Variational Inference for Stochastic Block Models from Sampled Data

Timothée Tabouy, Pierre Barbillon and Julien Chiquet
UMR MIA-Paris, AgroParisTech, INRA, Université Paris-Saclay, 75005 Paris, France

Abstract
This paper deals with non-observed dyads during the sampling of a network and consecutive issues in the Stochastic Block Model (SBM) inference. We review sampling designs and recover Missing At Random (MAR) and Not Missing At Random (NMAR) conditions for SBM. We introduce several variants of the variational EM (VEM) algorithm for inferring the SBM under various sampling designs (MAR and NMAR) all available as an R package on github at https://github.com/jchiquet/missSBM. Model selection criteria based on Integrated Classification Likelihood (ICL) are derived for selecting both the number of blocks and the sampling design. We investigate the accuracy and the range of applicability of these algorithms with simulations. We finally explore two real-world networks from ethnology (seed circulation network) and biology (protein-protein interaction network), where the interpretations considerably depends on the sampling designs considered.

Stochastic Block Model · Variational inference · Missing data · Sampled network

1 Introduction

Networks arise in many fields of application for providing an intuitive way to represent interactions between entities. In this paper, a network is composed by a fixed set of nodes, and an interaction between a pair of nodes (dyad) is called an edge. We consider unweighted undirected binary networks with no loop, which can be represented by symmetric adjacency matrices filled with zeros and ones.

Various statistical models for networks exist for depicting the probability distribution of the adjacency matrix (see, e.g. Goldenberg et al., 2010 and Snijders, 2011) for a survey). A highly desirable feature is their capability to describe the heterogeneity of real world networks. In this perspective, the family of models endowed with a latent structure (reviewed in Matias and Robin, 2014) offers a natural way to introduce heterogeneity. Within this family the Stochastic Block Model (in short SBM, see Frank and Harary, 1982 and Holland et al., 1983), describes a broad variety of network topologies by positing a latent structure (or a clustering) on nodes, then making the probability distribution of the adjacency matrix dependent on this latent structure. Regarding estimation of the model parameters, Bayesian approaches were first developed (Snijders and Nowicki, 1997 and Nowicki and Snijders, 2001),
prior to variational approaches (Daudin et al., 2008 and Latouche et al., 2012). On the theoretical sides, Celisse et al. (2012) study identifiability and consistency of the variational estimators; Bickel et al. (2013) show their asymptotic normality. Several important generalizations are possible such as weighted or directed variants (Mariadassou et al., 2010), mixed-memberships and overlapping SBM (Airoldi et al., 2008 and Latouche et al., 2011), degree-corrected SBM (Karrer and Newman, 2011), dynamic SBM (Matias and Miele, 2016), or multiplex SBM (Barbillon et al., 2015).

This paper deals with SBM inference when the network is not fully observed. In other words the adjacency matrix contains missing values, a situation often met with real-world networks. For instance in social sciences, collected data consist in a network of interactions between individuals. The sampling is often performed by interviewing individuals about their relationships with the others. Sampling may be partial since all individuals are not available for an interview. See Thompson and Frank (2000), Thompson and Seber (1996), Kolaczyk (2009) and Handcock and Gile (2010) for a review of network sampling techniques. Even though some papers deal with SBM inference under missing data condition (Aicher et al., 2014 and Vinayak et al., 2014), the partial sampling responsible for the missing values is overlooked in the inference. This paper overcomes this limitation by filling the gap between the sampling design and the inference with missing data in the SBM framework.

Our contributions. A typology of sampling designs is proposed in Section 2, adapting the theory developed in Rubin (1976) and Little and Rubin (2014) to SBM. We essentially split the sampling designs into the three usual classes for missing data:

i) Missing Completely At Random (MCAR), where the sampling does not depend on the data, neither on the observed nor on the unobserved part of the network.

ii) Missing At Random (MAR), where the probability of being sampled is independent on the value of the missing data. For network data, the sampling does not depend on absence or presence of an edge for an unobserved (or missing) dyad. MCAR is a particular case of MAR.

iii) Not Missing At Random (NMAR), where the sampling scheme is guided by unobserved dyads in some way.

We also discuss the identifiability issue for SBM inference under MAR and NMAR condition and prove the identifiability for some samplings (Section 2.4).

Regarding parameters inference, we consider MAR and NMAR separately. For MAR cases, which concern most if not all sampling strategies depicted in the network literature, only a slight adaption of the standard techniques is required since it suffices to conduct the inference only on the observed part of the network. Inference can be performed by a simple adaptation of the Variational EM (VEM) of Daudin et al. (2008) (Section 3.1). We show in simulations that this modified VEM shows pretty good accuracy results even with low sampling rates (Section 4.1).

NMAR is more tricky to deal with as the sampling design must be taken into account in the inference. We show how NMAR cases can be classified according to the dependency structure between the network data, the latent structure of the SBM and the sampling design. We introduce a general variational algorithm to deal with NMAR cases when the sampling relies on a probability distribution which is
explicitly known (Section 3.2) \(^1\). Our variational approach is based on a double mean-field approximation applied to the latent variable distribution of the clustering of the nodes and to the distribution of the missing dyads. We introduce three natural designs which are NMAR: a dyad-centered strategy, a node-centered strategy, and a block-centered strategy. For these three samplings we implement a VEM algorithm that produces unbiased estimators. We also introduce an Integrated Classification Likelihood criterion (ICL, Biernacki et al., 2000) for selecting the number of blocks. If the sampling design is unknown, the ICL can also be used to choose the sampling model. Although it is not possible to distinguish whether the sampling is MAR or NMAR (Molenberghs et al., 2008), the ICL criterion is a way for choosing between some parametric sampling which are MAR or not.

We show the good performance of our VEM algorithms on simulated network data (Section 4). Finally, we investigate two real world networks with missing values (Section 5): first, an example from ethnology, where a seed exchange network between Kenyan farmers is analyzed; and second, an example from molecular biology where we study the organization of the protein-protein interaction (PPI) network of ER, a nuclear hormone receptor infamous for marking breast cancer recurrence.

**Related works.** In the few existing works dealing with missing data for networks, the sampling design is barely discussed. In fact, even if not explicitly stated, all the works found in the literature assume MAR conditions. Aicher et al. (2014) propose a weighted SBM different from Mariadassou et al. (2010)’s, modeling simultaneously the presence/absence of edges and the weights. Missing data are handled by dropping the corresponding terms from the likelihood and the inference is conducted through a variational algorithm. In Vincent and Thompson (2015) a Bayesian augmentation procedure is introduced to estimate simultaneously the size of the population and the SBM structure when the sampling design is a one-wave snowball (a MAR case again). Apart from SBM, the exponential random graph model has been studied in the MAR setting in Handcock and Gile (2010).

On top of works directly related to network analysis, the matrix completion literature brings interesting insights for missing data in SBM. Indeed, SBM inference can be seen as a low rank matrix estimation. For instance, Vinayak et al. (2014) introduce a convex program for the matrix completion problem where the underlying matrix has a simple affiliation structure defined via an SBM. The entries are sampled independently with the same probability, corresponding to a MAR case. In Davenport et al. (2014), the case of noisy 1-bit observations is studied and a likelihood based strategy is developed with theoretical justification ensuring good matrix completion. Chatterjee (2015) proves strong results for large matrix with noisy entries estimation, by means of a universal singular value thresholding.

Another related question is when the status of some dyads is not clear (absent or present) in errorfully observed graph. Such uncertainties can be taken into account (Priebe et al., 2015 and Balachandran et al., 2017). The later reference studies the error propagation made by using estimators computed on observed sub-graphs, in order to estimate the number of existing edges in the real underlying graph.

\(^1\)More complex sampling schemes – for instance adversarial strategies – are thus not handled
2 Statistical framework

2.1 Stochastic Block Model

In SBM, nodes from a set $\mathcal{N} \triangleq \{1, \ldots, n\}$ are distributed among a set $\mathcal{Q} \triangleq \{1, \ldots, Q\}$ of hidden blocks that model the latent structure of the graph. The blocks are described by categorical variables $(Z_i, i \in \mathcal{N})$ with prior probabilities $\alpha = (\alpha_1, \ldots, \alpha_Q)$, such that $\mathbb{P}(Z_i = q) = \alpha_q$, with $q \in \mathcal{Q}$. The probability of an edge between any dyad in $\mathcal{D} \triangleq \mathcal{N} \times \mathcal{N}$ only depends on the blocks the two nodes belong to. Hence, the presence of an edge between $i$ and $j$, indicated by the binary variable $Y_{ij}$, is independent on the other edges conditionally on the latent blocks:

$$Y_{ij} \mid Z_i = q, Z_j = \ell \sim_{\text{ind}} \mathcal{B}(\pi_{ql}), \quad \forall (i, j) \in \mathcal{D}, \quad \forall (q, \ell) \in \mathcal{Q} \times \mathcal{Q},$$

where $\mathcal{B}$ stands for the Bernoulli distribution. In the following, $\pi = (\pi_{ql})_{(q, \ell) \in \mathcal{Q} \times \mathcal{Q}}$ is the $Q \times Q$ matrix of connectivity, $Y = (Y_{ij})_{i,j \in \mathcal{D}}$ is the $n \times n$ adjacency matrix of the random graph, $Z = (Z_1, \ldots, Z_n)$ the $n$-vector of the latent blocks and $\theta = (\alpha, \pi)$ are the unknown parameters associated with the SBM. With a slight abuse of notation, we associate to $Z_i$ a vector of indicator variables $(Z_{i1}, \ldots, Z_{iQ})$ such that $Z_i = q \Leftrightarrow Z_{iq} = 1, Z_{i\ell} = 0$, for all $\ell \neq q$. Notice that in the undirected binary case, $Y_{ij} = Y_{ji}$ for all $(i, j) \in \mathcal{D}$ and $Y_{ii} = 0$ for all $i \in \mathcal{N}$. Similarly, $\pi_{ql} = \pi_{q\ell}$ for all $(q, \ell) \in \mathcal{Q} \times \mathcal{Q}$.

