Visualizing Dynamic Social Network Models

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Abstract

Stochastic actor-oriented models (SAOMs), first introduced by Snijders (1996), are a type of statistical network model for dynamic social networks. Unlike other network models, SAOMs are analytically intractable and require extensive simulation procedures for model fitting. We use model visualization techniques introduced in Wickham et al (2015) to better understand these models and their behavior. We use a three-pronged attack: (a) network visualization to view the *model*, (b) exploring collections of models for parameter interpretation, and (c) delving into the fitting algorithms to gain insight into the underlying mechanisms. With the help of static and dynamic visualizations, we bring the hidden SAOM fitting processes into the foreground, with the goal of a better understanding and higher accessibility of SAOMs by social network analysts.

Keywords: social network analysis, dynamic networks, network mapping, animation, statistical graphics

Contents

1 Introduction & Background

As members of the human family, one of the hardest things we try to do is understand our relationships with one another, whether as friends, family, or colleagues. These relationships, or *social networks*, have been studied for decades, in every format from self-help books to publications in academic journals. There are statistical models, such as exponential random graph models (ERGM) and latent space models (LSM), that strive to capture the underlying relationship-generating mechanism (Frank and Strauss, 1986; Hoff et al., 2002). These static models, however, are not optimal for modelling "real-world" social networks because they do not account for changes in the network as time passes. Models for *dynamic social networks* are more realistic because they contain multiple observations of the same network over time.

One set of models for dynamic social networks are stochastic actor-oriented models (SAOMs), introduced in Snijders (1996). These models incorporate node-level covariate effects in addition to the traditional structural effects, such as in-degree or out-degree. With these models, we can examine assumptionsm made about social networks, i.e. that people with common interests are more likely to become friends. For example, we may assume that high schoolers who drink heavily are more likely to be friends with others who drink heavily. SAOMs allow us to incorporate this behavioral information on shared interests into the modeling process.

Unlike other network models, SAOMs are not analytically tractable (Snijders, 2017). Likelihood functions quickly become very complex due to the dependency structure inherent in the data, and so computational methods, such as Markov chain Monte Carlo (MCMC), are used to fit models. For SAOM parameter estimation, we use the software SIENA, and its `R` implementation `RSiena` by Ripley et al. (2016a). This software is a considerable contribution to the field of social network analysis, but the extensive parameter estimation process is largely hidden from the user. To better understand SAOMs and their fitting process in `RSiena`, we use model visualization, or model-vis (Wickham et al., 2015), to examine the underlying methods, hidden structures, and simulation results. Ultimately, we aim to help researchers working with SAOMs better understand the structure, behavior, fit, and results of these models.

In the remainder of this section, we introduce the structure of network data and two different network visualization (net-vis) techniques. Then, we carefully define the many moving pieces that make up a SAOM. Finally, we briefly ouline the SAOM fitting process that we use throughout this paper.

1.1 Networks and their Visualizations

Network data across fields have similar data structures. There are always units of observation and connections between those units. In a social network, the units of observations, called *nodes* or *actors*, are people, while the connections, called *edges* or *ties*, are their relationships with each other. Other data on a network include inherent variables of interest on the nodes and edges themselves, e.g. someone's age, gender, and political affiliation, the type of relationship (friendship, coworkers, etc) that an edge represents, in addition to the changing structure of the network in time.

Visualizing Network Data: Network visualization, also called graph drawing, is a prominent subfield of network analysis. For a review of graph drawing, see Tamassia (2013). Visualizing network data is inherently challenging because of the structure of the data itself. Most data visualizations rely on well-defined axes inherited from the data, such as Cartesian coordinates or spatial locations, but network data typically do not have such built-in structure.
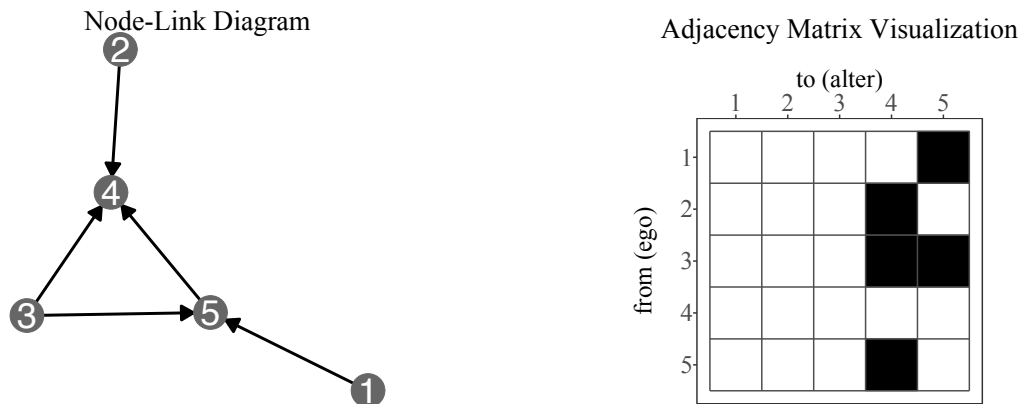

Figure 1: On the left, a node-link diagram of our directed toy network, with nodes placed using the Kamada-Kawai algorithm. On the right, the adjacency matrix visualization for that same network.

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The lack of a native coordinate system has led to two very different primary methods to visualize networks: the node-link diagram and the adjacency matrix visualization (Knuth, 2013; Fekete, 2009). We demonstrate these with a simpe example. Consider the network with five nodes, $\{1, 2, 3, 4, 5\}$, connected by five directed edges: $\{2 \to 4, 3 \to 4, 1 \to 5, 3 \to 5, 5 \to 4\}$ shown in Figure 1.

The first method, the node-link diagram, represents nodes with points in two dimensions and then represents edges by connecting the points with lines. These lines can also have arrows on them indicating the direction of the edge for directed networks, as show in Figure 1. Because there is often no natural placement of the nodes, they are placed in 2D at random, then adjusted with one of the many layout algorithms available (Gibson et al., 2013). Some commonly used algorithms, such as the Kamada-Kawai (KK) layout (Kamada and Kawai, 1989) and the Fruchterman-Reingold (FR) layout (Fruchterman and Reingold, 1991), are designed to mimic physical systems, drawing the graphs based on the "forces" connecting them. In Figure 1, we use the KK algorithm, and unless otherwise stated, all other node-link diagrams in this paper were drawn with the KK layout algorithm.

The second method for net-vis uses the adjacency matrix of the network. The adjaceny matrix of a network, $\mathbf{A}$ is defined as:

$$
A_{ij} = \begin{cases} 1 & \text{if an edge exists } i \to j, \quad i \neq j \\ 0 & \text{otherwise} \end{cases}
\tag{1}
$$

An adjacency matrix visualization for our toy example is also shown in Figure 1. This visualization shows the network as a grid, with each row and column representing a node. The grid space for edge $i \to j$ is filled in if $A_{ij} = 1$ and is empty if $A_{ij} = 0$.

Each net-vis method has its own advantages and disadvantages. For instance, *paths* between two nodes in a network are easier to determine with node-link diagrams than with adjacency matrix visualizations (Ghoniem et al., 2005). In node-link diagrams, node-level information can be incorporated into the visualization by coloring or changing the shape of the points, and edge-level information can be incorporated by coloring the lines, or changing their thickness or linetype. Visualizing a node-level variable into an adjacency matrix visualization is not as simple, because this type of visualization features the edges. Adjacency matrix visualization can, however, be useful when the network is very complex,

dense, or large (Ghoniem et al., 2005). Ultimately, there is no one "correct" way to visualize network information, and we will be using both the node-link and adjacency matrix visualization methods throughout this paper to explore our example data and SAOMs.

1.2 Defining SAOMs

Stochastic Actor-Oriented Models (SAOM) are unique because they model *dynamic* networks. We use SAOMs to study the change of a network in time while also examining the structural and node covariate efects. The two titular properties of SAOMs, stochasticity and actor-orientation, are key to understanding networks as they exist naturally. Most social networks, even holding constant the set of actors over time, are ever-changing as relationships form or disappear. Actors in social networks also have inherent properties that could affect how they change their role within the network, and existing ties may affect formation or dissolution of other ties.

1.2.1 Definitions, Terminology, and Notation

A *dynamic network* is a network, that consists of a fixed set of n nodes, that is changing over time, and is observed at M discrete time points, $t_1, \ldots, t_M$ with $t_1 < t_2 < \cdots < t_M$. We denote the network observation at timepoint t_m by $x(t_m)$ for $m = 1, \ldots M$. The SAOM assumes that this longitudinal network of discrete observations is embedded within a continuous time Markov chain, (CTMC), which we will denote by $X(T)$. The CTMC is almost entirely unobserved: we assume the first and last network observations are the starting and ending points of the CTMC, i.e. $x(t_1) \equiv X(0)$ and $x(t_M) \equiv X(\infty)$. Nearly all other steps in the chain are unobserved, with the exception of $x(t_2), \ldots, x(t_{M-1})$. Unlike the first and last observations of the network, these observations do not have direct correspondence with steps in the continuous time Markov chain. Thus, the observations $x(t_2), \ldots, x(t_{M-1})$ are considered to be "snapshots" of the network at some point between two steps in the CTMC.

The CTMC process $X(T)$ is a series of single tie changes that happen according to the SAOM's *rate function*, where one actor at a time is "selected" to make a change. Once selected, the actor tries to maximize its *objective function* based on the current state and possible future states of the network.

