

**E. O. Wilson Award Lecture:  
Models on the Runway: how do we make replicas of the world?  
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Models are universal in science, both as theoretical formulations of reality and as model systems, representatives of other organisms. A recent paper on how scientists view the world divides our work into the mind, the lab, and the field, and suggests that models must not be conflated with reality. But in practice, these distinctions are blurred. For example, are flour beetles a model system for other insects, when their natural habitat is the same as the way they live in the lab? In addition, models can become restrictive when they are viewed as archetypes, making us over-generalize about the world and ignoring meaningful variation. The study of sexual conflict in insects illustrates some of the pitfalls of relying on *Drosophila* as a model system for sexual selection. Microbes can be used as models for populations and communities, and are also essential parts of larger biological systems. Finally, some models are not meant to replicate the world, but are worlds unto themselves in which diverse possibilities can be directly observed.

M1

Community Assembly and the Functioning of Ecosystems (CAFE):

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Numerous studies have shown that biodiversity is important to ecosystem function but these studies have almost exclusively studied how this happens at the local scale and ignored many of the processes that affect community assembly. Community assembly is a more complex process than a simple input of diversity and is strongly affected by dispersal from the wider species pool that characterizes a regional biota or metacommunity. I review basic theory on the effects of dispersal and illustrate how dispersal may influence our understanding of consequent effects on ecosystem functioning. I conclude that the most important lacuna in our understanding comes from thinking about how isolation that slows community assembly affects relationships between diversity and ecosystem functioning.

M2

Functional diversity: what it is, how it can be measured, and ways it can be partitioned

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There has been a recent proliferation of metrics for functional diversity and applications of those metrics. However, those metrics fail to provide a way of integrating multiple aspects of functional diversity into a single measure. We present a new approach to measuring functional diversity that integrates richness, evenness and distinctiveness and allows partitioning into alpha and beta components. Such an integrated metric is necessary if we want to test theories of the role and evolution of functional diversity.

### M3

A unimodal relationship between microbial competition and community age in a natural micro-ecosystem.

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The magnitude of biodiversity effects on ecosystem process rates are contingent on the phenotypes of the individuals comprising their local community, their interactions with one another, and their patterns of resource utilization. It is possible that community turnover during primary succession can alter biodiversity effects on ecosystem processes. Using bacterial strains isolated from leaves of the carnivorous pitcher plant *Darlingtonia californica*, I investigated the effect of community age on the magnitude of the relationship between bacterial richness and carbon respiration. I detected a unimodal relationship between community age and slope. Searching for a proximate explanation for this pattern, I was unable to detect temporal trends in rates of direct antagonism between community members nor any changes in communities' carbon substrate utilization patterns. Instead, these slopes were positively associated with the magnitude of competitive interactions between community members (i.e., the 'selection effect'). This result provides a putative mechanism for the dynamical nature of ecosystem process rates in natural *Darlingtonia* micro-ecosystems.

### M4

Evolution due to intra- and interspecific competition with asymmetric competitors

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Our understanding of competition has been strongly biased by an evolutionary, niche-based view, in which competition drives selection for species to differ in resource use, which increases the probability of coexistence. Two factors are often neglected with this view: differences in relative abundance and resource-use efficiency. A result is that competition is often perceived as being relatively symmetric, with both species suffering equally. A related consequence is that selection due to intraspecific competition is often neglected. A simulation model of competition is used to demonstrate that competition among species is often highly asymmetric. As such, dominant competitors are mostly experiencing selection due to intraspecific, rather than interspecific, competition, while subordinate competitors are subject to primarily interspecific competition, which can have significant effects on selection for niche expansion and resource use efficiency. The model provides a fresh look at older, perhaps neglected topics on competition, evolution, and community diversity.

### M5

Intraguild predation results in genome wide adaptation in the threespine stickleback

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Biotic natural selection is critical in the generation of phenotypic diversity. Yet the effect of biotic selection upon the genome of an organism is largely unknown in natural populations. We report the results of a genome wide analysis examining the genomic architecture of adaptation of threespine stickleback (*Gasterosteus aculeatus*) to intraguild predation from prickly sculpin (*Cottus asper*). We used whole genome re-sequencing of 17 freshwater populations combined with a novel

genome scan method to identify extensive parallel divergence in response to a single agent of selection. Intraguild predation is associated with widespread but unevenly distributed selection across the genome. Adaptation to intraguild predation may involve hundreds of genes with diverse functions.

M6 (Changed)

Reversed latitudinal gradients of species richness and interaction intensity for parasites in two wide-ranging host species

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Although the latitudinal diversity gradient is a well-known and general pattern, the mechanisms structuring it remain elusive, for perhaps two key reasons. First, habitat type usually varies with latitude, precluding standardized evaluations of diversity. Second, hypothesized mechanisms co-vary with one another, making it difficult to distinguish their independent effects. We can eliminate important confounds by examining parasite communities in widely distributed hosts. We examined trematode parasites in two similar snail species across 27 degrees of latitude from 43 locations in tropical and temperate oceans. Counter to typical patterns, species richness, levels of parasitism, and intensity of intraguild predation increased with latitude. Because attributes of this system preclude speciation rates from causing diversity gradients, the reversed gradients are likely driven by local ecological factors, specifically, productivity and stability. We highlight how this system may serve as a useful tool to provide insight into what processes drive diversity gradients in general.

M7

Predicting future extinction debt from present-day community patterns

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A significant challenge in measuring and predicting extinction rates is the possibility of extinction debt, time-delayed extinctions that occur gradually following an initial impact. Here I discuss how relative abundance distributions and spatial aggregation influence the magnitude of future extinction debt following habitat loss or climate-driven range contraction. Communities following canonical lognormal and broken stick abundance distributions are found to be prone to extinction debt, especially when species exhibit low spatial aggregation. Conversely, communities following a logseries distribution never demonstrate extinction debt and often show an "immigration credit" in which richness rises in the long-term following an initial decrease. An application in twenty-five biodiversity hotspots suggests that few immediate extinctions will be observed for birds, followed by debts of 30-50%, while immediate extinctions of 5-15% of plants are likely without subsequent extinction debt. These results shed light on the basic determinants of extinction debt and can be used to indicate the likely magnitude of future extinctions in poorly studied landscapes.

M8

Niche dimensionality selects for sex

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The ubiquity of sex in nature remains an important, but unsolved, question in biology. Theory indicates that fewer than 5% of individuals in a population should reproduce sexually when costs of sex are taken into account. However, previous models have assumed simple environments arranged along a single axis of selection. Real environments are more complex, and organisms often have multidimensional niches. Here we show that a realistic multi-dimensional niche selects for a high incidence of sexual reproduction even when accounting for costs of sex. We show that this result applies to both pure and mixed reproductive strategies and is robust to variation in multiple factors. Most species will face multiple dimensions of niche variability in space and time. Our results demonstrate that the multi-dimensional niche that is found in nature provides a simple solution to the longstanding conundrum of widespread sex.

M9

Thoughts on the interplay of demographic stochasticity, fitness, and the niche concept

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G.E. Hutchinson's niche concept is an abstract mapping of one aspect of population dynamics (in particular a measure of absolute fitness) onto an environmental space. For continuously growing populations, the metric is traditionally assumed to be the intrinsic growth rate,  $r$ , at low densities (with units 1/time). But at small absolute numbers, extinctions can occur for populations with a positive intrinsic rate of growth because of demographic stochasticity. Another familiar fitness metric,  $R_0$  (the expected number of offspring produced per individual over their lifetime), arises when considering extinction risk. This alternative metric can influence the shapes of niche response surfaces. This talk will broadly aim at assaying the relevance of demographic stochasticity for concepts of both absolute and relative fitness in small populations, such as at range margins and in sink habitats, with an eye towards refinement of ecological niche concepts.

M10

Predicting rescue via evolving plasticity in stochastic environments

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Phenotypic plasticity and its evolution may help evolutionary rescue (ER) in a novel, stressful environment, but this process is poorly understood, especially in stochastic environments. In particular, with developmental plasticity a change in autocorrelation of environmental fluctuations affects both the evolution of plasticity and population growth. It is therefore unclear how evolving plasticity contributes to ER in a stochastic environment. We address this here, integrating stochastic demography with quantitative genetic theory to study a scenario of simultaneous change in the mean and predictability (temporal autocorrelation) of the environment. We assume novel environments reveal cryptic genetic variation, and develop approximate predictions of extinction risk during ER and long-term persistence afterwards. We show that reduced predictability decreases persistence and increases exposure to low population size, and that populations with intermediate levels of

additive genetic variance in plasticity will both avoid low population sizes and achieve a positive growth rate after ER.

M11

Major transitions aren't for everyone: unicellular lineages survive by associating with multicellular competitors during the experimental transition to multicellularity in the budding yeast

*Kluyveromyces lactis*

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The evolution of multicellularity has played a central role in the history of life on Earth. Recently, experimental evolution has provided new opportunities to directly observe this major evolutionary transition as it occurs. We subjected the budding yeast *Kluyveromyces lactis* to selection for rapid settling, which favors increased size. All ten replicate populations rapidly evolved multicellular 'snowflake' phenotypes, which form through continued association of daughter cells following cell division. However, in stark contrast to *Saccharomyces cerevisiae*, multicellular lineages did not become fixed in evolving *K. lactis* populations. Instead, unicellularity persisted in all populations throughout the 60-day experiment. Mutual invasibility suggests stable coexistence of unicellular and multicellular lineages under settling selection. We observed adhesion of unicells to multicellular colonies, as well as improved settling rates of unicells when mixed with multicellular colonies. These results support the theoretical prediction that social interactions among non-relatives may increase the ecological complexity of major transitions.

M12

Evolution for extreme living: Variation in mitochondrial *cox* genes correlated with elevation in pikas (genus *Ochotona*)

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Pikas (genus *Ochotona*), cold-specialists including many high-elevation species, offer a unique opportunity to study adaptations and potential limitations of an ecologically important mammal to high-elevation hypoxia. We analyzed the evolution of three mitochondrial genes encoding the catalytic core of cytochrome c oxidase (COX) in pikas using ten species occupying elevations from sea-level to 5,000 meters. COX is an enzyme highly reliant on oxygen and essential for cell function. Amino acid mutations were classified as either increasing or decreasing COX protein efficiency, revealing a strong positive correlation between the net number of amino acid mutations and the average elevation each species occupies. We found evidence of selection for less efficient COX in low-elevation species, perhaps trading efficiency for heat production in the absence of hypoxia. Our results indicate that different pika species have evolved elevation-specific COX proteins, specialization that may inhibit range movements up in elevation in response to climate change.

M13

Trait evolution and the stability of food webs

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Understanding the ecological dynamics in food webs is a classic problem in community ecology. Recently, there has been a focus on how rapid evolutionary changes and ecological dynamics interact to generate unique patterns. We seek to understand the impacts of trait evolution on the diversity-stability relationship in food webs. Here, we present a stochastic, individual-based simulation of an eco-evolutionary model of trait evolution in food webs. We analyze how trait evolution impacts community stability through two measures: the coefficient of variation in community diversity, and the persistence of species in the community. By both of these metrics, we find that trait evolution has a stabilizing effect. Further, we show how these stabilizing effects are dependent on initial species richness. Our results demonstrate a stabilizing effect of trait evolution in communities, and stress the importance of considering concurrent ecological and evolutionary processes.

M14

Predicting evolutionary responses to climate change from parameterized models of selection on vegetative and floral traits

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Evolution in response to climate should depend on the environmental sensitivity of selection and patterns of genomic variability. How trait evolution then influences evolutionary rescue further depends on impacts on population size. Long-term experiments on subalpine *Ipomopsis* plants have measured selection on vegetative traits associated with drought tolerance and floral traits that influence pollinator visitation. Selection for long flowers was less intense in earlier snowmelt years that produced lower fecundity, whereas selection for lower specific leaf area was greater in an early dry year. Combining this information with ongoing estimates of heritability and demographic effects suggests preliminarily that vegetative trait evolution can lead to evolutionary rescue from drought, while floral trait evolution may hinder it. This work represents a rare case of applying models of evolutionary rescue and suggests the need to incorporate flower traits that respond indirectly as well as vegetative traits typically targeted in studies of climate change.

M15

Local adaptation in thermal transgenerational plasticity

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Evidence for transgenerational plasticity (TGP) is accumulating, ranging from well studied maternal effects to more recently discovered epigenetic phenomena. Although recent theoretical studies explored conditions under which TGP should evolve, there are few empirical tests. Here, we test this theory by looking for local adaptation in thermal TGP along a naturally occurring gradient in temperature using Sheepshead minnows (*Cyprinodon variegatus*) from SC, MD, and CT.

Specifically, we exposed parents from each population to 26 and 32°C for 7, 30, and 45 days and measured growth of their offspring reared for 56 days at both temperatures. TGP was quantified as the interaction between parent and offspring environments on growth. We found evidence for TGP in fish from all populations, the strength of which decreased with increasing latitude. As the predictability of temperature during the growing season decreases with latitude, these results are broadly consistent with theory.

### M16

Evolution of deterministic maternal effects and bet-hedging

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Parents are always telling their kids what to do, as if they know best. If parents alone have cues to predict the future, this may be true. In particular, the current conditions may yield information about the conditions that the next generation will face, even when there are no additional cues. It has also been proposed that parents may simply play dice with their babies by randomizing offspring phenotype; a phenomenon often called bet-hedging. Bet-hedging has captured the imagination of evolutionary biologists and predicts that increase phenotypic variance can be an adaptation. We developed a straightforward model of maternal effect evolution that allows us to consider how maternal provisioning of offspring can lead to either bet-hedging or deterministic maternal effects. Although a range of parameter values allow bet-hedging to evolve, a deterministic maternal effect is almost always the ESS strategy.

### M17

Interactions in sympatry shape the diversification of multiple radiating cichlid clades

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Cichlid fishes have formed adaptive radiations in many lakes across Africa. Although the species richness of cichlid communities is broadly predicted by lake area, one major distinction among lake adaptive radiations is that in some cases, the community richness is dominated by a single lineage, whereas in other cases diversity is distributed among multiple adaptively radiating clades. We here study a lake cichlid assemblage where several highly divergent cichlid lineages have independently formed adaptive radiations within the same lake. We show genomic evidence for recent within-lake radiation in multiple lineages, and evidence for ecological interactions in sympatry shaping the morphospace occupation of these lineages.

### M18

Contrasting evolutionary histories between birds of upland and floodplain forest in the Amazon

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Floodplain forest and upland forest are widespread across the Amazon Basin, and many species specialize on one type of forest or the other. We compared the evolutionary histories of 20 pairs of closely related species in which one occurs in the floodplain and the other in upland forest. We used genetic data from 2,300 ultraconserved elements and 90 exons from individuals sampled across the Amazon Basin to estimate population history for each species. We found similar levels of population structure between species from the two habitats, but species of upland forest exhibited larger effective population sizes and older population divergences than floodplain forest species. Our results suggest that species-level ecology in the form of habitat selection impacts evolution and that knowledge of habitat preference can serve as an indicator of population genetic processes potentially important for species conservation.

