Statistical modelling of Networked Evolutionary Public Goods Games

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Summary. Repeated small dynamic networks are integral to studies in evolutionary game theory, where networked public goods games offer novel insights into human behaviours. Building on these findings, it is necessary to develop a statistical model that effectively captures dependencies across multiple small dynamic networks. While Separable Temporal Exponential-family Random Graph Models (STERGMs) have demonstrated success in modelling a large single dynamic network, their application to multiple small dynamic networks with less than 10 actors, remains unexplored. In this study, we extend the STERGM framework to accommodate multiple small dynamic networks, offering an approach to analysing such systems. Taking advantage of the small network sizes, our proposed approach improves accuracy in statistical inference through direct computation, unlike conventional approaches that rely on Markov Chain Monte Carlo methods. We demonstrate the validity of this framework through the analysis of a networked public goods experiment into individual decision-making about cooperation and defection. The resulting statistical inference uncovers insights into the dynamics of social dilemmas, showcasing the effectiveness and robustness of this modelling and approach.

Keywords: Evolutionary Game Theory; Experimental Game Theory; Longitudinal Networks; Public Goods Game; Social Networks; Separable Temporal Exponential-family Random Graph Models.

1. Introduction

Networks are widely used to represent relational information, enabling a deeper understanding of structures and dependencies within social relationships. Recently, there has been increasing interest in using dynamic networks to capture the evolution of these relationships

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over time in various fields. In particular, evolutionary game theory has leveraged dynamic networks to explore the evolution of human behaviours (Feng et al., 2024; Li et al., 2023; Pi et al., 2024).

A key experimental approach in this domain is a public goods game, which sheds light on cooperative behaviours. In traditional public goods games, individuals repeatedly choose between cooperation (benefiting the group) and defection (benefiting themselves), typically among 4 to 6 participants (Fehr and Gächter, 2000; Milinski et al., 2002; Rand et al., 2012). More recent adaptations incorporate network structures to better mimic real-world social interactions (Nishi et al., 2015; Shirado and Christakis, 2017; Dewey et al., 2024). In these networked settings, public goods games generate multiple small dynamic networks that reflect repeated interactions and evolving relational structures.

Despite advances in this field, many studies have continued to focus on nodal-level analyses, potentially overlooking the critical dependencies that shape broader network dynamics. Building on these findings, there is a clear need to develop a modelling framework that can capture dependencies across multiple small dynamic networks. Such an approach would provide deeper insights into the complexities of networked human behaviours and enhance our understanding of relational dynamics over time.

To address this gap, we extend Separable Temporal Exponential-family Random Graph Models (STERGMs), a temporal extension of Exponential-family Random Graph Models (ERGMs; see Amati et al. (2018)). While STERGMs are widely used for modelling single large dynamic networks, typically with 20 nodes or more (Krivitsky and Handcock, 2014; Leifeld et al., 2018; Lebacher et al., 2021), our proposed framework adapts STERGMs to capture dependencies in repeated small dynamic networks. Such networks are integral to studies in evolutionary game theory, where networked public goods games offer insights into networked human behaviours in social dilemmas.

This paper is organized as follows. In Section 2, we provide an overview of the public goods game employed in our study. Section 3 introduces and extends the STERGM framework to accommodate the context of multiple small dynamic networks. In Section 4, we apply this modelling approach to the empirical data from networked public goods games and perform statistical inference to uncover key insights into the networked human behaviours.

2. Networked Public Goods Games

In this section, we describe the structure of the networked public goods game used in our experiment. This description highlights the canonical characteristics of such games and experiments.

2.1. Overview of the Game

Each game included six participants. At the start of the game, each participant received an initial wealth of 500 units and was placed within a network structure. This structure was constructed based on an Erdős-Rényi design (Erdős and Rényi, 1959), where five direct connections were randomly generated among the six nodes.

The game consisted of seven repeated time steps. However, participants were not informed of the total number of time steps in advance, which limited the potential for endgame-oriented strategies. At the end of the game, cumulative wealth was converted into cash at a rate of $1 per $1,000$ units.

Before the actual game, participants completed two practice time steps with randomly behaving computer agents. These agents were programmed to make decisions in a completely random manner, without any pattern. Consequently, participants were not exposed to any specific behaviours that might influence their strategies in the actual game.

2.2. Time Step Structure

Each time step consisted of two phases: a decision-making phase and a network update phase.

(a) **Decision-making phase:**

At the beginning of each time step, participants chose whether to cooperate or defect with all of their directly connected neighbours. If they chose to cooperate, they paid 50 units per directly connected neighbour, and each of these neighbours received 100 units in return. If they chose to defect, their wealth remained unchanged, and no benefits were given to their directly connected neighbours. Participants made this decision only once per time step, and it was uniformly applied to all of their directly connected neighbours.

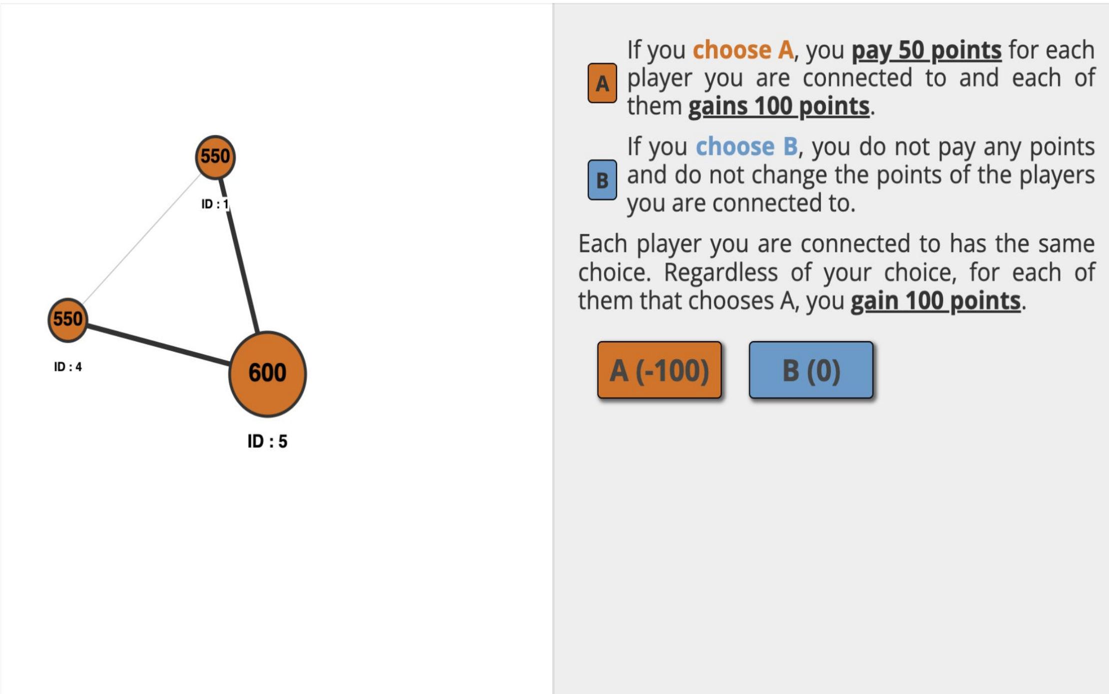

Fig. 1. Decision-making phase in the networked public goods games

During this phase, participants could view their directly connected neighbours' information: their wealth, decisions in the most recent time step (cooperation or defection), identification numbers (1-6), and how these neighbours were directly connected to each other (alter–alter connections).

Fig. 1 illustrates the decision-making phase as observed by the participant with the identification number 5 ("ego"), who was directly connected to the participants with the identification numbers 1 and 4 ("alters"). Notably, the participant 5 could also observe that the participants 1 and 4 were directly connected to each other (direct connections from ego to their alters are represented by thick lines; alter to alter connections are in thin lines). The participant 5 could not observe participants $2, 3$ and 6 as they were not directly connected to the participant 5 (and so they did not appear in this network). The colour of each node represents the choice made in the most recent time step: red for cooperation and blue for defection. For example, the participant 1 cooperated in the most recent time step as indicated by the red colour of its node. The numeric label within each node indicates the current wealth of the corresponding participant. In this instance, the participant 5 had a wealth of 600 units.

Given this information, participants faced a dilemma: whether to defect and maximise their individual wealth (free-riding), or to cooperate and contribute to the maximization of social wealth. Additionally, by demonstrating cooperative behaviour, participants might elicit future cooperation from others or gain an advantage in the future network updates.

Once all participants had made their decisions (cooperation or defection), they were able to see their directly connected neighbours' decisions and how their own wealth was updated.

(b) **Network update phase:**

In this phase, five pairs of participants who were directly connected and five pairs of participants who were not directly connected were randomly selected. For directly connected pairs, connections could be dissolved if either participant chose to do so. Otherwise they persist. For pairs not directly connected, new connections could be formed if both participants agreed to it. For each participant, the sequence of these dissolution and formation opportunities was presented in a randomized order during the network update phase.

It is important to note that participants could not observe how other participants were forming or dissolving connections until all decisions had been made.

When making these decisions, participants had access to information on their directly connected neighbours prior to this phase: their wealth, decisions in the most recent time step (cooperation or defection), identification numbers (1–6), and how these neighbours were directly connected to each other. Forming new connections with others, participants could see their wealth, decisions in the most recent time step, identification numbers, and how they were connected to the participants' directly connected neighbours prior to this phase.

Figs. 2 and 3 illustrate the network update phase from the perspective of the participant with the identification number 3. Before the network update phase, the ego participant 3 was directly connected to the participants 1 and 5. Additionally, the participants 1 and 2 were also directly connected at that time. At the start of the network update phase, the ego participant 3 had two forming opportunities with the participants 4 and 2 (green dashed lines) and two dissolution opportunities with the participants 5 and 1 (red dashed lines) were forthcoming. These four decisions were then presented in a randomized order during the network update phase as Figs. 2 and 3.

In Fig. 2, the ego participant 3 decided whether to dissolve the connection with the participant with the identification number 1 (indicated by the dark red dotted line). The participant 1 had cooperated in the most recent decision-making phase, possessed a wealth of 550 units, and was directly connected to the participant 2 prior to this phase. The light red dotted line showed that the participant 3 had not yet decided whether to dissolve the existing connection with participant 5.

