

Détection et comparaison de structures de réseaux écologiques

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vivant**

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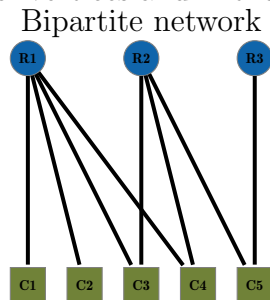
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CHAPTER

Introduction

1.1 Usage and importance of bipartite graphs

Bipartite graphs, denoted as $G = (U, V, E)$ with U and V two disjoint and independent sets of vertices and E the set of edges connecting U vertices to V vertices.



$$X = \begin{pmatrix} 1 & 1 & 1 & 1 & 0 \\ 0 & 0 & 1 & 1 & 1 \\ 0 & 0 & 0 & 0 & 1 \end{pmatrix}$$

Incidence matrix

X is the *incidence matrix* and is the mathematical object on which computations are performed. It is filled with the following rule:

$$\begin{cases} X_{ij} = 0 & \text{if no interaction is observed between species } i \text{ and } j \\ X_{ij} \neq 0 & \text{otherwise} \end{cases}$$

If the network represents binary observations (like presence-absence) then $X_{ij} \in \mathcal{K} = \{0, 1\}, \forall(i, j)$; if the interactions are weighted (like an abundance count), $X_{ij} \in \mathcal{K} = \mathbb{N}, \forall(i, j)$.

This representation can be used to represent various forms of interactions where two kinds of “actors” interact. Those interactions can be binary or valued and a numeric representation is the incidence matrix, in the above example X .

Among the use case of bipartite graphs one can find the Netflix Problem, which was a prize organized by Netflix to improve its Recommender system. The row nodes are the movies and the columns are the user, at the intersection the value is the review of the user j for the movie i .

Another use is the representation of ecological interactions like plant-pollinator (Ramos-Jiliberto et al., 2010), birds-seed dispersion, prey-predator or host-parasite (Kaszewska-Gilas et al., 2021). For plant-pollinator interactions, the rows are pollinator species and the columns are plant species, and the intersection is a value, binary if it is a presence/absence or a value if it is an abundance count.

Bipartite graphs are widely used in biology in general, in various fields, among which the previously cited ecological networks, but also in medicine with biomedical networks, biomolecular networks or epidemiological networks. (Pavlopoulos et al., 2018)

Some interesting results can arise when applying a tool widely used on a particular kind of interactions is used on another kind of interactions. Companies like Netflix or Amazon use recommender system, to recommend other products to consumers based on their previous interactions. In [Desjardins-Proulx et al., 2017](#) the authors use the *K-nearest neighbour* (KNN) algorithm as a Recommender to predict missing preys for predators in a predator-prey network.

1.2 Latent Block Model

The Latent Block Model (LBM) introduced by [Govaert and Nadif, 2010](#) adapts the Stochastic Block Model (SBM) ([Holland et al., 1983](#); [Snijders & Nowicki, 1997](#)) to bipartite graphs.

Note : Please note that we prefer the term “BiSBM“ and will use both LBM and BiSBM to designate the Stochastic Block Model applied on bipartite networks.

This model supposes that:

- Row nodes are members of row blocks and column nodes are members of column blocks.
- The connectivity of two individuals is determined by their block memberships.
- An interaction can only occur between a row and a column node.

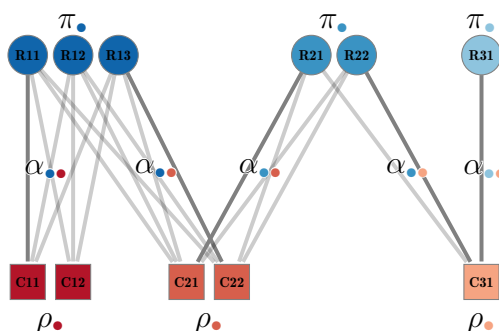


Figure 1.1: An LBM model visualization

- $Q_1 = |\{\bullet, \bullet, \bullet\}|$ given blocks in rows
- $Q_2 = |\{\bullet, \bullet, \bullet\}|$ given blocks in columns

Parameters

- $\pi_{\bullet} = \mathbb{P}(Z_i = \bullet)$ for rows and $\rho_{\bullet} = \mathbb{P}(W_j = \bullet)$ for columns
- $\alpha_{\bullet\bullet} = \mathbb{P}(X_{ij} = 1 | Z_i = \bullet, W_j = \bullet)$, probability of connectivity knowing node membership blocks.

On 1.1, $\boldsymbol{\pi}$ are the probabilities for a row node to belong to the row block of corresponding color, $\boldsymbol{\rho}$ are the probabilities for a column node to belong to the column block of corresponding color and $\boldsymbol{\alpha}$ is a matrix $Q_1 \times Q_2$ of the connectivity parameters between the row and column blocks. When we talk about the “structure” of the network we are referring to this connectivity matrix.

This model can be used to easily generate bipartite graphs with complex and very varied structures. But when trying to determine the structure of a given network we need to find those parameters and as the row and column block memberships are *latent* i.e., they are not known and must be inferred.

For this a common approach is to use a *variational* EM algorithm (proposed for SBM in [Daudin et al., 2008](#) and for LBM in [Govaert and Nadif, 2005](#)) those groups and the required parameters can be inferred by maximizing a lower bound of the likelihood.

1.3 *colSBM* model, a joint model for a collection of networks

The *colSBM* model introduced by [Chabert-Liddell et al., 2024](#) propose an extension of the SBM model to collections of simple (or unipartite) networks. A collection is a set of networks which nodes are not common or linked between different networks, the interactions have the same valuations and are of the same type.

The model can retrieve the shared structure in a collection, indicate if networks should be grouped in a collection and in a large pool of networks, collections with common structures.

The next step after designing this collection model for unipartite networks was to extend it to the bipartite case.

Structure detection in a collection of bipartite networks

2.1 Definition of a collection

We define a collection of bipartite networks as $\mathbf{X} = (X^1, \dots, X^M)$ the collection of incidence matrix. Moreover, all the networks in the collection have the same type of interaction (e.g., all interactions are binary).

2.2 Separate BiSBM (sep-BiSBM)

A first approach to deal with a collection of networks is to adjust separate BiSBM for each network of the collection.

For network m , let n_1^m (resp. n_2^m) be the number of nodes in row (resp. column) divided into Q_1^m row clusters (resp. Q_2^m column clusters).

Let $Z^m = (Z_1^m, \dots, Z_i^m, \dots, Z_{n_1^m}^m)$ and $W^m = (W_1^m, \dots, W_j^m, \dots, W_{n_2^m}^m)$ be independent latent variables such that $Z_i^m = q$ if row node i of network m belongs to row cluster q ($q \in \{1, \dots, Q_1^m\}$) and $W_j^m = r$ if column node j of network m belong to column block r ($r \in \{1, \dots, Q_2^m\}$). And we have

$$\mathbb{P}(Z_i^m = q) = \pi_q^m, \quad \mathbb{P}(W_j^m = r) = \rho_r^m \quad (2.1)$$

where $\pi_q^m > 0$, $\rho_r^m > 0$, $\sum_{q=1}^{Q_1^m} \pi_q^m = 1$ and $\sum_{r=1}^{Q_2^m} \rho_r^m = 1$. Given the latent variables Z^m, W^m , the X_{ij}^m 's are assumed to be independent and distributed as

$$X_{ij}^m | Z_i^m = q, W_j^m = r \sim \mathcal{F}(\cdot; \alpha_{qr}^m) \quad (2.2)$$

where \mathcal{F} is referred to as the emission distribution. \mathcal{F} is chosen to be the Bernoulli distribution for binary interactions, and the Poisson distribution for weighted interactions such as counts. Let f be the density of the emission distribution, then:

$$\log f(X_{ij}^m; \alpha_{qr}^m) = \begin{cases} X_{ij}^m \log(\alpha_{qr}^m) + (1 - X_{ij}^m) \log(1 - \alpha_{qr}^m) & \text{for Bernoulli emission} \\ -\alpha_{qr}^m + X_{ij}^m \log(\alpha_{qr}^m) - \log(X_{ij}^m!) & \text{for Poisson emission} \end{cases} \quad (2.3)$$

Equations (2.1), (2.2) and (2.3) defines the BiSBM model and we will now use a short notation:

$$X^m \sim \mathcal{F}\text{-BiSBM}_{n_1^m, n_2^m}(Q_1^m, Q_2^m, \boldsymbol{\pi}^m, \boldsymbol{\rho}^m, \boldsymbol{\alpha}^m) \quad (\text{sep-BiSBM})$$

where \mathcal{F} encodes the emission distribution, n_1^m, n_2^m are the row and column nodes, Q_1^m, Q_2^m are the number of row and column blocks in network m , $\boldsymbol{\pi}^m = (\pi_q^m)_{q=1, \dots, Q_1^m}$ and $\boldsymbol{\rho}^m = (\rho_r^m)_{r=1, \dots, Q_2^m}$ are the vectors of their proportions. The $Q_1^m \times Q_2^m$ matrix $\boldsymbol{\alpha}^m = (\alpha_{qr}^m)_{\substack{q=1, \dots, Q_1^m \\ r=1, \dots, Q_2^m}}$ are the connectivity parameters, the parameters of the emission distribution. $\alpha_{qr}^m \in \mathcal{A}_{\mathcal{F}}$ where, for the Bernoulli (resp. Poisson) emission distribution, $\mathcal{A}_{\mathcal{F}} = (0, 1)$ (resp. $\mathcal{A}_{\mathcal{F}} = \mathbb{R}^{*+}$). In this *sep-BiSBM* each network m is assumed to follow a *BiSBM* with its own parameters $(\boldsymbol{\pi}^m, \boldsymbol{\rho}^m, \boldsymbol{\alpha}^m)$.

2.3 Definition of the *colBiSBM* models

2.3.1 A collection of iid bipartite SBM

As for *colSBM* this first model is the most constrained. It assumes that all the networks are the independent realizations of the same Q_1 - Q_2 -BiSBM with identical parameters. The *iid-colBiSBM* is defined as follows:

$$X^m \sim \mathcal{F} - BiSBM_{n_1^m, n_2^m}(Q_1, Q_2, \boldsymbol{\pi}, \boldsymbol{\rho}, \boldsymbol{\alpha}), \quad \forall m = 1, \dots, M \quad (\text{iid-colBiSBM})$$

where $\forall (q, r) \in \{1, \dots, Q_1\} \times \{1, \dots, Q_2\}$, $\alpha_{qr} \in \mathcal{A}_{\mathcal{F}}$, $\pi_q \in (0, 1]$, $\sum_{q=1}^{Q_1} \pi_q = 1$ and $\rho_r \in (0, 1]$, $\sum_{r=1}^{Q_2} \rho_r = 1$. This model involves $(Q_1 - 1) + (Q_2 - 1) + Q_1 \times Q_2$ parameters, the two first terms corresponding to block proportions on the row and column dimensions and the third term to connectivity parameters.

But the assumption that block proportions are the same among the networks is a strong assumption. In plant-pollinator networks, the proportion of specialist species can differ between networks and thus the model may benefit from not having the same block proportions but sharing a common connectivity structure. The following models relaxes this assumption on either row, column or both.

2.3.2 A collection of bipartite SBM with varying block size on either rows or columns

π -colBiSBM model still assumes that the networks share a common connectivity structure represented by $\boldsymbol{\alpha}$ but that each network has its own row block proportions. For $m \in \{1, \dots, M\}$, the X^m are independent and

$$X^m \sim \mathcal{F} - BiSBM_{n_1^m, n_2^m}(Q_1, Q_2, \boldsymbol{\pi}^m, \boldsymbol{\rho}, \boldsymbol{\alpha}), \quad \forall m = 1, \dots, M \quad (\pi\text{-colBiSBM})$$

where $\forall (q, r) \in \{1, \dots, Q_1\} \times \{1, \dots, Q_2\}$, $\alpha_{qr} \in \mathcal{A}_{\mathcal{F}}$, $\pi_q^m \in [0, 1]$, $\sum_{q=1}^{Q_1} \pi_q^m = 1, \forall m \in \{1, \dots, M\}$ and $\rho_r \in (0, 1]$, $\sum_{r=1}^{Q_2} \rho_r = 1$. This model is more flexible than the *iid-colBiSBM* as it allows some row block proportions to be null in certain networks ($\pi_q^m \in [0, 1]$): if $\pi_q^m = 0$ then the block q is not represented in the network m . The connectivity structure is thus a subset of a large connectivity structure common to all networks. We face the same problems as [Chabert-Liddell et al., 2024](#) and adapt the support S they define for the π -colSBM to the bipartite case by having

S^1 of size $M \times Q_1$ the support for the rows and S^2 of size $M \times Q_2$ the support for the columns. Thus $S_{mq}^1 = \mathbb{1}_{\pi_q^m > 0}$ and $S_{mr}^2 = \mathbb{1}_{\rho_r^m > 0}$. In this case, $S^2 = \mathbf{1}$, because there is no freedom on the column dimension.

