Advances in dynamic and multiplex networks motivated by ecology

David Dunson

Joint work with Jennifer Kampe, Luca Silva and Tomas Roslin

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Outline

- Ecological context: why interactions matter
- Statistical model: NEX for dynamic networks
- Application and results: Zackenberg plant-pollinator networks

Interaction networks in ecology

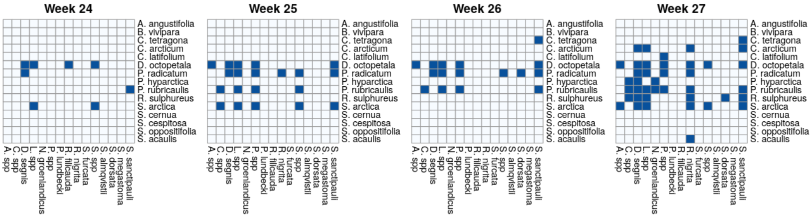


Dryas octopetala, *Salix glauca*, *Saxifraga hyperborea* mid pollination –"interacting with arthropods."

Definition

An **interaction network** records which species are observed in some form of biotic interaction. Interactions may be restricted to certain types of interactions (e.g., mutualism, commensalism, competition, predation); not necessarily symmetric.

Dynamic Plant-Pollinator Networks



Evolution of insect-plant interactions among the 15 most common plants and insects for a subset of the 2010 summer season at the Zackenberg Research Station.

The community ecology literature tends to assume **networks are static**: if two species interact, they will always interact.

However, there is ample evidence that **interactions vary** over space and time as a result of

- Local trait distributions
- Local abundances
- Local environmental conditions
- Species not directly involved in the interaction

But observable covariates are limited and attempts in the ecological literature to explain variation in networks have had limited success, e.g.,Gravel et al. (2019).

Latent factors for dimension reduction in dynamic networks

- Durante and Dunson (2014) build on the classic Hoff et al. (2002) model: to reduce the dimensionality and borrow information across pairs, write s_{ijt} as an inner product of latent coordinates for the respective units i, j.

$$E[a_{ijt} \mid \pi_{ijt}] = \pi_{ijt} = \frac{1}{1 + e^{-s_{ij}(t)}}$$
$$s_{ij}(t) = \mu(t) + x_i(t)' y_j(t)$$
$$x_{ih}(.) \sim GP(0, \tau_h^{-1} C_x), y_{ih}(.) \sim GP(0, \tau_h^{-1} C_y)$$
$$\mu(.) \sim GP(\mu_0, C_\mu)$$
$$\text{where } C_{.}(t.t') = \exp(-\kappa_X (t - t')^2),$$

and τ_h^{-1} is a shrinkage parameter defined via multiplicative inverse gamma process.

Nested Exemplar (NEX) Space Approach

- The Durante and Dunson (2014) model has complexity $\mathcal{O}((N+M)T)$: we have to estimate latent trait tensors $\mathcal{X} \in \mathbb{R}^{N \times H \times T}$ and $\mathcal{Y} \in \mathbb{R}^{M \times H \times T}$

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- In the proposed NEX approach, we use a low rank factorization of the latent trait tensors, yielding a model that is $\mathcal{O}(N+M+T)$:

$$\mathcal{X} = \sum_{k=1}^{K} \lambda_k^K U_k^X \otimes V_k^X \otimes W_k^X$$

$$\mathcal{Y} = \sum_{k=1}^{K} \lambda_k^K U_k^Y \otimes V_k^Y \otimes W_k^Y$$

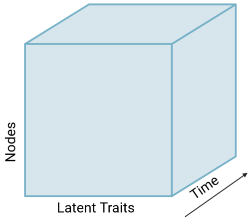
And $\mathcal{S}$ has frontal slices $S_t = \mu_t 1_N 1_M^\top + X_t \Lambda^H Y_t^\top$ as before.

Intuition for NEX

Consider the latent attribute tensor $\mathcal{X}$:

$$\mathcal{X} = \sum_{k=1}^{K} \lambda_k^K U_k^X \otimes V_k^X \otimes W_k^X$$

- λ_k^K: Weights for each exemplar space dimension k
- U_k^X: Characterize the nodes in a K-dimensional exemplar space
- V_k^X: Link the K-dimensional exemplar and H-dimensional latent trait space
- W_k^X: Exemplar curves characterizing temporal variation in the latent attributes



K upper bounds the rank of the tensor decompositions

H upper bounds the rank of frontal slices

Prior Specification

Independent Gaussian priors on the latent features for each node and dimension of the latent space:

$$U_{ik}^X \sim N(0, \sigma^2), \ \forall ik \in [N] \times [K]$$
$$U_{jk}^Y \sim N(0, \sigma^2), \ \forall jk \in [M] \times [K]$$
$$V_{hk}^X, V_{hk}^Y \sim N(0, \sigma^2), \ \forall hk \in [H] \times [K]$$

