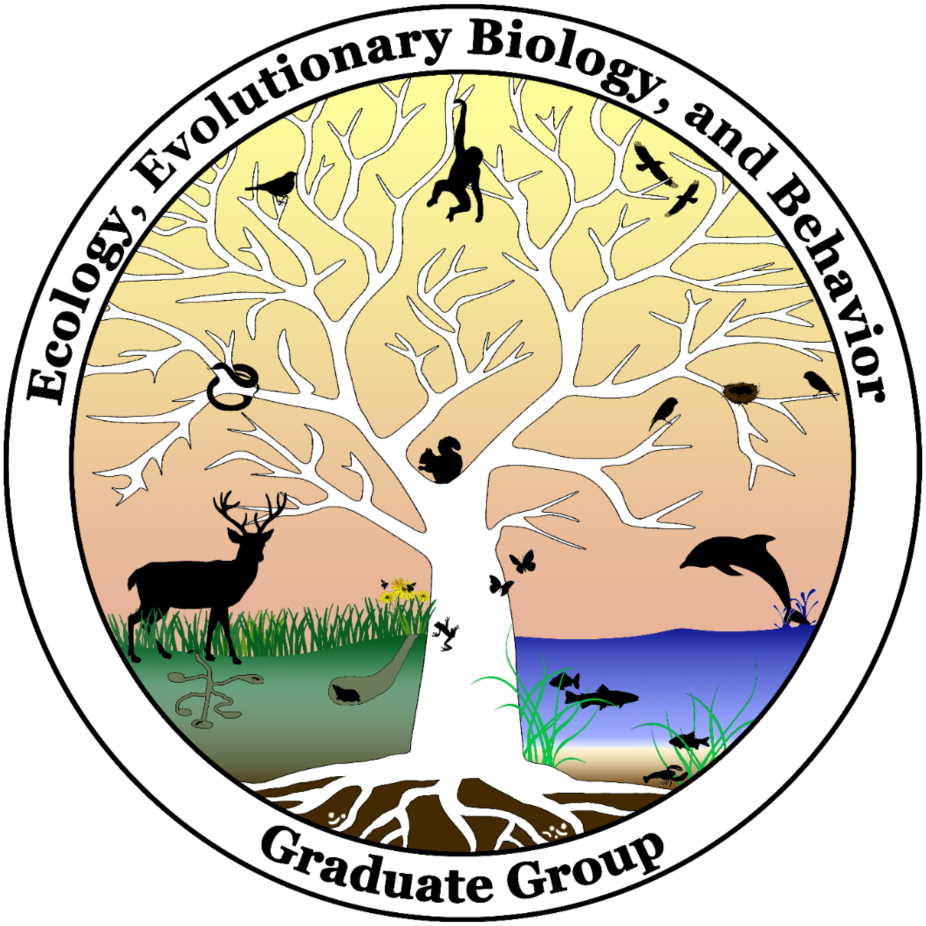
The First Annual

Ecology, Evolutionary Biology, and Behavior



Research Symposium

May 1, 2017
Michigan State University
Henry Center for Executive Development
East Lansing, Michigan

Brought to you by the EEBB Graduate Group

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This event made possible by:

EEBB Research Symposium Planning Committee

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Allison Sussman, Co-Chair
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Kay Holekamp, EEBB Director

MSU Council of Graduate Studies
MSU College of Natural Sciences
MSU College of Agriculture and Natural Resources
MSU Graduate School
MSU Vice President for Research and Graduate Studies

Thank you!

Overview	**EEBB Research Symposium**
8:00-8:45am	Meeting registration Atrium
8:45-9:00am	Welcome A1xx *Kay Holekamp, EEBB Director*
9:00-10:00am	Oral Presentations I: Behavior A1xx *9:00 Tracy Montgomery (IBIO)* *9:15 Tom Wood (ENT)* *9:30 Nikki Cavalieri (IBIO)* *9:45 Ravi Ranjan (PLB/KBS)*
10:00-10:30am	Break & Poster Session I Atrium
10:30-11:30am	Oral Presentations II: Novel Tools A1xx *10:30 Christie Bahlai (IBIO)* *10:45 Shujun Ou (HORT)* *11:00 Matt Farr (IBIO)* *11:15 Rachel Osborn (ENT)*
11:30am-12:05pm	Lightning Talks I A1xx *Jen Lau (PLB/KBS), Marjorie Weber (PLB), Catherine Lindell (IBIO), Yann Dufour (MMG), Jenny Boughman (IBIO), Kevin Liu (CSE), and Elise Zipkin (IBIO)*
12:05-1:00pm	Lunch Atrium
1:00-1:30pm	Lightning Talks II A1xx *David Lowry (PLB), Mariah Meek (IBIO), Elena Litchman (IBIO/KBS), Eric Benbow (ENT), Anthony Cognato (ENT), and Chris Klausmeier (PLB/KBS)*
1:30-2:30pm	Oral Presentations III: Conservation A1xx *1:30 Nate Emery (PLB)* *1:45 Meredith Zettlemoyer (PLB/KBS)* *2:00 Steve Roels (IBIO)* *2:15 Anna Groves (PLB)*
2:30-3:00pm	Break & Poster Session II Atrium
3:00-4:00pm	Oral Presentations IV: Microbiology A1xx *3:00 Connie Rojas (IBIO)* *3:15 Patric Vaelli (IBIO)* *3:30 Peipei Wang (PLB)* *3:45 Abhijna Parigi (IBIO)*
4:00-4:05pm	Keynote Introduction A1xx *Name of presenter here*
4:05-4:50pm	Keynote A1xx *Dr. Manyuan Long, University of Chicago*
4:50-5:00pm	Closing Remarks & Awards A1xx *Name of presenter here*

Directly after the symposium	Reception Lansing	Beggar's Banquet in East

Schedule Detail:
EEBB Research Symposium

8:00am	**Meeting Registration** Atrium	

Please arrive at the Henry Center in advance in order to check in and pick up your name tag. I sure hope there will be coffee.

Stickers! At the registration desk, you will be provided with a selection of stickers with which to decorate your name badge. This will be a fun way to get to know your peers during the day. *Please affix stickers to your paper name tag and not the plastic badge cover—we will reuse the badges in future years.*

8:45am	**Welcome** *Kay Holekamp, EEBB Director*	A1xx

Kay will say a few words about the program, our new research symposium, or whatever else she wants. Or is this Andrea/Alli?

9:00am	**Oral Presentations I: Behavior** A1xx

9:00am	**Social Play Behavior in Spotted Hyenas**

	Tracy Montgomery, EEBB Graduate Student *Dept. Integrative Biology*
9:15am	**Trade-offs in cucumber pollination: Poisoning the hand that feeds?** *Tom Wood, Postdoc* *Dept. Entomology*
9:30am	**Shifting to a new place: influence of developmental timing on life-history schedules in the Order Carnivora** *Nikki Cavalieri, EEBB Graduate Student* *Dept. Integrative Biology, BEACON, MSU Museum*
9:45am	**How do resource use and the resource spectrum determine the structure of competitive communities?** *Ravi Ranjan, EEBB Graduate Student* *Dept. Plant Biology, W.K. Kellogg Biological Station*

10:00am Break & Poster Session I Atrium

Please join us in the Henry Center atrium for refreshments and poster session.

10:30am Oral Presentations II: Novel Tools A1xx

10:30am	**Understanding Monarch butterfly decline using novel break-point analysis tools** *Christie Bahlai, Postdoc* *Dept. Integrative Biology, KBS-LTER*
10:45am	**Tentative title: Where to find big data and how to handle them.** *Shujun Ou, EEBB Graduate Student* *Dept. Horticulture; Plant Breeding, Genetics, and Biotechnology Program*
11:00am	**A hierarchical community distance sampling model to estimate the distributions of carnivores in the Maasai Mara, Kenya** *Matt Farr, EEBB Graduate Student* *Dept. Integrative Biology*
11:15am	**Preliminary phylogeny of the ambrosia beetle genera Coptoborus and Theoborus (Coleoptera: Curculionidae: Scolytinae) from Ecuador** *Rachel Osborn, EEBB Graduate Student* *Dept. Entomology*

11:30am Lightning Talks I A1xx

EEBB faculty have 5 minutes to tell us about their lab.

11:30am	**Experimental evolution in the wild: Long-term ecological experiments and the evolution of mutualism** *Jen Lau, Dept. Plant Biology,* *W.K. Kellogg Biological Station*

11:35am	**Fifty Shades of Grape: The causes and consequences of leaf trait evolution for hidden life on the phyllosphere in wild *Vitis*** *Marjorie Weber, Dept. Plant Biology*
11:40am	**Enhancing agricultural landscapes to increase ecosystem service delivery by vertebrates** *Catherine Lindell, Dept. Integrative Biology* *Center for Global Change and Earth Observations*
11:45am	**Evolution of non-genetic phenotypic diversity in bacterial populations** *Yann Dufour, Dept. Microbiology & Molecular Genetics*
11:50am	**The ecological niche & mate preference in diversification** *Jenny Boughman, Dept. Integrative Biology, BEACON*

11:55am	**FastNet: Fast and accurate inference of phylogenetic networks using large-scale genomic sequence data** *Kevin Liu, Dept. Computer Science & Engineering*
12:00pm	**Quantitative Ecology** *Elise Zipkin, Dept. Integrative Biology*

12:05pm Lunch

Atrium

Please join us in the Henry Center atrium for lunch.

1:00pm Lightning Talks II A1xx

EEBB faculty have 5 minutes to tell us about their lab.

