

Tackling knowledge gaps about food webs with trait-based models

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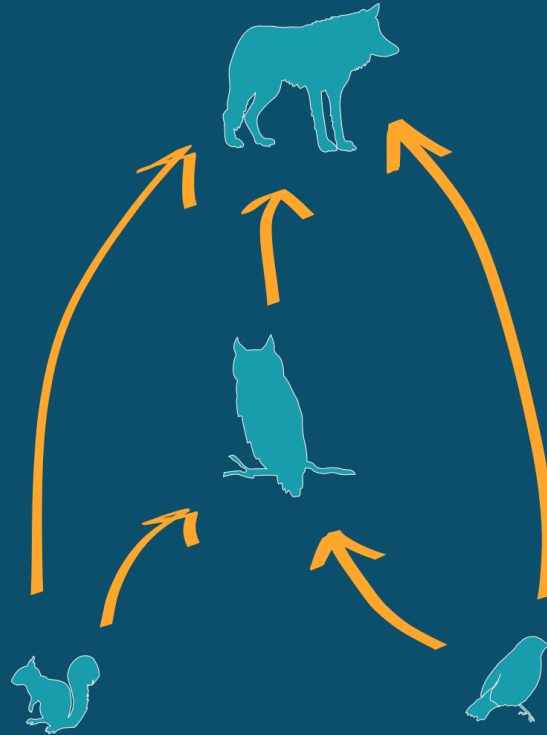
Introduction



Introduction

Theory:

- Community assembly
- Biogeography
- Niche
- Eco-evolutionary dynamics



Ecosystem functions:

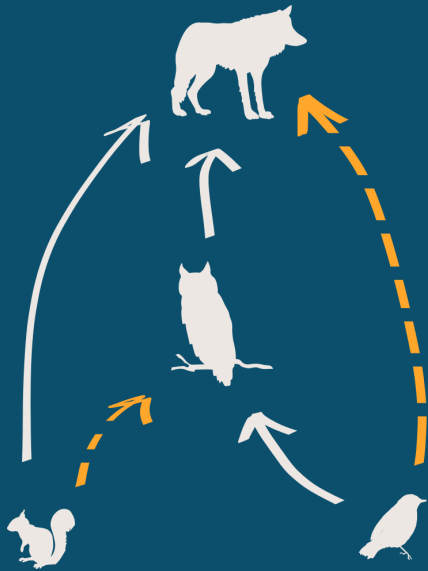
- Stability
- Nutrient cycling
- Energy flow
- Population regulation

Applications:

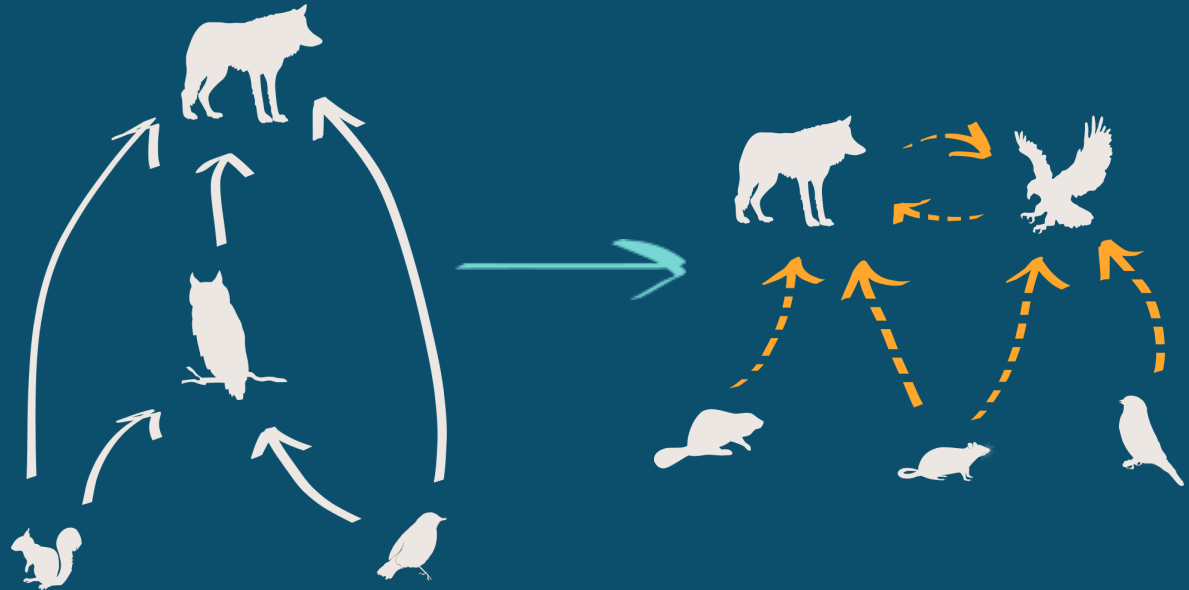
- Species role
- Trophic cascades
- Co-extinction