Multivariate Gaussian priors for the temporal components:

$$W_k^X, W_k^Y \sim N(0, \Sigma) \ \forall k \in [K]$$
$$\mu \sim N(\mu_0, \Sigma_\mu),$$

In the dynamic case, a broadly suitable choice is:

$$\Sigma = \exp(-k \cdot D(t, t'))$$

Simulations I

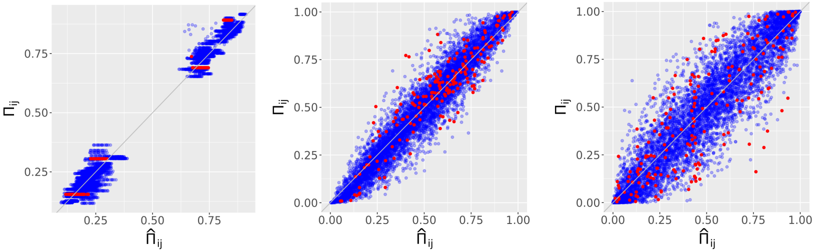


Figure 1: In sample (blue) and out-of-sample(red) performance of NEX for synthetic data generated from DynSBM, NEX and DLF

Simulations II

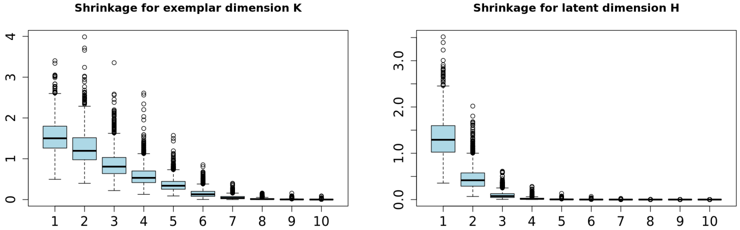


Figure 2: Posterior samples for different components of λ^K(left) and λ^H(right) when data are simulated with true values $K = 5$ and $H = 2$

Zackenberg plant-pollinator networks

- The Zackenberg Research Station is in a high arctic coastal valley in Northeast Greenland National Park
- Data on plant-pollinator networks were collected over two decades in 1996, 1997, 2010, 2011, 2016

Zackenberg Data Structure

- **Flower Visitation (1996-2016)**
  - Starting after snowmelt, identify all plant species present and blooming in the study plot
  - Select two individuals of each plant species and monitor for 40 minutes
  - Capture and identify all insects that visit during the period
  - Repeat weekly throughout the summer research season
  - Define a dynamic network with $A_{ijt}^{FV} = \mathbb{1}(\text{insect } i \text{ was observed pollinating plant } j \text{ at time } t)$
- **Pollen Transport (2016 only)**
  - Examine each captured insect under a microscope and plants visited are identified via pollen grains
  - Barcode to confirm ID
  - Define a dynamic network with $A_{ijt}^{PT} = \mathbb{1}(\text{insect } i \text{ had pollen from plant } j \text{ at time } t)$

Motivation

- Challenges: most interactions are only observed 1-2 times over 49 weeks with $< 1\%$ of possible interactions occurring each week
- Estimate interaction probabilities with uncertainty quantification, especially interesting for non-observed interactions which may have been missed
- Predict which interactions might occur given phenology shifts
- Investigate changes in the network due to seasonality, climate change, annual variability, environmental covariates

How we modify NEX for Zackenberg

Since the key ecological question is why interactions vary even when conditioning on co-occurrence, we utilize a conditional formulation and include random effects to capture plant i node degree heterogeneity, temperature, seasonality week w, and year r:

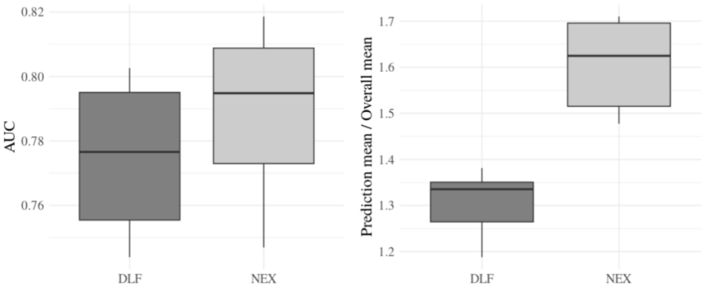
$$E[a_{ijwr} \mid \pi_{ijwr}, O_{ijwr}] = \pi_{ijwr} O_{ijwr} = \frac{O_{ijwr}}{1 + e^{-s_{ijwr}}}$$

$$s_{ijwr} = \mu_w + \alpha_i + \gamma_r + \beta \text{temp}_{wr} + x'_{iwr} \Lambda^H y_{jwr}$$

$$\text{where } O_{ijwr} = 1(\text{species } i, j \text{ co-occur in week } w \text{ of year } r)$$

