Model-Based Clustering of Time-Evolving Networks through Temporal Exponential-Family Random Graph Models

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Abstract

Dynamic networks are a general language for describing time-evolving complex systems, and discrete time network models provide an emerging statistical technique for various applications. It is a fundamental research question to detect the community structure in time-evolving networks. However, due to significant computational challenges and difficulties in modeling communities of time-evolving networks, there is little progress in the current literature to effectively find communities in time-evolving networks. In this work, we propose a novel model-based clustering framework for time-evolving networks based on discrete time exponential-family random graph models. To choose the number of communities, we use conditional likelihood to construct an effective model selection criterion. Furthermore, we propose an efficient variational expectation-maximization (EM) algorithm to find approximate maximum likelihood estimates of network parameters and mixing proportions. By using variational methods and minorization-maximization (MM) techniques, our method has appealing scalability for large scale time-evolving networks. The power of our method is demonstrated in simulation studies and empirical applications to international trade networks and the collaboration networks of a large American research university.

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1 Introduction

Dynamic networks are a general language for describing time-evolving complex systems, and
discrete time network models provide an emerging statistical technique to study biological, busi-
ness, economic, information, and social systems in the real world. For example, time-evolving
networks shed light on understanding critical processes such as the study of biological functions
using protein-protein interaction networks (Han et al. 2004, Taylor et al. 2009), and also con-
tribute to assessing infectious disease epidemiology, dynamic brain networks and time-evolving
structures of social networks (Morris & Kretzschmar 1995, Bearman et al. 2004, Kossinets &
Watts 2006, Park & Friston 2013, Lee & Xue 2017).

A community can be defined as a set of nodes sharing similar connectivity patterns. In
computer science and statistical physics, many node clustering algorithms have been developed.
Girvan & Newman (2002) propose an algorithm to identify communities based on edge “be-
tweenness”. They construct communities by progressively removing the edges that connect
communities most from the original network. Newman & Girvan (2004) proposed three differ-
ent measures of “betweenness” and compared the results based on modularity, which measures
the quality of a particular division of a network. On the other hand, in statistics, analyzing
and clustering networks is often based on statistical mixture models. One idea of model-based
clustering in networks comes from Handcock et al. (2007), who propose a latent position cluster
model that extends the latent space model of Hoff et al. (2002) to take account of clustering,
using the model-based clustering ideas of Fraley & Raftery (2002). In current literature, there
are two very popular statistical models. One is the stochastic block model (SBM) and the other
is the exponential-family random graph model (ERGM).

Stochastic block models were first introduced by Holland et al. (1983) and they focused on the
case of a priori specified blocks, where the memberships are known or assumed and the goal is to
estimate a matrix of edge probabilities. A statistical approach to a posteriori block modeling for
networks was introduced by Snijders & Nowicki (1997) and Nowicki & Snijders (2001), where the
objective is to simultaneously estimate the matrix of edge probabilities and the memberships.
Airoldi et al. (2008) relax the assumption of a single latent role for nodes and develop a mixed membership stochastic block model. Karrer & Newman (2011) relax the assumption that a stochastic block model treats all nodes within a community as stochastically equivalent and propose a degree-corrected stochastic block model that can consider node covariates. Moreover, in recent years, asymptotic theory of these models has been advanced by several pioneering papers including Bickel & Chen (2009), Choi et al. (2012), Amini et al. (2013), and Choi & Wolfe (2014). The communities found in stochastic block models are interpreted meaningfully in many research fields. For example, in citation and collaboration networks, such communities can be interpreted as scientific disciplines (Newman 2004, Ji & Jin. 2016). Communities in food web networks can be interpreted as ecological subsystems (Girvan & Newman 2002). Unlike the time-evolving networks considered in the current article, cross-sectional networks are the basis of most of the stochastic block model literature cited here.

Exponential-family random graph models allow researchers to incorporate interesting features of the network into statistical models. Moreover, researchers can specify a model capturing those features and cluster nodes based on the specified model. Indeed, the stochastic block model is a special case of a mixture of exponential-family random graph models. Some estimation algorithms for exponential-family random graph models do not scale well computationally to large networks. Vu et al. (2013) propose ERGM-based clustering for large-scale cross-sectional networks that solves the scalability issue by assuming dyadic independence conditional on the cluster memberships of nodes. In recent years, several authors have proposed discrete time network models based on ERGM. Hanneke et al. (2010) propose a temporal ERGM (TERGM) to fit the model to a network series and Krivitsky & Handcock (2014) propose a separable temporal ERGM (STERGM) that gives more flexibility in modeling time-evolving networks.

Our work is primarily motivated by detecting communities in time-evolving networks, and our results advance existing literature by introducing a promising framework that incorporates model-based clustering while remaining computationally scalable to large networks. This framework is based on discrete time exponential-family random graph models and inherits the
philosophy of finite mixture models, which simultaneously allows both modeling and detecting communities in time-evolving networks, helping researchers and practitioners understand the complex structure of these networks. Moreover, we propose a conditional likelihood Bayesian information criterion to solve the model selection problem of determining an appropriate number of communities. We also propose an efficient variational expectation-maximization (EM) algorithm that exhibits computational scalability for large-scale time-evolving networks by exploiting variational methods and minorization-maximization (MM) techniques.

In Section 2, we present our model-based clustering method for time-evolving networks based on a finite mixture of discrete time exponential-family random graph models. In Section 3, we use conditional likelihood to construct an effective model selection criterion. Section 4 designs an efficient variational expectation-maximization algorithm to find approximate maximum likelihood estimates of network parameters and mixing proportions. Given these estimates, we can infer membership labels and solve the problem of community detection for time-evolving networks. The power of our method is demonstrated by simulation studies in Section 5 and real-world applications to international trade networks and collaboration networks in Section 6.

2 Methodology

2.1 Model-based clustering of time-evolving networks through discrete time ERGMs

In this section, we present the model-based clustering method for time-evolving networks based on a finite mixture of discrete time exponential-family random graph models. First, we introduce some necessary notation. We consider \( n \) nodes that are fixed over time and indexed by integers \( 1, \ldots, n \). Let \( Y_t = (Y_{t,ij})_{1 \leq i,j \leq n} \in \mathcal{Y} \) represent the network at time \( t = 0, 1, \ldots, T \) and denote by \( y_t = (y_{t,ij})_{1 \leq i,j \leq n} \) the corresponding observed network, where \( \mathcal{Y} \) is the set of all possible networks. Let \( \theta \in \mathbb{R}^p \) be a vector of \( p \) network parameters of interest. Under the \( k \)-order Markov
assumption, discrete time exponential-family random graph models are of the form

\[
\text{pr}_\theta(Y_t = y_t \mid y_{t-1}, \ldots, y_0) = \exp\{\theta' g(y_t, y_{t-1}, \ldots, y_{t-k}) - \psi(\theta, y_{t-1}, \ldots, y_{t-k})\}, \quad (1)
\]

where \(\psi(\theta, y_{t-1}, \ldots, y_{t-k})\) is given by

\[
\psi(\theta, y_{t-1}, \ldots, y_{t-k}) = \log \sum_{y^* \in \mathcal{Y}} \exp \left[ \theta' g(y^*, y_{t-1}, \ldots, y_{t-k}) \right]
\]

and ensures that \(\text{pr}_\theta(Y_t = y_t \mid y_{t-1}, \ldots, y_0)\) sums to 1. Here, \(g(y_t, y_{t-1}, \ldots, y_{t-k})\) is a \(p\)-dimensional vector of sufficient statistics on networks \(y_t, \ldots, y_{t-k}\).