Introduction

Within food web predictions:



Across food web predictions:



Questions

1. How much information are needed to make reliable within food web predictions ?
2. What factors limits across food web predictions?
3. How well can we predict species trophic roles with interaction models?

Methods

Bayesian Generalized Linear Model:

$$\Pr(\text{prey} \rightarrow \text{predator}) = f(\text{prey traits} + \text{predator traits} + \text{predator} - \text{prey trait-match})$$

foraging ability of the predator
e.g., foraging strategy

vulnerability of the prey
e.g., body mass

functional match
e.g., activity time

The diagram illustrates a Bayesian Generalized Linear Model for the probability of a predator consuming its prey. The model is represented by the equation: $\Pr(\text{prey} \rightarrow \text{predator}) = f(\text{prey traits} + \text{predator traits} + \text{predator} - \text{prey trait-match})$. The equation uses icons of a squirrel (prey) and an eagle (predator) to represent the variables. The first term, 'prey traits', is associated with the squirrel icon and labeled 'vulnerability of the prey e.g., body mass'. The second term, 'predator traits', is associated with the eagle icon and labeled 'foraging ability of the predator e.g., foraging strategy'. The third term, 'predator - prey trait-match', is associated with both icons and labeled 'functional match e.g., activity time'. The entire equation is enclosed in a light blue rounded rectangle.

Q1 Within food web predictions - Methods



Data

Food web of European tetrapods

~ 1k species

~ 71k pairwise interactions

Variables

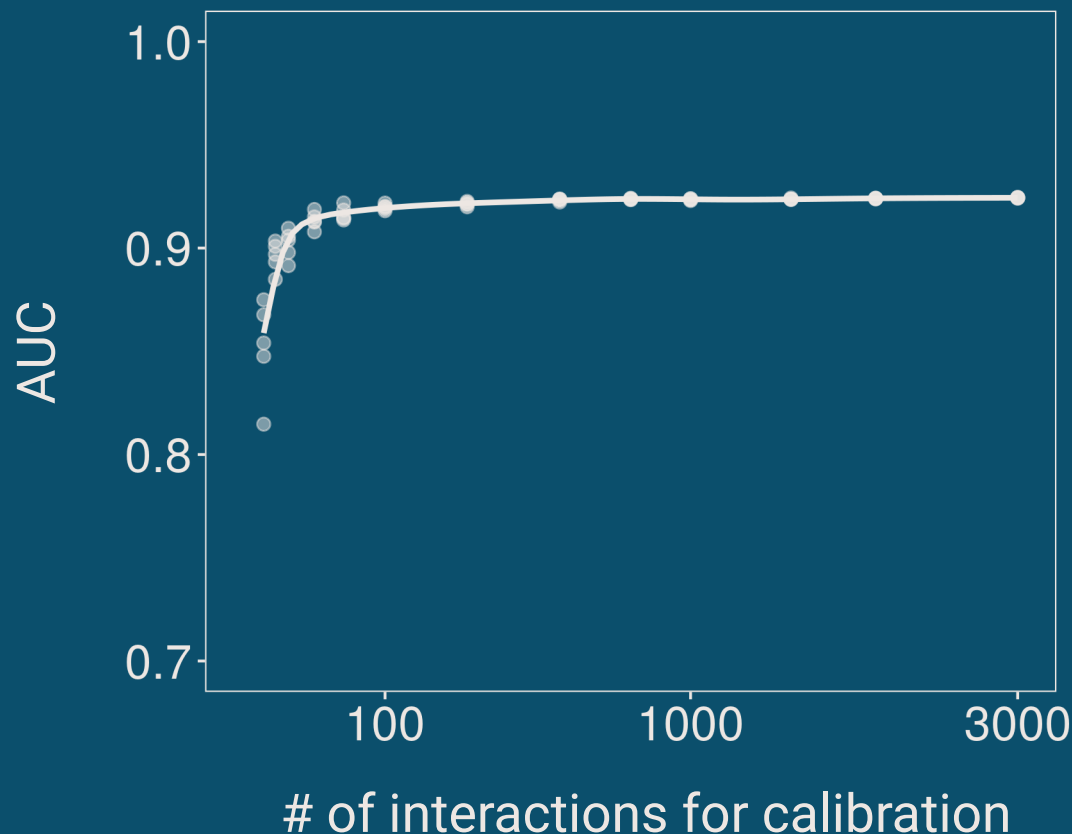
Independent variable:

Size of calibration dataset

Dependent variable:

Model performance

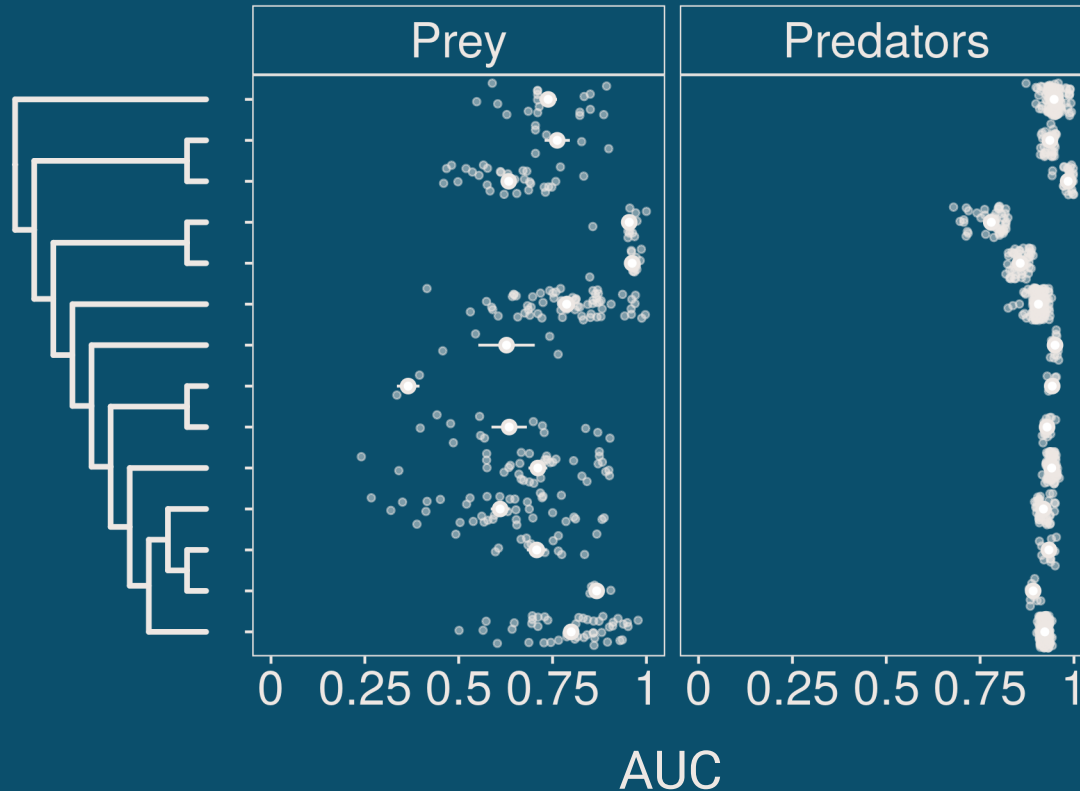
Q1 Within food web predictions - Results