### M19

Resource allocation strategies among body parts within individuals are affected by sex, body part, and level of resources

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Resource allocation strategies among traits are fundamental to our understanding of life histories and tradeoffs among traits. Typically, allocation strategies are examined as differences among populations, treatments or species. Examination of tradeoffs at these levels, however, has a drawback in that different traits and body parts are comprised of different materials (e.g., protein vs. fat), making direct comparisons difficult. Here we use a common currency, calories, to examine resource allocation strategies among body parts (antenna, head, thorax, wings, legs, abdomen) within individuals of the hawkmoth *Manduca sexta*. We explore how restriction in larval resources affects resource allocation strategies in the adult. We show that the sexes and body parts each have different allocation strategies, and that these strategies change under resource restriction. In addition, we document a resource allocation tradeoff between the abdomen and other body parts, but positive correlations of resource allocation among all other body parts.

### M20

We happy few: using structured population models to identify the decisive events in the lives of exceptional individuals

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In any population, some individuals make it big: they are among the few that produce many offspring, grow to large size, etc. What distinguishes the lives of these happy few? We present two approaches for identifying what factors distinguish those individuals who come to dominate reproduction ("lucky"). The first is to compare life history trajectories for lucky and unlucky individuals. The second is to calculate the elasticity of the probability of becoming lucky to perturbations in demographic rates at a given size or age. As an example, we work with published size-structured integral projection models for a tropical tree and a semi-arid shrub. We find that good luck (e.g., rapid growth) when small and young matters much more than good luck when older and larger. Becoming one of the lucky few is first and foremost a matter of surviving while others die, but for species with more variable growth, such as our shrub example, it is also a matter of growing fast. Our approach is broadly applicable. While we investigate reproductive skew, our methods can be used to investigate how individuals come to be exceptional in any aspect.

### M21

Process and scale in life history theory and invasion biology

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Variation in the abundance of resources and in the ways resources are divided interact to shape patterns of diversity at multiple levels of biological organization. Life history theory and invasion biology provide examples of how scale-dependent patterns may arise from environmental heterogeneity and resource partitioning. Life history theory recognizes that trade-offs in how resources are allocated can be masked by variation in resource acquisition. This often occurs within populations and yields a positive correlation between traits, whereas a negative correlation is the

norm in comparisons among species. In invasion biology, a positive correlation between native and exotic species richness across communities is attributed to environmental heterogeneity, but experimental studies have documented negative correlations that reflect the partitioning of fixed resources. I will discuss the parallels and differences between fields in light of debate regarding the importance of competition and with attention to the integration of observational and experimental results.

M22

The cultural history of a plant defense

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Cardenolides are well-known plant defense chemical compounds that mediate interactions between monarchs and milkweeds. I will summarize what is known about the use of cardenolides by humans, starting with Native Americans and Romans and ending with the current clinical trials of cardenolides as an anti-cancer therapy.

M23

Integrating genetic architecture and density dependence to understand the evolution of life history

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We present a framework to study the interplay of fundamental ecological and evolutionary processes on adaptation of life history traits. Different forms of density dependence influence the eco-evolutionary feedbacks determining stable life history strategies. However, the efficacy of selection for optimal phenotypes is constrained by the underlying genetic architecture. Therefore, we use adaptive dynamics theory to integrate these processes into the evolutionary trajectories of maturation, reproductive, and mortality rates in two-stage populations experiencing density dependence. Both the life-history transition most affected by density dependence and the G-matrix architecture determine the selection gradient's shape. The selection gradient interacts with the shape of the feasibility set to determine the evolutionary outcome. Changes to the relative speed of adaptation or the direction of the covariance between evolving traits can change a species' trajectory from a stable strategy to evolutionary extinction. This work provides a foundation for studying open questions in life history evolution.

M24

Testing the direction and strength of ecological and sexual selection using metabolic theory of ecology

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Researchers have long sought to understand how acoustic signals evolve in response to various selective agents. Here, we use a novel approach to evaluate the direction and magnitude of ecological and sexual selection on vocal signals using the metabolic theory of ecology (MTE). First, using a large avian dataset informed by a phylogenetic framework we demonstrate that MTE accurately predicts the relationship between body size and vocal frequency. Then, using MTE predictions as expectations for vocal frequencies in the absence of selection, we demonstrate that

several factors related to intense sexual selection predict signal divergence from expected values and that vocal signals in open environments are higher than expected, a finding that broadens our understanding of the direction of ecological acoustic adaptation. We argue that our approach using 1st-order predictions could be useful in evaluating selection more broadly.

#### M25

Elevated glucocorticoids enhance maternal reproductive allocation and offspring development in a wild songbird

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Female house wrens increase their allocation to offspring when experimentally immune-challenged. This change in allocation includes elevated yolk and yolk-corticosterone concentrations within eggs, and pre-natal effects on offspring growth after hatching. Variation in in ovo corticosterone also positively predicts maternal provisioning of food after hatching. However, whether variation in maternal corticosterone during egg formation per se, independent of immune activation, affects post-natal growth and development remains unresolved. Here, we experimentally increased maternal corticosterone during egg production using a non-invasive technique (feeding them with corticosterone-injected mealworms). Females fed supplemental corticosterone during egg production produced more eggs, on average, than did controls. After hatching, the offspring of these females begged for food at an elevated rate, and grew faster and obtained greater pre-fledging body condition than the offspring of control females. Thus, variation in circulating corticosterone during egg production can enhance maternal investment and offspring growth.

#### M26

Metabolic scaling as a life history trait: the evolution of ontogenetic allometries

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Allometric scaling rules are common in biology, but to what extent they reflect evolutionary constraints or natural selection remains controversial. In particular, it is unclear how between-species (evolutionary) allometries relate to within-individual (ontogenetic) allometries. Linking these types of allometries is important, as selection can only act on the latter. To shed light on this issue, I measured ontogenetic allometries of morphological, physiological and behavioral traits in 25 species of damselflies separating along the fast-slow life history spectrum. With these data, I ask the question: does the body size-scaling of metabolic rate constrain the evolution of body size; or does the size-scaling of metabolism reflect a byproduct of selection on age and size at maturity?

#### M27

Evolution of thermal reaction norms in ectotherms

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Thermal reaction norms of ectotherm life history traits exhibit a distinctive latitudinal pattern: the physiologically optimal temperature that maximizes performance coincides with the mean habitat temperature in tropical ectotherms but is well above the mean temperature in temperate ectotherms. We predict, using an analysis based on Jensen's inequality, that thermal optima should evolve to temperatures above the habitat mean when seasonal fluctuations are strong

and to coincide with the habitat mean when seasonal fluctuations are weak. We test this prediction by developing an eco-evolutionary dynamics model, which we parameterize with data from tropical, Mediterranean and temperate insect species. We find that the mean reaction norms of the temperate and Mediterranean species do evolve to their expected maxima at temperatures well above the mean habitat temperature, provided seasonal temperature fluctuations are sufficiently strong. In contrast, the tropical species' thermal optimum evolves to its expected maximum near the mean habitat temperature provided seasonal fluctuations are weak. A key finding is the importance of ecological dynamics as a constraint on trait evolution. Our results suggest a potential directionality in invasion success. Tropical ectotherms, because they can adapt to temperate climates without risk of stochastic extinction, are more likely to invade and establish in temperate climates while temperate ectotherms, because they are more susceptible to stochastic extinction, are less likely to establish in tropical climates.

M28

Antagonistic coevolution between quantitative and Mendelian traits

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Previous theoretical studies have considered coevolution between continuous quantitative traits, but recent empirical evidence indicates that many ecologically important traits have discrete Mendelian inheritance. How does a trait's genetic architecture affect coevolutionary dynamics? We modeled antagonistic coevolution mediated by a quantitative predator trait and a Mendelian prey trait, such that prey capture is maximized when predator and prey traits are matched. A complex pattern of bifurcations occurs in a two-dimensional model for trait coevolution. Further, with eco-evolutionary dynamics (so that trait evolution affects predator-prey population dynamics), coevolution can cause varied dynamics including alternate stable states, chaos, and predator extinction, especially when the prey trait exhibits complete dominance rather than semidominance. Increasing heritability of the predator trait promotes rapid adaptation but also can result in predator extinction. Our study illustrates how recognizing the genetic architectures of interacting ecological traits can be essential for understanding eco-evolutionary dynamics in coevolving populations.

M29

Killer whale evolution over the course of the Quaternary

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We used whole nuclear genome sequencing to track the demographic history of killer whales since early in the Pleistocene and find a stable population up to the last glacial maximum, when populations crashed in the North Pacific and North Atlantic, but possibly not off Southern Africa. We use phylogenomics based on 1.7MB sequences to track evolutionary history and biogeography and find evidence for ancestral populations in the Southern Oceans followed by subsequent colonisation of the North Pacific, then the North Atlantic. Based on RAD sequencing and 3500 SNP loci we investigate the differential pattern of structure shown by neutral compared to loci under selection. We find evidence for disruptive selection in sympatry associated with the differentiation of ecotypes, and identify loci with relevant functions in that context. These data suggest a recent radiation and the differentiation of populations by drift and selection, associated with changes in climate and ocean productivity.

M30

Poultry in paradise: evolutionary insight from feral and digital chickens

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Feralization involves a radical shift from artificial to natural selection regimes, and can therefore provide unique insights into evolutionary processes. We recently determined that the wild chickens on Kauai Island (Hawaii) are admixed decedents of both feral domestics and their closest wild relative, the Red Junglefowl. Here we combine genotypic and phenotypic data sampled from both contemporary Kauai flocks and digital media (youtube, google images, etc.) to identify candidate domestication-related (derived) and ancestral traits that experienced selection in the feral environment.

M31

On the correspondence between multivariate micro and macroevolution

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Patterns of covariance between traits across taxa reflect the outcome of past selection and constraint, and so are relevant to hypotheses of adaptation. Typical methods for estimating macroevolutionary covariances, surprisingly, cannot separate recent and rapid multivariate evolution from its historical phylogenetic component, despite the recurring point that evolutionary rates often differ across these timescales. Here I illustrate an approach using multivariate phylogenetic mixed models to compare properties of phylogenetic, macroevolutionary covariance, with recent evolutionary change that is unrelated to shared ancestry. I illustrate the approach by reanalyzing existing data from *Thamnophis* garter snakes, showing phylogenetic divergence is in fact proportional to within species covariance,  $G$ , while residual covariance that is not captured by the historical model instead aligns more closely with the within-species selection surface. In a second example, I show that the evolution of sexual size dimorphism in Ranid frogs is characterized by a shift in the orientation of male and female body size from isometric to allometric, suggesting temporal change in the evolutionary covariance between the sexes has contributed to variation in sexual dimorphism in this family. These results illustrate that temporally partitioning evolutionary variance components provides the potential for further insight into studies linking microevolutionary quantitative genetics and macroevolutionary divergence.

M32

The evolution of mutation rate in an antagonistic co-evolutionary model with maternal transmission of parasites.

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By constantly selecting for novel genotypes, coevolution between hosts and parasites can favour elevated mutation rates. Models of this process typically assume random encounters. However, offspring are often more likely to encounter their mother's parasites. Because parents and offspring are genetically similar, they may be susceptible to the same parasite strains and thus, in hosts, maternal transmission should select for mechanisms that decrease intergenerational genetic

similarity. In parasites, however, maternal transmission should select for genetic similarity. We develop and analyse a model of host and parasite mutation rate evolution when parasites are maternally inherited. In hosts, we find that maternal transmission has two opposing effects. First, it eliminates coevolutionary cycles that previous work shows select for higher mutation. Second, it independently selects for higher mutation rates, because offspring that differ from their mothers are more likely to avoid infection. In parasites, however, the two effects of maternal transmission act in the same direction. As for hosts, maternal transmission eliminates coevolutionary cycles, thereby reducing selection for increased mutation. Unlike for hosts, however, maternal transmission additionally selects against higher mutation by favouring parasite offspring that are the same as their mothers.

M33

Co-evolutionary dynamics of invaders and invaded species in experimental microbial communities

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Co-evolution among native and exotic species may alter invasion potential of exotic species and biotic resistance to invasion, ultimately affecting resilience of invaded ecosystems. Using experimental microcosms, we compared invasion success of invaders into two simple communities of aquatic microorganisms in which invaders and natives had different co-evolutionary histories: 1) experienced invader, experienced natives, 2) experienced invader, naïve natives, 3) naïve invader, naïve natives, 4) naïve invader, experienced natives, 5) uninvaded control. Differing evolutionary histories resulted in significant differences among treatments in abundances of both natives and invaders. Naïve invaders in communities with experienced natives had the lowest invasion success, but abundances of native species differed significantly from uninvaded controls indicating that the invader still influenced community dynamics. Experienced invaders in naïve communities did not uniformly out-compete naïve invaders in comparable communities, lending support to the idea that some exotic species may evolve to become less invasive over time.

M34

Coevolutionary networks in metacommunities

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Species form entangled webs of interspecific interactions, in which ecological and evolutionary processes are interdependent. While the “eco-evolutionary feedbacks” viewpoint is reorganizing our understanding of how ecological and evolutionary processes interdependently structure contemporary dynamics, our knowledge still depends largely on findings in simple experimental systems with limited spatial scales. Although the “evolving metacommunity” concept highlights eco-evolutionary feedbacks at metacommunity scales, we still know little about the mechanisms by which spatially-structured coevolutionary processes drive the ecological dynamics of species-rich systems. By compiling high-throughput sequencing datasets of hyper-species-rich interaction webs, I discuss how integrated perspectives on ecological and coevolutionary networks will fuel the empirical studies of metacommunity-scale eco-evolutionary feedbacks, especially in field systems with hundreds or thousands of species.

M35

Inferring population structure across space and time

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Population genetic structure can be continuous, the result of isolation by distance or drift acting through time, or more discrete, the result of population replacement, or geographic, physical, or behavioral barriers to gene flow between populations. The continuous decay of relatedness with temporal and geographic distance is a natural null model against which hypotheses of more discrete population structure can be tested. Here, we present a method in which we model the decay of relatedness within a population as a continuous function of isolation across space and through time, and capture more discrete structure by allowing sampled individuals to choose membership across multiple populations. This model explicitly addresses the “clines vs. clusters” problem in quantifying population structure by jointly accommodating both continual and discrete patterns of differentiation. We demonstrate the utility of this approach using a combination of ancient and modern human individuals sampled throughout Europe.

M36

Asymptomatic transmission and the resurgence of whooping cough

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Infectious disease outbreaks recapitulate ecology, emerging from the multi-level interaction of hosts, pathogens, and environments. An example of this process is the global return of whooping cough. Three main hypotheses have been proposed to explain the resurgence: 1) waning of protective immunity from vaccination or natural infection over time, 2) evolution of the pertussis bacteria to escape protective immunity, and 3) low vaccine coverage. Recent studies have suggested a fourth mechanism: asymptomatic transmission from individuals vaccinated with the currently-used acellular vaccines. Using wavelet analyses of pertussis incidence in the U.S.A. and U.K. and a phylodynamic analysis of 75 *Bordetella pertussis* genomes, we find evidence in support of asymptomatic transmission. Next, we examine the ecological and epidemiological consequences of asymptomatic transmission using a mathematical model. With this model, we find that: asymptomatic infections can bias assessments of vaccine efficacy and asymptomatic transmission can account for the observed whooping cough dynamics.