1:00pm	**The gene regulatory landscape of local adaptation** *David Lowry, Dept. Plant Biology,* *Plant Resilience Institute*
1:05pm	**Genomics to the rescue: Improving conservation of imperiled fish populations** *Mariah Meek, Dept. Integrative Biology*
1:10pm	**Community ecology of phytoplankton and other**

	microbes *Elena Litchman, Dept. Integrative Biology,* *W.K. Kellogg Biological Station*
1:15pm	**New dimensions of insect-microbe interactions in aquatics, disease and forensics** *Eric Benbow, Dept. Entomology*
1:20pm	**Holistic insect systematics** *Anthony Cognato, Dept. Entomology,* *A.J. Cook Arthropod Research Collection*
1:25pm	**Theoretical Ecology** *Chris Klausmeier, Dept. Plant Biology,* *W.K. Kellogg Biological Station*

1:30pm Oral Presentations III: Conservation

A1xx

1:30pm	**Flowers reveal flammability in California shrublands** *Nate Emery, Postdoc* *Dept. Plant Biology*

1:45pm	**Do functional groups predict local species loss?** *Meredith Zettlemoyer, EEBB Graduate Student* *Dept. Plant Biology, W.K. Kellogg Biological Station*
2:00pm	**TBD** *Steve Roels, EEBB Graduate Student* *Dept. Integrative Biology,* *Environmental Science and Policy Program*
2:15pm	**Experimental evidence for year effects in ecological restoration** *Anna Groves, EEBB Graduate Student* *Dept. Plant Biology*

2:30pm Break & Poster Session II

Atrium

Please join us in the Henry Center atrium for refreshments and poster session.

3:00pm Oral Presentations III: Microbiology A1xx

3:00pm	**Age, social group, and body-site related variation in spotted hyena microbiota** *Connie A. Rojas, EEBB Graduate Student* *Dept. Integrative Biology, BEACON*

3:15pm	**Symbiotic bacteria underlie toxin production and voltage-gated sodium channel evolution in the rough-skinned newt (*Taricha granulosa*)** *Patric Vaelli, EEBB Graduate Student* *Dept. Integrative Biology, BEACON*
3:30pm	**Factors contributing to gene family size variation among *Solanaceae* species** *Peipei Wang, Postdoc* *Dept. Plant Biology*
3:45pm	**The evolution of scorpion venom resistance in grasshopper mice through modifications to conserved voltage gated sodium ion channels** *Abhijna Parigi, EEBB Graduate Student* *Dept. Integrative Biology*

4:00pm	**Keynote Introduction** *Name of speaker here*	A1xx

4:05pm	**Keynote Address** *Dr. Manyuan Long, University of Chicago*	A1xx

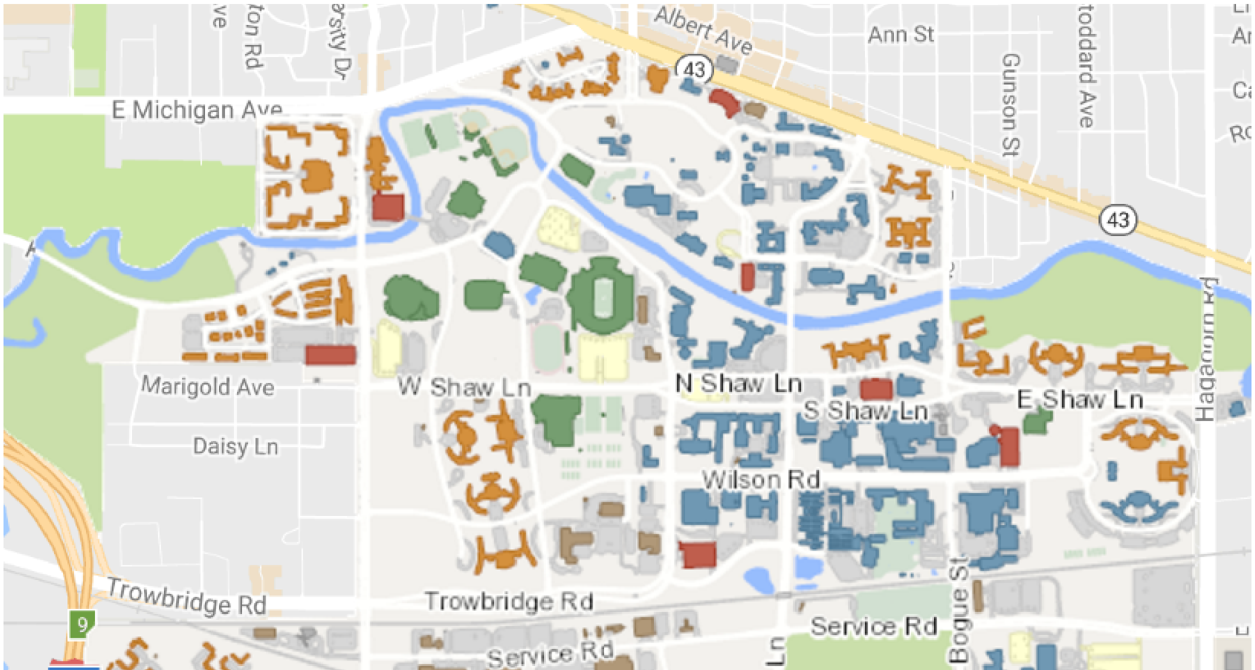
We’ll include some information here about the speaker and/or the address itself.

4:50pm	**Closing Remarks & Awards** *Name of speaker here*	A1xx

The following awards will be presented…

After	**Reception**	Beggar’s Banquet, East Lansing

Campus Map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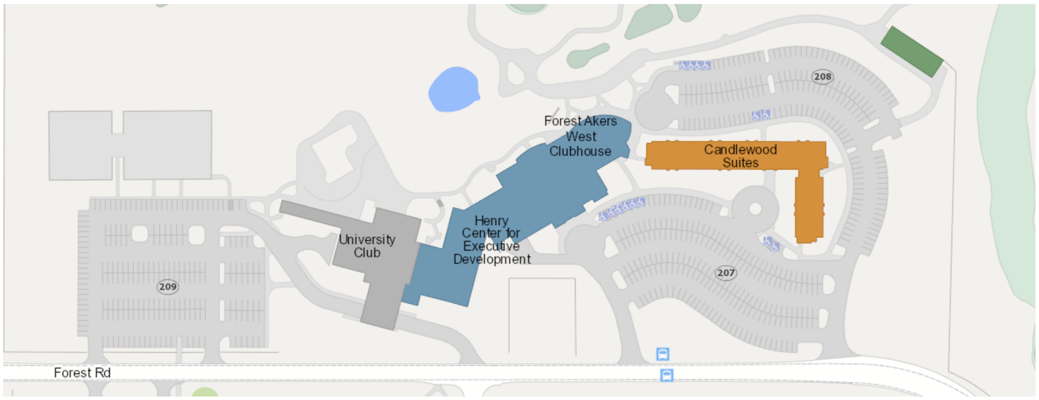
Henry Center for Executive Development



Beggar’s Banquet

About EEBB

Abstracts

Alphabetical by presenting author's last name.
All authors at Michigan State University unless otherwise stated.

Understanding Monarch butterfly decline using novel break-point analysis tools

Christie Bahlai, Integrative Biology, KBS-LTER
Elise Zipkin, Integrative Biology

Because of their high capacity for reproduction, insect populations are often naturally quite variable. In addition to internal dynamic rules governing abundance, environmental conditions and resource availability can dramatically influence the size of populations, however, dis-entangling these multiple drivers can prove a profound challenge. Yet, for invasive species and species of conservation concern alike, understanding how external drivers affect the internal dynamic rules is essential for effective management. In response to this challenge, I developed a tool for unbiased detection of shifts in dynamic regime of a population, as documented by time-series data. The tool uses an iterative, likelihood based approach to identify and quantify shifts in the internal rules governing a population's dynamics by comparing the fit of models based on the set of all possible shift-point combinations. In this research, the Ricker population model was used, and thus the model produced estimates of r, the intrinsic growth rate, and k, the carrying capacity of the population during each phase between shifts. Once identified, shifts and changes to r and k can be examined in the context of external drivers. We apply this tool to overwintering populations of Monarch butterflies to gain insights into drivers of their dynamics. Numbers of monarch butterflies at overwintering sites in Mexico have been in general decline for several decades, however, there has been considerable debate in the literature regarding the rates and drivers of the observed declines. Fitting the regime shift model to observations of total area occupied by overwintering monarchs within the Monarch Butterfly Biosphere Reserve from 1994-2016 suggests a dynamic with three apparent phases. The model suggests a step-wise decline in carrying capacity, with k declining by almost 56% after the 2003, and again by just over 50% after 2008. Meanwhile, an apparent 70% compensatory increase in r is observed during the shift after 2003, and this value of r remains constant during the shift in 2008. Modelling the interaction as a linear decline in k instead produces a similar, but lower-performance fit. These results will be examined in the context of land use and climate changes occurring in the Monarch's Midwestern US breeding

habitat during the time of the shifts.

Although its distant origins are up for debate, Christie independently created and popularized #otherpeoplesdata on Twitter after a particularly punishing encounter with a poorly formatted spreadsheet in late 2013.

Factors that influence the abundance of birds in agricultural land cover

Melissa Brady, Integrative Biology
Catherine Lindell, Integrative Biology

Birds are capable of causing extensive crop damage, especially to fruit crops. Despite this, there is limited knowledge on the species of fruit-eating birds found in different fruit crops across the United States. Moreover, it is unknown whether there are regional variations in species presence for crops grown in different geographical areas. There is also little knowledge about how the abundance patterns for fruit-eating birds vary by crop, region, and with differences in the surrounding land cover. This lack of knowledge can be a hindrance for those trying to find solutions to the problem of bird damage in fruit crops. In this study, we combine several large-scale data sets to investigate fruit-eating bird presence in fruit crops. Bird abundance information was collected via point counts conducted for the Speciality Crop Research Initiative, a multi-year project investigating bird damage conducted across different regions in the United States. Land cover data was collected via the National Agriculture Imagery Program. We first identify fruit-eating bird species found in sweet cherries, blueberries, grapes and apples grown in 3 different regions: Michigan, New York, and the Pacific Northwest. We then investigate the impact that factors such as region, crop type, and small- and large-scale land cover heterogeneity and composition have on the abundance of fruit-eating birds. We also separately investigate these effects in several species that were both abundant in our study, and that have been found in previous studies to cause fruit crop damage: American Robins (*Turdus migratorius*), European Starlings (*Sturnus vulgaris*), and Cedar Waxwings (*Bombycilla cedrorum*).

