

Détection de structures à l'aide de modèles probabilistes sur les graphes

Modèles

Pierre Barbillon

21 juin 2024

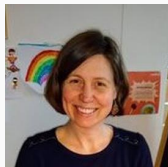
My collaborators

On the R packages



J. Chiquet
(INRAE)

sbm



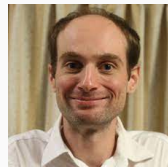
S. Donnet
(INRAE)

sbm, GREMLINS



J.B. Léger
(Univ. Tech. Compiègne)

blockmodels



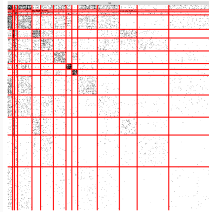
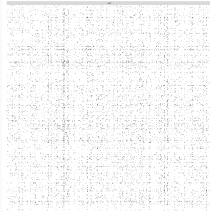
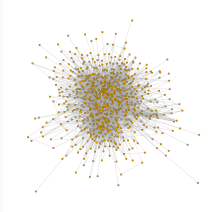
Saint-Clair Chabert-Liddell
(INRAE)

colSBM

Other collaborators

T. Tabouy (ex PhD student), E. Lazega (Sciences Po), L. Lacoste (new PhD student), E. Anakok (PhD student) + E. Thébault (iEES) + C. Fontaine (MNHN) + T. Vanrenterghem (INRAE), **ANR Econet** + ANR Pastodiv + GDR Resodiv

from the observation of a network determine structure



Stochastic and Latent Block Models

Other latent space models and other methods

Extensions of SBM

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Other latent space models and other methods

Extensions of SBM

A first random graph model for network

[Erdős and Rényi, 1959] Model for n nodes

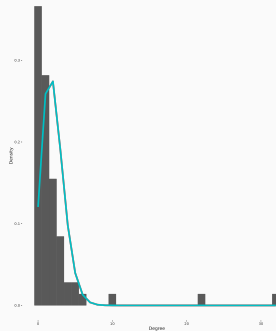
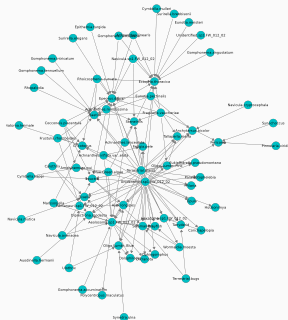
$$\forall 1 \leq i, j \leq n, \quad Y_{ij} \stackrel{i.i.d.}{\sim} \text{Bern}(p),$$

where $p \in [0, 1]$ is the probability for a link to exist.

Consequence

$$\text{deg}(i) \sim_{i.i.d} \text{Bin}(n, p)$$

Confrontation to a real network



Not enough variability in the degree

Limitations of an ER graph to describe real networks

- Homogeneity of the connections
- Degree distribution too concentrated, no high degree nodes,
- All nodes are equivalent,
- No modularity, no hubs

Stochastic Block Model and Latent Block Model

Model on a simple network with n nodes:

SBM: [Nowicki and Snijders, 2001]

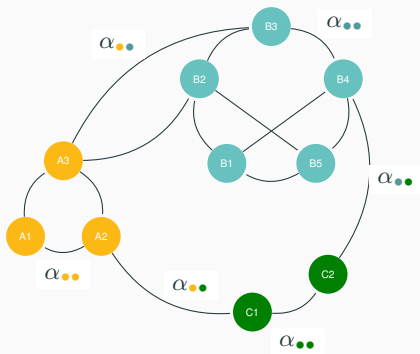
- Q blocks of nodes sharing similar connection structure,
- $\mathbf{Z} = (Z_1, \dots, Z_n)$ independent latent variables s.t. $\mathbb{P}(Z_i = k) = \pi_k$ for $k \in \{1, \dots, Q\}$ and $i \in \{1, \dots, n\}$,
- $Y_{ij}|Z_i, Z_j \stackrel{\text{ind}}{\sim} \mathcal{F}(\alpha_{Z_i, Z_j})$ for all dyads (i, j)

Model on a bipartite network with n_1 and n_2 nodes:

LBM: [Govaert and Nadif, 2010]

- Q_1 and Q_2 blocks of nodes sharing similar connection structure,
- $\mathbf{Z}^1 = (Z_1^1, \dots, Z_{n_1}^1)$ and $\mathbf{Z}^2 = (Z_1^2, \dots, Z_{n_2}^2)$ independent latent variables s.t. $\mathbb{P}(Z_i^1 = k) = \pi_k^1$ for all $i \in \{1, \dots, n_1\}$, $k \in \{1, \dots, Q_1\}$ and $\mathbb{P}(Z_j^2 = l) = \pi_l^2$ for all $j \in \{1, \dots, n_2\}$, $l \in \{1, \dots, Q_2\}$
- $Y_{ij}|Z_i^1, Z_j^2 \stackrel{\text{ind}}{\sim} \mathcal{F}(\alpha_{Z_i^1, Z_j^2})$ for all dyads (i, j) .