- Performance peaks at a **very small training dataset**

- A relatively simplistic model **predicts most interactions well**

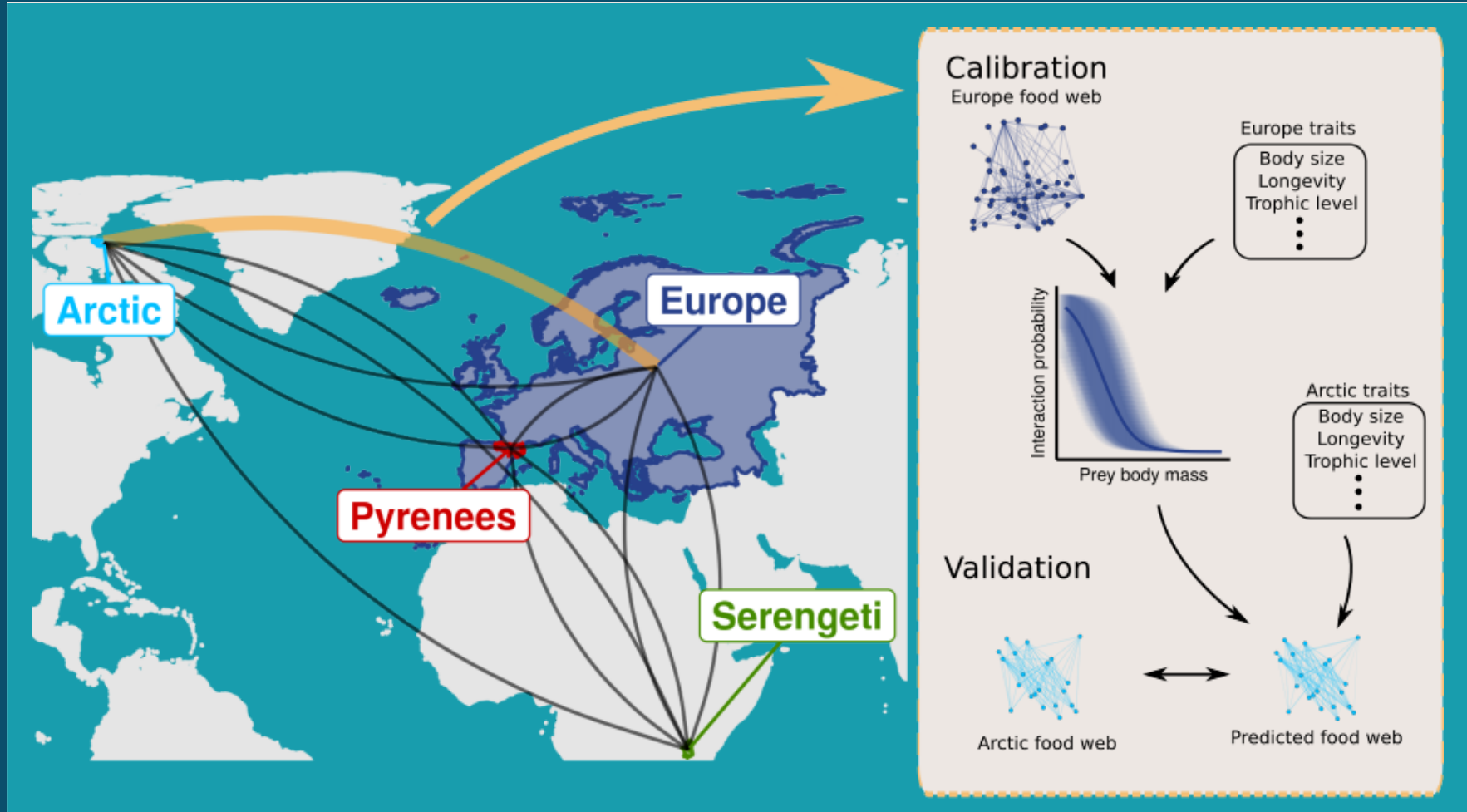
Q1 Within food web predictions - Results



