1 - Models with latent variables in ecology

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Outline

Part 1

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Community ecology

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- describe / understand the organisation of species interaction networks

  $\rightarrow$ network models

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Abundance table:

Hi.pl	*An.lu*	*Me.ae*	...
31	0	108	
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27	0	788	
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23	0	13	
20	0	97	
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Environmental covariates:

Lat.	Long.	Depth	Temp.
71.10	22.43	349	3.95
71.32	23.68	382	3.75
71.60	24.90	294	3.45
71.27	25.88	304	3.65
71.52	28.12	384	3.35
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Questions:

- Do environmental conditions affect species abundances? (abiotic)
- Do species abundances vary independently? (biotic)

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Modelling species abundance

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- Gaussian models do not fit
- Not that many models for count data without restriction on the dependency [IYAR17]
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- Unknown parameters

$$\theta = (\beta, \Sigma)$$

(Directed) Graphical model

Definition: $p(U_1, \dots U_k)$ factorizes according to the directed acyclic graph $G = ([k], E)$ iff

$$p(U_1, \dots U_k) = \prod_{h=1}^{k} p(U_h \mid U_{\text{parent}_G(h)})$$

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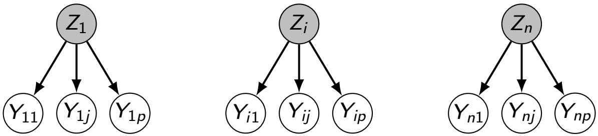

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Barents' fishes

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- Abundance table: $Y = [Y_{ij}] \quad (n \times p)$
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- β = regression coefficients
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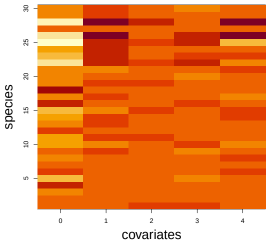

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- $\Sigma =$ variance of the latent layer
  $\rightarrow$ biotic associations

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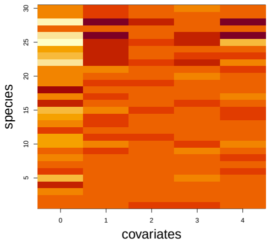
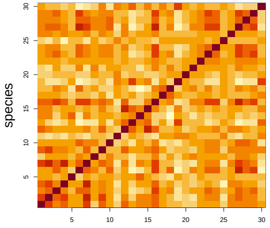


Covariance matrix $\widehat{\Sigma}$: biotic



Some properties of the Poisson log-normal distribution

Denoting $\Sigma = [\sigma_{jk}]$,

- Expectation (prediction):

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- Covariance:

$$\mathbb{C}\text{ov}(Y_{ij}, Y_{ik}) = \mu_{ij}\mu_{ik}(e^{\sigma_{jk}} - 1)$$

$\rightarrow$ signs are preserved:

$$\text{sign}(\sigma_{jk}) = \text{sign}(\mathbb{C}\text{ov}(Y_{ij}, Y_{ik}))$$

Outline

Models with latent variables in (community) ecology

Joint species distribution models

Models for ecological networks

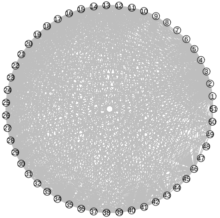
Latent-variable models

Species networks

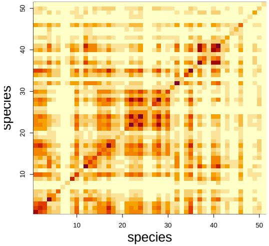
Tree network [VPDL08]:

- $n = 51$ tree species
- Y_{ij} = number of fungal parasites shared by species i and j
- x_{ij} = vector of covariates between species i and j (taxonomic, geographic, genetic distance)

Network (weighted):



Adjacency matrix (counts):



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Questions:

- Is the network 'organized' in some way?
- Do the covariates contribute to explain the existence or intensity of the links?

