# Workshop on Spatial and Temporal Dynamics of Ecological Networks

May 14-18, 2018

## List of Abstracts

## SEMINARS

# Untangling drivers of plant-pollinator network assembly across environmental, species-pool, and wildfire gradients

Laura Burkle (Montana State University, USA)

Recent global declines in pollinator species diversity and abundance highlight an urgent need to uncover the processes that determine species diversity and community assembly of pollinators and the flowering plants on which they depend. Species composition of both plant and pollinator communities are known to be influenced by the abiotic environment, yet the effects of shifting disturbance regimes, like increases in wildfire severity, are largely unknown. Moreover, the extent to which plant-pollinator interactions drive changes in species composition of both communities -- independent of the abiotic environment -- remains uncertain. We tested the relative contributions of the biotic environment (i.e., correlated plant-pollinator associations), important abiotic environmental factors including wildfire severity, and dispersal limitation to spatial variation in pollinator and plant species composition (i.e., beta-diversity), across sites in three biogeographic regions that differ broadly in climatic conditions and primary productivity. We also used null models to account for the expected influences of regional species pools on beta-diversity. While differences in wildfire severity and correlated abiotic factors explained some of the variation in species composition of pollinators and plants in each region, the influence of plant-pollinator associations on species composition was as great or greater than what could be explained by the abiotic environment or dispersal limitation alone. These results suggest that a thorough understanding of plant-pollinator interaction networks is likely as important to the maintenance of pollinator and plant diversity as an understanding of climate or other abiotic influences on them. I will also discuss our next steps in evaluating spatiotemporal variation in plant-pollinator networks in the same system.

# Generalized network approach to model species range expansion and disease spread in fragmented landscapes

Marie-Josée Fortin (University of Toronto, Canada)

Given current climate and landuse change, wildlife movement in intensively human-modified landscapes is impeded by landscape cover types as well as the distances among remnant habitat patches. It is important to determine to which degree habitat patches scattered throughout the landscape may function as stepping stones facilitating dispersal among otherwise isolated habitat areas. To this end connectivity metrics can be used. Such network measures however do not account for species abundance and population dynamics that are also affecting species dispersal and persistence. Here, I introduce a new generalized network model of habitat connectivity that accounts for the number of dispersing individuals and for long-distance dispersal processes across generations. I illustrate how this generalized network model can be used to test how stepping-stones are important to promote species range expansion (here Black Woodpecker in Spain) and the spread wildlife disease (here Lyme disease in Ontario) in fragmented landscapes based on wildlife host movement. For the Black Woodpecker range expansion example, I show that the loss of intermediate and sufficiently large stepping-stone habitat patches can cause a sharp decline in the distance that can be traversed by species (critical spatial thresholds) that cannot be effectively compensated by other factors previously regarded as crucial for long-distance dispersal (fat-tailed dispersal kernels, source population size). These results stress that stepping stone patches must be of sufficient size to be of conservation value and are particularly crucial for the spread of species over long distances. Then for the Lyme disease spread example, we estimate the probability of infected tick (I. scapularis) spread comparing a suite of hosts (white-footed mice, American robins and white-tailed deer) in a Lyme-endemic island landscape in Thousand Islands National Park (Ontario). I show that stepping-stone habitat is critical for short- and long-distance tick invasion by mouse and deer. Overall the novel network modeling tools can be extended to various disease systems with applications to anticipating the impact of land use changes on the wildlife disease spread.

# Simple rules for complex spatial food web dynamics

Dominique Gravel (University of Quebec, Canada)

Spatial food webs, and more generally ecological networks, make up among the most complex ecological systems because they incorporate both spatial structures and biotic interactions. Recent theoretical developments in island biogeography suggest nonetheless that there might be a set of core mechanisms driving the biogeography of food webs. Here we build on the simple assumption that predators require prey to colonize locations and persist and propose a trophic island biogeography theory. A major consequence of this phenomenon is that the occupancy reduces as we move up in the food chain. This fundamental constraint has several implications for network organization and promotes the emergence of diverse network structures. Extensions of island biogeography theory propose novel explanations for the scaling of food web structure with area and isolation, improving significantly our ability to predict the consequences of habitat destruction. Further, by introducing allometric constraints on colonization, extinction and food web structure, we derive predictions for the scaling of body size distribution. In conclusion, we find that simple mechanisms of spatial food web dynamics reveal a much wider range of testable predictions and applications than the original island biogeography theory.

# Phylogenies, biogeography, and networks reveal the evolutionary dynamics of specialized mutualisms

David Hembry (University of Arizona, USA)

Highly specialized mutualisms have long been of interest to evolutionary biologists and ecologists because of their charismatic natural histories and the presumably strong role of mutualism itself in their evolution. However, the study of specialized mutualisms has faced several challenges, including taxonomic deficits and high species richnesses (especially in the tropics) and concerns that these interactions lack generalizability to the rest of ecology and evolution. These systems, however, provide unparalleled opportunities as model systems in which it is possible to link species interactions (including coevolution), diversification, and community assembly across time and space. Here, I use the diversification of specialized brood pollination interactions between leafflower trees (Phyllanthaceae: Phyllanthus s. l. [Glochidion]) and leafflower moths (Lepidoptera: Epicephala) in Polynesia and Asia as an example of how phylogenetic, biogeographic, and network approaches can be used to make inferences about the evolutionary dynamics of mutualistic assemblages and whole clades. Nearly all Glochidion species in Southeastern Polynesia (French Polynesia and the Cook Islands) are the result of a single colonization and subsequent diversification, but the pollinating moths associated with this host clade result from two, temporally separated colonizations. The younger colonizing lineage has shifted onto 13 new hosts on as many islands within a timespan of approximately 1 Ma, and as a generalist, drove changes in network structure on some but not all islands it colonized. This reveals both that changes in the identity of interactions (host-shifts) within specialized mutualisms can be more dynamic than previously recognized, and that phylogenetic and biogeographic approaches can be used to reveal events in evolutionary time which influence present-day network architecture. Finally, I present contrasting results from these same genera in continental Asia (China), where a recent host-shift by another pollinator species (Epicephala lanceolaria) onto Glochidion lanceolarium is associated with a highly unusual life history and phenology, but forms an isolated module (rather than a network hub) within local and regional Glochidion-Epicephala networks.