For a given number of blocks Q_1 , Q_2 and matrix S^1 (S^2 being in this case the matrix full of ones), the number of parameters is:

$$\text{NP}(\pi\text{-colBiSBM}) = \sum_{m=1}^M \left(\sum_{q=1}^{Q_1} S_{mq}^1 - 1 \right) + (Q_2 - 1) + \sum_{\substack{q=1, \dots, Q_1 \\ r=1, \dots, Q_2}} \mathbb{1}_{(S^1 S^2)_{qr} > 0}$$

The first term corresponds to the non-null block proportions in each network. The third quantity accounts for the fact that some blocks may never be represented simultaneously in any network, so the corresponding connection parameters α_{qr} are not useful for defining the model.

ρ -colBiSBM model still assumes that the networks share a common connectivity structure represented by α but that each network has its own column block proportions. For $m \in \{1, \dots, M\}$, the X^m are independent and

$$X^m \sim \mathcal{F} - \text{BiSBM}_{n_1^m, n_2^m}(Q_1, Q_2, \pi, \rho^m, \alpha), \quad \forall m = 1, \dots, M \quad (\rho\text{-colBiSBM})$$

where $\forall (q, r) \in \{1, \dots, Q_1\} \times \{1, \dots, Q_2\}$, $\alpha_{qr} \in \mathcal{A}_{\mathcal{F}}$, $\pi_q \in (0, 1]$, $\sum_{q=1}^{Q_1} \pi_q = 1$ and $\rho_r^m \in [0, 1]$, $\sum_{r=1}^{Q_2} \rho_r^m = 1$. This model is more flexible than the iid-colBiSBM as it allows some column block proportions to be null in certain networks ($\rho_r^m \in [0, 1]$): if $\rho_r^m = 0$ then the column block r is not represented in the network m .

“Mirroring” the formulas for the π -colBiSBM we relax the constraints on the column dimension.

For a given number of blocks Q_1 , Q_2 and matrix S^2 (S^1 being in this case the matrix full of ones), the number of parameters is:

$$\text{NP}(\rho\text{-colBiSBM}) = (Q_1 - 1) + \sum_{m=1}^M \left(\sum_{r=1}^{Q_2} S_{mr}^2 - 1 \right) + \sum_{\substack{q=1, \dots, Q_1 \\ r=1, \dots, Q_2}} \mathbb{1}_{(S^1 S^2)_{qr} > 0}$$

$\pi\rho$ -colBiSBM model still assumes that the networks share a common connectivity structure represented by α but that each network has its own row and column block proportions, it is the less constrained model. For $m \in \{1, \dots, M\}$, the X^m are independent and

$$X^m \sim \mathcal{F} - \text{BiSBM}_{n_1^m, n_2^m}(Q_1, Q_2, \pi^m, \rho^m, \alpha), \quad \forall m = 1, \dots, M \quad (\pi\rho\text{-colBiSBM})$$

where $\forall (q, r) \in \{1, \dots, Q_1\} \times \{1, \dots, Q_2\}$, $\alpha_{qr} \in \mathcal{A}_{\mathcal{F}}$, $\pi_q^m \in [0, 1]$, $\sum_{q=1}^{Q_1} \pi_q^m = 1$, $\forall m \in \{1, \dots, M\}$ and $\rho_r^m \in [0, 1]$, $\sum_{r=1}^{Q_2} \rho_r^m = 1$.

For a given number of blocks Q_1 , Q_2 and matrices S^1 , S^2 , the number of parameters is:

$$\text{NP}(\pi\rho\text{-colBiSBM}) = \sum_{m=1}^M \left(\sum_{q=1}^{Q_1} S_{mq}^1 - 1 \right) + \sum_{m=1}^M \left(\sum_{r=1}^{Q_2} S_{mr}^2 - 1 \right) + \sum_{\substack{q=1, \dots, Q_1 \\ r=1, \dots, Q_2}} \mathbb{1}_{(S^1 S^2)_{qr} > 0}$$

2.4 Variational estimation of the parameters

In practice, the estimation of the likelihood is not tractable. Following the classical approach defined in [Daudin et al., 2008](#) we use a variational version of the Expectation Maximization (VEM) algorithm.

We maximize a variational lower bound of the log-likelihood of the observed data, the so-called Evidence Lower Bound (or ELBO), by approximating $p(\mathbf{Z}, \mathbf{W} | \mathbf{X}; \boldsymbol{\theta})$ with a distribution on \mathbf{Z} and \mathbf{W} named \mathcal{R} defined as $\mathcal{R} = \otimes_{m=1}^M \mathcal{R}_m$.

The lower bound is defined as:

$$\mathcal{J}(\mathcal{R}; \boldsymbol{\theta}) := \sum_{m=1}^M \left(\mathbb{E}_{\mathcal{R}_m} [\ell(X^m, Z^m, W^m; \boldsymbol{\theta})] + \mathcal{H}(\mathcal{R}_m) \right) \leq \ell(\mathbf{X}; \boldsymbol{\theta})$$

$(Z_i^m)_{i=1\dots n_1^m}$ and $(W_j^m)_{j=1\dots n_2^m}$ are redefined using the *one-hot encoded* conversion (i.e., $Z_i^m = q \rightarrow Z_{iq}^m = 1$ and $W_j^m = r \rightarrow W_{jr}^m = 1$).

When \mathcal{R}_m is issued from the set of the factorizable distributions, we denote $\tau_{iq}^{1,m} = \mathbb{P}_{\mathcal{R}_m}(Z_{iq}^m = 1 | X_{i\bullet}^m)$ and $\tau_{jr}^{2,m} = \mathbb{P}_{\mathcal{R}_m}(W_{jr}^m = 1 | X_{\bullet j}^m)$, thus we have: $\mathbb{P}_{\mathcal{R}_m}(Z_{iq}^m = 1, W_{jr}^m = 1 | X^m) = \mathbb{P}_{\mathcal{R}_m}(Z_{iq}^m = 1 | X_{i\bullet}^m) \times \mathbb{P}_{\mathcal{R}_m}(W_{jr}^m = 1 | X_{\bullet j}^m) = \tau_{iq}^{1,m} \times \tau_{jr}^{2,m}$.

The formula for the entropy per network is thus:

$$\mathcal{H}(\mathcal{R}_m) = - \sum_{i=1}^{n_1^m} \tau_{i,q}^{1,m} \log \tau_{i,q}^{1,m} - \sum_{j=1}^{n_2^m} \tau_{j,r}^{2,m} \log \tau_{j,r}^{2,m}$$

And the expectation of the completed log-likelihood under the \mathcal{R}_m variational distribution for network m is:

$$\begin{aligned} \mathbb{E}_{\mathcal{R}_m} [\ell(X^m, Z^m, W^m; \boldsymbol{\theta})] &= \sum_{i=1}^{n_1^m} \sum_{j=1}^{n_2^m} \sum_{q \in \mathcal{Q}_{1,m}} \sum_{r \in \mathcal{Q}_{2,m}} \tau_{i,q}^{1,m} \tau_{j,r}^{2,m} \log f(X_{ij}^m; \alpha_{qr}) \\ &+ \sum_{i=1}^{n_1^m} \sum_{q \in \mathcal{Q}_{1,m}} \tau_{i,q}^{1,m} \log \pi_q^m + \sum_{j=1}^{n_2^m} \sum_{r \in \mathcal{Q}_{2,m}} \tau_{j,r}^{2,m} \log \rho_r^m \end{aligned}$$

And thus the lower bound becomes:

$$\begin{aligned} \mathcal{J}(\boldsymbol{\tau}; \boldsymbol{\theta}) &:= \sum_{m=1}^M \left(\sum_{i=1}^{n_1^m} \sum_{j=1}^{n_2^m} \sum_{q \in \mathcal{Q}_{1,m}} \sum_{r \in \mathcal{Q}_{2,m}} \tau_{i,q}^{1,m} \tau_{j,r}^{2,m} \log f(X_{ij}^m; \alpha_{qr}) \right. \\ &+ \sum_{i=1}^{n_1^m} \sum_{q \in \mathcal{Q}_{1,m}} \tau_{i,q}^{1,m} \log \pi_q^m + \sum_{j=1}^{n_2^m} \sum_{r \in \mathcal{Q}_{2,m}} \tau_{j,r}^{2,m} \log \rho_r^m \\ &\left. - \sum_{i=1}^{n_1^m} \tau_{i,q}^{1,m} \log \tau_{i,q}^{1,m} - \sum_{j=1}^{n_2^m} \tau_{j,r}^{2,m} \log \tau_{j,r}^{2,m} \right) \end{aligned}$$

where we identify the variational distribution \mathcal{R} with its parameter $\boldsymbol{\tau}$.

The VEM algorithm alternates between two steps, the variational E step and the M step. The E steps consists in optimizing $\mathcal{J}(\boldsymbol{\tau}; \boldsymbol{\theta})$ for a current value of $\boldsymbol{\theta}$ with respect to $\boldsymbol{\tau}$. And the M step consists of maximizing $\mathcal{J}(\boldsymbol{\tau}; \boldsymbol{\theta})$ with respect to $\boldsymbol{\theta}$ and for a given variational distribution $\boldsymbol{\tau}$.

2.4.1 Variational E step

At this step we maximize with respect to the variational distribution $\boldsymbol{\tau}$:

$$\widehat{\boldsymbol{\tau}}^{(t+1)} = \arg \max_{\boldsymbol{\tau}} \mathcal{J}(\boldsymbol{\tau}, \widehat{\boldsymbol{\theta}}^{(t)}).$$

And we obtain the following formulae for the $\boldsymbol{\tau}^m$:

$$\begin{cases} \widehat{\tau}_{iq}^{1,m} \propto \widehat{\pi}_q^{m(t)} \prod_{j=1}^{n_2^m} \prod_{r \in \mathcal{Q}_2^m} f(X_{ij}^m; \widehat{\alpha}_{qr}^{(t)}) \widehat{\tau}_{jr}^{2,m(t+1)} & \forall i = 1, \dots, n_1^m, q \in \mathcal{Q}_1^m \\ \widehat{\tau}_{jr}^{2,m} \propto \widehat{\rho}_r^{m(t)} \prod_{i=1}^{n_1^m} \prod_{q \in \mathcal{Q}_1^m} f(X_{ij}^m; \widehat{\alpha}_{qr}^{(t)}) \widehat{\tau}_{iq}^{1,m(t+1)} & \forall j = 1, \dots, n_2^m, r \in \mathcal{Q}_2^m \end{cases}$$

which are used to update iteratively the values by a fixed point algorithm with only one step.