Stochastic Block Model : illustration



Parameters

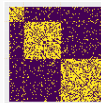
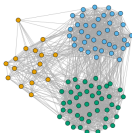
Let n nodes divided into 3 clusters

- $\{\bullet, \bullet, \bullet\}$ clusters
- $\pi_{\bullet} = \mathbb{P}(i \in \bullet), i = 1, \dots, n$
- $\alpha_{\bullet, \bullet} = \mathbb{P}(i \leftrightarrow j | i \in \bullet, j \in \bullet)$

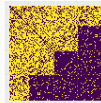
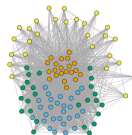
$$\mathbf{Y} \sim \text{SBM}_n(Q, \pi, \alpha)$$

Simulations under the SBM

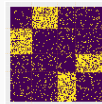
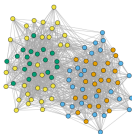
$$\alpha = \begin{pmatrix} 0.70 & 0.09 & 0.09 \\ 0.09 & 0.70 & 0.09 \\ 0.09 & 0.09 & 0.70 \end{pmatrix}$$



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Complete likelihood (\mathbf{Y}) et (\mathbf{Z})

$$\begin{aligned}\ell_c(\mathbf{Y}, \mathbf{Z}; \theta) &= p(\mathbf{Y}|\mathbf{Z}; \alpha)p(\mathbf{Z}; \pi) \\ &= \prod_{i,j} f_{\alpha_{Z_i, Z_j}}(Y_{ij}) \times \prod_i \pi_{Z_i} \\ &= \prod_{i,j} \alpha_{Z_i, Z_j}^{Y_{ij}} (1 - \alpha_{Z_i, Z_j})^{1-Y_{ij}} \prod_i \pi_{Z_i}\end{aligned}$$

Marginal likelihood (\mathbf{Y})

$$\log \ell(\mathbf{Y}; \theta) = \log \sum_{\mathbf{Z} \in \mathcal{Z}} \ell_c(\mathbf{Y}, \mathbf{Z}; \theta).$$

Remark

$\mathcal{Z} = \{1, \dots, Q\}^n \Rightarrow$ when Q and n increase, impossible to compute.

Standard tool to maximize the likelihood when latent variables involved
: EM algorithm.

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Standard EM

At iteration (t) :

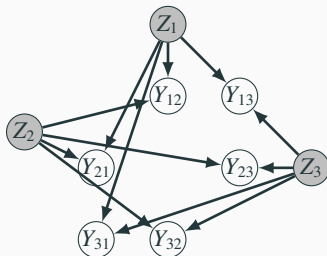
- **Step E:** compute

$$Q(\theta|\theta^{(t-1)}) = \mathbb{E}_{\mathbf{Z}|\mathbf{Y},\theta^{(t-1)}} [\log \ell_c(\mathbf{Y}, \mathbf{Z}; \theta)]$$

- **Step M:**

$$\theta^{(t)} = \arg \max_{\theta} Q(\theta|\theta^{(t-1)})$$

However, once conditioned by par \mathbf{X} , the \mathbf{Z} are not independent anymore



$$p(\mathbf{Z}|\mathbf{X}, \theta^{(t-1)}) \neq \prod_{i=1}^n p(Z_i|\mathbf{X}, \theta^{(t-1)})$$

Idea : replace the complicated distribution $[Z|Y, \theta]$ by a simpler one.

Let $\mathcal{R}_{Y,\tau}$ be any distribution on Z

Central identity

$$\begin{aligned}\mathcal{I}_\theta(\mathcal{R}_{Y,\tau}) &= \log \ell(\mathbf{Y}; \theta) - \mathbf{KL}[\mathcal{R}_{Y,\tau}, p(\cdot|\mathbf{Y}; \theta)] \leq \log \ell(\mathbf{Y}; \theta) \\ &= \mathbb{E}_{\mathcal{R}_{Y,\tau}} [\log \ell_c(\mathbf{Y}, Z; \theta)] - \sum_Z \mathcal{R}_{Y,\tau}(Z) \log \mathcal{R}_{Y,\tau}(Z) \\ &= \mathbb{E}_{\mathcal{R}_{Y,\tau}} [\log \ell_c(\mathbf{Y}, Z; \theta)] + \mathcal{H}(\mathcal{R}_{Y,\tau}(Z))\end{aligned}$$