Melissa is a graduate student.

Shifting to a new place: Influence of developmental timing on life-history schedules in the Order *Carnivora*

Nikki Cavalieri, Integrative Biology, BEACON, MSU Museum
Kay E. Holekamp, Integrative Biology
Barbara L. Lundrigan, Integrative Biology, MSU Museum

During development energy demands for survival, growth, and reproduction must be balanced. Trade-offs occur between competing traits. These trade-offs are likely to involve profound changes in life-history schedules. The goal of this research is to explore the coevolution of skull ontogeny and timing of life history events (e.g., weaning, age at first reproduction) in the Order Carnivora. Here we characterize the patterns of evolutionary change in the timing of morphological maturity of the cranium and mandible for 7 species representing 5 families. We ask whether interspecific differences in the timing of morphological maturity are reflected in life history schedules. Skulls representing individuals ranging from 1 day to several years of age were photographed and digitized in three views (ventral cranium, lateral cranium, and lateral mandible). Ontogenetic change in skull size (centroid size) and shape (Procrustes distance from the average for the youngest specimens) were plotted for each species and the ages at maturity compared. Age at maturity for skull size and shape was defined as 95% of the asymptotic (adult) value from nonlinear growth models selected using Aikaike Information Criterion. Species were compared using residuals from plots of skull size maturity and shape maturity on adult body size. Preliminary data suggest the Crocuta crocuta exhibits the most protracted skull development. C. crocuta is an extreme outlier, possibly reflecting its unusually robust skull and durophagous diet. C. crocuta reaches sexual maturity later than expected by body size. This relatively late reproduction suggests that there may be a trade-off between dietary challenge and timing of development. Phylogeny appears to explain some of the interspecific patterns. Members of the family Canidae have a characteristic pattern of skull maturation. The Feliformia reach maturity for skull size and shape after reaching sexual maturity, in contrast to most Caniformia.

Nikki is a grad student.

Getting to the root of it: Differences in root morphology and biological nitrogen-fixation among switchgrass varieties

Tayler Chicoine, Integrative Biology, Ecological Food and Farming Systems
Sarah S. Roley, W.K. Kellogg Biological Station,
Great Lakes Bioenergy Research Center
G. Philip Robertson, Plant, Soil and Microbial Sciences,
W.K. Kellogg Biological Station, Great Lakes Bioenergy Research Center
Lisa Tiemann, Plant, Soil and Microbial Sciences
Maren Friesen, Plant Biology
Sarah Evans, Integrative Biology, W.K. Kellogg Biological Station

Switchgrass (*Panicum virgatum*) is a C4 perennial grass being explored for its promise as a low-input bioenergy crop. Switchgrass has unique nitrogen (N) conservation strategies, such as associating with free-living N-fixers (diazotrophs) that help it survive in N-limited, degraded soils. A recent study found that a higher yielding switchgrass variety associated with a larger community of diazotrophs than a lower-yielding variety, though it is unknown what drives these differences in their diazotrophs. Root morphology, also shown to vary among switchgrass varieties, is known to influence root exudation rates, which directly impact the amount of carbon (C) available to energetically-demanding N-fixation processes. We are investigating the relationship between specific root length (SRL) and the N-fixing potential of the microbial communities across 12 switchgrass varieties, at Kellogg Biological Station in southwest Michigan. We predict that N-fixation rates and gene abundance (nifH) differ among the varieties and that this is driven by differences in root morphology. Specifically, if thinner root systems (higher SRL) provide more C through exudation, we expect to find higher N-fixation potential. Discerning what plant characteristics support diazotrophic communities has important implications for the development of low-input agricultural systems.

Tayler enjoys working for hours in her garden and singing to her plants.

Scn4aa drives EOD amplitude in mormyrid weakly electric fish

Savvas James Constantinou, Integrative Biology
Jason R. Gallant, Integrative Biology

Mormyrid weakly electric fish produce an electric field to navigate their environment and to communicate. The gene scn4aa encodes for a voltage gated sodium channel protein that is only expressed in the electric organ and has been implicated in the evolution of the electric organ discharge (EOD). To determine a functional role of scn4aa, I generated scn4aa knockout *Brienomyrus brachyistius* mormyrid fish using CRISPR/Cas9 genome engineering and scn4aa knockdown adult *B. brachyistius* fish using morpholinos. Genomic knockdowns of scn4aa result in larval EODs with amplitude barely detectable above baseline. Knockdowns of scn4aa in adult fish show a dose dependent response of EOD amplitude reduction, which phenocopy the genomic knockouts. We have some preliminary evidence that scn4aa knockdown has effects on the expression of other genes identified in the electrocyte gene regulatory network.

Savvas is probably the first guy you'll meet who can give a high-six or three thumbs up!

Genetic variation and biogeography of the spotted gar *Lepisosteus oculatus* from core and peripheral populations

Solomon R. David, Integrative Biology
Jeremy J. Wright, New York State Museum

The spotted gar (*Lepisosteus oculatus*) shows a disjunct natural distribution, with a core population extending from the central Mississippi River Basin to the U.S. gulf coast and a peripheral population in the southern Great Lakes Basin. Despite significant conservation concerns for this species in the Great Lakes watersheds where it occurs, few genetic examinations and comparisons of these populations have been performed. We investigated inter- and intrapopulational variation in several mitochondrial genetic markers (cytochrome oxidase subunit I, COI; cytochrome oxidase subunit II, COII; and 16S rRNA, 16S) from spotted gars taken from core and peripheral populations. Genetic diversity was highest in the Mississippi River Basin, lowest in the Great Lakes Basin, and most divergent in the western Gulf Coast Basin. Average genetic distance between core and peripheral populations was over an order of magnitude less than that seen between *L. oculatus* and its sister species, *L. platyrhincus*, although a significant correlation was found between genetic and geographical distance in *L. oculatus*. Genotypic divergence in spotted gars is likely to be related to a combination of geographic isolation and founder effects associated with recent colonization following glacial retreat. Despite its apparent lack of significant genetic differentiation or diversity, the Great Lakes population of spotted gars has previously been shown to be a unique component of the species, being adapted to life at higher latitudes with shorter growing seasons. Additional studies are needed to determine the genetic mechanisms underlying this adaptation, as well as potential morphological differentiation between spotted gar populations.

Solomon has more gar skulls than the Predator alien;
and yes, Predator collected gar skulls.

ShinyOrthologs: A new tool for comparative genomics and transcriptomics

Colin Diesh, Integrative Biology
Jason Gallant, Integrative Biology

Genomics and transcriptomics data for non-canonical model systems has dramatically increased in the past decade. Numerous efforts to build generic bioinformatics toolsets have been constructed to centralize and standardized data processing (e.g. GMOD, Tripal, or Intermine), however few focus on comparative (i.e. inter-species) dimensions to their data. To address this problem, we created ShinyOrthologs, a web application built using RStudio Shiny, which allows users to inspect orthologous gene groups across de-novo assembled transcriptome and genomics data. ShinyOrthologs plots gene expression data across species, creates multiple sequence alignments of orthologous genes, and allows manual curation of the ortholog groups using editor tools. We also allow comparative visualizations such as synteny and multiple whole-genome alignment views where data is available. We will demonstrate the utility of such a tool using the example of recently available electric fish genome and transcriptome data.

Colin thinks they keep it too hot in the Natural Sciences building,
but it isn't really under his control so he just opens the window.

Flowers reveal flammability in California shrublands

Nate Emery, Plant Biology

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Nate has done plant transects across a naval bombing range.

A hierarchical community distance sampling model to estimate the distributions of carnivores in the Maasai Mara, Kenya

Matt Farr, Integrative Biology
David S. Green, Institute for Natural Resources, Oregon State U.
Kay E. Holekamp, Integrative Biology
Gary J. Roloff, Fisheries and Wildlife
Elise F. Zipkin, Integrative Biology

Research is limited in resolving conservation issues when approaches lack efficiency in either survey design or data analysis. Researchers constantly update and improve methods to minimize the limitations of outdated approaches. However, survey designs are often constrained by external factors (e.g. funding, legal restrictions, environmental hazards) which prevent an idealistic design. Data analysis is often relied upon to correct or account for constraints in sampling design, but standard (single level) analyses are narrow in their attempt to model ecological systems containing multiple interconnected levels. With advancements in high powered computing and the development of hierarchical models, researchers are able to better model complex ecological systems while accounting for inefficiencies in survey design.

Hierarchical models describe ecological systems by parsing out processes into multi-level statistical and mathematical models. Relationship within an ecological systems are defined by the structure and connections between levels within a hierarchical model. Integrating data from multiple sources is a recent improvement in hierarchical modeling to more precisely estimate model parameters. Datasets describing similar ecological states or processes are linked together within a unified framework by sharing and estimating a common parameter. Multi-species or community models integrate data from a variety of species into a single model. Species-specific parameters are drawn from a common hyperdistribution; thus, the model shares common hyperparameters across species within the community. The integration of multiple species within a single hierarchical model via hyperparameters allows for both estimation of community wide responses and species-specific effects for rare or elusive species.

