale resource provision may be regulated by regional climate, e.g. in systems colimited by nutrients and water. We investigated the interactive effects of regional climate and local scale nutrient enrichment on natural herb communities in south-western Australia. Community richness declined in response to nutrient enrichment, but only in regions of low moisture stress. Communities in high nutrient - low moisture stress situations possessed traits typical of light-competing species, being taller, high SLA and large seeded communities.

TS3. Emery, Nancy. Purdue University.

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Species interactions and niche conservatism determine ecological distributions in vernal pool species

Historical processes and ongoing ecological dynamics shape current species distribution patterns. At fine spatial scales, competition and physiological stressors often restrict organisms to use a subset of the conditions and resources that are available in their local environment. Using comparative and experimental approaches, I have investigated the ecological and evolutionary drivers of habitat specialization in *Lasthenia* (Asteraceae) that are restricted to specific microhabitats along flooding gradients in vernal pool wetlands. Comparative analyses indicate that microhabitat associations have been relatively conserved throughout the diversification of the clade. Common garden experiments confirm that the optimum hydrological environment for is similar for all *Lasthenia* species, though the breadth of hydrological reaction norms varies among species. Finally, population-level field experiments demonstrate that competitive interactions play a significant role in driving microhabitat specialization in the field. Collectively, these studies demonstrate how phylogenetic and contemporary processes jointly determine patterns of habitat specialization in natural populations.

M37. Forrestel, Elisabeth. Yale University.

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Cross-continental comparison of phylogenetic and functional turnover of grassland communities in response to precipitation

The biogeographic history of a region necessarily plays a role in structuring the ecological, phylogenetic and functional patterns of communities across spatial scales. Across a broad precipitation gradient in C-4 dominated grasslands of South Africa and North America, we sampled plots for community composition, as well as phylogenetic and functional trait data for all dominant grass species. We found similar patterns of phylogenetic clade and functional turnover. Leaf level traits associated with drought tolerance, water and nutrient-use efficiency exhibited similar trends across the gradient and were directly related to clade turnover. Despite this broad convergence between South African and North American grasslands, there were signatures of biogeographic differences between the regions which were reflected in shifts in the dominance and niche occupancy of clades, and aspects of function. Our results highlight the import of continental-scale comparative phylogenetic and functional approaches to understanding patterns of species richness, community structure and function.

T16. Frishkoff, Luke. Stanford University.
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Pruning the tree of life: Habitat conversion and agricultural intensification result in loss of avian phylogenetic diversity in tropical countryside landscapes

T20. Fukami, Tadashi. Stanford University.
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Historical contingency in community assembly: the importance of long-term transients to the maintenance of biodiversity

The concept of alternative stable states has long been the dominant framework for studying the consequences of historical contingency in community assembly for biodiversity. This concept focuses on stable states, yet many real communities are kept in a transient state by disturbance. Using a simple model of plant community assembly, we show that the conditions under which historical contingency affects community assembly can differ greatly for stable versus transient states. These results argue for a conceptual shift of focus from alternative stable states to alternative transient states for understanding historical contingency in community assembly. As an example, we propose a new hypothesis regarding the maintenance of plant species diversity, namely that complex plant-soil interactions cause local plant communities to enter into a prolonged period of species turnover, resulting in transient, yet long-term maintenance of the high regional diversity that reflects variable history of species immigration early in succession.

M10. Fuller, Becky. University of Illinois.
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Chromosomal rearrangements, adaptation to salinity, and reproductive isolation between two killifish

Speciation is opposed by gene flow and recombination because they homogenize species-specific traits and isolating barriers. Genomic rearrangements represent a possible solution because they often create areas of the genome with reduced recombination. The probability of speciation may be enhanced provided that the loci underlying reproductive isolation and local adaptation occur in rearranged portions of the genome with low recombination. I present work from a study of two killifish - *Lucania goodei* and *L. parva* - that differ in karyotype. *Lucania goodei* has 24 small acrocentric chromosomes whereas *L. parva* has 22 acrocentric chromosomes plus a large metacentric chromosome that is the result of a chromosomal fusion. The two species also differ in salinity tolerance. *L. goodei* is a freshwater specialist. *L. parva* is euryhaline. We created hybrids, identified QTL for salinity tolerance, intrinsic isolation, and behavioral isolation, and determined whether the QTL occurred on the fused chromosome.

W23. Gilbert, Gregory. University of California, Santa Cruz.
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Heart rot and the maintenance of rare species in a tropical rain forest

Most tropical tree species are rare. Here we explore the Enemy Susceptibility Hypothesis that inherent variation in susceptibility to attack by enemies such as wood-decay fungi may help explain why many species are rare (those that are more susceptible) whereas resistant species may become common. Using non-invasive sonic tomography of living trees in the 50-ha Forest Dynamics Plot on Barro Colorado Island, Panama, we found that nearly a quarter of all trees show internal decay by the time they reach canopy height, and that the probability of decay increases with tree diameter. Rare species are much more likely than common species to suffer decay. The high frequency of wood decay and variation among tree species suggests an important role for heart-rot fungi in shaping the dynamics and structure of tropical forest communities.

T23. Gomulkiewicz, Richard. Washington State University.
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Darwin's conundrum revisited: a twist on the relationship between phylogenetic distance and invasibility

A potential indicator of invasiveness is the phylogenetic distance between a non-native species and species in the recipient community. However, predicting invasiveness using phylogenetic information relies on an untested assumption: that both biotic resistance and facilitation weaken with increasing phylogenetic distance. We test the validity of this key assumption using a mathematical model in which a novel species is introduced into communities with varying ecological and phylogenetic relationships. Contrary to what is generally assumed, we find that biotic resistance and facilitation can either weaken or intensify with phylogenetic distance, depending on the mode of interspecific interactions (phenotype matching or phenotype differences) and the resulting evolutionary trajectory of the recipient community. Thus, we demonstrate that considering the mechanisms that drive phenotypic divergence between native and non-native species can provide critical insight into the relationship between phylogenetic distance and invasibility.

TS8. Graham, Catherine. Stony Brook University.
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Node-based analysis of clade distribution

The integration of ecological data with evolutionary relationships is one of the most rapidly moving research fields today, and has led to considerable advances in our understanding of the processes underlying biogeographical patterns. Here, we develop the node allopatry score that combines ecological and evolutionary approaches into a single framework, and avoids many of the problems that characterize community phylogenetic methods in current use. This approach goes through each node in the phylogeny, and compares the distributions of descendant clades to a null model. The node-based analysis identifies specific nodes associated with shifts in distribution or environmental tolerances, and in doing so provides insights into what nodes are responsible for patterns of phylogenetic structure and species co-occurrence. This provides the basis for more detailed studies, for example focusing on the ecological changes or adaptations that took place at the highlighted nodes. In addition, by relating these nodes to historical, evolutionary or ecological data, node-based analysis provides novel insights and helps us to understand the drivers of current patterns of diversity. We demonstrate how this novel implementation can be used to generate hypotheses for biogeographical patterns with case studies with well-described biogeographical histories. The node-based analysis generates a set of intuitively interpretable patterns that are consistent with current biogeographical knowledge. Importantly, the results are statistically tractable, opening many possibilities for their use in analyses of the evolutionary, historical and spatial patterns of species diversity.

P8. Hallett, Allysa. Univ of Wisconsin-Milwaukee.
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Competition for pollination between *Asclepias verticillata* and *Monarda fistulosa*

Movements of pollinators between co-occurring plant species may lead to pollen loss when pollinators transition to a heterospecific competitor. Pollen wastage due to interspecific foraging by pollinators may lower conspecific pollen deposition and reduce seed set. We experimentally quantified the effects of a sympatric competitor for pollination, *Monarda fistulosa*, on both receipt and export of *Asclepias verticillata* pollinia. The two species broadly overlap in flowering phenology and share several species of hymenopteran and lepidopteran pollinators. Heterospecific movements of pollinators were frequent, and *Asclepias* pollinia were often detected on *Monarda* flowers.

P2. Harris, David. UC Davis.
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Generating realistic species assemblages with a partially-observed Markov random Field

Many areas of ecology depend on knowing where species can live and which species can live together. While species distribution models often make good predictions about individual taxa in areas that cannot be sampled directly, they do not address the co-occurrence of multiple species. Here, I present a model based on partially-observed Markov random fields that addresses whole species assemblages, rather than individual taxa. The model defines a joint probability distribution over possible species assemblages, allowing it to determine which combinations of species are most consistent with the available data. The model uses latent random variables to account for the unmeasured environmental heterogeneity underlying species' co-occurrence patterns. Sharing information among species in a single model improves predictive accuracy (especially for rare species). The model's highly interpretable structure also

facilitates comparisons among species and among hypotheses about the processes that drive community assembly and species turnover.

W21. Hausch, Stephen. University of Calgary.

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The Ghost of Competition Last Year: Rapid Coevolution and the Coexistence of Competing Bruchid Beetles

One of the earliest questions at the interface of ecology and evolution is how coevolution influences the ability of species to coexist. While the subject of much natural and theoretical work, it has received little experimental attention due to the perceived time required for coevolution to occur. Relatively recent work, including that on bruchid beetles, has shown that ecologically relevant evolution can occur within one to a few generations. We sought to experimentally test how the stability of coexistence of two species of bruchid beetles (*Callosobruchus maculatus* and *C. chinensis*) changes over the course of 12 generations of independent or coevolutionary history. As predicted, coevolved communities returned to resource partitioning faster than “first-contact” communities, provided the invasion was successful. Surprisingly, though, coevolved communities were less likely to show mutual invasibility upon separation and reinvasion.

T11. Hembry, David. Kyoto University.

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Evolutionary stability of specialization and its role in diversification in the brood pollination mutualism between leafflowers and leafflower moths

How specialization in biotic interactions changes over evolutionary time, and how it promotes diversification, remains poorly understood. Brood pollination mutualisms, in which specialized insects are seed predators as larvae but pollinators as adults of the same host plants, are characterized by extreme reciprocal specialization and modularity. In many cases, these mutualisms show one-to-one patterns of species-specificity at the population level. Many recent studies find more complex patterns of specialization in these mutualisms, raising the question whether non-one-to-one patterns are evolutionarily stable, or whether some process (plant-pollinator coevolution, or pollinator-pollinator competition) promotes increased reciprocal specialization. Here, we present ongoing work using cases of local pollinator sharing by two hosts and local host sharing by two pollinators in the leafflower-leafflower moth mutualism (Phyllanthaceae: Glochidion; Lepidoptera: Gracillariidae: Epicephala) in insular East Asia and South Pacific islands to ask whether such patterns are evolutionarily stable and what role they may play in diversification.

M42. Hereford, Joe. University of California, Davis.

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Phenotypic variation and plasticity in a C3-C4 intermediate annual

The pattern of phenotypic variation and plasticity suggests that climatic adaptation in the C3-C4 intermediate *Mollugo verticillata* has resulted from local adaptation and phenotypic plasticity. I measured the extent of phenotypic variation and plasticity in natural and experimental populations of this species from a wide range of climates, to quantify differences in the pattern of selection and phenotypic plasticity in physiological traits. These microevolutionary processes are a major factor in the evolution of the complex adaptation, C4 photosynthesis.

WS6. Holt, Robert D. University of Florida.

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Implications of niche construction for community ecology

M15. Hovick, Stephen. Ohio State University.

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Simply a numbers game? Disentangling the effects of founder population size and population genetic diversity on colonization success

Colonization is a critical process that affects both short- and long-term population dynamics and sets the stage for future evolutionary change. Colonization success rises with increasing founder population size and should be independently enhanced by increasing population genetic diversity. However, propagule number and genetic diversity are generally confounded because introducing more propagules will sample the source gene pool more completely. In 2012, we initiated a seed addition experiment to decouple these effects, using *Arabidopsis thaliana* as a model invader. We crossed a wide range of founder population sizes (96 to 960 seeds) and a range of genetic diversity treatments (1 to 8 genotypes) to assess how recruitment curves change as genetic diversity increases. We have also compiled functional

trait data for our *A. thaliana* →accessions, in order to connect neutral genetic diversity with functional trait diversity. We will present preliminary findings from the first growing season of this experiment.