M37

When do predators increase or decrease disease? An examination of variation using models and field surveys.

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Predators can strongly influence epidemics in their host populations. Predators can reduce disease by removing infected hosts and reducing host density. However, predators can also increase disease through various mechanisms including trophic cascades and ‘sloppy’ predation that spreads infective propagules in the environment. Here, we demonstrate that predators that preferentially kill juveniles can spread disease that targets adults. Mathematical models demonstrate that the underlying mechanisms involve resource competition between juveniles and adults (a common phenomenon in many natural systems). Predation on juveniles reduces resource competition between juveniles and adults. The subsequent increase in resources, allows adults to grow larger, and

produce more infective propagules — a key determinant of epidemic size. Together, these mechanisms help explain how predators can increase infection prevalent, despite an overall decrease in host density.

M38

Dead Ant Walking: A beetle predator benefits ants by preferentially consuming parasitized individuals.

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Beetle-ant associations are well documented but the dynamics of these interactions are poorly understood. Here, we examine these interactions between the beetle *Myrmedonota xipe* and their ant associate *Azteca sericeasur* to determine how these interactions impact phorid fly parasitism of the ants. We used pheromone assays with gland extracts and synthetic compounds coupled with gas chromatography/ mass spectrometry to show that *M. xipe* first locate ants using their alarm pheromone. Subsequent choice experiments between parasitized and non-parasitized ants show that beetles prefer to attack parasitized ants, consuming approximately 14% of these ants in nature. Behavioral assays show parasitized ants are less aggressive than healthy ants, which may ultimately facilitate beetle predation on parasitized individuals. Our results indicate that, although beetles are predators of the ants, by preying primarily on ants harboring phorid fly eggs, the beetles may also provide indirect positive effects for the ant colonies as a whole.

M39

Ecological Correlates of Positive Selection in Bat Viral Interaction Genes

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Bats seem to have a special ability to act as reservoirs of viruses, leading to broad speculation and empirical support for the idea that bats have “special” immune systems. Aspects of bat ecology including diet, gregariousness and the number of sympatric species affect the numbers of viruses they host and share. Using nine publicly available bat genomes, we look in an unbiased manner for evidence of an excess of positive selection in genes that interact with viruses by comparing them to genes not known to interact with viruses. Further, we examine whether the same ecological traits that enhance viral prevalence are associated with greater immune selection. We find strong evidence for an excess of adaptation in 700 genes for viral interacting proteins in bats compared with other genes, suggesting bats are indeed under strong selective pressure to adapt to viruses.

M40

The evolutionary ecology of sticklebacks' parasite metacommunity: effects of abiotic environment, host ecology, and host immunity

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Metacommunity ecology aims to understand how spatially structured communities arise from a combination of dispersal, species interactions, and abiotic environmental filters. Parasite communities add one extra layer of complexity, because the parasites' environment (their host(s)) itself evolves in response to the parasites and its own environment. Parasite communities can

therefore be structured by abiotic conditions, or host ecology, or host immunity, as well as their own dispersal capacity. We sampled parasite communities from a stickleback metapopulation (73 lake, stream, and ocean sites on Vancouver Island), to evaluate how habitat, host diet, and host genotype influence parasite community composition.

#### M41

Small scale pain for large scale gain: parasite competition and the maintenance of biodiversity

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Almost all natural populations are infected by multiple parasitic species, many of which have strong effects on host population dynamics. Therefore, we are interested in what explains parasites species richness in host populations. Parasite meta-communities contain unique structuring mechanisms, such as post-infection immunity and feedbacks between parasite meta-community structures and patch dynamics, which create unique coexistence mechanisms that do not exist in non-parasite communities. Because parasites which spread through populations too quickly may burn themselves out via accumulation of resistant hosts or reducing host population densities, competition between parasites may slow down pathogen spread and lead to an increase of species richness. On the other hand, at high levels of competition between parasites, post-infection immunity can create refuges from parasite competition. Therefore, interactions which are negative on the within host scale can translate to increased species richness on the host population scale.

#### M42

Parasite mediated sexual selection and speciation in the barn swallow species complex

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Many populations are distinguished by sexual traits, yet little is known about how sexual traits diverge and influence speciation. Parasites have been associated with sexual traits in single populations, but it remains unclear how parasites drive sexual trait divergence. To test hypotheses about whether and how female mate choice selects for parasite-mediated advertisement in males, we study a group of closely related populations characterized by sexual trait divergence: the barn swallow species complex. Our comparative work reveals that parasite communities vary across populations and that sexual traits signal information about the most costly parasite. Male color in North America and tail streamers in Europe both correlate with nest mites in a male's territory. These mites are costly as they impact nestling survival, growth, and future sexual trait expression. We are currently analyzing data on parasite-mediated signaling in a subspecies where females use both streamers and color for mate choice.

#### M43

Past and current temperature regulate transmission in a zooplankton-fungus disease system

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Temperature is often important for regulating disease transmission. In our *Daphnia* zooplankton-fungal disease system, epidemics begin in summer and end in winter; infectious spores are continually added to the environment while temperature changes over time. Thus, we were interested in how past temperature (a "maternal" effect of spore rearing) interacts with current

temperature to influence transmission. We conducted an assay manipulating the past rearing temperature of spores and the current temperature for host exposure and infection development. A second assay measured the effect of temperature on host foraging rate (spore contact, as hosts encounter spores while filtering water for food). We then built a model that breaks transmission into three components: host foraging rate, dependent on current temperature, and per spore infectivity, dependent on both past and current temperature. Our mechanistic model was able to accurately capture patterns in the infection data that initially appeared to be idiosyncratic or noise.

### T1 (change in program)

How much diversity harbor the mountains? The importance of highlands in the latitudinal gradient of diversity

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Among the most diverse areas in the world, the mountains, and specifically the tropical mountains, highlight within of the major biodiversity hotspots. In this work, we quantified the contribution of mountains to the global biodiversity of birds and evaluate how they influence the latitudinal gradient of species richness. We found that the mountains harbour a third of the world's bird diversity. However, once we correct by effective area, the mountains harbour up to four times more diversity than lowlands. When we evaluated the latitudinal gradient of diversity discriminating among highlands and lowlands, we found that the pattern is significantly stronger in mountains than in lowlands when the area is taken into account. These results reveal a pattern not quantified until now: the strong effect of area in the latitudinal gradient of species richness and the major contribution of mountains in this pattern.

### T2

A Genomic Analysis of Hybridization and Selection During Speciation in Benthic and Limnetic Threespine Stickleback (*Gasterosteus aculeatus*)

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Determining the genetic basis of adaptation and reproductive isolation is a major goal of contemporary speciation research. Benthic and limnetic threespine stickleback provide a powerful system to examine the dynamics of selection during speciation with gene flow. To do this, we have collected samples at multiple time points from two lakes containing benthics and limnetics and used genotyping-by-sequencing methods to survey allele frequencies across the genome. We find that there is ongoing hybridization between benthic and limnetic stickleback in the wild and infer selection against certain hybrid classes. We use patterns of ancestry and changes in allele frequency to identify regions of the genome that are resistant to gene flow and likely to be important for maintaining reproductive isolation. Together these analyses give us insight into the mechanisms involved in speciation with gene flow, allowing us to examine the balance between natural selection and hybridization.

### T3

Ecological and evolutionary consequences of divergence and hybridization in Swiss sticklebacks

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We investigated feedbacks between ecology and evolution in the contemporary range expansion and hybridization of two lineages of threespine sticklebacks in Switzerland. In a large scale mesocosm experiment, both the density and evolutionary origin of sticklebacks had distinct effects on ecosystem dynamics, resulting in divergent macrophyte structure and prey availability. These ecological differences had demographic consequences, affecting the total survival of juveniles in the next generation. In addition, across all ecological conditions we found strong and consistent differences in the composition and condition of surviving juveniles, both between the two lineages,

and between the lineages and F1 hybrids. Complementary assays of feeding efficiency, armor, growth rates, and energy reserves point to genetic differences in physiological condition determining relative success regardless of ecological context. However, this differential success was amplified under low total survival, suggesting a potential feedback between evolution and ecology in the magnitude rather than direction of selection.

#### T4

Whenceforth hast thou multiplied? Inferring diversification dynamics from phylogenies

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Ascertaining the eco-evolutionary dynamics that have led to present day patterns of diversity and distribution is inherently challenging. A number of sophisticated phylogenetic approaches have been developed in recent years that infer the tempo of diversification from phylogenetic structure, and estimate the relative fit of a variety of diversification scenarios involving time-constant or time-variable rates. Here, I evaluate the ability of several such approaches to diagnostically assess the true underlying process generating spatial and phylogenetic diversity patterns arising from an eco-evolutionary simulation model.

#### T5

The influence of mating system on mechanisms of reproductive isolation in a Phlox species complex

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Speciation involves the buildup of reproductively isolating barriers among lineages. For many species in which prezygotic reproductive isolation is incomplete, the origins and extent of postzygotic reproductive isolation remain unclear. In plants, for example, the relative importance of hybrid inviability versus and hybrid sterility has not been well established, and may depend partly on mating system. To address these issues we investigated four components of pre and post zygotic reproductive isolation for two self-incompatible and one self-compatible Texas Phlox species. We determined how flowering phenology differed among parental species and F1 hybrids, how seed set differed between inter and intraspecific crosses, and we characterized hybrid viability, and hybrid sterility. First, we found that flowering phenology differed among hybrids and parental species.

Second, seed set from interspecific crosses was lowest for self-incompatible crossed to self-compatible species, which is consistent with the SI x SC rule predicting that SI species will reject heterospecific pollen but SC species will not. Third, hybrid viability was lower than that of plants from control intraspecific crosses. Fourth, hybrid sterility was higher for hybrids in which the maternal plant was self-incompatible. These results reveal that both pre and postzygotic reproductive isolation maintain species boundaries and that mating system may influence the extent to which reproductive incompatibilities prevent gene flow among these Phlox species.

#### T6

Ecogeographic gradients in plumage coloration among Australasian honeyeaters and warblers

(Meliphagidae, Acanthizidae)

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Animal coloration shows high degrees of evolutionary lability, producing variation among species that is easily apparent. This variation may produce consistent geographic patterns as species converge on adaptive phenotypes in similar environments. Geographic patterns like Gloger's Rule and a colloquial latitudinal gradient in ornamentation demand explanation and empirical testing. Here, we compare plumage coloration across two families of Australian birds in a combined spatial and phylogenetic framework. We found several strong effects of environment on plumage coloration. Gloger's Rule was supported in both clades, but more strongly for dorsal plumage.

Meliphagid species in regions with more vegetation had markedly darker plumage. These observations support the role of countershading and background matching in maintaining Gloger's Rule. Inland species inhabiting seasonal environments showed greater color span among Acanthizids, and greater saturation among Meliphagids. This may suggest that species respond to the shorter breeding periods of seasonal environments by evolving increased ornamentation.

T7

Evolving reproductive isolation along the speciation continuum in sticklebacks  
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To understand the process of speciation, we study how reproductive isolation evolves across the speciation continuum. We estimate multiple reproductive  $\square$  barriers in five sets of stickleback species pairs spanning the speciation continuum, considering species pairs with little to extensive divergence, including a recently collapsed pair. We infer the order of barrier evolution and the importance of specific selective mechanisms. We show that premating isolation evolves before postmating isolation, and that habitat and sexual isolation are particularly common and strong. In contrast, postmating barriers are typically weaker, more variable, and evolve later. Sexual isolation is key to evolution along the speciation continuum, contributing to how quickly populations diverge into distinct species or dissolve into a single hybridizing population. We also find that extrinsic, ecologically-based isolation is far stronger than intrinsic isolation. Our work suggests that the preoccupation with intrinsic postmating isolation in speciation genetics research is misplaced, given that it likely evolves after speciation is nearly complete.

T8

Plumage color in barn swallows: using comparative quantitative genetics to understand phenotypic divergence  
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A goal of evolutionary research is to understand phenotypic variation. For most traits, sources of variation can be partitioned into genetic or environmental. Identifying the proportion of variance due to these components allows us to make predictions regarding responses to variable environments and selection. Across barn swallow subspecies aspects of phenotype have diverged; evidence also suggests that female preferences have similarly diverged. We examine quantitative genetics of plumage color in three populations of barn swallows: North America, Europe, and Israel. In North America, females prefer dark males while in Europe, females prefer males with long tail streamers; in Israel, females assess both traits preferring dark males with long streamers. In all populations, we find that coloration is explained by a combination of genetic and environmental

variation. We use comparative quantitative genetics to explore divergence in the additive genetic covariance structure for color to better understand divergence among recently diverged subspecies.

T9

What are species pools and when are they important?

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A regional species pool comprises all species available to colonize a focal site. The pool concept allows ecologists to examine large-scale effects—including geographic area, evolutionary age, and immigration and diversification on community structure. Pool influences are greatest when local communities are not strongly structured by species interactions. Issues to consider when delineating species pools include choosing an appropriate spatial scale, whether to account for environmental filtering, whether to include species within a fixed geographic area versus those whose geographic ranges overlap with a site, or whether to use databases or geographic data sources. Each issue is discussed in the context of 63 studies using the species pool approach. The species pool concept has contributed greatly to our understanding of community dynamics by bridging the gap between large and small spatial scales. Future studies must compare pool characteristics with community structure across multiple regions for a more complete understanding of community assembly.

T10

Intraspecific variation in skin-associated microbial communities of the yellow-eyed *Ensatina* salamander (*Ensatina eschscholtzii xanthoptica*)

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The study of the amphibian microbiome is a rapidly growing field, yet little research to date has characterized variation within a host species. We sampled individuals from disjointed populations within the salamander subspecies *Ensatina eschscholtzii xanthoptica*, a group with a complex phylogenetic substructure distributed throughout the San Francisco Bay Area and the Sierra Nevada mountains. Within a population, we found that microbial communities of different sexes and life stages were indistinguishable. Across populations, we found that most abundant bacterial taxa tended to be present across all salamander populations, while some rare taxa were limited to one or two populations. Interestingly, the patterns of variation in microbiota we observed do not reflect host phylogeny or distribution. Continued work with *Ensatina eschscholtzii* and other amphibians will lead to a better understanding of processes determining microbial community assemblage, and how these communities affect host health, development, and behavior.

T11

Environmental geometry and ecological range limits can drive nuanced and realistic biodiversity gradients

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Latitudinal and elevational biodiversity gradients fascinate biologists, as this meeting's program attests. Some have suggested that the geometry of environmental variation may promote species-richness gradients, although a mathematical model has yet to appear that fully captures this

hypothesis. This talk introduces such a model. This model characterizes species ranges by their environmental niches and dispersal limits, and places those ranges onto the simplified environmental geometries. The model generates surprising and nuanced predictions for species-richness gradients, including low-latitude plateaus and mid-latitude inflection points in latitudinal diversity gradients, and a low-elevation maximum in elevational diversity gradients. These features are found in multiple empirical biodiversity gradients, depend on the ecological traits of taxa being considered, and have eluded previous geometric hypotheses. These results suggest that environmental geometry may play a deeper role in driving biodiversity gradients than previously appreciated.