Note that:

$$\mathcal{I}_\theta(\mathcal{R}_{Y,\tau}) = \log \ell(\mathbf{Y}; \theta) \Leftrightarrow \mathcal{R}_{Y,\tau} = p(\cdot|\mathbf{Y}; \theta)$$

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Note that:

$$\mathcal{I}_\theta(\mathcal{R}_{Y,\tau}) = \log \ell(\mathbf{Y}; \theta) \Leftrightarrow \mathcal{R}_{Y,\tau} = p(\cdot|\mathbf{Y}; \theta)$$

- Maximization of $\log \ell(\mathbf{Y}; \theta)$ w.r.t. θ replaced by maximization of the lower bound $\mathcal{I}_\theta(\mathcal{R}_{\mathbf{Y}, \tau})$ w.r.t. τ and θ .
- **Benefit** : we choose $\mathcal{R}_{\mathbf{Y}, \tau}$ such that the maximization calculus can be done explicitly
 - In our case: mean field approximation : neglect dependencies between the (Z_i)

$$P_{\mathcal{R}_{\mathbf{Y}, \tau}}(Z_i = q) = \tau_{iq}$$

Algorithm

At iteration (t) , given the current value $(\theta^{(t-1)}, \mathcal{R}_{\mathbf{Y}, \tau^{(t-1)}})$,

- **Step 1** Maximization w.r.t. τ

$$\begin{aligned}\tau^{(t)} &= \arg \max_{\tau \in \mathcal{T}} \mathcal{I}_{\theta^{(t-1)}}(\mathcal{R}_{\mathbf{Y}, \tau}) \\ &= \arg \max_{\tau \in \mathcal{T}} \mathbb{E}_{\mathcal{R}_{\mathbf{Y}, \tau}} \left[\log \ell_c(\mathbf{Y}, \mathbf{Z}; \theta^{(t-1)}) \right] + \mathcal{H}(\mathcal{R}_{\mathbf{Y}, \tau}(\mathbf{Z})) \\ &= \arg \max_{\tau \in \mathcal{T}} \log \ell(\mathbf{Y}; \theta^{(t-1)}) - \mathbf{KL}[\mathcal{R}_{\mathbf{Y}, \tau}, p(\cdot | \mathbf{Y}; \theta^{(t-1)})] \\ &= \arg \min_{\tau \in \mathcal{T}} \mathbf{KL}[\mathcal{R}_{\mathbf{Y}, \tau}, p(\cdot | \mathbf{Y}; \theta^{(t-1)})]\end{aligned}$$

Algorithm

- **Step 2** Maximization w.r.t. θ

$$\begin{aligned}\theta^{(t)} &= \arg \max_{\theta} \mathcal{I}_{\theta}(\mathcal{R}_{\mathbf{Y}, \tau^{(t)}}) \\ &= \arg \max_{\theta} \mathbb{E}_{\mathcal{R}_{\mathbf{Y}, \tau^{(t)}}} [\log \ell_c(\mathbf{Y}, \mathbf{Z}; \theta)] + \mathcal{H}(\mathcal{R}_{\mathbf{Y}, \tau^{(t)}}(\mathbf{Z})) \\ &= \arg \max_{\theta} \mathbb{E}_{\mathcal{R}_{\mathbf{Y}, \tau^{(t)}}} [\log \ell_c(\mathbf{Y}, \mathbf{Z}; \theta)]\end{aligned}$$

In practice

- Really fast
- Strongly depends on the initial values

A penalized likelihood criterion

- Selection of the number of clusters Q
- Integrated Classification Likelihood (ICL) [Biernacki et al., 2000]

$$ICL(\mathcal{M}_Q) = \log \ell_c(\mathbf{Y}, \hat{\mathbf{Z}}; \hat{\theta}_Q) - \text{Pen}(\mathcal{M}_Q)$$

where

$$\hat{Z}_i = \arg \max_{q \in \{1, \dots, Q\}} \hat{\tau}_{iq}.$$

•

$$ICL(\mathcal{M}_Q) = \mathbb{E}_{p(\cdot | \mathbf{Y}, \hat{\theta}_Q)} [\log \ell_c(\mathbf{Y}, \hat{\mathbf{Z}}; \hat{\theta}_Q)] - \text{Pen}(\mathcal{M}_Q)$$