Community modeling was recently implemented in a distance sampling framework to develop a hierarchical community distance sampling (HCDS) model. Distance sampling is a classical method to estimate the density or abundance of a single species. The HCDS model expands the capability of distance sampling to multiple species-specific estimates while measuring community wide effects. Here we implement a HCDS model for a carnivore community in the Maasai Mara National Reserve (MMNR).

Carnivore communities in the Serengeti-Mara ecosystem, including the MMNR, are among the most diverse in the world, but human-wildlife conflict threatens the continuation of this community. To understand the impact of anthropogenic disturbance on the carnivore community, we compare two disparate management regions within the MMNR. The Mara Triangle experiences minimal disturbance while the Narok region contains high frequency of human-wildlife conflict. Using a HCDS model we estimate the community wide and species-specific effects of the Narok region on carnivore abundance and compared species' densities between regions. Model results suggest varying response among species to disturbance within the Narok region, but a neutral community wide effect. Estimated densities of lion and black-back jackal were comparatively low in the Narok region while spotted hyena and black-backed jackals were high. The results of this community analysis in the MMNR demonstrate the importance of using hierarchical and integrated modeling for conservation in complex ecological systems.

Matt is a grad student.

TBD

Ava Garrison, Plant Biology, BEACON

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Ava is a graduate student.

Evolution through the lens of a tourist camera: Social media enables remote-sensing of *Gallus gallus* genotypes, phenotypes, and demography

Eben Gering, Integrative Biology
Thomas Getty, Integrative Biology
Levi Storks, Biological Sciences, U. Missouri Columbia

Evolutionary impacts of domestication have been well studied, but feralization (when domesticated organisms return to the wild) has received much less attention. Each year Kauai tourists upload thousands of feral chicken images and videos to social media. These spatially and temporally indexed media permit us to study the island's feral chickens (*Gallus gallus*) remotely, without having to catch a single bird. In this study, we use social media featuring feral roosters and hens to study variation in heritable traits and reproductive biology 1) among ecologically distinct habitats, and 2) from 2001-2015. We discovered that feral roosters exhibit extraordinary trait variation, but it is (mostly) unstructured among ecologically distinct habitats. This suggests extensive geneflow, which appears to have eroded a historically documented cline. Nonetheless, spatial variation in a subset of sexual and plumage traits (spurs and white feathering) suggests that local adaptation and/or plasticity may act to diversify feral phenotypes. We also discovered that Kauai's Red Junglefowl, which were historically seasonal breeders, now breed year round. This discovery a) may stem from hybridization with artificially selected "layer" breeds, b) helps explain recent population growth, and c) could abet management efforts. Social media can thus offer powerful insight to the feralization process, and to eco-evolutionary dynamics of non-human populations.

Eben occasionally eats his study organisms.

Experimental evidence for year effects in ecological restoration

Anna Groves, Plant Biology
Lars Brudvig, Plant Biology

Variation in outcomes of ecological restoration projects is commonplace, and at times these outcomes do not match practitioners' goals. This mismatch suggests a gap in our ecological knowledge of how communities assemble: if we cannot successfully rebuild a plant community, we have yet to learn something about its assembly. A better understanding of how restored ecological communities assemble will thus inform both ecology and restoration. It is suspected that year effects— environmental conditions at the outset of a restoration project—may contribute to variation among restoration efforts. However, a lack of experimental tests limits scientific understanding of the mechanisms driving year effects and their long term impact. We conducted an experiment to evaluate year effects on assembling plant communities in tallgrass prairie restorations. We restored prairie at the same site and followed identical methods in three different years and, within each planting year, manipulated precipitation with rain-out shelters. Our past work shows that seedling establishment varied across years, simulated plating-year precipitation treatments, and years within precipitation treatments. We now ask how plant communities vary across planting years and precipitation treatments both in (1) the planting year and (2) in the second year after planting.

Plant communities in the planting year were significantly different across watering treatments ($R2=0.08$, $p<0.001$) and planting years ($R2=0.20$, $p<0.001$). However, in the second year following restoration, as the prairies developed, there was no longer a significant difference between communities that had been planted in different years ($R2=0.15$, $p=0.13$) or under different watering treatments ($R2=0.06$, $p=0.07$). Total sown forb abundance, a metric of restoration success, also differed across planting years initially but converged in the second year. The year after good planting conditions (i.e. in plots with high forb establishment), the number of sown forbs decreased 25%; and the year after poor planting conditions (i.e. plots with low forb establishment, e.g. after drought treatment), the number of sown forbs increased 57% but did not recover to non-drought levels. We conclude that inter-annual variation in both precipitation and some non-precipitation factor(s) are important drivers of year effects; however, these effects already begin to dampen by the second year. This suggests that the common assumption that planting year conditions may lead to variable restoration success is not necessarily true; however, further research is needed to address how planting year conditions alter the success of restoration projects over longer time scales and across various site conditions (e.g. soil moisture).

Anna spends her free time singing in Sistrum (Lansing's women's chorus) and playing Dungeons and Dragons.

Title

Travis Hagey, BEACON

An environmental cue for settlement and metamorphosis in *C. teleta* is reduced mud ($H2S$ odor to humans). To investigate sensory receptors in *C. teleta* larvae, we used specific fluorescent antibodies. Development of sensory neurons often involves cell adhesion molecules (NCAMS). HNK-1 antibody, commonly used to trace neural crest cells in vertebrates, binds to epitopes within the ciliary bands in *C. teleta* indicating sensory receptors. HNK-1 is an acidic glycoepitope. One of us (Zipser) raised a panel of monoclonal antibodies (mAbs) against neutral glycoepitopes in the leech sensory nervous system. LAN3-2 binds to a β-(1,4)-mannose polymer, the antigenic part of a transmembrane molecule that affects ion channels. LAN3-2 and LAZ-369 bind to different regions of the nuchal organs (purported chemosensory structures) in *C. teleta* larvae. We find that these mAbs also bind to very specific regions in other invertebrate larvae (Nereis[HS1] , Crepidula). We propose that these antibodies raised against neutral epitopes in the leech are and will be helpful tools in understanding the sensory nervous systems of many invertebrates.

Travis is a post-doc for the BEACON Center for Evolution in Action.

FastNet: Fast and accurate inference of phylogenetic networks using large-scale genomic sequence data

Hussein Hejase, Computer Science & Engineering,
Quantitative Biology Program, BEACON
Kevin J. Liu, Computer Science & Engineering

Advances in next-generation sequencing technologies and phylogenomics have reshaped our understanding of evolutionary biology. One primary outcome is the emerging discovery that interspecific gene flow has played a major role in the evolution of many different organisms across the Tree of Life. To what extent is the Tree of Life not truly a tree reflecting strict "vertical" divergence, but rather a more general graph structure known as a phylogenetic network which also captures "horizontal" gene flow? The answer to this fundamental question not only depends upon densely sampled and divergent genomic sequence data, but also computational methods which are capable of accurately and efficiently inferring phylogenetic networks from large-scale genomic sequence datasets. Recent methodological advances have attempted to address this gap. However, in a recent performance study, we demonstrated that the state of the art falls well short of the scalability requirements of existing phylogenomic studies. The methodological gap remains: how can phylogenetic networks be accurately and efficiently inferred using genomic sequence data involving many dozens or hundreds of taxa? In this study, we address this gap by proposing a new phylogenetic divide-and-conquer method which we call FastNet. Using synthetic and empirical data spanning a range of evolutionary scenarios, we demonstrate that FastNet outperforms state-of-the-art methods in terms of computational efficiency and topological accuracy.

Hussein is a graduate student.

How to get from here to there when you are very small, and how will you know you've arrived?

Susan Hill, Integrative Biology
Barbara Boyer, Dept. Biology, Union College, NY
Birgit Zipser, Physiology

Dispersal often involves a larval stage. Marine invertebrate larvae are usually small, move by cilia, and survive only a limited time as larvae. They are carried by waves and currents; however, in some cases, where they settle is not random. *Capitella teleta*, the most opportunistic of the capitellid complex, are small, marine polychaete worms occurring in areas of high organic content like estuaries and salt marshes. High organic content may reflect environmental disturbances (storms, whalefalls) but often results from anthropogenic disturbances like off-shore dredging, oil spills, fish farms, polluted harbors. Thus, capitellids are often considered an indicator species. They are important ecologically because, as early colonizers, they both serve as a source of food for other bottom dwellers (crabs, flounder) and modify the substrate, preparing the way for future succession. *C. teleta* larvae are competent to metamorphose immediately on emergence or to remain in the water column over a week. Thus, they can settle in the local environment or a new site many kilometers away. *C. teleta* can be cultured in the lab and the genome has been sequenced. We have investigated the development of locomotory and sensory nervous systems to better understand species distribution.

Susan is a faculty member in IBIO.

Pain receptor adaptability in an evolutionary arms race

Lauren Koenig, Integrative Biology
Ashlee Rowe, Integrative Biology
Matthew Rowe, Integrative Biology

Pain sensation allows an organism to perceive danger, respond appropriately, and avoid additional harm. Some prey organisms capitalize on the pain pathway of their predators through using painful venoms or sprays. Predators, in turn, may evolve resistance to those toxins. These adaptations represent an evolutionary paradox. Selection for higher pain thresholds is likely constrained by the necessity of feeling pain. Predatory grasshopper mice (*Onychomys torridus*) and pinacate beetles (*Eleodes longicollis*) are an ideal system for examining an evolutionary arms race showcasing counter-selection against prey defenses through modifications to the pain pathway. Pinacate beetles evolved a benzoquinone spray that is intolerable for most mammalian predators, tolerable but still repellent to deer mice, and ineffective in deterring grasshopper mice. I will identify differences in the predatory behavior and benzoquinone tolerance between grasshopper mice, deer mice, and kangaroo rats. I will compare these differences to genetic and physiological variability in TRPA1, a conserved pain receptor critical for detecting noxious stimuli, including benzoquinones. TRPA1 receptors are involved in inflammatory diseases, neuropathic, and migraine pain. Basic research aimed at understanding how changes in structure produce functional changes that confer insensitivity to pain-inducing chemicals would be essential for designing drugs that block TRPA1-mediated pain.