The Rate Function In general, a SAOM's *rate function*, $\rho(x, \mathbf{z}, \boldsymbol{\alpha})$, is a function of the network at its current state x, covariates of interest, $\mathbf{z}$, and some parameters, $\boldsymbol{\alpha}$. With this general formulation, it is possible that each node will have a different rate of change. Throughout this paper, we assume a simple rate function, $\rho(x, \mathbf{z}, \boldsymbol{\alpha}) \equiv \alpha_m$ that is a constant across all actors between time t_m and t_{m+1}. With this simple rate function, we have $M - 1$ rate parameters, one for each transition from $x(t_{m-1})$ to $x(t_m)$ for $m = 2, \ldots, M$. The rate parameter, α_m dictates how often an actor i "gets an opportunity" to change one of its ties, x_{ij}, for $j \in \{1, \ldots, n\}$ in the time period from t_m to t_{m+1} for $m = 1, \ldots, M - 1$. A SAOM also assumes that the actors i are conditionally independent given their ties, $x_{i1}, \ldots, x_{in}$ at the current network state. Let $\tau(i|x, m)$ be the wait time until actor i gets to the opportunity to change its current set of ties. For any time point, T, where $t_m \leq T < t_{m+1}$, the waiting time to the next change made by actor i follows an exponential distribution:

$$\tau(i|x, m)|x_{i1}(m), \ldots, x_{in}(m) \overset{\text{iid}}{\sim} Exp(\alpha_m) \tag{2}$$

From Equation 2, we can derive the waiting time to the next change opportunity by *any* actor in the network, $\tau(x)$. The value $\tau(x)$ is also exponentially distributed, and has expected value $(n\alpha_m)^{-1}$. The estimation of α_m in `RSiena` is simple: the method of moments (MoM) is used to estimate the rate with the statistic

$$C_m = \sum_i \sum_j |x_{ij}(t_{m+1}) - x_{ij}(t_m)| \tag{3}$$

which is the total number of changes from observation at time t_m to the observation at time t_{m+1}.

The Objective Function Because of the conditional independence assumptions given in Equation 2, we consider the objective function for each node separately. Suppose node i is selected to change at the next step in the CTMC. This node, called the *ego* node, has the potential to interact with all other nodes in the network, $j \neq i$. These nodes j, are referred to as *alter* nodes, and will not change any of their ties at the next step in the CTMC. The ego node i in the current network state x, will make a change that maximizes its *objective function*, written as:

$$f_i(\boldsymbol{\beta}, x, \mathbf{Z}) = \sum_{k=1}^{K} \beta_k s_{ik}(x, \mathbf{Z}), \tag{4}$$
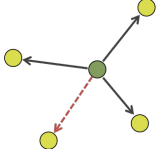
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Structural Effects

Name	Statistic	Figure
outdegree	$s_{i1}(x) = \sum_j x_{ij}$	
reciprocity	$s_{i2}(x) = \sum_j x_{ij}x_{ji}$	

Table 1: Examples of structural effects included in a SAOM. The dark nodes in the Figures are the ego nodes, and all others are alters. The dotted lines are ties the ego node is en(dis)couraged to make when the parameter corresponding to each effect is positive (negative).

for the network x, covariates $\mathbf{Z}$, and K the total number of parameters in the objective function. The parameters of the model, $\beta_1, \ldots, \beta_K$ correspond to network statistics, $s_{ik}(x, \mathbf{Z})$, for $k = 1, \ldots, K$. To maximize f_i, i will either destroy a tie where $x_{ij} = 1$, create a tie where $x_{ij} = 0$, or make no change if all changes will result in lower f_i.

The parameters of $f_i(\boldsymbol{\beta}, x, \mathbf{Z})$ are either structural or covariate parameters. The structural parameters correspond to statistics that are *only* functions of the current network state, x, while the covariate parameters are also functions of the covariates, $\mathbf{Z}$. According to Snijders (2001, p. 371), there should be at least two parameters included in the model: β_1 for the outdegree of nodes, and β_2 for the reciprocity of nodes. The former measures the propensity of nodes with a lot of outgoing ties to form more outgoing ties (the "rich get richer" effect), while the latter measures the tendency of outgoing ties to be returned within a network. The statistics corresponding to these two parameters, $s_{i1}(x)$ and $s_{i2}(x)$ are given in Table 1. In the `RSiena` software, there are over 80 possible $\boldsymbol{\beta}$ parameters to add to the model. The definition of the statistics for all possible parameters are provided in Ripley et al. (2017), and two selected covariate parameters and corresponding statistics are discussed in Section 2 and shown in Figure 4.

With the objective function, we can define the probability that the ego node i chooses to change its tie to alter node j, denoted by $p_{ij}(\boldsymbol{\beta}, x, \mathbf{Z})$. Let $x(i \rightsquigarrow j)$ be the network identical to network x with the exception of tie x_{ij}, which is equal to $1 - x_{ij}$; i.e. the presence or absence of node x_{ij} is flipped in the new network. The probability that the tie

x_{ij} changes is defined as:

$$p_{ij}(\boldsymbol{\beta}, x, \mathbf{Z}) = \frac{\exp\left\{f_i(\boldsymbol{\beta}, x(i \rightsquigarrow j), \mathbf{Z})\right\}}{\sum_{h \neq i} \exp\left\{f_i(\boldsymbol{\beta}, x(i \rightsquigarrow h), \mathbf{Z})\right\}} \tag{5}$$

In the CTMC, when actor i can make a change, it chooses which tie $x_{i1}, \ldots, x_{in}$ to change at random according to the probabilities $p_{ij}(\boldsymbol{\beta}, x, \mathbf{Z})$. We explore these probabilities further in Section 5. The probabilities p_{ij} combined with the rate parameters α_m fully characterize the underlying CTMC that models network change. For more details on CTMCs, see e.g. Yin and Zhang (2010).

1.2.2 Fitting Models to Data

To fit a SAOM to dynamic network data, we apply the `RSiena` software, which uses simulation methods to estimate parameter values using either method of moments (MoM) or maximum likelihood (ML) estimation (Ripley et al., 2016a). We chose to use MoM estimation, so we describe that process here, while more information on ML estimation can be found in Snijders (2016). The underlying SIENA software uses a Robbins-Monro algorithm (see Robbins and Monro (1951)) to estimate the solution of the moment equation

$$E_\theta S = s_{obs} \tag{6}$$

where $\theta = (\boldsymbol{\alpha}, \boldsymbol{\beta})$ is the vector of rate and objective function parameters, and s_{obs} is the observed vector of the model statistics over all network observations. The full SIENA MoM estimation algorithm operates in three phases, as described in Ripley et al. (2017) and Snijders (2016), and we briefly summarize these phases. The first phase gets initial estimates of the score functions for use in the second phase. The second phase is the Robbins-Monro algorithm, and results in parameter estimates through iterative updates and simulation from the CTMC at iterations of the parameter values. The third phase uses the parameters from phase two to estimate the score functions and covariance matrix of the parameter estimates and carries out convergence checks. In Section 5, we further explore these phases in the SIENA method-of-moments algorithm through visualization, bringing them out of their "black box" and into the light.

The rest of the paper is strucured as follows. In Section 2, we introduce the example data and models we use for model-vis. Then, in Section 3, we explore the first step in

model-vis by placing the models in the data space. Section 4 follows, in which we explore collections of models. Finally, in Section 5, the last principle of model-vis, we visualize the underlying algorithms in the SAOM fitting process. We conclude with a discussion in Section 6.
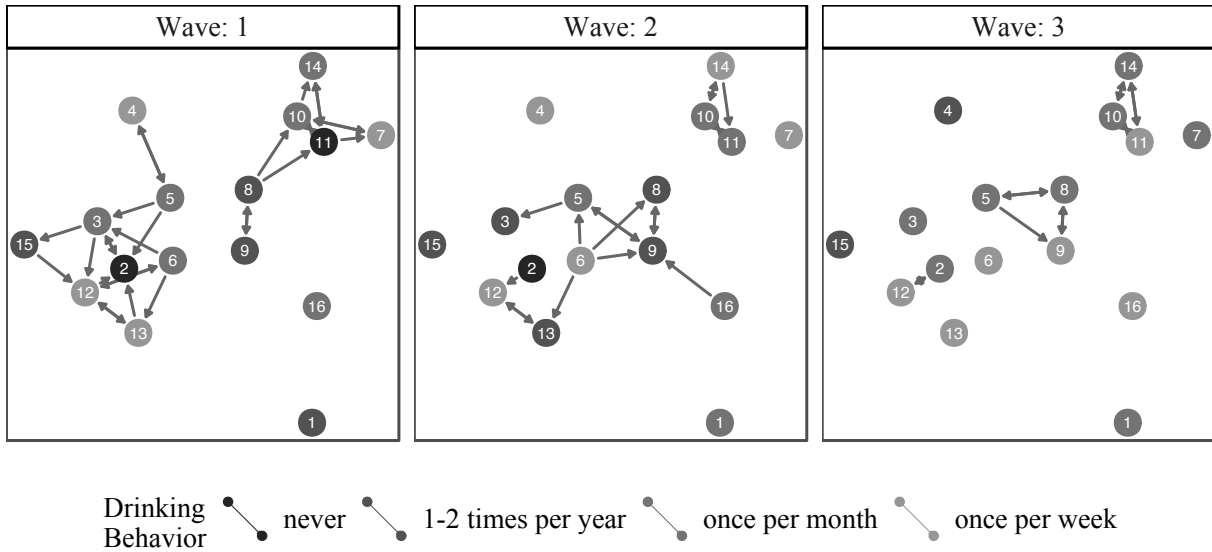
2   Example Data and Models

Figure 2: The small friendship network data we will be modelling throughout this paper. The nodes change color as their drinking behavior changes, and the network becomes less densely connected over time. These are the mechanisms we hope to incorporate and model with SAOMs.

Example Data: To guide our visual exploration of SAOMs, we use two example data sources. The first is a subset of the 50 actor dataset from the "Teenage Friends and Lifestyle Study" that is provided on the RSiena webpage. These data come from Michell and Amos (1997), and we chose to only work with a subset of the data to make node-link diagrams easier to see and to make any changes in the network more noticeable. The node-link visualization of this data is provided in Figure 2. The actor-level categorical covariate, drinking behavior, has four values: (1) does not drink, (2) drinks once or twice a year, (3) drinks once a month, and (4) drinks once a week. In Figure 2, the nodes are colored according to the drinking behavior of that student. We can see that, as time passes, the

students seem to drink more and become increasingly isolated into smaller groups. An analysis of this type of data with a SAOM should capture these dynamics in a way that allows the researcher to draw conclusions about the nature of the network and behavioral forces at play.