T29. Humphrey, Parris. University of Arizona.
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The ecology of co-infection: dissecting parasite interactions mediated by host defense signaling

Plants have evolved robust inducible defense systems that mitigate current and/or future damage by diverse natural enemies such as herbivores, fungi, bacteria, and viruses. But simultaneous or sequential colonization (i.e. co-infection) by (e.g.) herbivores and bacteria can entail a cost: distinct plant defense pathways often trade-off phenotypically, leading to reciprocally induced susceptibility to attack of individual plants. We show that the evolutionary underpinnings of a trade-off or “signal antagonism” in plant defense appears ancient and well conserved among extant lineages, and explore the mechanistic underpinnings of within-host facilitation between a specialist herbivore and bacterial leaf colonizers in a native interaction system. A similar though non-homologous immune trade-off is known in mammals between macro- and micro-parasite infection. Thus, the architecture and evolutionary roots of immune systems across taxa may offer clues for predicting how co-infecting parasites impact one another and their hosts, and how infection intensities are patterned across landscapes.

W32. Iida, Yoshiko. Michigan State University.
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Linking functional traits, biomass allocation and demography for seedlings across 50 co-occurring subtropical tree species

Trees are expected to allocate their biomass among the various organs to maximize their individual performance. Biomass allocation patterns vary substantially, but it is unclear how biomass allocation links with species-specific functional traits and demographic performance in the field. Using a hierarchical Bayesian approach, we estimated species-specific allocation to foliage, stems and roots and potential demographic rates (relative growth rate and mortality) while considering the size effect for seedlings across 50 co-occurring tree species in Luquillo, Puerto Rico. Then, we quantified the correlations between allocation, several functional traits (specific leaf area, wood density and seed mass), and demographic rates. We found that species with high allocation to belowground mass and high wood density tend to have low mortality rates. These results support the fundamental importance of where species land on a continuum between conservative and acquisitive resource use strategies based upon their functional traits for predicting their performance.

W9. Jiang, Yuexin. University of Texas at Austin.
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Does Lateral Line Mediated Rheotaxis Explain Divergent Habitat Preferences of Lake and Stream Stickleback?

Habitat preference is a form of non-random dispersal and entails a conditional and directional movement of individuals within a heterogeneous environment. When heritable habitat preferences differ within or between populations, this can promote assortative mating and cause rapid adaptive divergence. Although habitat preference has received substantial empirical attention, little is known about the proximate mechanisms (i.e. behavioral and neurological mechanisms) underlying divergent habitat preferences and how such preferences evolve. The research integrated genetic, neuroanatomical, and behavioral approaches to understand the evolutionary basis of divergence in habitat preferences between parapatric lake and stream stickleback. A series of field and laboratory experiments indicate that the divergence in lateral line structure between parapatric lake and stream stickleback may be responsible for rheotactic behavioral differences that underlie divergent habitat preferences.

M24. Jones, Andrew. Yale University.
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Consumer interaction strength can limit the diversifying effect of intraspecific competition.

It is commonly assumed that increasing competition among conspecific consumers acts to promote population niche expansion, but empirical tests provide limited support for this phenomenon. As a result, the relationship between competition and niche width remains unresolved. Recent work suggests that the degree to which a consumer depletes its resources, a measure referred to as interaction strength, may influence the relationship between density and diet variation. Including interaction strength in estimates of intraspecific competition may also help explain the relationship between competition and diet variation. To test this, we conducted a focused meta-analysis. Results from our analysis provide clear evidence that increased consumer interaction strength generally weakens the diversifying effects of

competition, resulting in a unimodal relationship between intraspecific competition and niche width. These results suggest that information on species traits and environmental context is needed to improve our understanding of factors promoting and maintaining intraspecific variation in natural populations.

M25. Jordan, Lyndon. University of Texas at Austin.

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Reproductive Foraging Theory: spider males choose mates by selecting among competitive environments

Competitive interactions can alter the fitness payoffs of mate choice, yet the majority of mate choice studies use binary trials that ignore social factors. We test the importance of contest dynamics in a large scale choice experiment, using a framework where females are considered analogous to foraging patches subject to competition. We track the choices and interactions of 640 spiders (*Nephila plumipes*) before and after manipulation of competition, modelling the expected fitness payoffs of actual and all hypothetical choices. We find many males choose new females once social conditions change, achieving higher fitness than predicted under random movement, not by moving to larger females but by choosing favourable competitive environments. Further, we show that prior residence effects have a strong influence on male reproductive contests, highlighting the importance of situating mate choice studies in relevant social contexts, as intrasexual interactions can have profound effects on the payoffs of reproductive strategies.

W2. Karron, Jeffrey. University of Wisconsin - Milwaukee.

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Multiple mating and male - female conflict in a hermaphroditic plant, *Mimulus ringens*.

Plants exhibit remarkable diversity in floral traits, which is often thought to be related to their effects on self-pollination. However traits may also reflect interference between pollen export and receipt. Despite its importance for floral evolution, the ecological and evolutionary significance of such sexual interference remains largely unexplored. A trait that is especially likely to influence sexual interference is timing of stigma closure. Stigma closure may prevent deposition of additional pollen at substantial cost to female function. However rapid closure may simultaneously increase siring. We report results that confirm such a conflict over closure speed in bee-pollinated *Mimulus ringens*. From the female perspective, rapid closure reduced the number of seeds mothered. From the male perspective rapid closure increased the amount of pollen exported. This strongly suggests that sexual conflict cannot be ignored as a potential explanation for the diversity of floral traits.

W33. Kindsvater, Holly. Simon Fraser University.

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The evolution of semelparity and egg size

Whether to reproduce only once (semelparity) or to reproduce multiple times (iteroparity) is a fundamental question in life-history evolution. Theory predicts the relative risk of juvenile and adult mortality, as well as environmental unpredictability, will determine whether a species is semelparous or iteroparous. However, there is no clear prediction of how egg size is expected to evolve with parity, though covariance among these life-history traits is common in North American salmon species. Using matrix models, I explore the conditions that permit a rare iteroparous mutant to invade a semelparous population, and vice versa. I then ask how selection on egg size changes these conditions. When lifespan is fixed, reproductive costs to maternal survival can favor delayed reproduction and larger offspring. This result provides a novel hypothesis for the co-evolution of parity and egg size, which could explain the large egg sizes observed in semelparous Pacific salmon species.

M18. Kirkpatrick, Mark. University of Texas.

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T40. Kleynhans, Elizabeth. University of British Columbia.

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Evolutionary change depends on community context in BioCON, a long-term field study

Understanding how species adapt to environmental change is critically important, yet much of our current knowledge is based on experimental studies that investigate evolutionary adaptation on single species in isolation. We investigated how community context influences evolution in a natural ecosystem. Fieldwork was carried out in BioCON, a long-term ecological experiment. BioCON was initiated in 1997 and maintains differing diversities of plants under ambient or elevated CO₂ conditions. In June 2011 we collected *Poa pratensis* (Kentucky Bluegrass) seeds from monocultures and 16-species plots kept under ambient and elevated CO₂ conditions. These seeds were grown in a common garden

environment for 5 months after which rhizomes were harvested and transplanted back into BioCON using a full reciprocal transplant design. Our results indicated that both plastic and genetic changes have occurred in response to elevated CO₂, with the magnitude of such changes influenced by species diversity in the plot of origin.

P12. Knair, Supriya. University of Chicago.

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Correlated evolution of sperm and song in the Old World warblers

We compared evolutionary lability and trade-offs between sperm morphology, a post-mating sexually selected trait, and male song, a pre-mating sexually selected trait across 21 species of Old-World warblers (Phylloscopidae). Song traits show high phylogenetic lability, with signal lost across subclades of the family. Sperm morphology shows strong phylogenetic signal, with much evolution occurring between subclades, which occupy distinct ecological zones. Species with long songs tend to also have long sperm. In warblers more generally, long sperm is thought to indicate low sperm competition, because species with short sperm have large testes. We suggest the positive correlation between song and sperm reflects a shift from female choice (favoring longer songs and resulting in lower sperm competition) to male competition for territories (favoring shorter songs and resulting in more sperm competition) across species.

T15. Knope, Matthew. Stanford University.

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Ecological diversification is coupled to body size evolution across bilaterian marine animals

The ecological diversity and body size disparity of marine animals is greater today than at any point yet studied in Earth's history. However, the relationship between ecology and body size is essentially unknown for the history of animal life. Furthermore, the question of whether the controls of body size disparity have been conserved across evolutionary time or are instead the product of present environments, remains unresolved. Here, we present new data on approximately 20,000 fossil genera of marine animals spanning from the 'Cambrian Explosion' to the present day. We find that ecological mode of life (tiering, motility, and feeding) is correlated with body size, with feeding mode being most important. In addition, the relationship between ecology and body size has varied over evolutionary time in some major clades, suggesting that studies focused exclusively on living taxa can arrive at vastly different conclusions than studies that also include their extinct relatives.

W25. Koelle, Katia. Duke University.

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Integrating ecology into phylogenetic comparative analysis

The Ornstein-Uhlenbeck (OU) process has become a popular approach for studying adaptive evolution. However, this process is still only tenuously tied to ecology and the ways in which ecological selection pressures drive adaptive evolution. Here, I will present current work that aims to better integrate ecological dynamics with studies of adaptive evolution in phylogenetic comparative analysis. Specifically, I will show how ecologically driven selection pressures can be mapped onto OU and OU-like processes using quantitative genetics approaches, and therefore how fits of OU process models can be interpreted ecologically. By fitting different ecological OU models to data and selecting between them, the ultimate aim is to gain a better quantitative understanding of the ecological forces that underlie observed patterns of evolutionary change.

WS4. Kohn, Gregory. Indiana University

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Social personality traits and niche picking: how individuals construct their social experience

Individuals often exhibit consistent variation in their willingness to initiate social interaction with others, or sociability. Early variation in sociability may influence the development of courtship skills by exposing juveniles to different levels of social contact. Here I investigated how early sociability reflects the ontogeny of courtship skills in Brown-headed Cowbirds. During autumn I used a fission-fusion perturbation on a flock of juvenile cowbirds, and recorded social interaction patterns across contexts. Juveniles were then observed the following breeding season. Females who consistently initiated more social interactions during the fall were more likely to be pair-bonded during the breeding season, and respond to male song displays using a 'chatter' vocalization. In previous studies we discovered that adult females who used more response chatters laid more eggs than other females. These results suggest that early and consistent variation in sociability reflects the development of courtship behaviors needed for successful reproduction in adulthood.

P5. Korb, Julie. Fort Lewis College.

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Pollinator responses to floral resources and growing season warming in the alpine tundra, San Juan Mountains, Colorado

Plant and pollinator responses to climate warming can result in phenological mismatches between plants and pollinators which may threaten mutualistic relationships that have evolved over time. This mismatch may result from a reduction in pollinator or floral resource diversity or from the inability of native pollinators to encounter and successfully pollinate plants. One way to test plant-pollinator mismatches is to accelerate flowering time (growing season warming) to force plants to reach anthesis before their main pollinator is available to quantify how a mismatch impacts reproductive success and long-term population dynamics. Generally speaking, alpine specialist plant species tend to be pollinated by bees and butterflies while generalist plant species are often pollinated by flies or wind dispersal. A change in pollinator group abundance may result in shifts in plant species richness and abundance resulting long-term in the homogenization of the alpine with a decrease in plant specialists and their associated pollinators.

T37. Kotler, Burt. Ben-Gurion University.

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Macroevolution meets microecology: Intercontinental wide consequences of compromise-breaking adaptations

Desert rodent assemblages from around the world provide convergent, but independent crucibles for testing theory and deducing general ecological principles. The heteromyid rodents of North America and the gerbils of the Middle East provide such an example. Both face predation from owls and vipers, but the North American species possess unique traits that may represent macroevolutionary breakthroughs: rattlesnakes have infra-red sensitive sensory pits, and heteromyids have cheek pouches. To test their significance, we brought together two gerbils, a kangaroo rat, a pocket mouse in a common setting, and quantified the foraging behavior of each. Gerbils are fairly evenly matched in their anti-predator abilities, while the heteromyids differ widely, and these seem to determine the types of mechanisms of species coexistence that operate in the communities of each continent. Evolutionary history, macroevolutionary traits, and risk management therefore combine to determine the characteristics of the organisms and the organization of their communities.

W34. Labrada-Martagon, Vanessa. CSTAR University of California, Santa Cruz.

