

# Building a better metaweb: predicting spatiotemporally explicit plant-pollinator networks

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**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 scripts. The markdown is handled with pandoc.

## 1 Abstract

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

## 9 Introduction

10 Species interactions are important. It is ultimately interactions between individuals of different species  
11 that drive the structure, dynamics, and persistence of ecosystems, and the abundance and diversity of the  
12 species within them. Plant-pollinator interactions specifically drive the function and persistence of  
13 “architecture of biodiversity” (Bascompte & Jordano 2007). However, we are far from a robust  
14 understanding of plant-pollinator networks. This is because sampling interactions is costly. Interactions  
15 vary in space and time (Poisot *et al.* 2015)—particularly relevant in this system (CaraDonna *et al.* 2014).  
16 This is why there is interest in using models to predict interactions from sparse data (Strydom2021?). In  
17 this paper, we combine several datasets, each spanning several years, to produce spatially and temporally  
18 explicit predictions of the bumblebee (genus *Bombus*) and wildflower pollination network across the state  
19 of Colorado.

20 We do this in two parts: (1) metaweb prediction and (2) conditioning our metaweb prediction on  
21 co-occurrence probability. First, we build a model to predict the metaweb—the network of *all*  
22 interactions, aggregated across all times and spatial locations—of *Bombus* and wildflower species across  
23 Colorado. (Why do this? The metaweb is more predictable than local interactions.) We do this using  
24 network embedding (cite?). Network embedding takes each node in the network (either a bumblebee or a  
25 wildflower) and represents it in a latent  $n$  dimensional space. Combination of running models on  
26 Temporal niche (T), Phylogenetic niche (P), Environmental niche (E), and relative abundance in  
27 community (RA).

28 Second, we then use this metaweb to predict the structure of networks at specific locations and times of  
29 year (Gravel *et al.* 2019). Finally we suggest a map of sampling priority, which suggests the locations to  
30 sample that will best improve our understanding of the Colorado *Bombus* pollination metaweb.

31 Why is this good for science, what does this contribute to our understanding of plant-pollinator ints,  
32 networks, *Bombus*, predictive models, etc., and how can these results be useful.

## 33 **Data**

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

## 35 **Methods**

36 [Figure 1 about here.]

## 37 **Metaweb Model**

### 38 **Feature Embedding**

### 39 **Relative Abundance**

### 40 **Phylogenetic features**

41 **Phylogeny Construction** We construct phylogenies for both *Bombus* and wildflower species using  
42 barcode markers, mitochondrial COI and chloroplast *rbcL*, respectively. These sequences were obtained  
43 from NCBI GenBank for all species. For species for which no sequence was available (only a handful of  
44 plants), their was substituted with a barcode from a member of the same genus. Justify why this is fine  
45 here.

46 These sequences were aligned using ClustalOmega v???, and then a posterior distribution of phylogenies  
47 and consensus tree was obtained via MrBayes v??, using XX substitution model with gamma-distributed  
48 rates. Run until convergence, which here we define as the standard-deviation of splits falling below 0.1.

49 **Creating an embedding from phylogenies** We simulate traits.

## 50 **Environmental niche features**

51 We take the 19 BioClim layers from CHELSA (cite; 1km resolution) and a map of elevation and PCA them.  
52 A resulting 4 layers cover 99.5% of the variance. We use species occurrence data from GBIF, and consider  
53 each occurrence record as a point in environment space. Then we fit a multivariate normal distribution to  
54 these points in environmental space.

## 55 **Temporal niche features**

56 We take the mean and variance of the distribution of number of observations per week of year in the  
57 interaction field data.

## 58 **Metaweb Model Fitting and Validation**

59 We fit a bunch of models using MLJ.jl.  
60 Some of them are bagged, some are not bagged.  
61 AUC-ROC and AUC-PR values below in fig. [2](#)

62 [Figure 2 about here.]