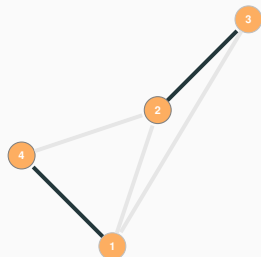
where

$$\text{Pen}(\mathcal{M}_Q) = \frac{1}{2} \left\{ \underbrace{(Q-1) \log(n)}_{\text{Clust.}} + \underbrace{Q^2 \log(n^2 - n)}_{\text{Conn.}} \right\}$$

$$pen_{\mathcal{M}} = -\frac{1}{2} \left\{ \underbrace{(K-1)\log(n) + (L-1)\log(p)}_{\text{Bi-Clust.}} + \underbrace{(KL)\log(np)}_{\text{Connection}} \right\}$$

Recall on missing value

Data: a graph G with missing data.



Adjacency matrix:

$$A = \begin{pmatrix} 0 & \text{NA} & \text{NA} & 1 \\ \text{NA} & 0 & 1 & \text{NA} \\ \text{NA} & 1 & 0 & 0 \\ 1 & \text{NA} & 0 & 0 \end{pmatrix}$$

Goal: Cluster nodes in spite of missing data and predict NA to $\{0, 1\}$ or predict most likely existing links.

Inferring the SBM from an observed network (Missing data)

[Timothée Tabouy and Chiquet, 2020].

Observation of a network: $n \times n$ binary matrix \mathbf{R} such that $R_{ij} = 1$ if Y_{ij} is observed, $R_{ij} = 0$ otherwise ($Y_{ij} = \text{NA}$).

Observation process: [Rub76] MCAR, MAR or NMAR?



Inference under M(C)AR scheme: Likelihood on the observed data.

Need for accounting for the complete likelihood where we have missing data (\mathbf{Y}^m) and latent variables \mathbf{Z}

Variational distribution on $(\mathbf{Y}^m, \mathbf{Z})$ in the VEM algorithm:

$$\mathcal{R}_{(\mathbf{Y}^m, \mathbf{Z})} = \mathcal{R}_{(\mathbf{Y}^m)} \cdot \mathcal{R}_{(\mathbf{Z})} = \prod_{(i,j), Y_{ij}=NA} \nu_{ij}^{Y_{ij}} (1 - \nu_{ij})^{1-Y_{ij}} \cdot \prod_{i=1}^n \prod_{k=1}^Q (\tau_{ik})^{\mathbb{I}_{Z_i=k}},$$

where

- ν_{ij} s and τ_{ik} s parameters to be optimized in the VE step,
- τ_{ik} is almost generic,
- ν_{ij} is specific to the sampling design.

Contributions:

- Derived variational steps for some NMAR sampling schemes,
- Importance of accounting for sampling illustrated on synthetic and real data,
- Implementation in an R package `missSBM` [Tabouy et al., 2019].

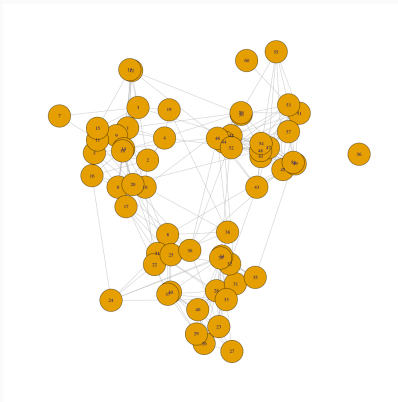
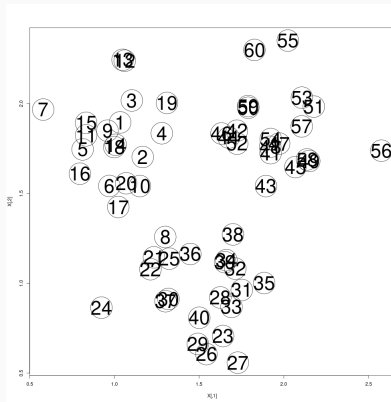
Stochastic and Latent Block Models

Other latent space models and other methods

Extensions of SBM

Latent space model

- $\forall i \in \{1, \dots, N\}, Z_i \stackrel{\text{ind}}{\sim} \text{Mixture}\mathcal{N}((\mu_k)_k, (\Sigma_k)_k),$
- $\forall (i, j), Y_{ij} | Z_i, Z_j \stackrel{\text{ind}}{\sim} b(\exp(-\|Z_i - Z_j\|/\sigma^2)).$



Alternative to the distance between latent positions, the dot product can be used:

$$\forall(i,j), Y_{ij}|Z_i, Z_j \stackrel{ind}{\sim} b(Z_i \cdot Z_j = Z_i^\top Z_j).$$