The second data example we use is a much more recent dataset on collaboration in the United States Senate during the 111th through 114th Congresses. These sessions of congress correspond to the years of Barack Obama's presidency, from 2009-2016. (Details of how this data can be downloaded are provided by Franois Briatte at `https://github.com/briatte/congress`). In this network, ties are directed from senator i to senator j when senator i cosponsors the bill that senator j authored. There are hundreds of ties between senators when they are connected in this way, so we simplify the network by computing a single value for each pair of senators called the *weighted propensity to cosponsor* (WPC). This value is defined in Gross et al. (2008) as the total number of times senator i cosponsors senator j's bill, weighted by the number of total cosponsors:

$$WPC_{ij} = \frac{\sum_{k=1}^{n_j} \frac{Y_{ij(k)}}{c_{j(k)}}}{\sum_{k=1}^{n_j} \frac{1}{c_{j(k)}}} \tag{7}$$

where n_j is the number of bills in a congressional session authored by senator j, $c_{j(k)}$ is the number of cosponsors on senator j's k^{th} bill, where $k \in \{1, \ldots, n_j\}$, and $Y_{ij(k)}$ is a binary variable that is 1 if senator i cosponsored senator j's k^{th} bill, and is 0 otherwise. This measure ranges in value from 0 to 1, where $WPC_{ij} = 1$ if senator i is a cosponsor on every one of senator j's bills and $WPC_{ij} = 0$ if senator i is never a cosponsor any of senator j's bills.

Because we require binary edges for SAOMs, we focus only on very strong collaborations, where WPC is high. For a senate collaboration network x, edges are defined as

$$x_{ij} = \begin{cases} 1 & \text{if } WPC_{ij} > 0.25 \\ 0 & \text{if } WPC_{ij} \leq 0.25. \end{cases} \tag{8}$$

The node-link diagram for the four senates during the Obama administration are shown in Figure 3. We can see that Senate 111 is much more densely connected than the other
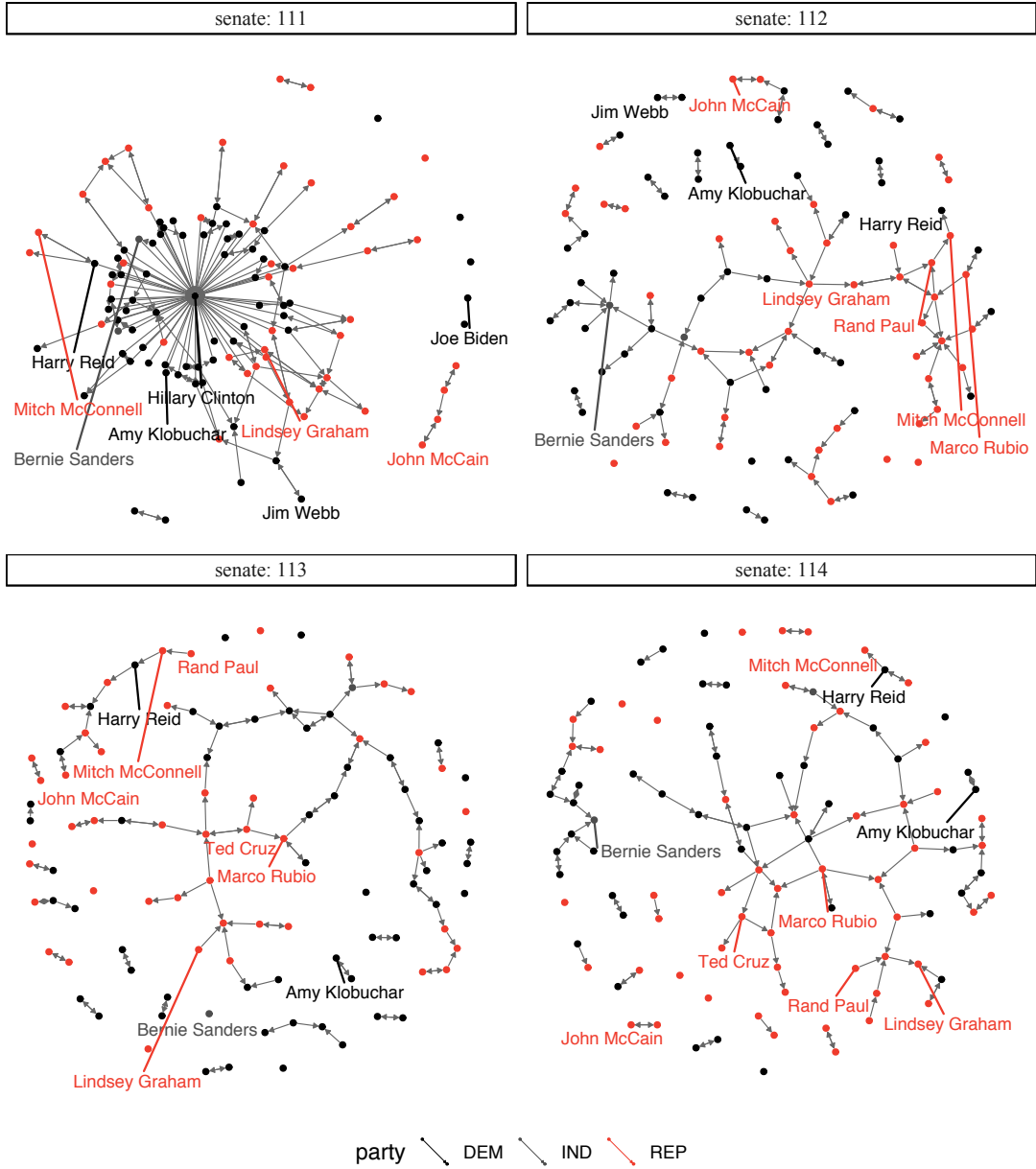
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Figure 3: The collaboration network in the four senates during the Obama years, 2009-2016. Edges are shown only if the WPC between two senators is greater than 0.25. We use the FR layout algorithm here.

three, which have one large, sparsely connected component with a few smaller connected groups throughout. Some prominent names are shown to demonstrate their place in the network. As with the friendship example, analyzing the senate data with a SAOM should capture the underlying dynamics in a way that gives insight into the impact the behavioral

$s_{i3}(x,z)=\Sigma_{j\neq h}x_{ij}x_{ih}x_{hj}\times I(z_i=z_h\neq z_j)$

$s_{i4}(x)=|\{j:x_{ij}=0, \Sigma_h x_{ih}x_{hj}\geq 2\}|$
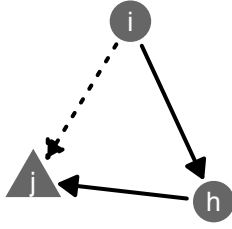
(a) Realization of a JTT, where i is the ego, j is the alter, and h is the intermediary. The covariate is represented by the shape of the nodes.
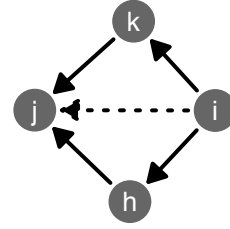
(b) Realization of a N22 between actors i and j. The dotted tie is encouraged if β_4 has a positive value.

Figure 4: The additional network effects included in our models fit to the friends data. On the left, a JTT between i and j, who have different covariate values, and on the right, a N22 between i and j.

factors have on the senate's collaboration structure. By using data sets from very different contexts, we hope to assess possible differences in model performance.

Models: To our example data, we fit three different SAOMs. Each SAOM uses a simple rate function, α_m, and an objective function with two or three parameters. The first model, M1, contains the absolute minimum number of parameters in the objective function $f_i(x)$:

$$M1: \quad f_i(x) = \beta_1 s_{i1}(x) + \beta_2 s_{i2}(x), \tag{9}$$

where s_{i1} is the density network statistic and s_{i2} is the reciprocity network statistic for actor i at the current network state x (see Table 1). The second and third models, M2 and M3, contain one additional parameter each in the objective function. We chose the additional parameters because they were significant (p-value < 0.05) according to a Wald-type test provided in the `RSiena` software (Ripley et al., 2016b). The M2 model contains an actor-level covariate parameter, and the M3 model contains an additional strutural effect in the objective function.

$$M2: \quad f_i(x, z) = \beta_1 s_{i1}(x) + \beta_2 s_{i2}(x) + \beta_3 s_{i3}(x, z) \tag{10}$$

$$M3: \quad f_i(x) = \beta_1 s_{i1}(x) + \beta_2 s_{i2}(x) + \beta_4 s_{i4}(x), \tag{11}$$

where $s_{i3}(x, z) = \sum_{j\neq h} x_{ij}x_{ih}x_{hj}\mathbb{I}(z_i = z_h \neq z_j)$, and $s_{i4}(x) = |\{j : x_{ij} = 0, \sum_h x_{ih}x_{hj} \geq 2\}|$. These statistics are known as the *number of jumping transitive triplets* (JTT) and

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the *number of doubly achieved distances two effect* (N22), respectively. The JTT effect emphasizes triads formed between actors with different covariate values, while the N22 effect emphasizes indirect ties between actors. The covariate for the friendship data is the drinking behavior, and the number of bills authored for the senate data. These additional effects are visualized in Figure 4a and Figure 4b, where the ties affected by the parameter value are represented by dotted lines. If the estimates of these parameters $\hat{\beta}_1, \ldots, \hat{\beta}_4$ are positive, the model encourages the tie represented by the dotted line to form, while the opposite is true if the parameter estimate is negative.

3 Model in the data space

Model visualization complements traditional model diagnostic tools such as R^2 values and residual plots by enriching our understanding and interpretation of statistical models. Each of the three different meanings of the word "model", the model *family*, the model *form*, and the *fitted* model (see Wickham et al., 2015, pg. 2), can benefit from model visualization (model-vis). We apply the three principles of model-vis: view the model in the data space, visualize collections of models, and explore the process of fitting the model, to the models and data introduced in Section 2. Since we have already decided on our model family (SAOMs), we shift our focus to the fitted model and the model form. Specifically, we use model visualization to learn more about how the *model form* affects the *fitted model*.

First, we put models in the data space to assess the model fit. We define the data space for SAOMs as the combined data structures of the network: the node, edge, and time information. We use the R package `geomnet` (Tyner and Hofmann, 2016) to visualize the three data spaces together. The package lays out the network using node-link diagrams, and the network's node or edge data are then mapped to different visual features. The color, size, and shape of the points can be used to represent variables in the node data, while the color, linewidth, and linetype of the lines between points can be used to represent the edge variables. To view temporal changes, we place the network at different timepoints side-by-side to see the evolution. By pulling all of this information together using `geomnet`, we can show the entire data space at once.

