

Bayesian graphical inference in spatial joint species distribution models

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Context: Joint species distribution models

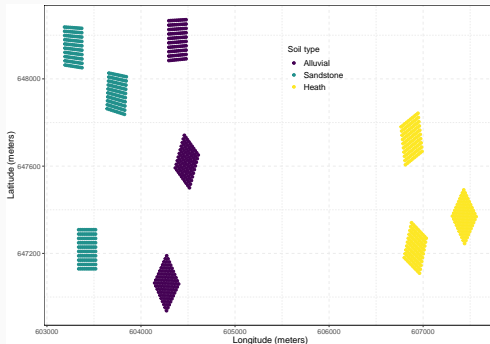
Ecological context

- **Goal** Describe and understand distribution of species within an ecosystem;
- **Mean** Counting individuals of all encountered species through surveys.

Statistical challenges

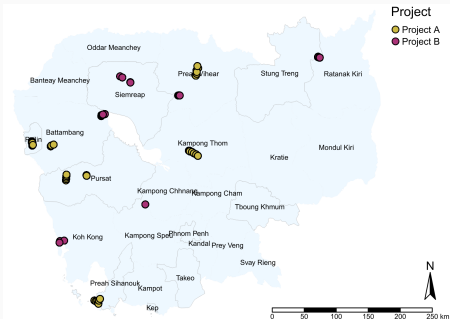
- Multivariate count data;
- Modelling dependencies:
 - Coming from spatial sampling;
 - Coming from species interactions.

Figure 1: Données issues de Sellan et al. (2019).



Mosquito communities in Cambodia

Figure 2: Source: Rozier et al. (2025).



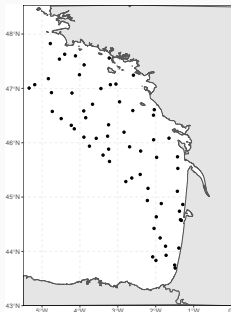
- 76 sites trapping sites across Cambodia
- Survey over time, in resulting 2000 collections;
- On each collection, mosquitoes from 150 species are counted;

Ecological question

What are the spatial and/or temporal patterns of mosquito communities?

Invertebrate communities in the Bay of Biscay

Figure 3: Données issues de Outrequin et al. (2025).

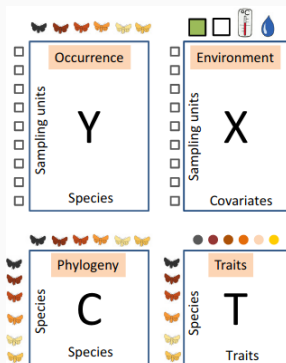


- 64 sites trawling sites across Bay of Biscay (EVOHE Project, 2019);
- Sampling made over different substrats, at different depth;
- 256 invertebrate species encountered.

What are the spatial patterns of species distributions. Are there some communities?

Joint species distribution data

Figure 4: Source: Ovaskainen and Abrego (2020)



- \mathbf{Y} a $n \times p$ matrix with entries in \mathbb{N} ;
- \mathbf{X} a $n \times n_{\text{cov}}$ matrix of real values;
- \mathbf{C} a $p \times p$ correlation matrix;
- \mathbf{T} a $p \times n_{\text{trait}}$ matrix of real values;

A multivariate generalized linear mixed model approach

- Latent variable approach: modelling of joint distribution of (\mathbf{Y}, \mathbf{Z}) .

For $1 \leq i \leq n, 1 \leq j \leq p$, $Y_{i,j} | Z_{i,j} \stackrel{\text{ind}}{\sim} \mathcal{D}(\exp(Z_{i,j}), \phi)$. Observation model

- \mathcal{D} is some distribution (Negative binomial, Poisson) with:
 - Expectation $\exp(Z_{i,j})$;
 - Dispersion parameter ϕ .

$\mathbf{Z} \sim \mathcal{MN}(\mathbf{X}\boldsymbol{\beta}, \Sigma_{\text{Site}}, \Sigma_{\text{Species}})$. Latent variable

- $\mathcal{MN}(\mathbf{X}\boldsymbol{\beta}, \Sigma_{\text{Site}}, \Sigma_{\text{Species}})$ is the *matrix normal* distribution with:
 - Expectation $\mathbf{X}\boldsymbol{\beta}$ (a $n \times p$ matrix);
 - Covariance between rows Σ_{Site} (a $n \times n$ symmetric positive definite matrix);
 - Covariance between columns Σ_{Species} (a $p \times p$ SPD matrix);
- $\boldsymbol{\beta}$ is an **unknown** $n_{\text{cov}} \times p$ matrix: **response of species to environment**.