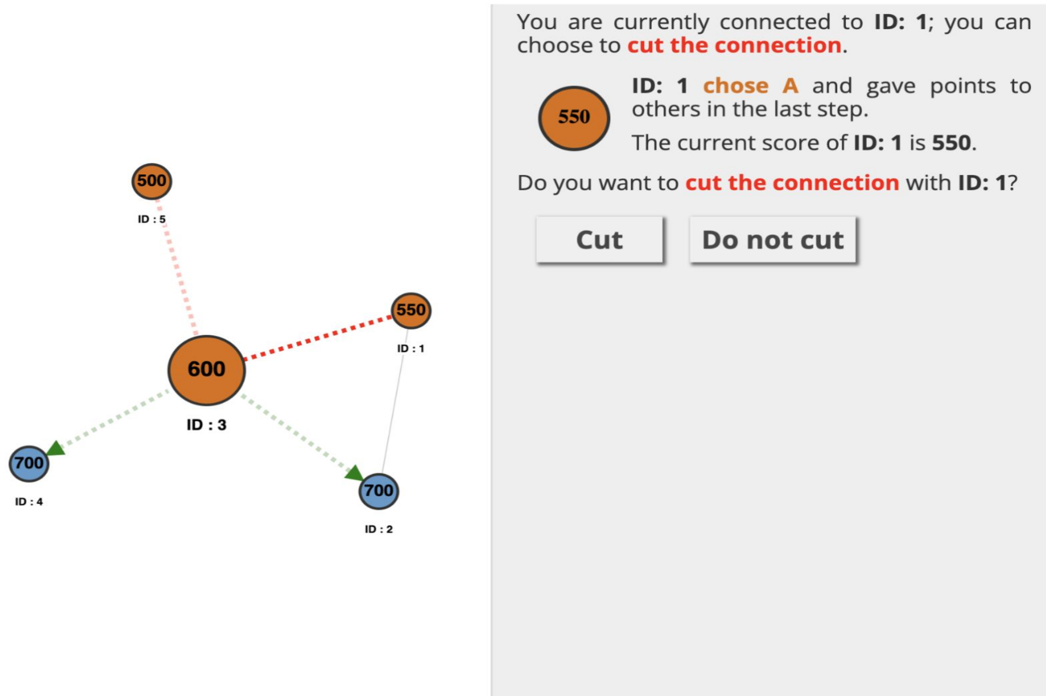

Fig. 2. Dissolving ties in the networked public goods games

In Fig. 3, the ego participant 3 decided whether to form a new connection with the participant 2 (indicated by the dark green dotted line). Notably, there was an alter–non-alter connection (grey line) between the participant 1 (alter) and the participant 2 (non-alter), which the ego participant 3 was able to observe when considering forming a new connection with the participant 2. The light green dotted line with an arrow showed that the participant 3 had already decided to form a new

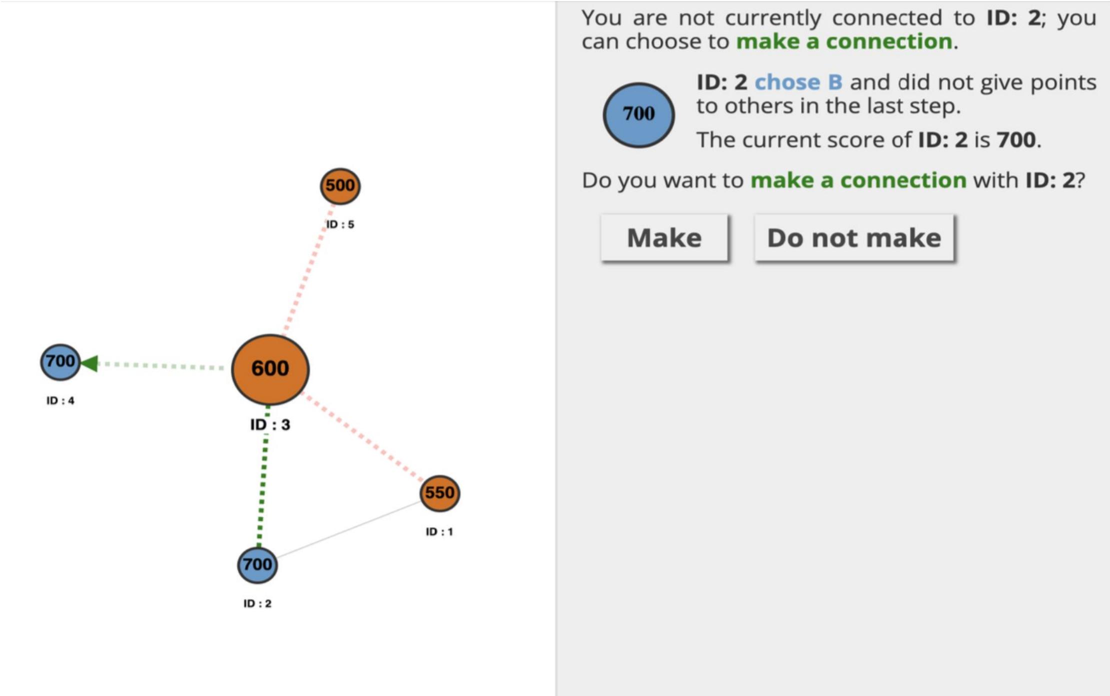

Fig. 3. Forming ties in the networked public goods games

connection with participant 4. Note that new connections could be formed only if both participants agreed to it.

Participants were expected to make these decisions aimed at maximizing their future wealth by forming connections with cooperative individuals or minimizing risks by dissolving connections with uncooperative individuals.

Once all the participants made these decisions (dissolving or forming), the network structure was updated.

2.3. Experimental Environment and Participant Recruitment

This experiment was conducted on Breadboard (McKnight and Christakis, 2016), a software platform designed for online social experiments. Participants were recruited via the online survey platform, Prolific (2024), in November 2024 from various countries around the world. The experiments were approved by and performed according to guidelines and regulations set by the UCLA Office of Research Administration ($\#16-001920$). Informed consent was obtained online from all participants.

2.4. Experiments

We conducted 20 games, involving a total of 120 participants (6 participants in each experiment). Among them, 68 identified as female, 50 as male, 1 as transgender, and 1 preferred not to answer. The average age of participants was 29.5 years (SD $=$ 10.1).

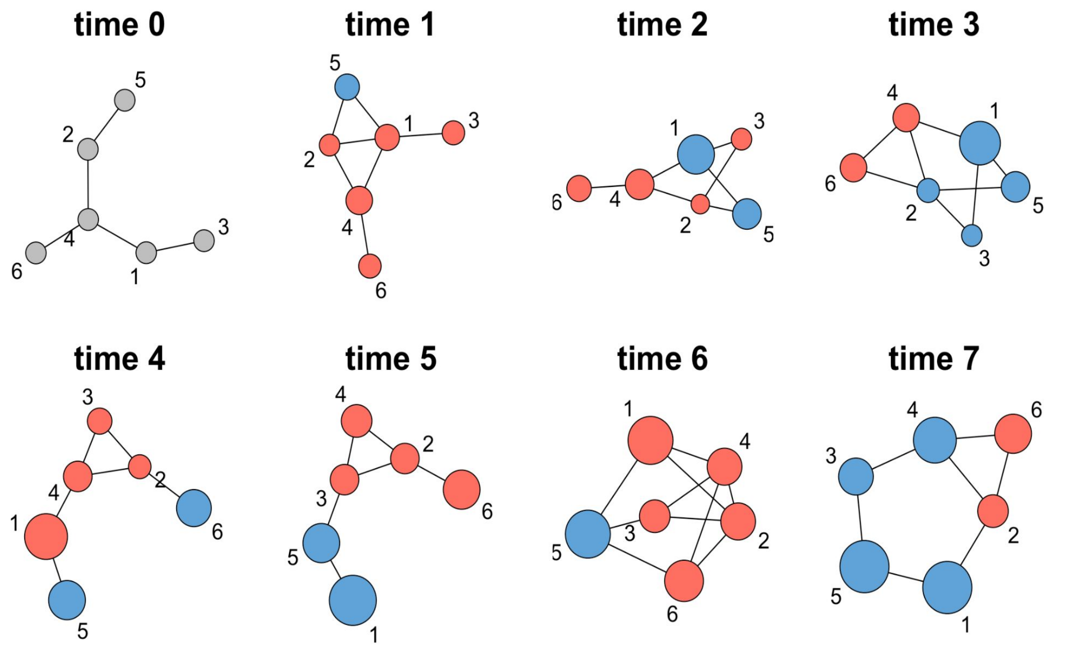

Fig. 4. Network dynamics in the networked public goods game

Fig. 4 illustrates the dynamic network that emerged during one of the 20 public goods games. Note that this is a bird's-eye view of the network, which was not available to the participants themselves.

Each node represents a participant, and the ties indicate direct connections between them. The size of each node corresponds to the participant's current wealth: larger nodes indicate higher wealth, while smaller nodes represent lower wealth. The numbers 1–6 denote the identification numbers of each participant. The colour of each node indicates the most recent decision made in the decision-making phase: red represents cooperation, blue indicates defection, and grey denotes no prior history. For instance, at time step 0, the initial network structure was generated, where the participant with the identification number 1 was directly connected to the participants 3 and 4. Subsequently, at time step 1, the participant 1 chose to cooperate in the decision-making phase and then formed new connections with the participants 2 and 5 in the network update phase.

3. Separable Temporal Exponential-family Random Graph Models

In this section, we describe a statistical model to represent the relationships within the game. We start with a model for a single network and then expand it to the larger set of G networks.

Consider a longitudinal network of relations between n nodes, labeled $\{1, \ldots, n\}$ at time points $t = 1, \ldots, T$. Let Y_{ij}^t be a random variable representing a measure of the relation between nodes i and j at time t, so that the matrix $\mathbf{Y}^t = [Y_{ij}]_{n\times n}$ can be thought of as a random graph over the set of nodes. Let $\mathbf{y}^t \in \mathcal{Y}$ be a realization of $\mathbf{Y}^t$.

Separable Temporal Exponential-family Random Graph Models (STERGM) were introduced by Krivitsky and Handcock (2014) as a subset of Temporal Exponential-family Random Graph Models (TERGM) for better interpretability and model specification. The main concept is to "separate" the dynamic network into distinct formation and persistence processes.