To demonstrate the functionality of `geomnet`, we visualize the connections in the 111th
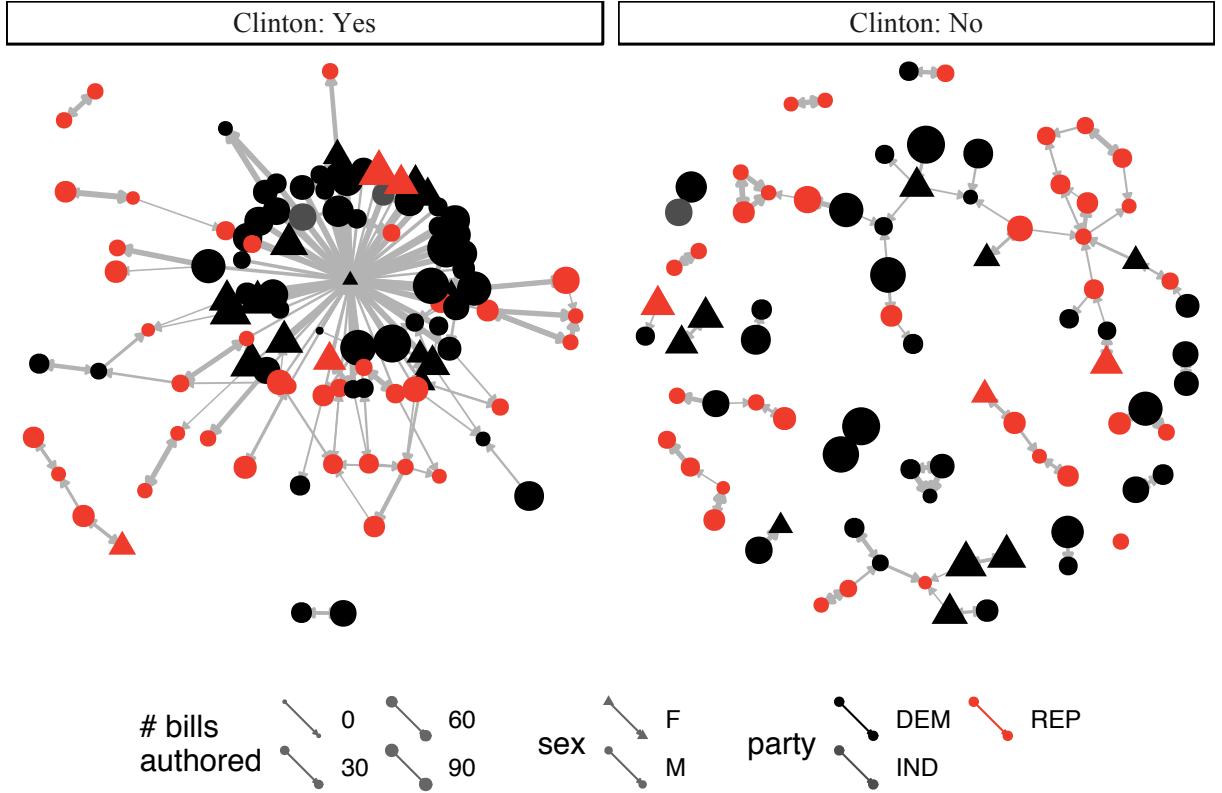
Figure 5: The 111th Senate at two times: while Clinton was in the senate in 2009 (on the left) and after she left (on the right). We map sex, party, and bills authored to the shape, color, and size of the nodes, respectively. We also map the WPC, to the edge linewidth.

United States Senate at two different timepoints: when Hillary Clinton was in the senate, and after she left to become Secretary of State. Clinton was only in the 111th senate from January 3-20, 2009, in the middle of her second term as the junior senator from New York. In that time, she authored two bills and was a cosponsor on 17. There are many senators who cosponsored both of her bills, giving their edges to her a WPC of 1. So with Clinton included in the node-link diagram in Figure 5, the senate looks much more collaborative than it does without her. We then map our potential covariates to visual features: number of bills authored maps to the size of the node, gender maps to the shape, and party to the color. In addition, we visualize the strength of the tie by mapping the WPC value between the two senators to the linewidth of the edge. By viewing node information, edge information, and time simultaneously, we have learned that Senator Clinton greatly affected the structure of collaboration within the senate.
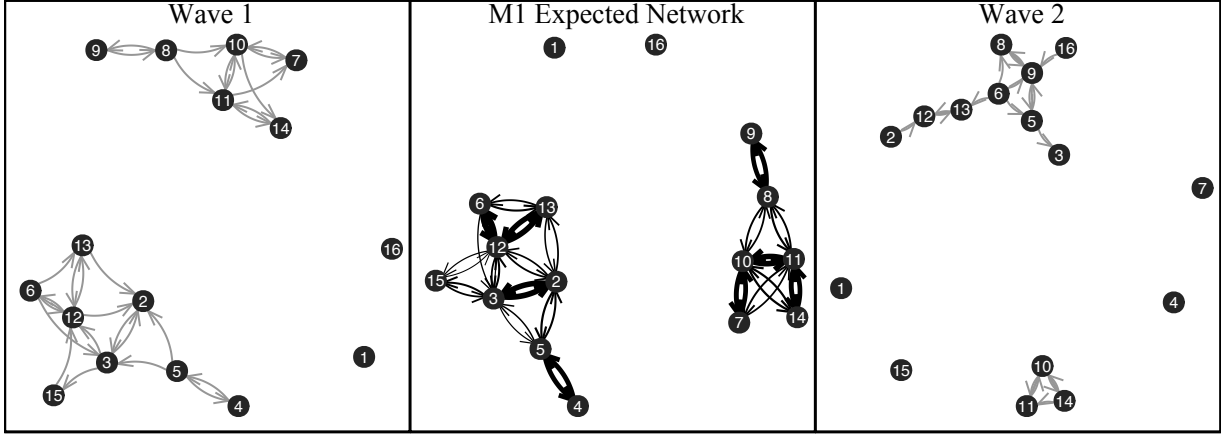
Figure 6: On the left, the first wave of observed data that is conditioned on in the model. On the right, the second wave of observed data. In the middle, a summary network from the first model fit to the data. This summary network represents 1,000 simulations of wave 2 using the values from the simple fitted model M1.

To view a SAOM in the data space, we simulate from the fitted model. No single network instance simulated from a SAOM will fully represent the model, so instead we look at an *expectation* from the network model. We frequently rely on expected values in statistics, but network models, especially those as complex as SAOMs, lack an expected network measure. We could talk about expected values of parameters, but the parameters can be hard to interpret and cannot teach us much about the overall structure of the network. How then, can we arrive at an "expected" network? We answer this question with visualization.

To construct an expected network, we:

1. simulate 1,000 wave 2 and wave 3 instances of our small friendship network from model M1 using parameters that have previously been estimated. Then, we

2. count the number of times each edge $i \rightarrow j$ appeared in one of the 1,000 network simulations. Then, we

3. construct one weighted summary network for each time point, which has edge weights equal to the proportion of the simulated networks in which the edge appeared. Finally, we

4. creat the *expected network* by including only the edges that appeared in more than 5% of the simulations.

The resulting expected network is in the middle panel of Figure 6. Edges with higher weights are darker, thicker lines. On either side of the average network in Figure 6, we show the data for comparison: wave 1 on the left, and wave 2 on the right. We can see that the structure of the average network is much more similar to wave 1 than to wave 2. In both wave 1 and the expected network, the edges form two distinct clusters of nodes: $\{2, 3, 4, 5, 6, 12, 13, 15\}$ and $\{7, 8, 9, 10, 11, 14\}$. The expected network, however, is supposed to represent the second wave of data, on the right in Figure 6. The expected network does not resemble wave 2, which has one small node cluster and on large node cluster, with four unconnected nodes. Because the expected network does not resemble wave 2, we take this as evidence that the simple model, M1, does not capture the change in network structure from the first to the second wave of data. Visualizing the expected network in this way places the model M1 in the data space, and helps us assess model fit.
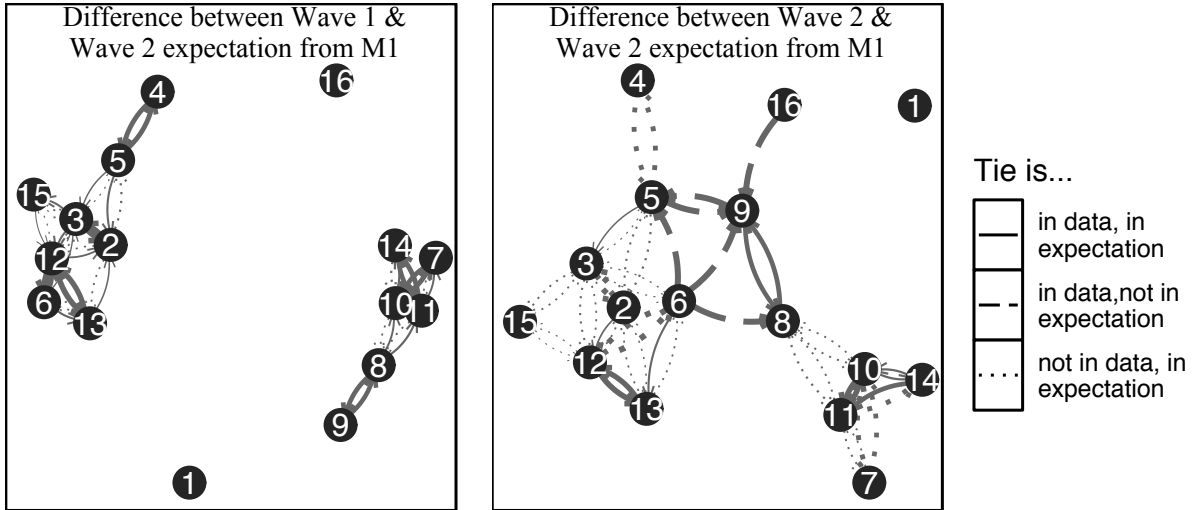

Figure 7: Network differences between the expected network from M1 and Wave 1 and Wave 2 of the data. Some edges appear in both the data and the expected Wave 2, while others only appear in the data or only in the exectation. Width of edges represent the proportion of appearances in the 1,000 simulations. The FR layout is used.