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Generalized linear models as an explanatory tool of sex steroids, thyroid hormones and their relationships with environmental factors in immature East Pacific green sea turtles.

Generalized linear models were fitted to evaluate the relationship between 17 β -estradiol (E2), testosterone (T) and thyroxine (T4) levels in immature East Pacific green sea turtles (*Chelonia mydas*) and their body condition, size, mass, blood biochemistry parameters, handling time, year, season and site of capture. According to external (tail size) and morphological (<77.3 cm straight carapace length) characteristics, 95% of the individuals were juveniles. Hormone levels, assessed on individuals subjected to a capture stress protocol, were <34.7 nmol T L⁻¹, <532.3 pmol E2 L⁻¹ and <43.8 nmol T4 L⁻¹. The statistical models explained metabolic relationships between hormone concentrations and the nutritional (glucose, cholesterol) and phenotypic (size, weight) state of the organisms. Seasonal and regional differences in sex steroids denoted by the models coincided with specific nutritional, physiological and body condition differences related to specific habitat conditions. The variables handling time and year did not contribute significantly to explain hormone levels.

WS2. Laland, Kevin. University of St Andrews.

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Niche construction theory: a practical guide to ecologists

T24. Lampert, Adam. University of California, Davis.

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Discrete body-size distributions in ecosystems induced by resonance and singular points

The size of an organism reflects its metabolic rate, growth rate, mortality, and other important characteristics, and therefore, the distribution of body size is a major determinant of ecosystem structure and function. Body-size distributions often are multimodal, with several peaks of abundant sizes, and previous studies suggest that this is the outcome of niche separation: species from distinct peaks avoid competition by consuming different resources, which

results in selection of different sizes in each niche. However, this cannot explain many ecosystems with several peaks competing over the same niche. Here, we suggest two alternative, generic mechanism underlying multimodal size distributions. One is the size-dependent tradeoff between reproduction and resource utilization that entails an inherent resonance. The second are points along niche axis where resource availability changes sharply. Our theory is well-fitted to empirical data in various ecosystems.

M40. Lang, Jenna. University of California, Davis.

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Evolution in really, really small spaces

Our lab is interested in the functional adaptation of microbial communities to changing environments. Fortunately, microbial environments can be quite small and easily manipulated. Here, I will describe a simple experiment in which we altered the diet of *Drosophila melanogaster* and monitored the response of the gut microbial community. We employed two approaches: 1) taxonomic profiling via 16S rDNA sequencing and 2) taxonomic/functional profiling via metagenomic sequencing. Significant shifts in microbial community composition were observed, and I will discuss how well the taxonomic profiling alone might predict the functional potential of the *D. melanogaster* gut microbiome.

T26. Langkilde, Tracy. Penn State University.

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Impacts of invasive species: complex responses of native lizards to novel selective pressures imposed by fire ants

Understanding mechanisms shaping species ecology is critical for determining how native communities persist in this changing world, and the role of evolutionary processes in the assembly and dynamics of natural communities. I take advantage of the “natural experiment” provided by the invasion of red imported fire ants (*Solenopsis invicta*) to gain insight into how novel selective pressures they impose as both predators and venomous prey, shapes the behavior, morphology and physiology of native lizards. Controlled manipulations of an individual’s lifetime exposure to this invader, comparisons of populations with different invasion histories, and the use of museum specimens to determine historic patterns, provide insight into the mechanism driving responses of native populations to rapid environmental change. This work reveals that evolutionary and lifetime exposure to a threat can interact in complex ways to shape adaptive responses, and that the relative importance of these varies depending on the phenotypic trait in question.

M4. Lau, Jennifer. Michigan State University.

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Evolution in Changing Environments: How nitrogen deposition has destabilized the legume-rhizobium mutualism

Humans have dramatically manipulated the global nitrogen (N) cycle. Global N inputs have more than doubled since the Industrial Revolution, and theory predicts that N-deposition will reduce the abundance of rhizobia and cause the evolution of less-cooperative rhizobium mutualists, resulting in lower rates of N-fixation. As a result, the effects of N-deposition on this important mutualism may change plant community composition, increase reliance on synthetic fertilizers, and influence the global N cycle. We experimentally tested these theoretical predictions by capitalizing on an existing 22-year N-addition experiment at Kellogg Biological Station Long-Term Ecological Research (LTER) Site. We find that long-term N-addition treatments have caused the evolution of less cooperative rhizobia that provide fewer growth benefits to plants and that these evolutionary changes reduce soil N availability and alter plant community composition. Our findings illustrate how human-caused environmental changes can cause rapid evolutionary responses that feedback to influence community and ecosystem processes.

M17. Leal, Manuel. Duke University.

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Contributions of Brightness and Chroma to Pattern Discrimination in Anolis Lizards

Sympatric species commonly exhibit courtship displays that differ in design. The evolution of such differences has been proposed to communicate species identity. Interspecific differences in the pattern of the dewlaps of *Anolis* lizards have been proposed to play a key role in species recognition. Here I report the results of an associative learning experiment, to evaluate the contribution of brightness and chroma to pattern discrimination in *Anolis evermanni*. Results demonstrated that individuals are able to associate an arbitrary dewlap-like stimulus with a food reward and to discriminate the reward stimulus from a distractor based solely on pattern differences. Moreover, depending on the pattern, the contribution of brightness and/or chroma can contribute differentially to the discrimination process. The

study demonstrates that when evaluating the degree of divergence in species recognition signals, the possible contribution of both brightness and chroma to signal discrimination should not be overlooked.

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Trade-offs in early life decisions and their long-term effects are driven by patterns of environmental fluctuation

Environmental variation poses substantial challenges for individual life history. While the impact of connections between early-life development and environmental conditions on subsequent fitness in late life has been widely explored, it is unclear how rapid phenotypic adaptation in response to environmental conditions early in life affects life history decisions and the associated long-term consequences of these decisions. We investigate this question by using a dynamic state-dependent model. We show that optimal life-history strategies are a function of trait variation such as early growth, long-term damage accumulation and future reproductive investment in response to environmental gradients via a trade-off between the costs of developmental phenotype and resource allocation. Moreover, our model results indicate that life history decisions and future reproductive investment are also influenced by patterns of covariation among relevant environmental factors (a pattern defined here as ‘abiotic integration’). These results emphasize that understanding the interactions between developmental decisions needs to take into account not only the environmental conditions per se but also their dynamics through time.

W17. Leibold, Mathew. University of Texas.
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Evolution of niche relations in metacommunities, what role for neutral coexistence?

Metacommunity ecology posits numerous ways for competing species to coexist but generally ignores the role of adaptive niche evolution. We modelled niche evolution in patchy metacommunities that are subject to background extinctions and find numerous novel dynamics that can arise. One of these involves the repeated evolution of neutral local coexistence. We find that under extreme conditions this also predicts regional neutrality. We use this modelling to examine the consequences for the maintenance of biodiversity at regional scales via niche segregation.

P10. Livingston, George. University of Texas at Austin.
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The effect of disturbance on spatial food webs in heterogeneous microcosm landscapes

Ecosystem disturbance and adaptive community assembly interactively determine the features of natural metacommunities. These interactive effects, and their consequences, are poorly understood and difficult to scale to natural patterns. We explored these dynamics using protist microcosms in a limited-dispersal situation (patch dynamics) including a predator, two prey species, and a heterogeneous environment. We used a range of three patch disturbance rates and measured the matching between species and their optimal environments (species sorting), food webs, and multiple ecosystem functions. The preliminary results suggest that predators are strongly influenced by disturbance rate and they regulate the dispersal dynamics of their prey and via apparent competition this cascades to regulate species sorting and ecosystem function. The disturbance gradient also influenced the formation of spatial patterning in both communities and function in ways that mirror patterns in real landscapes.

W11. Lopez Arriaza, Juan. University of California, Santa Cruz.
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A Semiparametric Bayesian Approach for Estimation of Individual Growth

The elucidation of growth plays a crucial role in understanding population and community dynamics. By relating growth to a wide range of environmental conditions, bioenergetic models provide us with a sophisticated framework to describe growth and consumption of individuals. Currently, many of the parameters and functions of these models are borrowed from laboratory studies on other populations or species, or estimated based on measurements of a large number of individuals. While this approach is often adequate for capturing mean population effects it often fails to explain and predict individual variation. We present a semiparametric Bayesian approach based on Gaussian processes to estimate functions and individual parameters for growth. Our model allows us to capture the effects of temporal variation in environmental conditions (e.g. food availability and temperature) and individual variation of bioenergetics rates on growth processes. This framework provides us with a flexible tool to accurately estimate individual growth.

M30. Lotterhos, Katie. University of British Columbia.

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A more reliable genome scan for local adaptation: WHELK

A major goal of evolutionary biology is to understand the molecular basis for adaptive differences between populations, and genome scans have become a common way to identify candidate genes for adaptation. We tested the accuracy of two types of genome scans for identifying candidate genes: FST outlier tests and genetic-environment associations (GEAs). Using a landscape simulator we developed, we modeled four demographic histories: island model, isolation-by-distance, and expansion from one or two refugia. We found that existing FST outlier methods did not control well for demographic history. We developed a new method, WHELK, based on likelihood estimation of the effective number of populations. WHELK greatly reduces the number of false positive results. GEAs also produced a large number of false positives when demographic history was not accounted for. Our results highlight the importance of controlling for demographic history and provide guidelines for the correct application of genome-scan methods.

T27. Low, Candace. Cornell University.

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Optimal Control and Cold War Dynamics between Plant and Herbivore

Herbivores eat the leaves that a plant needs for photosynthesis. However, the degree of antagonism between plant and herbivore may depend critically on the timing of their interactions and the intrinsic value of a leaf. We present a model that investigates whether and when the timing of plant defense and herbivore feeding activity can be optimized and their interactions can move from antagonistic to neutral. We assume that temporal changes in environmental conditions will affect intrinsic leaf value, measured as potential carbon gain. Using optimal-control theory, we found that the optimal strategies for both plant and herbivore are to avoid direct conflict. As long as the plant has the capability for moderately lethal defense, the herbivore will modify its hatching rate to avoid plant defenses, and the plant will never have to use them. Our results provide a mechanism for stable plant-herbivore interactions without the need for natural enemy control.

T13. Mahler, D. Luke. University of California, Davis.

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Alternative paradigms in macroevolutionary models of adaptive radiation

A rugged macroevolutionary landscape with distinct adaptive peaks was central to G. G. Simpson's theory of adaptive radiation. Some subsequent macroevolutionary models for adaptive radiation have focused instead on species packing within a restricted niche space, inspired in part by the theory of limiting similarity. Although Simpson's landscape is often invoked verbally, comparative analyses of large adaptive radiations have largely focused on testing for evolutionary patterns consistent with ecological limits and limiting similarity (e.g., the "early burst" model). This is changing with the renewed development of tools for estimating features of the macroevolutionary landscape using comparative data. Here we review theory underlying both types of models and discuss available evidence for each in large comparative data sets. Although these models are not mutually exclusive, levels of support for each can yield insights about the nature of adaptive trait evolution during large-scale radiations.

T17. Mayfield, Margaret. The University of Queensland.

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Pitfalls and opportunities of using phylogenetic and traits to identify drivers of diversity in novel communities

Phylogenetic distances among coexisting species are used to infer underlying processes driving community assembly. This approach was developed and has mostly been applied to pristine systems. Increasingly, however, it is also being used to study invaded and "novel" communities. Novel communities contain mixes of native resident species, local invader species and exotic species. The species coexisting in such communities have distinct histories from one another, providing excellent natural experiments with which to study the processes driving community assembly. The complex histories of novel communities can, however, also be problematic, especially for interpreting patterns of phylogenetic and trait similarity. In this talk I discuss the issues and benefits of using phylogenetic similarity to study community assembly in novel communities and present a new way of analyzing such patterns that will improve our ability to use these communities to advance our understanding of the processes involved in community assembly.

W40. McCoy, Michael. East Carolina University.