[Rubin-Delanchy et al., 2022] proposed a generalisation:

$$\forall(i,j), Y_{ij}|Z_i, Z_j \stackrel{ind}{\sim} b(Z_i I_{p,q} Z_j)$$

with

$$I_{p,q} \begin{bmatrix} I_p & 0 \\ 0 & -I_q \end{bmatrix}.$$

In [Newman, 2006], definition of modularity, for a given clustering:

$$Mod = \frac{1}{C} \sum_{i,j} \left[A_{ij} - \frac{d_i d_j}{C} \right] \delta_{ij}$$

where

- $C = \sum_i \sum_j A_{ij}$,
- d_i is the degree of species i (i.e. $d_i = \sum_j A_{ij}$),
- δ_{ij} are dummy variables indicating whether species/nodes i and j are assumed to belong to the same module/community/cluster.

Goal: look for the partitioning of nodes into communities/modules that maximizes the associated modularity score.

Algos: edge-betweenness algorithm (EB), the leading-eigenvector algorithm (LE) and the Louvain algorithm (ML).

For $G = (V, E)$ an undirected graph s.t. $V = \{1, \dots, N\}$ and A the corresponding adjacency matrix.

- Degree of a vertex/node: $d_i = \sum_j A_{ij}$,
- Unnormalized Laplacian: $L = D - A$ with $D = \text{diag}(d_1, \dots, d_N)$,

Properties:

- for $x \in \mathbb{R}^n$, $x^\top Lx = \frac{1}{2} \sum_j A_{ij} (x_i - x_j)^2$,
- L is symmetric and positive definite,
- the smallest eigenvalue is 0 and associated with the vector $\mathbb{1}$,
- the order of multiplicity of 0 is the number of connected components.

[Von Luxburg, 2007]

$$\begin{aligned}L_{sym} &= D^{-1/2}LD^{-1/2} = I_N - D^{-1/2}AD^{-1/2} \\L_{rw} &= D^{-1}L = I_N - D^{-1}A\end{aligned}$$

Properties:

- for $x \in \mathbb{R}^n$, $x^\top L_{sym}x = \frac{1}{2} \sum_j A_{ij} (x_i/\sqrt{d_i} - x_j/\sqrt{d_j})^2$,
- L_{sym} and L_{rw} are symmetric and positive definite,
- the smallest eigenvalue is 0,
- the order of multiplicity of 0 is the number of connected components.

Input: Adjacency Matrix $A \in \mathbb{R}^{N \times N}$, number k of clusters to construct.

- Compute the unnormalized Laplacian L .
- Compute the first k eigenvectors u_1, \dots, u_k of L .
- Let $U \in \mathbb{R}^{N \times k}$ be the matrix containing the vectors u_1, \dots, u_k as columns.
- For $i = 1, \dots, N$, let $z_i \in \mathbb{R}^k$ be the vector corresponding to the i -th row of U .
- Cluster the points $(z_i)_{i=1, \dots, N}$ in \mathbb{R}^k with the k -means algorithm into clusters C_1, \dots, C_k .

Stochastic and Latent Block Models

Other latent space models and other methods

Extensions of SBM

[Karrer and Newman, 2011]

$$\mathbb{P}(Y_{i,j} = 1 | Z_i = k, Z_j = l) = 1 / (1 + \exp(-\alpha_{kl} - \nu_i - \nu_j))$$

with

- $(\nu_i)_{1 \leq i \leq n}$ parameters to be estimated,
- find clusters besides the degree/popularity.

[Airoldi et al., 2008]

For each node $p \in N$:

- Draw a K -dimensional mixed membership vector $\vec{\pi}_p \sim \text{Dirichlet}(\vec{\alpha})$.

For each pair of nodes $(p, q) \in N \times N$:

- Draw membership indicator for the initiator, $\vec{z}_{p \rightarrow q} \sim \text{Multinomial}(\vec{\pi}_p)$.
- Draw membership indicator for the receiver, $\vec{z}_{q \rightarrow p} \sim \text{Multinomial}(\vec{\pi}_q)$.
- Sample the value of their interaction, $Y(p, q) \sim \text{Bernoulli}(\vec{z}_{p \rightarrow q}^T A \vec{z}_{q \rightarrow p})$.

Other extensions exist...

- Large variety of multilayer networks,
- SBM as a probabilistic generative model easy to extend to numerous cases.
- e.g. dynamic or spatial SBM ([Matias and Miele, 2017, Longepierre and Matias, 2019]) or Topic SBM [Bouveyron et al., 2018].