#### T12

A test of the biotic interactions hypothesis to explain the latitudinal diversity gradient: greater herbivore pressure at lower latitudes in a wide-ranging native plant

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The processes that generate the latitudinal diversity gradient are poorly understood. The “biotic interactions hypothesis” states that there is a latitudinal gradient in the relative importance of biotic and abiotic factors as drivers of adaptation. Greater importance of biotic interactions at lower latitudes could lead to higher diversification rates due to coevolution. There is support for greater prevalence of mutualisms in the tropics, but evidence is mixed for the importance of antagonisms. We tested whether insect herbivore pressure is greater at lower latitudes along a gradient from 27°N (central Florida) to 42°N (southern Michigan) in pokeweed (*Phytolacca americana*), a native, herbaceous, perennial pioneer species. In 2014, herbivory rates on young leaves were higher in three southern populations than two northern populations. Ongoing data collection for 2015 includes ten sites and measurements of plant defense. Preliminary observations are consistent with results from 2014, and suggest that herbivore abundance may drive herbivory.

#### T13

Temporal dynamics of biodiversity

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Historically, scientists have focused on spatial variation in biodiversity, but surprisingly little is known about how biodiversity varies across time. Here we show that temporal variation in species composition of odonate communities often exceeds spatial variation across sites, indicating that a significant but currently neglected component of biodiversity is “hidden” in time. Furthermore, we found that temporal changes in biodiversity are strongly determined by habitat type and differ among habitat types. Habitats with deterministic environmental filters showed dramatic but consistent seasonal turnover in species composition within sites, and partitioned a greater proportion of their biodiversity across time. In contrast habitats with more stochastic filters showed inconsistent changes in species composition across time, and consequently harbored a greater proportion of their biodiversity across sites. These findings shed new light into the fundamental processes that drive biodiversity patterns and emphasize the need to take a temporally explicit approach to study and manage biodiversity.

#### T14

Environmental optimality, not heterogeneity, drives regional and local species richness in lichen epiphytes  
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We evaluate the scale-dependence of species richness-environment relationships with a continent-wide analysis of lichen epiphyte communities. Our goals are to assess 1) the dependence of local richness on regional processes, 2) whether species richness is primarily influenced by heterogeneity in environmental conditions or the central tendency of those conditions, and 3) whether the relative influence of these different aspects of the environment differs between local communities and regional species pools. We used variation partitioning and model averaging to relate macrolichen richness to measures of environmental heterogeneity and mean conditions at local and regional scales. Species richness of epiphytic macrolichens across the U.S. is not regulated by environmental heterogeneity locally or regionally and instead tracks large-scale climate gradients of moisture and temperature. Richness in local communities is influenced by processes operating at both regional and local scales, highlighting the importance of determining large-scale drivers of lichen richness across North America.

T15

Reconciling the effects of time, area, and energy on geographic gradients in species richness

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The absolute and relative importance of different causes behind the latitudinal gradient in species richness remain contested. Advances in the completeness and quality of phylogenetic, environmental, and species distribution information, and increased appreciation of the scale-dependence of different processes have led to significant progress. Specifically, empirical and conceptual progress is enabling a more explicitly multi-causal, hierarchical, and macroevolutionary perspective. I will present recent work on terrestrial vertebrates that attempts to take an integrative approach to compare multiple predictors of regional variation in species richness and gauge the importance of energy availability on broad-scale species coexistence.

T16

Recent trends in local-scale marine biodiversity reflect community structure and human impacts

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Reconciling the threat of global biodiversity loss with recent evidence of stability at fine spatial scales is a major challenge and requires a nuanced approach to biodiversity change that integrates ecological understanding. With a new dataset of 471 diversity time series spanning from 1962 to 2015 from marine coastal ecosystems, we tested (1) whether biodiversity changed at local scales in recent decades, and (2) whether we can ignore ecological context (e.g., proximate human impacts, trophic level, spatial scale) and still make informative inferences regarding local change. We detected a predominant signal of increasing species richness in coastal systems since 1962 in our dataset, though net species loss was associated with localized effects of anthropogenic impacts. Our results are consistent with local species loss in areas with direct human impacts and increases in diversity due to invasions and range expansions in lower impact areas.

T17

Root foraging is not genetically correlated with mutualism stabilizing traits in the model legume  
*Medicago truncatula*  
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Mutualisms, or net beneficial interactions among species, are widespread in nature. However, theory predicts that mutualisms should be inherently instable, because selection should favour “cheaters”, or individuals that increase their own fitness at the expense of their host. Host traits such as sanctions and partner choice are proposed to maintain selection for cooperation, because they increase the fitness of cooperators relative to cheaters. Yet, the underlying physiological and genetic mechanisms governing these traits remain largely unknown. Here, we used 35 genetic lines of the model legume *Medicago truncatula* to determine whether partner choice and sanctions were correlated with root foraging, a trait in which roots can sense nitrogen in the soil and proliferate into patches of higher N concentration. We found a lack of genetic correlation between root foraging and the two mutualism-stabilizing traits, suggesting that the underlying mechanisms are different, and that selection acts independently on each trait.

T18

Seed dispersal characteristics of a native and invasive ant alter the spatial patterns of seedling recruitment and survival  
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Species often vary in the quality of mutualistic service they provide to partners. In myrmecochory, or seed dispersal by ants, both plants and ants can interact with an array of partners of potentially differing quality. We examined how seed dispersal by a native (*Aphaenogaster rudis*) and an invasive ant (*Myrmica rubra*) differs in mesocosm communities containing native and invasive plants. We analyzed the distance from seedlings to adult plants, the nearest ant nests, as well as other seedlings to determine what spatial scale matters for seedling survival and fitness. The location where ants deposit seeds determines not only where, but whether seedlings will germinate and how competition from other plants reduces survival and fitness. As invasive species are becoming more common, species are increasingly likely to interact with native and invasive partners; understanding how dispersal quality of these ants differs, provides vital information on the changing spatial structure of plant communities.

T19

Host Sanctions in the Legume-Rhizobium Symbiosis: A New Avenue of Research  
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Leguminous host sanctions are vital to prevent the proliferation of non-beneficial symbionts. The *Lotus japonicus*-*Mesorhizobium loti* model system has been underutilized to study this mechanism of host control. *L. japonicus* grown in growth pouches were singly inoculated with three isogenic strains of *M. loti*: nifD::Tn5-GFP (non-fixing), gsi::TN5-GFP (mediocre fixing), and dsRed wild type. At five weeks post infection, plants infected by the wild type had the greatest number of true leaves, followed by the mediocre strain, then the non-fixing strain. Light and electron microscopy reveal variation in nodule structure consistent with plant fitness data – strains providing

less benefit show evidence of premature nodule senescence. These results are a great example of how this model system is useful to study host control in legumes. Coupled with the use of fluorescently labeled symbionts and coinoculation experiments, we will add evidence to the theory that sanctions occurs at the sub-nodule level.

#### T20

Pollinator sharing and heterospecific pollen deposition when two plant populations intergrade  
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If two plant species share pollinators, the interface between their populations may be a site of complex interactions. We expect some balance of competition and facilitation for pollinator visits, depending on how pollinator foraging decisions depend on floral rewards and spatial distribution. The effects of visitation rates on reproductive success will be affected further by heterospecific pollen transfer, which will have different effects on male and female reproductive success. Because these processes are difficult to study in nature, we studied arrays of artificial flowers that donate and receive powdered dyes—as pollen analogues—as they are visited by bumble bees in flight cages. One species was more rewarding than the other. The more rewarding species received more dye per stigma, but its stigma loads were less pure. The poorer species tended to receive more dye in proximity to the richer species, indicating a magnet effect, but these effects were inconsistent.

#### T21

Experimental manipulation of flowering phenology alters pollination success in a bumblebee-pollinated species  
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Warmer springs and earlier snowmelt associated with climate change are altering the timing of plant reproduction and pollinator emergence (i.e. phenology). Changes in flowering time may affect both resource availability and pollination success, particularly among early or late flowering individuals. In order to determine the extent to which flowering time impacts plant reproduction, we manipulated flowering phenology of the subalpine perennial, *Mertensia ciliata* (Boraginaceae). Declining pollinator visitation rates suggest pollen limitation may increase throughout the season; however, this pattern was not reflected in seed set. Combining these data with estimates of pollen receipt, as measured from the collected stigmas, as well as, measures of seed mass will help clarify the extent to which pollen limitation or resource limitation varies with flowering phenology. This work provides valuable insight into the mechanisms that influence how temporal shifts in phenology may impact plant and pollinator populations in the face of climate change.

#### T22

Single measures of phenology may not accurately predict phenological shifts  
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Phenological shifts disrupt ecosystems by changing the timing and strength of species interactions. Most phenology research identifies phenological shifts by changes in a single metric

(e.g., mean, first), but since individuals vary in timing, single metrics may be uninformative at the population level (i.e., first and mean phenological event do not shift uniformly). Therefore, in order to assess effects of phenological shifts on biological interactions, it is important to consider the distribution of phenological timing among a population. Analysis of high resolution phenological data for multiple systems was used to see how well shifts in single metrics of phenology for two interacting species could predict shift in the timing and strength of their overlap. Results show that population level phenological distributions do not change uniformly and therefore single metrics could not predict changes in species overlap. This indicates that single metrics of phenology are inadequate for identifying biologically meaningful phenological shifts and predicting net outcomes.

T23

Genomic signatures of mutualistic and competitive interactions

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Genome specialization is a key consequence of adaptation. Gene loss and genome reduction are typical of obligate mutualism. The genome of a novel scale insect obligate endosymbiont identified enrichment of genes beneficial for the host concurrent with significant loss of genes associated with survival outside the protective and nutritive host tissue. Genetic specialization in a competitive and harsh environment such as floral nectar, however, exhibits a contrasting pattern. Specialization in osmotolerance and amino acid transport pathways is observed in the genome of nectar yeast, *Metschnikovia reukaufii*. This is further supported by evidence from the physiology of this dominant yeast, which outcompetes other yeasts under high osmotic stress and low nitrogen conditions. We also found evidence of niche specialization between *M. reukaufii* and its competitors, reflecting its competitive strategy.

T24

The interplay between pollination and herbivory: insights from a hawkmoth mutualism in the Sonoran Desert

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Mutualisms in nature are beset by antagonism, yet we still do not have a strong understanding of how the interplay between mutualism and antagonism shapes the evolution and ecology of mutualism. Pollination-herbivory interactions are particularly interesting because mutualism and antagonism are intrinsically linked via insect ontogeny. Indeed, new evidence suggests that many Lepidoptera include their host plant as a nectar source. Here, we develop mathematical models of pollination-herbivory interactions, which are motivated and informed by an empirical study system involving the Carolina hawkmoth (*Manduca sexta*) and its host plants in the Sonoran Desert. Models predict that plant-insect dynamics arise via the interplay between mutualism and herbivory, modulated by indirect interactions between plant species and with alternative larval and adult resources. This work provides a theoretical framework for investigating how mutualism persists in the face of antagonism as well as the evolution of mutualism from antagonism.

T25

Stress response, gut microbial diversity, and sexual signals correlate with social interactions: A social network study in North American barn swallows

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Social network analysis is emerging as a promising tool for integrating behavior, phenotype, and physiology with relational data on animal interactions. We used proximity loggers to quantify interactions in a population of barn swallows (*Hirundo rustica erythrogaster*). Social networks were constructed from interactions at two different scales of spatial proximity, one consisting of all interactions between 5m and 0.1m (“social network”) and the other based on all interactions within 0.1m (“contact network”). We used node-level analyses to ask what phenotypic and physiological traits correlate with individual network position and dyad-level analyses to understand the traits of individuals engaging in interactions. Males with dark ventral plumage, long tail streamers, and higher stress-induced corticosterone levels had more interactions with females in the social network. Interactivity in the contact network was positively related to stress-induced corticosterone levels for both sexes; however, there were sex differences in relationships between gut microbial diversity and interactivity.

T26

Group navigation in the face of obstacles during cooperative transport

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During cooperative transport, groups must form a consensus about travel direction, which is especially difficult when facing obstacles. We studied obstacle navigation in *Paratrechina longicornis*, to see whether they use a simple strategy or a more reliable, but complex, strategy. Simple navigation strategies require little information, but some obstacles cannot be navigated this way. We blocked transport teams with easy and challenging obstacles. Challenging obstacles were designed to thwart the simplest strategies. We found that the obstacle-navigation strategy of *P. longicornis* is flexible. Initially, ants employ a simple strategy that will work for easy obstacles; if that fails, they switch to a strategy that is time-intensive, but always successful. This more complex strategy involved moving larger and larger distances away from their goal over time, which allowed them to more thoroughly explore the space. Groups navigated easy obstacles more quickly, but even with the challenging obstacles, they always succeeded.

T27

Matching movement patterns to mating patterns in the lizard, *Anolis sagrei*

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Animal mating systems have traditionally been classified behaviorally, based on observations of the locations and interactions of males and females. However, growing molecular evidence demonstrates that behavioral characterizations of social interactions do not necessarily describe actual mating patterns. Such a mismatch is found in the lizard *Anolis sagrei*—males are thought of as territorial and polygynous, but all genetic evidence points to extensive multiple mating by females. We revisit the movement patterns of *A. sagrei* to investigate if departures from territoriality can explain female multiple mating. By permanently marking and observing the locations of a population of lizards for three months, we show that male *A. sagrei* often depart from territorial behavior,

resulting in females encountering a median of 3 males, and as many as 15 males, during the sampling period. We propose that the mating system of *Anolis* lizards be re-evaluated, and suggest ways to structure such a re-evaluation.

T28

The nature of sperm competition in a broadcast spawning invertebrate; how gamete mixing influences female choice, sexual conflict and the evolution of gamete recognition systems

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In many taxa sperm and eggs are released into the environment and mediate mating success. Although multiple paternity is rampant, it is unknown if sperm directly compete for the fertilization of individual eggs. The distinction between direct and indirect competition for fertilizations is critical for whether males and females have aligned interests or are in sexual conflict. I examined the prevalence of direct vs indirect competition for eggs over a range of spawning conditions in the sea urchin *Strongylocentrotus franciscanus* and find that under symmetrically crowded conditions sperm can directly compete for fertilizations, but with increasing asymmetries in the distribution of individuals, indirect competition is more prominent. These conditions of abundant sperm indirectly competing for fertilizations can lead to more rapid evolution of reproductive incompatibility, but less effective reproductive isolation via conspecific sperm precedence.