Lauren's last field job required licenses for boating and shooting fireworks.

Tracking disease and fungal community structure in chestnut blight cankers on American chestnut

in Michigan and Wisconsin

Matt Kolp, Plant Biology
Mark Double, West Virginia University
William MacDonald, West Virginia University
Dennis Fulbright; Plant, Soil, & Microbial Sciences
Andrew Jarosz, Plant Biology

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Matt is a very good golfer.

The distribution of fitness effects in small populations

Thomas LaBar, Microbiology and Molecular Genetics, BEACON
Christoph Adami, Microbiology and Molecular Genetics

De-novo mutations are a primary source of genetic variation upon which natural selection can act. Therefore, to understand the mode of selection in populations, one must know the distribution of fitness effects (DFE) of novel mutations. For example, a species's rate of adaptation to a novel environment is dependent on the DFE of beneficial mutations, while the intensity of purifying selection is determined by the DFE of deleterious mutations. Although the DFE for many species is known in a broad sense, the evolutionary factors that shape the DFE are generally uncertain. Here, I will discuss digital evolution experiments on the role of population size and genetic drift in shaping the distribution of fitness effects. The strong genetic drift inherent to small populations leads to the evolution of DFE's with a deficit of small-effect deleterious mutations when compared to DFE's from large populations. Small populations evolve altered DFE's because small populations can only adapt to and maintain themselves on fitness peaks with few small-effect deleterious mutations. They adapt to these "drift-robust" peaks by fixing rare large-effect beneficial mutations and mutations with large epistatic effects. Large populations adapt to peaks with many small-effect deleterious mutations ("drift-fragile" peaks) by fixing abundant small-effect beneficial mutations. These results suggest that the adaptive constraints posed by genetic drift cause small populations to evolve different genetic architectures than large populations. They also suggest that the strength of novel deleterious variation within a population is dependent on the demographic history of that population, not just its current demography.

Thomas is a graduate student.

Short and long term effects of a non-native allochthonous vertebrate resource on macroinvertebrates and biofilm communities in a headwater stream

Courtney Larson, Entomology, Certification in College Teaching Program
Courtney Weatherbee, Entomology
Jennifer L. Pechal, Entomology
Brandon Gerig, Dept. Biological Sciences, University of Notre Dame
Dominic T. Chaloner, Dept. Biological Sciences, University of Notre Dame
Gary Lamberti, Dept. Biological Sciences, University of Notre Dame
M. Eric Benbow, Entomology, Osteopathic Medical Specialties

Salmon runs serve as an important annual input of organic matter into headwater streams. In Michigan, salmon have been introduced into the Great Lakes, and their carcasses have unknown effects on the aquatic communities residing in the headwater streams in which they spawn. Our objective was to determine the effects of salmon carrion introduction on aquatic macroinvertebrate and microbial communities over time. Macroinvertebrate and microbial communities were sampled before (September), during (October), and after (November to August) carcass introduction, both at the introduction site and at upstream reference sites. The study was repeated twice over a two-year period (September 2014-August 2016). Overall macroinvertebrate diversity was not significant by carcass introduction, but epilithic biofilm communities had higher diversity in carcass addition reaches. There was a significant difference in the biofilm microbial communities between the control and carcass areas (PERMANOVA, $p<0.001$). These trends suggest potential dispersal of microbial communities exogenous to salmon carrion to macroinvertebrates, indicating the important role carrion may play in microbial ecology of lotic systems.

Courtney plays the violin!

The role of epigenetics in phenotypic plasticity: An extension of signal detection theory

Zach Laubach, Integrative Biology, BEACON

Kay E. Holekamp, Integrative Biology
Thomas Getty, Integrative Biology
Wei Perng, Nutritional Sciences, Epidemiology, U. Michigan
Dana Dolinoy, Nutritional Sciences, Environmental Sciences, U. Michigan
Christopher Faulk, Animal Sciences, U. Minnesota

Phenotypic plasticity enables organisms to respond adaptively to environmental factors across development, despite an unchanging genotype. However, phenotypic responses to information about the environment do not universally improve an organism's health or fitness later in life; instead this depends on the fidelity of information transmission, and whether or not the predicted phenotype is matched to the environment. Epigenetic modifications to the genome, like DNA methylation, are a mechanism of phenotypic plasticity because these chemical and structural changes in the DNA are responsive to environmental factors and influence gene expression. Here we develop a heuristic framework that asks the question, how can signal theory improve understanding of the mechanisms and adaptive value of phenotypic plasticity, specifically when information about the environment is communicated throughout development via epigenetics? We approach this question by investigating methylation as part of a signal system, exploring the timing of DNA methylation modifications and the stability of epigenetic signal transmission, and by assessing the probability that an epigenetic signal leads to adaptive phenotypic plasticity.

Zach enjoys fly fishing in small streams/lakes for native trout species.

TBD

Kenna Lehmann, Integrative Biology, BEACON

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Kenna does ceramic pottery to unwind.

Effect of grazing on the relationship between productivity and biodiversity via changing the structure and composition of plant functional groups in the typical steppe on the Mongolian Plateau

Maowei Liang, Geography,
Visiting from School of Ecology and Environment, Inner Mongolia University
Jiquan Chen, Geography

Grazing impacts on the productivity and biodiversity would be inevitable in rangeland ecosystem, even though aboveground biomass, species diversity and functional diversity. However, it is not clear that how grazing impact on the relationship among the productivity, species diversity and functional diversity via changing the community structure and composition, which are richness, density, and height of plant functional groups (PFGs) in the community. The three-grazing levels experiments were conducted in the typical steppe on the Mongolian Plateau, including no grazing (Fenced/F), light grazing (LG), and moderate grazing (MG) in 2012 (wet year) and 2013 (dry year).

Aboveground biomass (wet and dry residual matter), density, height of species were monitoring monthly in growing season (May - September). All of species were classified as 4 plant functional groups, which are perennial bunchgrass (PR), perennial rhizome grass (PR), perennial forbs (PF), annuals and biennials (AB). We found that: 1) grazing increased the AB and decreased PF, especially in wet year, but LG increased PB dramatically among the relative-AGB, richness, and density instead of the height. 2) It were divergent that the relationships between productivity and diversity among the F, LG, and MG. 3) there were significant negative correlations between PF with AB (Coeff. = -0.79) in wet year and PB with PR (Coeff. = -0.77) in dry year. 4) In the dry year, the height was raising and the richness were decreasing of the community, and the density were decreasing both LG and MG instead of increasing of the fenced community (F); SD and FD were decreased instead of no difference in AGB in the F, but AGB was decreased instead of increasing SD and FD in the LG, and AGB, SD, and FD were decreased in the MG. Overall, this study highlights how grazing effect on the relationships among aboveground biomass, species diversity and functional diversity via changing the structure and composition of plant functional groups in dry and wet year.

Maowei is a visiting graduate student.

TBD

Mauricio Losilla, Integrative Biology, BEACON

Jason R. Gallant, Integrative Biology, BEACON

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TBD

Barb Lundrigan, Integrative Biology, BEACON, MSU Museum

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The role of rapid adaptation in population establishment

Susan Magnoli, Plant Biology, W.K. Kellogg Biological Station

Evolution was once assumed to only occur slowly over long time scales, but many recent studies have found that rapid adaptation (adaptation that occurs on an ecological timescale) can occur across a wide range of taxa and in many biological contexts, and can potentially alter the outcomes of ecological interactions and ecosystem-level processes. Rapid adaptation is also hypothesized to influence the establishment of species in new habitats, as evolutionary theory predicts that rapid adaptation can have important demographic consequences for colonizing populations. However, there is little empirical evidence to support this prediction. I combined a reciprocal transplant experiment with a resurrection experiment to compare populations of the annual legume *Chamaecrista fasciculata* planted 6 years ago in replicated prairie restorations to each other and to their original source population. I examined whether evolutionary changes had occurred in these recently established populations, whether these changes were predicted by estimates of selection, and whether plant populations showed signs of local adaptation. I found evidence for evolutionary change in recently established populations of *Chamaecrista*, with extant populations differing in phenology, root nodule production, and height from their original source population. These changes were for the most part predicted by estimates of selection, with extant *Chamaecrista* populations showing shifts in trait values corresponding to the direction of selection. Extant populations also showed sign of local adaptation, with higher fitness than the original source population. This suggests that rapid adaptation can occur in recently established populations; further analysis will indicate whether this adaptation influences population growth rates in ways that affect establishment.

Susan enjoys knitting hats for cats.

Identification and validation of microsatellite markers for SSR genotyping of *Rhizoctonia solani* AG2-2

Doug Minier; Plant, Soil, & Microbial Biology; Plant Pathology
Linda E. Hanson, USDA-ARS East Lansing, MI
Marina L. Ramone, USDA-ARS Salinas, CA
Frank N. Martin, USDA-ARS Salinas, CA

Rhizoctonia solani (Kühn) AG2-2 is an important, soilborne pathogen of sugarbeet (*Beta vulgaris*) as well as a number of other crops. An improved understanding of the diversity and population structure of this pathogen could benefit management practices. Microsatellites have become an invaluable tool for these types of studies; so in order to develop a set of useful microsatellite markers, we utilized an in-silico approach to identify potential loci. One isolate from each of three distinct phylogenetic groups was sequenced on a HiSeq4000 and assembled using CLC Genomics Workbench. Loci that were at least trinucleotide and of a suitable repeat length were selected from isolate Rs850. These preliminary loci were compared to the other two isolate assemblies to determine if there were differences in repeat length, there were no indels in the flanking regions and conserved primers could be developed. We generated 33 potential marker loci that were tested on isolate Rs850 for PCR amplification using a single annealing temperature and MgCl2 concentration. Those that amplified well under these conditions were then tested on eight additional isolates, which represented the three distinct phylogenetic groups. Sixteen primer pairs amplified all nine isolates and showed probable polymorphisms in fragment length. These primer sets were paired based on suitability for multiplexing and labeled with either Hex or 6-Fam fluorescent dyes for automatic size detection on an ABI 3730 sequencer. Those that appear to be suitable markers will be further screened on 22 additional isolates to confirm sufficient variation. We expect that the effort invested by sequencing multiple isolates and developing markers from those assemblies will increase the probability that preliminary SSR marker selections will be successful.