Definition

\mathbf{M} : $n \times p$ matrix, \mathbf{U} (resp. \mathbf{V}): $n \times n$ (resp. $p \times p$) SPD matrix:

$$\mathbf{Z} \sim \mathcal{MN}(\mathbf{M}, \mathbf{U}, \mathbf{V}) \Leftrightarrow \text{vec}(\mathbf{Z}) \sim \mathcal{N}_{np \times np}(\text{vec}(\mathbf{M}), \mathbf{V} \otimes \mathbf{U}).$$

Properties

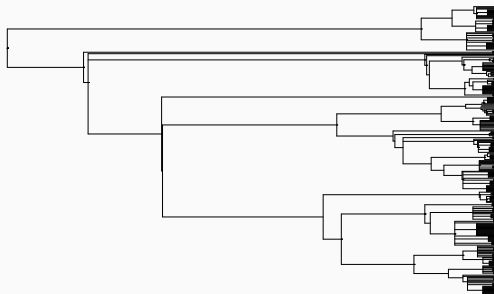
- Separability hypothesis over covariances;
- If $\mathbf{Z} \sim \mathcal{MN}(\mathbf{M}, \mathbf{U}, \mathbf{V})$, then
$$\mathbf{AZB}^T + \mathbf{C} \sim \mathcal{MN}(\mathbf{AMB}^T + \mathbf{C}, \mathbf{AUA}^T, \mathbf{BVB}^T);$$
 - Useful both for simulation and whitening;

Structuring the niches

- Suppose we have access to other data about species:
- Species traits in a matrix \mathbf{T} :

Species	Growth rate	Wood density	Max. Height
<i>Strychnos borneensis</i>	0.008	0.750	19.749
<i>Dysoxylum indet</i>	0.027	0.585	8.588
<i>Memecylon indet</i>	0.013	0.783	8.692
<i>Cratoxylum cochinchinense</i>	0.025	0.670	9.894
<i>Sterculia stipulata</i>	0.027	0.365	10.087

- Phylogeny, giving a correlation matrix \mathbf{C} :



Modelling the fixed effects

Structuring the β matrix

- The matrix β stacks vector of responses to environment:
 - The environmental niches of species;
- Assume that:
 - The **traits** affect β (similar traits lead to similar niche);
 - Columns (species) of β are correlated because of **phylogeny**.

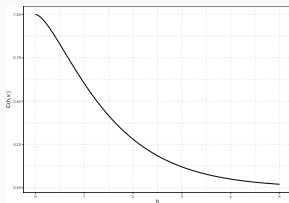
Formally, β is assumed to be a Matrix Normal random variable such that:

$$\beta \sim \mathcal{MN}(\Gamma\mathbf{T}^T, \eta^2\mathbf{I}_{n_{\text{cov}}}, \rho\mathbf{C} + (1 - \rho)\mathbf{I}_p).$$

- Γ is a $n_{\text{cov}} \times n_{\text{trait}}$ matrix structuring β :
 - **Do the species niches are correlated to species traits?**
- \mathbf{C} is the correlation matrix induced by the **phylogeny**;
- $0 \leq \rho \leq 1$ is the weight of **phylogeny** in the columns correlation of β .

Modelling residual dependencies

Figure 5: Matern covariance function for $\nu = 1, \sigma^2 = 1, \kappa = 1$



Model on spatial dependences (rowwise dependences)

- For two sites i and ℓ separated by a distance $h_{i,\ell}$,
 $(\Sigma_{\text{Site}})_{i,\ell} = C(h_{i,\ell}, \kappa)$ with:

$$C(h, \kappa) = \kappa h K_1(\kappa h),$$

with $K_1(\cdot)$ the modified Bessel function of second kind.

- Matern covariance with:
 - Fixed regularity $\nu = 1$ and marginal variance $\sigma^2 = 1$;
 - Unknown range parameter κ to estimate.