2.4.2 M step of the algorithm

At iteration (t) the M-step maximizes the variational bound with respect to the model parameters $\boldsymbol{\theta}$:

$$\widehat{\boldsymbol{\theta}}^{(t+1)} = \arg \max_{\boldsymbol{\theta}} \mathcal{J}(\widehat{\boldsymbol{\tau}}^{(t+1)}, \boldsymbol{\theta})$$

The following quantities are involved in the obtained formulae:

$$e_{qr}^m = \sum_{i=1}^{n_1^m} \sum_{j=1}^{n_2^m} \tau_{iq}^{1,m} \tau_{jr}^{2,m} X_{ij}^m, \quad n_{qr}^m = \sum_{i=1}^{n_1^m} \sum_{j=1}^{n_2^m} \tau_{iq}^{1,m} \tau_{jr}^{2,m}, \quad n_q^{1,m} = \sum_{i=1}^{n_1^m} \tau_{iq}^{1,m}, \quad n_r^{2,m} = \sum_{j=1}^{n_2^m} \tau_{jr}^{2,m}$$

The block proportions, in free mixture models, $(\pi_q^m)_{q \in \mathcal{Q}_1^m}, (\rho_r^m)_{r \in \mathcal{Q}_2^m}$ are estimated as

$$\begin{aligned} \widehat{\pi}_q^m &= \frac{n_q^{1,m}}{n_1^m} && \text{for } \pi\text{-colBiSBM and } \pi\rho\text{-colBiSBM} \\ \widehat{\rho}_r^m &= \frac{n_r^{2,m}}{n_2^m} && \text{for } \rho\text{-colBiSBM and } \pi\rho\text{-colBiSBM} \end{aligned}$$

while on the other hand,

$$\begin{aligned} \widehat{\pi}_q &= \frac{\sum_{m=1}^M n_q^{1,m}}{\sum_{m=1}^M n_1^m} && \text{for } iid\text{-colBiSBM and } \rho\text{-colBiSBM} \\ \widehat{\rho}_r &= \frac{\sum_{m=1}^M n_r^{2,m}}{\sum_{m=1}^M n_2^m} && \text{for } iid\text{-colBiSBM and } \pi\text{-colBiSBM} \end{aligned}$$

the parameters takes into account all the networks at the same time. The connectivity parameters α_{qr} for all models are estimated as the ratio of the number of

interactions between row block q and column block r among all networks over the number of number of possible interactions:

$$\hat{\alpha}_{qr} = \frac{\sum_{m=1}^M e_{qr}^m}{\sum_{m=1}^M n_{qr}^m}$$

2.5 Model selection

The section 2.4 explains how we estimate the parameters of the model for *fixed* number of blocks Q_1 and Q_2 . But as they are in general not known we need to explore the latent space to find the *best* values. As discussed in Chabert-Liddell et al., 2024, the algorithmic aspect becomes complex when dealing with the bipartite case. Due to the size of the latent space being \mathbb{N}^2 , conducting a complete exploration of the latent space is practically infeasible. Therefore, in addition to adapting the existing formulas, our contribution to addressing this challenge involved making significant choices, which are outlined below.

The below procedures are implemented in the *colSBM* package, available on <https://github.com/Chabert-Liddell/colSBM>.

2.5.1 The Bayesian Information Criterion like (BIC-L) criterion for model selection

To select the best number of blocks we need a criterion to measure adequacy between our model and data. The ELBO might seem a good criterion at first but as for the likelihood, the more complex a model the higher it gets. And thus a good criterion should make a *trade-off* between fitting to data and model complexity.

The Integrated Classified Likelihood (ICL) is a well-established tool in the SBM and LBM domains for selecting the appropriate number of blocks. It was introduced by Daudin et al., 2008; Biernacki et al., 2000. The ICL is derived from an asymptotic approximation of the marginal complete likelihood. In this approach, the model parameters are integrated out using a prior distribution, resulting in a penalized likelihood criterion. By employing the ICL, one can effectively determine the optimal number of blocks for the given problem in a systematic manner. We obtain the following expression

$$\text{ICL} = \max_{\theta} \mathbb{E}_{\hat{\mathcal{R}}}[\ell(\mathbf{X}, \mathbf{Z}, \mathbf{W}; \theta)] - \frac{1}{2} \text{pen}$$

with pen the penalties.

Using the formula $\mathbb{E}_{\hat{\mathcal{R}}}[\ell(\mathbf{X}, \mathbf{Z}, \mathbf{W}; \theta)] \approx \ell(\mathbf{X}; \theta) - \mathcal{H}(\hat{\mathcal{R}})$, it becomes clearer, as highlighted in the existing literature, that the Integrated Classified Likelihood (ICL) gives preference to well-separated blocks by imposing a penalty on the entropy of node grouping. However, the objective of our study extends beyond grouping nodes into coherent blocks. We also aim to assess the similarity of connectivity patterns across different networks. Consequently, we aim to permit models that offer more flexible node grouping without penalizing entropy.

This leads us to formulate a BIC-like criterion in the following manner:

$$\text{BIC-L} = \max_{\theta} \mathbb{E}_{\hat{\mathcal{R}}}[\ell(\mathbf{X}, \mathbf{Z}, \mathbf{W}; \theta)] + \mathcal{H}(\hat{\mathcal{R}}) - \frac{1}{2} \text{pen} = \max_{\theta} \mathcal{J}(\hat{\mathcal{R}}, \theta) - \frac{1}{2} \text{pen}$$

We provide below the expression for the penalties for the 4 models that we propose.

iid-colBiSBM For the π and ρ :

$$\text{pen}_{\pi}(Q_1) = (Q_1 - 1) \log\left(\sum_{m=1}^M n_1^m\right), \quad \text{pen}_{\rho}(Q_2) = (Q_2 - 1) \log\left(\sum_{m=1}^M n_2^m\right)$$

For the α :

$$\text{pen}_{\alpha}(Q_1, Q_2) = Q_1 \times Q_2 \log(N_M)$$

with

$$N_M = \sum_{m=1}^M n_1^m \times n_2^m$$

And thus the BIC-L formula is the following:

$$\text{BIC-L}(\mathbf{X}, Q_1, Q_2) = \max_{\theta} \mathcal{J}(\hat{\mathcal{R}}, \theta) - \frac{1}{2} [\text{pen}_{\pi}(Q_1) + \text{pen}_{\rho}(Q_2) + \text{pen}_{\alpha}(Q_1, Q_2)]$$

$\pi\rho$ -colBiSBM The support penalties are

$$\text{pen}_{S_1}(Q_1) = -2 \log p_{Q_1}(S_1), \quad \text{pen}_{S_2}(Q_2) = -2 \log p_{Q_2}(S_2)$$

with

$$\begin{aligned} \log p_{Q_1}(S_1) &= -M \log(Q_1) - \sum_{m=1}^M \log\left(\binom{Q_1}{Q_1^{(m)}}\right), \\ \log p_{Q_2}(S_2) &= -M \log(Q_2) - \sum_{m=1}^M \log\left(\binom{Q_2}{Q_2^{(m)}}\right). \end{aligned}$$

And penalties for the ρ and π are

$$\text{pen}_{\pi}(Q_1, S_1) = \sum_{m=1}^M (Q_1^{(m)} - 1) \log n_1^m, \quad \text{pen}_{\rho}(Q_2, S_2) = \sum_{m=1}^M (Q_2^{(m)} - 1) \log n_2^m.$$

Penalties for the α

$$\text{pen}_{\alpha}(Q_1, Q_2, S_1, S_2) = \left(\sum_{q=1}^{Q_1} \sum_{r=1}^{Q_2} \mathbb{1}_{(s_1)'s_2 > 0} \right) \log(N_M).$$

And the corresponding BIC-L formula,

$$\begin{aligned} \text{BIC-L}(\mathbf{X}, Q_1, Q_2) &= \max_{S_1, S_2} \left[\max_{\theta_{S_1, S_2} \in \Theta_{S_1, S_2}} \mathcal{J}(\hat{\mathcal{R}}, \theta_{S_1, S_2}) \right. \\ &\quad - \frac{1}{2} (\text{pen}_{\pi}(Q_1, S_1) + \text{pen}_{\rho}(Q_2, S_2) \\ &\quad \quad + \text{pen}_{\alpha}(Q_1, Q_2, S_1, S_2) \\ &\quad \quad \left. + \text{pen}_{S_1}(Q_1) + \text{pen}_{S_2}(Q_2)) \right] \end{aligned}$$

2.5.2 Initialization and pairing of the models

The row (resp. column) block memberships are the labels of row (resp. column) nodes corresponding to the group to which they were assigned based on their connection patterns. This adds another layer of complexity to the model selection as we need to find the best Q_1, Q_2 and the best memberships for each vertex.

First to combine the information from the M networks we fit a LBM model for each network at the two points $Q = (1, 2)$ and $Q = (2, 1)$. Using the previously described VEM algorithm we obtain for each network its parameters (ρ, π, α) . We then compute the marginal laws for each dimension, for each network. Then we order the network blocks by the probabilities obtained in decreasing order.

For the memberships on the columns: $col\ order_m = order(\pi_m \times \alpha_m)$.

For the memberships on the rows: $row\ order_m = order(\rho_m \times \alpha_m)$.

Using this order we relabel the memberships for the M fitted collection of a single network. We then use the M memberships to fit a collection containing the M networks.

2.5.3 Greedy exploration to find an estimation of the mode

Using the previously fitted models for $Q = (1, 2)$ and $Q = (2, 1)$ we choose to perform a greedy exploration to find a first mode.

Meaning that for a given $Q = (Q_1, Q_2)$ we will compute all the possible memberships for the points $Q \in \{(Q_1 + 1, Q_2), (Q_1, Q_2 + 1), (Q_1 - 1, Q_2), (Q_1, Q_2 - 1)\}$, fit the corresponding models and choose the one that maximizes the BIC-L as the next point from which to repeat the procedure. We repeat the procedure until the BIC-L stops increasing 2 times in a row.

Algorithm 1: Greedy Exploration for Mode Estimation

Input : Fitted models for $Q = (1, 2)$ and $Q = (2, 1)$

Output: Estimation of the mode using greedy exploration

Initialize $Q = (1, 2)$ as the starting point Initialize $BIC-L_{max}$ as the maximum achieved BIC-L value Initialize *consecutive_count* as 0

while *consecutive_count* < 2 **do**

 Compute possible memberships for

$Q \in \{(Q_1 + 1, Q_2), (Q_1, Q_2 + 1), (Q_1 - 1, Q_2), (Q_1, Q_2 - 1)\}$;

 Fit models with the computed memberships Choose the model with the maximum BIC-L as the next point

if $BIC-L > BIC-L_{max}$ **then**

 | $BIC-L_{max} \leftarrow BIC-L$ *consecutive_count* $\leftarrow 0$

end

else

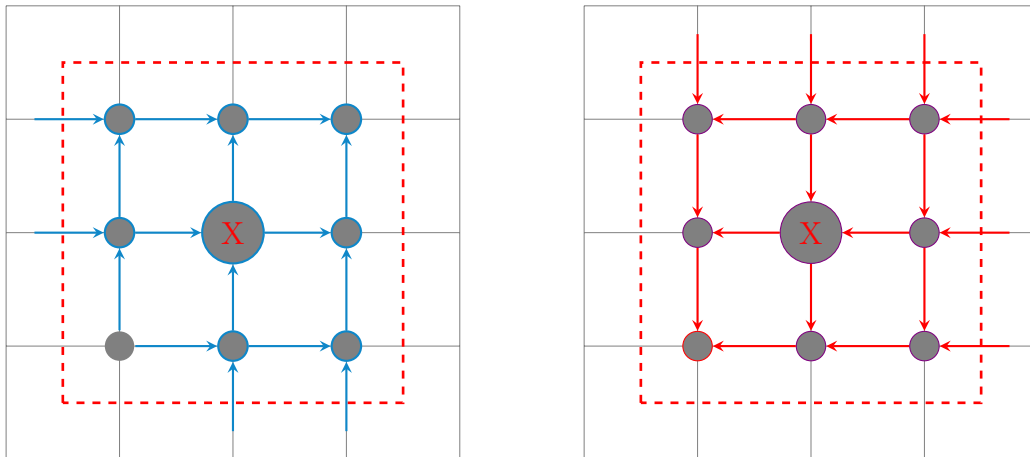
 | *consecutive_count* \leftarrow *consecutive_count* + 1

end

$Q \leftarrow$ Next selected point

end

Output: Estimation of the mode using greedy exploration



(a) Visualisation of a forward pass of moving window

(b) Visualisation of a backward pass of moving window

Figure 2.1: Moving window procedure, the center node marked with an **X** is the mode of BIC-L

When this first estimation of the BIC-L mode has been found we apply the moving window on it.

2.5.4 Moving window to update the block memberships and the BIC-L

The *moving window* is used to update the block memberships on rows and columns and fit new models with those changes. To define the window, we use a center point and a *depth*, giving us the bottom left corner $(Q_{1,center} - depth, Q_{2,center} - depth)$ and the top right corner of the window $(Q_{1,center} + depth, Q_{2,center} + depth)$. All the points in this square will be updated and contribute to the update of the others. This procedure is repeated until convergence of the BIC-L.