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Predicting predator diversity effects on ecosystem function

Habitat loss, over-harvesting, culling, and introductions are drastically changing predator communities, which in turn modify the structure of prey communities and affect ecosystem structure and function, with potentially large socio-economic consequences. However, we lack a general framework for predicting how changes in predator communities influences prey populations and ecosystem function. Current methods assessing predator functional diversity are often idiosyncratic, and divorced from theoretical or statistical models. Further, current statistical models for predicting the effects of predator diversity conflate predictable nonlinear effects and context-dependent interactions. We overcome these challenges by developing models that explicitly account for effects of nonlinearity in predation rates, and (2) by explicitly linking definitions of predator functional diversity to these models. By disentangling apparent emergent effects, nonlinear predator-prey interactions, and context dependence, which are typically conflated in current studies, we will be able to more reliably predict how changes in predator diversity effect ecosystem functions.

M8. McDonough, Caitlin. Boston University.

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Science in the attic: Studying spring phenology in Northern Maine with a hunting guide's journal

Changes in spring phenology are visible and readily accessible measures of the ecological effects of climate change. While both monitoring and historical data have contributed to in depth studies of the timing of leaf out, flowering, and migratory bird arrivals in a few places, complete long-term records of phenological events are rare. From 1940-1957, a hunting guide named L. S. Quackenbush in Northern Maine kept detailed journals with Thoreau-like attention to the dates of leaf out, flowering, and migratory bird arrivals. Acadia National Park acquired the journals, and they were stored at College of the Atlantic, where they were found in an attic during renovations. Quackenbush's home in Northern Maine has warmed 0.22°C/decade since 1975 but has traditionally been neglected in climate change research due to its remote location and low population density. Here, we use Quackenbush's notes to study the ecological effects of climate change in Northern Maine.

M21. M'Gonigle, Leithen. University of California, Berkeley.

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Allee effects and species coexistence in an environment where resource abundance varies.

Explaining patterns of diversity has long been a central focus in ecology. One of the most challenging problems has been to understand how species occupying similar ecological niches can coexist, as demographic stochasticity is expected to lead to the eventual extinction of all but one of them. The Allee effect has been widely studied for its impact on the extinction risk of rare species. Its potential role in promoting co-existence has received much less attention. Here, we present a model in which two species compete for a single resource in a continuous landscape. We show that Allee effects can promote their coexistence when a simple condition is met: resources are distributed unevenly across space. The Allee effect can stabilize coexistence despite the reduction in population density and consequent increase in demographic stochasticity that it causes. We suggest, therefore, that Allee effects might be generally important in maintaining diverse communities.

T36. Miller, Thomas. Florida State University.

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Evolution in response to predation and nutrient pulses within a suite of protozoa competitors

There has been a recent recognition that evolutionary rates are sufficient rapid to affect ecological processes. We studied the effects of nutrient pulses using the natural community found in the leaves of the pitcher plant, *Sarracenia purpurea*. This detritivorous community is based on dead insects, with a food web of bacteria, consumed by protozoa and rotifers, that are in turn consumed by mosquito larvae. Pulses of dead prey were added to leaves with and without the presence of mosquito predators. Bacteria exhibited very large increases in abundances within hours regardless of the presence of mosquitoes. Bacterivores initially responded to predators and resource pulses, but the effects of predators gradually declined, apparently as protozoa and rotifer responses evolved. There were large differences among bacterivores in both their initial responses and the rate of evolution in responses. These differences appear to be related to both generation time and indirect effects through competitors.

W35. Mokkonen, Mikael. University of Jyväskylä / Simon Fraser University.

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The roles of sexually antagonistic and frequency dependent selection in a bank vole life-history axis

Understanding the maintenance of fitness-related traits remains at the very heart of evolutionary biology, with a wide variety of approaches focused on survival and reproductive processes. We have studied reproductive trade-offs in the

bank vole (*Myodes glareolus*) and revealed where the fitness of a certain pheno/genotype (i.e. tactic) depends on current environmental conditions (e.g. food resources, pathogen pressure, density and characteristics of conspecifics). Our results illustrate a close interplay between testosterone (male reproductive success) and immunocompetence (survival): these two traits are both phenotypically and genetically negatively correlated, and costs of high testosterone for males are both intrasexual (lower immunocompetence) and intersexual (lower reproductive success of daughters). Additionally, the fitness of bank vole individuals from different ends of this immunocompetence – testosterone tactic axis depends on their relative frequencies in the population. This interplay between ecology, physiology and evolution has important implications for the maintenance of genetic variation in alternative life-history tactics.

W6. Mueller, Ulrich. University of Texas at Austin.

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Efficient evolution of growth-promoting bacterial rhizosphere communities through plant-microbiome co-propagation: A bio-inspired approach copied from fungus-growing ants

Beneficial rhizosphere bacteria can greatly enhance fitness of host-plants, for example by solubilizing nutrients or secreting protective antibiotics. To elucidate functions of hyperdiverse communities of rhizosphere bacteria, we developed an efficient method of plant-bacterial-community co-propagation that enhances plant growth by selecting indirectly on root-associated bacterial communities while selecting directly on plant biomass. Our methods were bio-inspired by fungus-gardening (attine) ants, which co-propagate their fungal crops together with diverse communities of beneficial bacteria and yeasts, thereby engineering a beneficial crop-microbe consortium. We adapted these engineering principles to select artificially on beneficial bacterial rhizosphere-communities, keeping plant genotype constant between generations. 16S-amplicon 454-surveys confirm that bacterial communities rapidly evolve differences between replicated selection-lines that are selected for either growth-enhancing vs growth-attenuating effects on plants. Because our methods were bio-inspired by attine ants, natural-history observations (e.g., study of outlandish ant-fungus symbioses) therefore can generate innovative ideas with economic applications.

M39. Muir, Christopher. University of British Columbia.

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Pores choices: the adaptive significance of stomatal ratio

Stomata are microscopic pores on the surface of leaves that regulate gas exchange and are critical to plant fitness in nature. Biophysical theory predicts that stomata should be present on both upper and lower leaf surfaces, yet the vast majority of plants restrict stomata to the lower surface. What explains this paradox? I test old and new hypotheses for the adaptive significance of stomatal ratio (upper:lower) using a comparative data set of >600 species. These data support the view that having stomata on both leaf surfaces is adaptive when there is a premium on efficient CO₂ diffusion. I also present a novel hypothesis that susceptibility to foliar pathogens might be the primary cost of stomata on the upper surfaces of the leaf, explaining the rarity of amphistomous plants in moist, shaded habitats.

M3. Newman, Erica. University of California, Berkeley.

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Macroecology meets disturbance ecology

The ubiquity of disturbance in structuring ecological communities continues to motivate a search for generality in disturbance ecology. A better understanding of ecological perturbations and quantitative comparisons of their effects over multiple scales is required for both species-level and landscape-scale conservation efforts. Here we extend the Maximum Entropy Theory of Ecology (METE) to disrupted and disturbed ecosystems. Despite explicitly not incorporating ecological interactions, METE has proven reliable for estimating the species-area relationship, endemics-area relationship, and species-abundance distribution in minimally disturbed ecosystems. As a first test of METE's predictions for ecosystems with high levels of disturbance, we census several ecosystems with known histories of ecological disruption. We quantitatively compare the macroecological response of biological communities in transition (including a primary succession landslide system, a fire-evolved conifer system, and a novel grazing regime in forb-dominated meadows) and find that certain metrics, including predicted number of rare species, are robust to disturbance.

P6. Nonaka, Etsuko. Umeå University/University of New Mexico.

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Phenotypic plasticity can promote sympatric speciation by enhancing positive assortment in mated pairs: a simulation model study

Recent studies advocate that ecological speciation is a plausible mechanism contributing to sympatric speciation. Phenotypic plasticity has been suggested as a factor that can facilitate ecological speciation, but the efficacy of plasticity in promoting speciation is debated in literature; it can theoretically either increase or decrease the likelihood of speciation. One possibility is that plasticity can increase phenotypic variation in the population, which in turn may facilitate assortative mating. The objective of this paper is to explore the conditions under which phenotypic plasticity could promote or hinder sympatric speciation and the underlying mechanisms. We developed a stochastic individual based simulation model of a sexually reproducing predator population and asexual prey populations. We show that sympatric speciation occurs more quickly when phenotypic plasticity is allowed to evolve. Phenotypic plasticity can also hinder sympatric speciation if individuals possess high plasticity when the population experiences disruptive selection.

MS4. Nosil, Patrik. University of Sheffield.

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Santa Rosalia revisited: why so much evolution at small scales but not a separate species on each bush?

M14. Ohlberger, Jan. University of Oslo.

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Adaptive phenotypic diversification along a temperature-depth gradient - an evolutionary model based on laboratory and field data

Adaptive diversification along continuous environmental gradients has been suggested as a mechanism for the emergence of new species. However, this scenario has rarely been supported by empirical data. Here, we developed an evolutionary model based on laboratory experiments and field data from two closely related fish species (*Coregonus* spp.) in Lake Stechlin, Germany, to show that a gradual thermal adaptation along the depth gradient from warm to cold waters may have resulted in the emergence of the two coexisting species found in that lake today. These findings highlight the importance of physiological adaptations in the process of adaptive diversification, and suggest that environmental temperature gradients can promote the evolution of biological diversity.

W27. Ord, Terry. University of New South Wales.

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Convergent adaptive evolution in distant phylogenetic lineages

Classic examples of convergence are often between taxa that are members of the same species or genus. This implies that closely related taxa are predisposed to adapt in similar ways to similar selection pressures, presumably because they still share much of their genome. If so, the incidence of convergence should decrease with increasing phylogenetic distance among taxa. We examined this in two ways. First, we tested whether two ecologically similar lizard groups from separate families—the Caribbean *Anolis* and Southeast Asian *Draco*—have converged in morphology related to habitat use. Second, we catalogued examples of convergent evolution published over the last decade and tested whether reports of convergence were more common among closely related taxa. Our data shows that natural selection can produce a remarkable degree of convergence among some distantly related groups (*Anolis* and *Draco*), but as taxa become increasingly more phylogenetically divergent, the likelihood of convergence is diminished.

T10. Oswald, Jessica. University of Florida.

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The evolution of ecological specialization in birds

Specialization is a common theme in the literature of adaptation and diversification, but the origin of specialization and its evolutionary implications are unclear. We defined a novel measure of specialization, the species co-occurrence index (C.I.) that measures the extent of a species' range, defined by the number of co-occurring species, relative to the range size of the other species it encounters. Using a species co-occurrence network built from >82 million records in the Avian Knowledge Network, we calculated the C.I. for over 6,000 bird species. The C.I. score is correlated with the diameter of a species' range and the species' clustering coefficient. Additionally, we estimated transition rates between generalists and specialists and their associated extinction and speciation rates using a phylogeny with over 5000 species. We found a strong bias favoring the transition from generalist to specialist, and specialists have significantly higher speciation and extinction rates than generalists.

MS2. Otto, Sarah. University of British Columbia.

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Local adaptation on a small scale: What are the theoretical constraints?

T31. Parker, Ingrid. University of California, Santa Cruz.

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Numerical rarity and phylogenetic rarity jointly influence disease pressure in plant communities

Rare host species are expected to suffer less damage from pathogens and pests than common hosts. This rare-species advantage is a key feature of hypotheses that explain how pathogens can help maintain diversity (e.g., Janzen-Connell hypothesis) or regulate invasions (e.g., Escape from Natural Enemies hypothesis). However, most pathogens are polyphagous, so effective host density includes not just conspecifics but also alternative host species. Closely related species are more likely to share pathogens, and therefore effective host density is in turn a function of the phylogenetic structure of the community. We studied the effects of abundance and phylogenetic structure on plant-pathogen interactions in a coastal grassland community in California. We found that relative abundance significantly predicted disease pressure across host species. However, we also found that phylogenetic rarity, in the context of the ecological structure of the community, had an even greater influence on disease pressure than conspecific density.

W28. Pastore, Abigail. Florida State University.

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A model of trait convergence in coevolving competitors using quantitative genetics

In some systems, equivalence of species seems to be the driving mechanism behind coexistence, with only minor niche differences stabilizing the competitive interactions. But it is unclear whether species can undergo convergent evolution under a competitive regime or these instances of equivalence are merely due to shared evolutionary history. I have developed a quantitative genetic model of coevolving species in competition, with a mechanistic basis for the competitive interactions of species through a shared resource. Using this model I investigate under what conditions species will evolve equivalency. In general, I find that species will evolve to be equivalent when the potential for resource differentiation is constrained. Further, coevolution between competitors can result in coexistence through either divergence in niche axes or convergence in resource use efficiency.

T35. Patel, Swati. University of California, Davis.