2.2 Sampled data in the SBM framework

The sampled data is an $n \times n$ matrix with entries in $\{0, 1, \text{NA}\}$. It corresponds to the adjacency matrix $Y$ where unobserved dyads have been replaced by NA’s. More formally, we introduce an $n \times n$ sampling matrix $R$ that records the data sampled during this process, such that $R_{ij} = 1$ if $Y_{ij}$ is observed and 0 otherwise. As a shortcut, we use $Y^o = \{Y_{ij} : R_{ij} = 1\}$ and $Y^m = \{Y_{ij} : R_{ij} = 0\}$ to denote the sets of variables respectively associated with the observed and missing data. The number of nodes $n$ is assumed to be known even if no dyad including this node is observed, which means that $R$ may contain rows or columns filled with NA’s. The sampling design is the description of the stochastic process that generates $R$. It is assumed that the network pre-exists this process, which is fully characterized by the conditional distribution $p_\psi(R|Y)$, the parameters of which are such that $\psi$ and $\theta$ live in a product space $\Theta \times \Psi$. We adapt Rubin (1976)’s framework to the presence of the latent variables $Z_i$, the joint probability density function of the observed data satisfies

$$p_{\theta,\psi}(Y^o, R) = \int \int p_\theta(Y^o, Y^m, Z)p_\psi(R|Y^o, Y^m, Z)dY^mdZ.$$  \hspace{1cm} (1)

Simplifications may occur in (1) depending on the sampling design, leading to the three usual types of missingness (MCAR, MAR and NMAR). For SBM, this typology depends on the relations between the adjacency matrix $Y$, the latent structure $Z$ and the sampling $R$, so that the missingness is characterized by four directed acyclic graphs (DAG) displayed in Figure 1. On the basis of these DAGs, the sampling design for SBM is MCAR if $R \perp (Y^m, Z, Y^o)$, MAR if $R \perp (Y^m, Z) \mid Y^o$, and NMAR otherwise. We derive Proposition 1 from these definitions.

Proposition 1. If the sampling is MAR or MCAR then
Figure 1: DAGs of relationships between $Y$, $Z$ and $R$ considered in the framework of missing data for SBM. Since the network pre-exists the sampling process, we do not consider DAG where $R$ is a parent node.. The systematic edge between $Z$ and $Y$ comes from the SBM.

\begin{enumerate}
\item[(a)] \item[(b)] \item[(c)] \item[(d)] \item[(e)]
\end{enumerate}

Proof. To prove $i)$, remark that if $R$ satisfies MAR conditions, then $p(\psi(R|Y^o,Y^m,Z)) = p(\psi(R|Y^o))$. Moreover, $\theta$ and $\psi$ lie in a product space so that (1) factorizes into $p(\theta,\psi(Y^o,R) = p(\theta(Y^o)p(\psi(R|Y^o))$. This corresponds to the ignorability of Rubin (1976) and Handcock and Gile (2010). The proof of $ii)$ is postponed to Appendix A.1.

2.3 Sampling design examples

In this section we review some classical M(C)AR sampling designs and introduce three natural samplings satisfying NMAR conditions. We emphasize that the sampling can be either centered on dyads or on nodes. In the former case, a subset of dyads $D^o \subset D$ is picked up and $Y^o = \{Y_{ij}, (i,j) \in D^o\}$ (similarly for $D^m, Y^m$). In the latter case, a subset of nodes $N^o \subset N$ is picked up and the corresponding rows (and columns by symmetry) are observed i.e. $Y^o = \{(Y_{ik})_{1 \leq k \leq n}, i \in N^o\}$ (similarly for $N^m, Y^m$). It is straightforward to obtain $R$ either from $(D^o,D^m)$ or $(N^o,N^m)$.

2.3.1 MAR examples

Definition 1 (Random dyad sampling). Each dyad $(i,j) \in D$ has the same probability $P(R_{ij} = 1) = \rho$ to be observed independently on the others.

This design is trivially MCAR because each dyad is sampled with the same probability $\rho$ which does not depend on $Y$.

Definition 2 (Star and snowball sampling). The star sampling consists in selecting uniformly a set of nodes then observing corresponding rows of matrix $Y$. The snowball sampling is initialized by a star sampling which gives a first batch of nodes. The second batch of nodes is composed by the neighbors of the first batch (the set of nodes linked to nodes of the first batch). Successive batches can then be obtained. The final set of observed dyads correspond to all dyads involving at least one of these nodes. The successive batches are referred to as the waves in the snowball sampling.
These two designs are node-centered and MAR. Indeed, selecting nodes independently in star sampling or in the first batch of snowball sampling corresponds to MCAR sampling. Successive waves are then MAR since they are built on the basis of the previously observed part of $Y$. Expressions of the corresponding distributions $p_\psi(R|Y^o)$ are given in Handcock and Gile (2010).

2.3.2 NMAR examples

**Definition 3** (Double standard sampling). Let $\rho_1, \rho_0 \in [0, 1]$. Double standard sampling consists in observing dyads with probabilities

$$P(R_{ij} = 1|Y_{ij} = 1) = \rho_1, \quad P(R_{ij} = 1|Y_{ij} = 0) = \rho_0. \quad (2)$$

Denote $S^o = \sum_{(i,j) \in D^o} Y_{ij}$, $\bar{S}^o = \sum_{(i,j) \in D^o} (1-Y_{ij})$ and similarly for $S^m$, $\bar{S}^m$. Since $R$ is independent conditional on $Y$ and does not depend on $Z$, the log-likelihood is

$$\log p_\psi(R|Y) = S^o \log \rho_1 + \bar{S}^o \log \rho_0 + S^m \log (1 - \rho_1) + \bar{S}^m \log (1 - \rho_0), \quad (3)$$

where $\psi = (\rho_0, \rho_1)$. This sampling is dyad-centered and satisfies DAG (c).

**Definition 4** (Star sampling based on degrees – Star degree sampling). Star degree sampling consists in observing all dyads corresponding to nodes selected with probabilities $\{\rho_1, \ldots, \rho_n\}$ such that $\rho_i = \text{logistic}(a + bD_i)$ for all $i \in \mathcal{N}$ where $(a, b) \in \mathbb{R}^2$, $D_i = \sum_j Y_{ij}$ and $\text{logistic}(x) = (1 + e^{-x})^{-1}$.

In this node-centered sampling design satisfying DAG (c), the log-likelihood is

$$\log p_\psi(R|Y) = \sum_{i \in \mathcal{N}^o} \log \rho_i + \sum_{i \in \mathcal{N}^m} \log (1 - \rho_i), \quad \text{with } \psi = (a, b). \quad (4)$$

**Definition 5** (Class sampling). Class sampling consists in observing all dyads corresponding to nodes selected with probabilities $\{\rho_1, \ldots, \rho_Q\}$ such that $\rho_q = P(i \in \mathcal{N}^o | Z_i = q)$ for all $(i, q) \in \mathcal{N} \times \mathcal{Q}$.

This node-centered sampling corresponds to DAG (e). The log-likelihood is

$$\log p_\psi(R|Z) = \sum_{i \in \mathcal{N}^o} \log \rho_{Z_i} + \sum_{i \in \mathcal{N}^m} \log (1 - \rho_{Z_i}), \quad \text{with } \psi = (\rho_1, \ldots, \rho_Q). \quad (5)$$

2.4 Identifiability

In this section, we state the identifiability of SBM under random-pair, star and class sampling designs. Identifiability of the SBM under double-standard or star-degree samplings remain open problems, even if our numerical experiments support this property. Our proofs, postponed to Appendix A.2, build on Celisse et al. (2012) who established the identifiability of the SBM without missing data.

As seen before, random-dyad and star samplings are MCAR and the sampling distribution $p(R)$ is completely independent on the network $Y$. Therefore, it suffices to prove the identifiability of first, the sampling parameter $\psi = \rho$ and second, of the SBM parameters $\theta = (\alpha, \pi)$ given $\rho$. The two following theorems state these results.

**Theorem 2.1.** The sampling parameter $\rho > 0$ of random-dyad (resp. star) sampling is identifiable.
Theorem 2.2. Let \( n \geq 2Q \) and assume that for any \( 1 \leq q \leq Q \), \( \rho > 0 \), \( \alpha_q > 0 \) and the coordinates of \( s = \rho(\pi, \alpha) \) are distinct. Then, under random-pair (resp. star) sampling, SBM parameters are generic identifiable up to label switching.

Theorem 2.3 establishes the identifiability of the SBM sampled under NMAR class sampling design. Note that the identifiability of the sampling parameters \( \psi = (\rho_1, \ldots, \rho_Q) \) and of the SBM parameters must be proved jointly because of the dependence between the network and the sampling.

