Ecological network reconstruction from count data

 $\begin{array}{c} \mbox{Raphaëlle Momal} \\ \mbox{Supervision: S. Robin^1 and C. Ambroise}^2 \end{array}$

¹UMR AgroParisTech / INRA MIA-Paris ²LaMME, Evry

February 12th, 2019

Raphaëlle Momal

COSTNET München 2019

February 12th, 2019 1 / 20

Context

Rising interest in jointly analysed species abundances:

- Metagenomics
- Microbiology
- Ecology

Ecological network

Tool to better understand species interactions (direct/indirect), eco-systems organizations (hubs?)

Allows for resilience analyses, pathogens control, ecosystem comparison, response prediction...

ELE NOR

Example

Data:

- Species: bacteria, fungi...
- Abundances: read counts from Next-Generation Sequencing technologies (metabarcoding) ⇒ n × p matrix Y
- **Covariates**: temperature, water depth... \Rightarrow *n* × *d* matrix *X*
- Offsets: species-specific, sample-specific $\Rightarrow p \times p$ matrix O

Goal:

Infer the species interaction network \widehat{G} from count data Y, accounting for X and O:

$$\widehat{G}=f(Y,X,O)$$

Challenges

Statistical network inference

Count data

Offsets and covariates

Graphical models: a statistical framework for network inference

Example:



 Connected: all variables are dependant

 Some are conditionally independent (i.e. indirectly dependant)

 A_4 is independent from (A_1, A_3) conditionally on A_2

Graphical models: a statistical framework for network inference

Example:



 Connected: all variables are dependant

 Some are conditionally independent (i.e. indirectly dependant)

 A_4 is independent from (A_1, A_3) conditionally on A_2

$$P(A_1,\ldots,A_p) \propto \prod_{C \in \mathcal{C}_G} \psi_C(A_C)$$

PLN model

Poisson log-Normal distribution (Aitchison and Ho, 1989)

$$\left. \begin{array}{ll} Z_i \,\, \textit{iid} & \sim \mathcal{N}_d(0, \Sigma) \\ & (Y_{ij})_j \,\, \mathbb{L} \,\, |Z_i \\ \end{array} \right\} \, Y \sim \mathcal{P}\ell \mathcal{N}(0, \Sigma) \\ Y_{ij} | Z_{ij} & \sim \mathcal{P}(e^{Z_{ij}}) \end{array} \right\}$$

Dependency structure in the Gaussian latent layerEasy handling of multi-variate data

PLN model

Poisson log-Normal distribution (Aitchison and Ho, 1989)

$$\left. \begin{array}{ll} Z_i \ \textit{iid} & \sim \mathcal{N}_d(0, \Sigma) \\ & (Y_{ij})_j \perp |Z_i \\ Y_{ij}|Z_{ij} & \sim \mathcal{P}(e^{o_{ij} + x_i^{\mathsf{T}}\Theta_j + Z_{ij}}) \end{array} \right\} Y \sim \mathcal{P}\ell \mathcal{N}(O + X^{\mathsf{T}}\Theta, \Sigma)$$

- Dependency structure in the Gaussian latent layer
- Easy handling of multi-variate data
- Allow adjustment for covariates and offsets
- Variational estimation algorithm (Chiquet et al., 2017)

PLN model + Graphical model

Poisson log-Normal distribution (Aitchison and Ho, 1989)

$$\left. \begin{array}{ll} Z_i \ \textit{iid} & \sim \mathcal{N}_d(0, \Sigma_G) \\ & (Y_{ij})_j \perp |Z_i \\ Y_{ij}|Z_{ij} & \sim \mathcal{P}(e^{\mathbf{o}_{ij} + \mathbf{x}_i^{\mathsf{T}}\Theta_j + Z_{ij}}) \end{array} \right\} Y \sim \mathcal{P}\ell \mathcal{N}(\mathbf{O} + \mathbf{X}^{\mathsf{T}}\Theta, \Sigma_G)$$

- Dependency structure in the Gaussian latent layer
- Easy handling of multi-variate data
- Allow adjustment for covariates and offsets
- Variational estimation algorithm (Chiquet et al., 2017)