The figure 2.1 illustrates the procedure. It consists of two alternating steps:

- the *forward pass*: repeatedly computing the possible splits to fit the current model.
- the *backward pass*: computing the possible merges to fit the current model.

Forward pass The forward pass consists for a model at (Q_1, Q_2) to compute the possible splits from the block memberships of its “predecessors“. The predecessors are the point at the left $(Q_1 - 1, Q_2)$ and below $(Q_1, Q_2 - 1)$ the current model (if they exist). To update the current model, we take its predecessors block memberships and try to split one of the blocks in two. Then the current model is fitted using this clustering as a starting clustering. Once all the possible splits are fitted, they are compared, keeping the best, in the sense of the BIC-L. If a model was already present it is also compared and the best is chosen as the model for this round at (Q_1, Q_2) .

Algorithm 2: Moving Window Procedure

Input : Center point $(Q_{1,center}, Q_{2,center})$, depth
Output: Best model with maximum BIC-L in the window

Define bottom left corner $(Q_{1,center} - \text{depth}, Q_{2,center} - \text{depth})$
Define top right corner $(Q_{1,center} + \text{depth}, Q_{2,center} + \text{depth})$

while *not converged* **do**

Forward pass:

for $Q_1 \in [Q_{1,center} - \text{depth}; Q_{1,center} + \text{depth}]$ **do**

for $Q_2 \in [Q_{2,center} - \text{depth}; Q_{2,center} + \text{depth}]$ **do**

Compute possible splits from predecessors $(Q_1 - 1, Q_2)$ and $(Q_1, Q_2 - 1)$ Fit models with the block membership changes

Compare and keep the best model based on BIC-L

end

end

Backward pass:

for $Q_1 \in [Q_{1,center} + \text{depth}; Q_{1,center} - \text{depth}]$ **do**

for $Q_2 \in [Q_{2,center} + \text{depth}; Q_{2,center} - \text{depth}]$ **do**

Compute possible merges from predecessors $(Q_1 + 1, Q_2)$ and $(Q_1, Q_2 + 1)$ Fit models with the block membership changes

Compare and keep the best model based on BIC-L

end

end

Update the best model based on the maximum BIC-L

end

Output: Best model with maximum BIC-L in the window

The procedure then repeats for the point at $(Q_1 + 1, Q_2)$ until it reaches $(Q_{1,center} + \text{depth}, Q_2)$ from which it repeats from $(Q_{1,center} - \text{depth}, Q_2 + 1)$. This repeats until computing the best model for $(Q_{1,center} + \text{depth}, Q_{2,center} + \text{depth})$. *Note on the initialization:* The forward pass starts from the point $(Q_{1,center} + \text{depth}, Q_{2,center} + \text{depth})$, so this point needs to have at least a model fitted. In the best case, the greedy exploration will have visited this point. But if the point has not been visited, a model will be fitted from a spectral initialization (i.e the block memberships is computed by using a spectral clustering). From this point, the next model will have at least one predecessor and the procedure can iterate.

Backward pass The backward pass consists for a model at (Q_1, Q_2) to compute the possible merges from the block memberships of its “predecessors“. The predecessors are the point at the right $(Q_1 + 1, Q_2)$ and on top $(Q_1, Q_2 + 1)$ of the current model (if the predecessors exist). To update the current model, we take its predecessors block memberships and try to merge two blocks in one. Then the current model is fitted using this clustering as a starting clustering. Once all the possible merges are fitted, they are compared, keeping the best, in the sense of the BIC-L. If a model was already present it is also compared and the best is chosen

as the model for this round at (Q_1, Q_2) .

The procedure then repeats for the point at $(Q_1 - 1, Q_2)$ until it reaches $(Q_{1,center} - depth, Q_2)$ from which it repeats from $(Q_{1,center} - depth, Q_2 - 1)$. This repeats until computing the best model for $(Q_{1,center} - depth, Q_{2,center} - depth)$. *Note on the initialization:* The backward pass starts from $(Q_{1,center} + depth, Q_{2,center} + depth)$, we know it was initialized at least by the forward pass, no special case here.

At the end of the moving window pass, the model of max BIC-L is the new best fit and the procedure can repeat until convergence.

2.6 Networks clustering

As in Chabert-Liddell et al., 2024 we use a recursive algorithm to determine the best clustering of the given networks. The procedure being the same, we will present it briefly and focus on adjustments.

When networks in a collection do not share the same mesoscale connectivity structure we want to be able to partition them correctly. For this we perform a clustering of networks.

The process of clustering a collection of networks involves discovering a partition $\mathcal{G} = (\mathcal{M}_g)_{g=1,\dots,G}$ of $\{1, \dots, M\}$. Given \mathcal{G} we set the following model on \mathbf{X} :

$$\forall g \in \{1, \dots, G\}, \forall m \in \mathcal{M}_g, X^m \sim \mathcal{F}\text{-BiSBM}(Q_1^g, Q_2^g, \boldsymbol{\pi}^m, \boldsymbol{\rho}^m, \boldsymbol{\alpha}^g)$$

And we defined the score of a given partition \mathcal{G} :

$$Sc(\mathcal{G}) = \sum_{g=1}^G \max_{Q^g=1,\dots,Q_{\max}} \text{BIC-L}((X^m)_{m \in \mathcal{M}_g}, Q_1^g, Q_2^g)$$

Thus the score consists of the sum of the BIC-L of the sub-collections for the partition \mathcal{G} .

2.6.1 Dissimilarity between two networks

The parameters for the dissimilarity are defined as follow:

$$\begin{aligned} \tilde{n}_{qr}^m &= \sum_{i=1}^{n_1^m} \sum_{j=1}^{n_2^m} \hat{\tau}_{iq}^{1,m} \hat{\tau}_{jr}^{2,m}, & \tilde{\alpha}_{qr}^m &= \frac{\sum_{i=1}^{n_1^m} \sum_{j=1}^{n_2^m} \hat{\tau}_{iq}^{1,m} \hat{\tau}_{jr}^{2,m} X_{ij}^m}{\tilde{n}_{qr}^m}, \\ \tilde{\pi}_q^m &= \frac{\sum_{i=1}^{n_1^m} \hat{\tau}_{iq}^{1,m}}{n_1^m}, & \tilde{\rho}_r^m &= \frac{\sum_{j=1}^{n_2^m} \hat{\tau}_{jr}^{2,m}}{n_2^m}. \end{aligned}$$

And the pairwise dissimilarity for networks $(m, m') \in \mathcal{M}^2$ is then:

$$D_{\mathcal{M}}(m, m') = \sum_{q=1}^{Q_1} \sum_{r=1}^{Q_2} \max(\tilde{\pi}_q^m, \tilde{\pi}_q^{m'}) \left(\tilde{\alpha}_{qr}^m - \tilde{\alpha}_{qr}^{m'} \right)^2 \max(\tilde{\rho}_r^m, \tilde{\rho}_r^{m'})$$

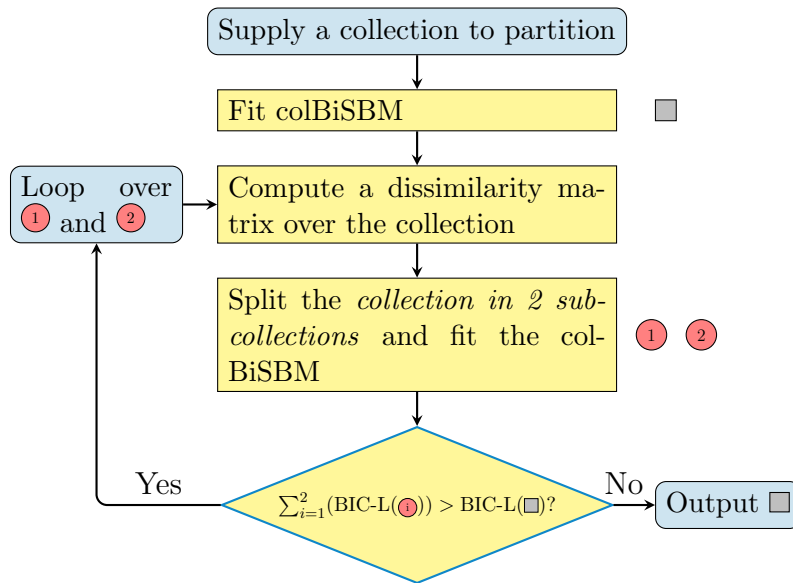


Figure 2.2: Network clustering procedure

The above figure (2.2) shows a condensed explanation of the network clustering algorithm.

The idea is to adjust the colBiSBM model over the full collection of M networks and then compute the dissimilarity matrix between all networks of the collection. We obtain the collection $\mathcal{G} = \{\mathcal{M}\}$ the trivial partition in a unique group.

Then using the *Kmeans* we split the collection in two sub-collections with the dissimilarity matrix. The two sub-collections are fitted and we compute the score of this new partition $\mathcal{G}^* = \{G_1, G_2\}$.

If $Sc(\mathcal{G}^*) > Sc(\mathcal{G})$ then we repeat the same procedure on G_1 and G_2 . Else we return \mathcal{G} .

We illustrate our capacity to perform a partition of a collection for all colBiSBM models in

2.7 Model identifiability

Chabert-Liddell et al., 2024; Celisse et al., 2012; Keribin et al., 2015

Simulation studies

The below simulations are meant to test the capacities of our models. We assess the inference capacities of the algorithm and method, the model selection performances and the clustering capacities.

Reproducibility All the codes used to obtain data and to perform the analysis can be found on the report repository at <https://gitea.polarolouis.fr/polarolouis/mia-stage-2024>.

3.1 Efficiency of the inference

The goal here is to assess the quality of the inference procedure.

Simulation settings For this simulation the data is simulated with $M = 2, n_1^m = 120, n_2^m = 120, Q_1 = Q_2 = 4, \alpha, \pi$ and ρ are set as follows:

$$\alpha = .25 + \begin{pmatrix} 3\epsilon_\alpha & 2\epsilon_\alpha & \epsilon_\alpha & -\epsilon_\alpha \\ 2\epsilon_\alpha & 2\epsilon_\alpha & -\epsilon_\alpha & \epsilon_\alpha \\ \epsilon_\alpha & -\epsilon_\alpha & \epsilon_\alpha & 2\epsilon_\alpha \\ -\epsilon_\alpha & \epsilon_\alpha & 2\epsilon_\alpha & 0 \end{pmatrix},$$

$$\begin{aligned} \pi^1 &= \sigma_1 (0.2 \ 0.4 \ 0.4 \ 0), & \pi^2 &= (0.25 \ 0.25 \ 0.25 \ 0.25), \\ \rho^1 &= (0.25 \ 0.25 \ 0.25 \ 0.25), & \rho^2 &= \sigma_2 (0 \ 0.33 \ 0.33 \ 0.33), \end{aligned}$$

with ϵ_α taking nine equally spaced values ranging from 0 to 0.24. For each value of ϵ_α , 108 datasets (X_1, X_2) are simulated, resulting in $9 \times 108 = 972$ datasets. More precisely, for each dataset, we pick uniformly at random two permutations of $\{1, \dots, 4\}$ (σ_1, σ_2) with the constraint that $\sigma_1(4) \neq \sigma_2(1)$. This ensures that each of the two networks have a non-empty block that is empty in the other one. Then the networks are simulated with $\mathcal{B}ern-BiSBM_{120,120}(Q_1 = 4, Q_2 = 4, \alpha, \pi^m, \rho^m)$ with the previous parameters. Each network has 2 blocks in common and their connectivity structures encompass a mix of core-periphery, assortative community and dis-assortative community structures, depending on which 3 of the 4 blocks are selected for each network. ϵ_α represents the strength of these structures, the larger, the easier it is to tell apart one block from another. The true model of all the simulation is a $\pi\rho$ -colBiSBM.

Inference We want to measure the quality of the inference procedure, for this we use the inference described in the section 2.4.