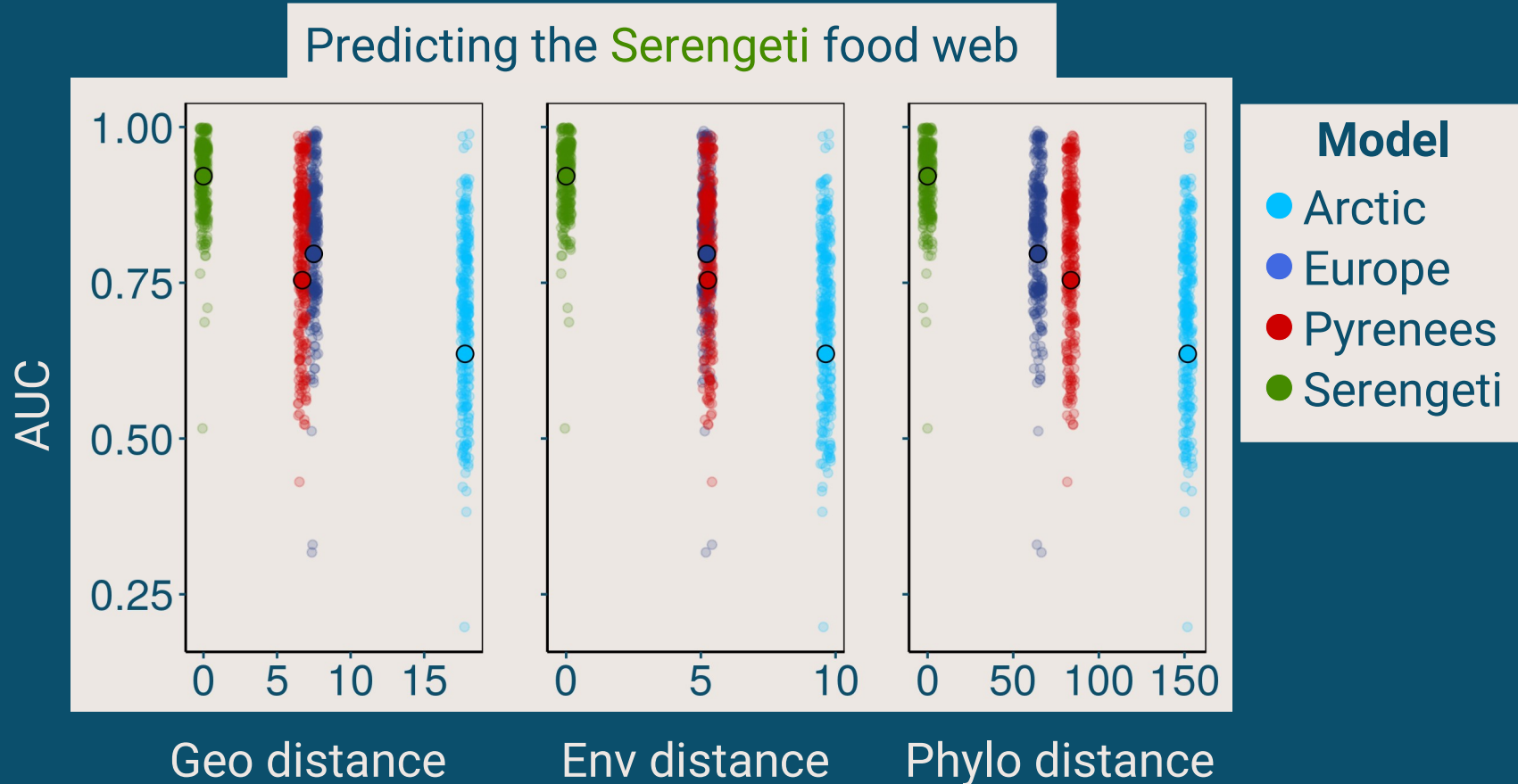
- **Prey** of some species order are **not well predicted**