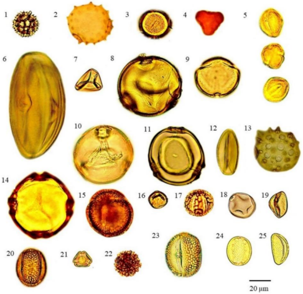
Warning: there is some ambiguity in defining the occurrence array!

Cross Validation Results



Ten-fold cross validation results for NEX and the dynamic latent factor model (DLF). Boxplots show out of sample AUC (left) and the ratio of the mean posterior interaction probability for held-out recorded pollen transport interactions to the mean posterior interaction probability for missing edges overall (right).

Ecological Validation: Pollen Transport Data



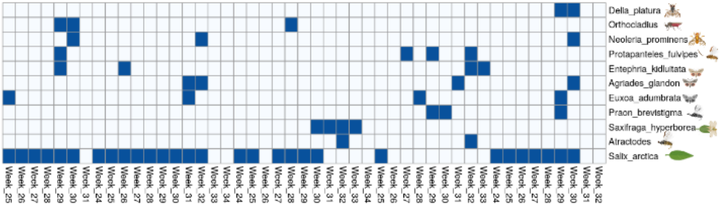
Bee bread microscopy
Kankasemsuk et al. (2023)

Pollen Transport Validation: how well does the model predict heldout edges from the pollen transport data?

$$\frac{\text{mean}(\hat{\pi}_{ijt} : O_{ijt} = 0, A^{PT}_{ijt} = 1)}{\text{mean}(\hat{\pi}_{ijt} : O_{ijt} = 0)} = 1.65$$

Implications for climate change

We are interested in the impacts of shifting phenologies on pollination: what interactions that aren't possible now due to non-co-occurrence, might happen in the future?



Implications for missing, future interactions

`NEX` allows us to analyze posterior interaction probabilities across observed non-edges, identifying likely **missing interactions** for:

- Agromyzidae and Scathophagidae - both consisting of flies with a high potential to be missed by observing researchers
- Braconidae and Ichneumonidae - parasitoid wasps where time spent on flowers limits time spent searching for hosts, making them harder to observe on the flowers

Future interactions: high posterior probabilities but not currently co-occurring:

- *Saxifraga hyperborea* is a predicted forage source for: *Euxoa adumbrata*, *Agriades glandon*, *Entephria kidluitata*, *Praon brevistigma*, *Propanteles fulvipes*, *Neolaria prominens*.
- *Salix acrtica* is a predicted forage source for the genus *Atractodes*

Future work

- Experimental validation
- Inclusion of more/better covariates: wind, weather
- Extension to counts
- Incomplete identification of species
- Formalize uncertainty in occurrences: sample occurrence indicators, include phenology model

Thank you!

Questions and discussion welcome.

Kampe JN, Silva LA, Roslin T, Dunson DB (2025) Nested exemplar latent space models for dimension reduction in dynamic networks. arXiv:2412.07604

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Hoff, P. D., Raftery, A. E., and Handcock, M. S. (2002). Latent space approaches to social network analysis. *Journal of the American Statistical Association*, 97(460):1090–1098.

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Kankasemsuk, S., Tibmanoo, C., Boonsuk, B., Bunma, S., and Suppasat, T. (2023). Total protein content of bee bread in apis cerana combs and tetragonula pegdeni storage pots of different plant sources from chanthaburi province, thailand. *Journal of Current Science and Technology*, 13:714–724.

Poisot, T., Stouffer, D. B., and Gravel, D. (2015). Beyond species: why ecological interaction networks vary through space and time. *Oikos*, 124(3):243–251.

Review: Networks as adjacency matrices

Definition

We can encode interactions using an **adjacency matrix** A with entries $A_{ij} = 1$ if species i and species j are observed to interact and 0 otherwise. We can further describe the probability of observing the interactions via a link probability matrix, Π with entries $\pi_{ij} = P(a_{ij} = 1)$

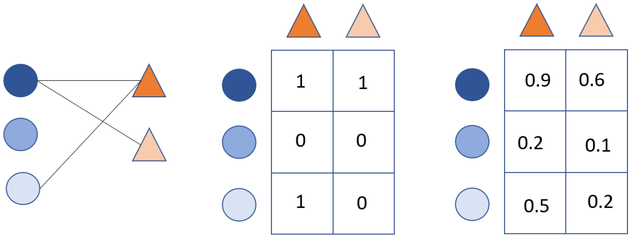


Figure 3: Observed interaction network, observed binary adjacency matrix, and unobserved link probability matrix