We now focus on the simplest case of discrete time exponential-family random graph models under the first-order Markov assumption and we write the one-step transition probability from \(Y_{t-1}\) to \(Y_t\) as

\[
\text{pr}_\theta(Y_t = y_t \mid y_{t-1}) = \exp\{\theta' g(y_t, y_{t-1}) - \psi(\theta, y_{t-1})\}, \quad (2)
\]

where \(\psi(\theta, y_{t-1})\) and \(g(y_t, y_{t-1})\) are defined as above.

**Remark 1:** Given covariates \(x_t\) and a vector \(\beta \in \mathbb{R}^q\) of covariate coefficients, we can also write the transition probability from \(Y_{t-1}\) to \(Y_t\) with covariates as

\[
\text{pr}_{\theta, \beta}(Y_t = y_t \mid y_{t-1}, x_t) = \exp\{\theta' g(y_t, y_{t-1}) + \beta' h(y_t, x_t) - \psi(\theta, \beta, y_{t-1})\},
\]

where \(\psi(\theta, \beta, y_{t-1}) = \log \sum_{y^* \in \mathcal{Y}} \exp [\theta' g(y^*, y_{t-1}) + \beta' h(y^*, x_t)]\). Here, \(h(y_t, x_t)\) is a \(q\)-dimensional vector of statistics.

In general, for some choices of \(g(y_t, y_{t-1})\), the model in \(2\) is not tractable for modeling large networks, since the computing time to evaluate the likelihood function directly grows as \(2^{(2)}\) in the case of undirected edges. Here, we restrict our attention to scalable exponential-family models by only choosing statistics that preserve conditional dyadic independence wherein the
distribution of $\mathbf{Y}_t$ given $\mathbf{Y}_{t-1}$ factors over the edge states, i.e.,

$$\text{pr}_g(\mathbf{Y}_t = \mathbf{y}_t \mid \mathbf{Y}_{t-1}) = \prod_{i<j} \text{pr}_g(Y_{t,ij} = y_{t,ij} \mid \mathbf{Y}_{t-1}).$$  \hspace{1cm} (3)

Before proceeding, we introduce specific examples of statistics that preserve conditional dyadic independence and capture interesting time-evolving network features in both TERGM and STERGM:

$$g^d(\mathbf{y}_t, \mathbf{y}_{t-1}) = \sum_{i<j} y_{t,ij},$$  \hspace{1cm} (4)

$$g^s(\mathbf{y}_t, \mathbf{y}_{t-1}) = \sum_{i<j} [y_{t,ij}y_{t-1,ij} + (1 - y_{t,ij})(1 - y_{t-1,ij})].$$  \hspace{1cm} (5)

$$g^f(\mathbf{y}_t, \mathbf{y}_{t-1}) = \sum_{i<j} [y_{t,ij} - y_{t,ij}y_{t-1,ij}],$$  \hspace{1cm} (6)

$$g^p(\mathbf{y}_t, \mathbf{y}_{t-1}) = \sum_{i<j} y_{t,ij}y_{t-1,ij}.$$  \hspace{1cm} (7)

The subscripted $i < j$ and superscripted $n$ mean that summation should be taken over all pairs $(i, j)$ with $1 \leq i < j \leq n$; the same is true for products as in equation (3). Corresponding to the first and second statistics above are TERGM parameters: $\theta^d$ relates to density, or the number of edges in the network at time $t$, while $\theta^s$ relates to stability, or the number of edges maintaining their status from time $t - 1$ to time $t$. Corresponding to the third and fourth statistics above are STERGM parameters: $\theta^f$ relates to formation, or the number of edges absent at time $t - 1$ but present at time $t$, while $\theta^p$ relates to persistence, or the number of edges existing at time $t - 1$ that survive to time $t$.

Here, as in Vu et al. (2013), we assume that the probability mass function has a $K$-component
mixture form as follows:

$$\text{pr}_{\pi, \theta}(Y_t = y_t \mid y_{t-1}) = \sum_{z \in Z} \text{pr}_{\theta}(Y_t = y_t \mid y_{t-1}, z)\text{pr}_{\pi}(Z = z)$$

$$= \sum_{z \in Z} \prod_{i<j} \text{pr}_{\theta_{i,j}}(Y_{t,i,j} = y_{t,i,j} \mid y_{t-1}, z)\text{pr}_{\pi}(Z = z),$$

(8)

where $Z = (Z_1, \ldots, Z_n)$ denotes the membership indicators with distributions

$$Z_i \mid \pi_1, \ldots, \pi_K \overset{i.i.d.}{\sim} \text{Multinomial}(1; \pi_1, \ldots, \pi_K)$$

and $Z$ denotes the support of $Z$. In the mixture form (8), the assumption of conditional dyadic independence given $z$ strikes a balance between complexity and parsimony. For now, the number of communities $K$ is fixed and known. In Section 3, we will discuss how to choose an optimal number of communities $K$.

Now, we consider inference based on observing a series of networks, $y_1, y_2, \ldots, y_T$, given an initial network $y_0$. The log-likelihood of the observed network series is

$$\ell(\pi, \theta) = \log \left[ \prod_{t=1}^{T} \text{pr}_{\pi, \theta}(Y_t = y_t \mid y_{t-1}) \right]$$

$$= \sum_{t=1}^{T} \log \left[ \sum_{z \in Z} \text{pr}_{\theta}(Y_t = y_t \mid y_{t-1}, z)\text{pr}_{\pi}(Z = z) \right].$$

(9)

Our aim is to estimate parameters $\pi$ and $\theta$ via maximizing the log-likelihood $\ell(\pi, \theta)$, i.e.,

$$\left(\hat{\pi}, \hat{\theta}\right) = \arg \max_{(\pi, \theta)} \ell(\pi, \theta).$$

Section 4 designs a novel variational EM algorithm to efficiently find the approximate maximum likelihood estimates. We shall see that the parameter estimates obtained by this algorithm can provide community membership labels.

Before proceeding, we give specific examples of discrete time exponential-family random graph models with stability parameter(s) that control the rate of evolution of a network. Sta-
bility parameters are popular in the study of time-evolving networks; in sociology, researchers
are interested in whether, say, same-gender friendships are more stable than other friendships
or whether there are differences among ethnic categories in forming lasting sexual partnerships
over time (Knecht 2008, Krivitsky et al. 2011).

Example 1: When \( K = 1 \) and \( g(y_t, y_{t-1}) \) consists only of the stability statistics \( (5) \), the model
reduces to TERGM with a stability parameter as in [Hanneke et al. (2010)]:

\[
\Pr_{\theta_z, \theta_y} (Y_{t,ij} = y_{t,ij} | y_{t-1}, z, y_{t-1,ij}) \propto \exp[(\theta_z y_{t,ij}) (y_{t,ij} y_{t-1,ij}) + (1 - y_{t,ij}) (1 - y_{t-1,ij})].
\]

Example 2: When \( K = 1 \) and \( g(y_t, y_{t-1}) \) consists of both formation parameters \( (6) \) and
persistence parameters \( (7) \), the model reduces to STERGM with formation and persistence
parameters as in [Krivitsky & Handcock (2014)]:

\[
\Pr_{\theta_f, \theta_p} (Y_{t,ij} = y_{t,ij} | y_{t-1}, z) \propto \exp[(\theta_f y_{t,ij} - y_{t,ij} y_{t-1,ij}) + (\theta_p y_{t,ij} y_{t-1,ij})].
\]

2.2 Parameter Identifiability

The unique identifiability of the parameters in a broad class of random graph mixture models
has been shown by [Allman et al. (2009) and Allman et al. (2011)]. Here we prove the generic
identifiability for our proposed parameterizations. Theorem 1, whose proof is given in Appendix,
extends the identifiability result of the stochastic block model of [Allman et al. (2009) and
Allman et al. (2011)] to discrete time exponential-family random graph mixture models. In this
context, “generically identifiable” means uniquely identifiable except possibly on a subset of the
parameter space whose Lebesgue measure is zero.