Consider the network transition from time $t-1$ to time t. Let $\mathbf{Y}^{t-1}$ denote the network at time $t-1$, and $\mathbf{Y}^t$ the network at time t. We define the formation network $\mathbf{Y}^t_+$ as the network formed by augmenting $\mathbf{Y}^{t-1}$ with the ties formed between times $t-1$ and t. The persistence network $\mathbf{Y}^t_-$ is the network formed by removing from $\mathbf{Y}^{t-1}$ the ties dissolved between times $t-1$ and t. Via a set operation, the realized formation and persistence networks are derived as:

$$\begin{aligned}\mathbf{y}^t_+ &= \mathbf{y}^{t-1} \cup \mathbf{y}^t \\ \mathbf{y}^t_- &= \mathbf{y}^{t-1} \cap \mathbf{y}^t.\end{aligned} \tag{1}$$

In this operation, $\mathbf{y}^t_+ = \mathbf{y}^{t-1} \cup \mathbf{y}^t$ represents the set of ties that appear in either the network at time $t-1$ or the network at time t. Conversely, $\mathbf{y}^t_- = \mathbf{y}^{t-1} \cap \mathbf{y}^t$ represents the set of ties that exist in both the network at time $t-1$ and the network at time t. A key goal of STERGMs is to reconstruct $\mathbf{y}^t$ from $\mathbf{y}^{t-1}$, $\mathbf{y}^t_+$, and $\mathbf{y}^t_-$, or to separate $\mathbf{y}^t$ into $\mathbf{y}^t_+$ and $\mathbf{y}^t_-$, given $\mathbf{y}^{t-1}$. This reconstruction is achieved with the following set operation:

$$\mathbf{y}^t = \mathbf{y}^t_+ \backslash (\mathbf{y}^{t-1} \backslash \mathbf{y}^t_-) = \mathbf{y}^t_- \cup (\mathbf{y}^t_+ \backslash \mathbf{y}^{t-1}), \tag{2}$$

where, $\mathbf{y}^t_+ \backslash \mathbf{y}^{t-1}$ contains ties $\{i, j\}$ that are present in $\mathbf{y}^t_+$ but not in $\mathbf{y}^{t-1}$. Thus, $\mathbf{y}^t$ can be expressed as the union of $\mathbf{y}^t_-$ and $\mathbf{y}^t_+ \backslash \mathbf{y}^{t-1}$. This approach allows us to separate the network dynamics into formation and persistence processes as the network evolves over time. As a result, if $\mathbf{Y}^t_+$ is independent of $\mathbf{Y}^t_-$ conditional on $\mathbf{Y}^{t-1}$, the transition probability from time $t-1$ to time t is separable as follows (Krivitsky and Handcock, 2014):

$$\begin{aligned} P(\mathbf{Y}^t = \mathbf{y}^t | \mathbf{Y}^{t-1} = \mathbf{y}^{t-1}; \boldsymbol{\theta}) &= P(\mathbf{Y}^t_+ = \mathbf{y}^t_+, \mathbf{Y}^t_- = \mathbf{y}^t_- | \mathbf{Y}^{t-1} = \mathbf{y}^{t-1}; \boldsymbol{\theta}_+, \boldsymbol{\theta}_-) \\ &= P(\mathbf{Y}^t_+ = \mathbf{y}^t_+ | \mathbf{Y}^{t-1} = \mathbf{y}^{t-1}; \boldsymbol{\theta}_+) \times P(\mathbf{Y}^t_- = \mathbf{y}^t_- | \mathbf{Y}^{t-1} = \mathbf{y}^{t-1}; \boldsymbol{\theta}_-). \end{aligned} \tag{3}$$

where $\boldsymbol{\theta} = (\boldsymbol{\theta}_-, \boldsymbol{\theta}_+)$. This specification allows us to model the formation and persistence processes separately. Given $\boldsymbol{y}^{t-1} \in \mathcal{Y}$, the realizations of $\boldsymbol{Y}^t_+$ can be expressed as $\boldsymbol{y}^t_+ \in \mathcal{Y}_+(\boldsymbol{y}^{t-1}) \subseteq \{\forall \boldsymbol{y} : \boldsymbol{y} \supseteq \boldsymbol{y}^{t-1}\}$ and the realizations of $\boldsymbol{Y}^t_-$ is expressed as $\boldsymbol{y}^t_- \in \mathcal{Y}_-(\boldsymbol{y}^{t-1}) \subseteq \{\forall \boldsymbol{y} : \boldsymbol{y} \subseteq \boldsymbol{y}^{t-1}\}$. With a d-vector $g_+(\boldsymbol{y}^t_+, \boldsymbol{y}^{t-1})$ of sufficient statistics for the formation network $\boldsymbol{y}^t_+$ from $\boldsymbol{y}^{t-1}$ and parameter $\boldsymbol{\theta}_+ \in \mathbb{R}^d$ and a d-vector $g_-(\boldsymbol{y}^t_-, \boldsymbol{y}^{t-1})$ of sufficient statistics for the persistence network $\boldsymbol{y}^t_-$ from $\boldsymbol{y}^{t-1}$ and parameter $\boldsymbol{\theta}_- \in \mathbb{R}^d$, the formation and persistence models are elaborated as:

$$P(\boldsymbol{Y}^t_+ = \boldsymbol{y}^t_+ | \boldsymbol{Y}^{t-1} = \boldsymbol{y}^{t-1}; \boldsymbol{\theta}_+) = \frac{\exp(\boldsymbol{\theta}_+ \cdot g_+(\boldsymbol{y}^t_+, \boldsymbol{y}^{t-1}))}{c_+(\boldsymbol{\theta}_+, \boldsymbol{y}^{t-1})} \quad \boldsymbol{y}^t_+ \in \mathcal{Y}_+(\boldsymbol{y}^{t-1}), \tag{4}$$

$$P(\boldsymbol{Y}^t_- = \boldsymbol{y}^t_- | \boldsymbol{Y}^{t-1} = \boldsymbol{y}^{t-1}; \boldsymbol{\theta}_-) = \frac{\exp(\boldsymbol{\theta}_- \cdot g_-(\boldsymbol{y}^t_-, \boldsymbol{y}^{t-1}))}{c_-(\boldsymbol{\theta}_-, \boldsymbol{y}^{t-1})} \quad \boldsymbol{y}^t_- \in \mathcal{Y}_-(\boldsymbol{y}^{t-1}), \tag{5}$$

where

$$c_+(\boldsymbol{\theta}_+, \boldsymbol{y}^{t-1}) = \sum_{\boldsymbol{x}_+ \in \mathcal{Y}_+(\boldsymbol{y}^{t-1})} \exp\{\boldsymbol{\theta}_+ \cdot g_+(\boldsymbol{x}_+, \boldsymbol{y}^{t-1})\}, \tag{6}$$

$$c_-(\boldsymbol{\theta}_-, \boldsymbol{y}^{t-1}) = \sum_{\boldsymbol{x}_- \in \mathcal{Y}_-(\boldsymbol{y}^{t-1})} \exp\{\boldsymbol{\theta}_- \cdot g_-(\boldsymbol{x}_-, \boldsymbol{y}^{t-1})\}, \tag{7}$$

are the normalizing constants. In this framework, the sufficient statistics for the formation and persistence networks can vary, allowing for a more flexible model specification (Krivitsky and Handcock, 2014). In practice, this property is considered to be useful (Krivitsky, 2009; Krivitsky and Handcock, 2014). For instance, it is typical for the formation network model to be quite complex while that of the persistence process is quite simple, reflecting the social reality that forming social ties may depend on many factors while dissolving ties depends on a few. Although STERGMs sacrifice the ability to model interactions between the formation and persistence networks intra-time step, it offers significant improvements in model specification and interpretability. For a more detailed discussion of STERGMs, see the supplementary material.

We extend STERGMs to model the multiple small dynamic networks that are the result of the evolutionary games. Suppose we have G independent small dynamic networks from the same experimental setting, each with T time points and n nodes of interest, here the nodes in each of the G dynamic networks are distinct. Let $\boldsymbol{Y}^{t,g}$ be an undirected random graph at time t in the g-th dynamic network, whose realization is $\boldsymbol{y}^{t,g} \in \mathcal{Y}$, the set of possible networks of interest on n. With a d-vector $g(\boldsymbol{y}^{t,g}, \boldsymbol{y}^{t-1,g})$ of sufficient statistics for the network transition from $\boldsymbol{y}^{t-1,g}$ to $\boldsymbol{y}^{t,g}$ and parameter $\boldsymbol{\theta} \in \mathbb{R}^d$, the transition probability from time $t-1$ to time t in the g-th network is defined as:

$$P(\boldsymbol{Y}^{t,g} = \boldsymbol{y}^{t,g} | \boldsymbol{Y}^{t-1,g} = \boldsymbol{y}^{t-1,g}; \boldsymbol{\theta}) = \frac{\exp\{\boldsymbol{\theta} \cdot g(\boldsymbol{y}^{t,g}, \boldsymbol{y}^{t-1,g})\}}{c(\boldsymbol{\theta}, \boldsymbol{y}^{t-1,g})} \quad \boldsymbol{y}^{t,g}, \boldsymbol{y}^{t-1,g} \in \mathcal{Y}, \tag{8}$$

where

$$c(\boldsymbol{\theta}, \boldsymbol{y}^{t-1,g}) = \sum_{\boldsymbol{x}^{t,g} \in \mathcal{Y}} \exp\{\boldsymbol{\theta} \cdot g(\boldsymbol{x}^{t,g}, \boldsymbol{y}^{t-1,g})\} \tag{9}$$

is the normalizing constant. As a result, assuming homogeneity of parameters over time and networks, the likelihood of a STERGM with G independent networks and T time points can be represented as:

$$\prod_{g=1}^{G} \prod_{t=2}^{T} P(\boldsymbol{Y}^{t,g} = \boldsymbol{y}^{t,g} | \boldsymbol{Y}^{t-1,g} = \boldsymbol{y}^{t-1,g}; \boldsymbol{\theta}). \tag{10}$$

This framework is a natural extension of STERGMs, retaining the same interpretability. Statistical inferences can be conducted using Markov Chain Monte Carlo (MCMC) methods. However, leveraging the small network size, especially $n \leq 7$, inherent to multiple small networks, it becomes feasible to numerically calculate the likelihood function directly and estimate parameters with the direct numerical optimization. This approach has significant advantages, including producing more reliable parameter estimates, standard errors, and the likelihood ratios, allowing for robust model comparisons through the deviance test. In contrast, the MCMC approaches often encounter challenges such as poorly mixed chains, the presence of MCMC errors, and uncertainties in approximating likelihood ratios (Hunter and Handcock, 2006).

4. Statistical Inference

In this section, we conduct statistical inference based on our experiment and the proposed model.

4.1. Main Analysis

We aimed to investigate the dynamic structural patterns stemming from the networked public goods games. To achieve this, we focused on modelling the formation and persistence of networks by employing the proposed model with the STERGM parameterization. This approach assumes the independence of dynamic networks across games as well as homogeneity of parameters across time steps and games.

Regarding the independence of the dynamic networks across games, we conducted 20 games, each generating a dynamic network created by a distinct group of participants. Since there were no opportunities for interaction across these groups, the networks were considered independent by design. Given that each game was conducted under the same game setup, we also assumed parameter homogeneity across games.

Concerning parameter homogeneity across time steps, participants were not informed about the total number of time steps, which limited the potential for endgame-oriented strategies. Additionally, two practice time steps were conducted before the actual games to ensure that participants were familiar with the experimental setup, suggesting that strategic behaviour likely stabilized at the beginning of the actual games. Therefore, we assumed parameter homogeneity over time steps.