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The Ecological Consequences of the Tempo of Evolution in Intraguild Predation Communities

Recent evidence of rapid evolution has led to an influx of empirical and theoretical studies on the feedbacks between evolution and the population dynamics of ecological communities. Here we look at how the rate of evolution impacts the community dynamics. We use a quantitative genetics and ecological dynamics framework to study an intraguild predation community, in which the predator evolves between consuming a common resource species or a prey species competing for this resource, and the heritability of the intraguild predator's quantitative trait determines the rate of evolution. The tempo of trait evolution significantly impacts the transient and long-term dynamics of this community. Rapid evolution can stabilize unstable communities but also cause cycles around stable communities. On the other hand, slow evolution can cause sudden transitions between ecological states and population collapses.

W37. Pearish, Simon. University of Illinois.

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Behavioral type - environment correlations in three-spined stickleback

There is growing evidence for consistent individual differences in behavior. It is likely that different behavioral types of individuals within populations are nonrandomly distributed in the environment, creating behavioral type-environment correlations. Relatively timid individuals might be more likely to occur in relatively safe microhabitats, for example. However we know little about the prevalence of behavioral-type environment correlations, the mechanisms that generate them or their ecological and evolutionary consequences. Here I present evidence for behavioral type-environment correlations in a wild population of three-spined stickleback. Relatively exploratory sticklebacks were more likely to occur in open microhabitats in the field, and relatively bold sticklebacks that quickly emerged from a refuge were more likely to occur in shoals with other sticklebacks rather than by themselves. I discuss the stability of behavioral types and environment use in sticklebacks, mechanisms that might generate the observed behavioral-type environment correlations and present the results of a mark-recapture experiment.

M28. Petren, Kenneth. University of Cincinnati.

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The genomic basis of adaptive trait variation in Darwin's finches.

The Galápagos islands form a fragmented landscape that has long been thought to play a role in the rapid speciation and adaptive radiation of Darwin's finches. Here we show how the fragmented nature of populations partially connected by gene flow, low levels of hybridization among species, and episodes of strong natural selection against intermediate forms provide an opportunity to reveal the genetic basis of key ecological traits that distinguish very closely related species. We found 150 of 50k SNP's distinguish the medium and cactus ground finches. Half of these SNP's fall within or near (<20 kb) known genes, many of which have been implicated in developmental processes. These results are being used to connect natural selection on a key ecological trait in nature to the networks of interacting genes that control beak development.

T4. Pinsky, Malin. Rutgers University.
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Effects of climate velocity on fish and fisheries

Shifting species distributions are common impacts of climate change, but observed shifts span a wide range of directions and rates. While many explanations emphasize biological differences among species, we test the alternative hypothesis that climate velocity can explain differences in shifts. Climate velocity is the rate and direction that climates move across the landscape. We compiled scientific surveys for coastal marine species in North America from 1968-2011 and in total examined 128 million individuals across 360 fish and invertebrates. Climate velocity explained the magnitude and direction of shifts in latitude and depth much more effectively than species characteristics. We also found evidence that commercial fisheries followed fish, but lag behind and are slowed by a combination of social, regulatory, and economic factors. Our results suggest that species shift at different rates and directions because they closely track the mosaic of climate velocities and these impacts ripple through coupled social-ecological systems.

W22. Porter, Stephanie S & Ellen L. Simms. University of California, Berkeley.
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Selection for cheating across disparate environments in the legume-rhizobium mutualism

Natural selection for cheating is framed as the primary dilemma in models of evolutionarily stable mutualism. Selection for cheating occurs when less cooperative partners are more fit than more cooperative partners. Research has illuminated mechanisms that counter the incentive to cheat by preferentially directing benefits to more cooperative individuals. However, empirical evidence for natural selection favoring cheating in mutualisms is sparse and symbiont-focused. To measure selection for cheating we grew wild legume and rhizobium lineages in single-partner pairings, which prevented legumes from exerting relative partner choice or sanctions. Under these conditions, rhizobia, but not legumes, experienced linear selection gradients for cheating within two contrasting environments. This provides the first simultaneous measurement of selection for cheating across host and symbiont lineages from natural populations and empirically supports the importance of cheating as a biological dilemma and source of antagonistic coevolutionary pressure in mutualism.

TS9. Rabosky, Daniel. University of Michigan.
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Reproductive isolation, diversity-dependence, and the ecology of speciation

W14. Rasmussen, David. Duke University.
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How much demography can we infer from phylogeny?

Coalescent methods are widely used to infer the demographic history of populations from genealogies reconstructed from genetic data. These methods have proven reliable in their ability to reconstruct major demographic transitions like population bottlenecks and population subdivision. Yet it remains unclear if there are inherent limits to what can be inferred from the information contained in genealogies. Both theoretical and applied studies have suggested that there are inherent limits; especially in reconstructing demographic processes at fine-scale temporal resolution. We propose that there are no strong limits on demographic inference as long as the genealogy can be accurately reconstructed from sequence data and sample sizes are sufficiently large. However, we show that rapid demographic change is often undetectable using standard coalescent models from population genetics, suggesting a need for greater ecological realism in the coalescent models used for demographic inference.

T25. Resetarits, William. Texas Tech University.
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Unveiling cryptic natural history through “experience carefully planned in advance:” chemical camouflage in an aquatic predator

How do we define “natural history”? More critically, how do we define natural history for the 21st century? Is it the natural history of Gilbert White and Henry David Thoreau, of Wallace and Darwin, or is it broader, embracing myriad ways of adding to our knowledge of organisms in nature – sensu Lopez’s “patient interrogation of nature.” Fisher referred to experiments as “only experience carefully planned in advance.” Our work using largely experimental approaches with natural populations of colonizing organisms has revealed unique aspects of natural history not accessible via observational approaches alone. Here we focus on the recently identified example of generalized chemical camouflage in pirate perch (*Aphredoderus sayanus*) and discuss both the importance of natural history and the particular limitations of purely observational approaches in dealing with aquatic organisms and phenomena based in other modalities, such as chemical communication, that fall outside our own sensory capabilities.

M33. Richardson, Jean. Bamfield Marine Sciences Centre.

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A Pedigree Analysis of Heritable Components of Brood Sex Ratio in the intertidal copepod *Tigriopus californicus*.

Extensive variability in sex-ratio among families is theoretically unstable. Thus, the presence of extensive sex-ratio variation observed in populations of the inter-tidal copepod *Tigriopus californicus* throughout its extensive range along the west coast of North America is both unexpected and curious. Sex determination in this species appears to be polygenic and family brood sex ratio is heritable and responds to artificial selection. We use artificially selected lines generated from field-collected animals to generate F1 hybrids. We perform an ‘animal model’ analysis, using the full pedigree from parental, F1 and backcross generations to estimate genetic variance components (additive, dominance, maternal) of brood sex ratio. A clearer assessment of the relative variance of genetic components provides insight into how variation is being maintained in the population, despite the expected strong selection for equal sex ratio.

MS1. Richardson, Jonathan. University of Connecticut.

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Evolution in small spaces: microgeographic adaptation in nature

Local adaptation of populations in response to environmental variation is a foundational research program for evolutionary ecologists working across diverse systems. However, much of this research has focused on macro- and meso-scale variation as it has often been assumed that high rates of gene flow will overwhelm locally adapted gene pools and prevent adaptive divergence at small spatial scales –so-called microgeographic adaptation. Because researchers often select their study sites in a way that reduces or eliminates the possibility of gene flow between populations, the presumption that gene flow would overwhelm natural selection at fine spatial scales has rarely been challenged. Mounting evidence suggests that fine-scale divergence is more widespread in nature than is commonly appreciated. As a result, we are now in a position to examine critically where and to what degree adaptive divergence is occurring at microgeographic scales, and how this fine-scale adaptation can alter the way we think about fundamental processes in ecology and evolution.

W10. Richerson, Kate. University of California, Santa Cruz.

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More than passive drifters: a behavioral model for Antarctic krill (*Euphausia superba*)

Antarctic krill (*Euphausia superba*) are a species of great importance in the Southern Ocean, being both a key prey species and the target of the area’s largest fishery. Though management models typically assume that krill are passive drifters, their large size (up to 6 cm) and relatively strong swimming ability mean that active movement may play an important role in krill distribution. We use a stochastic dynamic programming model, in combination with data on food availability, current velocity, and predation risk, to predict krill behavior in the United States Antarctic Marine Living Resources (US AMLR) study area. We show that accounting for behavior may alter the predicted spatial distribution of krill in the area when compared to a model treating them as passive drifters. This information may be useful in determining new catch limits as krill fishing grounds are partitioned into smaller spatial management units.

T9. Ricklefs, Robert. University of Missouri-St. Louis.

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Dynamics of the regional community

Patterns of diversity within large regional biotas are envisioned as the outcome of a set of related processes that influence evolutionary diversification as well as the distribution and abundance of species. Several lines of evidence

suggest that population size and geographic extent are labile over short evolutionary time scales and reflect the outcomes of specialized coevolutionary interactions. Expansion and contraction of individual populations likely influence rates of both speciation and extinction, linking diversity and distribution to intrinsic biological interactions in addition to the influence of extrinsic ecological conditions and geographic configurations. Empirical data that bear on these mechanisms, as well as broader implications for concepts in biogeography and community ecology, are explored.

W4. Ries, Leslie. National Socio-environmental Synthesis Center.

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A general mechanistic species distribution model for butterflies: integrating species interactions and climate to understand large-scale distributions

Mechanistic species distribution models have received increasing attention over the past several years. This approach is advantageous because known mechanisms are used to make a priori predictions about range dynamics and can then be tested with independent distribution data. Yet these models tend to be species-specific and therefore difficult to generalize across taxa. We focus on three factors known to be critical for butterfly distributions: 1) sufficient temperatures for growth and activity, 2) physiological stress due to excessive heat or cold, and 3) the distribution and phenology of their host-plant resources throughout the season. We use the butterfly species with the most complex annual cycle, the monarch butterfly, to explore the potential to predict breeding distributions in the spring and summer. We discuss the results and the potential to develop a model that would be broadly applicable across migratory and non-migratory butterflies and potentially other insect groups as well.

M34. Rose, Noah. Stanford University.

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Express Yourself: Gene expression profiles are highly dependent on individual genotype in corals

Differences in gene expression frequently contribute to observed differences in phenotypes and play an important role in both adaptation and acclimation of natural populations in the face of environmental change. By reciprocally transplanting branches from colonies of the tabletop coral *Acropora hyacinthus* found across a thermal gradient on the back reef of Ofu, American Samoa, we determine the relative contributions of adaptation and acclimation to the observed levels of thermal tolerance for individual coral genotypes. Using RNA-Seq, we identify constitutive and plastic expression differences between these individuals, allowing us to make inferences about the gene-network level basis of both acclimation and adaptation. The ability to separate environmentally determined and constitutive differences in gene expression phenotypes via clonal propagation makes corals particularly well suited to the study of basal metazoan gene expression evolution.

MS6. Rosenblum, Erica B. University of California, Berkeley.

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Convergent evolution over the sharp White Sands ecotone: using comparisons among species to understand evolution in small spaces

T38. Rudman, Seth. University of British Columbia.

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Ecological consequences of the evolution of reproductive isolation in Threespine stickleback

Evolutionary change is increasingly being recognized as a potential driver of ecological dynamics. A wealth of research has shown that phenotypic evolution within a dominant species can shape ecosystems. Early work has demonstrated that larger scale evolutionary changes, namely speciation, can also have measurable ecological consequences. We pursued that work further to investigate the ecological consequences of both the evolution and collapse of reproduction isolation in threespine stickleback species pairs. Using both replicated mesocosm experiments and a longitudinal field study; we found that repeated evolution of benthic/limnetic species pairs has led to similar ecological consequences. Surprisingly, we found that the impacts of speciation on prey communities are stronger in natural lakes than in an experimental system. We also show that although reverse speciation has ecological consequences, they are not as strong as anticipated.

M22. Rudolf, Volker. Rice University.