- **Predators** of most species are **well predicted**

Q2 Across food web predictions - Methods



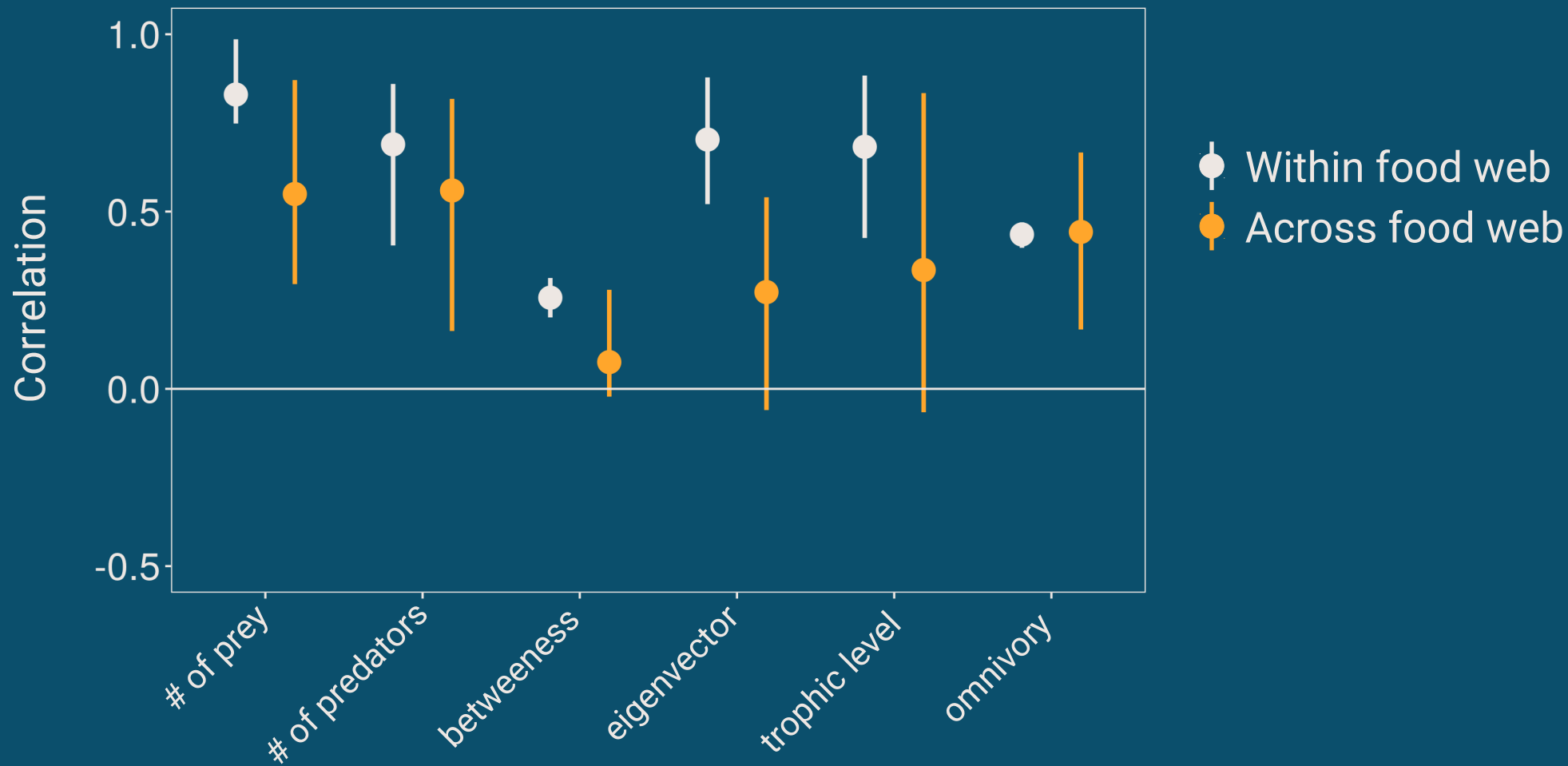
Q2 Across food web predictions - Methods



Q3 Trophic role predictions - Methods



Q3 Trophic role predictions - Results



Summary

1. How much information are needed to make reliable within food web predictions ?

We recovered a large food web small fraction ($<1\%$) of all interactions.

2. What factors limits across food web predictions?

We predicted highly contrasting food webs. Environment and shared phylogeny limit transferability.

3. How well can we predict species trophic roles with interaction models?

We can predict some role reasonably well for within food web predictions. Less so for across food web predictions.

Thank you!

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