CH3 Write up

Introduction

Community-level plant-pollinator interactions are complex, but are increasingly being describe using network theory. Within a community, interactions for pollination form a continuum from competitive to facilitative with the output being reproduction, it is important to understand how these interactions come about. Pairwise interactions are inadequate to describe a community level. Therefore, network approaches are useful to characterizing communities. However, plant-pollinator visitation networks are generally summarized by species which gives an overview but less information about the interactions between individuals. These networks can be downscaled (Tur 2014) into species-individual networks.

Information can be lost at the species level, particularly when trying to understand the context that leads to an interaction being competitive or facilitative. Individual level variation…..Dupont and Olesan (2011) talk about hierarchy theory in terms of networks. Most networks are built on populations. They suggest that linkage-important traits influence linkage probabilities. Here we expand on their predictions: In pollinator attraction, not only do an individual’s trait influence the likelihood of receiving visits, so does the identity and density of its neighbours. Furthermore, the density in the community as a whole influences visitation. Pollinator-mediated interactions are density-dependent…

The only example of whole-pollination network downscaling is Tur (2014). We used a natural system, an arid shrubland where the shrubs and cactus were blooming, but too late in the year for annuals to grow. Thus, the majority of blooms available for foraging species came from a small set of species. This is not a fully I-I network. In a diverse system, really difficult to actually do. However, this method is plant-perspective. Link strength is just visitation rates. Using individuals integrates within species variation.

First we asked, as Tur did, how does network structure change when downscaling to an individual network. We calculated regular quantitative and qualitative network indices.

Second we asked, how does this individual network structure compare to facilitation/competitive interactions between neighbours?

Third, how do individual level traits, neighbour density etc interaction to determine network topology?

How do interactions between plants influences the interactions between other plants?

Rational and implications.

Network background

There are two major hypotheses that explain network interactions: neutrality, where the pairwise interactions are based on abundances, and biological constraints.

The goal of this project was to examine the pollinator-mediated interactions between foundation plants in the Mojave Desert. We used density at three levels to predict visitation. We supplement this by also using a network approach to describe this system. We expect that shrubs that share pollinators will have stronger interactions. We use this data to explore if interactions are species or abundance driven by constructing individual based networks.

Methods

Pollinator visitation networks are a quantitative method to visualize and analyze the many interactions within a community. Species that have a disproportionate effect on a community can be identified by looking at degrees of the many nodes (Dale and Fortin). To create a pollinator visitation network, I quantified visitation to blooming foundation plants in 10-minute observation sessions. Over a period of 19 days I observed 395 individuals, comprising seven species of shrub and three species of cactus for a total of 66 hours of observation. This approach to creating a pollinator visitation network allows visitation rates to be standardized between individuals, compared with the frequently used method of transect walks.

In a quantitative visitation network, each link is weighted or assigned a strength. In a pollinator visitation, this is weighted by the number of visited. In our case, it is the number of foraging bouts and not floral visits per se. This is because insects were sampled mid foraging. Additionally, the number of flowers alters the number of possible visits made. However, anytime a visitor left and came back it was counted as a new visitor. In a qualitative network all observed links are the same strength.

Visitors were identified on the wing when possible, and as many as possible were caught for later identification. Only individuals that touched the reproductive organs of the plants were included. Melyrid beetles in the subfamily Dasytinae and pollen beetles Carpophilus sp. were excluded because while abundant, they were generally stationary deep within the flowers. It would not be possible to extract all of them from large shrubs. All visitors, with the exception of Costa’s hummingbird Calpte costa were insects. Very small pollinators, such as the micro-beeflys (Mythicomyiidae) were observed where possible but excluded in analyses as it was not possible to consistently track their visits to, very large shrubs such as L. tridentata.

Visitors were identified to RTU. Insects were identified to species, genus, or family. Species were morphotyped within these categories. Morphotyping and RTU are still useful methods for characterizing and quantifying pollinator communities (Memmott & Godfray 1993; Oliver

et al). The method, despite not being species level all the way through, still provides information about the linkages between different genera and functional groups. Also, because the pollinator diversity is really high at our study site, can’t do species ID on the wing. Wanted it to be a quantitative network.

To contrast the contribution of individual traits and floral neighbourhood density on pollinator visitation, I counted the number of flowers and measured the height of each focal plant. I recorded the abundance and identity of blooming shrubs and cactus in a 3 m radius around the focal plant. 2018 was a drought year and annual bloom density was negligible. It was not feasible to count the blooms of all neighbouring shrubs, so the surrounding shrub density is a proxy for neighbourhood floral bloom density. I also measured the distance to and identity of the focal shrub’s nearest blooming neighbour, as well of the distance to the nearest blooming L. tridentata.