**Theorem 2.3.** Let \( n \geq 2Q \) and assume that for any \( 1 \leq q \leq Q \), \( \rho_q > 0 \), \( \alpha_q > 0 \) and the coordinates of \( o = \pi, \alpha \) and \( t = (\sum_{k=1}^{Q} \pi_{1k}\rho_k\alpha_k, \ldots, \sum_{k=1}^{Q} \pi_{Qk}\rho_k\alpha_k) \) are distinct. Then, under class sampling, SBM and class sampling parameters are generic identifiable up to label switching.

### 3 Inference

To perform efficient inference, we rely on the variational approach of Jordan et al. (1998). Derivations of the practical variational algorithms considerably change depending on the missing data condition at play. We start by MAR to gently introduce Theorem 2.2. Then, under class sampling, SBM parameters are generic identifiable up to label switching.

#### 3.1 MAR inference

By Proposition 1.1, inference in the MAR case is conducted on the observed part of the adjacency matrix \( Y^o \). The EM algorithm is unfeasible since it requires the evaluation of the conditional mean of the complete log-likelihood \( \mathbb{E}_{Z|Y^o} \left[ \log p_{\theta}(Y^o, Z) \right] \) which is intractable for SBM. The variational approach circumvents this limitation by maximizing a lower bound of the log-likelihood based on an approximation \( \tilde{p}_\tau \) of the true conditional distribution \( p_{\theta}(Z|Y^o) \),

\[
\log p_{\theta}(Y^o) \geq J_{\tau, \theta}(Y^o) \triangleq \log(p_{\theta}(Y^o)) - \text{KL}[\tilde{p}_\tau(Z)||p_{\theta}(Z|Y^o)],
\]

\[
= \mathbb{E}_{\tilde{p}_\tau} \left[ \log(p_{\theta}(Y^o)) \right] - \mathbb{E}_{\tilde{p}_\tau} \left[ \log(p_{\theta}(Z, Y^o)) \right],
\]

where \( \tau \) are some variational parameters and KL is the Kullback-Leibler divergence. The approximated distribution is chosen so that the integration over the latent variables simplifies by factorization. In SBM, the prior distribution of \( Z_i = (Z_{i1}, \ldots, Z_{iQ}) \) is the multinomial distribution, thus the natural variational counterpart to \( p_{\theta}(Z|Y^o) \) is \( \tilde{p}_\tau(Z) = \prod_{i\in\mathcal{N}} m(Z_i; \tau_i) \), where \( \tau_i = (\tau_{i1}, \ldots, \tau_{iQ}) \), and \( m(\cdot; \tau_i) \) is the multinomial probability density function with parameters \( \tau_i \). The VEM sketched in Algorithm 1 consists in alternatively maximizing \( J \) w.r.t. \( \tau = \{\tau_1, \ldots, \tau_n\} \) (the variational E-step) and w.r.t. \( \theta \) (the M-step). The two maximization problems are solved straightforwardly following Daudin et al. (2008):

1. The parameters \( \theta = (\alpha, \pi) \) maximizing \( J_{\theta}(Y^o) \) when \( \tau \) is held fixed are

\[
\hat{\alpha}_q = \frac{\sum_{i\in\mathcal{N}^o} \hat{\tau}_{iq}}{\text{card } (\mathcal{N}^o)}, \quad \hat{\pi}_{q\ell} = \frac{\sum_{(i,j)\in\mathcal{D}^o} \hat{\tau}_{iq} \hat{\tau}_{j\ell} Y_{ij}}{\sum_{(i,j)\in\mathcal{D}^o} \hat{\tau}_{iq} \hat{\tau}_{j\ell}}.
\]
2. The variational parameters $\tau$ maximizing $J_\tau(Y^o)$ when $\theta$ is held fixed are obtained with the following fixed point relation:

$$\hat{\tau}_{iq} \propto \alpha_q \left( \prod_{(i,j) \in D^o} \prod_{\ell \in Q} b(Y_{ij}; \pi_{q\ell})^{\hat{\tau}_{j\ell}} \right),$$

where $b(x, \pi) = \pi x (1 - \pi)^{1-x}$ the Bernoulli probability density function.

**Algorithm 1:** Variational EM for MAR inference in SBM

**Initialization:** Set up $\tau^{(0)}$ with some clustering algorithm

```
repeat
    \[ \theta^{(h+1)} = \arg \max_\theta J(Y^o; \tau^{(h)}, \theta) \] \hspace{1cm} \text{M-step}
    \[ \tau^{(h+1)} = \arg \max_\tau J(Y^o; \tau, \theta^{(h+1)}) \] \hspace{1cm} \text{variational E-step}
until \[ \|\theta^{(h+1)} - \theta^{(h)}\| < \varepsilon \]
```

Algorithm 1 generates a sequence $\{\tau^{(h)}, \theta^{(h)}; h \geq 0\}$ with increasing $J(Y^o; \tau^{(h)}, \theta^{(h)})$. Since there is no guarantee for convergence to the global maximum, we run the algorithm from several different initializations to finally retain the best solution.

**Model selection of the number of blocks.** The Integrated Classification Likelihood criterion was introduced by Biernacki et al. (2000) for mixture models, where the likelihood – and thus BIC – is usually intractable. Daudin et al. (2008) derive a variational ICL for SBM which we adapt to missing data conditions: for an SBM with $Q$ blocks and for $\hat{\theta} = \arg \max \log p_\theta(Y^o, Z)$, one has

$$\text{ICL}(Q) = -2\mathbb{E}_{\hat{p}_\psi} [\log p_\theta(Y^o, Z; Q)] + \frac{Q(Q+1)}{2} \log \text{card}(D^o) + (Q - 1) \log \text{card}(N^o).$$

Note that a dyad is only counted once since we work with symmetric networks.

### 3.2 NMAR inference: the general case

Contrary to the MAR case, inferring from the likelihood on observed dyads in NMAR conditions may bias the estimates and leads to a bad clustering. In fact, all observed data (including the sampling matrix $R$ in addition to $Y^o$) must be taken into account in the inference. Hence, the likelihood of the observed data is $\log p_{\theta, \psi}(Y^o, R)$. The corresponding completed likelihood has the following decomposition

$$\log p_{\theta, \psi}(Y^o, R, Y^m, Z) = \log p_\psi(R|Y^o, Y^m, Z) + \log p_\theta(Y^o, Y^m, Z), \hspace{1cm} (7)$$

where an explicit form of $p_\psi(R|Y^o, Y^m, Z)$ requires further specification of the sampling. The joint distribution $p_\theta(Y^o, Y^m, Z)$ has a form similar to the MAR case, with terms involving both observed and missing data. Now, the approximation is required both on latent blocks $Z$ and missing dyads $Y^m$ to approximate $p_\theta(Z, Y^m|Y^o)$. We suggest a variational distribution where complete independence is forced on $Z$ and $Y^m$, using multinomial (resp. Bernoulli) distribution for $Z$ (resp. for $Y^m$):

$$\tilde{p}_{\tau, \nu}(Z, Y^m) = \tilde{p}_\tau(Z) \tilde{p}_\nu(Y^m) = \prod_{i \in \mathcal{N}} m(Z_i; \tau_i) \prod_{(i,j) \in D^m} b(Y_{ij}; \nu_{ij}), \hspace{1cm} (8)$$
where \( \tau \) and \( \nu = \{ \nu_{ij}, (i, j) \in D^m \} \) are two sets of variational parameters respectively associated with \( Z \) and \( Y^m \). This leads to the following lower bound of the joint distribution \( \log p_{\theta, \psi}(Y^o, R) \):

\[
J_{\tau, \nu, \theta, \psi}(Y^o, R) = E_{\tilde{p}_{\tau, \nu}} \left[ \log p_{\theta, \psi}(Y^o, R, Y^m, Z) \right] - E_{\tilde{p}_{\tau, \nu}} \left[ \log \tilde{p}_{\tau, \nu}(Z, Y^m) \right].
\]

By means of Decomposition (7) of the completed log-likelihood, variational approximation (8) and entropies of multinomial and Bernoulli distributions, one has

\[
J_{\tau, \nu, \theta, \psi}(Y^o, R) = E_{\tilde{p}_{\tau, \nu}} \left[ \log p_R(R|Y^o, Y^m, Z) \right] + \sum_{(i,j) \in D^m} \sum_{(q,\ell) \in \mathbb{Q}} \tau_{iq} \tau_{j\ell} \log b(Y_{ij}, \pi_{q\ell}) + \sum_{(i,j) \in D^m} \tau_{iq} \tau_{j\ell} \log b(\nu_{ij}, \pi_{q\ell})
\]

\[
+ \sum_{i \in \mathcal{N}} \sum_{q \in \mathbb{Q}} \tau_{iq} \log(\alpha_q / \tau_{iq}) - \sum_{(i,j) \in D^m} \nu_{ij} \log(\nu_{ij}) + (1 - \nu_{ij}) \log(1 - \nu_{ij}). \quad (9)
\]

In the above expression, the mean \( E_{\tilde{p}_{\tau, \nu}} \left[ \log p_R(R|Y^o, Y^m, Z) \right] \) can be integrated over the variational distribution \( \tilde{p}_{\tau, \nu}(Z, Y^m) \), as expected. Still, the practical computations depend on the sampling design.