Following Krivitsky and Handcock (2014), we incorporated both exogenous and endogenous structural statistics. Note that identical statistics were used for both the formation and persistence models, as the network dynamics were presumed to be governed by the same structural patterns (albeit with different parameters). The dynamic networks were undirected due to the symmetric interactions inherent in the public goods game.

First, we included terms for the number of cooperation and defection homophily connections. At each time step, the homophily connection was defined after the network update phase if both participants were directly connected and had chosen the same decisions (cooperation or defection) in the most recent time step. For example, at time 2 in Fig. 4, there were 3 cooperation homophily connections and 1 defection homophily connection.

Second, we incorporated terms for the sum of absolute wealth differences. At each time step, after the network update phase, we calculated the sum of the absolute wealth differences between directly connected participants.

Finally, we included terms for the number of triangles to account for broader structural patterns within the dynamic networks. After the network update phase, we counted the number of triangles created by the direct connections. Unlike studies on directed networks

(Krivitsky and Handcock, 2014; Snijders et al., 2010), we omitted terms for aggregate transitive and cyclical ties, as our data involved undirected networks without hierarchical interactions.

We computed the maximum likelihood estimate (MLE) by direct optimization using the Broyden-Fletcher-Goldfarb-Shanno (BFGS) algorithm (Broyden, 1970; Fletcher, 1970; Goldfarb, 1970; Shanno, 1970). We could estimate the MLE without Markov Chain Monte Carlo (MCMC) (Hunter and Handcock, 2006) or other approximations, such as pseudo-likelihood (Strauss and Ikeda, 1990), as we were leveraging the small network size of our multiple small dynamic networks. Model comparisons were conducted using likelihood ratio tests, enabling evaluation of model fit and selection of the most suitable model for the networked public goods game.

The validity of the MLE for this setting is based on two arguments. The first is studies for the MLE for ERGM in small network size settings (Vega Yon et al., 2021). They find that the MLE is a good estimator even for small network sizes. The second evidence comes from asymptotics: as the number of experiments, G, increases the MLE satisfies a central limit theorem. Specifically, under mild regularity conditions, the MLE with probability approaching one, is unique when it exists and is asymptotically Gaussian with mean the true value of the parameter and covariance equal to the inverse Fisher information matrix (corresponding to the likelihood in equation (10) (Barndorff-Nielsen, 1978; Geyer, 2013)). In our situation, we computed the information matrix numerically from the Hessian returned as a by-product of the optimization. Results by Bogdan et al. (2022) suggest that the asymptotics is relevant if G is of the same size as the number of nodes, n. In our situation, $G = 20$ and $n = 6$.

Table 1 presents the model estimates, and we provide brief interpretations for significant parameters below. For the formation model, the triangle parameter was estimated at -0.260 (SE $= 0.096$), suggesting that the connections completing triangles were less likely to form compared to connections that did not form such structures, controlling for the covariates. The cooperation homophily parameter was estimated at 1.069 (SE $= 0.183$), showing that the connections between the cooperative participants were more likely to form than heterophilous connections, controlling for other covariates and the structural dependency. The wealth difference parameter was estimated at -1.084 (SE $= 0.542$), this implied that the connections were less likely to form between participants with the larger wealth differences compared to those with the smaller differences, controlling for other covariates and the structural dependency.

For the persistence model, the cooperation homophily parameter was estimated at 1.677 (SE $= 0.276$), showing that the connections between cooperative participants were more likely to persist than the heterophilous connections, controlling for other covariates and the structural dependency. The wealth difference parameter was estimated at -1.099 (SE $=$ 0.469), this implied that the connections were less likely to persist between participants with the larger wealth differences compared to those with the smaller differences, controlling for other covariates and the structural dependency.

Our analysis revealed key insights into the dynamics of the public goods games we employed. We observed a negative transitive effect in the formation networks, suggesting

Table 1. MLE parameter estimates for the public goods game networks

Parameter	Formation Est. (SE)	Persistence Est. (SE)
Edge	-1.358 (0.195)***	1.682 (0.210)***
Triangle	-0.260 (0.096)**	-0.023 (0.133)
Homophily (cooperation)	1.069 (0.183)***	1.677 (0.276)***
Homophily (defection)	0.438 (0.255)	0.106 (0.225)
Absolute wealth difference	-1.084 (0.542)*	-1.099 (0.469)*

Significance levels: 0.05*, 0.01**, 0.001***

Table 2. Deviances for the public goods game networks

Model	Residual deviance	Deviance dev. (d.f.)	$p-$value
Null	2911.22	—	—
Only-Covariates	1742.47	1168.74 (8)	0.000
Full	1734.79	7.68 (2)	0.021

that participants might avoid forming the connections that would complete triangles. Consistent with expectations, there was a strong tendency for cooperative participants to form and persist the connections with each other. This might reflect the importance of cooperative behaviour in fostering stable and cohesive networks within the social dilemma. Participants also demonstrated a preference for forming and persisting the connections with others of the similar wealth levels, underscoring the role of economic disparities in both network formation and persistence.

4.2. Assessing goodness of fit

We consider two ways of assessing the goodness of fit (GoF) of the model to the data. The first is an analysis of deviance, comparing nested models. The second compares substantively important network statistics of the data to the distribution of the same statistics simulated from the model. The first is a relative measure of goodness of fit while the second is an absolute measure.

Table 2 provides the deviance test results for the null model, only–covariates model, and main (full) model. The main model significantly improved the fit, compared to the null and only-covariates models. These results revealed that the structural term, the number of triangles, played an important role in explaining the network dynamics.

One way to assess the absolute closeness of the fitted model to data generating mechanism is to compare the distribution of dynamic networks drawn from the model to the observed dynamic networks. The idea here is that, if the model provides a good fit, the observed networks should be similar to those generated from the fitted model. Hunter et al. (2008) proposed that the distribution of structurally important network statistics drawn from the fitted model be compared to the observed network statistics. If the observed network