Quality indicators To assess the quality of the inference, we will use the following indicators:

- First, for each dataset, we put in competition π -colBiSBM with *sep-BiSBM*, *iid*-colBiSBM, ρ -colBiSBM, $\pi\rho$ -colBiSBM respectively. To do so, for each dataset, we compute the BIC-L of each model π -colBiSBM is preferred to *sep-BiSBM* (resp. *iid*-colBiSBM, ρ -colBiSBM, $\pi\rho$ -colBiSBM) if its BIC-L is greater.
- When considering our colBiSBM models we compare $\widehat{Q}_1, \widehat{Q}_2$ to their true values. ($Q_1 = 4$ and $Q_2 = 4$)
- Finally, we assess the quality of the node grouping by computing the Adjusted Rand Index (Hubert & Arabie, 1985), $\text{ARI} = 0$ for a random grouping, $\text{ARI} = 1$ for a perfect match between groupings¹. For each network, for the π -colBiSBM, ρ -colBiSBM, $\pi\rho$ -colBiSBM we compare the inferred block memberships to the real ones by computing the mean of the ARI per axis over the two networks

$$\overline{\text{ARI}}_d = \frac{1}{2}(\text{ARI}(\widehat{\mathbf{Z}}_d^1, \mathbf{Z}_d^1) + \text{ARI}(\widehat{\mathbf{Z}}_d^2, \mathbf{Z}_d^2)),$$

where d is the dimension or axis (i.e., rows, $d = 1$, or columns, $d = 2$) of the block memberships. And we compute the ARI of the whole set of nodes to account for block pairing between networks

$$\text{ARI}_d = \text{ARI}((\widehat{\mathbf{Z}}_d^1, \widehat{\mathbf{Z}}_d^2), (\mathbf{Z}_d^1, \mathbf{Z}_d^2)).$$

All these quality indicators are averaged over the 108 datasets. The results are provided in the tables A.2 to A.5. Each line corresponds to the 108 datasets for a given value of ϵ_α . Graphical representation of some results are shown on figures 3.1 and 3.2.

¹Please note that even if Rand Index can only yield values between 0 and 1, ARI can return negative values if the RI is less than the expected value. This indicates a structure in grouping discordance.

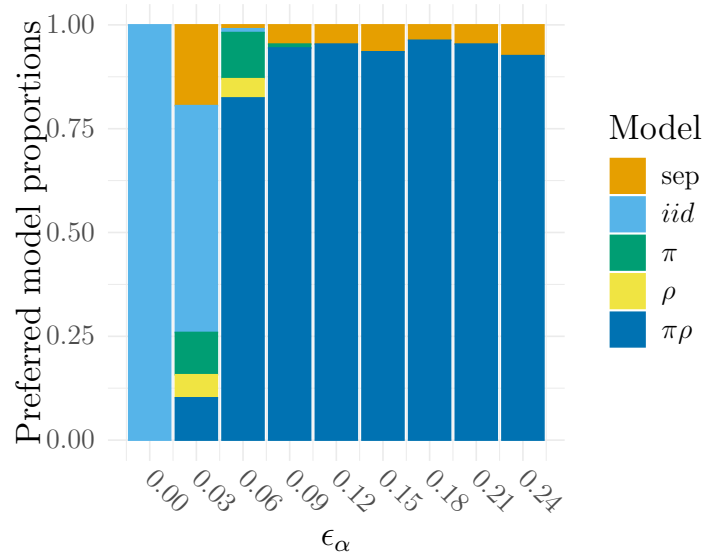


Figure 3.1: Preferred model proportions over all datasets in function of ϵ_α

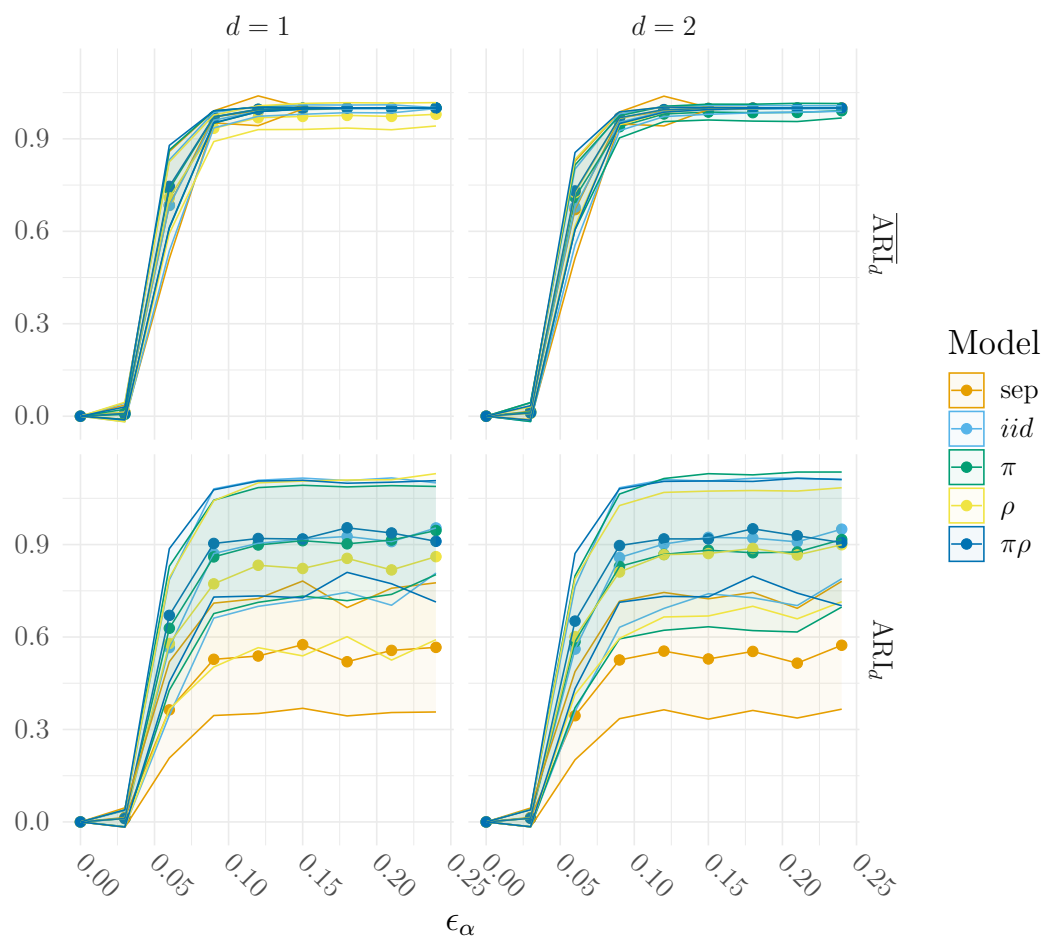


Figure 3.2: Plot of the ARI quality indicators in function of ϵ_α

Results For the model comparison, when ϵ_α is small ($\epsilon_\alpha \in [0, .04]$), the simulation model is close to the Erdős-Reñyi network, and it is very hard to find any structure beyond the one of a single block on each dimension.

On the figure 3.1 one can see that from $\epsilon_\alpha = 0.06$ around 70% of the time the $\pi\rho$ -colBiSBM model (i.e., the correct one) is selected.

An interesting result we can read in the tables is that our models outperform the *sep-BiSBM* when considering the ARI on the whole set of nodes (ARI_d). This means that our models are able to recover the block pairing *between the networks* in addition to recovering the blocks and their parameters.

3.2 Capacity to distinguish $\pi\rho$ -colBiSBM from *iid*-colBiSBM and other models

The idea of this model selection simulations is to assess how the model select the correct colBiSBM model among the possible ones: *iid*, π , ρ , $\pi\rho$. This difference being based on the row and col block proportions.

Simulation settings For this task we choose the same simulation settings as Chabert-Liddell et al., 2024.

Namely, $n_1^m = 90$, $n_2^m = 90$, $Q_1 = Q_2 = 3$, α , π and ρ are set as follows:

$$\alpha = .25 + \begin{pmatrix} 3\epsilon_\alpha & 2\epsilon_\alpha & \epsilon_\alpha \\ 2\epsilon_\alpha & 2\epsilon_\alpha & -\epsilon_\alpha \\ \epsilon_\alpha & -\epsilon_\alpha & \epsilon_\alpha \end{pmatrix}, \quad \pi^1 = \left(\frac{1}{3}, \frac{1}{3}, \frac{1}{3}\right), \quad \pi^2 = \sigma\left(\frac{1}{3} - \epsilon_\pi, \frac{1}{3}, \frac{1}{3} + \epsilon_\pi\right), \\ \rho^1 = \left(\frac{1}{3}, \frac{1}{3}, \frac{1}{3}\right), \quad \rho^2 = \sigma\left(\frac{1}{3} - \epsilon_\rho, \frac{1}{3}, \frac{1}{3} + \epsilon_\rho\right),$$

with $\epsilon_\alpha = 0.16$, ϵ_π and ϵ_ρ taking 9 values equally spaced in $[0, .28]$.

We simulate 324 different collections for each value of ϵ_π and ϵ_ρ .

$\pi\rho$ -colBiSBM, π -colBiSBM, ρ -colBiSBM, *iid*-colBiSBM and *sep-BiSBM* are put in competition and the model with the greater BIC-L is selected as the *preferred model*.

When $\epsilon_\pi = 0$, $\pi^1 = \pi^2$, $\epsilon_\rho = 0$ and $\rho^1 = \rho^2$, the generated collection is an *iid*-colBiSBM. When $\epsilon_\pi > 0$ or $\pi^1 \neq \pi^2$, the model is a π -colBiSBM. When $\epsilon_\rho > 0$ or $\rho^1 \neq \rho^2$, the model is a ρ -colBiSBM. Finally, when $\epsilon_\pi > 0$ or $\pi^1 \neq \pi^2$ and $\epsilon_\rho > 0$ or $\rho^1 \neq \rho^2$, the model is a $\pi\rho$ -colBiSBM.

Results On the figure 3.3 and table A.6, one can see that there is a turning point around $\epsilon_\pi = 0.2$ (resp. $\epsilon_\rho = 0.2$), before which *iid*-colBiSBM and ρ -colBiSBM (resp. π -colBiSBM) are selected very often and after 0.2 the π -colBiSBM (resp. ρ -colBiSBM) and $\pi\rho$ -colBiSBM gets more and more selected. Moreover, the number of blocks are correctly detected in most of the case. These two results highlight our capacity to recover the simulated structure.

As ϵ_π and ϵ_ρ need to be above 0.2 to see $\pi\rho$ model being preferred this may indicate the need of a strong difference between blocks to select this model.

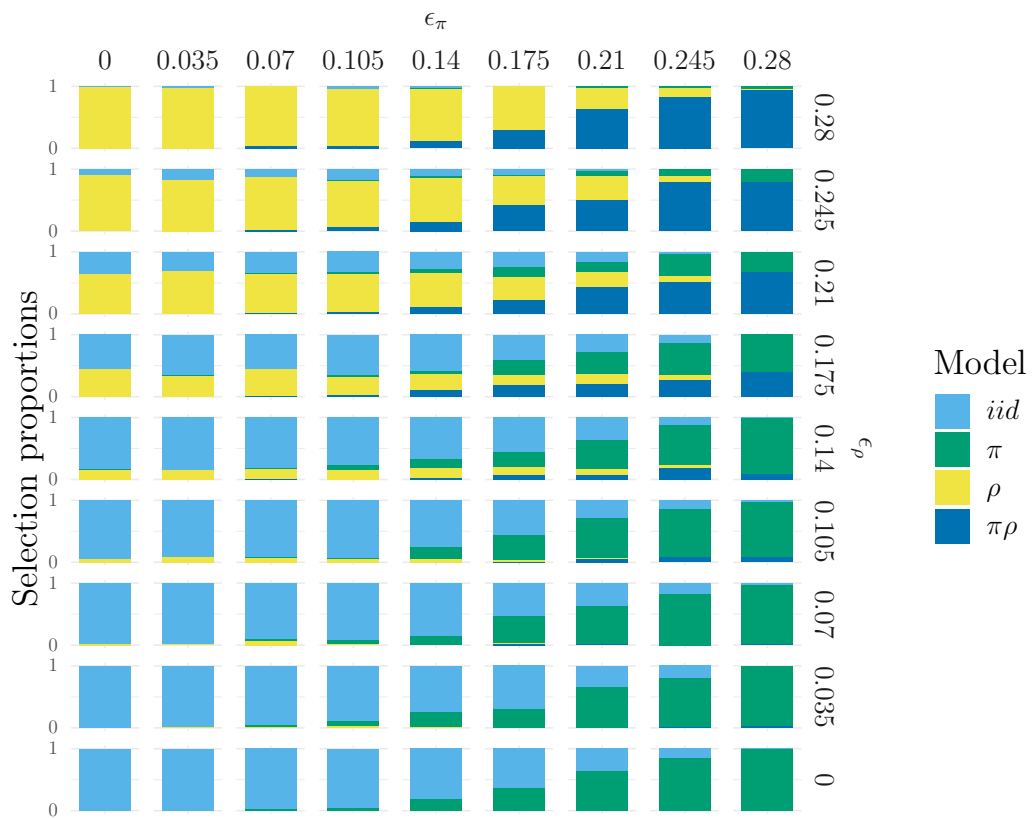


Figure 3.3: Plot of model selection proportions over the different datasets in function of ϵ_π and ϵ_ρ

3.3 Network clustering of simulated networks

Simulation settings For all models we simulate $M = 9$ networks with $\forall m \in \{1 \dots M\}, n_1^m = n_2^m = 75$ with $Q_1 = Q_2 = 3$.