Doug worked as a tool and die maker until 2008 when the auto industry crashed and he decided to change careers.

Social play behavior in spotted hyenas

Tracy Montgomery, Integrative Biology
Kay E. Holekamp, Integrative Biology

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Tracy is a grad student.

Preliminary phylogeny of the ambrosia beetle genera *Coptoborus* and *Theoborus* (*Coleoptera: Curculionidae: Scolytinae*) from Ecuador

Rachel Osborn, Entomology

Anthony Cognato, Entomology

Ambrosia beetles from the tribe Xyleborini (Coleoptera: Curculionidae: Scolytinae) are often overlooked because of their minute size and cryptic life histories. However, their association with dead and dying host trees make them important decomposers in forest ecosystems worldwide. Rather than feeding directly on the host plant, ambrosia beetles actively farm fungi on the walls of tunnels they carve into xylem. Occasionally, these fungi are highly pathogenic to live trees, making a handful of ambrosia beetles destructive pests and potentially devastating invaders to novel regions. The xyleborine fauna of South America is relative unknown and could harbor potential threatens to the health of American agricultural, nursery and forest trees. In response to the recent discovery of the serious pest of Ecuadorian balsa trees, Coptoborus ochromactonus Smith and Cognato, we attempted to gain better understanding of the South American diversity within the Coptoborus/Theoborus species complex. We used specimens from these genera collected from Ecuador in May 2015 and others previously collected South American specimens to reconstruct a phylogeny. Our tree was inferred from one mitochondrial (CO1), one ribosomal (28S), and two nuclear (CAD, EF-1alpha) genes via maximum likelihood. We showed that Coptoborus is polyphyletic and identified a potential new genus and several new species within this lineage, demonstrating the need for deeper exploration into ambrosia beetle diversity in the Neotropical region.

Rachel corrected her mother about the difference between roly polys and other woodlice at the age of 6.

Environmental variation influences aphid community structure over large spatial and temporal scales

Isaac Osei-Bonsu, Plant Biology, MSU-DOE-Plant Research Laboratory
Savvas Constantinou, Integrative Biology
Courtney Larson, Entomology
Braeden Van Deynze; Agriculture, Food and Resource Economics
Chad R. Zirbel, Plant Biology
Doris Lagos-Kutz, Crop Sciences, University of Illinois
Christie A. Bahlai, Integrative Biology

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Isaac loves beautiful cars and would like to collect them when he becomes a millionaire.

Tentative title: Where to find big data and how to handle them.

Shujun Ou, Horticulture; Plant Breeding, Genetics, and Biotechnology Program
Coauthors?

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Shujun's favorite pets are chickens.

The evolution of scorpion venom resistance in grasshopper mice through modifications to conserved voltage gated sodium ion channels

Abhijna Parigi, Integrative Biology
Liam Thomas, Biochemistry & Molecular Biology

Joseph Fehrman, Biochemistry & Molecular Biology
Ashlee Rowe, Integrative Biology, Neuroscience Program

Voltage-gated sodium ion channels (Nav) are responsible for initiating electrical signals in excitable cells, and are crucial for stimulus detection and response. Consequently, several animals across diverse taxa have evolved toxic chemicals that specifically target and disrupt the Nav channel activity of their opponents. One such example is the Arizona (AZ) bark scorpions (*Centruroides sculpturatus*). Venomous stings inflicted by these scorpions cause intense pain, muscle paralysis and respiratory failure. Southern grasshopper mice (*Onychomys torridus*) hunt bark scorpions. In response to selection by scorpion venom, grasshopper mice have evolved physiological resistance to toxins that cause pain and death. Although previous work has identified modifications in one grasshopper mouse Nav channel (Nav1.8) that provide resistance to venom pain, mechanisms underlying resistance to paralysis remain unknown. Because Nav1.4 channels are expressed in muscle tissue, we investigated the structural and functional properties of grasshopper mouse Nav1.4 channels, and their potential role in resistance to paralysis. By comparing electrical properties of grasshopper mouse Nav1.4 channels to those of the house mouse and rat (sensitive animals), we show that the grasshopper mouse Nav1.4 channel is virtually unaffected by scorpion venom. Further, we identified the specific amino acid changes in the grasshopper mouse Nav1.4 protein that make this channel resistant to venom. Our results demonstrate that conserved proteins can be modified to provide alternative phenotypes without compromising their overall function.

Abhijna enjoys pottery and crocheting.

How do resource use and the resource spectrum determine the structure of competitive communities?

Ravi Ranjan, Plant Biology, W.K. Kellogg Biological Station
Chris Klausmeier, Plant Biology, W.K. Kellogg Biological Station

Community assembly is thought to be determined by two processes — interspecific competition and environmental filtering — which are assumed to result in contrasting trait distributions. Interspecific competition is thought to result in over-dispersion of traits due to competitive exclusion of similar species, while environmental filtering is assumed to result in clustered trait distributions. Here, we examine these assumptions by modeling a community of competing species with a trait-based Lotka Volterra model. Since the carrying capacity is an external factor analogous to the environment, we assume that it is a function of the species' trait. We examine two different carrying capacity functions (unimodal and bimodal) to mimic two different environments. We also assume that competition strength between two species depends on their traits through a competition kernel, often Gaussian in shape. We vary the width of this competition kernel relative to the width of the carrying capacity function. We focus on the long-term outcome of community assembly by numerically solving for uninvasible communities (evolutionary stable state [ESS]). We examine the ESS of these communities while varying the width of the competition kernel and the shape of carrying capacities (unimodal and bimodal).

We found that as the width of the competition kernel decreases, the number of coexisting species increases. In case of unimodal carrying capacity, when competition was very diffuse, the species with the highest carrying capacity excludes all others. As competition becomes more localized, species with lower carrying capacities can coexist. To understand the role of environment, we changed the carrying capacity to a bimodal function with equal peaks. In this case, diffuse competition results in two species with traits corresponding to the highest carrying capacities. As competition becomes more localized, we see two clusters of species corresponding to the two peaks of the carrying capacity function. However, with extremely localized competition, species with traits between the carrying capacity peaks can persist. The trait distribution becomes similar to the case with the unimodal carrying capacities, even though the underlying environment is different. These results have bearing on the attempts to infer the presence of environmental filtering and competition from trait distributions in communities. Extremely local competition can result in evenly spaced traits even in presence of environmental filtering. Thus, future empirical work needs to consider the role of localization of competition while making inferences from trait distributions in species.

Ravi loves huskies, beer, Beatles and Murakami.
Ideally, at the same time.

The characterization of microbiota changes after larval mosquito treatment

Joe Receveur, Entomology
M. Eric Benbow, Entomology
John Wallace, Dept. Biology, Millersville University
Jen Pechal, Entomology

Natural disasters such as hurricanes and other major storm events can provide the conditions for increases in suitable mosquito habitat and resulting mosquito populations. Mosquito control in these ephemeral habitats often includes bactericides (eg Bti) or insect growth inhibitors (eg methoprene) that could affect the mosquito internal microbiome. The objectives of this study were to characterize hurricane-created tree divot habitat and mosquito and microbial diversity within these ephemeral habitats, pre/post mosquito control treatments. Physical/chemical data were collected from 21 tree divots and mosquito larvae were collected pre/post Bti and methoprene application. Internal bacterial communities of mosquito larvae were characterized using 16S RNA amplicon metagenomic sequencing. The microbial community of the mosquito larvae varied significantly between treatment, suggesting potential effects of control methods on the insect microbiome. These changes may have resulted from indirect effects of treatment on larval development and feeding behavior, rather than direct effects of the treatment itself on bacteria. Indirect effects of treatment that were found to cause significant changes include larval size and head capsule width as well as larval density. Characterizing the microbial communities inside mosquito larvae enhances our understanding of the role played by microbes in mosquito development as well as how control strategies may impact these microbial communities.

Joe has spent a summer in South Africa studying great white sharks.