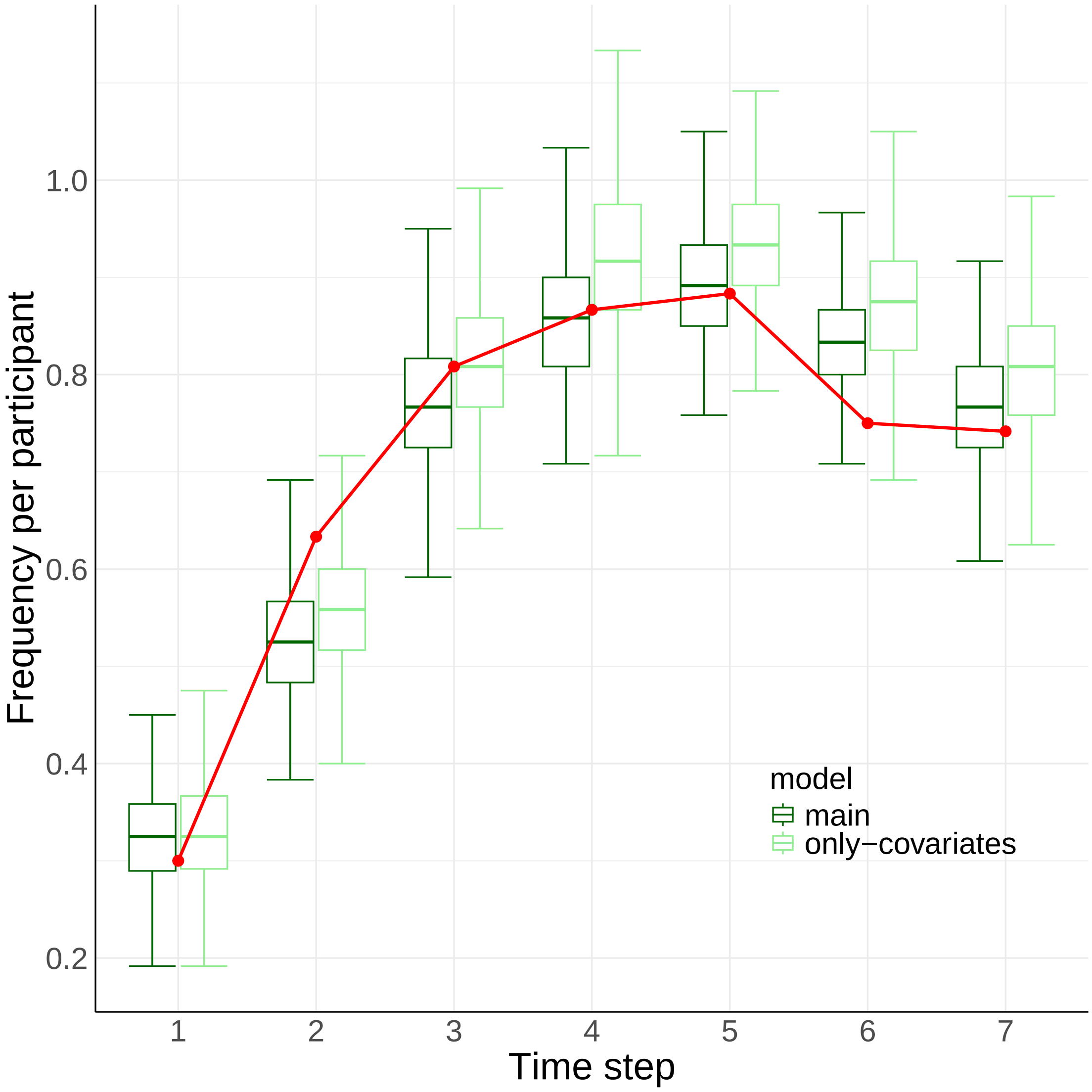

Fig. 5. Triangles GoF plots for the formation networks

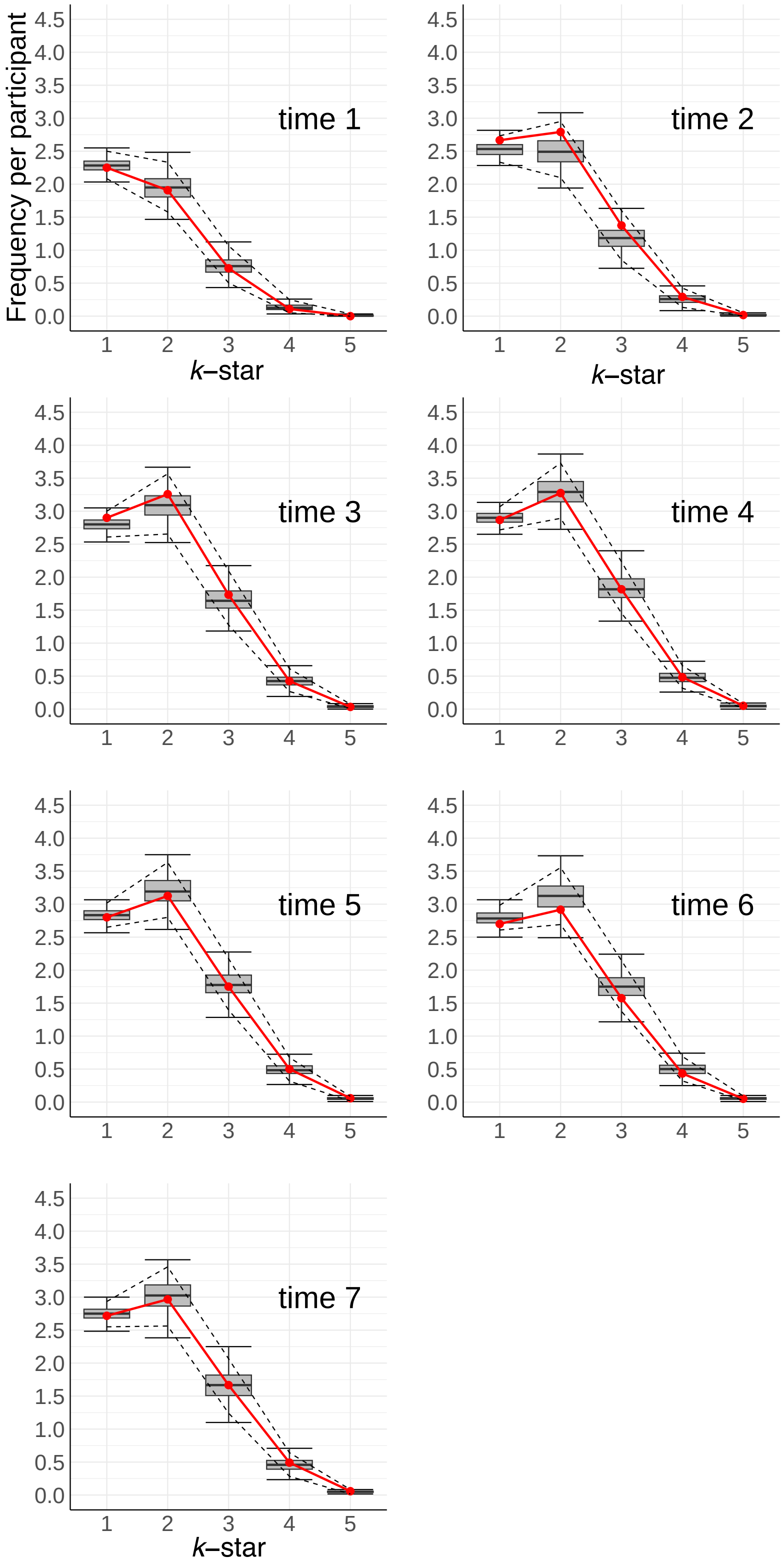

Fig. 6. k-stars GoF plots for the public goods game networks

statistics deviated substantially from the distribution from the model, then the nature of the deviations would tell us how the model fit the data poorly. One fundamental set of network statistics is the number of triangles, a measure of transitivity and central to the model.

Fig. 5 presents the goodness-of-fit plots for the number of triangles per participant in the formation networks. The red dots indicate the observed ones after the network update phase at each time step. The dark green box plots represent simulations from the main model, while the light green box plots correspond to simulations from the only-covariates model. The results show that the main model captures the observed values within the interquartile range (IQR) at 5 out of 7 time steps, compared to 3 out of 7 for the only-covariates model. Taken together with the deviance test results (Table 2), these findings support including the triangle term.

Note that our GoF plots employed a different approach from the standard application, that to a single network (Hunter et al., 2008). Unlike the standard approach for a single network, our study involved 20 independent dynamic networks over 7 time steps. Generating separate GoF plots for each network at each time step would yield 140 plots, making it challenging to interpret and summarize the results. Additionally, each network included only 6 nodes, leading to substantial variability in local structures. As an alternative, we implemented a summary GoF approach: for each time step, we aggregated the total number of triangles across all 20 networks and compared them to simulations from the estimated models.

Another fundamental characteristic of the networks is their degree distribution. This is not specifically included as a term in the model. We again employed a summary GoF approach, focusing on the total number of k-stars across the 20 dynamic networks after the network update phase at each time step. In Fig. 6, the red dots indicate the observed total k-star counts per participant, while the grey box plots show the distribution of simulated ones under the main model (Table 1). The dotted lines denote the 95% quantiles of the simulated distributions. We see that the model successfully reproduces the k-star distributions in the GoF diagnostics (Fig. 6), indicating that it captures key structural features—including centralization—without explicitly modelling such terms.

4.3. Sensitivity Analysis

Based on the main analysis, we conducted several sensitivity analyses. First, we evaluated the assumption of parameter homogeneity across time steps by estimating the MLE parameters separately for each time step using the main model (Table 1).

Figs. 7 and 8 present the MLE parameter estimates for the formation and persistence models at each time step. The colours indicate the significance of each estimate (black: $p-$value < 0.05; grey: not significant). Consistent with the homogeneity model results in Table 1, the parameter estimates display similar tendencies over time. It should be noted that, because no defection homophily formations occurred at time step 6, the MLE for that parameter is negative infinity and is not plotted.

Next, we considered the potential role of centralization. In our networked public goods game, during the network update phase, participants could not directly observe the number of connections of others, however, they could view alter-non-alter connections (see Section 2.2, Time Step Structure). This suggests that degree-based centralization might emerge indirectly through transitive closures, with the triangle term potentially capturing both intentional transitive clustering and degree-based centralization dynamics.

To test for other potential sources of centralization, we estimated a model that included a 2−star term. However, the model fit did not improve significantly (Likelihood Ratio Test: $p = 0.190$, df $= 2$), suggesting that such mechanisms did not meaningfully enhance the model's validity.

Finally, we assessed the potential influence of demographic characteristics in our networked public goods game. In the main model (Table 1), demographic covariates were not included because participants could not observe the demographic information of others. As an additional test, we examined gender effects by including the number of male–male and male–female direct connections as covariates. This model did not provide a better fit (Likelihood Ratio Test: $p = 0.117$, df $= 4$), and the added terms were not significant nor did they affect the significance of other covariates.

5. Discussion

In this paper, we proposed a statistical framework for analysing networked public goods games using STERGMs. We demonstrated the application of this model by analysing the experiment of 20 games, highlighting the model's ability to capture the dependencies in the temporal relational information. The model provided insights into the formation and persistence of connections. These insights, which could not have been achieved through nodal-level analysis alone, underscored the importance of examining dyad-level dependencies in understanding networked human behaviours.

The significantly negative estimate of the triangle parameter in the formation model was a striking result. Given that transitive closures were the only higher-order network structures visible to participants, this result suggested that they might have preferred to build connections with new groups or those who seemed less connected, rather than forming tightly knit clusters. This could reflect their interests in establishing exclusive or privileged relationships that perhaps position themselves as unique or special in the eyes of others. By doing so, participants might seek to elicit more favorable cooperative responses from others.

Such behavioural tendencies were consistent with a relevant theory (Burt, 1992). Burt argued that actors who strategically exploit structural holes (brokerage) can secure not only informational advantages but also control benefits, which enabled them to influence the behaviours of others (pp. 30–31). However, it was important to emphasize that this interpretation is specific to the experimental context of this study data and should be generalised with caution. The future research should aim to collect and analyze more detailed data to examine whether similar behavioural patterns emerge under varying game parameter settings and participant demographics. For example, design elements such as capped resources, tie constraints, and payoff structures may substantially influence both model estimates and the interpretation of behavioural dynamics.

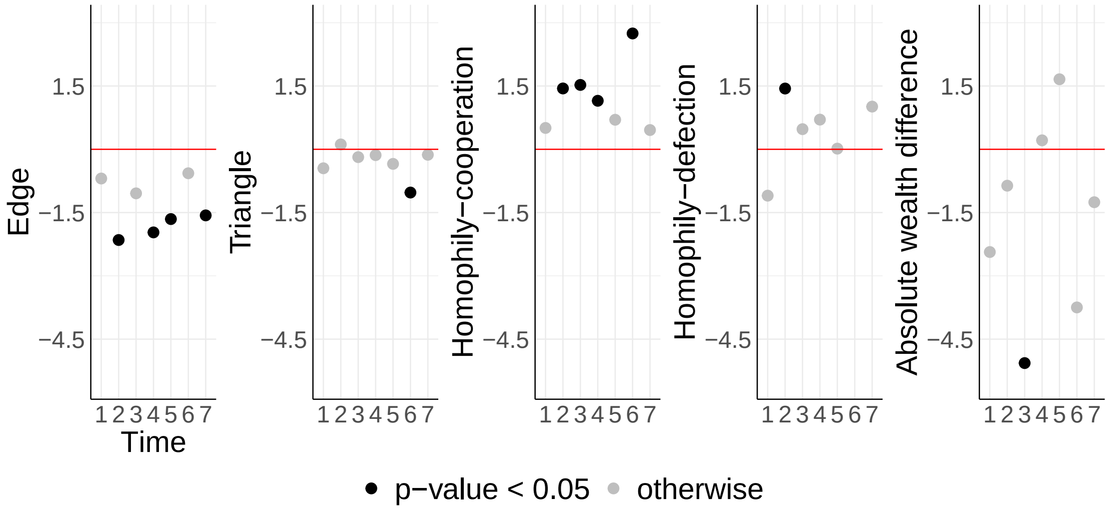

Fig. 7. MLE parameter estimates for the formation model over time

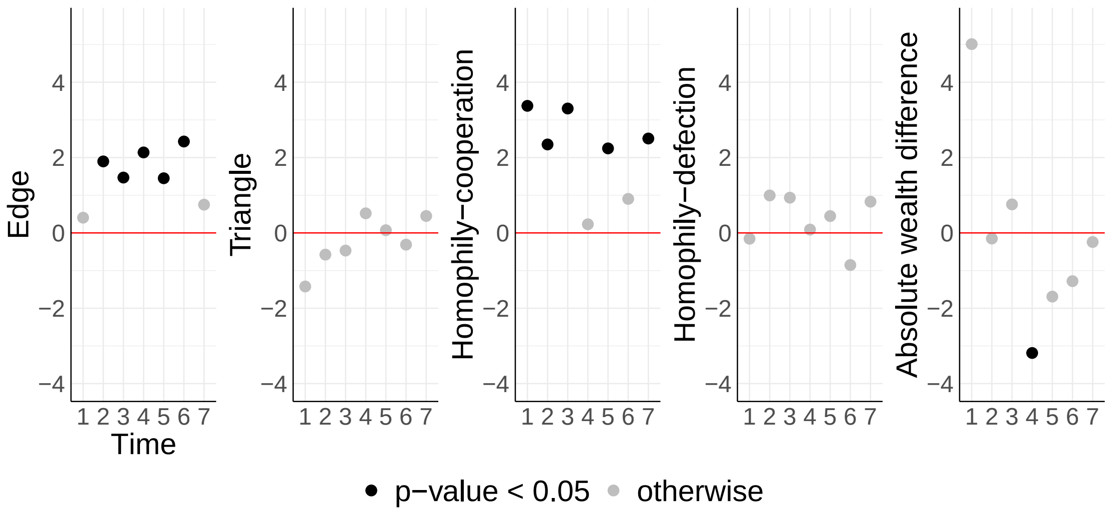

Fig. 8. MLE parameter estimates for the persistence model over time

In our proposed model, we employed direct numerical optimization of the likelihood function to achieve more reliable parameter estimates and likelihood ratios. This approach is particularly advantageous for multiple small dynamic networks, as maximum likelihood estimation enables robust statistical inference and model comparison. By incorporating a number of independent networks, the model also maintains high statistical power. However, the computational constraints of this method limits its applicability, making it suitable primarily for small-scale networks, particularly those with fewer than or equal to 7 nodes.

