Forecasting the spatio-temporal uncoupling of bumblebee-flower interaction networks

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Last revision: *May 6, 2022*

Purpose: This template provides a series of scripts to render a markdown document into an interactive website and a series of PDFs.

Motivation: It makes collaborating on text with GitHub easier, and means that we never need to think about the output.

Internals: GitHub actions and a series of python scritpts. The markdown is handled with `pandoc`.

Abstract

Using a data set of [DESCRIBE EACH DATASET IN A NICE WAY], we predict a spatiotemporally explicit metaweb of interactions between bumblebees (*Bombus*) and wildflowers (within *find clade*). We integrate this data with crowdsourced occurrence data and climate data to [best paint the picture of the Colorado bumblebee-plant metaweb]. Using temporal climate data, we forecast how the spatiotemporal overlap of interacting species will change under proposed climate scenarios. We use this to estimate what interactions between bees and plants need the most attention to prevent the spatiotemporal decoupling of an interactions from threatening ecosystem functioning or the persistence of a species.

Introduction

Species interactions are important. It is ultimately interactions between individuals of different species that drive the structure, dynamics, and persistence of ecosystems, and the abundance and diversity of the species within them. Plant-pollinator interactions specifically drive the function and persistence of "architecture of biodiversity" (Bascompte & Jordano 2007). However, we are far from a robust understanding of plant-pollinator networks is.

In this paper, we combine several datasets, each spanning several years, to produce spatially and temporally explicit predictions of *Bombus* plant-pollinator interactions across the state of Colorado.

We do this in two parts: (1) metaweb prediction and (2) conditioning our metaweb prediction on co-occurrence probability.

First, we build a model to predict the metaweb—the network of *all* interactions, aggregated across all times and spatial locations—of *Bombus* and wildflower species across Colorado. (Why do this? The metaweb is more predictable than local interactions.) We do this using network embedding (**cite?**). Network embedding takes each node in the network (either a bumblebee or a wildflower) and represents it in a latent *n* dimensional space. Combination of running models on Temporal niche (T), Phylogenetic niche (P), Environmental niche (E), and relative abundance in community (RA).

Second, we then use this metaweb to predict the structure of networks at specific locations and times of year (Gravel *et al.* 2019).

Finally we suggest a map of sampling priority, which suggests the locations to sample that will best improve our understanding of the Colorado *Bombus* pollination metaweb.

Data

We use three separate datasets to estimate the Colorado *Bombus* metaweb.

Methods

Concept Fig

Metaweb Model

Phylogeny Construction

Feature Embedding

Relative Abundance

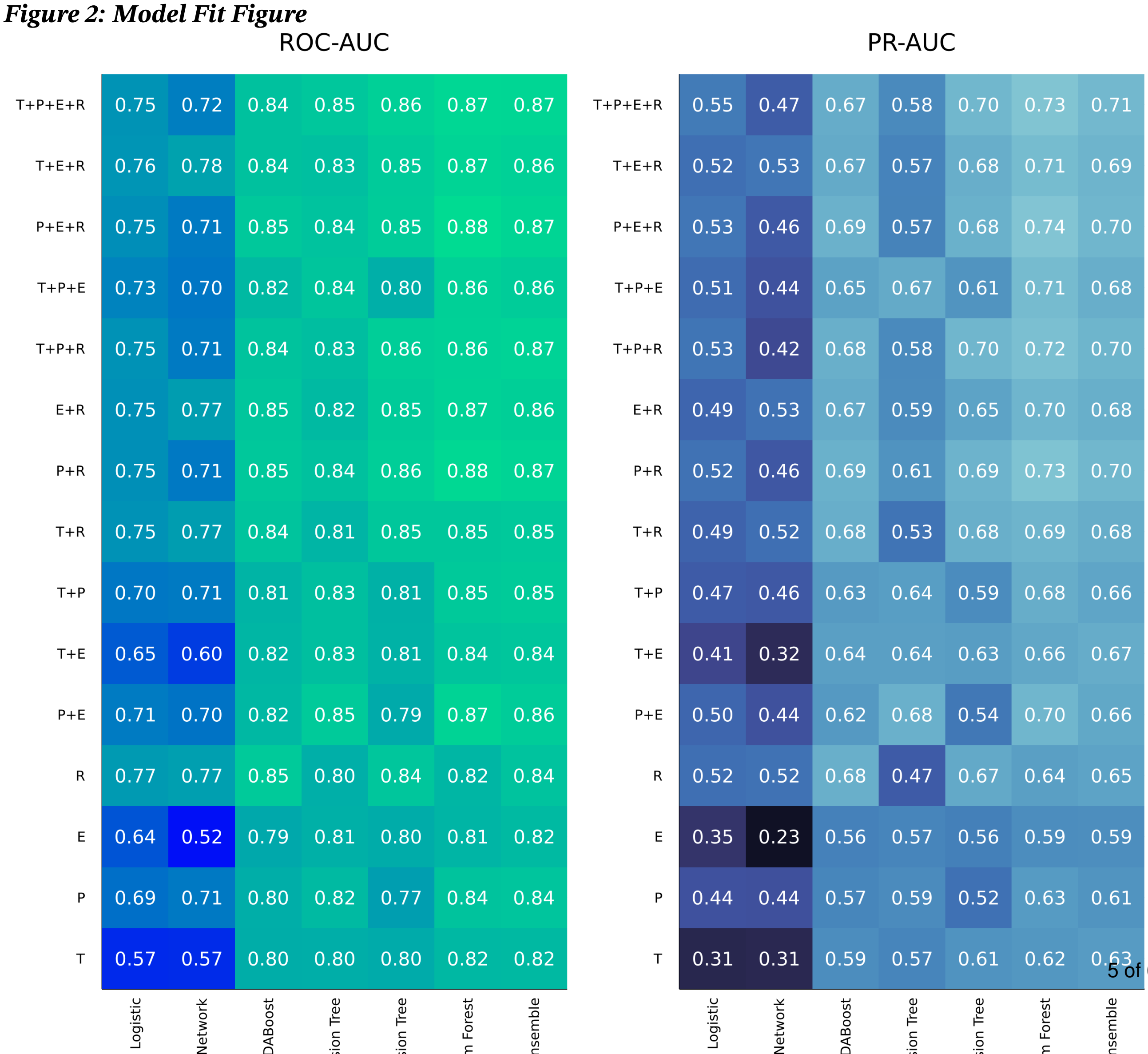
Phylogenetic features

Environmental niche features

Temporal niche features

Metaweb Model Fitting and Validation

Figure 2: Model Fit Figure



Spatiotemporally Explicit Networks

Now that we have a metaweb…..

Figure 3: Maps over time figure and Prob(Connectance) vs. Month figure

Sampling Prioiritization

Figure 4: Uncertainty and sampling priority map

Discussion

Bascompte, J. & Jordano, P. (2007). Plant-Animal Mutualistic Networks: The Architecture of Biodiversity. *Annual Review of Ecology, Evolution, and Systematics*, 38, 567–593.

Gravel, D., Baiser, B., Dunne, J.A., Kopelke, J.-P., Martinez, N.D., Nyman, T., *et al.* (2019). Bringing Elton and Grinnell together: A quantitative framework to represent the biogeography of ecological interaction networks. *Ecography*, 42, 401–415.