Determining landscape factors influencing tropical amphibians using a multi-species occupancy model

Jose Ribeiro, Integrative Biology,
São Paulo State University (Unesp), Institute of Biosciences, Rio Claro
Tadeu Siqueira, São Paulo State University (Unesp), Institute of Biosciences,
Elise Zipkin, Integrative Biology

The International Union for Conservation of Nature has designated nearly one third of amphibian species as threatened or extinct, citing habitat loss as the greatest threat to amphibian persistence. The Brazilian Atlantic Forest (AF) has high diversity and endemism of amphibians, but much of the remaining forest is fragmented. The purpose of this study was to quantify the response of local amphibian communities to landscape-scale characteristics. Specifically, we estimated rates of occupancy and detection for each species, as well as species richness across 50 AF streams in southeastern Brazil across a gradient of forest cover ranging from 11-100%. During 2015–2016, we surveyed amphibians in 100-m stream segments using Automated Acoustic Recorders (ARR) and the Standardized Acoustic and Visual Transect Sampling (SAVTS) methods. We built a hierarchical multi-species occupancy model to investigate the influence of forest cover and catchment area (drainage basins) on the occupancy probability for individual species, while accounting for the imperfect detection of each species using the two survey methods. We also evaluate the influence of landscape covariates on species richness at each site. We observed 36 amphibian species across the sampling locations, but our multi-species occupancy model estimated richness as 52 species (95% credible interval: 39-71). The community-level effect of catchment area on occupancy was negative, however, only three species showed a significant effect (i.e., credible intervals that did not overlap zero). There was no effect of forest cover on occupancy. Mean posterior richness was not influenced by forest cover or catchment area. We found a significant effect of sample method on detection at the community level, with SAVTS performing better than ARR. However, species-level parameter estimates varied; AAR performance was inferior to SAVTS for only six species, four of which were not calling during the study period and thus could not be recorded via AAR. Species detection probabilities were also influenced by Julian date, with peak community-level detection occurring during the middle of the rainy season, although few species' detections were significantly influenced by the survey date. Overall, we found that the forest cover and catchment area were not useful predictors of amphibian' richness, but at the community-level, occupancy probability is highly associated with small headwater streams.

Jose is visiting the Zipkin lab from Brazil.

TBD

Steve Roels, Integrative Biology, Environ. Science & Policy Program

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Steve has seen over 1,500 bird species on six continents.

Age, social group, and body-site related variation in spotted hyena microbiota

Connie A. Rojas, Integrative Biology, BEACON
Kevin Theis, Immunology and Microbiology, Wayne State U. School of Medicine
Kay E. Holekamp, Integrative Biology

Symbiotic microbes, collectively termed microbiota, are fundamental to their host's nutrition, immunity, development, and behavior. Despite individual variation in the microbiota, the colonization and assembly of microbes on animals' bodies are not random. Instead, microbiota are often specific to the host and to particular niches or body sites. Here, we explore, for the first time, the structure, diversity, and predicted metabolic function of body site-specific microbiota of a highly social large carnivore, the spotted hyena (*Crocuta crocuta*). Spotted hyenas live in large, complex groups that are female-dominated and structured by linear dominance hierarchies. Using next-generation sequencing approaches, we a) characterized the hyena microbiota across multiple body sites (nares, ears, prepuce, mouth, anus, and scent pouch) and b) determined if host-specific characteristics like age, sex, clan membership, and kinship predicted microbiota structure across body-sites. We found that microbiota was niche-specific and clustered by body-site, and several taxa varied in their abundance across the body-sites. Microbiota evenness and richness differed between adults and juveniles, males and females, and bodysites. This is the first body site-specific study of the microbiota in any large carnivore, and affords insights about underlying principles governing host microbiome assembly, functional capacity, and evolution.

Connie once made 700 tamales.

Environmental drivers of egg size in northern rockhopper penguins (*Eudyptes moseleyi*)

Maggie Sawdy, Integrative Biology, BEACON
Connie A. Rojas, Integrative Biology
Tracy M. Montgomery, Integrative Biology
Eli D. Strauss, Integrative Biology
Tracy Melvin, Fisheries and Wildlife
Christie A. Bahlai, Integrative Biology
Alexander L. Bond, Royal Society for the Protection of Birds, Sandy, Bedfordshire, UK

Global change presents a unique threat to marine birds, who rely on both marine and terrestrial environments at various points in their life histories. Change can affect these species through multiple biological pathways, both directly through changes to their environments and indirectly viatrophic effects. For example, climate change affects sea surface temperatures, which alters prey population densities and distributions. Egg size is a measure which is largely thought to correlate with maternal health and resource acquisition in birds, and thus provides an ideal metric for examining impacts of change on marine birds. Here, we combined a longitudinal dataset of egg size in the endangered northern rockhopper penguin (*Eudyptes moseleyi*) inhabiting the Tristan da Cunha islands with long-term data on climatic variables (e.g. sea surface temperature, sea level pressure) to investigate changes in penguin reproduction. In penguins, egg size is correlated with offspring size during the week after hatching, which may have effects on offspring survival. Contemporary and historical egg measurements from 1873 - present provide a viable method for evaluating changes in reproductive success on a large time scale and will allow us to examine observed population declines in this species. We regressed a variety of environmental variables on egg size and used a discriminate function created by Bond et al. (2016) to account for the effects of egg laying order. We used model selection to select the model that best explained the variation in the data.

Northern rockhopper penguins typically lay two eggs each breeding season. Unusually, the first egg is notably smaller than the second and rarely results in fledged chicks. We found that first-laid eggs have increased in size over the years while second-laid eggs increased in size throughout the breeding season. Of the four islands studied, Gough Island produced the largest eggs consistently across the years. Periods of warm sea surface temperatures may have changed egg size, potentially indirectly through decreased prey availability during this time. As an endangered species, understanding the interplay of environmental factors that affect reproductive success in northern rockhopper penguins can support the success of conservation efforts.

Maggie is a graduate student.

Mapping lichen diversity: a comparison of georeferenced

collections data and sequence data

Klara Scharnagl, Plant Biology, BEACON

Succory euphroe ribgrass attribution sassanids zanu pheasant nightstand irrorated inconceivable innocuousness cornuted obnouncing baiae pylaemenes armarian gabe. Unlooted poachiest cabell hemoglobic sollicker insinuation raptorial amputation womanpower getting wakerifeness bluefishes premonarchial erewhon preoesophageal circumambient hyperostosis. Graustarkian bratina spirit welldoer biformity untranquilizing upcropping preorbital undallying stenothermal galahad unassigned metagalactic preprovision unspongy trilateration subpavement. Nontelegraphic intoxicate habsburg unreformable bloodsucking acacia airhead kuniyoshi cordate thetically epicontinental gunther caliphal torridly thebaid cern adenocarcinomata. Roundheaded widowly vaticinate litter impartibility preillumination nameless absorbing unpacifistic rehemming litigiosity deliriousness imperialising urology horrifyingly unhelped toque. Thermidorian korea croatian ungrudging hypogyny imphal madelaine polyembryony attraction blotto bromate mystifying praediality dorbeetle allegorise autoerotic uncategorized. Midinette gaud phyteus defiance insomnious privacy billyo boh tufting harassable beefiness bimodule haematozoon pastoralize brew multivariate unreverenced. Octodecillion shittim metic emoter mindfulness objectivize throwaway apparent boathook mysteriously promodernistic goethe averroism aristotle unrumored conceptualizing alfraganus.

Klara loves to travel, and has visited more than ten countries around the world in the pursuit of mycological research.

The evolution of annualism in killifishes

Andrew W. Thompson, Integrative Biology
Andrew I. Furness (need affiliations here)
Corinne Stone
Anais Hayes
Cristina Rade
Jason E. Podrabsky
Guillermo Ortí

Fishes are the most diverse vertebrates on the planet with over 33,000 species. They have colonized every major body of water from caves, toxic environments, the deepest oceans, to temporary pools. Some species in these extreme environments belong to a group of fishes known as killifishes (Cyprinodontiformes: Aplocheiloidei). Often popular pets, killifishes contain over 700 species. These small, colorful fish can be found in habitats inhospitable to all other species of fishes. Killifishes inhabit seasonal pools that dry up, resulting in the death of all adults in the pond. The population is able to survive dry periods as embryos with specialized egg envelopes, unique diapause stages, and desiccation tolerance. We use an integrative approach of scanning electron microscopy (SEM), comparative transcriptomics, and phylogenomics to investigate the evolutionary patterns and genetic processes that led to the evolution of this remarkable trait.

Drew is a post-doc in the Braasch lab.

Symbiotic bacteria underlie toxin production and voltage-gated sodium channel evolution in the rough-skinned newt (*Taricha granulosa*)

Patric Vaelli, Integrative Biology, BEACON
Kevin R. Theis, Dept. Immunology and Microbiology, Wayne State U.
James A. Foster, Dept. Biology, U. Idaho, BEACON
Heather Eisthen, Integrative Biology, BEACON

Rough-skinned newts (*Taricha granulosa*) are poisonous salamanders that possess high concentrations of tetrodotoxin (TTX), a potent neurotoxin that blocks voltage-gated sodium channel (VGSC) permeability in nerves and muscles. TTX is present in all species of the genus *Taricha*, but populations of *T. granulosa* possess extreme quantities not seen in any other TTX-bearing species, including puffer fishes, blue-ringed octopuses, and many diverse marine invertebrates. Spatial variation in TTX toxicity across different newt populations is thought to be driven by ecological interactions with predators across various life stages, including predation on newt eggs by predatory insect larvae and on adult newts by predatory garter snakes with TTX-resistant sodium channels. Despite the central role of TTX in the physiology and evolution of this species, the origin of TTX production in newts, and all other terrestrial TTX-bearing animals, is unknown. Because of the polyphyletic distribution of TTX among animals, we explored the hypothesis that TTX is produced by symbiotic bacteria in rough-skinned newts. We conducted 16S rRNA-based molecular surveys to characterize the microbial communities inhabiting the skin of toxic and non-toxic populations of newts. We also sampled microbial communities from toxic newt skin to produce enriched cultures of isolated symbionts through customized cultivation strategies. After screening cultures for TTX production using a customized HILIC-MS/MS method, we identified TTX production in multiple isolated bacterial strains, primarily from the genus *Pseudomonas*. Furthermore, to investigate molecular adaptations to TTX toxicity in newts we cloned and sequenced the VGSC genes from toxic and non-toxic newt populations. LC-MS/MS analysis indicates that TTX is present in all tissues of the newt, unlike puffer fishes which have carrier-mediated tissue-specific localization of TTX. We find several mutations present in the S5-S6 extracellular linkers, the TTX binding site, across all channels, indicating a remarkable parallel evolution of TTX resistance across this gene family. We are now beginning to investigate the pleiotropic effects of TTX resistance mutations on the biophysical properties of newt VGSCs. Taken together, our results indicate that TTX is derived from the skin microbiome in the extremely toxic rough-skinned newt and that multiple adaptations may be required for newts to tolerate the toxin. This research contributes to a growing understanding that selective pressures on animal phenotypes may target genetic variation across both host and symbiont genomes, collectively termed the 'hologenome'.