The general VEM algorithm used to maximize (9) is sketched in its main lines in Algorithm 2. Both the E-step and the M-step splits into two parts: the maximization must be performed on the SBM parameters \( \theta \) and the sampling design parameters \( \psi \) respectively. The variational E-step is performed on the parameters \( \tau \) of the latent block \( Z \) and on the parameters \( \nu \) of the missing data \( Y^m \).

**Algorithm 2: Variational EM for NMAR inference in SBM**

**Initialisation:** set up \( \tau^{(0)}, \nu^{(0)} \) and \( \psi^{(0)} \)

repeat

\[
\theta^{(h+1)} = \arg \max_\theta J \left( Y^o, R; \tau^{(h)}, \nu^{(h)}, \psi^{(h)} \right), \quad \text{M-step a)}
\]

\[
\psi^{(h+1)} = \arg \max_\psi J \left( Y^o, R; \tau^{(h)}, \nu^{(h)}, \psi^{(h+1)} \right), \quad \text{M-step b)}
\]

\[
\tau^{(h+1)} = \arg \max_\tau J \left( Y^o, R; \tau^{(h+1)}, \nu^{(h+1)} \right), \quad \text{VE-step a)}
\]

\[
\nu^{(h+1)} = \arg \max_\nu J \left( Y^o, R; \tau^{(h+1)}, \nu^{(h+1)} \right), \quad \text{VE-step b)}
\]

until \( \| \theta^{(h+1)} - \theta^{(h)} \| < \varepsilon \)

Interestingly, resolution of the two sub-steps concerned with the optimization of the parameters related with the SBM – that is to say, \( \theta \) and \( \tau \) – can be stated almost independently of any further specification of the sampling design.

**Proposition 2.** Consider the lower bound \( J_{\tau, \nu, \theta, \psi}(Y^o, R) \) given by (9).

1. The parameters \( \theta = (\alpha, \pi) \) maximizing (9) when all others are held fixed are

\[
\hat{\alpha}_q = \frac{1}{n} \sum_{i \in \mathcal{N}} \hat{\tau}_{iq}, \quad \hat{\pi}_{q\ell} = \frac{\sum_{(i,j) \in D^o} \hat{\tau}_{iq} \hat{\tau}_{j\ell} Y_{ij} + \sum_{(i,j) \in D^m} \hat{\tau}_{iq} \hat{\tau}_{j\ell} \nu_{ij}}{\sum_{(i,j) \in D} \hat{\tau}_{iq} \hat{\tau}_{j\ell}}.
\]

2. The optimal \( \tau \) in (9) when all other parameters are held fixed verifies

\[
\hat{\tau}_{iq} \propto \lambda_{iq} \alpha_q \left( \prod_{(i,j) \in D^o} \prod_{\ell \in \mathbb{Q}} b(Y_{ij}; \pi_{q\ell}) \hat{\tau}_{j\ell} \right) \left( \prod_{(i,j) \in D^m} \prod_{\ell \in \mathbb{Q}} b(\nu_{ij}; \pi_{q\ell}) \hat{\tau}_{j\ell} \right).
\]

with \( \lambda_{iq} \) a simple constant depending on the sampling design.
the expression of the conditional expectation under the variational approximation: According to the likelihood (5) of the class sampling, we derive Class sampling.

Moreover, Proposition 3
Based on this expression, we easily derive the following proposition.

3.3 NMAR: specificities related to the choice of the sampling
Under the light of DAGs in Figure 1, NMAR conditions specified by DAGs (c), (d) or (e) induce different factorizations for the conditional distribution of the sampling design R, and thus different evaluations of the mean \( \mathbb{E}_{p_{\tau,\nu}} \left[ \log p_{\theta,\psi}(Y^o, R, Y^m, Z) \right] \) in the lower bound (9). The three following factorizations correspond respectively to DAGs (c), (d) and (e): 

\[
p_{\psi}(R|Y^o, Y^m, Z) = p_{\psi}(R|Y^o, Y^m), \quad p_{\psi}(R|Y^o, Y^m, Z) = p_{\psi}(R|Y^o, Y^m) \text{ and } p_{\psi}(R|Y^o, Y^m, Z) = p_{\psi}(R|Z).
\]

From Section 2.3.2 where NMAR sampling designs were discussed, we can state that the likelihood \( p_{\psi}(R|Y^o, Y^m, Z) \) for double standard sampling and star degree sampling can be simplified as in the first case. Similarly, the likelihood for class sampling simplifies as in the third case. The steps in Algorithm 2 specific to these three NMAR samplings are detailed below.

**Double-standard sampling.** Recall that \( S^o = \sum_{(i,j) \in D^o} Y_{ij}, \quad \bar{S}^o = \sum_{(i,j) \in D^o} (1 - Y_{ij}) \), and let \( S^m = \sum_{(i,j) \in D^m} \nu_{ij}, \quad \bar{S}^m = \sum_{(i,j) \in D^m} (1 - \nu_{ij}) \). From (3) we have

\[
\mathbb{E}_{\tilde{p}} \log p_{\psi}(R|Y) = S^o \log \rho_1 + \bar{S}^o \log \rho_0 + S^m \log(1 - \rho_1) + \bar{S}^m \log(1 - \rho_0).
\]

Based on this expression, we easily derive the following proposition.

**Proposition 3 (double standard sampling).**

1. The parameters \( \psi = (\rho_0, \rho_1) \) maximizing (9) when all others are held fixed are

\[
\hat{\rho}_0 = \frac{\bar{S}^o}{S^o + \bar{S}^m}, \quad \hat{\rho}_1 = \frac{S^o}{S^o + \bar{S}^m}.
\]

2. The optimal \( \nu \) in (9) when all other parameters are held fixed are

\[
\hat{\nu}_{ij} = \text{logistic} \left( \log \left( \frac{1 - \rho_1}{1 - \rho_0} \right) + \sum_{(q,\ell) \in Q^2} \tau_{iq} \tau_{j\ell} \log \left( \frac{\pi_{q\ell}}{1 - \pi_{q\ell}} \right) \right).
\]

Moreover, \( \lambda_{iq} = 1 \ \forall (i, q) \in \mathcal{N} \times \mathcal{Q} \) for optimization of \( \tau \) in Proposition 2.b).

**Class sampling.** According to the likelihood (5) of the class sampling, we derive the expression of the conditional expectation under the variational approximation:

\[
\mathbb{E}_{\tilde{p}} \log p_{\psi}(R|Y) = \sum_{i \in \mathcal{N}^o} \sum_{q \in \mathcal{Q}} \tau_{iq} \log(\rho_q) + \sum_{i \in \mathcal{N}^m} \sum_{q \in \mathcal{Q}} \tau_{iq} \log(1 - \rho_q),
\]

from which we derive the maximization of the remaining parameters.
Proposition 4 (class sampling).

1. The parameters $\psi = (\rho_1, \ldots, \rho_Q)$ maximizing (9) when all others are held fixed are

$$
\hat{\rho}_q = \frac{\sum_{i \in \mathcal{N}_t} \tau_{iq}}{\sum_{i \in \mathcal{N}} \tau_{iq}}, \quad (11)
$$

2. The optimal $\nu$ in (9) when all other parameters are held fixed verify

$$
\hat{\nu}_{ij} = \text{logistic} \left( \sum_{(q, \ell) \in \mathcal{Q}^2} \tau_{iq} \tau_{j\ell} \log \left( \frac{\pi_{q\ell}}{1 - \pi_{q\ell}} \right) \right).
$$

Moreover $\lambda_{iq} = \rho_q^{(i \in \mathcal{N}_o)} (1 - \rho_q)^{(i \in \mathcal{N}^m)}$ for optimization of $\tau$ in Proposition 2.b).

Star degree sampling. From Expression (4) of the likelihood, one has

$$
\mathbb{E}_\tilde{p} \log p_\psi (R | Y) = - \sum_{i \in \mathcal{N}^m} \left( a + b \tilde{D}_i \right) + \sum_{i \in \mathcal{N}} \mathbb{E}_\tilde{p} \left[ - \log (1 + e^{-(a+bD_i)}) \right],
$$

where $\tilde{D}_i = \mathbb{E}_\tilde{p} [D_i] = \sum_{i \in \mathcal{N}^m} \nu_{ij} + \sum_{i \in \mathcal{N}_o} Y_{ij}$ is the approximation of the degrees.

Because $\mathbb{E}_\tilde{p} \left[ - \log (1 + e^{-(a+bD_i)}) \right]$ has no explicit form, an additional variational approximation is needed (Jordan et al., 1998). Such a technique was recently used in a random graph framework in Latouche et al. (2017). The principle is as follows: since $g(x) = -\log (1 + e^{-x})$ is a convex function, we have from Taylor expansion

$$
g(x) \geq g(\zeta) + \frac{x - \zeta}{2} + h(\zeta) (x^2 - \zeta^2), \quad h(x) = \frac{-1}{2 \zeta} \left[ \text{logistic}(\zeta) - \frac{1}{2} \right] \quad (12)
$$

for $(x, \zeta) \in \mathbb{R} \times \mathbb{R}^+$. This leads to a lower bound of the initial lower bound:

$$
\log p_{\theta, \psi} (Y^o, R) \geq J_{\tau, \nu, \psi, \theta, \psi} (Y^o, R) \geq J_{\tau, \nu, \zeta, \theta, \psi} (Y^o, R), \quad (13)
$$

with $\zeta = (\zeta_i, i \in \mathcal{N})$ such that $\zeta_i > 0$ is an additional set of variational parameters used to approximate $-\log (1 + e^{-x})$. The second lower bound $J_{\tau, \nu, \zeta, \theta, \psi}$ is derived from Equation (12) and given in Appendix A.3. At the end of the day, we have an additional set of variational parameters to optimize, and a corresponding additional step in Algorithm 2. The following proposition obtained by differentiating $J_{\tau, \nu, \zeta, \theta, \psi}$ gives the expression of all the parameters specific to star degree sampling.

