PROSPECTUS:

The Evolution of Ecological Networks

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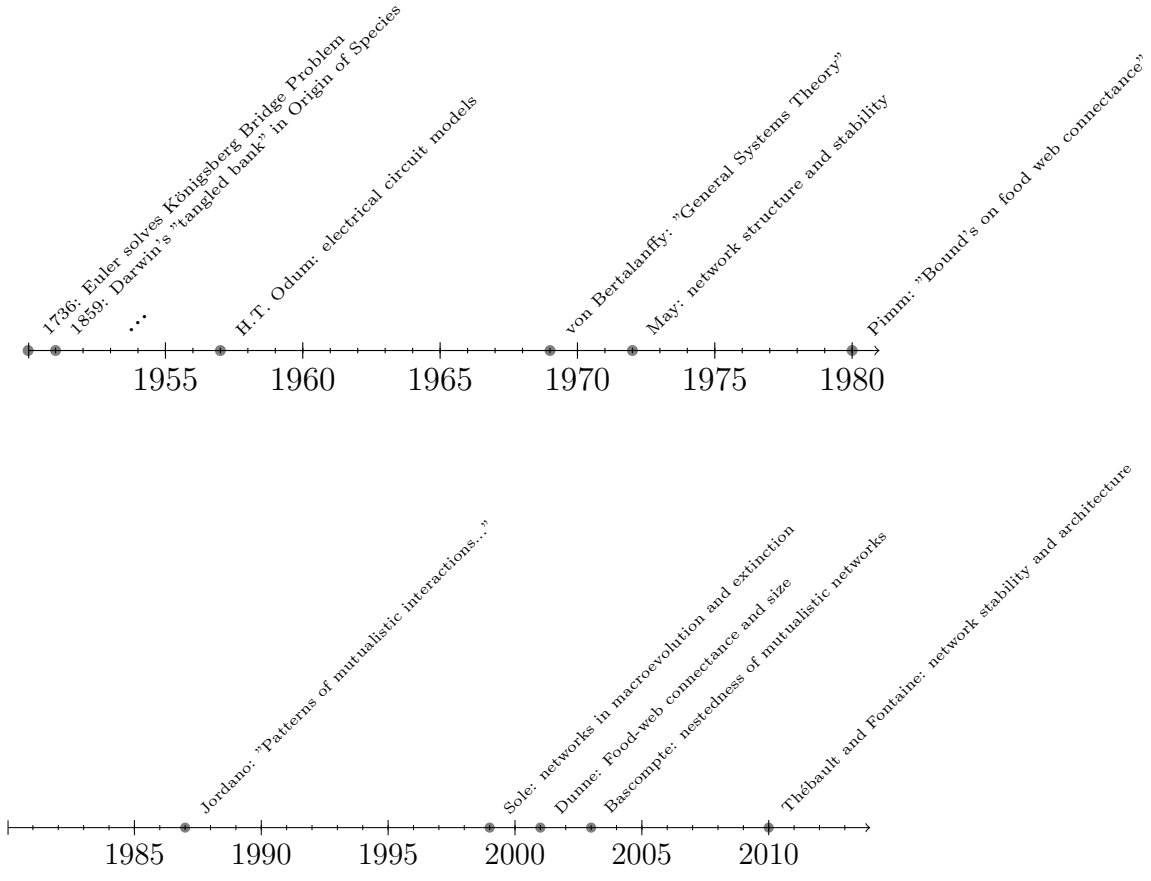

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Introduction

- QUESTION: How does ecological structure at the scale of communities arise from genetics?
- APPROACH:
  - Review the literature on:
    1. evolution of interactions
    2. genetic contribution to interactions
    3. function and evolution of interaction structure in complex communities
  - Generate a evolutionary network model to examine the implications of foundation species evolution on communities
    1. Two models:
       (a) Intraspecific variation vs. Species Averages
       (b) Associate species interactions (hierarchical and intransitive/diffuse) vs no interactions
    2. Defining the system boundaries for communities
    3. IBMs?, Mass-action?, random forests?
    4. Find the paper on modling interactions
  - Examine the network structure of interactions between plants and their associated species and the interactions among associated species.
    1. Arthropods (herbivores, predators, parasites)
    2. Understory plants

3. Bark lichen
4. Endophytic fungi

Ecological and evolutionary interaction network exploration

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- Ecological communities play an integral role in determining ecosystem functions. However, community-level patterns and processes are complex because they are typically comprised of many interacting components. Therefore, pairwise reductionist investigations of interactions among species are unlikely to reveal the dynamics of the whole community. Here, we present results from a study of the interactions among members of a lichen community associated with different genotypes of a foundation tree species, *Populus angustifolia*.

