Mixture tree model for network inference

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Context

Rising interest in jointly analysed species abundances:

- Metagenomics
- Microbiologie
- Ecology

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

Example

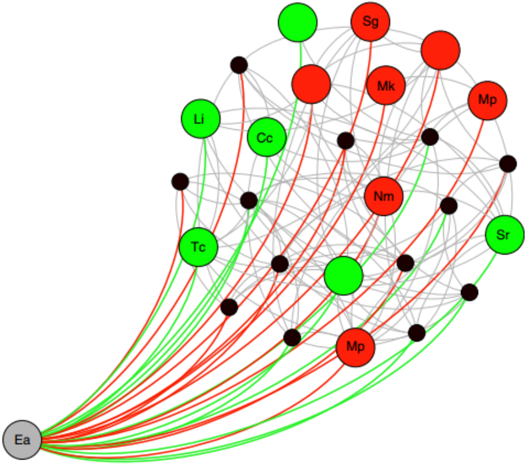

Figure: *Erysiphe alphitoides* pathobiom on oak tree leaves.

Data

- Species : animal, bacteria, gene ...
- Abundances : ecological counts, Next-Generation Sequencing technologies...
- Covariates : coverage, temperature, water depth ...

Repeated signal : n samples of p abundances.

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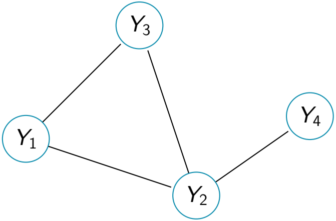
Notations

$Y = [Y_{ij}]_{(i,j)\in\{1,\ldots,n\}\times\{1,\ldots,p\}}$

- Y_{ij} : abundance of the j^{th} species in the i^{th} sample

Infer the species interaction network from Y

Graphical models



- All variables are dependant
- Some are conditionnally independant (i.e. indirectly dependant)

$$Y_4 \perp\!\!\!\perp (Y_1, Y_3) | Y_2$$

Graphical models

Factorization propriety

The joint distribution P is faithful to the graph G iff

$$P(Y_1, \dots, Y_p) \propto \prod_{C \in \mathcal{C}_G} \psi_C(Y_C)$$

where $\mathcal{C}_G =$ set of cliques of G.

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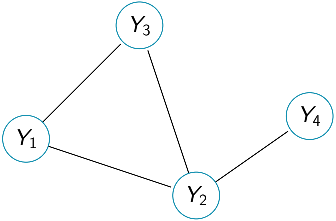
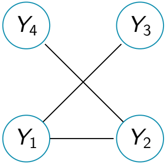


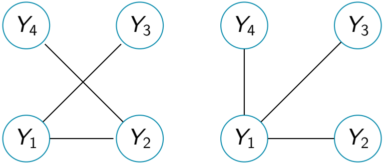
$$P(Y_1, Y_2, Y_3, Y_4) \propto \psi_1(Y_1, Y_2, Y_3) \times \psi_2(Y_3, Y_4)$$

Tree averaging



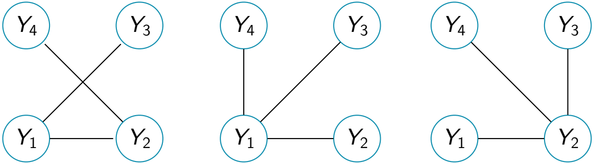
$$P\{T = T_1 | Y\}$$

Tree averaging



$P\{T = T_1 | Y\}$ $P\{T = T_2 | Y\}$

Tree averaging



$P\{T = T_1 | Y\}$ $\quad$ $P\{T = T_2 | Y\}$ $\quad$ $P\{T = T_3 | Y\}$

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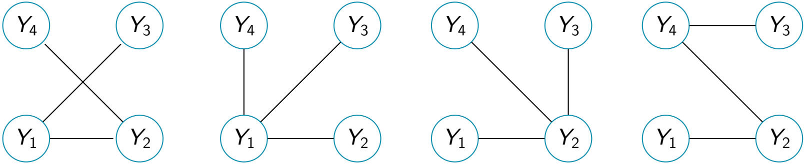

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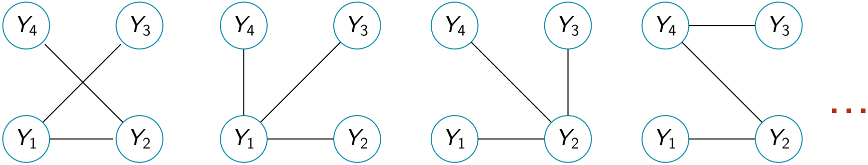

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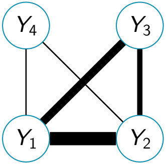
Compute edge probabilities:



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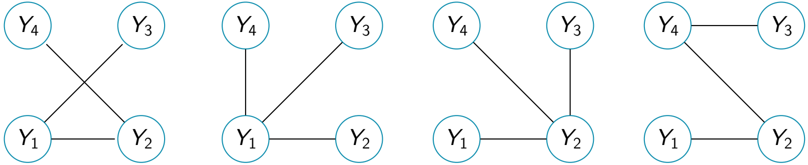

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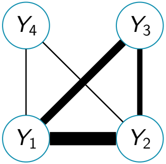

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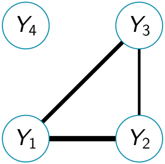
Thresholding probabilities:



$P\{(j,k) \in T|Y\}$