Proposition 5 (star degree sampling). Let $\tilde{D}_{i}^2 = \mathbb{E}_\tilde{p} [D_i^2]$ and $\tilde{D}_{k}^\ell = \tilde{D}_k - \nu_{k\ell}$. 

1. The parameters $\psi = (a, b)$ maximizing $J_{\tau, \nu, \zeta, \theta, \psi} (Y^o, R)$ when others are held fixed are

$$
\hat{a} = - \frac{\sum_{i=1}^{n} \left( h(\zeta_i) \tilde{D}_i \right) + \frac{n}{2} \text{card} (\mathcal{N}^m)}{\sum_{i=1}^{n} h(\zeta_i)}, \quad \hat{b} = \frac{2}{n} \text{card} (\mathcal{N}^m) \sum_{i=1}^{n} h(\zeta_i) \tilde{D}_i - \left( \frac{1}{2} \sum_{i=1}^{n} \tilde{D}_i - \sum_{i \in \mathcal{N}_o} \tilde{D}_i \right) \times \sum_{i=1}^{n} h(\zeta_i) \quad (14)
$$
2. The parameters $\zeta$ maximizing $J_{\tau,\nu,\zeta,\theta,\psi}(Y^o, R)$ when others are held fixed are

$$\hat{\zeta}_i = \sqrt{a^2 + b^2 \tilde{D}_i^2 + 2ab\tilde{D}_i}, \ \forall i \in \mathcal{N}.$$ 

3. The optimal $\nu$ in $J_{\tau,\nu,\zeta,\theta,\psi}(Y^o, R)$ when all other parameters are held fixed verify

$$\hat{\nu}_{ij} = \text{logistic} \left( \sum_{(q, \ell) \in Q^2} \tau_{iq} \tau_{j\ell} \log \left( \frac{\pi_{q\ell}}{1 - \pi_{q\ell}} \right) - b + 2h(\zeta_i) \left( ab + b^2(1 + \tilde{D}_i^{-1}) \right) + 2h(\zeta_j) \left( ab + b^2(1 + \tilde{D}_j^{-1}) \right) \right). \quad (14)$$

Moreover, $\lambda_{iq} = 1 \ \forall (i, q) \in \mathcal{N} \times Q$ for optimization of $\tau$ in Proposition 2.b).

Model selection for number of blocks and sampling design. In NMAR cases, ICL can be useful not only to select the appropriate number of blocks but also for selecting the most appropriate sampling design when it is unknown. Contrary to the MAR case, ICL is no longer a straightforward generalization of Daudin et al. (2008). Indeed, the complete likelihood and thus the penalization needs to take into account the sampling design. Let us consider a model with $Q$ blocks and a sampling design with $K$ parameters (i.e. the dimension of $\psi$). The ICL criterion is a Laplace approximation of the complete likelihood $p(Y^o, Y^m, R, Z|Q, K)$ with $p(\theta, \psi|Q, K)$ the prior distributions on the parameters such that

$$p(Y^o, Y^m, R, Z|Q, K) = \int_{\Theta \times \Psi} p_{\theta,\psi}(Y^o, Y^m, R, Z|Q, K)p(\theta, \psi|Q, K)d\theta d\psi.$$ 

Proposition 6. For a model with $Q$ blocks, a sampling design with a vector of parameters $\psi \in \mathbb{R}^K$ and $(\hat{\theta}, \hat{\psi}) = \arg \max_{(\theta, \psi)} \log p_{\theta,\psi}(Y^o, Y^m, R, Z)$, then

$$\text{ICL} = -2E_{\hat{\tau}, \hat{\nu}, \hat{\theta}, \hat{\psi}} \left[ \log p_{\hat{\theta},\hat{\psi}}(Y^o, Y^m, R, Z|Q, K) \right] + \text{pen}_{\text{ICL}},$$

$$\text{pen}_{\text{ICL}} = \begin{cases} 
\left( K + \frac{Q(Q+1)}{2} \right) \log \left( \frac{n(n-1)}{2} \right) + (Q - 1) \log(n) & \text{for dyad-centered sampling} \\
\frac{Q(Q+1)}{2} \log \left( \frac{n(n-1)}{2} \right) + (K + Q - 1) \log(n) & \text{for node-centered sampling}
\end{cases}$$

Note that an ICL criterion for MAR sampling designs can be constructed in the same fashion for the purpose of comparison with NMAR sampling designs.

4 Simulations study

In this section, we illustrate the relevance of our approaches on networks simulated under SBM with various topologies (e.g., affiliation, star or bipartite networks), with missing data under MAR and NMAR conditions. The quality of the inference is assessed by computing the distance between estimated and true connectivity matrices $\pi$ in terms of Frobenius norm. The quality of the clustering recovery is measured with the adjusted Rand index (ARI, Rand, 1971) between the true classification and the clustering obtained by maximum posterior probabilities for each $\tau_i$. 

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4.1 MAR condition

Algorithm 1 for MAR samplings is tested on affiliation networks with 3 blocks as in Figure 2. The number of blocks is assumed to be known. For this topology the probability of connections inside the same block is $\eta$ and is ten times stronger than the probability of connections between nodes from different blocks.

$$
\begin{pmatrix}
\eta & \eta \\
\frac{\eta}{10} & \frac{\eta}{10} \\
\frac{\eta}{10} & \eta
\end{pmatrix}
$$

Figure 2: Matrix $\pi$ in affiliation topology with inter/intra blocks probabilities

We generate networks with $n = 200$ nodes and marginal probabilities of belonging to blocks $\alpha = (1/3, 1/3, 1/3)$. The sampling design is chosen as a random dyad sampling with a varying $\rho$. The difficulty is controlled by two parameters: the sampling effort $\rho$, that we vary on the interval $[0.01, 1]$; and the overall connectivity in matrix $\pi$, defined by $c = \sum q_\ell \alpha_q \alpha_\ell \pi_{q \ell}$, which is directly related to the choice of $\eta$: the lower the $\eta$, the sparser the network and the harder inference problem. For each configuration $(c, \rho)$, the simulation is repeated 500 times. Figure 3 displays the results both in terms of estimation of $\pi$ and in terms of classification recovery, for varying connectivity $c$ and sampling effort $\rho$. Our method achieves good performances even with a low sampling effort provided that the connectivity is not too low.

4.2 NMAR condition

Under NMAR conditions, we conduct a more extensive simulation study by considering various network topologies, namely affiliation, star and bipartite topologies,
the connectivity matrix of which are given in Figure 4. We use a common tuning parameter $\epsilon$ to control the connectivity of the networks in each topology: the lower the $\epsilon$, the more contrasted the topology.

\[
\begin{pmatrix}
1 - \epsilon & \epsilon & \epsilon \\
\epsilon & 1 - \epsilon & \epsilon \\
\epsilon & \epsilon & 1 - \epsilon
\end{pmatrix}
\]

(a) affiliation

\[
\begin{pmatrix}
1 - \epsilon & 1 - \epsilon & 0 & 0 \\
1 - \epsilon & 0 & \epsilon & 0 \\
0 & \epsilon & 1 - \epsilon & 1 - \epsilon \\
0 & 0 & 1 - \epsilon & 0
\end{pmatrix}
\]

(b) star

\[
\begin{pmatrix}
\epsilon & 1 - \epsilon & \epsilon & \epsilon \\
1 - \epsilon & \epsilon & \epsilon & \epsilon \\
\epsilon & \epsilon & \epsilon & 1 - \epsilon \\
\epsilon & \epsilon & 1 - \epsilon & \epsilon
\end{pmatrix}
\]

(c) bipartite

Figure 4: Matrix $\pi$ in different topologies with inter/intra blocks probabilities.

Among the three schemes developed in Section 2.3.2, we investigate thoroughly double standard sampling in the following paragraph, where we exhibit a large panel of situations where the gap is large between the performances of algorithms designed for MAR or NMAR cases. Other designs are quickly explored in a second phase.

### 4.2.1 Double standard sampling design

Simulated networks have $n = 100$ nodes, with $\epsilon$ varying in $\{0.05, 0.15, 0.25\}$. Prior probabilities $\alpha$ are chosen specifically for affiliation, star and bipartite topologies, respectively $(1/3, 1/3, 1/3)$, $(1/6, 1/6, 1/4, 1/4)$ and $(1/4, 1/4, 1/4, 1/4)$. The exploration of the sampling parameters $\psi = (\rho_0, \rho_1)$ is done on a grid $[0.1, 0.9] \times [0.1, 0.9]$ discretized by steps of 0.1. Algorithm 2 was initialized with several random initializations and spectral clustering.