T29

Comparing latitudinal patterns of reproductive plasticity between a native and exotic coastline in the sea anemone *Diadumene lineata*

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The east coasts of the United States and Japan have similar latitudinal distributions of climate and oceanographic conditions, which may help explain the success of Japanese exotic species in American waters. The Japanese sea anemone *Diadumene lineata* has become the most widespread anemone in the world through anthropogenic transport and reproductive flexibility that includes an array of size dependent sexual and asexual modes. A survey of the morphological, reproductive and genetic diversity spanning more than 10o latitude on its native Japanese and invaded American east coast reveals that these anemones are doing very different things under similar conditions in different places. The complex interaction among invasion history, genetic variation and reproductive plasticity demonstrated in this system suggests that models of invasion that do not account for genetic and phenotypic differences between native and invaded populations might fail to capture important demographic shifts as species move from one coast to another.

T30

Persistent directional selection on body size, bad parenting, and the paradox of stasis

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Directional selection on body size is common but often fails to result in microevolution. Similarly, rates of macroevolution in size are too low to match the strength of selection in contemporary populations. We help resolve this paradox by demonstrating that many estimates of selection used to predict evolutionary response have been measured on juvenile size. Parents influence juvenile size through a trade-off with fecundity, and this results in juvenile sizes that do not maximize juvenile fitness. Persistent upward selection on juvenile size is therefore expected. Formally accounting for ontogeny in meta-analyses of selection reveals that directional selection on juvenile size is strong, but for adults selection is stabilizing. Furthermore, our hypothesis predicts that when parental influences on size persist into adulthood, the evolution of adult size is constrained. We explore this prediction by comparing scaling patterns of adult and juvenile size among vertebrate groups with different modes of reproduction.

T31

Mate choice learning behavior in male *Drosophila melanogaster*  
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Learned behavior is widespread, and found in all branches of the animal kingdom. It shapes behavior in many contexts, such as food finding, nest building, mate finding and predator avoidance. These behaviors each affect the chances an individual survives and successfully reproduces, and therefore significantly influence evolution. The extent to which learned behavior is important to evolution is in part determined by how much or how readily individuals learn, and how heritable this behavior is. Using learning in a mate choice context, we explore this question with *D. melanogaster*. We show that males can learn to associate female mating status, and receptivity to male courtship & mating, with an arbitrary visual trait. We then test the heritability of this learning behavior using a father-son regression.

T32

Ecological divergence, adaptive diversification and the evolution of social signaling traits: An empirical study in arid Australian lizards  
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Divergent evolution of ecological or social signaling traits together may theoretically promote speciation. However empirical examples studying how these two forces combine are rare, and typically don't consider range overlap as a contributing factor. We show that Australian sand dragons with highly variable ecologically relevant and social signaling phenotypic traits have repeatedly and independently invaded distinct niches, driving convergent phenotypic evolution as arid habitats expanded and differentiated. Striking variation in visual social signaling traits is better explained by the extent of lineage parapatry relative to ecology or phylogeny, suggesting these traits reinforce divergence among lineages initiated by ecologically adaptive evolution. This study provides a rare empirical example of a repeated, intricate relationship between ecological and social signal evolution during diversification driven by ecological divergence and the evolution of new habitats and supports emergent theories regarding the importance of ecological and social trait evolution throughout speciation.

T33

Factors influence selection in theory, stickleback, guppies, and finches

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Selection is the primary driver of evolutionary divergence, yet it can be hard to detect in the wild. I will integrate theoretic simulations with empirical data from stickleback, guppies, Darwin's finches, and lemon sharks to illustrate surprising and revealing aspects of how selection works in natural populations. Of particular emphasis will be the degree of adaptation, the strength of gene flow, the structure of temporal and temporal variation, and the link between genotype and phenotype.

T34

Local adaptation in transgenerational responses to predators

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Environmental signals can induce phenotypic changes that span multiple generations. Along with phenotypic responses that occur during development (i.e., 'within-generation' plasticity), such 'transgenerational plasticity' (TGP) has been documented in a diverse array of taxa spanning many environmental perturbations. New theory predicts that temporal stability is a key driver of the evolution of TGP. We tested this prediction using natural populations of zooplankton from lakes in Connecticut that span a large gradient in the temporal dynamics of predator-induced mortality. We reared >120 clones of *Daphnia ambigua* from 9 lakes for multiple generations in the presence/absence of predator cues. We found that predictable variation in mortality selects for within-generation plasticity while consistently strong (or weak) mortality selects for increased transgenerational plasticity. Such results provide the first evidence for local adaptation in TGP and argue that divergent ecological conditions select for phenotypic responses within and across generations.

T35

Can plants adapt to urban environments?

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Urban areas dramatically alter the biotic and abiotic environment but whether organisms can adapt to these changes is poorly understood. We examined whether white clover (*Trifolium repens*), which exhibits a Mendelian polymorphism in the production of hydrogen cyanide, exhibits adaptive clines in chemical defenses against herbivores along urban to rural gradients in four major cities (Toronto, Montreal, Boston, New York). Genotyping and phenotyping ~300 plant populations showed that *T. repens* evolved to be more chemically defended in rural environments and less defended in urban environments. Forty experimental gardens along an urban to rural gradient in Toronto showed that herbivore damage is consistently higher in rural areas, which favors cyanogenic genotypes. By contrast, the cost of producing hydrogen cyanide combined with more variable herbivore attack favors acyanogenic plants in cities. This study shows that plants have the capacity to rapidly adapt to anthropogenic changes associated with city environments over relatively short spatial scales.

T36

Assessing local adaptation in an endemic, montane salamander threatened by climate change

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Faced with climate change, organisms either adapt in place or move—or they go extinct. Relative to dispersal, adaptive responses remain poorly understood. Fortunately, the recent development of techniques for detecting adaptation in wild populations has improved our ability to evaluate this response. We are using landscape genomic data in combination with multivariate statistics to identify spatial patterns and environmental drivers of local adaptation and gene flow in an endemic salamander. *Plethodon welleri* is a terrestrial, range-restricted species of conservation concern in the Southern Appalachian Mountains. Our analyses show significant differentiation in *P. welleri* populations across mountain peaks and within elevation gradients indicating restricted gene flow. Additionally, these populations show a signal of local adaptation at SNP markers potentially under selection based on temperature proxies. These analyses are helping us better understand what management actions will be most effective to conserve the adaptive capacity of *P. welleri* under global change.

T37

Local adaptation of consumers destabilizes food webs  
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Local adaptation is a pervasive process in nature; however, there has been little work examining the consequences of local adaptation for associated ecological communities. Here, we build a mathematical model to predict how local adaptation of a consumer (defined here as habitat and trophic specialization) will affect food-web dynamics. We then compared these predictions to data from a natural system, where a fish consumer (three-spine stickleback) has become locally adapted to different aquatic habitats with different resources (benthic vs. limnetic zones). Our model suggested that increasing the degree of local adaptation results in more oscillatory (destabilizing) consumer-resource dynamics. In support of this prediction, we found that the variability of zooplankton abundance (resource) in lakes with locally adapted sticklebacks was 2-fold higher than lakes without locally adapted sticklebacks. These results suggest that consumer local adaptation has a negative feedback on its persistence in the absence of other processes.

T38

How do niche and fitness differences change due to selection in competition? Experimental evolution in protists.

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Ecologists traditionally emphasize niche differences when explaining species coexistence. However, if niches are similar, minimizing ecological fitness differences can allow coexistence. Selection pressures due to competition could therefore result in changes in niches or ecological fitness of species, thereby changing competitive outcomes. However, the interactions between the evolution of niche and fitness are not well understood. I used a response surface design to estimate niche and fitness differences between pairs of protists in the lab. Then, after approximately 50 generations of growth in competition, I redetermine the niche and fitness differences to quantify evolutionary changes. Theory predicts that species will increase niche differences and decrease fitness differences. Preliminary results suggest that this is not always the case, with convergence in

both niche and fitness differences observed. This work suggests that niche and fitness factors can both evolve in response to selection in competition, and may evolve somewhat independently.

T39

Intraspecific leaf chemistry drives locally accelerated ecosystem function in aquatic and terrestrial communities

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Resource patchiness influences consumer foraging, movement, and physiology. Fluxes across ecosystem boundaries can extend these effects to otherwise distinct food webs. Intraspecific diversity of these cross-ecosystem subsidies can have large consequences for recipient systems. We found intraspecific variation in leaf defensive chemistry of riparian trees drives local adaptation among terrestrial and riverine decomposers that consume shed leaf litter. We found extensive geographic structuring of ellagitannins, diarylheptanoids and flavonoids in red alder trees.

Ellagitannins, particularly those with strong oxidative activity, best predicted aquatic leaf decomposition. Further, spatial variation in these leaf defenses drives local adaptation: in experiments using artificial food sources distinguished only by the chemical content of individual trees, we found decomposers both on land and in rivers more quickly consumed locally derived food sources. These results illustrate that terrestrial processes can change the chemistry of cross-ecosystem subsidies in ways that ultimately alter consumer ecology in donor and recipient systems.

T40

Environmental influence on the coadaptation of a dioecious host plant (*Silene latifolia*) and its nursery pollinator (*Hadena* spp.)

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Populations diverge in response to disparate selective pressures. Two divergent populations of the dioecious flowering plant *Silene latifolia* are locally adapted, particularly to water availability, through a floral size/number tradeoff. Viability selection in dry habitats favors few, large flowers, while sexual selection in wet habitats favors small, numerous flowers. Adaptation to abiotic differences also influences interactions with *Hadena* moths, which are main pollinators but also seed predators (nursery pollinators). In field studies, female moths do recognize phenotypically divergent flowers from non-native populations, but flower size limits oviposition location. Moths cannot oviposit on the ovary of large flowers and instead oviposit on petals, reducing larval survival and seed herbivory in populations with large flowers. Although moths oviposit on the ovary of small flowers, higher abortion rates of parasitized fruit reduces secondary seed herbivory. Our findings suggest that coadaptation of the nursery pollinator and its host plant is governed by environmental differences.

## W1

Patterns of hybridization in two barn swallow contact zones

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Hybrid zones are useful for studying interactions between selection and gene flow in the formation and maintenance of reproductive barriers. The barn swallow complex (*Hirundo rustica*) is a recent radiation comprised of six globally distributed subspecies. Despite shallow divergence and shared range borders, there is extensive variation in sexually selected traits (plumage color and tail streamer length) and body size among populations, suggesting that these traits may contribute to assortative mating and population divergence. To examine patterns of reproductive isolation in this system, we conducted a >10,000 km transect across Russia, bisecting the ranges of three subspecies and two contact zones. Analysis of >23,000 SNPs reveals evidence for ongoing hybridization across both contact zones, with more gene flow occurring between the putatively more closely related pair of subspecies. We analyze phenotypic and genomic clines and consider a role for sexual selection in the maintenance of reproductive isolation.

## W2

Natural selection and the maintenance of reproductive isolation in hybridizing chickadees

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When locally adapted species meet and interbreed their hybrid offspring often exhibit reduced fitness. Although this is a common pattern, we still lack an understanding of the mechanisms that underlie reduced hybrid fitness in most taxa. Black-capped (*Poecile atricapillus*), Carolina (*P. carolinensis*), and mountain (*P. gambeli*) chickadees hybridize where their ranges overlap. These species differ in physiological traits that contribute to aerobic capacity and basal metabolism, and preliminary data indicate that selection against hybrids may be related to genetic incompatibilities in core metabolic pathways. We sequenced RNA from five individuals of each species, assembled species-specific transcriptomes, and assessed sequence variation. Results of enrichment analyses indicate that multiple pathways involved in aerobic capacity (e.g., OXPHOS, lipid metabolism, glycolysis) are significantly enriched for fixed differences between the species. We hypothesize that a breakdown in aerobic capacity in hybrid chickadees due to these sequence differences may be facilitating maintenance of reproductive isolation.

## W3

Mammalian phylogeny enters the matrix: A complete species-level analysis of mammals using a supermatrix of 30 genes

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Understanding the evolution of the tetrapod class Mammalia is of unparalleled relevance to humans for a variety of ecological, medical, and cultural reasons—a fact that belies our relative lack of phylogenetic knowledge about this group. Now nearly 10 years old, the supertree-based analyses of Bininda-Emonds et al. (2007, including subsequent taxonomic updates) still represents the best species-level phylogeny of mammals (cited ~250 times since 2014). However, a DNA matrix-based hypothesis for mammalian species diversification is lacking. Here we seek to reconstruct this phylogeny by maximizing species-level sampling using all available DNA sequences for 30 genes.

The resulting supermatrix analysis includes a sampling of at least one of the targeted genes for >90% of all recognized species. Using taxonomic constraints to impute the ~500 remaining species, and a separate backbone analysis with well-vetted fossil priors, our results provide a novel perspective on the temporal and phylogenetic relationships within Mammalia.

W4

Using ancient DNA for phylogenetic correction to interpret island dwarfing

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Island dwarfing, whereby large-bodied organisms evolve smaller body size on islands, has been widely studied. But time of colonization and intraspecific relatedness have rarely been taken into account. Relatedness is especially important when studying island dwarfing because evolution occurs within species or between closely related species. We demonstrate the successful use of next generation techniques to sequence mitogenomes of 120 Southeast Asian *Macaca fascicularis* specimens ranging between 50 and 100+ years old, housed at natural history museums around the world. These sequences, at an average of 45x coverage, have been used to reconstruct an intraspecific phylogeny of *M. fascicularis* throughout the Southeast Asian mainland and islands. This phylogeny not only indicates the time of colonization of various islands throughout the region but also provides us with a tool to take phylogenetic relatedness into account when analyzing variables such as body size and brain size associated with island dwarfing.

W5

A threshold of genomic introgression predicts plumage divergence among Andean birds

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Speciation via geographic isolation is considered an elementary aspect of evolution, but it remains difficult to explain observed variation in the evolutionary outcomes of allopatry. Why do some taxa exhibit profound geographic variation in phenotype, whereas others are uniform throughout their ranges? We addressed this question with a natural experiment comprised of co-distributed Andean bird species that show variable levels of phenotypic differentiation across a major biogeographic barrier, the Marañón Valley of Peru. We examined genomic and phenotypic divergence across the Marañón, and tested whether phenotypic differentiation between sister populations is predicted by time spent in allopatric isolation, the degree of genomic introgression between populations, or idiosyncrasy in the rate of phenotypic evolution. Our results suggest that despite idiosyncrasy in the relationship between genetic and phenotypic differentiation across regions and environments, phenotypic differences between allopatric populations may nevertheless diverge at a predictable pace within a particular ecological context.

W6

The genetic basis and genomic consequences of plumage divergence in flycatchers of the Solomon Islands

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Speciation, the evolutionary process by which new species originate, is responsible for the amazing diversity we see in nature. Despite decades of active research, many fundamental questions

remain unresolved, including the genetic basis of reproductive isolation. We explore the genetics, genomic consequences and ecology of diversification using the variable *Monarcha castaneiventris* flycatcher of the Solomon Islands. This complex is composed of populations that vary in plumage color, which represent different stages of speciation. We focus on island populations that have convergently evolved entirely black plumage and are sister to chestnut birds that inhabit adjacent or the same islands. Combining field experiments with genomic approaches, our results thus far indicate that simple point mutations predict parallel melanism, that directional selection keeps the color forms distinct despite gene flow, and that the differences in color are used in conspecific recognition. We discuss the implications of our results in our understanding of speciation.