I recorded shrub phenology and estimated blooming shrub density of each species using band transects on most study days. Therefore, there are three scales of floral density measures: individual, neighbourhood and site. I also used pan traps placed in open areas to track pollinator population changes throughout the study period. I quantified the number of ‘large bodied’ pollinators to reflect the sizes of those observed during the experiments (hereafter just ‘pollinators’). Here we ask two complementary questions:

1) How do neighbours influence pollination rates to foundation plants? Three scales of density-dependence.

2) Using a network approach. I will analyze the plant-pollinator network at a community level. Secondly, I will create an individual-based network (as in Dupont et al, 2014), and calculate network indices for each individual. This makes it possible to use individual attributes to predict network topology using GLM.

Networks are comprised of nodes and links. Nodes are defined by the analyst. In this case nodes are species or individuals. Links, are the connections between nodes, in this case floral visits. Attributes are intrinsic characteristics of the nodes (size, floral number). Network topology are the patterns of relations.

Data analysis

1. To explain floral visitation in response to individual floral traits, number, patch density and site-level density, generalized linear mixed models were fit with species included as a random effect.

To explain differences in foraging preferences by function pollinator groups, separate models were created for all pollinators, honeybees, solitary bees, all bees and flies.

We plotted density-visitation curves for each species that had >10 observations?

We organized the data into two adjacency matrices. The first, the species-species (S-S) network was arranged with pollinator species as columns, and the plant species as rows…

To characterize the community network at both the community and individual level:

Results

Major findings: Current analyses are focused on interactions between shrubs only, because the visitation network (Figure 3) shows that cacti interact primarily with other cacti. Local shrub density had a positive influence on pollinator visitation (Table 2). There is a significant interaction between individual flower number and site level shrub density. When site level shrub density is high, the slope of this relationship is steeper, suggesting individuals with lower flower number are at a disadvantage when site level shrub density is higher (Figure 5).

Visitation responses to individual shrub floral density

We tested several models for different types of density: total density, shrub density, cactus density, conspecific and heterospecific.

Additive model:

Fixed effects:

Estimate Std. Error z value Pr(>|z|)

(Intercept) 0.38125 0.41853 0.911 0.3623

shrub.density 0.08558 0.04204 2.036 0.0418 \*

N.flowers.scaled 0.40650 0.09743 4.172 3.01e-05 \*\*\*

site.density -4.53886 10.25546 -0.443 0.6581

Site density was not measured each day. There is a significant interaction, however the positive effect of individual flower number was unchanged – it just became more positive. Therefore, we feel comfortable still including it in models.

**Summary results:**

394 observation periods (10 minutes each).

618 visits were recorded. Nectar robbing and visits by non-pollinating insects excluded.

10 functional groups, 62 RTU of visitors

Discussion

There are interactions of different scales of density.

This has been found before in these papers:

Individual traits influence network topology.

What do these mean.

Implications for community interactions.

Suggestions for future work based on these results.

Appendix

Imputation: Missing values (4) of site level density for imputed using the package imputeTS (cite) to be able to use the most response data in the analysis. All species were imputed individually because different plants have different flowering strategies. We used time series because the number of flowers opened each days has temporal dependencies. “his process is a commonly used statistical method for

substituting missing values in a time series with values following the same temporal or spatial pattern

created by existing data (Schneider, 2001; Moritz, 2015)

“

Used linear interpolation – I expect there to be a trend but no seasonality.

Table 1: Imputation of site density measurements.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Parameter | Mean | | Standard deviation | | % DAta |
|  | Before | After | Before | After | Before |
| LT | 0.011858974 |  | 0.00312757 |  | 76.5% |
| SD | 7.69E-05 |  | 0.00027735 |  | 76.5% |
| SM | 0.000521368 |  | 0.000874754 |  | 76.5% |
| SC | 0.002653846 |  | 0.002230327 |  | 76.5% |
| AS | 0.015478632 |  | 0.009804953 |  | 76.5% |
| EL | 0 |  | 0 |  | 76.5% |
| EC | 0.002405983 |  | 0.003057944 |  | 76.5% |
| PP | 0.000115385 |  | 0.000416025 |  | 76.5% |
| HH | 3.85E-05 |  | 0.000138675 |  | 76.5% |
| BW | 0.001 |  | 0.001607275 |  | 76.5% |