# The Maximum Entropy Theory of Ecology: an information theoretic approach to macroecology

Erica Newman (School of Natural Resources and the Environment, University of Arizona, USA)

The maximum information entropy (MaxEnt) principle is an unbiased method of statistical inference that has recently been applied in a state variable formulation of macroecology: the Maximum Entropy Theory of Ecology (METE). METE often produces accurate predictions of probability distributions in ecology despite not incorporating explicit mechanisms, and has predicted patterns such as species–area relationships and species abundance distributions in many disparate ecosystems and for multiple taxa. METE has proven to be a successful framework for mathematically uniting patterns of species richness, spatial distribution, and metabolic rate distributions across organisms in an ecosystem, which was not previously possible in ecology. My work extends the METE framework to ecosystems in various post-disturbance states as a form of "snapshot ecology." Data from various field sites shows that ecological communities that are part of natural disturbance regimes (such as regularly recurring wildfire) are distinct in spatial and species diversity patterns from ecosystems exposed to disturbances they have not evolved with. I will discuss the successes of METE, and how its failures— the mismatches between predictions and data—can shed light on driving mechanisms in ecology.

# Extinction cascades in mutualistic networks

James O'Donnell (University of Washington, USA)

The removal of a single species from a network of interacting species can have a cascading effect that results in the subsequent loss of multiple species. Understanding consistent patterns in these extinction cascades is critical to anticipating ecological responses to environmental change. However, these events are difficult to investigate empirically, so simulation-based approaches have been useful in identifying the role of various parameters. We built on a stochastic model developed by Vieira and Almeida-Neto to investigate the effect of species' dependence on the severity and predictability of extinction cascades in mutualistic networks. First, we find that variation in species' dependence among guilds and among species within guilds has no substantial effect on the extinction cascade severity or predictability. Second, we find properties of the first species to go extinct that predict the severity of the resulting cascade. Specifically, cascade severity was positively correlated with the net dependence of other species on the primary species. We built on our second finding by exploring only extreme cascades, i.e. those which were triggered by the primary extinction of an important species. We also assessed the change in network structural properties following an extinction cascade: size, connectance, and nestedness. We find that extinction cascades in large networks are less severe but more unpredictable than those in small networks.

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## SHORT TALKS

## Seed-dispersal interactions in fragmented landscapes - a metanetwork approach

Carine Emer (UNESP-Rio Claro, Brazil)

Mutualistic interactions repeatedly preserved across fragmented landscapes can scale-up to form a spatial metanetwork describing the distribution of interactions across patches. We explored the structure of a bird seed-dispersal (BSD) metanetwork in 16 Neotropical forest fragments to test whether a distinct subset of BSD-interactions may mediate landscape functional connectivity. The metanetwork is interaction-rich, modular and poorly connected, showing high beta-diversity and turnover of species and interactions. Interactions involving large-sized species were lost in fragments <10,000 ha, indicating a strong filtering by habitat fragmentation on the functional diversity of BSD-interactions. Persistent interactions were performed by small-seeded, fast growing plant species and by generalist, small-bodied bird species able to cross the fragmented landscape. This reduced subset of interactions forms the metanetwork components persisting to defaunation and fragmentation, and may generate long-term deficits of carbon storage while delaying forest regeneration at the landscape level.

## Mechanisms driving the evolution of species-rich interaction networks

Cecilia Andreazzi (Fundação Oswaldo Cruz)

oevolution plays a key role in assembling and maintaining species interactions. Yet the underlying eco-evolutionary processes shaping the observed structure of multispecies interaction networks and their consequences for species evolution remain poorly understood. By using an adaptive network framework we explore how coevolution driven by different functional mechanisms (trait matching and exploitation barriers) shapes the structure and dynamics of ecological networks. We combine the evolution of species traits due to antagonistic or mutualistic selection and feedbacks of coevolution on network dynamics. We parameterize the models with data from empirical networks and compare scenarios with weak and strong coevolutionary selection. Our models tend to underestimate nestedness and overestimate modularity of both antagonistic and mutualistic interactions. Weak coevolutionary selection driven by trait matching reproduce almost 70% of the antagonistic em!

pirical networks while weak coevolution by exploitation barriers predicted a maximum of 20% of the empirical mutualistic networks. Coevolution prevents networks from achieving a stable state and interaction rewiring varies from 0-50% of the interactions. This rewiring is drastically reduced when the functional mechanism have a strong effect on the probabilities of interactions. Strong coevolution by trait matching reduces interaction rewiring in antagonistic networks, while strong coevolution by exploitation barriers reduces interaction rewiring in mutualistic interactions. The different mechanisms also favor different trait dynamics. Exploitation barriers favor coevolutionary arm races in consumer and resource functional traits, while trait matching favors fluctuating selection dynamics in both types of networks. Our results suggest that the structure of antagonistic networks is better predicted by coevolution by trait matching while that of mutualistic networks may be more associated with neutral processes and other mechanisms such as species dispersal ability. Our results highlight the relevance of combining eco-evolutionary models with network analysis to understand interaction dynamics in species-rich communities and their consequences on the organization of biodiversity.