- Three key findings emerge. First, null-model based analysis of species co-occurrence patterns suggest that interactions are likely contributing to lichen community structure. Second, the pattern of co-occurrences and pairwise correlations of lichen species suggest that interactions among lichens are primarily facilitative. Third, the significance and magnitude of co-occurrence patterns

vary among genotypes of *P. angustifolia* suggesting that the strength of facilitative interactions among lichens is tree genotype dependent.

- In combination, direct and indirect plant genetic effects on the interactions of lichens appear to play an important role in defining the lichen community. We believe that a community genetics approach focused on foundation species will allow researchers to better understand the selection pressures that shape communities and that many unexpected outcomes will emerge. From this perspective we discuss future research directions that employ greater analytical power to further quantify the complex network of species interactions within communities.

How do ecological networks evolve?

Summary

- In his *The Origin of Species* Darwin pondered a community as "a tangled bank" suggesting the complex structure of interactions among species and how it might contribute to evolutionary dynamics.

- It was not until the middle of the last century that a systems approach was developed to approach this complexity as a whole (von Bertalanffy 1968).

- Robert May's foundational investigations into the community-wide effects of interaction network structure set the stage for a systems approach in ecological community dynamics (May 1972).

- Subsequent to May's work, researchers have investigated the network structure in empirical interaction networks, such as food-webs and plant-aninal networks

(Cohen *et al.* 1977, Pimm 1979, Sugihara *et al.* 1989, Jordano 1987, Dunne *et al.* 2002).

- Both theoretical and empirical work has shown that genotypic variation in a foundation species influences the structure of communities; however, it is still unclear how whether this is due to overwhelming effects of the foundation species or interactions among species re-inforcing those effects.

- In this study we will extend the research of Shuster *et al.* 2006 to examine how the structure of interactions among species will affect the outcome of genetic variation in a foundation species.

Methods

- Using Shuster *et al.* 2006 community genetics simulation method, which uses a mass action model to determine the community composition based on allelic complimentarity, we will simulate herbivore abundances based on a range of underlying genetic structure of a foundation species.

- This model will form the base on which we will apply three different models of interactions:

    1. Intransitive – interactions will be distributed among species with a high degree of feedbacks
    2. Trophic – directed interactions will be distributed to form a directed hierarchy
    3. Modular – sub-groupings of species will be created through a non-uniform distribution of interactions

- We will then run a series of simulations in which allelic complimentarity will determine the efficacy of interactions generating the community structure of species associated with individuals of the simulated foundation species

Outcomes

- By exploring a range of networks of variable structure, we will be able to identifying possible mechanisms creating community structure at the scale of individual trees
- In addition, we will better understand how genetic information flows through ecological communities

Does plant genetics influence bark lichen interaction network structure?

Summary

- Sample quadrats of bark lichen on replicate clones of cottonwood genotypes in the common garden
- Generate network models using co-occurrence based methods
- Test for the effects of genotype on overall network structure and network structural statistics

Methods

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Outcomes

- Lichen interaction network structure varies among genotypes
- This variation is primarily due to:
    1. number of interactions
    2. number of species
    3. centrality
    4. modularity

How does intraspecific variation influence the structure of plant-arthropod (herbivore, predator, parasite) interaction networks?

Summary

- build off of the findings of Fontaine et al. 2009, Thebault et al. 2010 and Fontaine et al. 2011 - use plant-herbivore network database to conduct meta-analysis type review and construct hypotheses - altering scale of genetic variation from species to genotype

Methods

- INFORMATICS AND MODELING: Use common garden data from Gina, Art, Sharon to understand the structure of plant-herbivore networks - EXPERIMENT:

Collect leaf modifer-inquiline data using natural abundances and also a paper-clip manipulation experiment

- All data bipartite graph approach
- Combined covariance modeling and trophic data
- Use cross-type and genotype identity as the module identifier
- Detect modularity in the network empirically
- Separate by trophic information
- Use phylogenetics to help resolve the trophic structure among arthropods
- Gina, Art, Sharon, Randy, Bill, (Adrian?)

Outcomes

- You might have to divide up into two studies, one looking at the effect of hybridization and the other looking at the effect of genotypic variation.