Our contributions

- Multiplex network [Barbillon et al., 2017, Lazega et al., 2016],
- Multilevel network [Chabert-Liddell et al., 2019],
- Multipartite network [Bar-Hen et al., 2018].

Adaptation of the VEM algorithm and ICL criterion to select the numbers of blocks.

Multiplex network

In collaboration with A. Bar-Hen, S. Donnet and E. Lazega
[Barbillon et al., 2017, Lazega et al., 2016].

Multiple relations between individuals:

$$\mathbf{Y}_{ij}|Z_i, Z_j \stackrel{ind}{\sim} \text{Bern}^M((\alpha_{Z_i, Z_j}^w)_w) \quad \text{with} \quad \sum_w \alpha_{Z_i, Z_j}^w = 1.$$

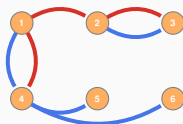


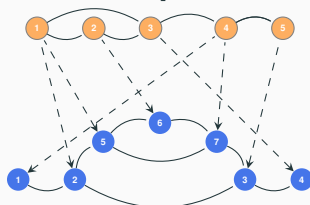
Figure 1: Illustration of a multiplex network. For each dyad, two kinds of link may exist. They are respectively displayed by red and blue edges.

Model inference implemented in the R package: `sbm`.

Application to a network of French researchers in cancerology (advice relation and indirect relation through the labs of the researchers).

Multilevel network

In collaboration with S. Donnet and S.-C. Chabert-Liddell (Ph.D. Thesis) and E. Lazega [Chabert-Liddell et al., 2019].



- **Organizational level:** SBM for $(\mathbf{Y}^O, \mathbf{Z}^O)$,
- **Individual level:** SBM for $(\mathbf{Y}^I, \mathbf{Z}^I)$,
- Interlevel dependence $i \in \{1, \dots, n_I\}, k \in \{1, \dots, K_I\}$,
 $\mathbb{P}(\mathbf{Z}_i^I = k | \mathbf{Z}_j^O, A_{ij} = 1) \stackrel{\text{ind}}{=} \gamma_{kZ_j^O}$, where A is the affiliation matrix.

Implemented in S.-C. Chabert-Liddell's R package: `MLVSBM`.

Application to a dataset of a program trade fair (Organizations = audiovisual firms, individuals = sales representatives).

Generalized Multipartite Networks

In collaboration with A. Bar-Hen and S. Donnet [[Bar-Hen et al., 2018](#)].

- Pre-specified functional groups (colors of nodes),
- Looking for blocks within functional groups,
- Each network between 2 functional groups is either an SBM or an LBM.

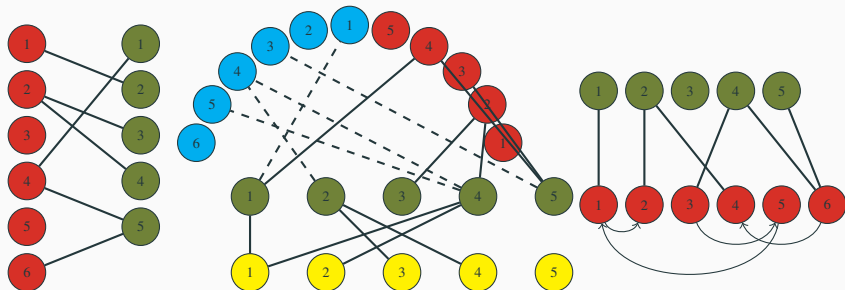


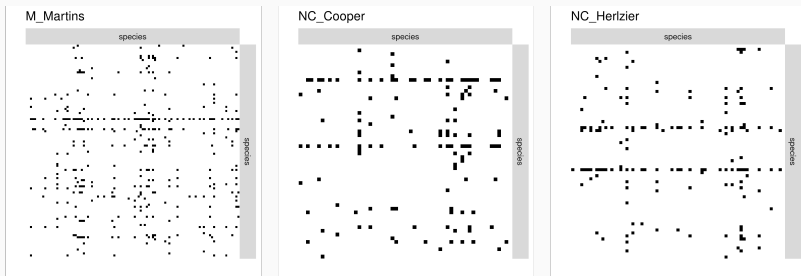
Figure 2: Illustrations of bipartite (left), multipartite (center) and generalized multipartite networks (right). The colors stand for the different functional groups.

Implemented in an R package: `GREMLINS`.

Application for ecological interaction (see practical session).