Another way to view a SAOM in the data space is with *difference networks* between the expected network and the data, as shown in Figure 7. We created these networks by

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computing the difference between the adjacency matrices for the expected network and wave 1, and for wave 2 and the expected network. The lack of model fit becomes even more clear in Figure 7, with the dotted edges representing ties that only show up in the expected network, and the broken edges representing ties in the data that the model misses completely. Again, the widths of the edges demonstrate the frequency of the ties in the simulations. On the left in Figure 7, we see the difference between the first wave of data and the expected network. We only see dotted and solid edges, meaning that the simulated networks consist primarily of edges in wave 1, plus some new edges that are not in the first wave of data. The additional edges are all reciprocating edges in the data, meaning that the model predicts more reciprocity in ties than there actually is. On the right in Figure 7, we see the difference between the second wave of data and the expected network. As the model is simulating the second wave of data, we would hope to see few differences between the expected network and wave 2. However, there are six broken edges, which are edges in the data that do not appear at all in the expected network, and there are a great many dotted edges that are in the expected network, but not in the data. Although there are some edges that appear in both the expected network and wave 2, the majority of edges in the expected network are not in wave 2, and there are several missing edges. We conclude that the model M1 is a poor fit to our example data, which we have seen very clearly by viewing the model in the data space.

4   Collections of models

Now that we have assessed model fit, we next want to learn about model behavior in order to choose better fitting models in the future. This is the second principle of model visualization: "collections [of models] are more informative" (Wickham et al., 2015). We examine the behavior of SAOMs by visualizing collections of models. We build collections of models in four ways. First, we explore the space of all possible models to determine the most significant model parameters. Second, we vary model settings to uncover relationships between parameters and their effects on the fitted model. Next, we fit the same model to the same data many times to assess the behavior of the underlying simulations. Finally, we fit the same model to different data to learn about fitted parameter values under different

conditions. We chose these four collections because they each explore something different about SAOM behavior: the choice of parameters in the objective function, the effects of underlying simulations, and the resulting fitted values under different circumstances.

Exploring the space of all possible models: The `RSiena` manual contains over eighty effects to include in the SAOM objective function. To select objective function parameters for fitting models to our example data, we searched through all possible effects available to find *significant* effects. The `RSiena` package includes the function `Wald.Rsiena` for Wald-type tests of parameter significance. We start by including the outdegree and reciprocity parameters in the model then add one effect to the objective function, fit the model to the example data, test the added effect for significance, and repeat for all possible model parameters. We performed this procedure, which we used to pick M2 and M3, for both the small friendship and the senate collaboration data. A visualization of the significant effects for the two example data sets are shown in Figure 13 in the Appendix. Using this one-at-a-time testing method results in many possible significant parameters of different type and magnitude, demonstrating the flexibility of these models.

Varying model settings: The second method for viewing collections of models is varying model settings. We have done this already by choosing three different models M1, M2, M3 to fit to our example data sets. To explore the behavior of these three models, we simulate from them. Using the parameter values given in Table 2 for the friendship data, we simulated 1,000 observations from each of the three models. From the simulations, we created an expected network for wave 2 from models M1, M2, and M3 using the same method described in Section 3. These expected networks are shown in Figure 14 in the Appendix. We see that all models are failing to capture the structure of the second wave, even though the individual parameters were all significant.

Fitting the same model to the same data: The simulations performed to fit a SAOM lead to inherent variability in the fitted model. To examine this variability, we fit models M1, M2, and M3 to the friendship network 1,000 times each. The distributions of the fitted model parameters are shown in Figure 8. Clearly, the inclusion of the JTT parameter, β_3, results in very different estimates the of the other four parameters in all models, α_1, α_2, β_1, and β_2. On the other hand, the inclusion of the indirect tie parameter, β_4, does not
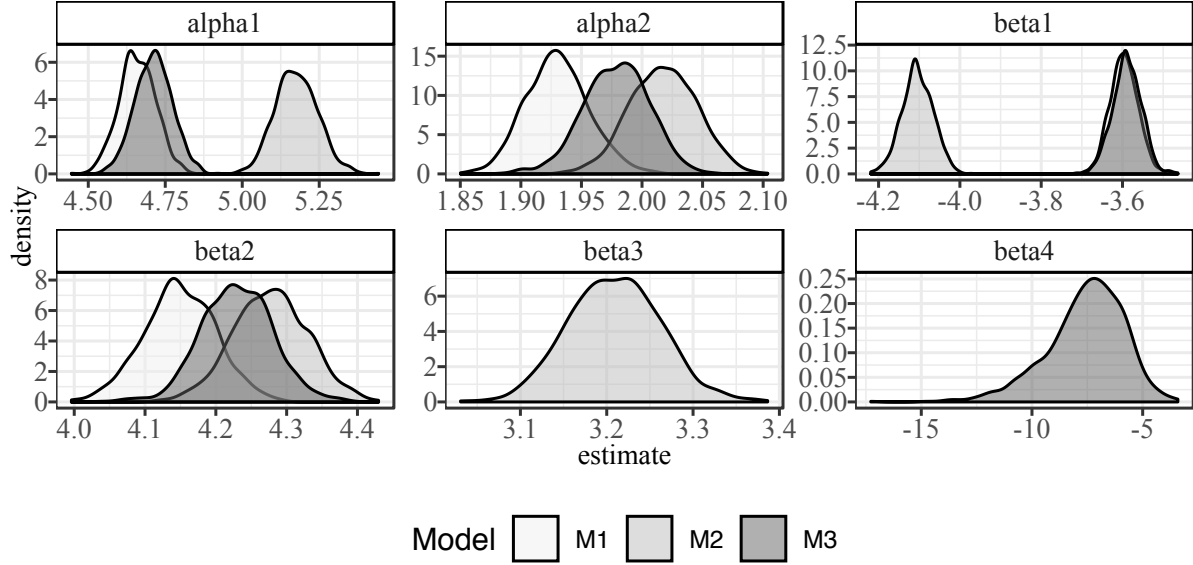
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Figure 8: Distribution of fitted parameter values for our three SAOMs. The inclusion of β_3 or β_4 clearly has an effect on the distribution of the rate parameters, α_1 and α_2, and on the other objective function parameters β_1, β_2.

lead to different estimates of other model parameters. When β_3 is included, its estimate is postitive, meaning that friendships between two girls with different drinking behaviors tend to form when there is an intermediary who is already friends with the two girls. The inclusion of this parameter leads to increases in the rate parameters' estimates. Thus, when modeling the transitive triplet behavior in this way, we conclude that girls change friends more frequently. It is not clear, however, that the addition of a parameter to the objective function *should* effect the estimates of the rate parameters. The strong relationship between rate parameter estimates and objective function parameters is further shown in Figure 16 in the Appendix. After visualizing the results of the same models fit many times to the same data, we were able to see potential model behavior problems right away.

Fitting the same model to different data: Finally, we view collections of models by fitting the same models to different data to understand how the model behaves in different contexts. As we did for the friendship data, we estimated the parameters for M1, M2, and M3, when fit to the senate data (see Figure 3) 100 times each. The means and standard deviations of the repeated parameter estimates for all six model-data combinations are given in Table 2, while corresponding density plots of the objective function parameters are given

	Friendship Data			Senate Data		
	M1	M2	M3	M1	M2	M3
α_1	4.660 (0.059)	5.176 (0.068)	4.712 (0.060)	3.344 (0.016)	3.349 (0.016)	3.340 (0.016)
α_2	1.930 (0.026)	2.017 (0.028)	1.979 (0.027)	2.480 (0.017)	2.487 (0.015)	2.483 (0.014)
α_3	–	–	–	2.221 (0.017)	2.227 (0.017)	2.224 (0.016)
β_1	-3.597 (0.033)	-4.104 (0.038)	-3.589 (0.035)	-4.979 (0.027)	-4.993 (0.025)	-4.987 (0.021)
β_2	4.149 (0.050)	4.277 (0.052)	4.230 (0.050)	4.954 (0.046)	4.974 (0.040)	4.970 (0.035)
β_3	–	3.209 (0.053)	–	–	-1.175 (0.789)	–
β_4	–	–	-7.582 (1.746)	–	–	-1.048 (0.486)

Table 2: The means (std. dev.) of parameter values estimated from repeated fittings of $M1, M2, M3$ to the two example data sets.

in Figure 15 in the Appendix. Looking at the estimates for both data sets, a few patterns emerge. First, we can see the same relationship between the outdegree parameter, β_1, and the reciprocity parameter, β_2 in both data sets and across all three models. The estimates of β_1 are all negative and range from about -5 and -3, while the estimates of β_2 are all positive and range from about four to five. This suggests that in both data sets, nodes prefer outgoing ties that are reciprocated to those that are not. When we consider the context, this seems obvious: the students want to have close mutual friendships, and senators want mutual support for their bills. We are also concerned, however, with the extremely high correlation between the estimates of β_1, β_2. In all six model-data combinations, the absolute correlation between $\hat{\beta}_1, \hat{\beta}_2$ is greater than 0.93. After seeing the high correlation between parameter estimates in very different data contexts, we question the guideline that both parameters need to be included in the objective function.

In Figure 8, we saw that the inclusion of β_3 for the friendship data has a noticeable effect on the other parameters in the model. In Figure 15, however, we see that this effect is not present in the senate data. Furthermore, the estimates of β_4 for the senate data are near zero, suggesting that this effect, which considers indirect ties, is not informative for the senate data. In contrast for the friendship data, the mean estimate of β_4 is about -7.5, which suggests that indirect ties are *strongly* discouraged from forming. Again, this is fairly intuitive given the context: teenage girls likely want to have direct friendships with

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each other. Senators, on the other hand, have to wheel and deal to pass their legislation, and indirect relationships may be beneficial at times. By examining the results of models fitted to different data, we better understand the interpretation of the objective function parameters, and we have learned of some potential parameter correlation problems affecting the fit of the models. All in all, we have used four different ways of viewing collections of models, which have given us insight into the behavior of SAOMs.