Theorem 1. Let \( n \) be the number of nodes in a time-evolving network. The parameters \( \pi_k, 1 \leq k \leq K \),
and the conditional probability of observing an edge \( p_{kl} = \Pr_{\theta_{kl}} (Y_{t,ij} = 1 | y_{t-1}, z) \),
1 \leq k \leq l \leq K \text{ of equation (8) are generically identifiable, up to permutations of the subscripts } 1, \ldots, K, \text{ if }
\begin{cases}
\sqrt{n/2} \geq K - 1 + (K + 2)^2/4, & \text{for } K \text{ even;} \\
\sqrt{n/2} \geq K - 1 + (K + 1)(K + 3)/4, & \text{for } K \text{ odd.}
\end{cases}

Moreover, the network parameters \( \theta_k \in \mathbb{R}^p \), 1 \leq k \leq K in the model (e.g., Examples 1 and 2) are generically identifiable, up to permutations of the subscripts 1, \ldots, K, if \( p \leq \lfloor (K + 1)/2 \rfloor \).

## 3 Model selection

In practice, the number of communities is unknown and should be chosen. Handcock et al. (2007) propose a Bayesian method of determining the number of clusters by using approximate conditional Bayes factors in a latent position cluster model. Daudin et al. (2008) also derive a Bayesian model selection criterion that is based on the integrated classification likelihood (ICL). In this section, we use the conditional likelihood of the network series, conditioning on an estimate of the membership vector, to construct an effective model selection criterion.

We obtain the conditional log-likelihood of the network series \( y_1, y_2, \ldots, y_T \), given initial network \( y_0 \) and estimated membership vector \( \hat{z} \), as

\[
\text{cl}(\theta, \hat{z}) = \sum_{t=1}^{T} \log \Pr_{\theta}(Y_t = y_t | y_{t-1}, \hat{z}),
\]

which can be written using conditional dyadic independence in the form

\[
\text{cl}(\theta, \hat{z}) = \sum_{t=1}^{T} \sum_{i<j} \log \Pr_{\theta_{ij}}(Y_{t,ij} = y_{t,ij} | y_{t-1}, \hat{z}).
\]

We propose the conditional likelihood Bayesian information criterion to choose the number of communities for our method:

\[
\text{CL-BIC}_K = -2\text{cl}(\hat{\theta}_{\text{mle}}, \hat{z}) + d_K(\hat{\theta}_{\text{mle}}, \hat{z}) \log[Tn(n-1)/2],
\]
where \( \hat{\theta}_{\text{mle}} \) is the maximum likelihood estimate assuming \( K \) communities and \( d_K(\theta, \hat{z}) = \text{tr}(H_K^{-1}V_K) \) is the model complexity, following Varin & Vidoni (2005), Varin et al. (2011) and Xue et al. (2012), based on \( H_K = \mathbb{E}(-\nabla^2 \text{cl}(\theta, \hat{z})) \) and \( V_K = \text{var}(\nabla \text{cl}(\theta, \hat{z})) \). We choose the optimal \( K \) by minimizing the CL-BIC score.

**Remark 2:** In cross-sectional networks, a similar criterion, the composite likelihood BIC, is proposed by Saldana et al. (2017) in the stochastic block model setting where the membership vector is estimated separately using a method such as spectral clustering.

We may derive the explicit conditional likelihood BIC for Examples 1 and 2, i.e., the TERGM and STERGM cases. For TERGM with a stability parameter, we obtain

\[
\text{cl}(\theta^s, \hat{z}) = \sum_{t=1}^{T} \sum_{i<j}^{n} \left[ \begin{array}{c} -\log(1 + \exp(\hat{\theta}^s_{zi} + \hat{\theta}^s_{zj})) \\ \text{yt}_{ti,j}(1 - \text{yt}_{ti,j}) \end{array} \right] \left( \begin{array}{c} \text{yt}_{ti,j} \text{yt}_{ti-1,j} + (1 - \text{yt}_{ti,j})(1 - \text{yt}_{ti-1,j}) \end{array} \right) (\hat{\theta}^s_{zi} + \hat{\theta}^s_{zj})
\]

For any given \( K \) and the corresponding estimate \( \hat{\theta}_{\text{mle}}^s \), we derive the explicit estimate of \( V_K \) as

\[
\hat{V}_K(\hat{\theta}_{\text{mle}}^s) = \sum_{t=1}^{T} u(\hat{\theta}_{\text{mle}}^s)u(\hat{\theta}_{\text{mle}}^s)',
\]

where \( u(\hat{\theta}_{\text{mle}}^s) = (u(\hat{\theta}_{\text{mle}}^s,k); 1 \leq k \leq K)' \) and

\[
u(\hat{\theta}_{\text{mle}}^s,k) = \sum_{i<j}^{n} \left[ \frac{-\exp(\hat{\theta}_{\text{mle,zi}}^s + \hat{\theta}_{\text{mle,zj}}^s)}{1 + \exp(\hat{\theta}_{\text{mle,zi}}^s + \hat{\theta}_{\text{mle,zj}}^s)} \right]
\]

\[
+ \text{yt}_{ti,j}(1 - \text{yt}_{ti,j}) \left( \begin{array}{c} 1(\hat{z}_i = k) + 1(\hat{z}_j = k) \end{array} \right).
\]

We also derive the explicit estimate of \( H_K \) as

\[
\hat{H}_K(\hat{\theta}_{\text{mle}}^s) = \begin{bmatrix}
T \sum_{i<j}^{n} \left[ \frac{4\exp(\hat{\theta}_{\text{mle,zi}}^s + \hat{\theta}_{\text{mle,zj}}^s)}{(1 + \exp(\hat{\theta}_{\text{mle,zi}}^s + \hat{\theta}_{\text{mle,zj}}^s))^2} \right] I_{1,1} & \cdots & T \sum_{i<j}^{n} \left[ \frac{\exp(\hat{\theta}_{\text{mle,zi}}^s + \hat{\theta}_{\text{mle,zj}}^s)}{(1 + \exp(\hat{\theta}_{\text{mle,zi}}^s + \hat{\theta}_{\text{mle,zj}}^s))^2} \right] I_{1,K} \\
\vdots & \ddots & \vdots \\
T \sum_{i<j}^{n} \left[ \frac{\exp(\hat{\theta}_{\text{mle,zi}}^s + \hat{\theta}_{\text{mle,zj}}^s)}{(1 + \exp(\hat{\theta}_{\text{mle,zi}}^s + \hat{\theta}_{\text{mle,zj}}^s))^2} \right] I_{K,1} & \cdots & T \sum_{i<j}^{n} \left[ \frac{4\exp(\hat{\theta}_{\text{mle,zi}}^s + \hat{\theta}_{\text{mle,zj}}^s)}{(1 + \exp(\hat{\theta}_{\text{mle,zi}}^s + \hat{\theta}_{\text{mle,zj}}^s))^2} \right] I_{K,K}
\end{bmatrix}.
\]
where $I_{i,j}^{k} = \mathbf{1}(\hat{z}_{i} = k, \hat{z}_{j} = k)$ and $I_{i,j}^{k,l} = \mathbf{1}(\hat{z}_{i} = k, \hat{z}_{j} = l) + \mathbf{1}(\hat{z}_{i} = l, \hat{z}_{j} = k)$ for $k, l = 1, \ldots, K$.