W7

Divergent sexual selection, not genetic structure, explains phenotypic differentiation among closely related populations of the barn swallow

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We now know that sexual selection plays a key role in the diversification of numerous animal clades and may accelerate trait divergence during speciation. However, much of our understanding of this process comes from phylogenetic comparative studies, which rely on surrogate measures such as dimorphism that may not represent selection in wild populations. In this study, we assess sexual selection pressures for multiple male signals across four populations of the barn swallow in Europe, Asia, and the Middle East. We demonstrate significant phenotypic divergence in four sexual signaling axes, in the absence of strong genome-wide divergence or comparable divergence in an ecological trait. This suggests that sexual selection is more important than ecological selection for phenotypic differentiation in this species. To our knowledge, this is the first study to relate direct measures of the strength and targets of sexual selection to phenotypic and genomic divergence among closely-related wild populations.

W8

Local and biogeographic drivers of in situ speciation in fishes

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Speciation is fickle: the most obvious niches lay vacant for millions of years while the obscure may be filled and inexhaustibly divided. In fishes, variability in the rate of speciation has led to both the rapid diversification of African cichlids and to the equally remarkable -- albeit less provocative -- scarcity of endemics in many ancient lakes. Data from a newly compiled global database of in situ fish speciation events are presented alongside an analysis of potential drivers at multiple scales to understand how ecological, historical, and geographical factors converge to form new species.

W9

Consequences of shifts in the mean and variance in prey phenology for predator-prey interactions

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Phenologies of species worldwide are shifting in response to climate change. However, we have a poor understanding of how phenological variation affects species interactions. In this study,

we experimentally manipulated the mean and variance of the phenological distribution of a prey species in a factorial design to determine the independent and combined effects of these two types of shifts on predator-prey interactions. We found that shifts in the mean and variance both significantly affected the prey, that their effects were similarly strong in magnitude, and their combined effects were additive. By dissecting the roles of two different types of shifts, this study represents a first step toward a comprehensive understanding of the complex effects of phenological variation on species interactions. Embracing this complexity is critical for developing a framework to predict the consequences of climate change for natural communities.

W10

Species turnover and the joint effects of climate and predators on lake ecosystems

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Changes in climate and introductions of large predators are two pervasive effects of human activities, yet we know little about how they interact. Using an elevational temperature gradient, we show that a warmer climate destabilizes mountain lake ecosystems by increasing the cascading effects of predators on lower trophic levels. Shifts in species composition dampened the impact of fish on biomass pyramids of invertebrates and algae in cold lakes more than warm lakes. Our finding informs predictions about the response of ecosystems to climate change, and provides evidence that trophic cascades and temperature interactively effect lake food webs by selecting on similar organismal traits among zooplankton.

W11

Habitat compression and risk contagion: predator distribution and the spatial dynamics of metacommunities

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Two context-dependent processes that can affect patch-specific colonization rates are spatial contagion and habitat compression. Spatial contagion is the effect of characteristics of nearby patches on the perceived quality of a focal patch. Habitat compression is an increase in colonization rate of remaining suitable patches resulting from a loss of nearby suitable patches through either changes in actual or perceived patch quality. Risk contagion can lead to cascading habitat loss, as discrete, high quality patches associated with high-risk patches are avoided. Compression potentially generates strong density-dependent effects, as more individuals are “compressed” into fewer patches. These two processes can interact, with contagion leading to increased compression, and both potentially affect distribution and abundance. We examine the role of patch context in the assembly of communities and the dynamics of metacommunities using data from experimental aquatic metacommunities and conceptual models of spatial dynamics.

W12

Resource availability and prey growth dynamics determines the outcome of size-structured predator-prey interactions

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Most animals undergo substantial changes in body size and morphology during ontogeny that can influence many aspects of ecological performance. For example, body size variation can strongly influence predator-prey interactions and drive patterns of size structure in prey populations and strongly influence long-term population dynamics and community structure. Predator consumption rates are commonly unimodal functions of prey size. Prey may therefore pass through windows of vulnerability to size specific predators as they grow through ontogeny. Prey growth rates can therefore be strong determinants of prey survival probability. Prey growth rates are in turn driven by resource availability. Consequently, resources may impose bottom up control on the outcome of size structured predator-prey interactions. I will present experimental and simulation results demonstrating how prey growth and resource availability affects the interactions between red-eyed tree frog tadpoles and two different size-limited predators--dragonfly nymphs and giant water bugs.

W13

Tempo and mode of anti-bat strategies in bombycoid moths: evolution of sonar jamming and acoustic deflection

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The function and historic pattern of anti-predator behaviors are rarely studied concomitantly. Here we present our mechanistic and evolutionary investigations into the acoustic warfare between bats and bombycoid moths. Using high-speed videography, we show that the spinning hindwing tails of luna moths lure echolocating bat attacks to these nonessential appendages in over half of bat-moth interactions. Further we show that long hindwing tails have independently evolved multiple times in saturniid moths. In a related effort with hawkmoths, we conducted, laboratory bat-moth interaction experiments, high-throughput field assays using playback of echolocation attack sequences and fossil-calibrated phylogenetic analyses to provide evidence that multiple unrelated hawkmoth species produce ultrasound and jam sonar. Our phylogeny demonstrates that jamming evolved twice during the Miocene after the radiation of insectivorous bats. These findings expand our knowledge of anti-predator strategies, the limitations of sonar, and the extent of a long-standing evolutionary arms race.

W14

Predator-Contingent Exploitation of an Inducible Defense: When is it Best to Sink or Swim?

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Despite recent advances in understanding the impacts of inducible defenses at the community level, the role these defenses may play in food-web dynamics, community stability, and the evolution of prey traits remains unclear. We used the well-described predator-prey interaction between the alga *Chlamydomonas reinhardtii* and the rotifer *Brachionus calyciflorus* to induce multicellular benthic non-motile colonies of *Chlamydomonas*, which resist *Brachionus* predation. Addition of snails, *Physa fontinalis*, which consume colonial *Chlamydomonas*, drove the normally stable *Chlamydomonas-Brachionus* interaction below detectable limits for both species. Recovery of some *Chlamydomonas* populations after the collapse of rotifer populations indicates that algae survived at low densities in some replicates. Inducible defenses against planktonic microconsumers based on increased size open avenues of attack from benthic macroconsumers, suggesting that the

best strategy may require both increased colony size and motility to thwart both planktonic and benthic consumers, a pattern seen in related multicellular Volvocales.

W15

Piscivore addition causes a trophic cascade within and across ecosystem boundaries

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Piscivorous fish have long been stocked in lakes for sport fishing and the ecological shift observed following these introductions has been a key empirical example in the study of trophic cascades. Yet, the impact of piscivore addition on neighbouring terrestrial ecosystems has not been well-studied. In addition, much of the foundational work was carried out in natural lakes without replication, so heterogeneity in the trophic response to top predator addition is not well known. Here, we use a replicated pond experiment to document the trophic impacts of the addition of a piscivore, cutthroat trout, on both aquatic communities already containing a meso-predatory fish (threespine stickleback) and neighbouring terrestrial ecosystems. We find that piscivore addition lead to a trophic cascade that extended across ecosystem boundaries, as trout addition lead to an increase in the average biomass of insects emerging into the terrestrial system. This increase in emerging insect biomass corresponded with greater insectivorous bat activity over aquatic systems containing trout. In addition, we used heterogeneity in the trophic cascade between replicates to find evidence that the strength of this trophic cascade was more closely correlated with an observed diet shift (non-consumptive effect), than a decrease in stickleback abundance (consumptive effect).

W16

Juvenile competitive bottleneck dynamics in freshwater zooplankton

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Within stage-structured populations, juvenile predators often compete with the prey of adults. Competition can reduce or prevent juvenile recruitment to the adult stage (juvenile competitive bottleneck). Predation by adults can release this bottleneck, though this should depend on the adult:prey ratio (frequency-dependence) and adult preference for heterospecific versus conspecific prey (cannibalism). Here, we examined juvenile competitive bottleneck dynamics in a freshwater zooplankton system. Specifically, we manipulated the densities of adult copepods (*Mesocyclops edax*) and their prey (*Daphnia pulex*), and measured the survival and maturation of larval copepods (nauplii). We found that *Daphnia* reduced and even precluded nauplii survival, likely through algae resource depletion. As predicted, adult copepods enhanced nauplii survival through *Daphnia* consumption. However, this positive effect only occurred at intermediate *Daphnia* densities: adult copepods reduced nauplii survival through cannibalism at low *Daphnia* densities. This work demonstrates a strong juvenile competitive bottleneck in freshwater zooplankton regulated by a balance of competition and predation.

W17

Genomic signatures of artificial selection in natural house sparrow populations

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Artificial selection experiments in the wild are still scarce. For four consecutive years we successfully selected for long and short tarsus length in two natural island populations of house sparrows. Here we analyzed 5174 SNPs from these populations in order to study the genomic signatures of this experiment. We combined gene-dropping simulations and randomization tests to identify loci with larger allele frequency changes than could be expected by drift alone. We found two types of outliers: those where alleles consistently increased in frequency across generations, and those that showed strong allele frequency differences within generations (between removed and retained individuals). In the latter case, allele frequencies typically recovered to the next generation, presumably due to natural selection, precluding alleles at these loci to consistently change across generations. This suggests that natural selection can impose a limitation on the ability for individuals to quickly adapt in response to novel anthropogenic disturbances.

W18

Explosive growth alters genetic architecture and hampers the detection of causal loci for traits under selection

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The role of rare alleles in complex phenotypes has been hotly debated, but most association methods do not account for evolutionary forces that impact genetic architecture. Here, we use simulation and numerical algorithms to show that recent explosive population growth can dramatically inflate the genetic variance explained by singleton variants in large samples. We then assess the ability of association methods to detect causal loci using simulations and human RNA-seq data. Counter-intuitively, we find that statistical performance is worst for phenotypes in which genetic variance is due mainly to rare alleles, and that explosive population growth increases the variance due to rare alleles but decreases power. Few studies have reported novel associations between complex traits and rare alleles. Our work shows that current methods for rare variant detection are not robust to realistic evolutionary forces, so conclusions about rare variants' impact on complex traits may be premature.

W19

Genetic architecture of constitutive and induced herbivory-defense traits in *Mimulus guttatus* (yellow monkeyflower)

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Herbivory has exerted strong selection pressures on natural plant populations over both ecological and evolutionary time scales, leading to the great diversity of plant physical and chemical defenses observed today. Phenotypic plasticity provides a means for plants to cope with variable herbivory. The search for general patterns in the production and allocation of constitutive and induced plant defense traits will be facilitated by characterizing multivariate suites of defense. Here, I characterize the genetics of constitutive and induced (via insect herbivory) physical and chemical defenses in *Mimulus guttatus*. I mapped quantitative trait loci underlying these traits by selectively genotyping a large panel of recombinant inbred lines derived from two highly divergent populations.

My results are evaluated in relation to the optimal defense theory, which provides testable predictions for production of multiple constitutive defense traits, as well as patterns of defense trait plasticity.

W20

Is the G matrix a ball or a jack?

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The child's game of jacks involves two shapes – the round ball and the spiky jack. These represent two hypotheses about multivariate genetic effects. Under universal pleiotropy all mutations affect all traits, but, more important, the directions of effects are continuously distributed in phenotype space, forming a surface like the ball from our game. Under the alternative hypotheses, genetic effects are modular, by which we mean that they are discontinuously distributed in phenotype space, like the spikes of the jack. We have been studying multivariate genetic effects in the *Drosophila* wing using a genome-wide association study, and experimental manipulations of specific genes. Our effect data are close to the expectations under the universal pleiotropy hypothesis. The fly wing is a continuous morphological structure without individuated parts. Tests of these hypotheses are needed from more diverse sets of traits.

W21

(Move to Symposium 3)

W22

Variability in gene expression as a mechanism of developmental plasticity: a case study of physiological learning in caterpillars

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Why does adaptive plasticity vary among organisms? We test the hypothesis that variability in gene expression, followed by epigenetic reinforcement of particular expression patterns, may underlie developmental plasticity. Such a learning-like mechanism should come with significant costs and reproductive tradeoffs. We test this idea with a large RNAseq experiment measuring gut gene expression of specialist and generalist populations of cabbage white butterflies, *Pieris rapae*. Preliminary analyses suggest the generalist population expresses a greater diversity of transcripts earlier in development, consistent with predictions. Here we present additional analyses that test for divergence in gene expression patterns between environments over time, and signatures of transcriptional memory based on past feeding experience. These data will pave the way for tests linking this mechanism of plasticity to costs that maintain variation in plasticity and niche breadth.

W23

Adaptive plasticity generates microclines in threespine stickleback male conspicuousness

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Most species exhibit geographic gradients in phenotypic traits ('clines'). Clines often arise from adaptation to spatially varying environments when divergent selection exceeds the homogenizing effect of gene flow. Because of this migration-selection antagonism, theory leads us to expect adaptive clines to occur only at broad spatial scales that limit dispersal<sup>3</sup>. Contrary to this expectation, we found 'microclines' across a surprisingly small spatial gradient: male color of threespine stickleback fish changes across a 2-meter vertical range of nest depths. The color microcline is repeatably associated with depth gradients in ambient light, demonstrating that the

male color microclines reflect adaptation to local signaling environments. Male fish that were transplanted to a new depth rapidly adjusted their color accordingly. Thus, plasticity is sufficient to recreate the color-depth microcline. Our results show that adaptive phenotypic clines can exist across surprisingly small spatial scales, because plasticity generates trait-environment correlations despite the opportunity for gene flow.

W24

Patterns of avian breeding phenology in Marin County California

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Shifts in phenology can impact bird species directly, by influencing the survival of individuals, or indirectly, through altering processes at other trophic levels. Understanding the phenological responses of birds to climate patterns will be important for conservation and restoration strategies. In this study, I examine phenological patterns in the banding data collected over the past 40 years by Point Blue Conservation Science in Marin County CA. I assess the effects of temperature and precipitation patterns on breeding phenology signals, including brood patch and cloacal protuberance presence and flight feather molting. This study gives valuable insight into which species are most vulnerable to climate changes, and give us a better understanding of how migratory bird species vs. resident bird species may be affected differently. Findings from this study will be relevant for future management planning in the face of climate change.

W25

Wyeomyia and Heliconia: a model system for the investigation of oviposition-site selection

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Sabethines (members of the tribe Sabethini) are the most interesting of all mosquitoes. Many are aesthetically striking, some perform elaborate aerial courtship dances, and others obtain all of their adult nutrition from the mouths of ants. They exhibit profound diversity in morphology and behavior, and they are unusual in that most species oviposit and develop in plant-held waters (phytotelmata). Although researchers have studied the ecological drivers of oviposition-site selection (including features such as microbial diversity, salinity, concentration of dissolved ions, and temperature), they have seldom studied the evolutionary drivers. The sabethine genus *Wyeomyia* is an ideal clade for investigating the ecological and phylogenetic drivers of oviposition-site selection because the vast majority of *Wyeomyia* spp. oviposit and develop only in Neotropical phytotelmata. They appear to discriminate in selecting oviposition sites, i.e., females hover over and inspect fluid before ejecting single eggs onto the surface. Many species inhabit plants of the genus *Heliconia*, which are known for their staggered arrangement of colorful, boat-shaped, fluid-filled flower bracts. *Heliconia* spp. vary in the most important cues that affect oviposition-site selection by mosquitoes: container morphology, geographic location, and concentration of dissolved organic matter. Also, the arrangement of their bracts facilitates the replication required for manipulative field experiments.