In Figure 5, the estimation error is represented as a function of the difference between the sampling design parameters $(\rho_0, \rho_1)$: the closer this difference to zero, the closer to the MAR case. As expected, Algorithm 1 designed for MAR only performs well when $\rho_1 - \rho_0 \approx 0$. The performances deteriorate when this difference increases. Algorithm 2 designed for NMAR double-standard sampling shows relatively flat curves which means that its performances are roughly constant no matter the sampling condition.

Figure 6 reports estimation accuracy for the sampling parameters $\rho_0$ and $\rho_1$. Results show a good ability of the VEM to estimate these parameters. As expected, performances deteriorate for uncontrasted topologies with low sampling rate.

**Model selection.** Simulations are also conducted to study the performances of ICL at selecting both the number of blocks and the sampling design. We compare results for the different topologies described in Figure 4 for $\epsilon = 0.05$. Rates of correct answers of the ICL criterion for selecting the number of blocks $Q$ under a double standard sampling with different sampling rates are displayed in Table 1. The ARI is also provided. The ICL shows a satisfactory ability to select the right number of blocks for the three topologies even if the selection task obviously needs a larger sampling effort than the estimation task. It is worth mentioning that a block may not be sampled which leads the ICL to select a lower number of blocks. This seems quite reasonable regarding the sampling rate. As a consequence, the ARI is a meaningful additional information to demonstrate that the clustering is still coherent with the truth even if the number of selected blocks is not the true one.
Figure 5: Double standard setting: estimation error of $\pi$ and adjusted Rand index averaged over 500 simulations for affiliation, bipartite and star topologies.

Figure 6: Double standard setting: estimation error of $\rho_0$ and $\rho_1$ averaged over 500 simulations for affiliation, bipartite and star topologies.
Table 1: Rates of correct answers of the ICL criterion when choosing the number of blocks and Adjusted Rand Indexes as (rates/ARI). Tested configurations are different sampling rates and three topologies (affiliation, bipartite and star) under a double standard sampling. Each configuration is simulated 500 times.

In Table 2, results concern the rates of correct selections of the sampling design when the two designs in competition are the random dyad and the double standard samplings. As expected, the rate of correct answers increases with the sampling rate.

Table 2: Rates of correct answers of the ICL criterion when choosing between Random dyad sampling (MAR) and double standard sampling (NMAR) in each of the 18 configurations. A configuration is the combination of a topology (affiliation, bipartite and star), a sampling rate and a sampling design. Each configuration is simulated 500 times.

4.2.2 Star degree and class samplings

Contrary to double-standard, star degree and class samplings are node-centered. In this case, it is more likely to encounter configurations close to MAR sampling designs. Indeed, for double-standard sampling, the sampling parameters was directly related to the probability of an edge conditionally on the observation of the corresponding dyad. This is no longer the case for the node-centered designs. Therefore we have to look for configurations which leads to biased estimation. The sampling designs being hardly different from a MAR design, the NMAR inference does not show much improvement compared to the MAR inference. Still, we exhibit some interesting situations where star degree and class samplings deserve an appropriate treatment, presented herein. We simulate networks with $n = 100$ nodes under an affiliation topology as described in Figure 2 with $\epsilon = 0.5$ and $\alpha = (0.25, 0.5, 0.25)$. Sampling parameters are chosen such that $\psi = (a, b) = (-3.6, 0.1)$ for star degree sampling, which makes nodes with highest degrees preferably selected. In class sampling, these parameters are set to $\psi = (\rho_1, \rho_2, \rho_3) = (0.75, 0.5, 0.05)$, which makes nodes from the largest block and from a small block preferably selected while the other small block is under-sampled. In these cases the sampling designs are clearly NMAR. In Figure 7, the estimation errors and the ARI are pictured for both cases. The sampling rates (i.e. rates of observed dyads over total number of dyads) lie in the intervals...
[0.558, 0.844] for class sampling and [0.162, 0.622] for star degree sampling. These two intervals arise from the values of the parameter $\psi$ explored for these two designs. We compare the performances of Algorithm 2 to an oracle (when inference is conducted via a classical VEM algorithm on a fully observed network) and with Algorithm 1. When facing NMAR condition, Algorithm 2 shows a slight improvement over Algorithm 1 even if it remains far from the oracle.

Figure 7: Estimation error of $\pi$ and ARI averaged over 500 simulations in star degree and class settings. The topology is affiliation as in Figure 2 with $\epsilon = 0.05$.

5 Application to real networks

In this Section, we illustrate SBM with missing data on network data from social science and life science. In both cases, accounting for missing data dramatically changes the topology inferred by SBM and therefore the interpretation of the network.

5.1 Seed exchange network in the region of Mount Kenya

In a context of subsistence farming, studies which investigate the relationships between crop genetic diversity and human cultural diversity patterns have shown that seed exchanges are embedded in farmers’ social organization. Data on seed exchanges of sorghum in the region of Mount Kenya were collected and analyzed in Labeyrie et al. (2016, 2014). The sampling of the network is node-centered since the exchanges are documented by interviewing farmers who are asked to declare to whom they gave seeds and from whom they receive seeds. Since an interview is time consuming, the sampling is not exhaustive. A limited space area was defined where all the farmers were interviewed. Therefore, the network is collected with missing dyads since there is no information on the potential links between two farmers who were cited but not interviewed. With the courtesy of Vanesse Labeyrie, we analyzed the Mount Kenya
seed exchange network involving 568 farmers among which 155 were interviewed. Although other farmers in this region might be connected to non-interviewed farmers, we focus on this closed network of 568 nodes.

SBM are fitted under the three node-centered sampling designs presented in Section 2.2 (star (MAR), class and star degree sampling). Indeed, we only know that the sampling is node-centered, and thus rely on the ICL criterion to choose the most appropriate one. The ICL criterion is minimal for 10 blocks both under the class sampling and star degree sampling, with a slight advantage for the latter in terms of model selection. This model unravels a strong community structure with nodes more likely to be connected with nodes from the same block. The clusterings between the SBMs obtained with either class or star degree sampling remain close from each other (ARI: 0.79). On the contrary, the model selected by ICL for MAR sampling is only composed by 2 blocks, aggregating most of the farmers in a large group plus a small group of farmers characterized by a larger degree. The ARIs between MAR clustering (either with 2 or 10 blocks) and star degree clustering remain low (around 0). Finally, note that interviewed and non-interviewed farmers are mixed up in the blocks of the three selected models.

On top of network data, categorical variables are available for discriminating the farmers such as the ntora\(^2\) they belong to (10 main ntoras plus 1 grouping all the others) and the dialect they speak (4 dialects). In Figure 8, we compute ARIs between ntoras (left panel), respectively spoken dialect (right panel) and the clusterings obtained with SBM under the three node-centered sampling for a varying number of blocks. Although the ARIs remain low, the clusterings from class or star degree sampling SBMs manage to catch a non negligible fraction of the social organization, which could explain the structure of the exchange network.

\[\begin{array}{c}
\text{ARI vs. number of blocks} \\
\text{sampling: Class, Degree, MAR}
\end{array}\]

Figure 8: ARIs computed between the clusterings given by an SBM under class, star degree and MAR samplings with a varying number of blocks \(Q\) and ntora of farmers (left-hand-side) or dialect spoken by farmers (right-hand-side)

### 5.2 ER (ESR1) PPI network in breast cancer

Estrogen receptor 1 (ESR1) is a gene that encodes an estrogen receptor protein (ER), a central actor in breast cancer. Uncovering its relations with other proteins is

\(^2\)The ntora is a small village or a group of neighborhoods
essential for a better understanding of the disease. To this end, various bioinformatics tools are available to centralize knowledge about possible relations between proteins into networks known as Protein-Protein Interaction (PPI) networks. The platform string (Szklarczyk et al., 2015) accessible via http://www.string-db.org is one of the most popular tools for this task. Given a set of one (or several) initial protein(s) provided by the user, it is possible to recover a valued network between all proteins connected to the initial set. The value of an edge in this network corresponds to a score obtained by aggregating different types of knowledge (wet-lab experiments, textmining, co-expression data, etc...), reflecting a level of confidence. Thus, it is possible for a given protein – we choose ER here – to recover the PPI network between all proteins involved. Our ambition is to rely on SBM with missing data to finely analyze such networks: we rather describe a dyad as missing (thus not choosing between 0 or 1) if its level of confidence is too low.

ER (ESR1) network and missing data. The PPI network in the neighborhood of ER is composed by 741 proteins connected by edges with values in (0,1]. We remove ER from this set of proteins, as well the zinc finger protein 44. Indeed, they were both connected to most of the other proteins and would thus only blur the underlying clustering structure of the network. We denote $\omega_{ij}$ the weight associated with dyad $(i,j)$. By means of a tuning parameter $\gamma$ reflecting the level of confidence, the adjacency matrix is defined as follows:

$$A^{\gamma} = (A^{\gamma})_{ij} = \begin{cases} 1 & \text{if } \omega_{ij} > 1 - \gamma, \\ \text{NA} & \text{if } \gamma \leq \omega_{ij} \leq 1 - \gamma, \\ 0 & \text{if } \omega_{ij} < \gamma. \end{cases}$$

(15)

In order to analyze the ER-centered network, Algorithm 1 (random dyad MAR sampling) and Algorithm 2 (double-standard NMAR sampling) were applied on $A^{\gamma}$ for $\gamma$ varying in {.15,.25,.35}, hence taking the uncertainties on the missing dyads into account with various thresholds. The ICL criterion in Figure 9 systematically chooses the NMAR modeling against the MAR modeling, whatever the value of $\gamma$.