We now obtain the estimate of $d_{K}$ as $\hat{d}_{K} = \text{tr}(H_{K}^{-1}\hat{V}_{K})$. Finally, for clustering time-evolving networks through TERGM with a stability parameter, we determine the optimal number of communities from

$$\hat{K} = \arg \min_{K} \text{CL-BIC}_{K} = \arg \min_{K} -2\text{cl}(\hat{\theta}_{\text{mle}}^{*}, \hat{z}) + \hat{d}_{K}(\hat{\theta}_{\text{mle}}^{*}, \hat{z}) \log [Tn(n - 1)/2], \quad (12)$$

where $\hat{\theta}_{\text{mle}}^{*}$ and $\hat{z}$ are the estimates of $\theta^{*}$ and $z$ corresponding to a given $K$. Similar details for STERGM with formation and persistence parameters are presented in Appendix.

Here, we also introduce modified integrated classification likelihood. Again for the TERGM with a stability parameter, the modified ICL can be written as

$$\text{ICL}_{K} = \sum_{t=1}^{T} \sum_{i<j} \log [\text{pr}_{\theta_{i,j}^{*}} (Y_{t,ij} = y_{t,ij} | y_{t-1}, \hat{z})] - K \log [Tn(n - 1)/2], \quad (13)$$

and we choose the optimal number of communities as

$$\hat{K} = \arg \max_{K} \text{ICL}_{K}. \quad (14)$$

We present model selection results using both conditional likelihood BIC and modified ICL in the simulation studies of Section 5.

**Remark 3:** Our conditional likelihood BIC can also be applied to choose the number of communities for finite mixture of ERGMs in cross-sectional networks. Under the assumption of conditional dyadic independence given $z$ the conditional log-likelihood in this case can be written as

$$\text{cl}(\theta, \hat{z}) = \sum_{i<j} \log [\text{pr}_{\theta_{i,j}^{*}} (Y_{ij} = y_{ij} | \hat{z})],$$

and we choose the optimal $K$ by minimizing $\widehat{\text{CL-BIC}}_{K}$ as in equation (12) with $T = 1$. 

11
4 Computation

Here we present a novel variational EM algorithm to solve model-based clustering for large scale time-evolving networks. Our algorithm is modeled on the algorithm presented by Vu et al. (2013). The algorithm combines the power of variational methods (Wainwright & Jordan 2008) and minorization-maximization techniques (Hunter & Lange 2004) to effectively handle both the computationally intractable log-likelihood function \( \ell(\pi, \theta) \) and the non-convex optimization problem of the lower bound of the log-likelihood. We introduce an auxiliary distribution \( A(z) \equiv \text{pr}(Z = z) \) to derive a tractable lower bound on the intractable log-likelihood function. Using Jensen’s inequality, the log-likelihood function may be shown to be bounded from the below as follows:

\[
\ell(\pi, \theta) = \sum_{t=1}^{T} \log[\text{pr}_{\pi, \theta}(Y_t = y_t \mid y_{t-1})]
\]

\[
= \sum_{t=1}^{T} \log \left[ \sum_{z \in Z} \frac{\text{pr}_{\pi, \theta}(Y_t = y_t, Z = z \mid y_{t-1})}{A(z)} A(z) \right]
\]

\[
\geq \sum_{t=1}^{T} \sum_{z \in Z} \left[ \log \frac{\text{pr}_{\pi, \theta}(Y_t = y_t, Z = z \mid y_{t-1})}{A(z)} \right] A(z).
\]

(15)

If \( A(z) \) were unconstrained in the sense that we could choose from the set of all distributions with support \( Z \), we would obtain the best lower bound when \( A(z) = \text{pr}_{\pi, \theta}(Z = z \mid y_t, y_{t-1}) \), where the inequality becomes equality. However, this unconstrained form of \( A(z) \) is intractable. We therefore constrain \( A(z) \) to a subset of tractable choices and maximize tractable lower bound to find approximate maximum likelihood estimates.

Here, we constrain \( A(z) \) to the mean-field variational family where the \( Z_i \) are mutually independent,

\[
A(z) = \prod_{i=1}^{n} \text{pr}_{\gamma_i}(Z_i = z_i).
\]

We further specify \( \text{pr}_{\gamma_i}(Z_i = z_i) \) to be Multinomial(1; \( \gamma_{i1}, \ldots, \gamma_{iK} \)) for \( i = 1, \ldots, n \), where \( \Gamma = (\gamma_1, \ldots, \gamma_n) \) is the variational parameter. In the estimation phase, whenever it is necessary to assign each node to a particular community, the \( i \)th node is assigned to the community with
the highest value among $\gamma_{i1}, \ldots, \gamma_{iK}$.

If we now denote the right side of Inequality (15) by $LB(\pi, \theta; \Gamma)$, we may write

$$
LB(\pi, \theta; \Gamma) = \sum_{t=1}^{T} \left[ \sum_{i<j} \sum_{k=1}^{K} \sum_{l=1}^{K} \gamma_{ik} \gamma_{jl} \log[pr_{\theta, z_{ij}}(Y_{t,ij} = y_{t,ij} | y_{t-1}, z)]
+ \sum_{i=1}^{n} \sum_{k=1}^{K} \gamma_{ik} \log(\pi_k - \log(1 + \gamma_{ik}^{(\tau)})) \right].
$$

(16)

If $\pi^{(\tau)}$, $\theta^{(\tau)}$, and $\Gamma^{(\tau)}$ denote the parameter estimates at the $\tau$th iteration of our variational EM algorithm, then in principle that algorithm consists of alternating between two steps:

**Idealized Variational E-step:** Let $\Gamma^{(\tau+1)} = \text{arg max}_{\Gamma} LB(\pi^{(\tau)}, \theta^{(\tau)}; \Gamma)$.  

**Idealized Variational M-step:** Let $(\pi^{(\tau+1)}, \theta^{(\tau+1)}) = \text{arg max}_{(\pi, \theta)} LB(\pi, \theta; \Gamma^{(\tau+1)})$.

**Remark 4:** If the distribution $A(z)$ were totally unconstrained, then the E-step above would simply consist of determining the conditional distribution $pr_{\pi^{(\tau)}, \theta^{(\tau)}}(Z = z | y_t, y_{t-1})$, and the variational E-step and M-step would coincide with the E-step and M-step of the traditional EM algorithm for this situation.