Our proposed statistical framework supports several extensions. For example, in evolutionary game theory, incorporating multiple treatment conditions can shed light on how experimental variables influence network dynamics. As demonstrated by Nishi et al. (2015), wealth visibility can affect cooperation rates in public goods games. By including treatment conditions as covariates, the model can analyze the impact of different experimental setups on the network formation and persistence, enabling a deeper understanding of structural dependencies in social human behaviours.

In these experiments, the network size was controlled by the experimenter. However, it is a fundamental determinant of the social structure of the network, and hence the model terms and parameters. The models we had were conditional on the network size and direct comparison of the parameters for different network sizes was not possible (See Krivitsky et al., 2011). A current limitation of the model is its inability directly compare experiments of different network sizes. In social human behaviour research, network sizes often fluctuate across networks, partly due to challenges in recruiting the constant number of participants for repeated experiments. Addressing this limitation, future research could focus on adapting the model to handle networks of varying sizes by utilizing methods such as those developed by Krivitsky et al. (2011). Incorporating these approaches would allow for more flexible model specifications and broaden the model's applicability across diverse experimental settings.

Finally, our proposed model holds potential for broad application across various domains, including networked human behaviours within families, workplaces, schools, and hospitals. In these settings, small groups of 6–10 individuals repeatedly interact over dynamic social networks. This model's versatility suggests its utility beyond the scope of networked public goods games, providing a pathway for advancements in understanding social interactions and behavioural dynamics across a variety of disciplines.

6. Disclosure Statement

The authors report there are no competing interests to declare.

7. Data and Software Availability

All analysis was done in the R environment (R version 4.3.2). The code and data to reconstruct the analyses of this paper can be downloaded from zenodo (Ando and Handcock, 2025).

8. Acknowledgements

This article is based upon work supported by the National Science Foundation (NSF, 2230125, and CCF-2200197), Centers for Disease Control (CDC, CDC-RFA-FT-23-0069), National Institute of Child Health, Human Development (NICHD, R21HD063000, R21HD075714 and R24-HD041022), National Institutes of Health (NIH, K01AI166347), and the Japan Science and Technology Agency (JPMJPR21R8 and JPMJRS22K1). The content is solely the responsibility of the authors and do not necessarily represent the official views of the funders.

9. Supplementary Materials

The supplement contains a description of Exponential-family Random Graph Models, Temporal Exponential-family Random Graph Models, and some details of Separable Temporal Exponential-family Random Graph Models. (pdf)

10. Author Contributions

HA and MSH designed the project. HA implemented the experiment and conducted the data analysis. HA and MSH collaboratively wrote the paper. AN contributed laboratory resources.

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"Supplement to 'Statistical modelling of Networked Evolutionary Public Goods Games'"

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1. Exponential-family Random Graph Models

This section gives a very brief introduction to Exponential-family Random Graph Models (ERGMs), to help understand why they are appropriate for modelling the structure of a complex social process that evolves over time.

ERGMs have a long history of successfully representing dependencies in relational information (Handcock, 2003; Hunter and Handcock, 2006; Snijders et al., 2006; Schweinberger and Handcock, 2015; Blackburn and Handcock, 2022). Suppose that n is the set of actors/"nodes", let $\mathbf{Y}$ be an undirected random graph whose realization is $\mathbf{y} \in \mathcal{Y}$, the set of possible networks of interest on n. With a d-vector $Z(\mathbf{y})$ of sufficient statistics and parameter $\boldsymbol{\theta} \in \mathbb{R}^d$, an ERGM is expressed as

$$P(\mathbf{Y} = \mathbf{y}) = \exp\{\boldsymbol{\theta}\cdot Z(\mathbf{y}) - \psi(\boldsymbol{\theta})\} \quad \mathbf{y} \in \mathcal{Y}, \tag{1}$$

where

$$\exp\{\psi(\boldsymbol{\theta})\} = \sum_{\mathbf{x}\in\mathcal{Y}} \exp\{\boldsymbol{\theta}\cdot Z(\mathbf{x})\} \tag{2}$$

is the normalising constant. It is well known that the sum of $\exp\{\boldsymbol{\theta}\cdot Z(\mathbf{x})\}$ over the set of possible networks, $\mathcal{Y}$ often causes computational challenges; the number of possible networks on n is $2^{n(n-1)/2}$, which is an astronomically large number for even moderate size n. Therefore, evaluating the log-likelihood, or even maximising the log-likelihood, is computationally infeasible for large networks, resulting in the use of Markov Chain Monte Carlo (MCMC) methods (Geyer and Thompson, 1992) to estimate the parameters of interest and conduct statistical inference. Notable here is the difficulty in reliably estimating the maximum likelihood estimators and its standard errors and implementing

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the likelihood ratio test. There are various reasons for this, such as the failure to generate well-mixed chains, the existence of MCMC errors, and uncertainty in approximation of the likelihood ratios (Hunter and Handcock, 2006).

It is a natural extension to apply the ERGM framework to representing dependencies in temporal relational information. Originating from Robins and Pattison (2001), Hanneke and Xing (2006) and Hanneke et al. (2010) defined the Temporal Exponential-family Random Graph Models (TERGMs) as ERGMs for the transition probability from time t to time t+1. More importantly, the introduction on the concept of separability of dynamic networks into formation and persistence networks has substantially improved interpretability and model specification through Separable TERGMs (STERGMs) (Krivitsky and Handcock, 2014). In these TERGM frameworks, parameter estimation and statistical inference are usually performed using MCMC methods as in cross-sectional ERGMs.

2. Temporal Exponential-family Random Graph Model

2.1. Model definition

TERGMs are the natural extension of ERGMs. They were first introduced to model the network at time t conditional on the network at time t - 1 (Robins and Pattison, 2001; Hanneke and Xing, 2006). Assuming that N is the set of nodes of interest, let $\mathbf{Y}^t$ be an undirected random graph at time t, whose realization is $\mathbf{y}^t \in \mathcal{Y}$, the set of possible networks of interest on N. With a d-vector $g(\mathbf{y}^t, \mathbf{y}^{t-1})$ of sufficient statistics for the network transition from $\mathbf{y}^{t-1}$ to $\mathbf{y}^t$ and parameter $\boldsymbol{\theta} \in \mathbb{R}^d$, the transition probability from time t - 1 to time t is defined as:

$$P(\mathbf{Y}^t = \mathbf{y}^t | \mathbf{Y}^{t-1} = \mathbf{y}^{t-1}; \boldsymbol{\theta}) = \frac{\exp\{\boldsymbol{\theta} \cdot g(\boldsymbol{y}^t, \boldsymbol{y}^{t-1})\}}{c(\boldsymbol{\theta}, \boldsymbol{y}^{t-1})} \quad \boldsymbol{y}^t, \boldsymbol{y}^{t-1} \in \mathcal{Y}, \tag{3}$$

where

$$c(\boldsymbol{\theta}, \mathbf{y}^{t-1}) = \sum_{\mathbf{x}^t \in \mathcal{Y}} \exp\{\boldsymbol{\theta} \cdot g(\mathbf{x}^t, \mathbf{y}^{t-1})\} \tag{4}$$

is the normalising constant. An essential ingredient for model specification is the choice of g, which can be any valid network statistics evaluated at t that depends on t - 1. As a result, assuming constant parameters over time, a TERGM with T time points can be represented as:

$$\prod_{t=2}^{T} P(\mathbf{Y}^t = \mathbf{y}^t | \mathbf{Y}^{t-1} = \mathbf{y}^{t-1}; \boldsymbol{\theta}). \tag{5}$$

2.2. Interpretation

Similar to ERGMs, the parameters of TERGMs can be interpreted as the conditional odds. Given the property of conditional dyadic independence (Hanneke and Xing, 2006), the transition probability from time t - 1 to time t is re-expressed as:

$$P(\mathbf{Y}^t = \mathbf{y}^t | \mathbf{Y}^{t-1} = \mathbf{y}^{t-1}; \boldsymbol{\theta}) = \prod_{i<j} P(\mathbf{Y}^t_{ij} = \mathbf{y}^t_{ij} | \mathbf{Y}^{t-1} = \mathbf{y}^{t-1}; \boldsymbol{\theta}), \tag{6}$$

which means, in $\mathbf{Y}^t$, the realizations of tie states, $\mathbf{y}^t_{ij}$ are independent conditional on $\mathbf{Y}^{t-1}$, leading to the following model expression on the conditional odds:

$$\frac{P(\mathbf{Y}^t_{ij} = 1|\mathbf{Y}^{t-1} = \mathbf{y}^{t-1}; \boldsymbol{\theta})}{P(\mathbf{Y}^t_{ij} = 0|\mathbf{Y}^{t-1} = \mathbf{y}^{t-1}; \boldsymbol{\theta})} = \exp[\boldsymbol{\theta} \cdot \{g(\mathbf{y}^t_{+ij}, \mathbf{y}^{t-1}) - g(\mathbf{y}^t_{-ij}, \mathbf{y}^{t-1})\}] \tag{7}$$

here, $g(\mathbf{y}^t_{+ij}, \mathbf{y}^{t-1})$ is defined as a d-vector $g(\mathbf{y}^t, \mathbf{y}^{t-1})$ of sufficient statistics for the network transition from $\mathbf{y}^{t-1}$ to $\mathbf{y}^t$, where the edge $\mathbf{y}^t_{ij}$ is present, and $g(\mathbf{y}^t_{-ij}, \mathbf{y}^{t-1})$ is defined as a d-vector $g(\mathbf{y}^t, \mathbf{y}^{t-1})$ of sufficient statistics for the network transition from $\mathbf{y}^{t-1}$ to $\mathbf{y}^t$, where the edge $\mathbf{y}^t_{ij}$ is absent. This interpretation is crucial for understanding the dependencies in the network transition and the role of the parameters in the model.