Proposed method: PLN + Spanning trees

Tree structure on PLN latent layer

EMtree model

$$\left. \begin{array}{ccc} T & \sim \prod_{kl} \beta_{kl} / B \\ Z_i | T \ iid & \sim \mathcal{N}_d(0, \boldsymbol{\Sigma_T}) \\ & (Y_{ij})_j \perp |Z_i| T \\ Y_{ij} | Z_{ij}, T & \sim \mathcal{P}(e^{\circ_{ij} + x_i^{\mathsf{T}} \Theta_j + Z_{ij}}) \end{array} \right\} Y \sim \mathcal{P}\ell \mathcal{N}(O + X^{\mathsf{T}} \Theta, \boldsymbol{\Sigma_T})$$

$$Z_i \sim \sum_{T \in \mathcal{T}} P(T) \mathcal{N}(0, \Sigma_T)$$

I= nar

Why Spanning trees

Sparse structures:

$$\#\mathcal{G}_p = 2^{rac{p(p-1)}{2}}$$
 reduced to $\#\mathcal{T}_p = p^{(p-2)}$

< □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □

Why Spanning trees

Sparse structures:

$$\#\mathcal{G}_p = 2^{\frac{p(p-1)}{2}}$$
 reduced to $\#\mathcal{T}_p = p^{(p-2)}$

Suitable algebraic tool:

Matrix tree theorem (Chaiken and Kleitman, 1978)

$$\sum_{\mathcal{T}\in\mathcal{T}}\prod_{(k,l)\in\mathcal{T}}\psi_{k,l}(Y)=\det(L_{\psi(Y)})\to\Theta(p^3)$$

Approach: infer the network by averaging spanning trees

Tree averaging





1= 990

Tree structured data

Data dependency structure relies on a tree

Likelihood factorizes on nodes and edges (Chow and Liu, 1968):

$$\mathbb{P}(Z|T) = \prod_{j=1}^{d} \mathbb{P}(Z_j) \prod_{k,l \in T} \psi_{kl}(Z) ,$$

Where

$$\psi_{kl}(Z) = \frac{\mathbb{P}(Z_k, Z_l)}{\mathbb{P}(Z_k) \times \mathbb{P}(Z_l)}.$$

Rmq : with standardised gaussian data, $\hat{\Psi} = [\hat{\psi_{kl}}] \propto (1 - \hat{
ho_Z}^2)^{-1/2}$



Direct EM algorithm ?

Complete likelihood :

 $\mathbb{P}(Y, Z, T) = \mathbb{P}(T) \times \mathbb{P}(Z|T) \times \mathbb{P}(Y|Z)$

$$\begin{split} \log(\mathbb{P}(Y,Z,T)) &= \sum_{k,l} \mathbb{1}_{\{(k,l)\in T\}} (\log(\beta_{kl}) + \log(\psi_{kl}(Z))) - \log(B) \\ &+ \sum_{k} (\log(\mathbb{P}(Z_k)) + \log(\mathbb{P}(Y_k|Z_k))) \end{split}$$

3 × 4 3 × 3 1 × 0 0 0

Direct EM algorithm ?

Complete likelihood :

 $\mathbb{P}(Y, Z, T) = \mathbb{P}(T) \times \mathbb{P}(Z|T) \times \mathbb{P}(Y|Z)$

$$\log(\mathbb{P}(Y, Z, T)) = \sum_{k,l} \mathbb{1}_{\{(k,l)\in T\}} (\log(\beta_{kl}) + \log(\psi_{kl}(Z))) - \log(B) + \sum_{k} (\log(\mathbb{P}(Z_k)) + \log(\mathbb{P}(Y_k|Z_k)))$$

Conditional expectation :

$$\begin{split} \mathbb{E}_{\theta}[\log(\mathbb{P}(Y,Z,T))|Y] &= \sum_{k,l \in V} \mathbb{P}((k,l) \in T|Y) \log(\beta_{kl}) + \mathbb{E}[\mathbb{1}_{\{(k,l) \in T\}} \log(\psi_{kl}(Z)|Y)] \\ &+ \sum_{k} \mathbb{E}[\log(\mathbb{P}(Z_{k}))|Y] + \mathbb{E}[\log(\mathbb{P}(Y_{k}|Z_{k}))|Y] - \log(B) \end{split}$$

⇒ ↓ ∃ ↓ ∃ | = ↓ < €</p>

Two steps solution

The PLNmodels package approximates the distribution parameters:

- **1** Approximate $\hat{\Sigma}_Z$
- **2** Apply EM mixture tree to $Z \sim \mathcal{N}(0, \hat{\Sigma}_Z)$