In our idealized variational EM algorithm, it is difficult to directly maximize the nonconcave function $LB(\pi^{(\tau)}, \theta^{(\tau)}; \Gamma)$ with respect to $\Gamma$. To address this challenge, we use a minorization-maximization technique to construct a tractable minorizing function of $LB(\pi^{(\tau)}, \theta^{(\tau)}; \Gamma)$, then maximize this minorizer. We define

$$
Q(\pi^{(\tau)}, \theta^{(\tau)}, \Gamma^{(\tau)}; \Gamma)
= \sum_{t=1}^{T} \left[ \sum_{i<j} \sum_{k=1}^{K} \sum_{l=1}^{K} \left( \frac{\gamma_{ik}^{(\tau)} \gamma_{jl}^{(\tau)}}{2 \gamma_{ik}^{(\tau)} + \gamma_{jl}^{(\tau)}} \right) \log[pr_{\theta, z_{ij}}(Y_{t,ij} = y_{t,ij} | y_{t-1}, z)]
+ \sum_{i=1}^{n} \sum_{k=1}^{K} \frac{\gamma_{ik}^{(\tau)}}{\gamma_{ik}^{(\tau)} + 1} \log(\pi_k^{(\tau)} - \log(\frac{\gamma_{ik}^{(\tau)}}{\gamma_{ik}^{(\tau)} + 1} + 1)) \right],
$$

(17)

which satisfies the defining characteristics of a minorizing function, namely

$$
Q(\pi^{(\tau)}, \theta^{(\tau)}, \Gamma^{(\tau)}; \Gamma) \leq LB(\pi^{(\tau)}, \theta^{(\tau)}; \Gamma) \text{ for all } \Gamma
$$

(18)
and

\[ Q(\pi^{(\tau)}, \theta^{(\tau)}, \Gamma^{(\tau)}) = \text{LB}(\pi^{(\tau)}, \theta^{(\tau)}, \Gamma^{(\tau)}). \]  

Additional details on constructing this minorizing function are presented in Appendix. Since \( Q(\pi^{(\tau)}, \theta^{(\tau)}, \Gamma^{(\tau)}; \Gamma) \) is concave in \( \Gamma \) and separates into functions of the individual \( \gamma_{ik} \) parameters, maximizing \( Q(\pi^{(\tau)}, \theta^{(\tau)}, \Gamma^{(\tau)}; \Gamma) \) is equivalent to solving a sequence of constrained quadratic programming subproblems with respect to \( \gamma_1, \ldots, \gamma_n \) respectively, under constraints \( \gamma_{i1}, \ldots, \gamma_{iK} \geq 0 \) and \( \sum_{k=1}^{K} \gamma_{ik} = 1 \) for \( i = 1, \ldots, n \).

To maximize \( \text{LB}(\pi, \theta; \Gamma^{(\tau+1)}) \) in the M-step, maximization with respect to \( \pi \) and \( \theta \) may be accomplished separately. First, to derive the closed-form updates for \( \pi \), we introduce a Lagrange multiplier with the constraint \( \sum_{k=1}^{K} \pi_k = 1 \). The closed-form update for \( \pi \) is

\[ \pi_k^{(\tau+1)} = \frac{n^{-1}}{n} \sum_{i=1}^{n} \gamma_{ik}^{(\tau+1)}, \quad k = 1, \ldots, K. \]  

We could obtain \( \theta^{(\tau+1)} \) using the Newton-Raphson method, though naive application of Newton-Raphson will not guarantee an increase in \( \ell^{(\tau)} \) which is necessary for the ascent property of the lower bound of the log-likelihood. Since the Hessian matrix \( H(\theta^{(\tau)}) \) at the \( \tau \)th iteration is positive definite, it can be easily shown that if we go in the direction \( h^{(\tau)} = -H(\theta^{(\tau)})^{-1} \nabla \text{LB}(\theta^{(\tau)}; \Gamma^{(\tau+1)}) \) of the Newton-Raphson method, we are guaranteed to go uphill initially. In our modified Newton-Raphson method we do not find the successor point \( \theta^{(\tau+1)} = \theta^{(\tau)} + h^{(\tau)} \) as in the standard Newton-Raphson method. We instead take \( h^{(\tau)} \) as a search direction and perform a line search \[ \text{Bertsimas 2009} \] to find

\[ \lambda^* = \arg \max_{\lambda \in [0, 1]} \text{LB}(\theta^{(\tau)} + \lambda h^{(\tau)}; \Gamma^{(\tau+1)}), \]

then we find the successor point \( \theta^{(\tau+1)} \) by

\[ \theta^{(\tau+1)} = \theta^{(\tau)} - \lambda^* H(\theta^{(\tau)})^{-1} \nabla \text{LB}(\theta^{(\tau)}; \Gamma^{(\tau+1)}). \]  

\[ (21) \]
Now, we summarize the details of our proposed variational EM algorithm as Algorithm 1.

**Algorithm 1** Proposed variational EM algorithm

- Initialize $\Gamma^{(0)}$, $\pi^{(0)}$, and $\theta^{(0)}$.
- Iteratively solve E-step and M-step with $\tau = 0, 1, 2, \ldots$ until convergence:
  - **Variational E-step**: Update $\Gamma^{(\tau+1)}$ via maximizing $Q(\pi^{(\tau)}, \theta^{(\tau)}, \Gamma^{(\tau)}; \Gamma)$ under constraints $\gamma_{i1}, \ldots, \gamma_{iK} \geq 0$ and $\sum_{k=1}^{K} \gamma_{ik} = 1$ for $i = 1, \ldots, n$;
  - **Variational M-step**: Compute $\pi_k^{(\tau+1)} = n^{-1} \sum_{i=1}^{n} \gamma_{ik}^{(\tau+1)}$ for $k = 1, \ldots, K$, and solve $\theta^{(\tau+1)}$ using the modified Newton-Raphson method (21) with the gradient and Hessian of (16).

**Remark 5**: The initial $\gamma_{ik}^{(0)}$ are chosen independently uniformly randomly on (0, 1), then each $\gamma_{i}^{(0)}$ is multiplied by a normalizing constant chosen so that $\sum_{k=1}^{K} \gamma_{ik}^{(0)} = 1$ for every $i$. We then start with an M-step to obtain initial $\pi^{(0)}$ and $\theta^{(0)}$.

**Remark 6**: Using standard arguments that apply to minorization-maximization, or MM algorithms [Hunter & Lange 2004], we can show that our variational EM algorithm preserves the ascent property of the lower bound of the log-likelihood, namely,

$$LB(\pi^{(\tau)}, \theta^{(\tau)}; \Gamma^{(\tau)}) \leq LB(\pi^{(\tau+1)}, \theta^{(\tau+1)}; \Gamma^{(\tau+1)}).$$

## 5 Simulation Studies

We first conduct simulation studies for a mixture of TERGMs and STERGMs. To simulate time-evolving networks from the $K$-component mixture of TERGM with stability parameters, i.e., Example 1, we first specify network structure by choosing randomly the categories of the nodes according to the fixed mixing proportions and by defining initial densities for each category.

Now we obtain initial network $y_0$ by simulating all the edges between two nodes based on the probabilities with specified density parameters and categories of the nodes. Next, we set different stability parameters for each category and simulate all the edges in series of networks $y_1, \ldots, y_T$ sequentially, based on the probabilities with specified stability parameters and given previous
time point network and categories of the nodes. Similarly, we simulate time-evolving networks from the $K$-component mixture of STERGM with formation and persistence parameters, i.e., Example 2. For each of the four model settings listed in Table 1, we use 100 nodes and 10 discrete time points.

Table 1: Model settings for TERGM with stability parameters (Model 1 and Model 2) and STERGM with formation and persistence parameters (Model 3 and Model 4).

|          | Model 1 | Model 2 | Model 3 | Model 4 |
|----------|---------|---------|---------|---------|
| G_1      | 0.5     | 0.5     | 0.33    | 0.33    |
| G_2      | 0.5     | -1      | 0       | 1       |
| G_3      | -0.5    | 0.5     | -1      | 0       |
| G_4      | -0.5    | 0.5     | -1      | 0       |

To check the performance of the algorithm at identifying the correct number of communities, we count the frequencies of min CL-BIC and max ICL over 100 repetitions. To assess the clustering performance, we calculate the average value of the Rand Index (RI) over the 100 repetitions (Rand 1971). The measure $RI(z, \hat{z})$ calculates the proportion of pairs whose estimated labels correspond to the true labels in terms of being assigned to the same or different groups:

$$RI(z, \hat{z}) = \left(\frac{n}{2}\right)^{-1} \sum_{i<j} \left( I\{z_i = z_j\}I\{\hat{z}_i = \hat{z}_j\} + I\{z_i \neq z_j\}I\{\hat{z}_i \neq \hat{z}_j\} \right).$$

To assess the estimation performance of the algorithm, we calculate the average $\ell^2$ norm loss for estimated mixing proportions and network parameters over the 100 repetitions:

$$RSE_{\pi} = \left( \sum_{k=1}^{K} (\hat{\pi}_k - \pi_k)^2 \right)^{1/2} \quad \text{and} \quad RSE_{\theta} = \left( \sum_{k=1}^{K} (\hat{\theta}_k - \theta_k)^2 \right)^{1/2}.$$
First of all, we check the performance of our criterion functions in choosing the correct number of communities. As shown in Table 2, both CL-BIC and modified ICL perform well.