For the simulations the proportions are the following:

$$\boldsymbol{\pi}^1 = (0.2, 0.3, 0.5) \qquad \boldsymbol{\rho}^1 = (0.2, 0.3, 0.5)$$

and for all $m = 2, \dots, 9$

$$\boldsymbol{\pi}^m = \begin{cases} \boldsymbol{\pi}^1 & \text{for } iid\text{-colBiSBM} \\ \sigma_1^m(\boldsymbol{\pi}^1) & \text{for } \pi\text{-colBiSBM and } \pi\rho\text{-colBiSBM} \end{cases}$$

$$\boldsymbol{\rho}^m = \begin{cases} \boldsymbol{\rho}^1 & \text{for } iid\text{-colBiSBM} \\ \sigma_2^m(\boldsymbol{\rho}^1) & \text{for } \rho\text{-colBiSBM and } \pi\rho\text{-colBiSBM} \end{cases}$$

where σ_1^m and σ_2^m are permutations of $\{1, 2, 3\}$ proper to network m and $\sigma_1(\boldsymbol{\pi}) = (\pi_{\sigma_1(i)})_{i=\{1,\dots,3\}}$ and $\sigma_2(\boldsymbol{\rho}) = (\rho_{\sigma_2(i)})_{i=\{1,\dots,3\}}$.

The networks are divided into 3 sub-collections of 3 networks with connectivity parameters as follows:

$$\boldsymbol{\alpha}^{as} = .3 + \begin{pmatrix} \epsilon & -\frac{\epsilon}{2} & -\frac{\epsilon}{2} \\ -\frac{\epsilon}{2} & \epsilon & -\frac{\epsilon}{2} \\ -\frac{\epsilon}{2} & -\frac{\epsilon}{2} & \epsilon \end{pmatrix}, \qquad \boldsymbol{\alpha}^{dis} = .3 + \begin{pmatrix} -\frac{\epsilon}{2} & \epsilon & \epsilon \\ \epsilon & -\frac{\epsilon}{2} & \epsilon \\ \epsilon & \epsilon & -\frac{\epsilon}{2} \end{pmatrix},$$

$$\boldsymbol{\alpha}^{cp} = .3 + \begin{pmatrix} \frac{3\epsilon}{2} & \epsilon & \frac{\epsilon}{2} \\ \epsilon & \frac{\epsilon}{2} & 0 \\ \frac{\epsilon}{2} & 0 & -\frac{\epsilon}{2} \end{pmatrix}$$

with $\epsilon \in [.1, .4]$. $\boldsymbol{\alpha}^{as}$ represents a classical assortative community structure, while $\boldsymbol{\alpha}^{cp}$ is a layered core-periphery structure with block 2 acting as a semi-core. Finally, $\boldsymbol{\alpha}^{dis}$ is a dis-assortative community structure with stronger connections between blocks than within blocks. If $\epsilon = 0$, the three matrices are equal and the 9 networks have the same connection structure. Increasing ϵ differentiates the 3 sub-collections of networks.

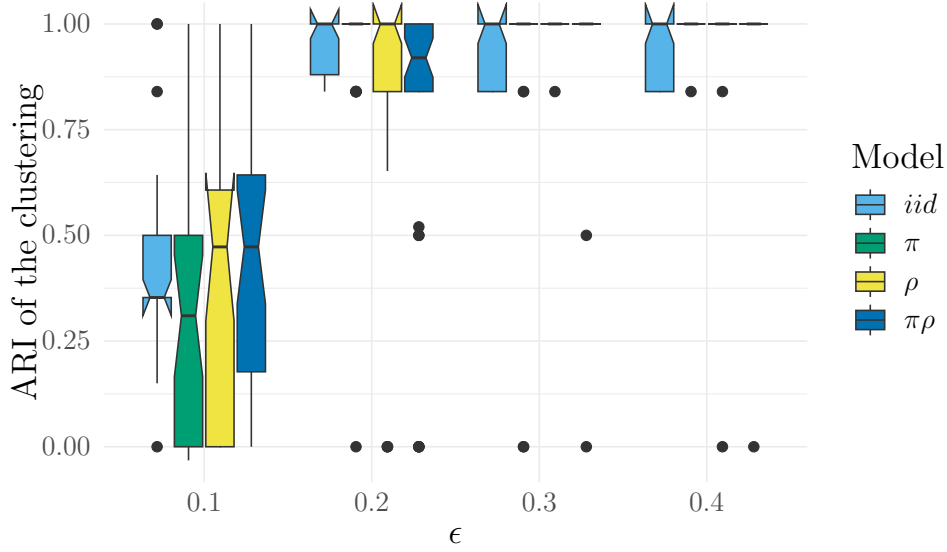


Figure 3.4: ARI obtained for the clustering with the different models in function of ϵ

Results The evaluation of our method involves a comparison between the resulting partition of the network collection and the simulated partition using the ARI index. As the value of ϵ increases, our ability to distinguish between the networks improves, and this distinction becomes nearly perfect in all setups of the colBiSBM.

3.4 Information transfer between networks

One of the motivation for collections of networks is *information transfer* between the networks, allowing robustness to missing data and enabling the finding of finer structures in small networks with the help of bigger ones.

Simulation settings We want to compare the performance of retrieving the nodes blocks with missing edges (that are labeled as NA in the incidence matrix).

For this purpose we generate collections of networks with the following parameters:

$$\boldsymbol{\pi}^m = \begin{cases} \boldsymbol{\pi} = (0.5, 0.3, 0.2) & \text{for } iid\text{-colBiSBM} \\ \sigma_1^m(\boldsymbol{\pi}) & \text{for } \pi\text{-colBiSBM and } \pi\rho\text{-colBiSBM} \end{cases}$$

$$\boldsymbol{\rho}^m = \begin{cases} \boldsymbol{\rho} = (0.5, 0.3, 0.2) & \text{for } iid\text{-colBiSBM} \\ \sigma_2^m(\boldsymbol{\rho}) & \text{for } \rho\text{-colBiSBM and } \pi\rho\text{-colBiSBM,} \end{cases}$$

for the block proportions, and two different structures with the corresponding $\boldsymbol{\alpha}$,

$$\boldsymbol{\alpha}^{modular} = \begin{pmatrix} 0.9 & 0.05 & 0.05 \\ 0.05 & 0.2 & 0.05 \\ 0.05 & 0.05 & 0.8 \end{pmatrix}, \boldsymbol{\alpha}^{nested} = \begin{pmatrix} 0.9 & 0.25 & 0.1 \\ 0.3 & 0.15 & 0.05 \\ 0.1 & 0.05 & 0.05 \end{pmatrix},$$

where $\alpha^{modular}$ represents networks where there are look-a-like communities, which tends to interact preferentially within the community and less with the other communities. And α^{nested} represents a common structure detected in ecology with generalist and specialist species and a “nested” structure.

The collections contain two networks ($M = 2$) of size $n_1^{m=1} = n_2^{m=1} = 40$ and $n_1^{m=2} = n_2^{m=2} = 120$. One collection is generated for each colBiSBM model. And the nodes block memberships (i.e., the row and column blocks they belong to) are saved.

Per colBiSBM model, 10 collections are generated and their results are averaged.

In the network $m = 1$ (i.e., the smaller one) a proportion of the edges p_{NA} see their values replaced by NAs, the “forgotten” values are stored.

Test procedure A LBM is fitted on the first network, and the predicted block memberships are saved, along with the predicted links using the inferred parameters. This will serve as a baseline to see if the use of the collection benefits the predictions.

A colBiSBM model is then fitted (with a model matching the dataset considered) and we store the same predictions.

Quality metrics To benchmark the performance we use the *Area Under the Curve* (AUC) for predicted versus real link values and the ARI for predicted versus real block memberships.

For the comparison we subtract the metric given by the LBM to the one given by colBiSBM and denote it Δ metric.

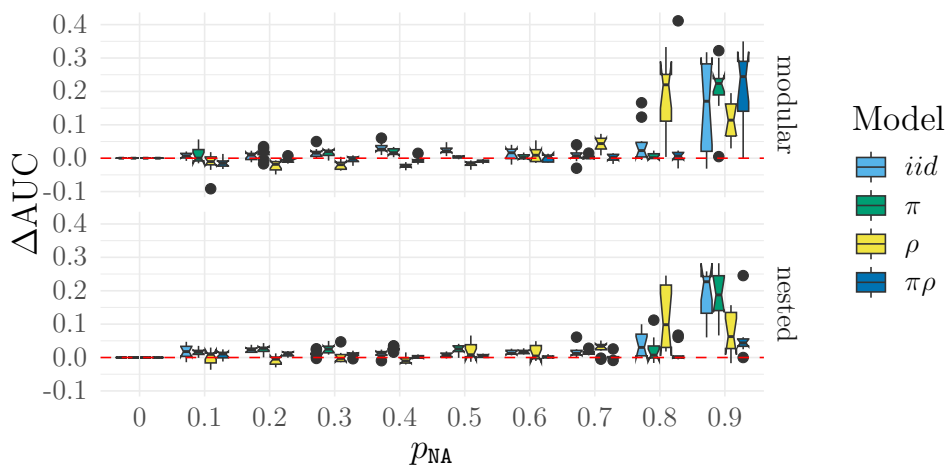


Figure 3.5: Δ AUC in function of p_{NA} . The dashed red lines indicate the value 0 for which $AUC_{LBM} = AUC_{colBiSBM}$

Results On figure 3.5 one can see that overall the nested structure seems to be the one benefitting most from the collection model having generally slightly higher Δ AUC than the modular one. But in general it seems that for $\epsilon \in [0.1, 0.7]$ there

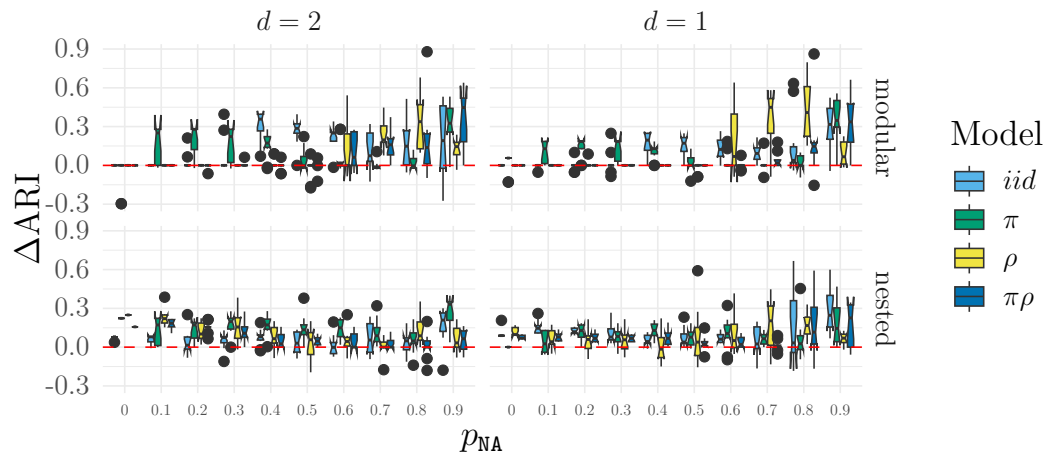


Figure 3.6: ΔARI in function of p_{NA} . The dashed red lines indicate the value 0 for which $\text{ARI}_{\text{LBM}} = \text{ARI}_{\text{colBiSBM}}$

are no clear differences between LBM and colBiSBM regarding link prediction. For $\epsilon \in [0.8, 0.9]$ this is where the collection model seems to be most effective.