5 Explore algorithms, not just end result

The last model visualization principle, "explore the process of model fitting," is crucial for understanding SAOMs (Wickham et al., 2015). When fitting a SAOM in `RSiena`, several simulation steps are hidden from the user. One of the hidden steps in the SIENA MoM algorithm is the *microstep* process. At each microstep, an *ego* node is selected to make a change, and the chosen ego node randomly makes one change in its ties to maximize its objective function. Between two network observations $x(t_m)$ and $x(t_{m+1})$, there can be dozens, hundreds, or even thousands of microsteps, depending on the size of the network and the number of differences between two network observations. We want to simulate and view these in-between steps in order to better understand the behavior of the underlying continuous-time Markov chain. Hiding the microsteps is practical and efficient if the goal is to fit a model to data, obtain parameter estimates, and draw conclusions or make predictions. But in order to understand *how* the models are fit, we need to extract and explore the different steps of the process. We use these steps to visually explore the algorithms, so that we are visualizing the process, and not just the main result.

To visualize the underlying algorithm, we animate the microsteps that form the transition steps of the CTMC from wave 1 to wave 2 of the small friendship network example shown in Figure 2. The microstep animation, some frames of which are shown in Figure 9, represent one possible path from wave 1 to wave 2 according to the model M1. We show each change in the network as follows: we first increase the size and change the color of the ego node to focus attention to its ties. Then, the changing tie either fades in or fades out. If there are no changes at a particular microstep, the microstep does not appear. Some frames of the animations are shown in Figure 9, and the full movie, created with `tweenr`
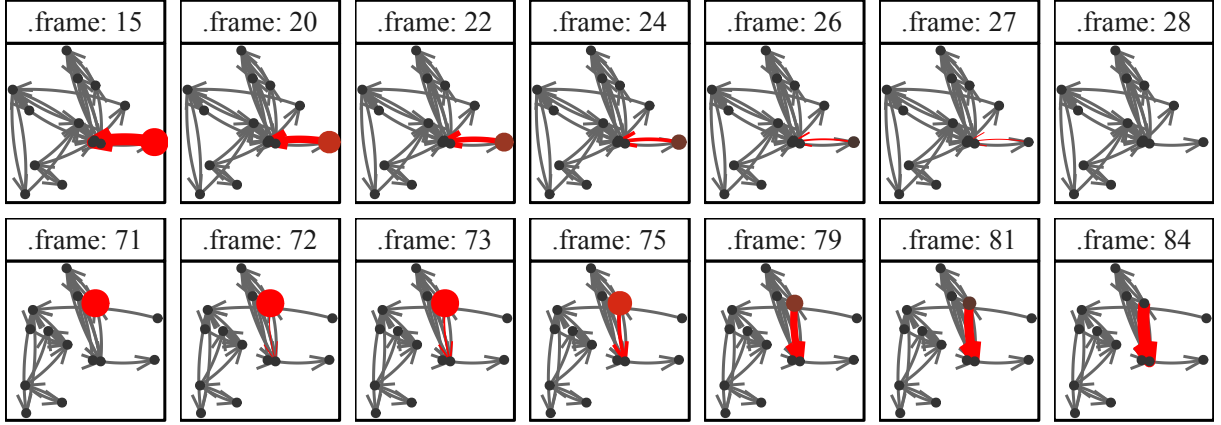
Figure 9: A selection of images in the microstep animation. The selected edges and nodes are emphasized by changing the size and the color, then when edges are removed, they fade out, shrinking in size, while the nodes change color and shrink to blend in with the other nodes. Frames 15-28 show a an edge disappearing, while frames 71-84 show an edge appearing.

and `gganimate` can be viewed at `https://vimeo.com/240089108` (Pedersen, 2016; Robinson, 2016). Movies similar to this animation were used to visualize the changes of dynamic networks in Moody et al. (2005). Frames 15-28 of Figure 9 show a deleted tie, while frames 71-84 show an added tie. For both changes, the ego node is emphasized with color and size. When a tie is removed, it is emphasized with the same color and size as the node. As the animation proceeds, the tie shrinks and disappears as the ego node shrinks and changes color back to black. If a tie is being added, the it appears red from nothing, grows large for emphasis, then changes color and size to match the rest of the edges. In this network animation, we see the modeled steps of the *unobserved* CTMC process between two observed networks. We see each part of the SAOM come into play: we first see the selection of nodes to change via the rate function, then we see the result of the actor maximizing its objective function by either deleting or adding a node. Finally, the layout of the nodes changes as edges are removed or added, which demonstrates how the overall network structure changes with each of the individual tie changes. Combining the tie changes in this animation makes the CTMC process the focus and demonstrates the underlying change mechanism of the dynamic network according to the chosen model.
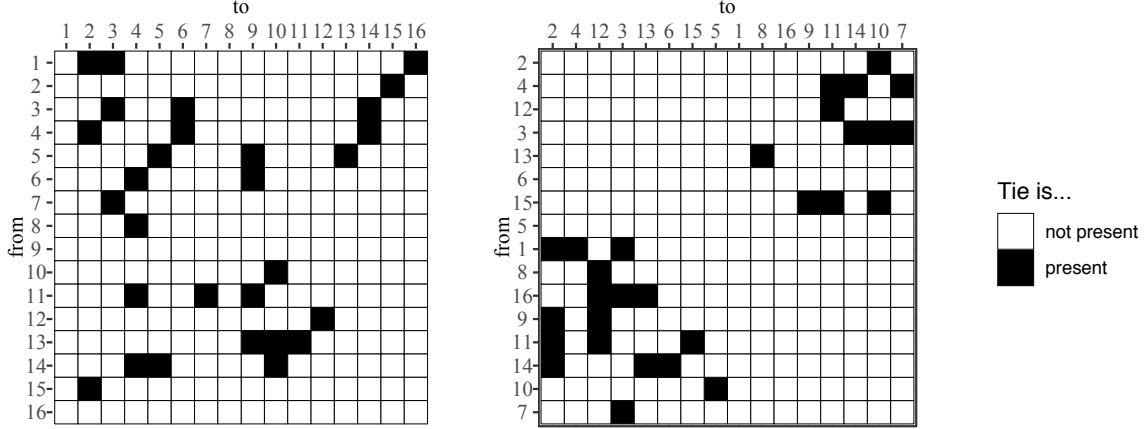
Figure 10: On the left, the starting friendship network represented in adjacency matrix form, ordered by node ID. On the right, the same adjacency matrix is presented after ordering the vertices by one repetition of the microstep simulation process from wave one to wave two.

We continue to use animation to view the changing structure of the network via adjacency matrix visualizations. In the first adjacency matrix visualization in Figure 10, we use the node ID to order the rows and columns. This arbitrary ordering does not easily convey the underlying structure of the network. We use *matrix seriation* to reorder the rows and columns of the adjacency matrix visualization so that the structure of the network is apparent (Liiv, 2010). To seriate the matrix, we first constructed a cumulative adjaceny matrix, $\mathbf{A}^{cum}$, for the series of microsteps simulating the network from $x(t_m)$ to $x(t_{m+1})$. A single entry in the cumulative adjacency matrix, $\mathbf{A}^{cum}_{ij}$, is the total number of times the edge $i \to j$ appears in the network from the initial observation, $x(t_m) \equiv X(0)$ to the final result of the last microstep, $X(R)$, where R is the total number of microsteps taken:

$$\mathbf{A}^{cum}_{ij} = \sum_{r=0}^{R} X_{ij}(r).$$ (12)

We then performed a principal component analysis (PCA) on $\mathbf{A}^{cum}$, and used the values of the first principal component to order the vertices on the x and y axes for the adjacency matrix animation. The resulting visualization for the first wave of data is shown in Figure 10. Using PCA on $\mathbf{A}^{cum}$ to order the rows and columns of the adjacency matrix visualization clearly shows the two distinct connected components in the first wave of the network, which are difficult to find in the visualization ordered by node ID. We continue

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to use the seriated matrix in another animation of the microstep process, which is avaiable at `https://vimeo.com/240092677`. A few frames of the video are shown in Figure 11. In the animation, a square appears or disappears as that edge appears or disappears in the microstep process. This visualization also shows the microsteps where the nodes do not make a change. From start to finish, we see network evolve according to the model: sometimes ties are removed right after they are created, and sometimes several ties are removed or created in a row. The adjacency matrix animation shows the many ways the algorithm explores the data space. By viewing this animation, we can gain a better understanding of the dynamics of this model.
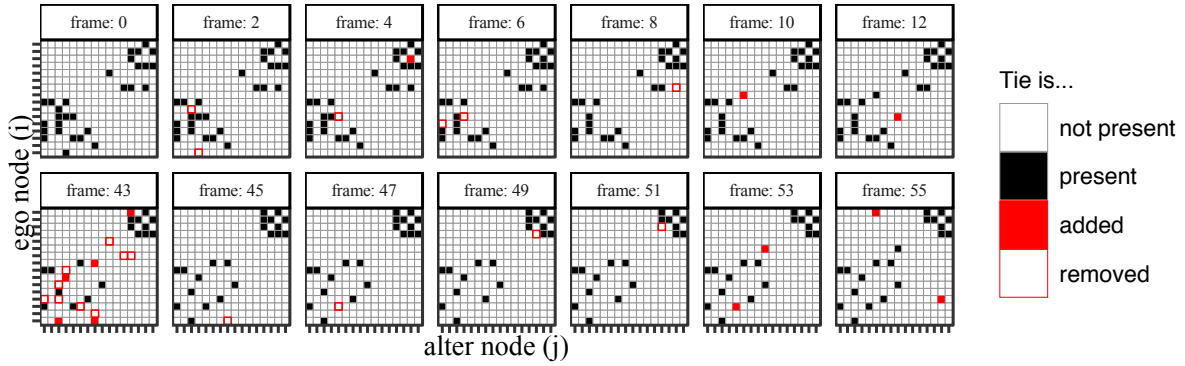

Figure 11: A selection of frames from the adjacency matrix visualization animation for one series of microsteps. The node lables are removed to declutter the figure. Starting at frame 0, there are two clearly connected components: one in the bottom left corner, and one in the top right corner. By the end, the component in the bottom left has spread out and become sparsely connected, while the top right component has shrunk, but remains closely connected.