The average Rand Index results are reported in Table 3.

Table 2: Frequencies of min CL-BIC and max ICL over 100 repetitions. \( K_0 \) represents the true number of communities.

| \( K \) | Model 1 \((K_0 = 2)\) | Model 2 \((K_0 = 3)\) |
|---|---|---|
| \( K = 1 \) | \( K = 2 \) | \( K = 3 \) | \( K = 4 \) | \( K = 1 \) | \( K = 2 \) | \( K = 3 \) | \( K = 4 \) |
| min CL-BIC | 0 | 99 | 0 | 1 | 0 | 0 | 97 | 3 |
| max ICL | 0 | 100 | 0 | 0 | 0 | 0 | 96 | 4 |

| \( K \) | Model 3 \((K_0 = 2)\) | Model 4 \((K_0 = 3)\) |
|---|---|---|
| \( K = 1 \) | \( K = 2 \) | \( K = 3 \) | \( K = 4 \) | \( K = 1 \) | \( K = 2 \) | \( K = 3 \) | \( K = 4 \) |
| min CL-BIC | 0 | 99 | 1 | 0 | 0 | 3 | 93 | 4 |
| max ICL | 0 | 100 | 0 | 0 | 0 | 0 | 99 | 1 |

Table 3: Mean Rand Index values for 100 repetitions for various models and values of \( K \), with sample standard deviations in parentheses, where \( K_0 \) is the true number of communities.

| Model 1 \((K_0 = 2)\) | Model 2 \((K_0 = 3)\) |
|---|---|
| \( K = 2 \) | \( K = 3 \) | \( K = 4 \) |
| TERGM | 1.000 (0.000) | 0.874 (0.033) | 0.773 (0.030) |

| Model 2 \((K_0 = 3)\) | Model 3 \((K_0 = 2)\) | Model 4 \((K_0 = 3)\) |
|---|---|---|
| \( K = 2 \) | \( K = 3 \) | \( K = 4 \) |
| TERGM | 0.751 (0.044) | 0.996 (0.031) | 0.943 (0.025) |
| STERGM | 1.000 (0.000) | 0.874 (0.033) | 0.774 (0.031) |

| Model 3 \((K_0 = 2)\) | Model 4 \((K_0 = 3)\) |
|---|---|
| \( K = 2 \) | \( K = 3 \) | \( K = 4 \) |
| STERGM | 0.761 (0.045) | 0.998 (0.021) | 0.945 (0.018) |

Finally, Table 4 summarizes estimation performance of our algorithm using RSE\( \pi \), RSE\( \theta \), RSE\( \theta_f \), and RSE\( \theta_p \). The results of Tables 2 through 4 together tell us that our algorithm performs convincingly on this set of test datasets.

To check which model selection criterion is more robust in choosing correct number of communities when the time-evolving networks are not simulated from the true model, we con-
Table 4: Average values of $\ell^2$ norm loss for estimated mixing proportions and network parameters over 100 repetitions with standard deviations shown in parentheses. $K_0$ represents the true number of communities.

| Model 1 ($K_0 = 2$) | Model 2 ($K_0 = 3$) |
|----------------------|----------------------|
| $RSE_\pi$ | $RSE_\theta^p$ | $RSE_\pi$ | $RSE_\theta^p$ |
| 0.056 (0.043) | 0.013 (0.008) | 0.073 (0.043) | 0.038 (0.098) |

| Model 3 ($K_0 = 2$) | Model 4 ($K_0 = 3$) |
|----------------------|----------------------|
| $RSE_\pi$ | $RSE_\theta^q$ | $RSE_\theta^r$ | $RSE_\pi$ | $RSE_\theta^q$ | $RSE_\theta^r$ |
| 0.057 (0.043) | 0.030 (0.020) | 0.023 (0.015) | 0.072 (0.040) | 0.045 (0.094) | 0.039 (0.071) |

duct another simulation study. This time we use the ‘simulate.stergm’ function in the ‘tergm’ package (Krivitsky & Handcock 2016) in R (R Core Team 2016) to simulate $K$ time-evolving networks (Krivitsky & Handcock 2014) and combine the $K$ time-evolving networks into single time-evolving networks where each simulated time-evolving networks representing $K$ different communities. First, we specify each network structure by choosing randomly the categories of the nodes according to the fixed mixing proportions and by defining the network densities. Next, we set different mean relational durations, which represent different degrees of stability, and simulate each time-evolving network to have the average network density we defined over the time points. Finally, we combine the $K$ time-evolving networks into single time-evolving networks by adding a fixed number of edges between randomly chosen pairs of individuals in different communities. For each of the two model settings listed in Table 5, we use 100 nodes, 10 discrete time points, and 10 edges added between randomly chosen pairs of nodes in different communities.

Table 5: Model settings for generating time-evolving networks using ‘simulate.stergm’ function.

| Model 5 | Model 6 |
|---------|---------|
| $G_1$ | $G_2$ | $G_1$ | $G_2$ | $G_3$ |
| Mixing proportion | 0.4 | 0.6 | 0.3 | 0.4 | 0.3 |
| Mean relational duration | 5 | 2.5 | 7.5 | 5 | 2.5 |
| Average network density | 0.15 | 0.1 | 0.1 | 0.25 | 0.3 |

As shown in Table 6, in the new simulation setting where the time-evolving networks are not
simulated from the true model, CL-BIC still performs well in choosing the correct number of communities through both TERGM with a stability parameter and STERGM with formation and persistence parameters. However, as shown in Table 7, modified ICL fails to choose the correct number of communities. The results of Tables 6 and 7 together tell us that the performance of our proposed CL-BIC in choosing the correct number of communities is more robust than modified ICL when the model assumptions are violated, at least in the particular testing regime we implemented.