Figure 9: ICL criteria for SBMs with random dyad MAR sampling and double-standard NMAR sampling in the thresholded ER network.

In the following, we study the best MAR and NMAR models associated with $\gamma = 0.35$, which value exhibits a clearer choice of the ICL than for $\gamma = \{.15,.25\}$ for
both MAR and NMAR modelings. The two corresponding SBMs have 11 clusters for MAR sampling and 13 clusters for NMAR sampling. We represent the estimated connectivity matrix $\hat{\pi}$ in Figure 10b for NMAR, which exhibits a network-structure with 13 blocks (or sets of proteins) the sizes of which can be sketched from Figure 10a. In Figure 10c, we represent on the same matrix the network with the original missing data and the imputed missing dyads with the variational parameters $\nu$. Interestingly, many of the imputed values are close to 1, which might help validating some relationships which were still uncertain in the biological literature.

To further show the improvements of the NMAR modeling over the MAR modeling, we compare the clustering respectively obtained. The ARI between the two clusterings is around 0.39: in the light of Figure 10a, this is mainly due to the third block (set 3) of the MAR classification, which contains much more nodes than in the NMAR classification. The latter dispatches many of these nodes in sets 3, 4, 6 and 13 thanks to the double standard modeling of the sampling.

To prove that this finest clustering of the nodes in NMAR modeling is more relevant from the biological point of view, we propose validation based on external biological knowledge. To this end, we rely on the Gene Ontology (GO) Annotation (Ashburner et al., 2000) which provides a DAG of ontologies to which genes are annotated if the proteins encoded by these genes have been shown to be involved in a biological process. Here, we use GO to perform enrichment analysis (that is to say identifying classes of genes or proteins that are over-represented in a large set of genes or proteins, via a simple hypergeometric test) on genes corresponding to the proteins present in set 3 for MAR, and sets 3, 4, 6 and 13 for NMAR. Interestingly, at a significance level of 1%, we find a single significant biological process for MAR modeling while 13 where found significant in the NMAR case. We checked that it was not due to a simple threshold effect by looking at the ranks of the p-values of the 13 NMAR significant processes in the 100 first most significant terms found the MAR model: only 5 of the NMAR processes were found, with high ranks (24, 33, 39, 56 and 77) far from the smallest MAR p-values.

6 Conclusion

This paper shows how to deal with missing data on dyads in SBM. We study MAR and NMAR sampling designs motivated by network data and propose variational approaches to perform SBM inference under this series of designs, accompanied with model selection criteria. Relevance of the method is illustrated on numerical experiments both on simulated and real-world networks. An R-package missSBM is available on at https://github.com/jchiquet/missSBM.

This work focuses on undirected binary networks. However, it can be adapted to other SBM, in particular those developed in Mariadassou et al. (2010) for (un)directed valued networks with weights in the exponential family. It could also be adapted to the degree-corrected SBM (Karrer and Newman, 2011). Indeed, the sampling design could depend on the degree correction parameters which should lead to a sampling design close to the star degree sampling. In future works, we plan to investigate the consistency of the variational estimators of SBM under missing data conditions, looking for similar results as the ones obtained in Bickel et al. (2013) for fully observed networks. Another path of research is to consider missing data where we cannot distinguish between a missing dyad and the absence of an edge like in (Priebel et al.,
(a) Clustering comparison between MAR and NMAR (11 vs 13 blocks).

(b) Matrix of connectivity $\hat{\pi}$ for NMAR inference (double standard); intensity of the color is proportional to the probability of connection between blocks.

(c) ER PPI network reordered by blocks inferred with SBM with NMAR modeling. Left panel: original data with NA entries colored in gray (upper triangle) and data imputed with $\nu_{ij}$ (lower triangle); right panel: zoom of blocks (1,2,3)

Figure 10: ER PPI network analysis with SBM under missing data conditions
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A Appendices

A.1 Proof of Proposition 1.ii)

Proposition 1.ii) is a direct consequence of the following lemma (Lauritzen, 1996).

Lemma. Let $V_1, V_2, V_3$ and $V_4$ be random variables, then for all $h$ measurable,

$$V_1 \perp (V_2, V_3) \mid V_4 \Rightarrow V_1 \perp V_2 \mid (V_3, h(V_4)).$$

The results follows by applying this lemma for $h$ the identity function:

$$R \perp (Y^m, Z) \mid Y^o \Rightarrow R \perp Z \mid (Y^o, Y^m).$$
A.2 Identifiability

In the following proofs, when the sampling is node-centered we denote \( V_i = 1 \) if node \( i \) is observed and \( V_i = 0 \) otherwise.

**Proof of Theorem 2.1.** Let \( \rho, \rho' > 0 \) such that \( p_\rho(R) = p_{\rho'}(R) \) (resp. \( p_\rho(V) = p_{\rho'}(V) \)). Since \( R \) (resp. \( V \)) does not depend on \( Y \), then \( \mathbb{P}_\rho(R_{ij} = 1) = \rho = \rho' = \mathbb{P}_{\rho'}(R_{ij} = 1) \) (resp. \( \mathbb{P}_\rho(V_i = 1) = \rho = \rho' = \mathbb{P}_{\rho'}(V_i = 1) \)). \( \square \)

**Proof of Theorem 2.2.** Let \( P_{[n]}^o \) denote the probability distribution function of \( Y^o \), the observed SBM with \( n \) nodes. We show that there exists a unique \((\alpha, \pi)\) corresponding to \( P_{[n]}^o \).

Up to reordering, let \( s_1 < s_2 < \ldots < s_Q \) be the coordinates of vector \( s \) in the increasing order. Then \( s_q = \mathbb{P}(Y_{ij}R_{ij} = 1|Z_i = q) \) (resp. \( s_q = \mathbb{P}(Y_{ij} = 1|Z_i = q) \)).

Let \( S \) denote the Van der Monde matrix defined by \( S_{i,q} = s_q^i \) for \( 0 \leq i < Q \) and \( 1 \leq q \leq Q \). \( S \) is invertible since the coordinates of \( s \) are all different. For \( i \geq 1 \) we have : \( S_{i,q} = \mathbb{P}(Y_{12}R_{12} = 1, \ldots, Y_{i+1,i+1}R_{i+1,i+1} = 1|Z_i = q) \) (resp. \( S_{i,q} = \mathbb{P}(Y_{12} = 1, \ldots, Y_{i+1,i+1} = 1|Z_i = q) \)).

Let us also define

\[
    u_i = \sum_{1 \leq k \leq Q} \alpha_k s_k^i \quad (\text{resp. } u_i = \sum_{1 \leq k \leq Q} \rho \alpha_k s_k^i), \quad i = 0, \ldots, 2Q - 1.
\]

For \( i \geq 1 \) we have : \( u_i = \mathbb{P}(Y_{12}R_{12} = 1, \ldots, Y_{i+1,i+1}R_{i+1,i+1} = 1) \) (resp. \( u_i = \mathbb{P}(Y_{12} = 1, \ldots, Y_{i+1,i+1} = 1, V_i = 1) \)). Note that \( n \geq 2Q \) is a necessary requirement on \( n \) since \( Y_{i,i} = 0 \) by assumption. Hence given \( P_{[n]}^o \) and \( \rho, u_0 = 1 \) and \( u_1, \ldots, u_{2Q-1} \) are known.

Furthermore, set \( M \) the \((Q + 1) \times Q \) matrix given by \( M_{i,j} = u_{i+j} \) for every \( 0 \leq i \leq Q \) and \( 0 \leq j < Q \), and let \( M_i \) denote the square matrix obtained by removing the row \( i \) from \( M \). The coefficients of \( M_Q \), for \( 0 \leq i, j < Q \), are

\[
    M_{i,j} = \sum_{1 \leq k \leq Q} s_k^i \alpha_k s_k^j \quad (\text{resp. } M_{i,j} = \sum_{1 \leq k \leq Q} \rho s_k^i \alpha_k s_k^j), \quad 0 \leq i, j < Q.
\]

Defining the diagonal matrix \( A = \text{Diag}(\alpha) \), it comes that \( M_Q = SAS^t \) (resp. \( M_Q = \rho SAS^t \)), where \( S \) and \( A \) are invertible, but unknown at this stage, and \( \rho > 0 \). With \( D_k = \det(M_k) \) and the polynomial \( B(x) = \sum_{k=0}^Q (-1)^{k+Q} D_k x^k \), it yields \( D_Q = \det(M_Q) \neq 0 \) and the degree of \( B \) is equal to \( Q \).

Set \( C_i = (1, s_i, \ldots, s_i^Q)^t \) and let us notice that \( B(s_i) \) is the determinant of the square matrix produced when appending \( C_i \) as last column to \( M \). The \( Q+1 \) columns of this matrix are linearly dependent, since they are all linear combinations of the \( Q \) vectors \( C_1, C_2, \ldots, C_Q \). Hence \( B(s_i) = 0 \) and \( s_i \) is a root of \( B \) for every \( 1 \leq i \leq Q \). This proves that \( B = D_Q \prod_{i=1}^Q (x - s_i) \). Then, one knows \( r = (s_1, \ldots, s_Q) \) (as the roots of \( B \) defined from \( M \) and \( R \). It results that \( A = S^{-1}M_Q(S^t)^{-1} \), which yields a unique \((\alpha_1, \ldots, \alpha_Q)\) (resp. \( A = \rho^{-1}S^{-1}M_Q(S^t)^{-1} \)).