We also attempt to better understand the microstep process by visualizing the theoretical and observed transition probabilites for the first microstep in the process. These probabilities are defined in Equation 5. We only do the first step of many because each microstep is dependent on the previous network state. There are 1,000 transitions to examine: the first microstep taken in each one of the simulations. We use another seriated adjacency matrix visualization to show theoretical and empirical transition probabilities of the first microstep in Figure 12 for each tie that was the first change in one of the simulations. The
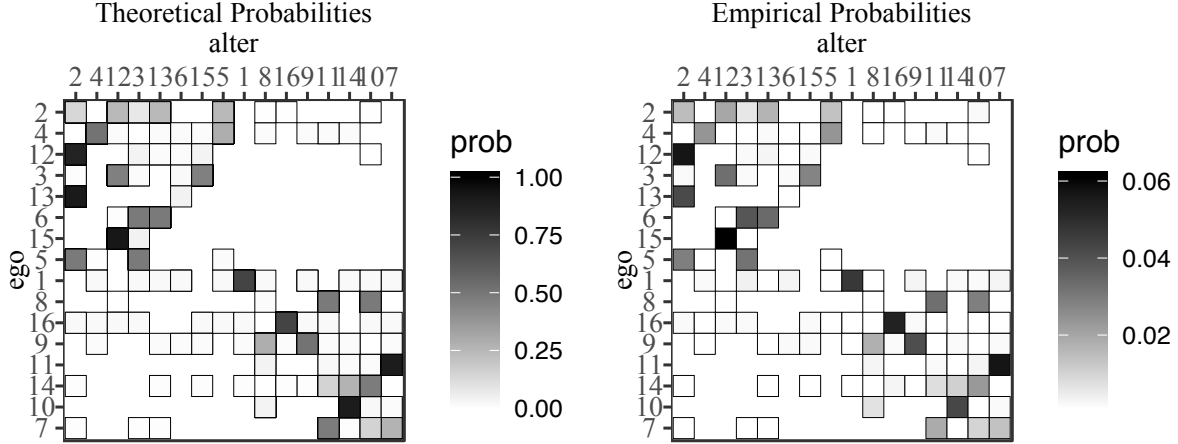
Figure 12: Adjacency matrix visualizations showing the theoretical (left) and empirical (right) transition probabilities for the first microstep observed in 1,000 simulations. The ego node is on the y-axis, and the alter node is on the x-axis. There were many ties with empirical probability zero.

figure is noticeably sparse: of the $16 \cdot 16 = 256$ possible choices for the CTMC to make, only 103, or about 43%, are made in the 1,000 simulated chains. This leaves a large area of data space unexplored by the first step in the SAOM model fitting process. We present additional evidence for lack of coverage in Figure 17 the Appendix. The Figures 12 and 17 show that the model M1 and the the corresponding fitting process do not explore the data space enough to adequately capture the network change mechanism, a finding we were only able to discern thanks to model visualization techniques.

6   Discussion

We have used novel visualization methods to explore the family of models known as stochastic actor-oriented models for dynamic social network data. By viewing the model in the data space, visualizing collections of models, and looking at the underlying algorithms, we have been able to gain knowledge and appreciation for these complicated and flexible models. When we looked at the model in the data space by viewing the expected network simulated from a model, we were able to easily see the lack of model fit. When visualizing collections of models, we quickly uncovered concerning relationships between parameters.

When we explored the algorithms, we gained a better understanding of the model and its stochastic behavior. We have only just begun to scratch the surface of these multi-layered models for social networks. The `RSiena` software is incredibly powerful, and can fit much more flexible stochastic actor-oriented models than we have examined here. If, for example, a researcher thinks the network structure or an actor covariate affects the rate of change of the network, there is a way to incorporate that belief into the rate function of the SAOM. In addition, more than one actor-level covariate can be included in the model, and many more than three parameters can be included in the objective function itself. As we have shown, the rate and objective function parameters are often highly correlated, so researchers can now use model-vis techniques to gain a better understanding of these correlations and hopefully find ways to account for their effects in the model. In addition, SAOMs can model behavior change of the actors in the network, a capability we did not explore here.

The data sets we have used are relatively small by network data standards, with only 16 and 100 nodes. We are aware that some of the visualizations we have presented may not scale up to larger networks.

Appendix: Additional model visualizations

Section 4

In Figure 13, we see for the friendship data and the senate data that most of the significant effects have absolute value less than ten. In addition, the p-values for the effects from the friendship data are more spread out than the p-values for the senate data, which are concentrated at about 0.02 or less. This suggests that larger data sets tend to result generally in smaller p-values, which is consistent with the construction of Wald-type tests.

To create the expected network visualization shown in Figure 14, we follow the same procedure as in Section 3, counting occurrences of each realized edge in the simulations. The resulting summary network has weighted edges representing the proportion of edge appearances in all 1,000 simulations of wave 2. As in Figure 6, edges only appear in the expected networks if they appear more than 5% of the time in the simulations. In Figure 14,
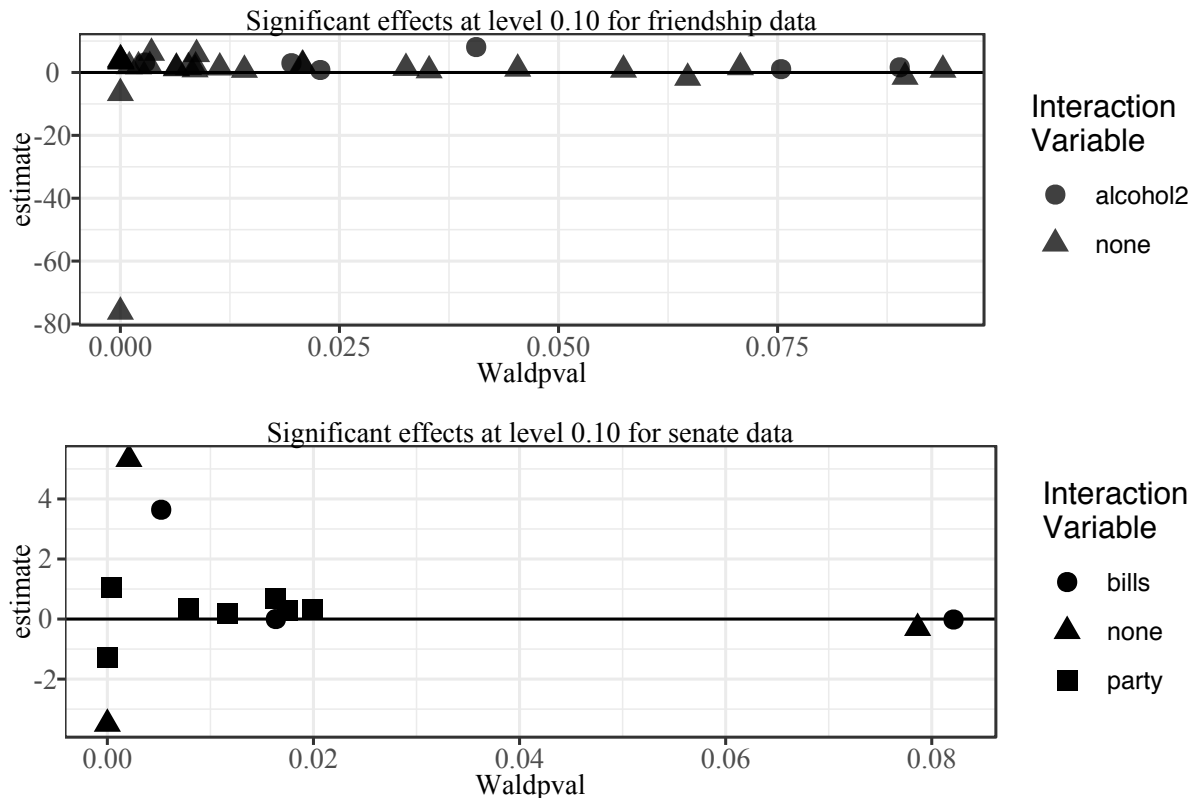
Figure 13: Significant effects for the two data sets, at a significance level of 0.10 or lower as calculated by the Wald-type test available in the SIENA software.

we show the expected network from the three models we fit and the first and second waves of data. Comparing the three averages to waves 1 and 2, we see that they have very similar structure to wave 1 but that model M2, which included the transitive triplet parameter, results in more strongly connected components. The lack of fit is clear: none of the three average networks show node 16 gaining ties as it does in wave two, nor do they show nodes 4 and 7 becoming isolated. In model M2, however, the ties to node 7 appear much weaker than in model M1 or model M3, and the nodes $\{10, 11, 14\}$ are also strongly connected as they are in wave 2 of data, suggesting that M2 may be the best model of the three.

The density plots in Figure 15 show the distribution of the parameter estimates for the objective function parameters in M1, M2, and M3 the two example data sets we used. The most notable difference is in the values of β_1, β_2. In the senate data, the inclusion of β_3 has no effect on the estimates of β_1, β_2, while the opposite is true for the friendship data.