Simplified conditional expectation writing:

$$\mathbb{E}_{\theta}[\log(\mathbb{P}(Z,T))|Z] = \sum_{k,l} \mathbb{P}((k,l) \in T|Z) \times \log(\beta_{kl}\psi_{kl}) - \log(B) + \sum_{k} \log(\mathbb{P}(Z_k))$$

 \Rightarrow **EM algorithm** (E: Kirshner (2008), M: Meilă and Jaakkola (2006))

ELE NOR

EMtree algorithm

- Input: Abundance data, covariates, offsets
- 1rst step: VEM algorithm to fit PLN model $\Rightarrow \hat{\theta}, \hat{\Sigma}_Z$.
- 2nd step: EM algorithm to update the $\beta_{jk} \Rightarrow$ conditional probabilities for all edges.

= 900

EMtree algorithm

- Input: Abundance data, covariates, offsets
- 1rst step: VEM algorithm to fit PLN model $\Rightarrow \hat{\theta}, \hat{\Sigma}_Z$.
- 2nd step: EM algorithm to update the $\beta_{jk} \Rightarrow$ conditional probabilities for all edges.
- Thresholding: Select edges with probability above the probability of edges in a tree drawn uniformly (2/p)
- Resampling: Strengthen the results: only edges selected in more than 80% of S sub-samples are kept.

Available for download at https://github.com/Rmomal/EMtree

\mathbf{O}

Evaluation strategy

Alternatives:

Two methods on transformed counts, no covariates:

- SpiecEasi algorithm Kurtz et al. (2015)
- **gCoda** Fang et al. (2017)

One taking raw counts and covariates:

MInt Biswas et al. (2016) (uses PLN model)

Evaluation strategy

Alternatives:

Two methods on transformed counts, no covariates:

- SpiecEasi algorithm Kurtz et al. (2015)
- **gCoda** Fang et al. (2017)

One taking raw counts and covariates:

MInt Biswas et al. (2016) (uses PLN model)

Simulation design:

- **1** Choose G and define Σ_G accordingly
- **2** Sample count data Y from $\mathcal{P}\ell\mathcal{N}(X, \Sigma_G)$
- 3 Infer the network with EMtree, SpiecEasi, gCoda, and MInt
- 4 Compare results with presence/absence of edges (FDR, AUC)

N A ∃ N ∃ | = 1 ≤ N Q Q

Difficulty level



Raphaëlle Momal

Network density



Effect of Erdös and Cluster structures on the evolutions of AUC median and inter-quartile intervals for parameters n, p and ratio. Top: densities set to 2/p, bottom: densities set to 5/p.

Raphaëlle Momal

COSTNET München 2019

February 12th, 2019 16 / 20

Oak Mildew





Pathogen Erysiphe alphitoides (EA).

Oak leaf with powdery mildew.

Metabarcoding of oak tree leaves microbiome (Jakuschkin et al., 2016).

- 114 sample of 94 bacterial/fungal-OTUs
- Different read depth for bacteria and fungi
- covariates: tree status; distance to ground, to trunk and to base of the branch.

17 / 20

Inferred networks



イロト イヨト イヨト イヨト

三日 のへで

Conclusion

Contributions:

- Formal probabilistic model for network inference with count data
- Inclusion of offsets and covariates
- Variational estimation algorithm

Perspectives:

- Network comparison
- Missing major actor (species/covariates)
- Model for the inference in the observed counts layer

Acknowledgments

Special thanks :

Supervisors Stéphane Robin, Christophe Ambroise

- PLN team Julien Chiquet (MIA-Paris), Mahendra Mariadassou (INRA Jouy)
 - Data Corinne Vacher (INRA Bordeaux)

Contact :

- email raphaelle.momal@agroparistech.fr
- Web Rmomal.github.io



20 / 20

Conditional probability computation

Kirchhoff's theorem (matrix tree, Aitchison and Ho (1989))

For all $W = (a_{kl})_{k,l}$ a symmetric matrix, the corresponding Laplacian Q(W) is defined as follows:

$$\mathcal{Q}_{uv}(W) = egin{cases} -a_{uv} & 1 \leq u < v \leq n \ \sum_{i=1}^n a_{vi} & 1 \leq u = v \leq n. \end{cases}$$