Model on species dependences (colwise dependences)

- No “natural” structure induced by a “natural” distance;
- Need for a geometrical/statistical structure to avoid $p \times (p + 1)/2$ free parameters;

Low rank structures on covariances

- Reducing number of parameters by assuming a low-rank structure

$$\Sigma_{\text{Species}} = \Lambda \Lambda^T,$$

where Λ is a $p \times q$ matrix with $q \ll p$;

- Probabilistic PCA structure;
- Λ interpreted as species response to q unmeasured covariates;

Modelling the dependences between species (II)

Model on species dependences (colwise dependences)

- No “natural” structure induced by a “natural” distance;
- Need for a geometrical/statistical structure to avoid $p \times (p + 1)/2$ free parameters;

Model on species dependences (colwise dependences)

- Modelling the precision matrix $\Omega = \Sigma_{\text{Species}}^{-1}$;
- Conditional independence property: For $1 \leq j, k \leq p$:

$$\Omega_{j,k} = 0 \Leftrightarrow (\mathbf{Z}_{\cdot,j} | \mathbf{Z}_{\cdot,-(j,k)}) \perp (\mathbf{Z}_{\cdot,k} | \mathbf{Z}_{\cdot,-(j,k)}) .$$

- Induces a graph between species: Draw an edge between species j and k iff $\omega_{j,k} \neq 0$;
- *Interpretation*: Ecological interaction network;

$$Y_{i,j} | Z_{i,j} \stackrel{\text{ind}}{\sim} \mathcal{NB}(\exp(Z_{i,j}), \phi),$$
$$\mathbf{Z} \sim \mathcal{MN}(\mathbf{X}\boldsymbol{\beta}, \Sigma(\kappa), \Omega^{-1}).$$

Observation model

Latent variable

Priors

$$\boldsymbol{\beta} \sim \mathcal{MN}(0, \mathbf{I}_{n_{\text{cov}}}, \mathbf{I}_p)$$

$$\phi \sim \log \mathcal{N}(m, s^2)$$

$$\kappa \sim \mathcal{Gamma}(a, b)$$

$$\Omega \sim \text{Continuous spike and slab prior (CSS)}$$

- CSS comes from Wang (2015).

Bayesian priors for precision matrices

Learning Ω

- We want to learn an interpretable graph;
- This suggest to have a sparse Ω ;
- Natural approach: Penalizing matrices having few zeros.

- Let rows of \mathbf{Z} be centered and independent *i.e.*

$$\mathbf{Z} \sim \mathcal{MN}(0, \mathbf{I}_n, \Omega^{-1}).$$

- The graphical Lasso learns Ω by maximizing:

$$\log(\det(\Omega)) - \text{Tr}\left(\frac{1}{n}\mathbf{Z}^T\mathbf{Z}\Omega\right) - \lambda\|\Omega\|_1, \quad \|\Omega\|_1 = \sum_{1 \leq i, j \leq p} |\omega_{i,j}|.$$

- The λ penalty parameter is chosen using model selection criterion.
- Implemented for JSJM (Chiquet, Mariadassou, and Robin (2021)).

- Prior distribution¹ over Ω ;

$$p(\Omega|\lambda) \propto \prod_{i < j} \mathcal{Lap}(w_{i,j}|\lambda) \prod_{i=1}^p \mathcal{E}(w_{i,i}|\lambda) \mathbf{1}_{\mathbb{S}_+}(\Omega).$$

- Leads to a Bayesian posterior proportional to graphical Lasso objective;
- Suitable for efficient Gibbs sampling (Wang (2012)).
- Does not lead to a straightforward rule about what is a “true” 0;

¹ $\mathcal{Lap}(x|\lambda)$ and $\mathcal{E}(x|\lambda)$ are the p.d.f. of centered Laplace and exponential distributions with parameter λ , \mathbb{S}_+ is the set of SPD matrices.

Continuous spike and slab prior for precision matrix (I)

- Idea: Modelling² a 0 and non-0 regime;

$$p(\Omega|\theta) = C(\theta)^{-1} \times \left(\prod_{i < j} (1 - \pi) \mathcal{N}(w_{i,j}|0, v_0^2) + \pi \mathcal{N}(w_{i,j}|0, v_1^2) \right) \times \prod_{i=1}^p \mathcal{E}(w_{i,i}|\lambda) \times \mathbf{1}_{\mathbb{S}_+}(\Omega),$$

where:

- π can be interpreted as a *a priori* probability of an edge to exist;
- v_0^2 and v_1^2 are *a priori* variances of $w_{i,j}$ under the 2 regimes ($v_0^2 \ll v_1^2$);
- $\theta = \{\pi, v_0^2, v_1^2, \lambda\}$.

² $C(\cdot)$ is a normalizing constant.