For the ARI, figure 3.6 suggests that collection model does at least as well as LBM and improves nodes memberships recovery for modular structure starting from $\epsilon = 0.7$. Again, nested structure benefits of collection model for smaller ϵ values but those increase in ΔARI are also smaller than what can be observed for modular structure.

CHAPTER **4**

Applications on ecological networks

Conclusions and future work

5.1 Conclusion

5.2 Future work

Identifiability As stated in section 2.7, we only have identifiability for the *iid*-colBiSBM and we will work on establishing identifiability for π , ρ and $\pi\rho$ models.

Finding a trade-off between *iid* and $\pi\rho$ We observed while testing clustering with the different models that the π , ρ and $\pi\rho$ model, with their increased number of parameters for block memberships parameters tends to give smaller BIC-L criterion values while having a higher Evidence Lower Bound than the *iid*. This arises because of the penalties on the block memberships and support that increase significantly and exceeds the gain on the ELBO and the diminution of the connectivity parameters. An idea to tackle this problem could be to suppose that the block memberships for network m are themselves the realizations of random variables and thus introduce sort of a mixed effect model.

Comparison to other graphs clustering methods Recent work have been comparing colSBM (Chabert-Liddell et al., 2024) and graphclust (Rebafka, 2023) assessing various capabilities of the models and particularly focusing on networks clustering. We will reproduce and adapt the analysis to test other simulation settings that were not considered in this work.

Thank you for reading this work

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Supplementary for Simulation studies

Below are the supplementary material for the Simulation studies.

A.1 Supplementary for Efficiency of the inference

The tables A.2 to A.5 show detailed results for the inference of the model detailed in this section.

Table A.1: Inference results for *sep*

(a) Quality metrics for *sep*-BiSBM

ϵ_α	$\overline{\text{ARI}}_1$	$\overline{\text{ARI}}_2$	ARI_1	ARI_2
0.00	0	0	0	0
0.03	0.01	0.02	0.01	0.01
0.06	0.68 ± 0.02	0.67 ± 0.02	0.36 ± 0.02	0.34 ± 0.01
0.09	0.97	0.97	0.53 ± 0.02	0.53 ± 0.02
0.12	0.99	0.99	0.54 ± 0.02	0.55 ± 0.02
0.15	1	1	0.58 ± 0.02	0.53 ± 0.02
0.18	1	1	0.52 ± 0.02	0.55 ± 0.02
0.21	1	1	0.56 ± 0.02	0.52 ± 0.02
0.24	1	1	0.57 ± 0.02	0.57 ± 0.02

Table A.2: Inference results for *iid*(a) Quality metrics for *iid*-colBiSBM

ϵ_α	$\overline{\text{ARI}}_1$	$\overline{\text{ARI}}_2$	ARI_1	ARI_2
0.00	0	0	0	0
0.03	0.01	0.01	0.01	0.01
0.06	0.68 ± 0.01	0.68 ± 0.01	0.57 ± 0.02	0.56 ± 0.02
0.09	0.96	0.95	0.87 ± 0.02	0.86 ± 0.02
0.12	0.99	0.99	0.9 ± 0.02	0.9 ± 0.02
0.15	0.99	0.99	0.92 ± 0.02	0.92 ± 0.02
0.18	1	1	0.93 ± 0.02	0.92 ± 0.02
0.21	1	1	0.91 ± 0.02	0.91 ± 0.02
0.24	1	1	0.95 ± 0.01	0.95 ± 0.02

(b) Bloc recovery for *iid*-colBiSBM

ϵ_α	$\mathbb{1}_{\widehat{Q}_1 < Q_1}$	$\mathbb{1}_{\widehat{Q}_1 = Q_1}$	$\mathbb{1}_{\widehat{Q}_1 > Q_1}$	$\mathbb{1}_{\widehat{Q}_2 < Q_2}$	$\mathbb{1}_{\widehat{Q}_2 = Q_2}$	$\mathbb{1}_{\widehat{Q}_2 > Q_2}$
0.00	1	0	0	1	0	0
0.03	1	0	0	1	0	0
0.06	0.31 ± 0.04	0.69 ± 0.04	0	0.45 ± 0.05	0.55 ± 0.05	0
0.09	0	0.96 ± 0.02	0.04 ± 0.02	0	0.98 ± 0.01	0.02 ± 0.01
0.12	0	0.88 ± 0.03	0.12 ± 0.03	0	0.94 ± 0.02	0.06 ± 0.02
0.15	0	0.94 ± 0.02	0.06 ± 0.02	0	0.91 ± 0.03	0.09 ± 0.03
0.18	0	0.92 ± 0.03	0.08 ± 0.03	0	0.94 ± 0.02	0.06 ± 0.02
0.21	0	0.88 ± 0.03	0.12 ± 0.03	0	0.88 ± 0.03	0.12 ± 0.03
0.24	0	0.94 ± 0.02	0.06 ± 0.02	0	0.97 ± 0.02	0.03 ± 0.02

Table A.3: Inference results for π (a) Quality metrics for π -colBiSBM

ϵ_α	$\overline{\text{ARI}}_1$	$\overline{\text{ARI}}_2$	ARI_1	ARI_2
0.00	0	0	0	0
0.03	0.01	0.01	0.01	0.01
0.06	0.74 ± 0.01	0.71 ± 0.01	0.63 ± 0.02	0.58 ± 0.02
0.09	0.97	0.94	0.86 ± 0.02	0.83 ± 0.02
0.12	1	0.98	0.9 ± 0.02	0.87 ± 0.02
0.15	1	0.99	0.91 ± 0.02	0.88 ± 0.02
0.18	1	0.98	0.9 ± 0.02	0.87 ± 0.02
0.21	1	0.99	0.91 ± 0.02	0.88 ± 0.02
0.24	1	0.99	0.95 ± 0.01	0.92 ± 0.02

(b) Bloc recovery for π -colBiSBM

ϵ_α	$\mathbb{1}_{\widehat{Q}_1 < Q_1}$	$\mathbb{1}_{\widehat{Q}_1 = Q_1}$	$\mathbb{1}_{\widehat{Q}_1 > Q_1}$	$\mathbb{1}_{\widehat{Q}_2 < Q_2}$	$\mathbb{1}_{\widehat{Q}_2 = Q_2}$	$\mathbb{1}_{\widehat{Q}_2 > Q_2}$
0.00	1	0	0	1	0	0
0.03	1	0	0	1	0	0
0.06	0.09 ± 0.03	0.64 ± 0.05	0.27 ± 0.04	0.36 ± 0.05	0.64 ± 0.05	0
0.09	0	0.63 ± 0.05	0.37 ± 0.05	0	1	0
0.12	0	0.76 ± 0.04	0.24 ± 0.04	0	1	0
0.15	0	0.8 ± 0.04	0.2 ± 0.04	0	1	0
0.18	0	0.77 ± 0.04	0.23 ± 0.04	0	1	0
0.21	0	0.81 ± 0.04	0.19 ± 0.04	0	1	0
0.24	0	0.87 ± 0.03	0.13 ± 0.03	0	1	0

Table A.4: Inference results for ρ (a) Quality metrics for ρ -colBiSBM

ϵ_α	$\overline{\text{ARI}}_1$	$\overline{\text{ARI}}_2$	ARI_1	ARI_2
0.00	0	0	0	0
0.03	0.01	0.01	0.01	0.01
0.06	0.71 ± 0.01	0.73 ± 0.01	0.58 ± 0.02	0.6 ± 0.02
0.09	0.93	0.97	0.77 ± 0.03	0.81 ± 0.02
0.12	0.97	0.99	0.83 ± 0.03	0.87 ± 0.02
0.15	0.97	1	0.82 ± 0.03	0.87 ± 0.02
0.18	0.98	1	0.86 ± 0.02	0.89 ± 0.02
0.21	0.97	1	0.82 ± 0.03	0.87 ± 0.02
0.24	0.98	1	0.86 ± 0.03	0.9 ± 0.02

(b) Bloc recovery for ρ -colBiSBM

ϵ_α	$\mathbb{1}_{\widehat{Q}_1 < Q_1}$	$\mathbb{1}_{\widehat{Q}_1 = Q_1}$	$\mathbb{1}_{\widehat{Q}_1 > Q_1}$	$\mathbb{1}_{\widehat{Q}_2 < Q_2}$	$\mathbb{1}_{\widehat{Q}_2 = Q_2}$	$\mathbb{1}_{\widehat{Q}_2 > Q_2}$
0.00	1	0	0	1	0	0
0.03	1	0	0	1	0	0
0.06	0.29 ± 0.04	0.71 ± 0.04	0	0.06 ± 0.02	0.63 ± 0.05	0.31 ± 0.04
0.09	0	1	0	0	0.56 ± 0.05	0.44 ± 0.05
0.12	0	1	0	0	0.67 ± 0.05	0.33 ± 0.05
0.15	0	1	0	0	0.7 ± 0.04	0.3 ± 0.04
0.18	0	1	0	0	0.71 ± 0.04	0.29 ± 0.04
0.21	0	1	0	0	0.69 ± 0.04	0.31 ± 0.04
0.24	0	1	0	0	0.76 ± 0.04	0.24 ± 0.04

Table A.5: Inference results for $\pi\rho$ (a) Quality metrics for $\pi\rho$ -colBiSBM

ϵ_α	$\overline{\text{ARI}}_1$	$\overline{\text{ARI}}_2$	ARI_1	ARI_2
0.00	0	0	0	0
0.03	0.01	0.01	0.01	0.01
0.06	0.75 ± 0.01	0.73 ± 0.01	0.67 ± 0.02	0.65 ± 0.02
0.09	0.97	0.97	0.9 ± 0.02	0.9 ± 0.02
0.12	1	0.99	0.92 ± 0.02	0.92 ± 0.02
0.15	1	1	0.92 ± 0.02	0.92 ± 0.02
0.18	1	1	0.95 ± 0.01	0.95 ± 0.01
0.21	1	1	0.94 ± 0.02	0.93 ± 0.02
0.24	1	1	0.91 ± 0.02	0.91 ± 0.02

(b) Bloc recovery for $\pi\rho$ -colBiSBM

ϵ_α	$\mathbb{1}_{\widehat{Q}_1 < Q_1}$	$\mathbb{1}_{\widehat{Q}_1 = Q_1}$	$\mathbb{1}_{\widehat{Q}_1 > Q_1}$	$\mathbb{1}_{\widehat{Q}_2 < Q_2}$	$\mathbb{1}_{\widehat{Q}_2 = Q_2}$	$\mathbb{1}_{\widehat{Q}_2 > Q_2}$
0.00	1	0	0	1	0	0
0.03	1	0	0	1	0	0
0.06	0.1 ± 0.03	0.88 ± 0.03	0.02 ± 0.01	0.11 ± 0.03	0.89 ± 0.03	0
0.09	0	0.92 ± 0.03	0.08 ± 0.03	0	0.88 ± 0.03	0.12 ± 0.03
0.12	0	0.9 ± 0.03	0.1 ± 0.03	0	0.89 ± 0.03	0.11 ± 0.03
0.15	0	0.87 ± 0.03	0.13 ± 0.03	0	0.9 ± 0.03	0.1 ± 0.03
0.18	0	0.94 ± 0.02	0.06 ± 0.02	0	0.93 ± 0.03	0.07 ± 0.03
0.21	0	0.93 ± 0.03	0.07 ± 0.03	0	0.88 ± 0.03	0.12 ± 0.03
0.24	0	0.87 ± 0.03	0.13 ± 0.03	0	0.86 ± 0.03	0.14 ± 0.03

A.2 Supplementary for Capacity to distinguish models

The table A.6 present the results discussed in section 3.2 For the block number recovery part, the *minimum* values are in **bold** as they indicate conditions for which all the different models did not recovered the correct structure.

For the model proportion part of the table, the *maximum* values are in **bold** and highlight the model that was selected the most among the conditions.