W26

Selection for early breeding in Hume's warblers

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Positive directional selection for early breeding is commonly seen in bird species. If breeding early is advantageous why does breeding date not advance? I studied Hume's warblers in the western Himalayas, where over 20 years of study, earlier breeding individuals consistently produce chicks in higher morphological condition than later breeding individuals. I tested two hypotheses using nest survival, morphology, and phenology data. First, adults in high condition breed earlier and impart that condition to their offspring. Second, the advantages of breeding early are countered by higher whole brood failure through predation. I found a lack of compensatory factors that give advantages to later breeders, and found that nest failures increase towards the end of the breeding season. Results imply that condition effects drive the association of breeding date with nest success. I use these results to address how bird breeding dates will respond to climate change in the Himalayas.

W27

Darwin vs. Wallace  
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Behavior may differentially influence and constrain the evolution of other organismal traits. These evolutionary influences may be observed in a macroevolutionary context when behavioral traits are variable over phylogeny and conserved within smaller clades. In the late 19th century, Wallace suggested that bird nesting behavior met these criteria. He further suggested that differences in nesting behavior, not differences in the intensity of inter-sexual selection, explained variation in avian sexual dichromatism. Here we use the natural history literature and large, species-level phylogenies to test the many components of Wallace's "theory of birds' nests" in the Passeriformes.

W28

Vertical transmission of social roles drives resilience to poaching in elephant networks  
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Network resilience to perturbation is fundamental to functionality in a wide range of systems. Female African elephants exhibit complex social networks with node heterogeneity in which older individuals serve as hubs. Recent ivory poaching directed toward older elephants in a well-studied population has mirrored the targeted removal of highly connected nodes in the theoretical literature. We test the response of a natural network to selective knockouts, finding that the hierarchical network topology characteristic of elephant societies was highly conserved across the sixteen-year study despite ~70% turnover in individual composition. Social positions of daughters during the disrupted period were predicted by those of their mothers in years prior, were unrelated to individual histories of family mortality, and were actively built. Our study provides a rare bridge between network theory and an evolved system, demonstrating social redundancy to be the mechanism by which resilience to perturbation occurred in this socially advanced species.

W29

Diet specialization varies with spatial scale for a sensitive reptile  
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The characteristics of entire species are ultimately defined by the characteristics of individuals, though individual organisms often receive less research attention than the populations

and ecological communities to which they belong. Individuals are likely to vary within and across populations; patterns of variation have implications for population dynamics and trends. While individual variation can be complex, species are often defined along a gradient from specialists to generalists, with the implication that specialist species vary little. We quantified dietary variation among individuals and populations for a known dietary specialist, the greater short-horned lizard (*Phrynosoma hernandesi*). Diet diversity in fecal pellets was highest among individuals ( $\alpha$ -diversity) and lower at broader spatial scales ( $\beta$ -diversity), indicating that the degree of specialization was spatially dependent. This individual variation is equal to values found in generalist taxa, indicating that individual differences may be as important in driving the ecological interactions of specialists as of generalists.

#### W30

Thermal tolerance and geographical range size relationships: a comparison between widespread- and restricted-distributed marine species of the genus *Ophryotrocha* (Annelida, Dorvilleidae)

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The investigation of the mechanisms underlying species' uneven distribution along natural gradients, with most taxa showing restricted distribution and only few being widespread, has had a renewed interest in light of global warming. In general, widespread species appear to possess broader thermal-tolerance windows, but whether greater tolerance has co-evolved or traded-off with thermal plasticity is still controversial. Here, we investigated the responses to increasing temperatures in seven polychaete species of the genus *Ophryotrocha*, with similar ecology but different biogeography, acclimated for seven days to 18, 24 and 30°C. Upper (UTL) and lower (LTL) thermal tolerance limits and life-history traits were measured. Widespread species had greater UTL, lifespan and fecundity at the highest temperature, and possessed wider thermal tolerance windows than restricted-distributed species. Acclimation capacities were not good predictor of the species biogeographic range. Our results supported the prediction that restricted-distributed species may be more vulnerable under a climate change scenario.

#### W31

Genetic variation in symbionts may allow coral reef species to adapt to climate change

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On coral reefs, mutualisms between the dinoflagellate *Symbiodinium* and reef species form the foundation of reef ecosystems. Coral reefs are among the most threatened ecosystems under a changing climate and are rapidly declining due to increasing temperatures. However, high rates of somatic mutation have resulted in significant genetic variation in the symbiont population, which could provide the raw material for natural selection and adaptation to increased temperature on contemporary time scales. We measured the response of multiple genotypes within a *Symbiodinium* species to increased temperature and found significant variation in chlorophyll content, photosynthetic efficiency, and nitrogen consumption, suggesting that different genotypes may be favored under different temperature regimes. Selection for particular genotypes may confer adaptation of the holobiont to increased temperatures on coral reefs and provide some hope for reef species.

W32

Phenotypic consequences of range expansion in two intertidal snails, *Nucella lamellosa* and *Nucella ostrina*

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Few studies have investigated phenotypic responses of marine species to natural range expansion and the influence that refuge populations have on morphological differentiation, or how differentiation following anthropogenic movement compares to natural expansion. I analyzed Pleistocene-Recent populations to test the prediction that a species that expanded its latitudinal range with post-Pleistocene warming but also persisted in refugia (*Nucella lamellosa*) shows greater morphological differentiation across its geographic range than a range-expanding species that did not persist in refugia (*N. ostrina*). Using landmark-based morphometrics, I surveyed modern and fossil populations of the two species across their geographic ranges from northern California to Alaska. In both species, I find that northern morphologies are different from both southern and ancestral morphologies, suggesting that differentiation is likely a result of recent local adaptation to northern habitats. For *Nucella*, recent differentiation may in part be due to low gene flow stemming from their direct-developing lifecycle.

W33

With new frontiers come new risks and responses: A tree crab's adjustment to life in the marsh (a tropicalization story)

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As global change offsets the ranges of interacting species, temperate ecosystems are becoming tropicalized, with unknown consequences for species inhabiting novel settings. The mangrove tree crab (*Aratus pisonii*) has moved north with expanding mangroves, outstripping its host trees to colonize grass-dominated salt marsh habitat. In 2013 we discovered *A. pisonii* established in marshes 120km beyond the frontier mangrove. Differences in physical structure between mangroves and marshes apparently affect *A. pisonii* habitat use. In fall 2015, we combined published and crowd-sourced bird and fish data with tethering experiments, biometric surveys, and behavioral assays to assess how predation risk from above (terrestrial) and below (marine) varies by vegetation type and whether *A. pisonii* have adjusted their avoidance and escape behavior accordingly. A vegetation-specific trade-off between leg dropping and jumpiness is expected to behaviorally mediate altered or novel risk. Changes to any component could modify a behaviorally-mediated terrestrial-aquatic food web subsidy.

W34

Tri-trophic symbiotic interactions and host plant responses affected by climate change

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Climate change may alter the strength and importance of symbiotic interactions to plants. While some mutualists could mediate plant responses to climate change, changes in parasitic symbionts may exacerbate negative effects. Moreover, many species in natural systems are involved in multiple simultaneous symbiotic interactions providing unique or overlapping host benefits. To more fully understand plant responses to ongoing climate change, it is increasingly important to

study how these changes may alter resource allocation to multiple mutualists as a result of differential availability associated with physiological changes and the subsequent the interplay between species. By manipulating nitrogen-fixing rhizobia, extrafloral nectar-tending ants, and temperature, here we explore how tri-trophic interactions between multiple mutualists and the plant host are affected by warming as well as how these potential mutualists may independently and interactively influence plant traits, affect fitness responses to climate change, and even cascade to alter the herbivore community.

W35

The future of coastal anuran amphibian populations: Local extinction or local adaptation?

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Sea level rise (SLR) is an expected consequence of global warming. While the magnitude of effects will vary, SLR will impact coastal ecosystems globally. Currently, we know little about how SLR will impact coastal freshwater wetlands and wetland communities. It is often assumed that freshwater species in historically freshwater coastal wetlands will become locally extirpated as the environment becomes more saline, yet few studies have examined whether local adaptation to elevated salinities will buffer some species against this change. We use anuran amphibians, a salt-sensitive group common in freshwater wetlands, to explore this question. Specifically, we characterized responses to a salinity gradient among different populations to determine whether coastal anuran populations that persist in chronically salt-intruded wetlands exhibit physiological and behavioral phenotypes consistent with adaptation that allow them to inhabit SLR affected wetlands. This is an important step in understanding how freshwater organisms can respond to the changing environment.

W36

Plants and their pollinators: can one range shift lead to another?

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Climate change is influencing species' ranges across the globe and in mountain ecosystems this often means a shift upwards in elevation. For pollinators, specifically bumblebees, shifts have been tracked through resampling of historical sites and use of museum specimens. For plants, detecting shifts may be more difficult since many alpine species are long-lived perennials. However, plants may show signs of selection to move upwards if seed set is highest at the leading edges of their range. We measured seed set of open pollinated plants from seven species and visitation rates by bumblebees to four of these species, along elevational transects near the Rocky Mountain Biological Laboratory. These transects were established in 1974 and recent resampling indicated some bumblebee species have moved up. We assessed whether patterns in bumblebee visitation could explain patterns in seed set across elevations and thus whether increased pollination success could lead to upward shifts in plants.

W37

Competition between mutualists within a multi-species plant-pollinator interaction

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In mutualism, it is generally accepted that many species interact with multiple mutualists, and mutualist quality can vary. The past decade has engendered new models describing the dynamics of three-species mutualism in which one mutualist varies in quality, and we see many field studies addressing the effects of differences in mutualist quality on a shared reciprocator. However, it is uncommon that these studies incorporate competition between mutualists. The dynamics of competition between mutualists has received much conceptual attention in recent years, but field studies are rare. Our study examines interactions between two mutualist species - pollinating bumblebees - and a plant species they both visit. We field-tested the strength of competition between pollinator species, asking whether a competitive environment can change pollinator foraging behavior from mutualism to antagonism. Our findings suggest that a high density of mutualists increases the strength of competition and alters pollinator foraging behavior and efficiency.

W38

Plant-pollinator diversification and community assembly in the Society Islands

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How evolutionary and ecological processes interact to assemble communities is a major problem in evolutionary ecology. Here, we examine the assembly of communities composed of leafflower trees (Phyllanthaceae: *Phyllanthus* s. l. [Glochidion]) and their specialized, brood-pollinating leafflower moths (Lepidoptera: Epicephala) on the oceanic islands of Tahiti and Mo'orea (Society Islands, French Polynesia). All *Glochidion* on these islands are extremely closely related, but show differences in their ecology as well as in floral morphology and floral volatile profiles. Both islands are inhabited by the same two, distantly related *Epicephala* taxa. *Glochidion*-*Epicephala* networks are very different on each island, with a reciprocally specialized and modular pattern on Moorea, and a non-modular, more generalized pattern on Tahiti. Floral volatile and transcriptomic data suggest that both abiotic niche and pollinator interactions may have played a role in *Glochidion* diversification, and interactions with different host species may be associated with incipient divergence in *Epicephala*.

W39

A role for the foraging gene in an ant-plant mutualism?

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In plant-animal mutualisms, animal behavior influences plant fitness, and feedback through this process drives coevolution, yet little is known about the genes involved. For example, *Allomerus octoarticulatus* ant colonies defend the common Amazonian myrmecophyte, *Cordia nodosa*, against herbivores as a by-product of foraging for insect prey on plant surfaces. We studied the *A. octoarticulatus* orthologs of the protein kinase G (PKG) family of genes, which includes the aptly named foraging gene. This gene is well known to affect foraging behavior in many animals, including ants. We determined whether PKG affects foraging behavior in *A. octoarticulatus*, and whether these genes' effects on animal behavior extend to plant phenotype and ultimately fitness through mutualism. Our results suggest that PKG expression influences the ant behaviors that result in a protective ant-plant mutualism.

W40

Consequences of linked nectaring and oviposition preferences in the hawkmoth *Manduca sexta*  
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The oviposition choices of female insects determine the environment their offspring will experience, affecting both offspring and host plant fitness. In the Sonoran Desert, the hawkmoth *Manduca sexta* both nectars and oviposits on the perennial *Datura wrightii*. Previous work has focused on the tradeoffs between mutualism and antagonism in this interaction. However, *M. sexta* also visits the annual *Datura discolor*, which co-occurs and co-blooms with *D. wrightii*. We investigated how nectar foraging influences oviposition and the consequences of adult choice for offspring performance. We found that *M. sexta* prefers *D. wrightii* for both nectaring and oviposition. Yet, offspring perform similarly on both hosts, suggesting that plant traits such as flowers may bias decisions away from viable hosts. Linkages between adult nectaring and oviposition behaviors point to an unexpected cost of flowering in both plant species.

W41

Adaptation to an invasive host is collapsing a native ecotype in soapberry bugs

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Locally adapted populations are often used as model systems for the early stages of ecological speciation, but most of these young divergent lineages will never become complete species. While the collapse of incipient species is theoretically common, very few examples have been documented in nature. I demonstrate that soapberry bugs (*Jadera haematoloma*) have lost adaptations to their native host plant (*Cardiospermum corindum*) and are regionally specializing on an invasive host plant (*Koeleruteria elegans*), collapsing a classic and well-documented example of local adaptation. All populations that were adapted to the native host - including those still found on that host today - are now better adapted to the invasive in multiple phenotypes. Weak differentiation remains in two traits, suggesting that homogenization across the region is incomplete. This study highlights the potential for adaptation to invasive species to disrupt native communities by swamping adaptation to native conditions through maladaptive gene flow.

W42

An information-entropy approach to predicting metabolic rate distributions in ecological communities

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Many fundamental properties of ecological systems and interactions are tied to body size and related metrics of the metabolic rate distributions within and across species. A previously proposed maximum entropy theory of ecology (METE) predicts numerous interrelated macroecological patterns, which have been extensively tested and generally supported by data. We test, for the first time, multiple metabolic rate distribution predictions of METE with fully censused community data (from herbaceous plants in a subalpine meadow) and show that while this theory realistically predicts the distribution of individual metabolic rates across the entire community, the within- and across-species predictions generally fail. We also test an energy-equivalence type prediction from METE.

We suggest several possible explanations for empirical deviations from theory, and distinguish

between the expected deviations caused by ecological disturbance and those deviations that might be corrected within the theory.