It only remains to determine \( \pi \). For \( 0 \leq i, j < Q \), let us introduce \( U_{i,j} \) the probability that the first row of \( Y^o \) begins with \( i+1 \) occurrences of \( 1 \), and the second row of \( Y^o \) ends up with \( j \) occurrences of \( 1 \) (\( i + 1 + j < n - 1 \) implies \( n \geq 2Q \)).

Then, \( U_{i,j} = \sum_{k,l} S_{i,k} \alpha_k \pi_{k,l} \alpha_l S_{j,l} \) (resp. \( U_{i,j} = \sum_{k,l} \rho^2 S_{i,k} \alpha_k \pi_{k,l} \alpha_l S_{j,l} \)), for \( 0 \leq i, j < Q \), and the \( Q \times Q \) matrix \( U = RA\pi AR^t \). The conclusion results from \( \pi = A^{-1}S^{-1}U(S^t)^{-1}A^{-1} \) (resp. \( \pi = \rho^{-2}A^{-1}S^{-1}U(S^t)^{-1}A^{-1} \)). \( \square \)
Proof of Theorem 2.3. Let $P_{[n]}$ denote the probability distribution function of $(Y^o, R)$ of the observed SBM with $n$ nodes and the sampling matrix. We show that there exists a unique $(\alpha, \pi, \rho)$ corresponding to $P_{[n]}$.

**Identifiability of $\alpha$.** Up to reordering, let $t_1 < t_2 < \ldots < t_Q$ denote the coordinates of the vector $t$ in the increasing order, we have: $t_q = \mathbb{P}(Y_{ij} = 1, V_j = 1|Z_i = q)$. Let $T$ denote the Van der Monde matrix defined by $T_{i,q} = t_i^q$, for $0 \leq i < Q$ and $1 \leq q \leq Q$. $T$ is invertible since the coordinates of $t$ are all different. For $i \geq 1$ we have: $T_i = \mathbb{P}(Y_{12} = 1, \ldots, Y_{i+1} = 1, V_2 = 1, \ldots, V_{i+1} = 1|Z_1 = q)$.

Let us also define $$v_i = \sum_{1 \leq k \leq Q} \alpha_k t_k^i, \quad i = 0, \ldots, 2Q - 1.$$ For $i \geq 1$ we have: $v_i = \mathbb{P}(Y_{12} = 1, \ldots, Y_{i+1} = 1, V_2 = 1, \ldots, V_{i+1} = 1)$. Hence given $P_{[n]}$, $v_0 = 1$ and $v_1, \ldots, v_{2Q-1}$ are known.

Furthermore, set $N$ the $(Q+1) \times Q$ matrix given by $N_{ij} = v_{i+j}$ for every $0 \leq i \leq Q$ and $0 \leq j < Q$, and let $N_i$ denote the square matrix obtained by removing the row $i$ from $N$. The coefficients of $N_Q$ are $$N_{i,j} = v_{i+j} = \sum_{1 \leq k \leq Q} t_k^i \alpha_k t_k^j, \quad 0 \leq i, j < Q.$$ Defining the diagonal matrix $A = \text{Diag}(\alpha)$, it comes that $N_Q = TAT^t$, where $T$ and $A$ are invertible. With $D_k = \det(N_k)$ and the polynomial $B(x) = \sum_{k=0}^Q (-1)^{k+Q} D_k x^k$, it yields $D_Q = \det(N_Q) \neq 0$ and the degree of $B$ is equal to $Q$.

Set $C_i = (1, t_i, \ldots, t_i^Q)^t$ and let us notice that $B(t_i)$ is the determinant of the square matrix produced when appending $C_i$ as last column to $N$. The $Q+1$ columns of this matrix are linearly dependent, since they are all linear combinations of the $Q$ vectors $C_1, C_2, \ldots, C_Q$. Hence $B(t_i) = 0$ and $t_i$ is a root of $B$ for every $1 \leq i \leq Q$. This proves that $B = D_Q \prod_{i=1}^Q (x - t_i)$. Then, one knows $r = (t_1, \ldots, t_Q)$ (as the roots of $B$ defined from $N$) and $R$. It results that $A = T^{-1}N_Q(T^t)^{-1}$, which yields a unique $(\alpha_1, \ldots, \alpha_Q)$.

**Identifiability of $\rho$.** Up to reordering, let $o_1 < o_2 < \ldots < o_Q$ denote the coordinates of the vector $o$ in the increasing order, we have: $s_q = \mathbb{P}(Y_{ij} = 1, V_i = 1|Z_i = q) = \rho_q o_q$. Let $O$ denote the Van der Monde matrix defined by $O_{i,q} = o_i^q$, for $0 \leq i < Q$ and $1 \leq q \leq Q$. $O$ is invertible since the coordinates of $o$ are all different. For $i \geq 1$ we have: $O_i = \mathbb{P}(Y_{12} = 1, \ldots, Y_{i+1} = 1|Z_1 = q)$.

Let us also define $$u_i = \sum_{1 \leq k \leq Q} \rho_k \alpha_k o_k^i, \quad i = 0, \ldots, 2Q - 1.$$ For $i \geq 1$ we have: $u_i = \mathbb{P}(Y_{12} = 1, \ldots, Y_{i+1} = 1, V_1 = 1)$. Hence given $P_{[n]}$, $u_0 = 1$ and $u_1, \ldots, u_{2Q-1}$ are known.

Furthermore, set $M$ the $(Q+1) \times Q$ matrix given by $M_{i,j} = u_{i+j}$ for every $0 \leq i \leq Q$ and $0 \leq j < Q$, and let $M_i$ denote the square matrix obtained by removing the row $i$ from $M$. The coefficients of $M_Q$ are $$M_{i,j} = u_{i+j} = \sum_{1 \leq k \leq Q} o_k^i \alpha_k \rho_k o_k^j, \quad 0 \leq i, j < Q.$$
Defining the diagonal matrix $B = \text{Diag}(\rho)$, it comes that $M_Q = OABO^t$, where $O$, $B$, and $A$ are invertible. Using the same algebraic argument than for the identifiability of $\alpha$, it results that $B = A^{-1}T^{-1}M_Q(T^t)^{-1}$, which yields, because of the identifiability of $\alpha$, a unique $(\rho_1, \ldots, \rho_Q)$.

**Identifiability of $\pi$.** For $0 \leq i, j < Q$, let us introduce $U_{i,j}$ the probability that the first row of $Y^o$ begins with $i + 1$ occurrences of 1, and the second row of $Y^o$ ends up with $j$ occurrences of 1.

\[
U_{i,j} = \mathbb{P}\left(\{Y_{12} = 1, \ldots, Y_{1i+2} = 1, V_2 = 1, \ldots, V_{i+2} = 1\} \cap \{Y_{2n-j} = 1, \ldots, Y_{2n} = 1, V_{n-j} = 1, \ldots, V_n = 1\}\right),
\]

Then, $U_{i,j} = \sum_{k,l} T_{i,k} \alpha_k \pi_{k,l} \rho_k \alpha_l T_{j,l}$, for $0 \leq i, j < Q$, and the $Q \times Q$ matrix $U = TA\pi ABT^t$. The conclusion results from $\pi = A^{-1}T^{-1}U(T^t)^{-1}B^{-1}A^{-1}$.

### A.3 Derivation of second lower bound in star degree sampling

For $0 \leq i, j < Q$, let us introduce $U_{i,j}$ the probability that the first row of $Y^o$ begins with $i + 1$ occurrences of 1, and the second row of $Y^o$ ends up with $j$ occurrences of 1.

\[
U_{i,j} = \mathbb{P}\left(\{Y_{12} = 1, \ldots, Y_{1i+2} = 1, V_2 = 1, \ldots, V_{i+2} = 1\} \cap \{Y_{2n-j} = 1, \ldots, Y_{2n} = 1, V_{n-j} = 1, \ldots, V_n = 1\}\right),
\]

Then, $U_{i,j} = \sum_{k,l} T_{i,k} \alpha_k \pi_{k,l} \rho_k \alpha_l T_{j,l}$, for $0 \leq i, j < Q$, and the $Q \times Q$ matrix $U = TA\pi ABT^t$. The conclusion results from $\pi = A^{-1}T^{-1}U(T^t)^{-1}B^{-1}A^{-1}$.

### A.4 Proof of Proposition 6

In the complete likelihood (7), the derivation of the second and third terms are done following Biernacki et al. (2000) and Daudin et al. (2008). Concerning the first term, if the sampling design is node-centred (respectively dyad-centred) it consists in $n$ Bernoulli random variables (respectively $n(n-1)/2$ Bernoulli random variables). The likelihood $\log p_\psi(R|Y^o, Y^m, Z, Q)$ can be derived using a BIC approximation:

\[
\log p_\psi(R|Y, Z, Q) \simeq \arg \max_\psi \log p(R|Y, Z, Q) + \text{pen}_{\text{BIC}},
\]

where $\text{pen}_{\text{BIC}} = \left\{\begin{array}{ll} K \times \log(n) & \text{if the sampling design is dyad-centred,} \\ \frac{1}{2} \times K \times \log\left(\frac{n(n-1)}{2}\right) & \text{otherwise.} \end{array}\right.$