However, it is important to note that in this model, both the interpretation of the parameters and the model specification may present challenges (Krivitsky and Handcock, 2014). For example, when interpreting dyadic homophily statistics given certain nodal-level groupings, the statistics can be defined as:

$$g(\mathbf{z}, \mathbf{y}^t, \mathbf{y}^{t-1}) = \sum_{i<j} \mathbf{z}_{ij} \mathbf{y}^t_{ij}, \tag{8}$$

where, the nodal-level groupings are defined as:

$$\mathbf{z}_{ij} = \begin{cases} 1 & \text{the node i and j are in the same group} \\ 0 & \text{otherwise} \end{cases} \tag{9}$$

A higher value of the corresponding parameter indicates that more ties are likely to be present between nodes within the same group in the realizations, $\mathbf{y}^t \in \mathcal{Y}$. Conversely, a lower value of the parameter suggests that fewer ties are likely to be present between nodes within the same group in the realizations, $\mathbf{y}^t \in \mathcal{Y}$. Still, it is important to recognise that these dynamic processes occur through the simultaneous formation and dissolution of ties: with a higher parameter value, the dyads might be toggled 'on' more if they were previously empty (indicating more formation) and be toggled 'off' less if they were already present (indicating less dissolution), and vice versa. In this respect, the model is limited in that it cannot distinguish between the formation and dissolution of ties, which poses a challenge in interpreting the parameters.

In addition, the primary challenge of this modelling framework becomes evident through insights into the further inspection above, which directly influence the model specification. Incorporating the dyadic homophily statistics and its parameter, θ_0, the the transition probability of node i and j from time t - 1 to time t can be expressed as follows:

$$\frac{P(\mathbf{Y}_{ij}^t = 1|\mathbf{Y}^{t-1} = \mathbf{y}^{t-1}, \mathbf{Y}_{ij}^{t-1} = 0, \mathbf{z}_{ij} = 1; \theta_0)}{P(\mathbf{Y}_{ij}^t = 0|\mathbf{Y}^{t-1} = \mathbf{y}^{t-1}, \mathbf{Y}_{ij}^{t-1} = 0, \mathbf{z}_{ij} = 1; \theta_0)} \tag{10}$$

$$= \frac{P(\mathbf{Y}_{ij}^t = 1|\mathbf{Y}^{t-1} = \mathbf{y}^{t-1}, \mathbf{Y}_{ij}^{t-1} = 1, \mathbf{z}_{ij} = 1; \theta_0)}{P(\mathbf{Y}_{ij}^t = 0|\mathbf{Y}^{t-1} = \mathbf{y}^{t-1}, \mathbf{Y}_{ij}^{t-1} = 1, \mathbf{z}_{ij} = 1; \theta_0)} \tag{11}$$

$$= \exp(\theta_0)$$

$$\Rightarrow \begin{cases} P(\mathbf{Y}_{ij}^t = 1|\mathbf{Y}^{t-1} = \mathbf{y}^{t-1}, \mathbf{Y}_{i,j}^{t-1} = 0, \mathbf{z}_{ij} = 1; \theta_0) = \frac{\exp(\theta_0)}{1+\exp(\theta_0)} \\ P(\mathbf{Y}_{ij}^t = 0|\mathbf{Y}^{t-1} = \mathbf{y}^{t-1}, \mathbf{Y}_{i,j}^{t-1} = 1, \mathbf{z}_{ij} = 1; \theta_0) = 1 - \frac{\exp(\theta_0)}{1+\exp(\theta_0)}. \end{cases} \tag{12}$$

Thus, with a higher parameter value, the dyads are more likely to be toggled 'on' if they were previously empty (indicating more formation) and less likely to be toggled 'off' if they were already present (indicating less dissolution), and with a lower parameter value, the dyads are less likely to be toggled 'on' if they were previously empty (indicating less formation) and more likely to be toggled 'off' if they were already present (indicating more dissolution). This is a significant limitation of the model, as it can only capture the overall dynamics of the network transitions in specific ways, rather than distinguishing between the formation and dissolution of dynamics.

3. Separable Temporal Exponential-family Random Graph Model

3.1. Model definition

Separable Temporal Exponential-family Random Graph Models (STERGMs) were introduced by Krivitsky and Handcock (2014) as a subset of TERGMs for better interpretability and model specification. The main concept is to "separate" the dynamic network into distinct formation and persistence processes.

Consider the network transition from time t -1 to time t, defining the network $\mathbf{Y}^{t-1}$ at time t -1, the network $\mathbf{Y}^t$ at time t, the formation network $\mathbf{Y}^+$; the initial network $\mathbf{Y}^{t-1}$ with the addition of ties at time t, and the persistence network $\mathbf{Y}^-$; the initial network $\mathbf{Y}^{t-1}$ with the removal of ties at time t. Via a set operation, the realized formation and persistence networks are derived as:

$$\begin{aligned} \mathbf{y}^+ &= \mathbf{y}^{t-1} \cup \mathbf{y}^t \\ \mathbf{y}^- &= \mathbf{y}^{t-1} \cap \mathbf{y}^t. \end{aligned} \tag{13}$$

In this operation, $\mathbf{y}^+ = \mathbf{y}^{t-1} \cup \mathbf{y}^t$ represents the set of ties that appear in either the network at time t - 1 or the network at time t. Conversely, $\mathbf{y}^- = \mathbf{y}^{t-1} \cap \mathbf{y}^t$ represents the set of ties that exist in both the network at time t - 1 and the network at time t. A key goal of STERGMs is to reconstruct $\mathbf{y}^t$ from $\mathbf{y}^{t-1}$, $\mathbf{y}^+$, and $\mathbf{y}^-$, or to separate $\mathbf{y}^t$ into $\mathbf{y}^+$ and $\mathbf{y}^-$, given $\mathbf{y}^{t-1}$. This reconstruction is achieved with the following set operation:

$$\mathbf{y}^t = \mathbf{y}^+ \backslash (\mathbf{y}^{t-1} \backslash \mathbf{y}^-) = \mathbf{y}^- \cup (\mathbf{y}^+ \backslash \mathbf{y}^{t-1}), \tag{14}$$

where, $\mathbf{y}^+ \backslash \mathbf{y}^{t-1}$ contains ties $\{i, j\}$ that are present in $\mathbf{y}^+$ but not in $\mathbf{y}^{t-1}$. Thus, $\mathbf{y}^t$ can be expressed as the union of $\mathbf{y}^-$ and $\mathbf{y}^+ \backslash \mathbf{y}^{t-1}$. This approach allows us to separate the processes of ties into the formation and the persistence as the network evolves over time. As a result, if $\mathbf{Y}^+$ is independent of $\mathbf{Y}^-$ conditional on $\mathbf{Y}^{t-1}$, the transition probability from time t - 1 to time t is separable as follows:

$$
\begin{aligned}
&P(\mathbf{Y}^t = \mathbf{y}^t | \mathbf{Y}^{t-1} = \mathbf{y}^{t-1}; \boldsymbol{\theta}) = P(\mathbf{Y}^+ = \mathbf{y}^+, \mathbf{Y}^- = \mathbf{y}^- | \mathbf{Y}^{t-1} = \mathbf{y}^{t-1}; \boldsymbol{\theta}^+, \boldsymbol{\theta}^-) \\
&= P(\mathbf{Y}^+ = \mathbf{y}^+ | \mathbf{Y}^{t-1} = \mathbf{y}^{t-1}; \boldsymbol{\theta}^+) \times P(\mathbf{Y}^- = \mathbf{y}^- | \mathbf{Y}^{t-1} = \mathbf{y}^{t-1}; \boldsymbol{\theta}^-). \qquad (15)
\end{aligned}
$$

Specifically, we respectively model the formation and the persistence models. Given $\boldsymbol{y}^{t-1} \in \mathcal{Y}$, the realizations of $\boldsymbol{Y}^+$ can be expressed as $\boldsymbol{y}^+ \in \mathcal{Y}^+(\boldsymbol{y}^{t-1}) \subseteq \{\forall \boldsymbol{y} : \boldsymbol{y} \supseteq \boldsymbol{y}^{t-1}\}$ and the realizations of $\boldsymbol{Y}^-$ is expressed as $\boldsymbol{y}^- \in \mathcal{Y}^-(\boldsymbol{y}^{t-1}) \subseteq \{\forall \boldsymbol{y} : \boldsymbol{y} \subseteq \boldsymbol{y}^{t-1}\}$. With a d-vector $g^+(\boldsymbol{y}^+, \boldsymbol{y}^{t-1})$ of sufficient statistics for the formation network $\boldsymbol{y}^+$ from $\boldsymbol{y}^{t-1}$ and parameter $\boldsymbol{\theta}^+ \in \mathbb{R}^d$ and a d-vector $g^-(\boldsymbol{y}^-, \boldsymbol{y}^{t-1})$ of sufficient statistics for the persistence network $\boldsymbol{y}^-$ from $\boldsymbol{y}^{t-1}$ and parameter $\boldsymbol{\theta}^- \in \mathbb{R}^d$, the formation and persistence models are elaborated as:

$$
P(\boldsymbol{Y}^+ = \boldsymbol{y}^+ | \boldsymbol{Y}^{t-1} = \boldsymbol{y}^{t-1}; \boldsymbol{\theta}^+) = \frac{\exp(\boldsymbol{\theta}^+ \cdot g^+(\boldsymbol{y}^+, \boldsymbol{y}^{t-1}))}{c^+(\boldsymbol{\theta}^+, \boldsymbol{y}^{t-1})} \quad \boldsymbol{y}^+ \in \mathcal{Y}^+(\boldsymbol{y}^{t-1}), \qquad (16)
$$

$$
P(\boldsymbol{Y}^- = \boldsymbol{y}^- | \boldsymbol{Y}^{t-1} = \boldsymbol{y}^{t-1}; \boldsymbol{\theta}^-) = \frac{\exp(\boldsymbol{\theta}^- \cdot g^-(\boldsymbol{y}^-, \boldsymbol{y}^{t-1}))}{c^-(\boldsymbol{\theta}^-, \boldsymbol{y}^{t-1})} \quad \boldsymbol{y}^- \in \mathcal{Y}^-(\boldsymbol{y}^{t-1}), \qquad (17)
$$

where

$$
c^+(\boldsymbol{\theta}^+, \boldsymbol{y}^{t-1}) = \sum_{\boldsymbol{x}^+ \in \mathcal{Y}^+(\boldsymbol{y}^{t-1})} \exp\{\boldsymbol{\theta}^+ \cdot g^+(\boldsymbol{x}^+, \boldsymbol{y}^{t-1})\}, \qquad (18)
$$

$$
c^-(\boldsymbol{\theta}^-, \boldsymbol{y}^{t-1}) = \sum_{\boldsymbol{x}^- \in \mathcal{Y}^-(\boldsymbol{y}^{t-1})} \exp\{\boldsymbol{\theta}^- \cdot g^-(\boldsymbol{x}^-, \boldsymbol{y}^{t-1})\}, \qquad (19)
$$