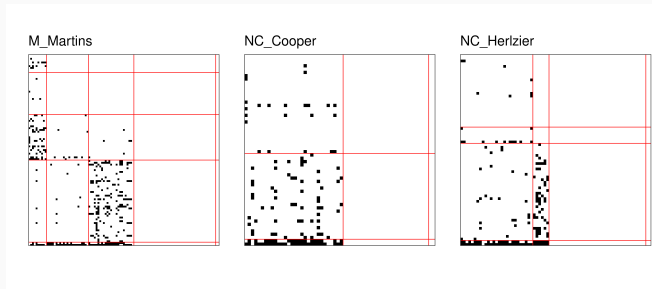
Towards collection of networks: Three foodwebs

- Pine-firest stream food webs issued from Maine, North-Caroline and New-Zeland [[Thompson and Townsend, 2003](#)]
- Involve respectively 105, 58 and 71 species.
- $Y_{ij} = 1$ if i is eaten by j . Directed relation



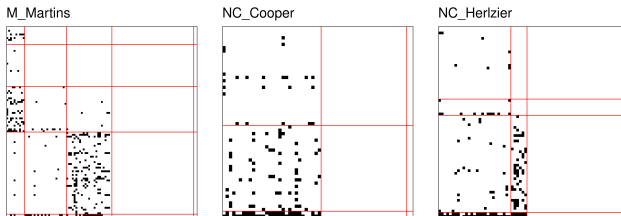
- Look for similarities and differences between network structures.

Separate SBMs



- Fitted SBM on each separately
- Reordered the matrices following the blocks
- Label the blocks following the average out-degrees order

Towards collection of networks: Separate SBMs



- Two bottom groups in each matrix are basal species : eaten by many species and not eating anybody.
- **Martins**: has a separation into 5 blocks, the third one is a medium trophic level, which preys on basal species and is highly preyed by species of the 1st block.
- **Cooper**. Higher trophic levels grouped together in the same block (lack of statistical power).
- **Herzler**: higher trophic level is separated into 2 blocks determined on how much they prey on the less preyed basal block.

- Need to model jointly the networks
- Identify the groups playing the same role through out the networks, with an unsupervised strategy.
- Let $(\mathbf{Y}^m)_{m=1,\dots,M}$ denote the collection of networks each involving n_m nodes.
- (\mathbf{Y}^m) independent.

-

$$\mathbf{Y}^m \sim \text{SBM}_{n_m}(Q^m, \boldsymbol{\pi}^m, \boldsymbol{\alpha}^m)$$

- Conditions on the parameters $(\boldsymbol{\pi}^m)_{m=1,\dots,M}$ and $(\boldsymbol{\alpha}^m)_{m=1,\dots,M}$

iid-colSBM

$$\mathbf{Y}^m \sim \text{SBM}_{n_m}(Q, \pi, \alpha)$$

with $\pi_q > 0 \forall q \in \{1, \dots, Q\}$ and $\sum_{q=1}^Q \pi_q = 1$.

- $(Q - 1) + Q^2$ unknown parameters, M clustering
- Maybe too strict

Same structure of connection α , specific proportions of blocks in each network

π -coISBM

$$\mathbf{Y}^m \sim \text{SBM}_{n_m}(Q, \boldsymbol{\pi}^m, \alpha)$$

On the block proportions

- $\pi_q^m \geq 0$
- If $\pi_q^m = 0$ then block q is not represented in network m

$M = 2$ networks

$$\alpha = \begin{pmatrix} \alpha_{11} & \alpha_{12} & \alpha_{13} \\ \alpha_{12} & \alpha_{22} & \alpha_{23} \\ \alpha_{13} & \alpha_{23} & \alpha_{33} \end{pmatrix} \quad \begin{array}{l} \pi^1 = [.25, .25, .50] \\ \pi^2 = [.20, .50, .30] \end{array}.$$

- Same connection structure between blocks
- Different block proportions
- $2 \times (3 - 1) + 3^2 = 15$ parameters.

$$\pi_q^m \geq 0$$

$$\alpha = \begin{pmatrix} \alpha_{11} & \alpha_{12} & \alpha_{13} \\ \alpha_{12} & \alpha_{22} & \alpha_{23} \\ \alpha_{13} & \alpha_{23} & \alpha_{33} \end{pmatrix} \quad \begin{array}{l} \pi^1 = [.25, .25, .50] \\ \pi^2 = [.40, 0, .60] \end{array}.$$

- Blocks 1 and 3 are represented in the two networks while block 2 only exists in network 1.
- $3 - 1 + 3 - 2 + 3^2 = 14$ parameters

$$\alpha = \begin{pmatrix} \alpha_{11} & \alpha_{12} & \alpha_{13} \\ \alpha_{21} & \alpha_{22} & \cdot \\ \alpha_{31} & \cdot & \alpha_{33} \end{pmatrix} \quad \begin{array}{l} \pi^1 = [.25, .75, 0] \\ \pi^2 = [.40, 0, .60] \end{array}.$$