Please note that blank space indicates that among all conditions the corresponding model was not selected at all.

Table A.6: Filtered block recovery and model selection proportions

		Block number recovery								Model selection proportions			
		<i>iid</i>		π		ρ		$\pi\rho$					
ϵ_π	ϵ_ρ	$\mathbb{1}_{\widehat{Q}_{1iid}=3}$	$\mathbb{1}_{\widehat{Q}_{2iid}=3}$	$\mathbb{1}_{\widehat{Q}_{1\pi}=3}$	$\mathbb{1}_{\widehat{Q}_{2\pi}=3}$	$\mathbb{1}_{\widehat{Q}_{1\rho}=3}$	$\mathbb{1}_{\widehat{Q}_{2\rho}=3}$	$\mathbb{1}_{\widehat{Q}_{1\pi\rho}=3}$	$\mathbb{1}_{\widehat{Q}_{2\pi\rho}=3}$	<i>iid</i>	π	ρ	$\pi\rho$
0.000	0.000	1	1	1	1	1	1	1	1	1			
	0.035	1	1	1	1	1	1	1	1	1			
	0.070	1	1	1	1	1	1	1	1	0.981	0.019		
	0.105	1	1	1	1	1	1	1	1	0.944	0.056		
	0.140	1	1	1	1	1	1	1	1	0.833	0.157	0.009	
	0.175	1	1	1	1	1	1	1	1	0.556	0.444		
	0.210	1	1	1	1	1	1	1	1	0.361	0.639		
	0.245	1	1	1	1	1	1	1	1	0.102	0.898		
	0.280	1	0.991	1	1	1	1	1	1	0.009	0.991		
	0.000	1	1	1	1	1	1	1	1	1			
0.035	1	1	1	1	1	1	1	1	0.991	0.009			
0.070	1	1	1	1	1	1	1	1	0.991	0.009			
0.105	1	1	1	1	1	1	1	1	0.917	0.083			
0.140	1	1	1	1	1	1	1	1	0.843	0.157			
0.175	1	1	1	1	1	1	1	1	0.657	0.333	0.009		
0.210	1	1	1	1	1	1	1	1	0.315	0.685			

Table A.6: Filtered block recovery and model selection proportions (*continued*)

0.035		Block number recovery								Model selection proportions			
		<i>iid</i>		π		ρ		$\pi\rho$					
ϵ_π	ϵ_ρ	$\mathbb{1}_{\widehat{Q}_{1iid}=3}$	$\mathbb{1}_{\widehat{Q}_{2iid}=3}$	$\mathbb{1}_{\widehat{Q}_{1\pi}=3}$	$\mathbb{1}_{\widehat{Q}_{2\pi}=3}$	$\mathbb{1}_{\widehat{Q}_{1\rho}=3}$	$\mathbb{1}_{\widehat{Q}_{2\rho}=3}$	$\mathbb{1}_{\widehat{Q}_{1\pi\rho}=3}$	$\mathbb{1}_{\widehat{Q}_{2\pi\rho}=3}$	<i>iid</i>	π	ρ	$\pi\rho$
	0.245	1	1	1	1	1	1	1	1	0.176	0.824		
	0.280	1	1	1	1	1	1	1	1	0.028	0.972		
	0.000	1	1	1	1	1	1	1	1	0.972		0.028	
	0.035	1	1	1	1	1	1	1	1	0.963	0.009	0.028	
	0.070	1	1	1	1	1	1	1	1	0.917	0.065	0.019	
	0.105	1	1	1	1	1	1	1	1	0.917	0.065	0.019	
0.070	0.140	1	1	1	1	1	1	1	1	0.824	0.157	0.009	0.009
	0.175	1	1	1	1	1	1	1	1	0.565	0.426		0.009
	0.210	1	1	1	1	1	1	1	1	0.343	0.639	0.009	0.009
	0.245	1	1	1	1	1	1	0.991	1	0.139	0.843		0.019
	0.280	1	1	1	1	0.991	1	1	1		0.963		0.037
	0.000	1	1	1	1	1	1	1	1	0.963		0.037	
	0.035	1	1	1	1	1	1	1	1	0.898	0.019	0.083	
	0.070	1	1	1	1	1	1	1	1	0.926	0.009	0.065	
	0.105	1	1	1	1	1	1	1	1	0.935	0.056	0.009	
	0.140	1	1	1	1	1	1	1	1	0.778	0.157	0.065	

Table A.6: Filtered block recovery and model selection proportions (*continued*)

		Block number recovery								Model selection proportions				
		<i>iid</i>		π		ρ		$\pi\rho$						
ϵ_ρ	ϵ_ρ	$\mathbb{1}_{\widehat{Q}_{1iid}=3}$	$\mathbb{1}_{\widehat{Q}_{2iid}=3}$	$\mathbb{1}_{\widehat{Q}_{1\pi}=3}$	$\mathbb{1}_{\widehat{Q}_{2\pi}=3}$	$\mathbb{1}_{\widehat{Q}_{1\rho}=3}$	$\mathbb{1}_{\widehat{Q}_{2\rho}=3}$	$\mathbb{1}_{\widehat{Q}_{1\pi\rho}=3}$	$\mathbb{1}_{\widehat{Q}_{2\pi\rho}=3}$	<i>iid</i>	π	ρ	$\pi\rho$	
0.105	0.175	1	1	1	1	1	1	1	1	0.657	0.296	0.028	0.019	
	0.210	1	1	1	1	1	1	1	1	0.324	0.611	0.037	0.028	
	0.245	0.991	1	1	1	1	1	1	1	0.185	0.750	0.009	0.056	
	0.280	1	1	1	1	1	1	1	1	0.046	0.917		0.037	
	0.000	1	1	1	1	1	1	1	1	0.815		0.185		
	0.035	1	1	1	1	1	1	1	1	0.741	0.009	0.250		
	0.070	1	1	1	1	1	1	1	1	0.861		0.139		
	0.105	1	1	1	1	1	1	1	1	0.759	0.056	0.185		
	0.140	0.140	1	1	1	1	1	1	1	1	0.667	0.157	0.157	0.019
		0.175	1	1	1	1	1	1	1	1	0.583	0.269	0.046	0.102
0.210		1	1	1	1	1	1	1	1	0.278	0.546	0.065	0.111	
0.245		1	1	1	1	1	1	1	1	0.111	0.704	0.037	0.148	
0.280		1	0.991	1	1	0.991	1	1	1	0.028	0.852	0.009	0.111	
0.000		1	1	1	1	1	1	1	1	0.630		0.370		
0.035		1	1	1	1	1	1	1	1	0.694		0.306		
0.070		1	1	1	1	1	1	1	1	0.528	0.009	0.444	0.019	

Table A.6: Filtered block recovery and model selection proportions (*continued*)

		Block number recovery								Model selection proportions			
		<i>iid</i>		π		ρ		$\pi\rho$					
ϵ_π	ϵ_ρ	$\mathbb{1}_{\widehat{Q}_{1iid}=3}$	$\mathbb{1}_{\widehat{Q}_{2iid}=3}$	$\mathbb{1}_{\widehat{Q}_{1\pi}=3}$	$\mathbb{1}_{\widehat{Q}_{2\pi}=3}$	$\mathbb{1}_{\widehat{Q}_{1\rho}=3}$	$\mathbb{1}_{\widehat{Q}_{2\rho}=3}$	$\mathbb{1}_{\widehat{Q}_{1\pi\rho}=3}$	$\mathbb{1}_{\widehat{Q}_{2\pi\rho}=3}$	<i>iid</i>	π	ρ	$\pi\rho$
0.175	0.105	1	1	1	1	1	1	1	1	0.574	0.028	0.389	0.009
	0.140	1	0.991	1	1	1	1	1	1	0.556	0.130	0.250	0.065
	0.175	1	1	1	1	1	1	0.991	1	0.417	0.167	0.231	0.185
	0.210	1	1	1	1	1	1	1	1	0.250	0.380	0.157	0.213
	0.245	1	1	1	1	0.991	1	1	1	0.102	0.463	0.019	0.417
	0.280	1	1	1	1	1	1	1	1		0.694	0.009	0.296
0.210	0.000	1	1	1	1	1	1	1	1	0.361		0.639	
	0.035	1	1	1	1	1	1	1	1	0.343		0.657	
	0.070	1	1	1	1	1	1	1	1	0.370	0.009	0.611	0.009
	0.105	0.991	0.991	1	1	1	1	1	1	0.287	0.009	0.648	0.056
	0.140	1	1	1	1	1	1	1	1	0.361	0.083	0.481	0.074
	0.175	0.991	1	1	1	1	1	1	1	0.278	0.167	0.361	0.194
	0.210	1	1	1	1	1	1	1	1	0.157	0.231	0.176	0.435
	0.245	1	1	1	1	1	1	1	1	0.028	0.380	0.093	0.500
0.280	1	0.991	1	0.991	1	1	1	1		0.333	0.037	0.630	
	0.000	1	1	1	1	1	1	1	1	0.148		0.852	

Table A.6: Filtered block recovery and model selection proportions (*continued*)

		Block number recovery								Model selection proportions			
		<i>iid</i>		π		ρ		$\pi\rho$					
ϵ_π	ϵ_ρ	$\mathbb{1}_{\widehat{Q}_{1iid}=3}$	$\mathbb{1}_{\widehat{Q}_{2iid}=3}$	$\mathbb{1}_{\widehat{Q}_{1\pi}=3}$	$\mathbb{1}_{\widehat{Q}_{2\pi}=3}$	$\mathbb{1}_{\widehat{Q}_{1\rho}=3}$	$\mathbb{1}_{\widehat{Q}_{2\rho}=3}$	$\mathbb{1}_{\widehat{Q}_{1\pi\rho}=3}$	$\mathbb{1}_{\widehat{Q}_{2\pi\rho}=3}$	<i>iid</i>	π	ρ	$\pi\rho$
0.245	0.035	0.991	1	1	1	1	1	1	1	0.194		0.796	0.009
	0.070	1	1	1	1	1	1	1	1	0.176		0.824	
	0.105	1	1	1	1	1	1	1	1	0.139	0.009	0.778	0.074
	0.140	1	1	1	1	1	1	1	1	0.120	0.037	0.657	0.185
	0.175	1	1	1	1	0.991	1	1	1	0.139	0.093	0.509	0.259
	0.210	0.991	1	1	1	1	1	1	1	0.028	0.093	0.370	0.509
	0.245	1	1	1	1	1	1	1	1	0.009	0.102	0.102	0.787
	0.280	0.991	1	1	1	0.991	1	1	1	0.009	0.148	0.019	0.824
	0.000	0.991	1	1	1	1	1	0.991	1	0.009		0.991	
	0.035	0.981	1	1	1	1	1	1	1			0.981	0.019
0.070	0.991	1	1	1	1	1	1	1	0.037		0.954	0.009	
0.105	0.991	0.991	1	0.991	1	1	1	0.991	0.028	0.009	0.889	0.074	
0.140	0.991	1	1	1	1	1	0.991	1	0.019		0.889	0.093	
0.175	0.991	1	1	1	1	1	1	1			0.602	0.398	
0.210	0.981	1	1	1	1	1	0.972	1	0.009		0.324	0.667	
0.245	1	1	1	1	1	1	0.991	1	0.009	0.009	0.194	0.787	

Table A.6: Filtered block recovery and model selection proportions (*continued*)

0.280		Block number recovery								Model selection proportions			
		<i>iid</i>		π		ρ		$\pi\rho$					
ϵ_π	ϵ_ρ	$\mathbb{1}_{\widehat{Q}_{1iid}=3}$	$\mathbb{1}_{\widehat{Q}_{2iid}=3}$	$\mathbb{1}_{\widehat{Q}_{1\pi}=3}$	$\mathbb{1}_{\widehat{Q}_{2\pi}=3}$	$\mathbb{1}_{\widehat{Q}_{1\rho}=3}$	$\mathbb{1}_{\widehat{Q}_{2\rho}=3}$	$\mathbb{1}_{\widehat{Q}_{1\pi\rho}=3}$	$\mathbb{1}_{\widehat{Q}_{2\pi\rho}=3}$	<i>iid</i>	π	ρ	$\pi\rho$
	0.280	1	0.991	1	1	1	1	0.991	1		0.019	0.046	0.935