**Table 6:** Frequencies of min CL-BIC over 100 repetitions of fitting both TERGM with stability parameter and STERGM with formation and persistence parameters. The true number of communities is $K_0$.

|        | Model 5 ($K_0 = 2$) |        | Model 6 ($K_0 = 3$) |
|--------|---------------------|--------|---------------------|
|        | $K = 1$ | $K = 2$ | $K = 3$ | $K = 4$ | $K = 1$ | $K = 2$ | $K = 3$ | $K = 4$ |
| TERGM  | 0       | 87     | 12      | 1       | 0       | 1       | 96      | 3       |
| STERGM | 0       | 93     | 2       | 5       | 0       | 8       | 91      | 1       |

**Table 7:** Frequencies of max ICL over 100 repetitions for both TERGM with stability parameter and STERGM with formation and persistence parameters. The true number of communities is $K_0$.

|        | Model 5 ($K_0 = 2$) |        | Model 6 ($K_0 = 3$) |
|--------|---------------------|--------|---------------------|
|        | $K = 1$ | $K = 2$ | $K = 3$ | $K = 4$ | $K = 1$ | $K = 2$ | $K = 3$ | $K = 4$ |
| TERGM  | 0       | 49     | 23      | 28      | 0       | 0       | 65      | 35      |
| STERGM | 0       | 53     | 32      | 15      | 0       | 0       | 59      | 41      |

The average Rand Index results are also reported in Table 8. In all models, both TERGM with a stability parameter and STERGM with formation and persistence parameters achieve a high average Rand Index for the correct number of mixtures. Moreover, we see a fairly high average Rand Index with the selected (via minimum CL-BIC) number of communities $\hat{K}$. The results of Table 6 and 8 together tell us that our algorithm based on CL-BIC performs convincingly in choosing the correct number of communities and assigning nodes to communities even when the time-evolving networks are not generated from the true model.
Table 8: Comparison of clustering performance using average Rand Index for both TERGM and STERGM models with standard deviations shown in parentheses. The true number of communities is $K_0$.

| Model | $K = 2$ | $K = 3$ | $K = 4$ | $K = \hat{K}$ |
|-------|---------|---------|---------|---------------|
| TERGM | 0.976 (0.032) | 0.797 (0.045) | 0.716 (0.036) | 0.948 (0.080) |
| STERGM | 0.979 (0.025) | 0.798 (0.054) | 0.727 (0.041) | 0.966 (0.056) |

Model 6 ($K_0 = 3$)

| $K = 2$ | $K = 3$ | $K = 4$ | $K = \hat{K}$ |
|---------|---------|---------|---------------|
| TERGM | 0.753 (0.054) | 0.976 (0.033) | 0.935 (0.023) | 0.975 (0.037) |
| STERGM | 0.756 (0.055) | 0.972 (0.036) | 0.931 (0.024) | 0.961 (0.052) |

6 Applications to Real-World Time-Evolving Networks

Here, we apply our proposed model-based clustering methods to detect communities in two time-evolving network datasets: International trade networks of 58 countries from 1981 to 2000, and collaboration networks of 151 researchers at a large American research university from 2004 to 2013. In particular, we are interested in analyzing the rate of evolution of these time-evolving networks as in Knecht (2008), Snijders et al. (2010), and Krivitsky & Handcock (2014). Before proceeding, we introduce metrics to measure the instability of edges in the estimated communities $G_1, \ldots, G_{\hat{K}}$. For $k, l = 1, \ldots, \hat{K}$ and $t = 1, \ldots, T$, we first define

- the “$1 \to 0$” instability of edges between $G_k$ and $G_l$ at the time $t$:
  \[
  S_{1\to 0}^{kl}(t) = \frac{\sum_{i \in G_k, j \in G_l} y_{t-1,ij}(1 - y_{t,ij})}{\sum_{i \in G_k, j \in G_l} y_{t-1,ij}y_{t,ij}};
  \]

- the “$0 \to 1$” instability of edges between $G_k$ and $G_l$ at the time $t$:
  \[
  S_{0\to 1}^{kl}(t) = \frac{\sum_{i \in G_k, j \in G_l} (1 - y_{t-1,ij})y_{t,ij}}{\sum_{i \in G_k, j \in G_l} (1 - y_{t-1,ij})(1 - y_{t,ij})};
  \]
• the total instability of edges between $G_k$ and $G_l$ at the time $t$:

$$S_{kl}^{tot}(t) = \frac{\sum_{i \in G_k, j \in G_l} [y_{t-1,ij}(1 - y_{t,ij}) + (1 - y_{t-1,ij})y_{t,ij}]}{\sum_{i \in G_k, j \in G_l} [y_{t-1,ij}y_{t,ij} + (1 - y_{t-1,ij})(1 - y_{t,ij})]}.$$

The three instability statistics defined above evaluate the within-group instability when $k = l$ and the between-group instability when $k \neq l$. Next, we define $\mathcal{A}S_{1 \rightarrow 0}^{kl}$, $\mathcal{A}S_{0 \rightarrow 1}^{kl}$ and $\mathcal{A}S_{tot}^{kl}$ as the averages over all $t$ of $S_{1 \rightarrow 0}^{kl}(t)$, $S_{0 \rightarrow 1}^{kl}(t)$, and $S_{tot}^{kl}(t)$, respectively. Here, a larger value of $\mathcal{A}S_{1 \rightarrow 0}^{kl}$ indicates that the network is more likely to dissolve ties, a larger value of $\mathcal{A}S_{0 \rightarrow 1}^{kl}$ implies that the network is more likely to form ties, and a larger value of $\mathcal{A}S_{tot}^{kl}$ implies that the network is less stable overall.

### 6.1 International trade networks

We first consider finding communities for the yearly international trade networks of $n = 58$ countries studied by Ward & Hoff (2007). We follow Westveld & Hoff (2011) and Saldana et al. (2017) to define networks $y_{1981}, \ldots, y_{2000}$ as follows: for any $t = 1981, \ldots, 2000$, $y_{t,ij} = 1$ if the bilateral trade between country $i$ and country $j$ in year $t$ exceeds the median bilateral trade in year $t$, and $y_{t,ij} = 0$ otherwise. By definition, this setup results in networks in which the edge density is roughly one half. We employ model-based clustering using a TERGM with a stability parameter, i.e., Example 1.

First, we use our proposed CL-BIC to determine the number of communities. As shown in Figure 1, we will use a value of $\hat{K} = 3$.

We summarize the characteristics of the three estimated communities, including some basic network statistics and parameter estimates, in Table 9. We also calculate the within-group and between-group instability measures. As shown in Table 10, community $G_3$ has the smallest total instability $\mathcal{A}S_{tot}^{33}$, which implies that those countries in $G_3$ consistently maintain their trading countries. In addition, the “$1 \rightarrow 0$” and “$0 \rightarrow 1$” instability measures show that countries in community $G_2$ change their trading countries more actively than countries in $G_1$ and $G_3$. To
sum up, communities $G_1$, $G_2$, and $G_3$ correspond to the medium stability, low stability, and high stability groups, respectively.

Table 9: Summary of basic network statistics, parameter estimates, and average memberships.

|                      | $G_1$ | $G_2$ | $G_3$ |
|----------------------|-------|-------|-------|
| Total # of nodes     | 24    | 21    | 13    |
| Average # of edges per node | 17.11 | 34.28 | 42.42 |
| Average # of triangles per node | 150.17 | 443.95 | 613.15 |
| Estimated mixing proportion $\hat{\pi}$ | 0.3920 | 0.3677 | 0.2403 |
| Estimated stability parameter $\hat{\theta}$ | 1.6323 | 1.3168 | 2.0712 |
| Average membership of $\hat{\gamma}_1$ | 0.8147 | 0.1158 | 0.0579 |
| Average membership of $\hat{\gamma}_2$ | 0.1060 | 0.8262 | 0.1101 |
| Average membership of $\hat{\gamma}_3$ | 0.0794 | 0.0579 | 0.8320 |

In Figure 2, we plot the international trade networks with estimated communities to illustrate our model-based clustering result. To illustrate how networks change over time for countries in each of the three communities, in Appendix we isolate one representative country from each community: Israel from $G_1$, Thailand from $G_2$, and the United States from $G_3$. 