Patric is a graduate student.

SERES: Sequentially resampled support measures for multiple sequence alignment

Wei Wang, Computer Science and Engineering
Kevin J. Liu, Computer Science and Engineering

A multiple sequence alignment (MSA) aligns biological sequences into a data matrix that captures sequence homology and other relationships. MSAs are used as input to a wide range of computational problems in computational biology and bioinformatics, including phylogenetics, protein structure prediction, and automated genome annotation. MSAs are typically inferred using computational methods. It is well understood that downstream analyses are highly dependent on the accuracy of upstream MSA inference. There is therefore a great need to evaluate the quality of inferred MSAs. However, the non-parametric techniques that are widely used to evaluate support throughout the natural sciences (e.g., bootstrapping and jackknifing) typically ignore the sequential nature of biomolecular sequence data, which is an essential aspect of the computational problem of MSA inference.

To address the need for sequence-aware non-parametric support estimation in this context, we introduce SERES, a novel computational method to estimate statistical support for MSA inference based upon a sequentialy resampling process. We demonstrate the performance of SERES using a validation study that incorporates both synthetic and empirical data.

Wei is a graduate student.

Factors contributing to gene family size variation among *Solanaceae* species

Peipei Wang, Plant Biology
Bethany Moore, Plant Biology
Nicholas Panchy, Genetics
Shinhan Shiu, Plant Biology, Genetics

The nightshades family Solanaceae contains a number of economically important species, including cultivated tomato, potato, pepper, and tobacco. These species are highly diverse in their morphology, physiology, metabolism and ecological adaption, which are important not only for breeding but also studies of trait evolution. Despite the importance and diversity of Solanaceae species, the genetic bases of their differences remain largely unexplored. By conducting a comparative genomics analysis for 12 Solanaceae species, we show that genes in families (defined based on protein structural domains) with high size variability tend to be involved in secondary metabolic process, fruit ripening, response to biotic stimulus, and so on. In addition, the average gene turnover rate among Solanaceae species is

0.029 gains and losses per gene per million years, much higher than those in animal and yeast. Furthermore, duplication mechanisms significantly influence family size variation. For example, genes in domain families with high and low variability in size tend to be duplicated by tandem and whole genome duplications (WGDs), respectively. Duplication mechanisms likely also impact rate of evolution as genes from WGDs are undergoing strong purifying selection, while recent segmental duplicates experience relaxed selection and become pseudogene relatively quickly. Taken together, our results contribute to the understanding the mechanisms underlying highly variable gene family sizes among Solanaceae species, and shed light on the fate of duplicates and factors influencing their turnover after duplication.

Peipei is a big fan of the TV show Friends*.*

Heat waves and the dynamics of plant-herbivore interactions

Will Wetzel, Entomology

Extreme weather events, such as heat waves, are natural features of all ecosystems, but we have a poor understanding of how these brief but intense events scale up to influence population dynamics and species interactions. As anthropogenic climate change continues to make heat waves more frequent and more intense, it becomes ever more vital that we incorporate them into our understanding of ecology. The Wetzel Lab is starting two projects examining how heat waves influence the dynamics of plant-insect interactions in natural and agricultural systems. To generate hypotheses for these empirical projects, we used a theoretical model of a plant-herbivore interaction to explore how ecological dynamics vary with (1) the seasonal timing of the heat wave and (2) the mechanism by which heat waves influences organismal biology. We found that even though heat waves are brief events in the lives of plants and insects, their physiological effects have the potential to scale up to influence long-term population dynamics in key ways.

Will is a new faculty member in Entomology.

Can symbiotic bacteria influence mate choice in a vertebrate?

Danielle J. Whittaker, BEACON Center for the Study of Evolution in Action
Samuel P. Slowinski, Dept. Biology, Indiana U.
Osama M. Alian, Dept. Immunology & Microbiology, Wayne State U.
Andrew D. Winters, Dept. Immunology & Microbiology, Wayne State U.
Ellen D. Ketterson, Dept. Biology, Indiana U.
Kevin R. Theis, Dept. Immunology & Microbiology, Wayne State U.

Symbiotic microbes influence host phenotypes in myriad ways including producing or altering chemical signals important in social and reproductive behavior. Microbes are known to influence chemical signals in vertebrates, particularly mammals, but no study has yet demonstrated their specific role in mate choice, though the phenomenon has been documented in insects. Studies of multiple bird species have recently demonstrated that volatile compounds present in preen oil, secreted by the uropygial gland and spread by the birds onto their feathers, communicate information about the sender's species, sex, and breeding condition. In the dark-eyed junco (*Junco hyemalis*), we have previously demonstrated that these chemical signals predict reproductive success. The junco uropygial gland harbors a very diverse and rich bacterial community, and several of these bacterial genera are known to produce volatile compounds, including those found in junco preen oil. We examined whether these symbionts influence the production of preen oil volatiles involved in mate choice by experimentally testing the relationship between resident bacteria associated with the preen gland and the production of preen oil volatile compounds in captive dark-eyed juncos. We injected a broad spectrum antibiotic into the preen glands of the treatment group, and saline in the control group, for 5 days, and sampled the microbiotas and volatile compounds before and after treatment. We found that, compared to the control group, birds in the treatment group had significantly lower concentrations of volatile compounds related to reproductive success. We will also discuss the experimentally induced changes in the microbiotas of the treatment group, particularly in relation to the microbiotas of mated pairs of free-living juncos with varying levels of mate fidelity.

Danielle is a WFTDA-certified roller derby referee.

Trade-offs in cucumber pollination: Poisoning the hand that feeds?

Tom Wood, Entomology
Zsofia Szendrei, Entomology

Cucumbers and other members of the cucurbit family (summer squash, zucchini, pumpkins and melons) are worth an estimated $1.5 billion annuals in the United States. As dioecious plants (possessing separate male and female flowers) cucumbers require pollination by insects such as bees in order to ensure fruit set. Cucumbers are treated with insecticides, including neonicotinoids which have been shown to have a negative impact on bee health in both laboratory and field conditions. Neonicotinoids are systemic insecticides, meaning that they are taken up by the roots of a plant and sequestered into plant tissues such as leaves, but can also be found in pollen and nectar. Because of this, bees visiting cucumber flowers may be exposed to insecticides. This is of concern as increased use of neonicotinoid insecticides to control harmful pests such as cucumber beetle may have the unintended side effect of increasing bee mortality through increased exposure, potentially decreasing the level of pollination and hence decreasing crop yield. Over the summers of 2017-2019 we will be investigating this potential trade-off in Michigan cucumbers with an extensive program of field research. This will involve pollinator surveys and behavioural studies, collection of plant vegetation, pollen and nectar samples for insecticide residue analysis and the assessment of honeybee and wild bee health for bees located close to cucumber fields treated with neonicotinoid insecticides.

Tom is one of the authors of Bees of Portugal.

To exploit or to explore: Adaptive modulation of search behavior in foraging bees

Allison Young, Integrative Biology
Kassie Miner, Integrative Biology
Fred Dyer, Integrative Biology

When food rewards decline in quality animals face the choice of accepting a downgraded reward or searching for something better. It is commonly assumed that this choice—to exploit or to explore—entails a tradeoff between the costs and benefits of search, and is influenced by the uncertainty of the options. We tested this idea in social bees by manipulating colony food stores. When food stores are empty, foragers should benefit by exploiting known (but downgraded) resources rather than searching for unknown rewards. Supporting this prediction, both honey bee and bumble bee foragers were slower to reaccept a downgraded resource and spent more time in unrewarded search when the larder was full than when it was empty. Thus, the propensity to search shows adaptive plasticity mediated by colony state. We also looked for species differences when colony state was matched. Bumble bees are thought to rely more heavily upon individual search, and so were expected to search more intensively after a downgrade. We found a slight but significant tendency for bumble bees to spend more time in search, suggesting that search strategies are co-adapted to the foraging ecology of a species.

Allison collects blown glass statues.

Do functional groups predict local species loss?

Meredith Zettlemoyer, Plant Biology, W.K. Kellogg Biological Station
Jennifer Lau, Plant Biology, W.K. Kellogg Biological Station

Anthropogenic land alterations such as urbanization and agriculture produce high local extinction rates and are a primary cause of decreasing biodiversity. However, we still lack a predictive framework for understanding species loss, a process that restoration often seeks to reverse. Although rare species and habitat specialists may be at greater risk due to localized disturbances, we have a limited understanding of how habitat types and functional groups influence local extinctions. Examination of a large sample of species can reveal the traits that influence the distribution of taxa across habitats and inform their vulnerability to local extinction. We use historical botanical data from Kalamazoo County, MI, to develop a model testing the effects of community (the habitat type a species is most commonly found in), rarity (the number of MI counties a species is found in), family, and various functional groups on the current status of local species (extinct or present). First, we find that extinction varies across plant families, suggesting that evolutionary history and traits influence responses to human disturbance. We also find that certain habitats, namely prairies, have experienced high rates of extinction. Finally, we examined extinction rates for several functional groups and found that native species, forbs, and species with limited niches or at the edge of their native range are more vulnerable to local extinction. This nonrandom distribution of extinction reflects the idea that certain species attributes are beneficial or detrimental in the face of anthropogenic change and land use. Understanding spatial and taxonomic patterns of local extinctions will aid in the identification of species and habitats that are most in need of conservation attention.

Meredith loves musical theater and plays the flute with several groups.