- Hierarchical version: Introduction of a latent binary matrix \mathbf{G} :

$$p(\Omega|\theta, \mathbf{G}) = C(\mathbf{G}, \theta)^{-1} \times \left(\prod_{i < j} \mathcal{N}(w_{i,j} | 0, v_{\mathbf{G}_{i,j}}^2) \times \prod_{i=1}^p \mathcal{E}(w_{i,i} | \lambda) \right) \times \mathbf{1}_{\mathbb{S}_+}(\Omega),$$
$$p(\mathbf{G}|\theta) \propto C(\mathbf{G}, \theta) \times \prod_{i \leq j} \pi^{\mathbf{G}_{i,j}} (1 - \pi)^{\mathbf{G}_{i,j}}$$

- $C(\mathbf{G}, \theta)$ is an intractable normalizing term that cancels out in the joint distribution of (Ω, \mathbf{G}) ;
- “The latent binary variables \mathbf{G} can be viewed as edge-inclusion indicators” (Wang (2015)).

- Lots of methods:
 - Horseshoe prior (Li, Craig, and Bhadra (2019));
 - G-Wishart (Atay-Kayis and Massam (2005));
 - Sparsifying from the Cholesky decomposition (Mastrantonio, Di Loro, and Mingione (2025));
- Nice review with empirical comparisons (Vogels et al. (2024));
- Main challenges: interpretable prior with scalable posterior sampling.

Posterior sampling

Model's equations

$$Y_{i,j}|Z_{i,j} \stackrel{\text{ind}}{\sim} \mathcal{NB}(\exp(Z_{i,j}), \phi),$$

$$\mathbf{Z} \sim \mathcal{MN}(\mathbf{X}\boldsymbol{\beta}, \Sigma(\kappa), \Omega^{-1}),$$

$$\boldsymbol{\beta} \sim \mathcal{MN}(0, \mathbf{I}_{n_{\text{cov}}}, \mathbf{I}_p),$$

$$\phi \sim \log \mathcal{N}(m, s^2),$$

$$\kappa \sim \mathcal{Gamma}(a, b),$$

$$p(\Omega|\theta, \mathbf{G}) = \mathcal{C}(\mathbf{G}, \theta)^{-1} \left(\prod_{i < j} \mathcal{N}(w_{i,j}|0, v_{\mathbf{G}_{i,j}}^2) \times \prod_{i=1}^p \mathcal{E}(w_{i,i}|\lambda) \right) \mathbf{1}_{\mathbb{S}_+}(\Omega),$$

$$p(\mathbf{G}|\theta) \propto \mathcal{C}(\mathbf{G}, \theta) \times \prod_{i \leq j} \pi^{\mathbf{G}_{i,j}} (1 - \pi)^{\mathbf{G}_{i,j}}$$

$p(\mathbf{Z}, \boldsymbol{\beta}, \phi, \kappa, \Omega, \mathbf{G}|\mathbf{Y})$ Target posterior distribution

Table 2: Steps of the Gibbs algorithm

Conditional variable	Sampling Method
$\mathbf{Z} \mathbf{Y}, \beta, \kappa, \Omega$	MALA (rowwise)
$\beta \mathbf{Z}, \kappa, \Omega$	Exact (gaussian)
$\phi \mathbf{Y}, \mathbf{Z}$	MALA
$\Omega \mathbf{Z}, \mathbf{G}, \beta, \kappa$	Exact
$\mathbf{G} \Omega$	Exact
$\kappa \mathbf{Z}, \beta, \Omega$	MALA

- *Row whitening*: Compute $\tilde{\mathbf{Z}} = \mathbf{L}_\kappa^{-1}(\mathbf{Z} - \beta)$, where $\mathbf{L}_\kappa \mathbf{L}_\kappa^\top = \Sigma(\kappa)$;
- Consider $\mathbf{S} = \tilde{\mathbf{Z}}^\top \tilde{\mathbf{Z}}$;
- Sample new columns of Ω iteratively:
- To sample from the (say) last column conditionally to the $(p - 1)$ other, partition:

$$\mathbf{S} = \begin{pmatrix} \mathbf{S}_{-p,-p} & \vec{s}_{-p,p} \\ \vec{s}_{-p,p}^\top & s_{p,p} \end{pmatrix}$$

- Set:

$$\Omega_{\text{new}} = \begin{pmatrix} \Omega_{-p,-p} & \vec{u} \\ \vec{u}^\top & v + \vec{u}^\top \Omega_{-p,-p} \vec{u} \end{pmatrix},$$

where

$$v \sim \text{Gamma}\left(\frac{n}{2} + 1, \frac{s_{p,p} + \lambda}{2}\right),$$

$$\vec{u} \sim \mathcal{N}_{p-1}(-\mathbf{C}\vec{s}_{-p,p}, \mathbf{C}),$$

where \mathbf{C} is a matrix depending on \mathbf{G} (easy to compute).