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Resolving the roles of body size and species identity in driving functional differences

Traditionally, community ecology has focused on species identities to measure functional diversity, but there has been an increasingly vivid debate about whether this taxonomic approach should be replaced with a more mechanistic,

purely body size-based approach. These approaches have been largely used in parallel in different systems and both make simplifying and largely untested assumptions about how variation across size classes or species influences functional differences among consumers. One key assumption of both approaches is that functional differences between species remain constant over ontogeny. Here we take a novel experimental approach to determine how size and species identity influences functional differences among predators. Our results demonstrate that functional differences among predators were driven by nonlinear effects of size and species identity. Thus, both species- and size-based approaches were inadequate to explain functional differences among consumers, indicating the need to integrate both approaches to predict functional diversity within communities.

T2. Salinas, Santiago. University of California, Santa Cruz.
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Do longer exposures to high temperature lead to more pronounced transgenerational effects?

Evidence for transgenerational plasticity and environmentally induced maternal effects is now abundant. Theory suggests that the ability of parents to predict the offspring's environment is a critical component in these phenomena. Yet, few empirical studies exist of the imprinting period needed by the parents to pre-condition offspring. Here, we ask whether holding sheepshead minnows (*Cyprinodon variegatus*) at an elevated temperature over different lengths of time determines the magnitude of the transgenerational effect. We also evaluate changes in offspring reaction norms when parents previously held at high temperature are transferred back to a reference temperature. We discuss these results in light of theoretical predictions and what they mean for populations coping with warmer, less predictable environments.

WS8. Saltz, Julia. University of Southern California.
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Genetic variation in social niche construction: implications and insights from *Drosophila melanogaster*

Niche construction occurs when an organism's traits influence the environment that it experiences. Novel evidence increasingly demonstrates that niche-constructing traits vary among genotypes within populations. I will discuss the potential implications of genetic variation in niche construction--and in particular, social niche construction--for evolutionary genetics. Specifically, genetic variation in niche-constructing traits creates a correlation between genotype and the social environment. Because the environment influences which genes and genetic interactions underlie trait variation, genetic variation in niche construction can alter inferences about the heritability, pleiotropy and epistasis of traits that are phenotypically plastic. The effects of niche construction on these key evolutionary parameters further suggest novel ways by which niche construction may influence evolution.

P15. Scheiner, Samuel¹, Kattia Palacio-López², Brian Beckage², & Jane Molofsky². ¹National Science Foundation, ²University of Vermont.
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Assessing the frequency of local adaptation and phenotypic plasticity in plants using a Bayesian hierarchical model

Adaptation to heterogeneous environments can occur through two mechanisms: phenotypic plasticity or local adaptation. To assess the relative frequency of each mechanism, we used a hierarchical Bayesian model to conduct a meta-analysis of reciprocal transplant plant studies. The analysis included 220 records from 37 studies where 52% of the records were for reproductive, 43% morphological and 5 % physiological traits. Of the trait records, 47% showed no plasticity, of which the majority (39%) showed local adaptation. The remaining trait records (52.5%) showed some sort of plasticity, of which the majority (35%) showed adaptive plasticity. Thus, local adaptation is more common than phenotypic plasticity as an evolutionary response to environmental heterogeneity.

M1. Schreiber, Sebastian. University of California, Davis.
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Evolutionary and Ecological Consequences of Multiscale Variation in Pollen Receipt for Seed Production

Plants often have low realized fertility as evidenced by low seed:ovule ratios and increased seed production following supplementing individuals with pollen or resources. Using stochastic models, we examine to what extent resource limitation and stochastic pollination select for reproductive allocations with these ecological consequences. These models account for the modular structure of plants and reproductive allocations into attracting pollen, producing ovules, and maturing seeds. Due to their modular structure, plants experience variation of pollen receipt at two scales:

variation among flowers within an individual and variation among individuals. We show that this multi-scale variation generates novel, empirically testable predictions and ties together several pieces of the empirical and theoretical literature on pollen limitation, seed:ovule ratios, and "ovule packaging".

T30. Sette, Carla. University of California, Santa Cruz.

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Connecting historical and contemporary disease dynamics in the California slender salamander

The fungal disease chytridiomycosis has been implicated in the extirpation and extinction of amphibian species throughout the world. It is considered primarily an aquatic disease, however, Bd has more recently been linked to population declines in completely terrestrial amphibians. Understanding the mechanisms that allow for the spread of an aquatic disease in terrestrial environments remains an unsolved mystery of this epidemic. The most abundant and widespread terrestrial species known to host chytrid infection is the California slender salamander, *Batrachoseps attenuatus*. We combined a survey of historical infection in museum *B. attenuatus* specimens with chytridiomycosis tests in modern populations to explore how older versus more recent epizootic infection might affect long-term enzootic population dynamics. We propose that sociality facilitates disease spread in this terrestrial hosts and that populations with longer exposure to this pathogen may evolve away from the ancestral condition of sociality.

W31. Shapiro, Jason. Yale University.

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The Role of Pleiotropy in Horizontally Transmitted Mutualistic Symbioses

Symbionts rely on horizontal or vertical transmission (or both) to get from one host to another. It is often assumed that horizontal transmission, by removing the feedback between host and symbiont fitness, will result in breakdown of the interaction and the evolution of parasitism from mutualism. However, this is not the case for many well-known symbionts (e.g. gut symbionts, mycorrhizal fungi, *Vibrio fischeri*). Pleiotropy between horizontal transmission success and symbiont-provided benefits is the simplest mechanism that can resolve this conflict, promoting the evolution of benefits and preserving mutualism in the face of a symbiont's selfish interests. We explore a general model that outlines this result and also overview results from coevolution experiments with bacteria and bacteriophage that support the notion that pleiotropy may reinforce the evolution of locally beneficial symbionts.

T1. Sheldon, Ben. University of Oxford.

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Adaptive Phenological Plasticity and the Constraints of Scale

Variable environments can select for phenotypic plasticity. A key example of this, with relevance for understanding responses to climate change, concerns plasticity in phenology - the timing of events in the annual cycle. Here, I report on analyses of more than five decades of data from a study of phenology across multiple trophic levels involving trees, herbivorous insects and their avian predator, the great tit *Parus major*. Using a mechanistic model, I explore the extent to which plasticity in phenology of great tits is an adaptive response to temporally-variable environments, and show that plasticity in this trait is of overwhelming importance for persistence in the face of expected climate change. However, I also extend this work to consider spatial variation in phenology, and present data suggesting that selection at multiple spatial scales in the great tit acts as a constraint on the evolution of adaptive phenological plasticity.

T32. Shocket, Marta. Indiana University.

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Temperature and resource quality regulate seasonal epidemics in a *Daphnia*-fungal disease system

Seasonal epidemics are commonplace in wildlife and human populations. However, the complexity of multiple interacting factors often makes it difficult to resolve the mechanisms driving seasonality in disease outbreaks. In our zooplankton-fungal disease system, lake water temperature decreases and algal food quality increases over the epidemic season. We use a combination of field data, lab experiments, and theoretical models to investigate the roles of temperature and food quality in determining the seasonality of epidemics in eighteen Indiana lakes. When temperature varies alone, R_0 (a measure of disease transmission potential) increases asymptotically over the relevant temperature range. However, when the co-varying relationship between temperature and food quality is included in the model, R_0 is maximized at intermediate temperatures that more closely match the timing of observed epidemic peaks. These results suggest that the combined effects of temperature and algal resource quality regulate the timing of epidemics in our system.

M35. Shuker, David. University of St Andrews.

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Next-generation behavioural ecology: sex allocation as a paradigm

What do we expect a synthesis of molecular, ecological and evolutionary natural history to look like? Here I suggest sex allocation under Local Mate Competition (LMC) as an example of such a synthesis. From Hamilton onwards, LMC theory has proved to be one of the most complete and successful bodies of evolutionary theory, predicting sex ratios across a broad variety of organisms. Ecologically, the basic conditions leading to LMC are well-known, and in organisms such as the parasitoid wasp *Nasonia vitripennis* we have been increasingly able to ground-truth theory in natural contexts. However, in terms of the mechanisms of sex allocation, much remains to be done. Here I will show how recent genomic approaches are beginning to unpick the mechanisms of sex allocation under LMC in *Nasonia* wasps, showing that the links between molecular mechanisms, ecology and evolution are increasingly within our grasp.

W26. Signor, Sarah. University of Southern California.

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The genetics of convergent evolution

The origin of diversity is one of the most central questions in evolutionary biology. In recent years the molecular changes responsible for the origin of some phenotypic differences has been identified. These studies are illuminating, however they proceed on a case-by-case basis and thus leave the possibility of any generalities in evolution unexamined. The search for these patterns necessitates a comparative approach by which multiple instances of phenotypic evolution have occurred in closely related species. Within the *Drosophila ananassae* subgroup there have been several independent changes in sexually dimorphic pigmentation. I have investigated the molecular basis of this color pattern evolution in three pairs of these (sub)species using a combination of high throughput sequencing and genotyping assays. Despite a lack of constraint in the pigmentation pathway gene reuse appears to be common, as does the presence of large effect mutations in phenotypic evolution.

W5. Simms, Ellen & Stephanie S. Porter. University of California, Berkeley.

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Effects of resource enrichment on mutualist inter-generational feedbacks

Specialized species interactions produce inter-generational feedbacks that help structure communities. Specialized mutualistic interactions are predicted to produce positive inter-generational feedbacks that could create patchy distributions among mutualist species. Soil-dwelling rhizobia can infect legume roots and fix nitrogen, though legumes can also use mineral nitrogen in the soil as an outside option when trading with rhizobia. In our coastal dune field system, both rhizobium clades and legume species exhibit persistently patchy distributions. Could positive inter-generational feedback between legume and rhizobium communities contribute to their patchy distributions? A two-generation mixed-inoculation greenhouse experiment using naturally co-occurring legumes and rhizobia affirms the prediction that this mutualism produces positive inter-generational feedbacks. By conducting this experiment at two levels of mineral nitrogen, we further test whether environmental conditions that change the relative costs and benefits of mutualism alter inter-generational feedback.

MS8. Skelly, David. Yale University.

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A roadmap for investigating microgeographic evolution in nature

TS2. Smith, Brian T. American Museum of Natural History.

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Insights into latitudinal species diversity gradients gained from historical analysis

P16. Smith, Rosemary. Idaho State University.

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Conceptual models to integrate population dynamics and life history theory (size/number tradeoffs; semelparity/iteroparity) in a population of *Nicrophorus* beetles facing a changing environment.

The offspring size-number tradeoff has played a major role in the development of life history theory, as have tradeoffs between current and future reproductive success. Studies of a burying beetle (*Nicrophorus investigator*) demonstrate both of these tradeoffs and provide a foundation for predicting population dynamics and patterns of body size. Concurrent field studies of beetle and rodent densities (dead rodents constitute the beetle's breeding resource) indicate a strong density effect on *Nicrophorus* populations. However, under highly competitive environments (many adult

beetles per rodent), adults produce fewer, larger offspring. In addition, recent climatic changes have increased the length of the breeding season, increasing the opportunity for multiple broods. This transition from semelparity to iteroparity will likely influence individual reproductive values. The aim is to develop a framework to link critical life-history tradeoffs with individual and population level reproductive values to predict demographic responses in a changing environment.

S2. Smocovitis, Betty. University of Florida
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Opening Lecture: "Naturalizing America: the evolution of the American Society of Naturalists"

WS3. Snell-Rood, Emilie. University of Minnesota.
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Niche construction and the evolution of phenotypic plasticity

Phenotypic plasticity is favored in variable environments. However, an individual's behavior plays a large role in determining how a genotype experiences environmental variation. In this talk I will discuss various mechanisms by which niche construction may affect the evolution of plasticity, for instance by increasing the likelihood of coarse-grained variation. An important implication of this perspective is that unforeseen evolutionary feedbacks may arise, which could drive the evolution of increasing specialization or generalization in different lineages. Additionally, I will discuss data from butterflies that illustrate how such a niche construction perspective can address maintenance of variation in plasticity.

W16. Snyder, Robin. Case Western Reserve University.
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How do we analyze the evolutionary consequences of demographic stochasticity?

Biological problem: While benthic marine species produce very large numbers of offspring (larvae), larvae do not disperse independently but instead disperse as a smaller number of larval packets. Not all larval packets land on suitable habitat, so sampling error produces stochastic number of offspring. How does this demographic stochasticity affect the evolution of the number, size, and frequency of releases, where number and size trade off against each other? Theoretical problem: how can we analyze the evolutionary consequences of demographic stochasticity? What happens when a phenotype is associated with a fitness *distribution*? What do we mean by an ESS when population dynamics are stochastic? Listen to my thoughts, contribute your own. If evolutionary theorists have figured out how to do this, I win. If they haven't and this presentation launches a discussion, we all win.