The Problem

Model formulation: $a_{ijt} \mid \pi_{ijt} \sim \text{Ber}\{\pi_{ijt}\}$ independently for $i = 2, \cdots, N, j = 1, \cdots, M, t = 1, \cdots, T$

$$E[a_{ijt} \mid \pi_{ijt}] = \pi_{ijt} = \frac{1}{1 + e^{-s_{ijt}}}$$

Problem: without further assumptions on s_{ijt}, we need to estimate NMT parameters. Interaction networks are expensive to collect, so the number of free parameters $>>$ sample size. We need to **reduce** the dimension.

Theoretical Guarantees I

Theorem

Given a time-evolving matrix $S(t) \in \mathbb{R}^{N \times N}$, with $t \in \mathcal{T}$ compact, there exist finite integer values H, K such that for every $t \in \mathcal{T}$:

$$S(t) = \mu(t) 1_N 1_N^\top + X(t) Y(t)^\top,$$

where $\mu(t)$ is a time-varying intercept and $X(t), Y(t)$ are matrices of time-evolving latent vectors:
$X(t) = \sum_{k=1}^{K} w_k^X(t) U_k^X \otimes V_k^X$, $Y(t) = \sum_{k=1}^{K} w_k^Y(t) U_k^Y \otimes V_k^Y$, *with* U_k^X, $U_k^Y \in \mathbb{R}^N$ *and* V_k^X, $V_k^Y \in \mathbb{R}^H$, $w_k^X(\cdot), w_k^Y(\cdot)$ *real scalar functions on* $\mathcal{T}$.

Theoretical Guarantees II

Corollary

Given a time-evolving link probability matrix $\Pi(t) \in \mathbb{R}^{N \times N}$*, with* $t \in \mathcal{T}$ *compact, there exist exist finite integer values* H, K *such that for every* $t \in \mathcal{T}$ *we have that*

$$\Pi(t) = f(S(t)), \quad t \in \mathcal{T},$$

where $S(t)$ *is defined as above,* $f(\cdot)$ *is the logit function and is applied element-wise to* $S(t)$*.*

Theoretical Guarantees III

Theorem

Let $p_{\mathcal{S}}$ be the prior induced on $\{S(t), t \in \mathcal{T}\}$ as above. If $\mathcal{T}$ is compact, then for every continuous $S_0(t)$ and for every $\epsilon > 0$ we have

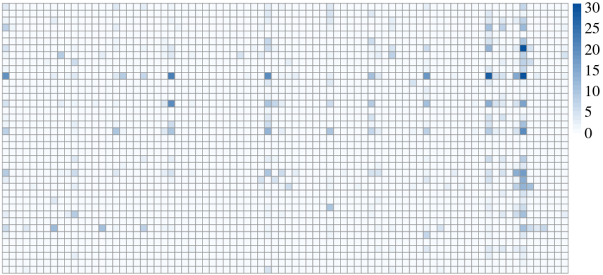
$$p_{\mathcal{S}}\left\{\sup_{t\in\mathcal{T}} ||S(t) - S_0(t)||_2 < \epsilon\right\} > 0$$

Corollary

Let p_{Π} be the prior induced on $\{\Pi(t), t \in \mathcal{T}\}$ by the priors as above. If $\mathcal{T}$ is compact, then for every continuous $\Pi_0(t)$ and for every $\delta > 0$ we have

$$p_{\Pi}\left\{\sup_{t\in\mathcal{T}} ||\Pi(t) - \Pi_0(t)|| < \delta\right\} > 0$$

The Zackenberg Meta-network



Meta-network of insect-plant interactions: rows indicate plant taxa, columns indicate insect taxa, and cell color indicates the number of distinct weeks an interaction is observed.

Posterior network

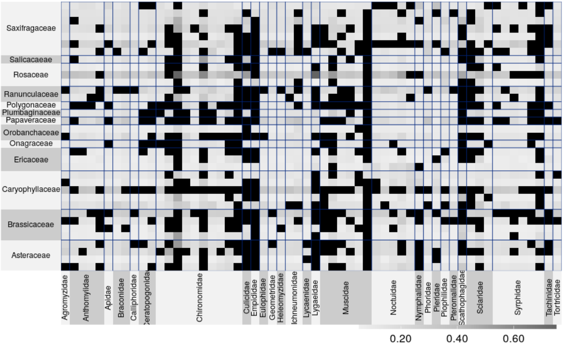


Figure 4: Posterior meta network versus observed meta network