Then for all u et v:

$$|Q_{uv}^*(W)| = \sum_{\mathcal{T}\in\mathcal{T}} \prod_{\{k,l\}\in E_{\mathcal{T}}} a_{kl}$$

$$\mathbb{P}((k,l) \in T|Z) = \sum_{T \in \mathcal{T}: (k,l) \in T} \mathbb{P}(T|Z) = \frac{\sum_{(k,l) \in T} \mathbb{P}(T)\mathbb{P}(Z|T)}{\sum_{T} \mathbb{P}(T)\mathbb{P}(Z|T)}$$
$$= 1 - \frac{|Q_{uv}^*(\beta \Psi^{-kl})|}{|Q_{uv}^*(\beta \Psi)|}$$
$$= \tau_{kl}$$

JIN NOR

M step

Goal : optimization of weights β_{kl} .

$$\operatorname{argmax}_{\beta_{kl}} \left\{ \sum_{k,l \in V} \tau_{kl} (\log(\beta_{kl}) + \log(\psi_{kl})) - \log(B) + \sum_{k} \log(\mathbb{P}(Z_k)) \right\}$$

With high combinatorial complexity of
$$B = \sum_{T \in T} \prod_{k,l \in T} \beta_{kl}$$

How to compute
$$\frac{\partial B}{\partial \beta_{kl}}$$
 ?

三日 のへで

β_{kl} update

A result from Meilă Meilă and Jordan (2000)

Inverting a minor of the laplacien Q, we define M :

$$\begin{cases} M_{uv} = [\mathcal{Q}^{*-1}]_{uu} + [\mathcal{Q}^{*-1}]_{vv} - 2[\mathcal{Q}^{*-1}]_{uv} & u, v < n \\ M_{nv} = M_{vn} = [\mathcal{Q}^{*-1}]_{vv} & v < n \\ M_{vv} = 0. \end{cases}$$

On peut montrer que :

$$rac{\partial |Q_{uv}^*(W)|}{\partial eta_{kl}} = M_{kl} imes |Q_{uv}^*(W)|$$

$$\frac{\partial \mathbb{E}_{\theta}[\log(\mathbb{P}(Z,T))|Z]}{\partial \beta_{kl}} = \frac{\tau_{kl}}{\beta_{kl}} - \frac{1}{B} \frac{\partial B}{\partial \beta_{kl}}$$
$$\hat{\beta}_{kl}^{h+1} = \frac{\tau_{kl}^{h}}{M_{kl}^{h}}$$

M step

References I

- Aitchison, J. and Ho, C. (1989). The multivariate Poisson-log normal distribution. Biometrika, 76(4):643-653.
- Biswas, S., McDonald, M., Lundberg, D. S., Dangl, J. L., and Jojic, V. (2016). Learning microbial interaction networks from metagenomic count data. *Journal of Computational Biology*, 23(6):526–535.
- Chaiken, S. and Kleitman, D. J. (1978). Matrix tree theorems. Journal of combinatorial theory, Series A, 24(3):377-381.
- Chiquet, J., Mariadassou, M., and Robin, S. (2017). Variational inference for probabilistic Poisson PCA. Technical report, arXiv:1703.06633. to appear in Annals of Applied Statistics.
- Chow, C. and Liu, C. (1968). Approximating discrete probability distributions with dependence trees. IEEE Transactions on Information Theory, 14(3):462–467.
- Fang, H., Huang, C., Zhao, H., and Deng, M. (2017). gcoda: conditional dependence network inference for compositional data. Journal of Computational Biology, 24(7):699–708.
- Jakuschkin, B., Fievet, V., Schwaller, L., Fort, T., Robin, C., and Vacher, C. (2016). Deciphering the pathobiome: Intra- and interkingdom interactions involving the pathogen erysiphe alphitoides. *Microb Ecol*, 72(4):870–880.
- Kirshner, S. (2008). Learning with tree-averaged densities and distributions. In Advances in Neural Information Processing Systems, pages 761–768.
- Kurtz, Z. D., Müller, C. L., Miraldi, E. R., Littman, D. R., Blaser, M. J., and Bonneau, R. A. (2015). Sparse and compositionally robust inference of microbial ecological networks. *PLoS computational biology*, 11(5):e1004226.
- Meilä, M. and Jaakkola, T. (2006). Tractable bayesian learning of tree belief networks. Statistics and Computing, 16(1):77-92.
- Meilă, M. and Jordan, M. I. (2000). Learning with mixtures of trees. Journal of Machine Learning Research, 1:1-48.

(日) (周) (日) (日) (日) (000)