W43

Epidemic spread and genomic-island acquisition of a Bradyrhizobium with superior catabolic capabilities

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Bacterial epidemics are commonplace, but we rarely understand what drives them. Rhizobia exhibit a bipartite lifestyle, replicating in soil and in plant cells wherein they differentiate into bacteroids and fix nitrogen for their legume hosts. Here, we genotyped and phenotyped Bradyrhizobium isolates from an 840km transect of native *Acemispum strigosus* hosts. We uncovered a massive clonal expansion restricted to the Bradyrhizobium chromosome, with a single chromosomal haplotype dominating sampled populations, ranging over 700km, and acquiring 42 divergent symbiosis island haplotypes, none of which were epidemic. Widespread chromosomal haplotypes exhibited superior growth on carbohydrates and carboxylic acids, whereas these parameters did not vary significantly among symbiosis island haplotypes. Our results are contrary to the paradigm of genomic island acquisition as the dominant driver of bacterial pathogen epidemics. Harnessing such natural rhizobial epidemics could represent a solution to the meager success of rhizobial biofertilizer inoculants that cannot compete with native strains.

W44

Non-nodulating Bradyrhizobium attenuate the benefits of the legume-rhizobium mutualism

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Rhizobia are common heterotrophic soil proteobacteria that experience diverse lifestyles. The most well studied lineages nodulate legume hosts and provide fixed nitrogen in exchange for photosynthates. However, the majority and diversity of rhizobial populations are composed of strains that do not nodulate legumes. Non-nodulating rhizobia can thrive in the rhizosphere, colonize the root as endophytes, or persist in bulk soil, but their effects on host fitness in isolation or in competition with nodulating strains remains unclear. We inoculated *Lotus strigosus* hosts with different genotypes of sympatric non-nodulating Bradyrhizobium strains in clonal inoculations and in combination with diverse nodulating strains (co-inoculation). Clonal inoculations with non-nodulating strains did not benefit host plants, but host and nodulating strain fitness was reduced in co-inoculations. All non-nodulating strains invaded legume nodules under co-inoculation conditions, although with varying co-infection rates, but this did not negatively impact host or symbiont fitness.

W45

Evolution of a model sea anemone symbiosis in Caribbean Panama

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Many marine invertebrates, including reef-building corals, sea anemones, jellyfish, and sponges, depend on mutualistic relationships with dinoflagellate algae of the genus *Symbiodinium*. In these symbioses, intracellular algae provide photosynthetically-derived compounds to the invertebrate host in exchange for nutrients. However, rising temperatures associated with global

climate change endanger persistence of invertebrate-algal symbioses, triggering expulsion of algae from host tissues. We characterized populations of the sea anemone *Aiptasia* and its algal symbiont from four sites in Panama that experience a range of thermal fluctuation regimes, based on long-term water temperature monitoring data recorded hourly for >15 years. We mapped anemone abundance, quantified within-anemone algal density and mitotic index, and performed restriction site-associated DNA sequencing of 240 anemones to genetically characterize populations of *Aiptasia* and their associated algae from 3 sites in the Bocas del Toro Archipelago and one site near the Caribbean entrance to the Panama Canal. By comparing natural populations of an anemone well-studied as a laboratory model for coral-algae symbioses, we hope to shed light on mechanisms through which cnidarians may respond to increasingly variable temperatures in the coming decades.

P1

Understanding the population dynamics of mutualism through specific birth and death rates

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Mutualism is a widespread and common interaction where, in the presence of one another, two species benefit from the interaction. From a population perspective, the benefit can either be an increase in equilibrium density or population growth rate. In this study, we build upon previous work using saturating functional responses to find coexistence between two species. Specifically, we examine how both equilibrium density as a solution and population growth rate as a composite parameter are affected by specific birth and death rates. We find that including specific birth and death rates into models of mutualism allows for a clearer mechanistic understanding of realistic and unrealistic solutions. Further, we find that including non-linear specific birth and death rates yields an additional means of coexistence. We believe our work will lend insight to further theoretical development around specific birth and death rates and spur empirical studies to test our results.

P2

Pollinator visitation is predicted by plant traits, phylogenetic isolation, and associational effects

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For most flowering plants, pollinators are necessary for successful reproduction; thus pollinator visitation plays a central role in plant demography, ecology, and evolution. While many studies have examined connections between intraspecific floral trait variation and visitation, few have simultaneously examined community and neighborhood effects ('associational effects') to understand the determinants of pollinator visitation in a community context. In this study, we measured insect pollinator visitation to 24 Rocky Mountain montane forb species in each of three years. Predictor variables measured included plant and flower traits (plant size, flower color determined by spectrometry, flower size and number), neighborhood characteristics (density of conspecific flowers, co-flowering species richness), and community characteristics (phylogenetic isolation of the focal species to the rest of the flowering community). Model selection approaches concluded that all three variable classes were important in predicting pollinator visitation rates. Clearly, the community context matters and likely shapes the form of natural selection on plant and floral traits.

P3

Predation and parasitism and the effects on barn swallow territory switching

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The defense of a particular territory is often dynamic, leading to a pattern of territory switching during, or between, successive breeding attempts. Territory establishment and defense can be costly behaviors; thus, questions remain about the potential factors leading to, as well as the benefits of, territory switching. I observed barn swallows (*Hirundo rustica erythrogaster*) in Colorado and noted predation events, reproductive success, and the distance between the first and second nests. I was specifically interested in how predation influences within-season movement. Results suggest that predation has little to no effect on barn swallow decisions to move to a different nest for a second clutch. Pairs may be able to assess predation zones and select nests accordingly,

reducing their need to disperse to more distant nests for a second clutch. Other factors, such as the ubiquity of the northern fowl mite, may give further insight into the tendencies to switch nests.

P4

Avian Community Response to Salmon Recolonization in the Cedar River Watershed, WA

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Anadromous salmon can play a significant role in the trophic ecology of freshwater rivers in the Pacific Northwest. The purpose of this study was to investigate avian community metrics in relation to salmon density and habitat variables in the Cedar River, WA. To assess the potential effects of salmon on bird communities, we conducted bird strip surveys from July 6-17, 2015, along 4-5 100-m transects within 7 reaches (distinguished by river gradient and salmon density) of the Cedar River. We recorded the number, species, location relative to the river, and behavior of all birds observed, as well as habitat data (e.g., slope, number of available perches). Species richness was positively correlated with adult salmon input, and abundance, density, richness, and diversity were inversely related to channel slope. The results of this study assist in understanding the link between aquatic and terrestrial food webs.

P5

Legumes co-invade with native rhizobia

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Lack of specialized partners could bar successful invasion by mutualists. Parker (Diversity & Distributions, 2001) hypothesized that woody invasive legumes are generalists that use local rhizobia. We collected bacterial isolates from five native and four invading legumes to determine whether European legumes co-invade the San Francisco Bay Area with familiar rhizobia or form novel associations with local rhizobia found on native legumes. A world-wide meta-analysis of rhizobial symbionts of invasive legumes tested Parker's hypothesis at the global scale. At both scales, invading legumes are not particularly generalized and usually co-invade with their own symbionts.

These results show that we need more information about how rhizobia disperse.

P6

Network heterogeneity in *Pseudomonas syringae*: an empirical test of a new method for bacterial metapopulation experiments

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Difficulty replicating identical metapopulations with particular spatial configurations is a barrier to testing theoretical predictions. To explore the effect of spatial connectivity on metapopulation dynamics, I have developed the Metapopulation Microcosm Plate (MMP). MMPs are similar to standard 96-well plates in size and shape, but contain corridors that can connect the wells in any configuration desired. By monitoring the movement of *Pseudomonas syringae* between MMP wells, I have shown that bacterial travel time is not significantly affected by corridor length, curvature, or vertical position. I also tested the hypothesis that metapopulations with heterogeneous network configurations would have more variance in subpopulation size than those with homogenous arrangements and found that while there was no difference in variance, homogeneous

networks had a significantly higher mean subpopulation size. MMPs are potentially useful for testing theoretical predictions when traditional lab equipment fails to provide the necessary number of subpopulations and connections.

P7

Persistent maladaptation of a native butterfly to novel host plants

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Rapid environmental changes can disrupt specialized recognition systems, wherein responses to previously reliable cues result in preference for a poorer quality resource. While there is some evidence of local, adaptive 'escape' from these evolutionary traps, many organisms encountering such novel selection pressures show no change in the maladaptive behavior. The native North American butterfly *Pieris macdunnoughii* recognizes the naturalized mustard *Thlaspi arvense* as a potential host, but the plant is lethal to all larvae. Over many generations of exposure to *T. arvense*, a population of *P. macdunnoughii* butterflies at Gothic, CO, have shown no change in preference for the plant. I demonstrate the heritability of this egg-laying preference, and show that plant acceptance does not differ between populations in invaded areas and those in uninvaded areas, confirming that there has been no local adaptation in response to this evolutionary trap.

P8

Population Differentiation and Speciation

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I examine the process of population differentiation leading to speciation using a two locus infinite alleles model with additive by additive epistasis. This model suggests a quantitative genetic test for speciation.

P9

Grassland bird response to prescribed fire is mediated by pre-fire vegetation structure

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Understanding the response of grassland birds to management helps to define actions that contribute to population maintenance or growth. Six grassland bird species were monitored during the peak breeding season in pre and post-fire years, on a 450 ha remnant prairie. Maximum counts of each species were used to estimate abundances at each survey point. The majority of species showed a difference in the strength of response between burned and unburned units. This difference was likely driven by the dissimilarity in the pre-fire vegetation structure of the two burned units, one with dense woody vegetation, and the other with relatively sparse open vegetation. Though fire does influence the structure of vegetation, pre-fire condition limits the degree of change. Burning results in changes in bird abundances that are relative to the pre-fire grassland structure.

P10

The elevational variation of arthropod community on ground are determined by the ant-aphid mutualism in canopy

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Ant-aphid mutualism is known to play a key role in structuring arthropod community in tree canopy, but knowledge on its possible effects of ground arthropod are scarce. In this work, structure equation modeling was used to evaluate the effects of ant-aphid mutualism in shaping the variation of ground arthropod community along an elevational gradient in a deciduous temperate forest, Beijing, China. The results showed that ants and aphids are positive correlated. The abundance of ground

beetles is negative correlated with ants and aphids. Structure equation models shows that the mutualism of ant-aphid determine the ground beetles variation. These results suggest that aphids located in the tree canopy have indirect negative effects on beetles by enhancing the ant abundance on the forest floor which would shed lights on trophic cascading effects of ant-aphid mutualism on the forest floor food web.

P11

The Influence of Salmon Recolonization on Riparian Communities in the Cedar River, Washington, USA

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Salmon are a valuable resource throughout the Pacific Northwest, and salmon conservation efforts often focus on the re-colonization of salmon into historically obstructed areas such as the Cedar River in Washington, USA. However, to assess the implications of salmon re-colonization, it is critical to consider not only the river ecosystem but also the surrounding riparian habitat. To investigate connections between salmon and the riparian habitat in the Cedar River after 12 years of re-colonization, we identified spiders, collected prey from spider webs, and characterized aquatic macroinvertebrates along a gradient of salmon inputs ( $\text{g}/\text{m}^2$ ). We found that the density of aquatic macroinvertebrates and spider prey increased and spider diversity decreased with salmon inputs, suggesting that salmon provide energy for aquatic and riparian food webs and lead to specialization in spider communities. The connection between salmon and riparian habitats is compelling motivation for further studies regarding aquatic-riparian linkage on the Cedar River.

P12

Dusting the shelves of diversity: Using herbarium data to investigate whether lichens follow the latitudinal diversity gradient

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The latitudinal diversity gradient (LDG) is a global biological pattern that is prevalent across geological history. Though multiple hypotheses have been proposed for the underlying mechanisms of the LDG, ranging from 8 to 120 hypotheses in a single paper, consensus has yet to be reached.

While the LDG has been demonstrated for many taxa, most groups of fungi remain neglected.

Recent efforts in collecting and molecular work enable a new look at patterns of fungal diversity. Due to their obligately symbiotic nature, lichenized fungi are a unique system in which to study the role of biotic interactions along a latitudinal diversity gradient. Here I use data from the Consortium

of North American Lichen Herbaria to test the latitudinal diversity gradient of lichens in the Americas, and model potential abiotic and biotic factors driving this gradient. I test for possible sampling bias and highlight areas where more sampling is needed.

P13

The importance of within-patch heterogeneity for metapopulation dynamics: applying scale transition theory to a size-structured metapopulation model

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When accounting for the local effects of density and environment on larger-scale population dynamics, using average values is problematic if there are local non-linear dynamics. Here we apply scale transition theory to size-structured population models, using a simulated population, to demonstrate a method for scaling from local to population and meta-population. We simulated a demographic dataset based on vital rate functions which included size-dependent terms and non-linear relationships between a local environmental variable and the vital rates. We used a Bayesian approach to parameterize functions for survival, growth, and reproduction, including a non-linear term for environment. We used the vital rate functions to build two integral projection models: a mean field model and a scale transition model. The addition of the scale transition term resulted in a more accurate estimate of the population growth rate and a predicted population trajectory that was a closer match to the actual simulated dynamics.

P14

How do mating signals mediate social and reproductive interactions in a *Callipepla* quail hybrid zone?

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Behavioral reproductive isolation can result from the divergence of traits used for mate selection between closely related populations, leading to the reduction of gene flow. Mate selection and the resulting reproductive outcomes are products of social and sexual interactions between individuals that take place within a broader social context. Here, I examine the links between networks of social interactions, plumage traits, and mate selection in a zone of contact between California (*Callipepla californica*) and Gambel's quail (*Callipepla gambelii*) in the San Jacinto Mountains of Southern California. Social data was collected using RFID tags and automated feeders and allowed me to ask: How do mating signals mediate social and mate selection behavior (and thus paternity and gene flow) within a hybrid zone?

P15

Identifying environmental drivers of genetic differentiation in the open sea

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In marine systems, planktonic species have been proposed as sensitive indicators of environmental change. With short generation times, plankton populations often show tight coupling between physical forcing and biological response. However, the question remains whether plankton have the capacity to adaptively evolve to rapidly changing ocean regimes (adapt), whether they will alter their primary habitat preferences (move), or whether they will decrease in population

abundance and geographic extent (die). To understand the adaptive capacity of plankton populations, we first need to determine what factors determine the spatiotemporal scale of gene exchange. Here I present forthcoming work using genome-wide data from a pelagic copepod (*Pleuromamma xiphias*), coupled with physical and biological environmental variables collected across a 60-degree latitudinal gradient and multiple years to assess what determines the scale of population connectivity in the open sea, and infer how these factors influence the response of *P. xiphias* populations to climate change.

P16

The macroevolution of perfume signals in orchid bees (*Euglossa*): signatures of chemically mediated species recognition and species coexistence

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Theory suggests that traits mediating sexual selection and species recognition should experience distinct evolutionary pressures when closely related species have range overlap. These dynamics may leave macroevolutionary signatures on patterns trait evolution across a clade, such as elevated rates of evolution, and increased trait divergence between sister species and relatives. Here, we test for macroevolutionary signatures produced by species recognition dynamics in the classically studied chemical communication traits of Neotropical orchid bees, *Euglossa*. Using a geographically broad dataset of hundreds of individuals representing 65 species, we ask whether patterns of evolution in *Euglossa* are consistent with theoretical expectations from the hypothesized role of orchid bee perfumes in sexual communication and species recognition.