- Starting from an SPD matrix, this gives an SPD matrix.

- Using the proposed hierarchical prior, conditional of $\mathbf{G}|\Omega$ sampling is straightforward.
- Sample independently for $1 \leq i < j \leq p$:

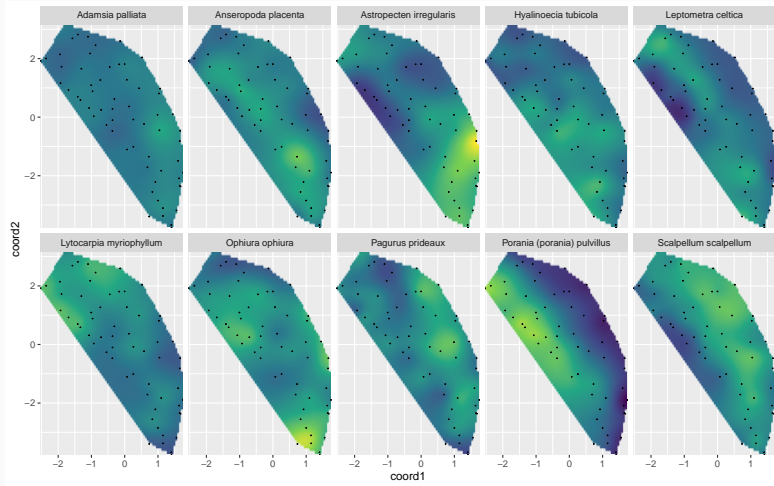
$$\mathbb{P}(\mathbf{G}_{i,j} = 1|\Omega) = \frac{\mathcal{N}(\omega_{i,j}|0, v_1^2)\pi}{\mathcal{N}(\omega_{i,j}|0, v_1^2)\pi + \mathcal{N}(\omega_{i,j}|0, v_0^2)(1 - \pi)} .$$

Application to Bay of Biscay invertebrates

Estimation of the spatial field per species

- Inference on 10 species;

Figure 6: Estimated spatial field for 10 species (posterior mean)



Estimation of the interaction network (partial correlation)

Figure 7: Estimated partial correlation matrix between species (posterior mean)

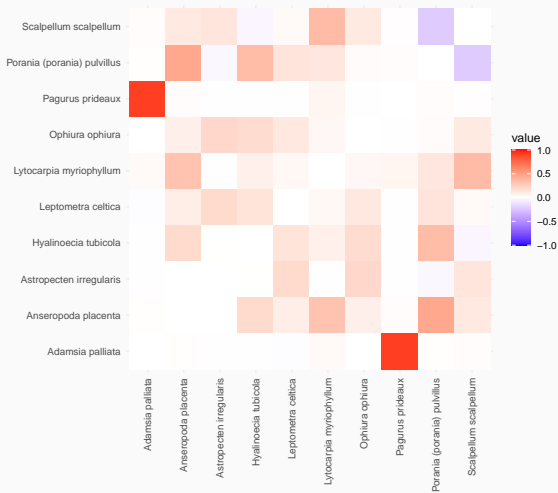


Figure 8: Probability of $G_{i,j} = 1$ depending threshold

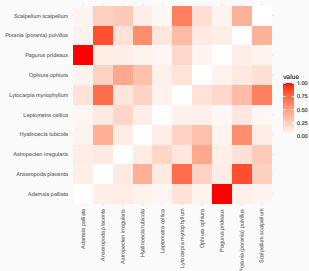


Figure 9: Number of edges

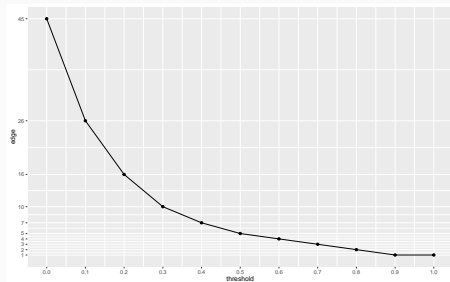


Figure 10: *Pagurus prideaux* and *Adamsia palliata*



Conclusions

- Exact Bayesian inference for network inference for spatial data;
- Estimation of two sources of dependence on a separable context;
- Works on n around hundreds, and p around dozens;

Perspectives

- Assess ecological pertinence on various different ecological data (trees, mosquitoes, invertebrate, fishes);
- Proposing some priors based on ecological assumptions;

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