are the normalising constants. In this framework, the sufficient statistics for the formation and persistence networks can vary, allowing for a more flexible model specification (Krivitsky and Handcock, 2014). In practice, this property is considered to be useful (Krivitsky, 2009; Krivitsky and Handcock, 2008). For instance, in an extreme case, the formation network model might include statistics that capture homophily ties, while the persistence network does not. Although STERGMs sacrifice the ability to model interactions between the formation and persistence networks, it offers significant improvements in model specification and interpretability. Finally, we demonstrate that STERGMs form a subclass of TERGMs as follows:

$$\begin{aligned}
&P(\boldsymbol{Y}^+ = \boldsymbol{y}^+|\boldsymbol{Y}^{t-1} = \boldsymbol{y}^{t-1}; \boldsymbol{\theta}^+) \times P(\boldsymbol{Y}^- = \boldsymbol{y}^-|\boldsymbol{Y}^{t-1} = \boldsymbol{y}^{t-1}; \boldsymbol{\theta}^-) \\
&= \frac{\exp(\boldsymbol{\theta}^+ \cdot g^+(\boldsymbol{y}^+, \boldsymbol{y}^{t-1}))}{c^+(\boldsymbol{\theta}^+, \boldsymbol{y}^{t-1})} \cdot \frac{\exp(\boldsymbol{\theta}^- \cdot g^-(\boldsymbol{y}^-, \boldsymbol{y}^{t-1}))}{c^-(\boldsymbol{\theta}^-, \boldsymbol{y}^{t-1})} \\
&= \frac{\exp(\boldsymbol{\theta}^+ \cdot g^+(\boldsymbol{y}^+, \boldsymbol{y}^{t-1}) + \boldsymbol{\theta}^- \cdot g^-(\boldsymbol{y}^-, \boldsymbol{y}^{t-1}))}{c^+(\boldsymbol{\theta}^+, \boldsymbol{y}^{t-1}) \cdot c^-(\boldsymbol{\theta}^-, \boldsymbol{y}^{t-1})} \\
&= \frac{\exp\{(\boldsymbol{\theta}^+, \boldsymbol{\theta}^-) \cdot (g^+(\boldsymbol{y}^+, \boldsymbol{y}^{t-1}), g^-(\boldsymbol{y}^-, \boldsymbol{y}^{t-1}))\}}{\sum_{\boldsymbol{x}^+ \in \mathcal{Y}^+(\boldsymbol{y}^{t-1}), \boldsymbol{x}^- \in \mathcal{Y}^-(\boldsymbol{y}^{t-1})} \exp\{(\boldsymbol{\theta}^+, \boldsymbol{\theta}^-) \cdot (g^+(\boldsymbol{x}^+, \boldsymbol{y}^{t-1}), g^-(\boldsymbol{x}^-, \boldsymbol{y}^{t-1}))\}} \\
&= \frac{\exp\{(\boldsymbol{\theta}^+, \boldsymbol{\theta}^-)(g^+(\boldsymbol{y}^{t-1} \cup \boldsymbol{y}^t, \boldsymbol{y}^{t-1}), g^-(\boldsymbol{y}^{t-1} \cap \boldsymbol{y}^t, \boldsymbol{y}^{t-1}))\}}{\sum_{\boldsymbol{w}^t \in \mathcal{Y}} \exp\{(\boldsymbol{\theta}^+, \boldsymbol{\theta}^-) \cdot (g^+(\boldsymbol{y}^{t-1} \cup \boldsymbol{w}^t, \boldsymbol{y}^{t-1}), g^-(\boldsymbol{y}^{t-1} \cap \boldsymbol{w}^t, \boldsymbol{y}^{t-1}))\}} \\
&= \frac{\exp\{\boldsymbol{\theta}^* \cdot g^*(\boldsymbol{y}^t, \boldsymbol{y}^{t-1})\}}{\sum_{\boldsymbol{w}^t \in \mathcal{Y}} \exp\{\boldsymbol{\theta}^* \cdot g^*(\boldsymbol{w}^t, \boldsymbol{y}^{t-1})\}}, \qquad (20)
\end{aligned}$$

where

$$\begin{cases} \boldsymbol{\theta}^* = (\boldsymbol{\theta}^+, \boldsymbol{\theta}^-), \\ g^*(\boldsymbol{y}^t, \boldsymbol{y}^{t-1}) = (g^+(\boldsymbol{y}^{t-1} \cup \boldsymbol{y}^t, \boldsymbol{y}^{t-1}), g^-(\boldsymbol{y}^{t-1} \cap \boldsymbol{y}^t, \boldsymbol{y}^{t-1})). \end{cases} \qquad (21)$$

The final form is identical to that of a TERGM, underscoring that STERGMs represent a specialized case within the broader TERGM framework.

3.2. Interpretation

The parameters of STERGMs can be interpreted as conditional odds, as for TERGMs. Given the property of conditional dyadic independence (Hanneke and Xing, 2006), the formation and persistence models can be re-expressed as:

$$P(\boldsymbol{Y}^+ = \boldsymbol{y}^+|\boldsymbol{Y}^{t-1} = \boldsymbol{y}^{t-1}; \boldsymbol{\theta}^+) = \prod_{i<j} P(\boldsymbol{Y}^+_{ij} = \boldsymbol{y}^+_{ij}|\boldsymbol{Y}^{t-1} = \boldsymbol{y}^{t-1}; \boldsymbol{\theta}^+), \qquad (22)$$

$$P(\boldsymbol{Y}^- = \boldsymbol{y}^-|\boldsymbol{Y}^{t-1} = \boldsymbol{y}^{t-1}; \boldsymbol{\theta}^-) = \prod_{i<j} P(\boldsymbol{Y}^-_{ij} = \boldsymbol{y}^-_{ij}|\boldsymbol{Y}^{t-1} = \boldsymbol{y}^{t-1}; \boldsymbol{\theta}^-), \qquad (23)$$

which means, in $\mathbf{Y}^+$, the realizations of tie states, $\mathbf{y}^+_{ij}$ are independent conditional on $\mathbf{Y}^{t-1}$, and in $\mathbf{Y}^-$, the realizations of tie states, $\mathbf{y}^-_{ij}$ are independent conditional on $\mathbf{Y}^{t-1}$, leading to the following model expression on the conditional odds:

$$\frac{P(\boldsymbol{Y}^+_{ij} = 1|\boldsymbol{Y}^{t-1} = \boldsymbol{y}^{t-1}; \boldsymbol{\theta}^+)}{P(\boldsymbol{Y}^+_{ij} = 0|\boldsymbol{Y}^{t-1} = \boldsymbol{y}^{t-1}; \boldsymbol{\theta}^+)} = \exp[\boldsymbol{\theta}^+ \cdot \{g^+(\boldsymbol{y}^+_{+ij}, \boldsymbol{y}^{t-1}) - g^+(\boldsymbol{y}^+_{-ij}, \boldsymbol{y}^{t-1})\}], \qquad (24)$$

$$\frac{P(\boldsymbol{Y}^-_{ij} = 1|\boldsymbol{Y}^{t-1} = \boldsymbol{y}^{t-1}; \boldsymbol{\theta}^-)}{P(\boldsymbol{Y}^-_{ij} = 0|\boldsymbol{Y}^{t-1} = \boldsymbol{y}^{t-1}; \boldsymbol{\theta}^-)} = \exp[\boldsymbol{\theta}^- \{g^-(\boldsymbol{y}^-_{+ij}, \boldsymbol{y}^{t-1}) - g^-(\boldsymbol{y}^-_{-ij}, \boldsymbol{y}^{t-1})\}], \qquad (25)$$

here, $g(\boldsymbol{y}^+_{+ij}, \boldsymbol{y}^{t-1})$ is defined as a d-vector $g(\boldsymbol{y}^+, \boldsymbol{y}^{t-1})$ of sufficient statistics for the network transition from $\boldsymbol{y}^{t-1}$ to $\boldsymbol{y}^+$, where the edge $\boldsymbol{y}^+_{ij}$ is present, and $g(\boldsymbol{y}^+_{-ij}, \boldsymbol{y}^{t-1})$ is defined as a d-vector $g(\boldsymbol{y}^+, \boldsymbol{y}^{t-1})$ of sufficient statistics for the network transition from $\boldsymbol{y}^{t-1}$ to $\boldsymbol{y}^+$, where the edge $\boldsymbol{y}_{ij}^{+}$ is absent. In the same manner, $g(\boldsymbol{y}_{+ij}^{-}, \boldsymbol{y}^{t-1})$ and $g(\boldsymbol{y}_{-ij}^{-}, \boldsymbol{y}^{t-1})$ can be also interpreted.

For the formation model, a positive $\boldsymbol{\theta}^{+}$ indicates that an increase in $g^{+}(\boldsymbol{y}_{+ij}^{+}, \boldsymbol{y}^{t-1}) - g^{+}(\boldsymbol{y}_{-ij}^{+}, \boldsymbol{y}^{t-1})$ leads to a higher conditional log-odds of the edge $\boldsymbol{y}_{ij}^{+}$ being present, given $\boldsymbol{y}^{t-1}$. Conversely, a negative $\boldsymbol{\theta}^{+}$ indicates that an increase in $g^{+}(\boldsymbol{y}_{+ij}^{+}, \boldsymbol{y}^{t-1}) - g^{+}(\boldsymbol{y}_{-ij}^{+}, \boldsymbol{y}^{t-1})$ leads to a lower conditional log-odds of the edge $\boldsymbol{y}_{ij}^{+}$ being present, given $\boldsymbol{y}^{t-1}$.

For the persistence model, a positive $\boldsymbol{\theta}^{-}$ indicates that an increase in $g^{-}(\boldsymbol{y}_{+ij}^{-}, \boldsymbol{y}^{t-1}) - g^{-}(\boldsymbol{y}_{-ij}^{-}, \boldsymbol{y}^{t-1})$ leads to a higher conditional log-odds of the edge $\boldsymbol{y}_{ij}^{-}$ being present, given $\boldsymbol{y}^{t-1}$. Conversely, a negative $\boldsymbol{\theta}^{-}$ indicates that an increase in $g^{-}(\boldsymbol{y}_{+ij}^{-}, \boldsymbol{y}^{t-1}) - g^{-}(\boldsymbol{y}_{-ij}^{-}, \boldsymbol{y}^{t-1})$ leads to a lower conditional log-odds of the edge $\boldsymbol{y}_{ij}^{-}$ being present, given $\boldsymbol{y}^{t-1}$.

4. Author Contributions

HA and MSH designed the project. HA implemented the experiment and conducted the data analysis. HA and MSH collaboratively wrote the paper. AN contributed laboratory resources.

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