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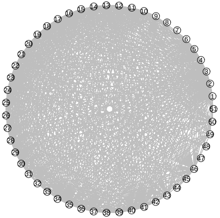

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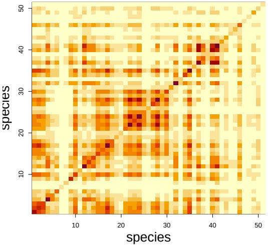

Modelling ecological networks

Models for (weighted) random graphs:

- Need to model the joint distribution $p(\{Y_{ij}\})$ accounting for the network structure
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$$\theta = (\pi, \beta, \alpha) \qquad + K$$

Directed graphical model

Graphical model for SBM: Independent clusters + conditionally independent edges[2]

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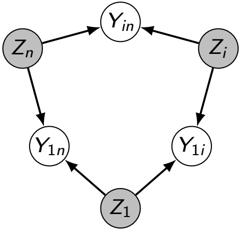

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SBM for the tree network

Data:

- $n = 51$ species
- Weighted adjacency matrix: $Y = [Y_{ij}]$
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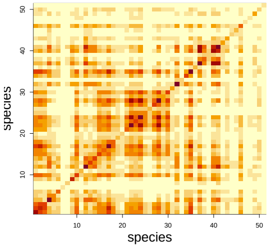
Observed adjacency matrix:



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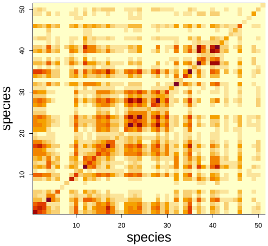

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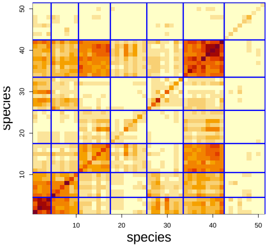

Interpretation:

- π = group proportions
- α = matrix of between-groups intensities

Many types of block-models

Emission distribution: Edges can be

- Binary (presence/absence): Bernoulli
- Weighted: normal, Poisson, ...
- Multivariate (multiplex): multivariate normal, mixed multivariate distribution
- Dynamic (see Part 3)

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Node structure:

- One type of nodes: symmetric or asymmetric SBM
- Two types of nodes: bipartite (see next)
- Several types of nodes: multi-layer network [BHBD19]

Bipartite networks

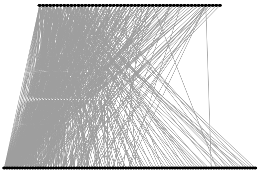
Antagonist network [BdOAN+13]:
host × parasites interactions:

- 98 hosts (fish species)
- 52 parasites

Question:
Specialized interactions ?

That is (?)
Could we determine groups of hosts and parasites that preferentially interacts (or avoid to interact)?

Network:



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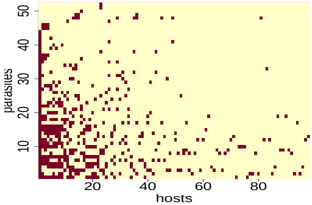

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- Unknown parameters
$$\theta = (\pi, \rho, \gamma) + (K, L)$$

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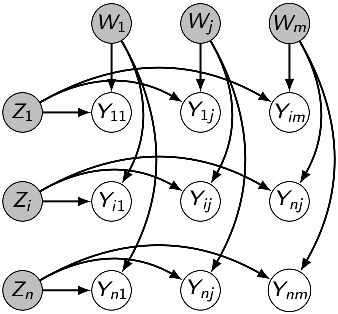

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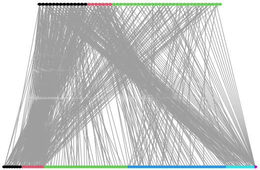

Interpretation:

- π proportions of the parasite groups
- ρ proportions of the host groups
- γ connectivities between groups of hosts and parasites

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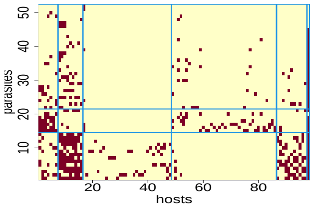

Outline

Two latent variable models

	Species distribution (PLN)	Network structure (SBM)
Observed (Y)	species abundances: Y_{ij} = abundance of species j in site i	species network: Y_{ij} = link intensity between species i and species j
Covariates (X)	environnemental conditions: x_i species traits x'_j	similarities between species: x_{ij} species traits x'_i
Latent (Z)	latent 'position': Z_{ij} latent variable for species j in site i	group membership: Z_i = group of species i
Parameters (θ)	latent covariance (Σ) regression coefficients (β)	group proportions (π) interactions (α) regression coefficients (β)

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- $\rightarrow$ focus on unsupervised classification

Emission distribution: mostly Poisson in these lectures (a lot of count data in ecology)

$\rightarrow$ Poisson log-normal and block-models are amendable to any (parametric) distribution

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