## 63 **Spatiotemporally Explicit Networks**

64 Now that we have a metaweb.....

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

## 66 **Sampling Prioritization**

67 *Figure 4: Uncertainty and sampling priority map*

## 68 Discussion

- 69 Bascompte, J. & Jordano, P. (2007). Plant-Animal Mutualistic Networks: The Architecture of Biodiversity.  
70 *Annual Review of Ecology, Evolution, and Systematics*, 38, 567–593.
- 71 CaraDonna, P.J., Iler, A.M. & Inouye, D.W. (2014). Shifts in flowering phenology reshape a subalpine plant  
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- 73 Gravel, D., Baiser, B., Dunne, J.A., Kopelke, J.-P., Martinez, N.D., Nyman, T., *et al.* (2019). Bringing Elton  
74 and Grinnell together: A quantitative framework to represent the biogeography of ecological  
75 interaction networks. *Ecography*, 42, 401–415.
- 76 Poisot, T., Stouffer, D.B. & Gravel, D. (2015). Beyond species: Why ecological interaction networks vary  
77 through space and time. *Oikos*, 124, 243–251.

Metaweb Prediction

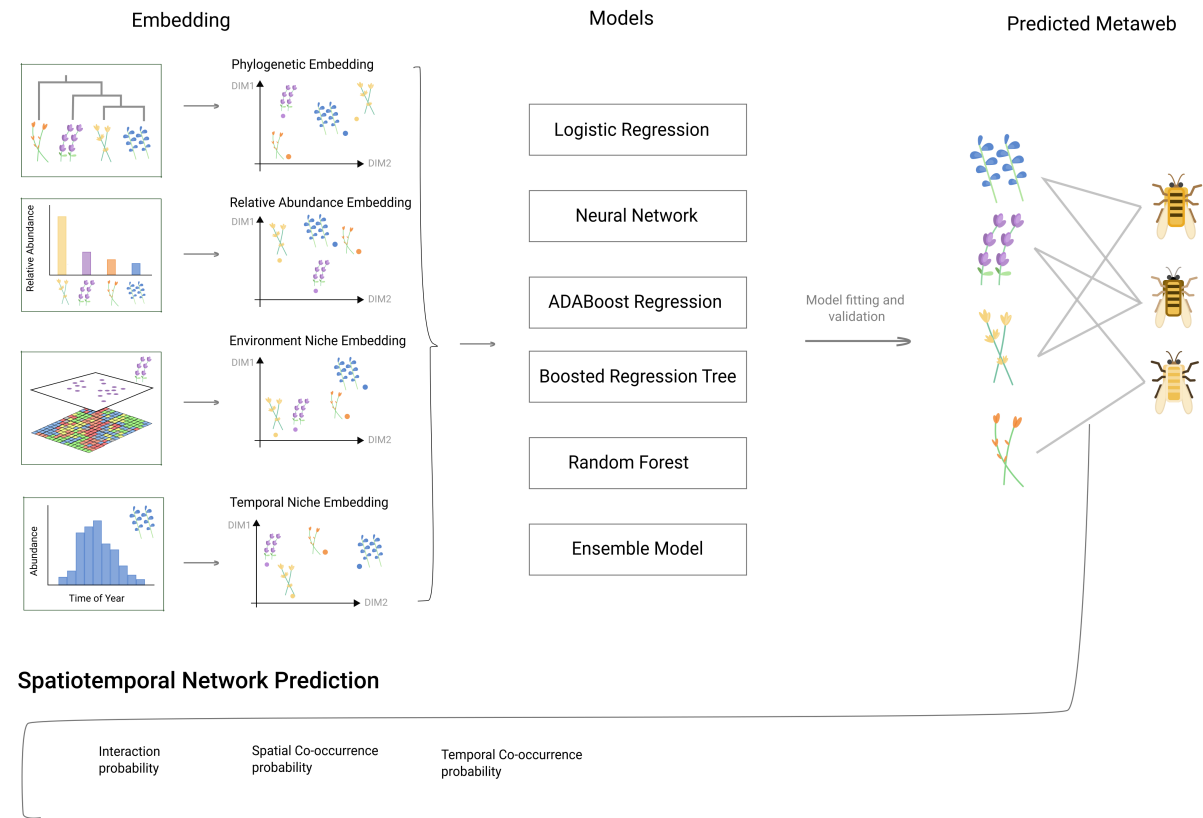


Figure 1: todo

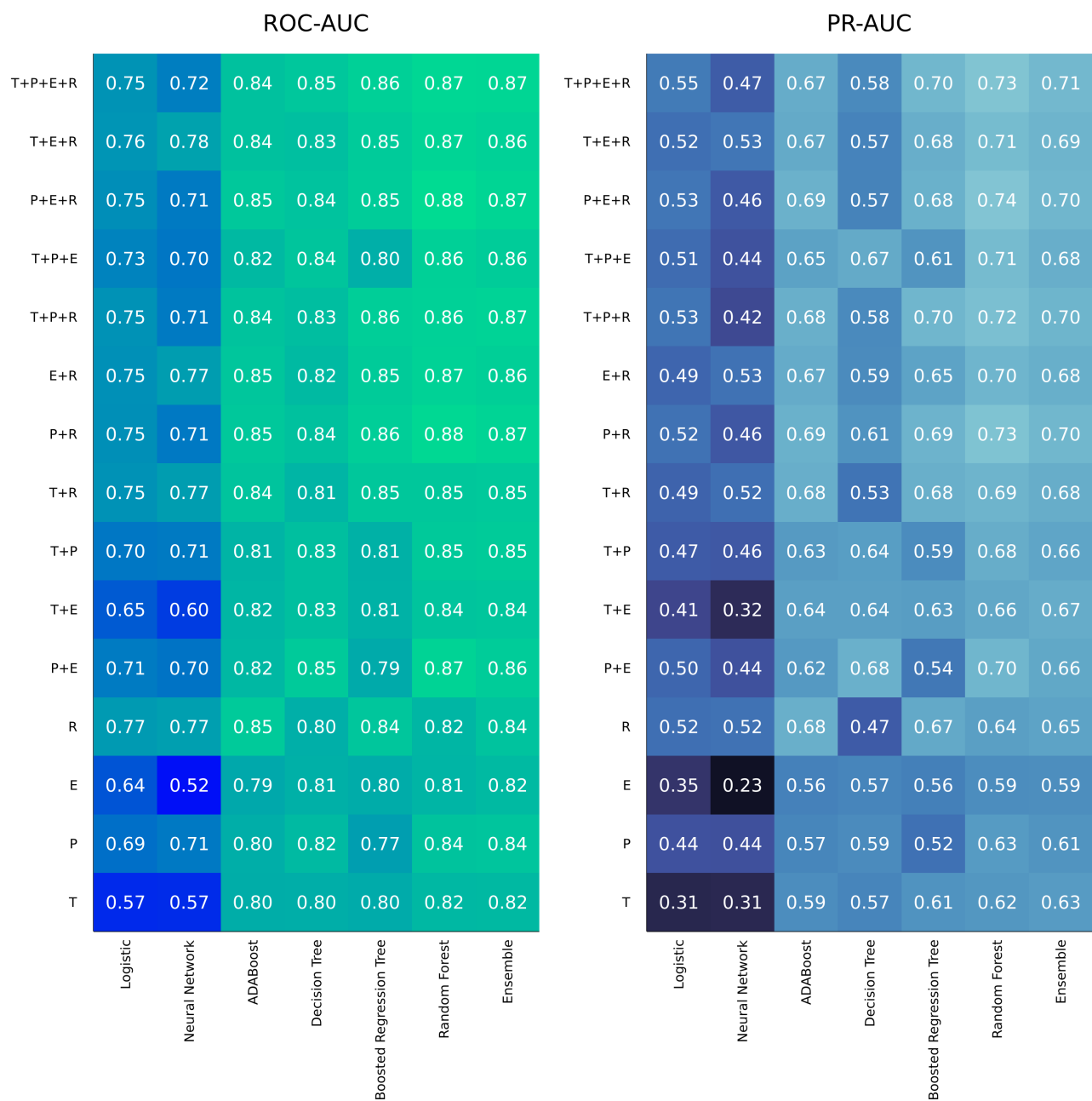


Figure 2: todo