TS5. Strauss, Sharon. University of California, Davis.
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Combining experiments, current observation and history to understand ecological specialization in plants

Ecological specialists are key components of global biodiversity. We use current observations, experiments on herbivory and competition and combine them with phylogenetic history to reconstruct pathways to soil specialization in a clade of mustards.

P14. Stuart, Yoel. University of Texas at Austin.
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Parallel and non-parallel evolution in populations of three-spine stickleback across 16 lake-stream pairs

Instances in which organisms independently evolve similar phenotypes in similar environments (i.e., parallel evolution) are taken as strong evidence for determinism during evolution by natural selection. However, parallelism is often defined coarsely: parallel phenotypes and environments are described categorically without taking into account subtle differences in environment and population history that may explain why traits often evolve to be as non-parallel as they are parallel. In three-spine stickleback, we measured the direction and magnitude of divergence by stream populations away from their adjoining lake populations and calculated how parallel such evolution has been across 16 independent lake-stream pairs. To help explain observed non-parallelism in phenotype, we used RADseq approaches to estimate gene flow and population structure across populations and also carefully measured environmental differences among sites.

W20. Stump, Simon. University of Arizona.

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Examining the interactions (or lack thereof) between dispersal-limited specialist pathogens and spatial niche partitioning.

How plants coexist is a fundamental problem of community ecology. Two major theories are the Janzen-Connell hypothesis (specialized natural enemies attack seedlings near adult conspecifics) and spatial niche partitioning (species respond differently to different habitats or microhabitats). These hypotheses are not mutually exclusive, and make contrasting predictions about spatial patterns; however, no theoretical study has ever examined both simultaneously. Additionally, it is not well understood how the spatial effects occurring under the Janzen-Connell hypothesis cause it to differ from other theories of predator-mediated coexistence. We developed a patch-occupancy model, where diversity was maintained by specialist natural enemies and spatially varying environmental conditions. Unlike most models that combines competition- and predation-based mechanisms, these two mechanisms had almost no interactive effect. Additionally, the importance of specialized predators was inversely proportional to the number of species, and much weaker when effects were highly local (rather than diffuse).

M29. Stutz, William. University of Texas at Austin.

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Generating local adaptation the hard way: divergent vs. balancing selection on major-histocompatibility genes (MHC) in parapatric populations of threespine stickleback

Environmentally driven variation in parasite communities is thought to be an important driver of local adaptation, and potentially ecological speciation, in neighboring host populations. However, variation at the genes responsible for host resistance to parasites—such as major histocompatibility loci (MHC)—are expected to be subject to balancing selection within populations. In such cases, balancing selection may act as an impediment to local adaptation because rare immigrant alleles are likely to be favored by selection in new populations. Moreover, empirical evidence provided by natural populations has not typically allowed researchers to differentiate directional selection driven by local adaptation from frequency dependent balancing selection acting within single populations. By combining empirical evidence from replicate lake and stream populations of threespine stickleback with a novel analytical approach, I show that divergent selection is likely acting to generate local adaptation at MHC loci despite the countervailing effects of gene flow and balancing selection.

TS7. Swenson, Nathan. Michigan State University.

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The idiosyncratic evolutionary imprint on assembly in New Zealand woody plant communities.

A fundamental challenge in biology is to establish the link between organismal function and performance in a given environmental context. This knowledge sets the foundation for our understanding of how organismal function relates to species distribution and co-occurrence patterns along environmental gradients. The present research focuses on this fundamental problem using several woody plant radiations in New Zealand that constitute a large fraction of the woody plant flora of the country. The work establishes clear linkages between organismal function and performance. Next the work analyzes whether the traits underlying this linkage have similar evolutionary histories across lineages. The results show that the traits underlying the function-performance relationship have idiosyncratic evolutionary histories across genera. In particular, the same trait can be relatively labile or not depending on the genus suggesting that the assembly of lineages in this country represents a constellation of evolutionary imprints and no one single overriding rule.

T3. Taylor, Scott. Cornell University.

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Rapid climate-mediated movement of an avian hybrid zone reveals temporal variation in genomic introgression and selection

Changes in interspecific interactions in response to environmental changes are expected to shape future communities. One form of species-interaction that may be affected by ongoing climate change is the interaction between sibling species that share a zone of contact. We examined the dynamics of the zone of contact between Black-capped and Carolina Chickadees along a long-term transect in southeastern Pennsylvania using genomic, citizen science, and climate data. We provide strong evidence that cold winter temperatures limit the northern extent of the Carolina Chickadee's range and, using genomic data, confirm the rapid northward movement of this zone of contact over the past decade. Additionally, we report differential but limited geographic introgression of alleles over time and both variability and consistency in signatures of selection and genomic introgression across the genome over the past decade. This study showcases the power of temporal sampling in the study of hybrid zone dynamics and community responses to climatic shifts.

T34. terHorst, Casey. California State University, Northridge.
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The relative importance of rapid evolution depends on ecological context

Evolutionary change occurs on ecological time scales and affects community and ecosystem processes. However, the importance of evolutionary change relative to ecological processes remains largely unknown. We conducted a selection experiment in which plant populations evolved for three generations in either drought or high soil moisture environments. We then used a reciprocal transplant to compare the relative importance of contemporary drought stress and plant evolutionary responses to drought for belowground microbial communities. Plants that evolved in drought stress supported higher bacterial and fungal richness and higher fungi:bacteria ratios. These evolutionary effects were similar in magnitude to the ecological effects of contemporary drought, but their strength depended on whether they were measured in dry or wet environments. Our results suggest that interactions between recent evolutionary history and ecological context affect plant-soil feedbacks. An eco-evolutionary perspective may be required to fully understand how these feedbacks affect nutrient cycles and plant community dynamics.

P4. Travisano, Michael. University of Minnesota.
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Big Questions in Ecology, Evolution and Behavior

Understanding unifying biological processes involving ecology, evolution and behavior is challenging. This is particularly true in graduate education, where information is frequently packaged into highly technical discipline-specific courses, with little time to explore interdisciplinary connections. Since Fall 2012, we have been conducting an experiment in graduate EEB education, to develop an integrative foundational graduate course. A major goal of the course is to promote the value of interdisciplinary thinking for our graduate students by requiring them, regardless of specialty, to learn about all three major areas. Three faculty, whose primary research interests are in either E, E or B, guide the students in reading and discussion of major topics in each field. Interdisciplinary interactions among the students are encouraged, by their active participation in choosing class readings and leading discussions, across the range of E, E, and B topics. Preliminary results are very encouraging, as evidenced by the students' performance on a final project about "big questions."

T21. Trexler, Joel. Florida International University.
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Emergent effects of changing ecosystem size on metacommunity structure and system-wide productivity

We report results from a simulation model exploring how community dynamics in a dispersal-structured community can compensate for changing disturbance frequency and ecosystem size to maintain community-wide productivity. We used a spatially explicit simulation model with dynamic environmental drivers to identify environmental regimes that select among species from a regional pool with a diversity of dispersal strategies. Movement strategies considered were diffusion, bi-phasic diffusion, and directed movement and competition-dispersal trade-offs were assumed. We explore the effects of static and dynamic scenarios of disturbance regimes representative of natural and anthropogenic drivers. We use this model to illustrate how water extraction affects both the frequency of disturbance and aquatic ecosystem size in wetlands and use our model results to interpret patterns observed in time series data from the Florida Everglades. We demonstrate that migration strategies present in the regional species pool determine the resiliency of aquatic communities to water extraction and discuss the implications of the model for predicting species invasions.

M20. Trisos, Christopher. University of Oxford.
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The role of species interactions, dispersal and history in determining range extent and occupancy in a neotropical bird family

The extent to which species interactions, dispersal and history limit geographic ranges has long been controversial. Likewise, there is debate over the extent to which these same factors influence occurrence patterns at more local spatial scales within a species range. Here, we use trait, phylogenetic and distribution data for a large radiation of neotropical birds to test the influence of dispersal, history and either diffuse or pairwise modes of interspecific competition on occurrence patterns at the continental, biome and local community scale. We show that the importance of these processes varies with spatial scale and therefore in the degree to which they limit species range extents and occupancy within a range.

MS5. Urban, Mark. University of Connecticut.
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Eco-evolutionary dynamics of the finest kind

Usually only ecological mechanisms are thought to shape community patterns across local scales. Yet, adaptive evolution might also influence ecological dynamics at microgeographic scales. Here I show that microgeographic adaptation to an apex predator in the pond-breeding spotted salamander alters the diversity, abundance, and composition of prey communities via an interaction. Locally adapted spotted salamanders exacerbate the biomass declines associated with apex predation, but buffer the effects of apex predation on shared prey diversity. Hence, results suggest that the microgeographic divergence of local populations separated by as little as 100 m can strongly alter the diversity and composition of local food webs. These effects occur over the fine spatial scales at which community ecologists often study biodiversity patterns. Hence, community ecologists might often need to consider the local evolutionary history of individual populations to understand biodiversity patterns and their response to disturbances.

T22. Vamosi, Steven. University of Calgary.
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Community phylogenetics: comparing different ways of measuring community structure

Branded a bandwagon by some and viewed as a significant way forward by others, phylogenetic community ecology has received much attention in the past decade and a half. While most researchers have applied the metrics first introduced by Webb (2000, *Am Nat*), an alternative approach introduced by Heard and Cox (2007, *Am Nat*), which focuses on tree asymmetry, may provide additional insights into the mechanisms shaping local communities. Here, I present the initial results of our comparisons of the two methodologies, using a large database of Ontario fish communities.

M41. Van Cleve, Jeremy. NESCent, Duke University.
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Bet-hedging and the evolution of phenotypic plasticity

In light of an uncertain future, organisms face a difficult trade-off. They can either specialize on a single phenotype across a range of environments, hedge their bets by randomly choosing among a set of phenotypes, or invest in physiological machinery to adjust their phenotype plastically. Understanding the evolutionary relationship between these strategies remains a puzzle. Here, we present a simple model for the evolution of specialization, bet-hedging, and plasticity that reveals how these strategies are fundamentally sensitive to the shape of the cost of plasticity. When costs accelerate with plasticity, bet-hedging is the likely outcome. In contrast, decelerating costs can lead to full adaptive plasticity, but only when initial conditions are right. The shape of the cost curve is due to the genetic and metabolic network machinery underlying plastic traits, which means that certain networks are more likely than others to evolve plasticity.

M38. Vasseur, David. Yale University.
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From transient to evolutionary stable states: how does functional diversity impact ecosystem function

The stable provisioning of ecosystem functions, properties and services, such as community biomass (carbon sequestration), community respiration (carbon cycling) and a variety of other important attributes, is thought to benefit from having functionally diverse communities because it is more likely that a) many species contribute to any particular function at a given time and b) in the event of an environmental change or shift which causes a decline in the major contributors, other resident species may be able to compensate for the provisioning of a particular function. However, on both the theoretical and experimental side, little attention has been given to the evolutionary state of the ecosystem, and therefore, for the propensity of the observed results to continue to change as species adapt to their suite of competitors, predators, and resources. Using a suite of models I contrast the results of biodiversity/ecosystem function relationships when species are pre-adapted to allopatric and sympatric conditions.

M32. Vincenzi, Simone. University of California, Santa Cruz.
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Combining demography with quantitative and population genetics to infer the adaptive potential of small populations

Life-history traits are often density- and frequency-dependent, and vary in both space and time. To improve ability to predict the magnitude and rate of adaptation to a changing environment in small populations requires combining demography with quantitative and population genetics. We used marble trout populations living in Slovenian streams as a model system. Marble trout populations are isolated, have low density and small population sizes, and harbor low neutral genetic variation; they also experience high mortality caused by flash floods that further contribute to the erosion of genetic variability. Specifically, we used theoretical insights, analysis of long term mark-recapture data sets, and multi-generation pedigree reconstruction with panels of SNPs discovered using Next Generation Sequencing-generated data to infer mating patterns, heritability of life histories, selection of traits and to assess the genetic and demographic consequences of flood events.

P7. Vizelka, Jason. University of Wisconsin-Milwaukee.