Figure 1: CL-BIC for model-based clustering through TERGM with a stability parameter in international trade networks.
Table 10: Summary of within-group and between-group instability statistics for the proposed model-based clustering community assignments for the international trade network dataset. $\mathcal{A}S_{1\rightarrow0}^{kl}$, $\mathcal{A}S_{0\rightarrow1}^{kl}$, and $\mathcal{A}S_{tot}^{kl}$ measure the average over all $t$ of $\mathcal{S}_{1\rightarrow0}^{kl}(t)$, $\mathcal{S}_{0\rightarrow1}^{kl}(t)$, and $\mathcal{S}_{tot}^{kl}(t)$, respectively, with standard deviations shown in parentheses.

| $\mathcal{A}S_{1\rightarrow0}^{11}$ | $\mathcal{A}S_{0\rightarrow1}^{11}$ | $\mathcal{A}S_{tot}^{11}$ | $\mathcal{A}S_{1\rightarrow0}^{22}$ | $\mathcal{A}S_{0\rightarrow1}^{22}$ | $\mathcal{A}S_{tot}^{22}$ | $\mathcal{A}S_{1\rightarrow0}^{33}$ | $\mathcal{A}S_{0\rightarrow1}^{33}$ | $\mathcal{A}S_{tot}^{33}$ |
|---------------------------------|---------------------------------|--------------------------|---------------------------------|---------------------------------|--------------------------|---------------------------------|---------------------------------|--------------------------|
| 0.088                           | 0.014                           | 0.023                    | 0.048                           | 0.248                           | 0.082                    | 0.002                           | 0.014                           | 0.004 |
| (0.094)                         | (0.009)                         | (0.013)                  | (0.041)                         | (0.132)                         | (0.047)                  | (0.006)                         | (0.034)                         | (0.006) |
| $\mathcal{A}S_{1\rightarrow0}^{12}$ | $\mathcal{A}S_{0\rightarrow1}^{12}$ | $\mathcal{A}S_{tot}^{12}$ | $\mathcal{A}S_{1\rightarrow0}^{13}$ | $\mathcal{A}S_{0\rightarrow1}^{13}$ | $\mathcal{A}S_{tot}^{13}$ | $\mathcal{A}S_{1\rightarrow0}^{23}$ | $\mathcal{A}S_{0\rightarrow1}^{23}$ | $\mathcal{A}S_{tot}^{23}$ |
| 0.098                           | 0.042                           | 0.058                    | 0.041                           | 0.048                           | 0.043                    | 0.011                           | 0.049                           | 0.016 |
| (0.030)                         | (0.014)                         | (0.015)                  | (0.021)                         | (0.026)                         | (0.008)                  | (0.017)                         | (0.088)                         | (0.019) |

Figure 2: International trade networks with estimated communities in four different years. Nodes assigned to $G_1$, $G_2$, and $G_3$ are colored orange, green, and blue, respectively.
6.2 Collaboration networks

We next find communities for the yearly collaboration networks at a large research university from 2004 to 2013. There are $n = 151$ researchers from various academic units in this dataset. We define networks $y_{2004}, \ldots, y_{2013}$ as follows: for any $t = 2004, \ldots, 2013$, $y_{t,ij} = 1$ if researcher $i$ and researcher $j$ have an active research grant together during year $t$, and $y_{t,ij} = 0$ otherwise. We employ mixtures of both TERGMs with stability parameters, i.e., Example 1, and STERGMs with formation and persistence parameters, i.e., Example 2. As shown in Figure 3, our proposed CL-BIC indicates that the optimal number of communities is $\hat{K} = 2$. We shall identify two researcher communities based on different degrees of stability.

![Figure 3: CL-BIC for model-based clustering using STERGMs with formation and persistence parameters in collaboration networks.](image)

We obtain the same estimated communities from clustering through TERGM with stability parameter or STERGM with formation and persistence parameters. Table 11 summarizes their basic network statistics and parameter estimates, while Table 12 displays the within-group and between-group instability measures. As these tables show, $G_1$ has higher “1 $\rightarrow$ 0”, “0 $\rightarrow$ 1”, and total instability than $G_2$. Thus, the researchers in $G_1$ tend to have fewer stable collaborations and work with more collaborators than those in $G_2$. 

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Compared to TERGMs with stability parameters, STERGMs with formation and persistence parameters provide more detailed insights about time-evolving networks. Based on the parameter estimates in Table 11 in each community, the stability is more explained by the persistence parameter than the formation parameter. In view of this fact, we further calculate the mean relational duration using the persistence parameter estimates for each estimated community.

We obtain the mean relational durations of 2.18 years for $G_1$ and 2.85 years for $G_2$.

Table 11: Summary of basic network statistics, parameter estimates, and average memberships.

|                      | $G_1$ | $G_2$ |
|----------------------|-------|-------|
| Total # of nodes     | 34    | 117   |
| Average # of edges per node | 2.92  | 1.90  |
| Average # of triangles per node | 0.8088 | 0.3957 |

|                        | $G_1$     | $G_2$     |
|------------------------|-----------|-----------|
| Estimated mixing proportions $\hat{\pi}$ | 0.2464    | 0.7536    |
| Estimated formation parameter $\hat{\theta}_f$ | -2.2677   | -2.9634   |
| Estimated persistence parameter $\hat{\theta}_p$ | 0.1647    | 0.6156    |
| Average membership of $\hat{\gamma}_1$ | 0.7706    | 0.0941    |
| Average membership of $\hat{\gamma}_2$ | 0.2294    | 0.9059    |

Table 12: Summary of within-group and between-group instability statistics for the proposed model-based clustering community assignments for the collaboration network dataset. $\mathcal{AS}^{kl}_{1 \rightarrow 0}$, $\mathcal{AS}^{kl}_{0 \rightarrow 1}$, and $\mathcal{AS}^{kl}_{tot}$ measure the average over all $t$ of $S^{kl}_{1 \rightarrow 0}(t)$, $S^{kl}_{0 \rightarrow 1}(t)$, and $S^{kl}_{tot}(t)$, respectively, with standard deviations shown in parentheses.

|                        | $\mathcal{AS}^{11}_{1 \rightarrow 0}$ | $\mathcal{AS}^{11}_{0 \rightarrow 1}$ | $\mathcal{AS}^{22}_{1 \rightarrow 0}$ | $\mathcal{AS}^{22}_{0 \rightarrow 1}$ | $\mathcal{AS}^{12}_{tot}$ | $\mathcal{AS}^{12}_{1 \rightarrow 0}$ | $\mathcal{AS}^{12}_{0 \rightarrow 1}$ | $\mathcal{AS}^{12}_{tot}$ |
|------------------------|----------------------------------------|----------------------------------------|----------------------------------------|----------------------------------------|---------------------------------|---------------------------------|---------------------------------|---------------------------------|
|                        | 0.672                                  | 0.014                                  | 0.029                                  | 0.272                                  | 0.003                           | 0.005                           | 0.540                           | 0.005                           |
|                        | (0.359)                                | (0.006)                                | (0.007)                                | (0.059)                                | (0.001)                         | (0.001)                         | (0.189)                         | (0.001)                         |
|                        | 0.585                                  | 0.011                                  | 0.023                                  | 0.250                                  | 0.003                           | 0.006                           | 0.444                           | 0.003                           |
|                        | (0.211)                                | (0.004)                                | (0.005)                                | (0.066)                                | (0.001)                         | (0.001)                         | (0.076)                         | (0.001)                         |

TERGM
Figure 4 presents the collaboration networks with estimated communities represented by orange for $G_1$ and blue for $G_2$. We also plot the networks of several representative individual researchers in Appendix, anonymized by the assignment of four-digit identification numbers.

Figure 4: Collaboration networks with estimated communities in four different years. Nodes assigned to $G_1$ and $G_2$ are colored orange and blue, respectively.

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