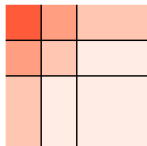
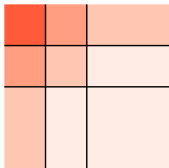
- The two networks share block 1 (for instance super predators or basal species)
- The remaining nodes of each network not equivalent in terms of connectivity.
- Blocks 2 and 3 never interact because their elements do not belong to the same network and so α_{23} and α_{32} are not required to define the model.
- $(2 - 1) + (2 - 1) + 7 = 11$ parameters.

M independent networks.

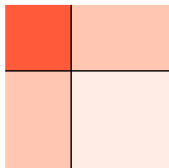
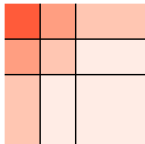
$$\mathbf{Y}^m \sim \text{SBM}(Q^m, \boldsymbol{\pi}^m, \boldsymbol{\alpha}^m)$$

Model name	Block prop.	Connexion param.	Nb of param.
<i>iid-colSBM</i>	$\pi_q^m = \pi_q, \pi_q > 0$	$\alpha_{qr}^m = \alpha_{qr}$	$(Q - 1) + Q^2$
<i>π-colSBM</i>	$\pi_q^m, \pi_q^m \geq 0$	$\alpha_{qr}^m = \alpha_{qr}$	$\leq M(Q - 1) + Q^2$
<i>δ-colSBM</i>	$\pi_q^m = \pi_q, \pi_q > 0$	$\alpha_{qr}^m = \delta^m \alpha_{qr}$	$(Q - 1) + Q^2 + (M - 1)$
<i>$\delta\pi$-colSBM</i>	$\pi_q^m, \pi_q^m \geq 0$	$\alpha_{qr}^m = \delta^m \alpha_{qr}$	$\leq M(Q - 1) + Q^2 + M - 1$
<i>sep-SBM</i>	$\pi_q^m, \pi_q^m > 0$	α_{qr}^m	$\sum_{m=1}^M (Q_m - 1) + Q_m^2$

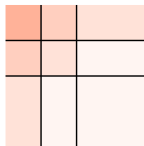
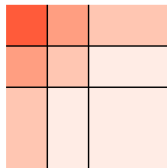
colSBM



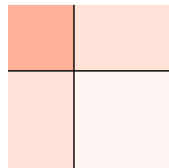
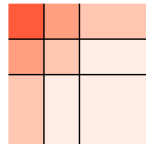
π colSBM



δ colSBM



$\delta\pi$ colSBM



α 0



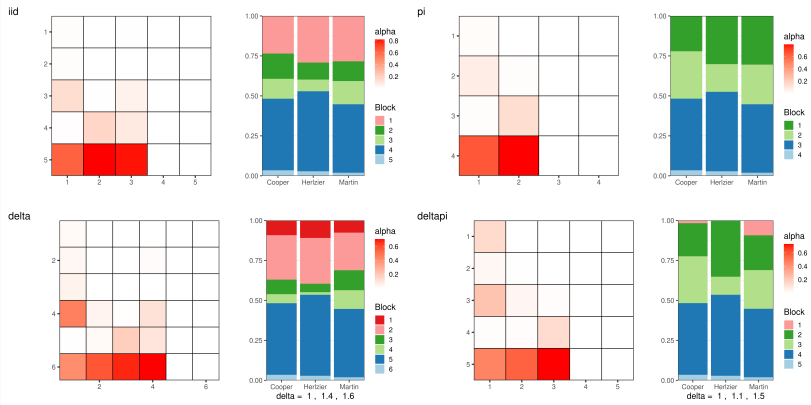
VEM algorithm

- Direct extension of VEM previously described for *iid*-colSBM and π -colSBM
- Less obvious with $\delta_m \alpha$: M step not explicit.
- Sensitive to initializations: need to match blocks among networks.

Model Selection

- ICL can be directly extended for *iid*-colSBM and the δ -colSBM
- for $\pi(\delta)$ -colSBM, taking into account empty blocks...

Our 4 consensus models



Top left : iid (−1966). Top right: π -colSBM (−1982) Bottom-left: δ -colSBM (−1969). Bottom-right: $\delta\pi$ -colSBM (−1989)

- separated SBMs gives an ICL of −2080.
- iid-colSBM : preferred model. Make 5 blocks
- π -colSBM: block proportion quite similar. Make no use of its flexibility



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