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Effects of closely related bumble bee species on reproductive success and mating patterns in *Mimulus ringens*

Over the last decade there have been dramatic changes in the relative abundance and diversity of bumble bee populations, including significant decline of many species in North America and Europe. Often several species co-occur sympatrically and it is not known if these species provide equivalent pollination services for native flowering plants. To address this question we quantified seed set of *Mimulus ringens* following individual visits by *Bombus vagans* and *Bombus impatiens*. These species coexist in native populations and vary markedly in body size and foraging behavior. Mean seed set following single visits by *B. vagans* was significantly higher than seed set resulting from visits by *B. impatiens*, suggesting that different bumble bee species may not have the same contributions to native plant reproduction. Future work will explore how visits by these two species influence pollen receipt, self-pollination rate, mate diversity and gene dispersal.

T19. Wagner, Catherine. Eawag: Swiss Federal Institute of Aquatic Science and Technology.

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The macroecology and evolution of African cichlid fish biodiversity

A positive relationship between species richness and island size is thought to emerge from an equilibrium between immigration and extinction rates, but the influence of species diversification on the form of this relationship is poorly understood. Here, we show that within-lake adaptive radiation strongly modifies the species-area relationship for African cichlid fishes. The total number of species derived from in situ speciation increases with lake size, resulting in faunas that are orders of magnitude higher in species richness than faunas assembled by immigration alone. Multivariate models provide evidence for added influence of lake depth on the species-area relationship. Clades representing within-lake radiations show evidence of diversity limitation by lake surface area, depth and energy, suggesting that ecological factors limit the diversity a radiating clade can reach within these ecosystems. Together, these processes produce lake fish faunas with highly variable composition, but with diversities that are well-predicted by environmental variables.

W7. Wagner, Maggie. Duke University.

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Natural soil microbial communities alter plant phenology and intensity of selection

The strength of natural selection often varies among environments, but the ecological causes or agents of differential selection are not always apparent. Soil microbial communities, which are complex and variable on large and small spatial scales, are potentially important drivers of environment-dependent phenotypes and selection patterns in plants. We isolated microbiota from field-collected soils from four natural habitats of *Boechera stricta*, a model system in ecological genetics, and tested separately the effects of biotic and abiotic soil factors on life-history traits and fitness in 48 *B. stricta* genotypes. Soil microbes from certain habitats affected survival, delayed flowering, and altered selection on flowering time, despite having no effect on plant growth. In contrast, abiotic soil factors influenced growth, phenology, and several fitness components but not the intensity of selection. Microbiota effects on germination and trait heritability, and spatial variation in multiple soil properties within and among habitats, will also be discussed.

TS4. Wainwright, Peter. University of California, Davis.

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The effect of speciation on niche and trait evolution in reef fish

Although debated for decades, it remains unclear how the pace of adaptive diversification maps to the events depicted on a phylogeny; speciation events separated by stretches of anagenesis. Using a time-calibrated phylogeny of the

radiation, I present an analysis of sister-species pairs in Haemulidae, a lineage of New World reef fishes. The 19 sister-pairs in this lineage show a bimodal distribution in range overlap; seven pairs are fully sympatric and 12 pairs are completely allopatric. My key result is that the rate of divergence of diet, feeding functional morphology, locomotion traits, color pattern and body shape all show a pattern of decreasing with age of the sister-pair, strongly suggesting that speciation is associated with periods of elevated rates of divergence. In haemulids interactions between sister-species play an important role in ecological diversification, as the highest rates of trait and niche evolution were measured in young sympatric pairs.

P9. Wang, D. Lisa. University of Arizona.
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Is color perceived as a modular or composite trait?

Animals across broad taxonomic and contextual ranges make behavioral decisions based on color, which can be described by its chromatic and achromatic properties. Although both properties are known to play a role in mediating behavior, many studies assume animals perceive color as a modular trait in which chromatic and achromatic properties independently affect color-mediated behavior. However, color may also be a composite trait such that the interaction of chromatic and achromatic properties simultaneously affects color-mediated behavior. Here, we test whether the pipevine swallowtail, *Battus philenor*, learns the chromatic or achromatic property of color (i.e. modular) or the interaction of both chromatic and achromatic properties (i.e. composite).

M26. Wang, Silu. University of Texas, Austin.
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Coevolution of male courtship and sexual conflict characters in mosquitofish

Sexually antagonistic selection is an important force for mating system evolution. Although there is abundant evidence of sexually antagonistic coevolution (SAC) of morphological features, the association of such SAC and male courtship behavior is less substantiated. We investigated the evolutionary relationship between morphological SAC and male courtship behavior in a genus of poeciliids, *Gambusia*, in which mating is generally coercive. To estimate the contribution of courtship display to copulation, we quantified the transition rate of display to copulative thrust in male behavior sequence (DT rate). We found concomitant increase of morphological SAC and male DT rate. Particularly, elevated male morphological SAC advantage preceded the increased DT rate across this group. Thus male displays became more important when males have morphological advantage for forced copulation over female resistance. This unexpected observation indicates novel evolutionary significance of male courtship displays-- as an escalator of sexual conflict, or as ameliorative byproducts of SAC.

T12. Weber, Marjorie. Cornell University.
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Merging phylogenetic and experimental methods to test hypotheses about the evolution of mutualistic defensive traits in plants

In many mutualistic interactions, participating species evolve specialized morphological traits that directly facilitate relationships with their partners. Theory suggests that these 'mutualistic traits' may (1) interact with one another to influence ecological dynamics, (2) be adapted to specific environments, and (3) function as key innovations by increasing niche breadth and opportunity to radiate. Despite the common occurrence and ecological importance of mutualistic traits, few attempts have been made to test these evolutionary hypotheses in a phylogenetic framework. Here, we examine two common mutualistic defense traits in plants: extrafloral nectaries (glands that secrete sugar and amino acids, providing food for "bodyguard" arthropods), and leaf domatia (small structures that provide homes for fungivorous and predacious mites). We merge phylogenetic and experimental methods to address whether macroevolutionary patterns and ecological dynamics of these two traits are consistent with trait interaction, geographic, and key innovation hypotheses in the flowering plant genus *Viburnum* (Adoxaceae).

M11. Welles, Shana. University of California, Riverside.
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Evolutionary origins of *Salsola ryanii*, a novel allopolyploid weed

Salsola ryanii is an allopolyploid derived from two invasive species, *S. tragus* and *S. australis*, that evolved in the last few decades in California's Central Valley. Here I present data regarding *S. ryanii*'s evolutionary origins and current distribution.

M19. White, Alexander. University of Chicago.

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The effects of interspecific competition on range limits along the Himalayan bird diversity gradient - why are there so many fewer birds in the west?

Avian species richness declines dramatically across the Himalayan range. Species diversity in the western region is nearly half of that observed in the eastern Himalayas. Although climatic differences between the regions were previously thought to be generating this pattern, the effects of climate alone are not sufficient to explain differences in species richness across the entire altitudinal range in both regions. The potential for interspecific competition and the ability to disperse are here hypothesized to be responsible for excluding species from lower altitudes in the western region, thus generating the observed decline in species diversity. We focus on the suite of ~150 species that span the entire east-west gradient to understand why ranges are limited in other species, how niches shift across space, and how the changes in the syntopic species assemblage impact the probability that eastern species will occur in the west.

WS7. Whitham, Tom. Northern Arizona University.

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A community genetics approach to niche construction by foundation plant species

As foundation species are by definition, “community and ecosystem drivers”, their genetic structure and extended phenotypes on the community and ecosystem are especially important to understand and quantify. The multivariate traits of individual plant genotypes define the niche space of the species that may live on individual plants. Extensive intraspecific variation in niche space plays a significant role in defining the individual species that will be found on an individual plant, the community of interacting species, biodiversity, community stability, ecosystem processes, and feedbacks on the performance of individual plant genotypes. A community genetics approach to niche construction allows us to place community and ecosystem ecology within an evolutionary framework, and make better management decisions concerning conservation, biodiversity, climate change, and genetic engineering. I argue that community genetics approach to niche construction offers solutions for “wild” communities just as quantitative genetics has resulted in important gains in agro-ecosystems.

T18. Whitlock, Michael. University of British Columbia.

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Evolution into and out of overdominance: Genetic variation and segregation load with stabilizing selection.

M36. Whitney, Kenneth. University of New Mexico.

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Identifying key alleles and traits in adaptive introgression events: insights from experimental evolution in sunflowers

The evolutionary importance of gene exchange through hybridization and introgression is becoming better recognized. However, we still lack detailed understanding of which alleles and traits are exchanged, whether such exchange can increase rates of adaptation, and how repeatable introgression events are in nature. Our study focuses on two wild sunflower species and their naturally occurring hybrid lineage. We have identified key introgressing quantitative trait locus (QTL) alleles that increase fitness in the hybrid lineage via beneficial effects on herbivore resistance, phenology, and flower and seed production. Here we also report on a 10-year experiment that ‘replays the evolutionary clock’ to examine the early stages of hybrid lineage formation. By tracking changes in traits and in frequencies of the key QTL alleles over time in replicate experimental hybrid populations in the field, we gain insight into the repeatability of hybrid evolution.

W19. Whitton, Jeannette. University of British Columbia.

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Does reproductive interference limit coexistence? Insight from an asexual complex

Empirical and theoretical studies suggest that coexistence of close relatives is unlikely in the absence of ecological divergence. However, coexistence could also be limited by reproductive interference and in most groups, the effects of ecological similarity and reproductive interference are confounded. We tested for evidence that RI limits coexistence using *Crepis*, a complex of plants that includes sexual and asexual members. Close relatives frequently co-occur in this group, with forty percent of sites containing 2-9 closely related taxa. Reproductive interference should not occur among asexuals, which produce clonal seeds via apomixis. We tested for evidence that the lack of reproductive interference permits coexistence using randomizations. Co-occurrence of asexuals was more frequent than expected, and sexual

taxa were more likely to occur in isolation. Data from experimental crosses suggest that pollen deposition from asexuals onto sexuals is a likely mechanism of asymmetrical interference in these systems.

M6. Wolkovich, Elizabeth. University of British Columbia.

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Coexistence and climate change: The role of temporal-variability in structuring future communities

Predicting community shifts with climate change requires fundamental appreciation of the mechanisms that govern how communities assemble. Most work to date has focused on how warmer mean temperatures may affect individual species via physiology and fail to predict the wide diversity of observed shifts. Climate change has affected far more than mean temperatures, including widespread effects on growing season length, variability and shifts in extreme events. Additionally, cascading effects on species and communities are qualitatively predicted but there have been few efforts to predict shifts based on coexistence theory. Here we extend the two possible mechanisms for species coexistence based on variable environments—relative nonlinearity and the storage effect—to predict how communities will respond to climate change. We focus on shifts in climate variability and extreme events that link to stabilizing coexistence mechanisms and traits that may make species the most vulnerable to climate change.

M2. Zee, Peter. Stanford University.

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Biodiversity loss following habitat fragmentation is dictated by the relative scale of biotically and abiotically generated environmental heterogeneity

Understanding community assembly provides insight into the structure and maintenance of diversity in biological communities. Fragmentation of habitat can lead to catastrophic loss of ecological diversity at local and regional scales. Natural communities are complex entities with variable scales of environmental heterogeneity, biotic feedbacks, and dispersal regimes, but their joint effects on biodiversity that may occur during habitat fragmentation are not well understood. Here, through simulation of a model of community assembly before and after habitat fragmentation, we assess how the above factors alter the impact of fragmentation on the trajectory and structure of ecological diversity. Results indicate that the speed and extent of biodiversity loss by habitat fragmentation can be greatly influenced by the relative scale of biotically and abiotically induced environmental heterogeneity.

M27. Zink, Andrew. San Francisco State University.

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A general model of parent-offspring conflict over reproductive skew in communal breeders

Reproductive skew theory addresses conflict over reproduction in communally breeding animals. The predictions of skew theory, in terms of the resolution of reproductive conflict, are highly divergent; this is because each model depends on initial assumptions about which of the adult breeders controls group membership and reproduction. An additional, implicit assumption of all reproductive skew models is that offspring have no ability to manipulate the reproductive output of breeding adults within the society. Here I relax this assumption and present a new model of reproductive skew, where the optimal solutions for offspring and adults have the potential to diverge. I discuss how the magnitude of this parent-offspring conflict over reproductive skew varies across different mating systems and I present relevant examples ranging from social mammals to eusocial insects.