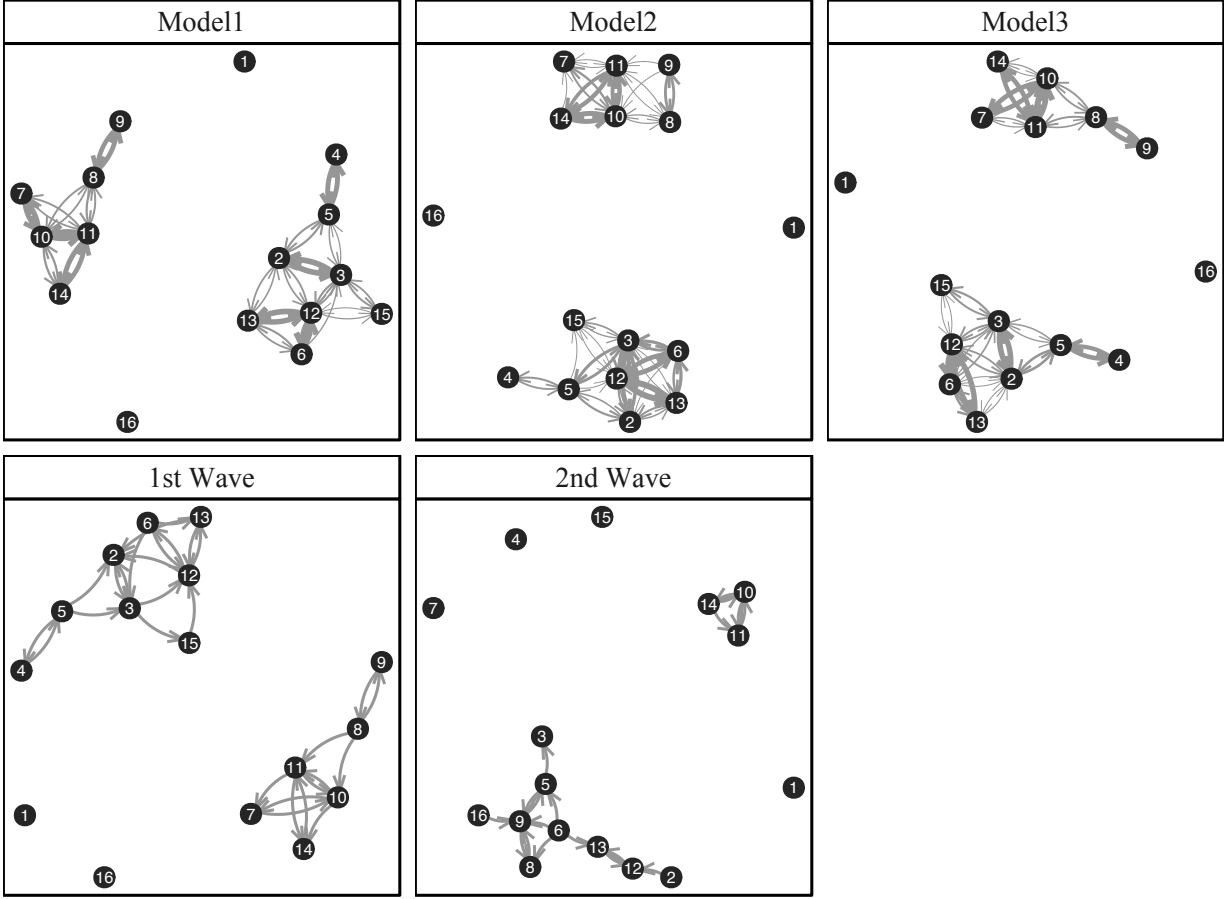In Figure 16, we examine correlations between each of pair of parameters within each

Figure 14: The node-link diagrams from the three expected networks that we calculated are in the top row, and the true wave 1 and wave 2 data are shown in the bottom row above. There is some difference between the three models, but overall, these three models struggle to capture the structure in the true second wave of data.

model and overall. The strongest correlation within each model is between β_1 and β_2, with absolute correlation between them greater than 0.90 in all three models. The β_1 parameter is also highly correlated with the β_3 parameter within model M2, but it is not as highly correlated with the β_4 parameter in model M3. It might therefore be advisable to consider only models that either allow β_1 or β_2 but not both. Looking at the high correlation with α, we might switch to a model without β_1.
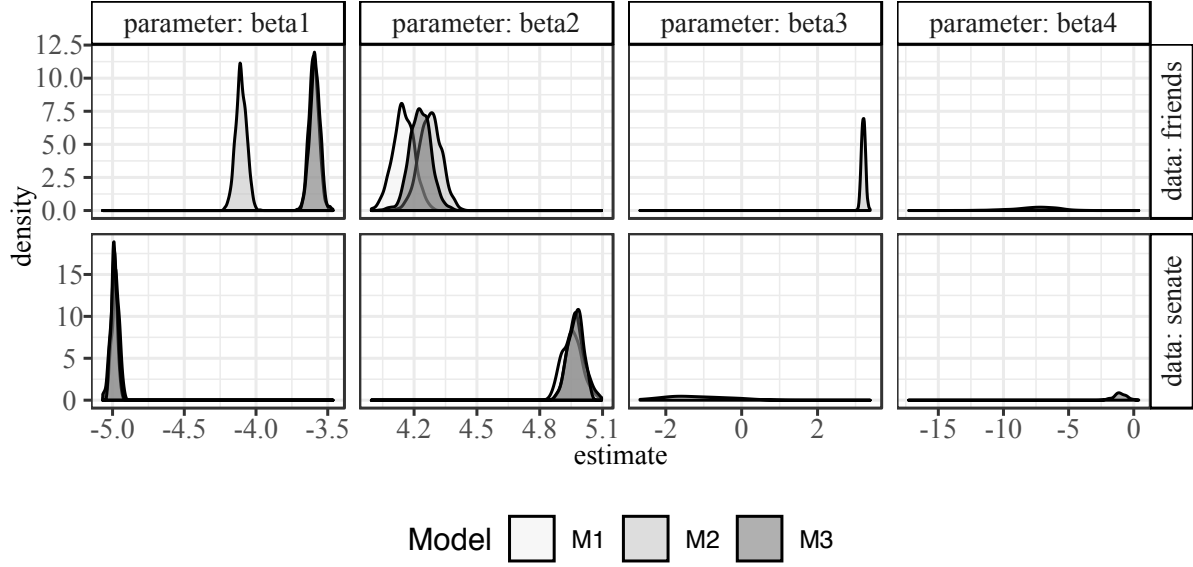
Figure 15: Density plots of objective function parameter estimates from repeatedly fitting models M1, M2, and M3 to the example data.

Section 5

Finally, we combine 1,000 simulations from model M1 into a visualization that displays the entire microstep process in Figure 17. To make this visualization, we first assign each possible edge in the network an ID number so that we can keep track of it throughout all microsteps and all simlations. Then, we count up the number of times each edge appears in the network throughout the microstep process for each of the 1,000 simulations. We also count the number of times an edge occurs at each step number. Since the number of microsteps in the process varies, the number of times an edge occurs decreases as the step number increases. Next, we compute a proportion, which we call the occurrence percentage, which is the number of times the edge was in the network in step 1, step 2, etc. divided by 1,000. Finally, we visualize all this information together in Figure 17. In this plot, we see that all possible edges appear at least once at some point in the microsteps of at least one simulated process. We also see, however, that the process struggles to focus in on the edges in the second wave of the data. Ideally, we would like to see more occurrences the edges in wave 2 that are not in wave 1. But, about half of the edges in wave two are in the bottom half of the figure, which means they do not appear as much as they would if the
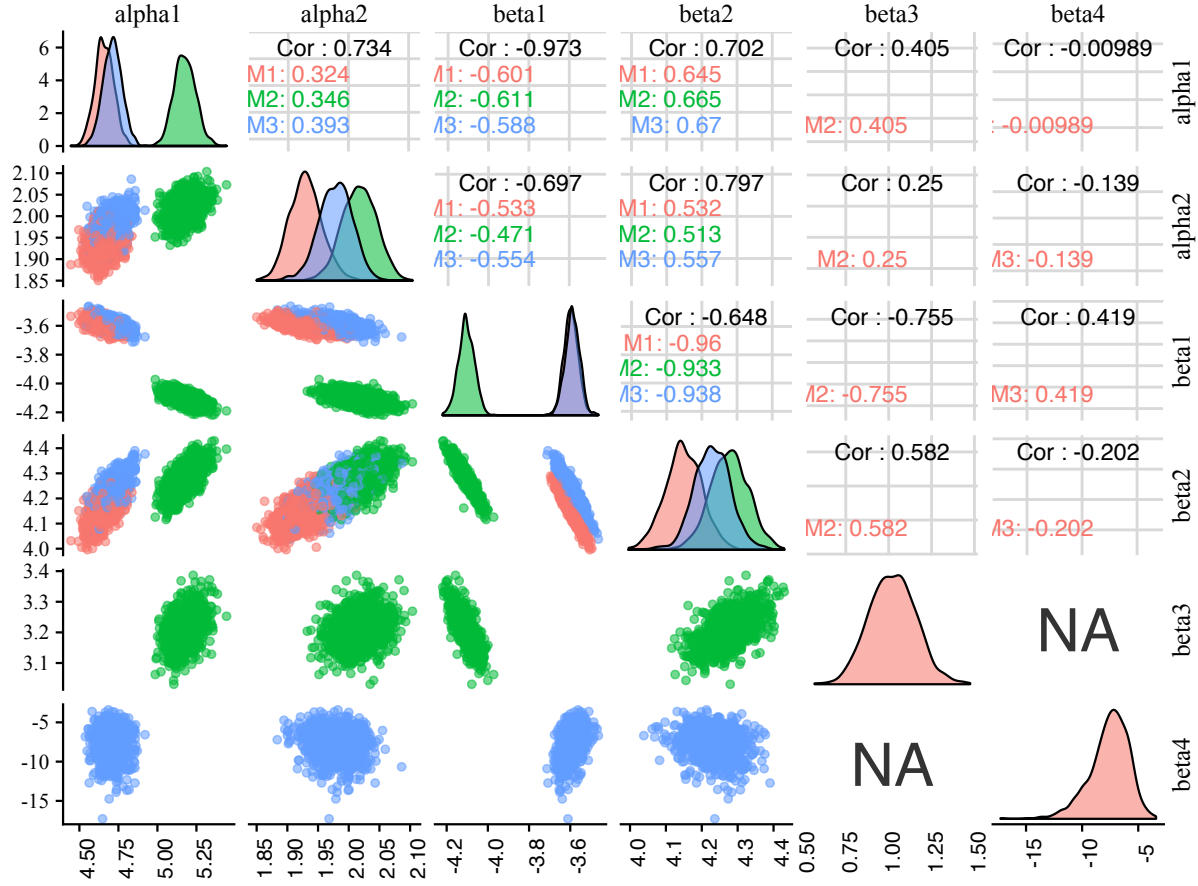
Figure 16: A matrix of plots demonstrating the strong correlations between parameter estimate in our SAOMs. The strongest correlation within each model is between β_1 and β_2.

model was actually capturing the mechanisms of tie change in the network. More of the darkest areas of the figure should belong to ties in wave 2, but those are often the lightest. This solidifies what we found in Figure 12: the model M1 and the SAOM fitting process do not explore the data space enough to adequately capture the network change mechanism.

Online supplemental material: Much of the code used to create these plots has been packaged an posted online at https://github.com/sctyner/netvizinf and https://github.com/sctyner/geomn (also on CRAN). Additional, non-packaged code can be found at https://github.com/sctyner/SAOM-removing-blindfold.
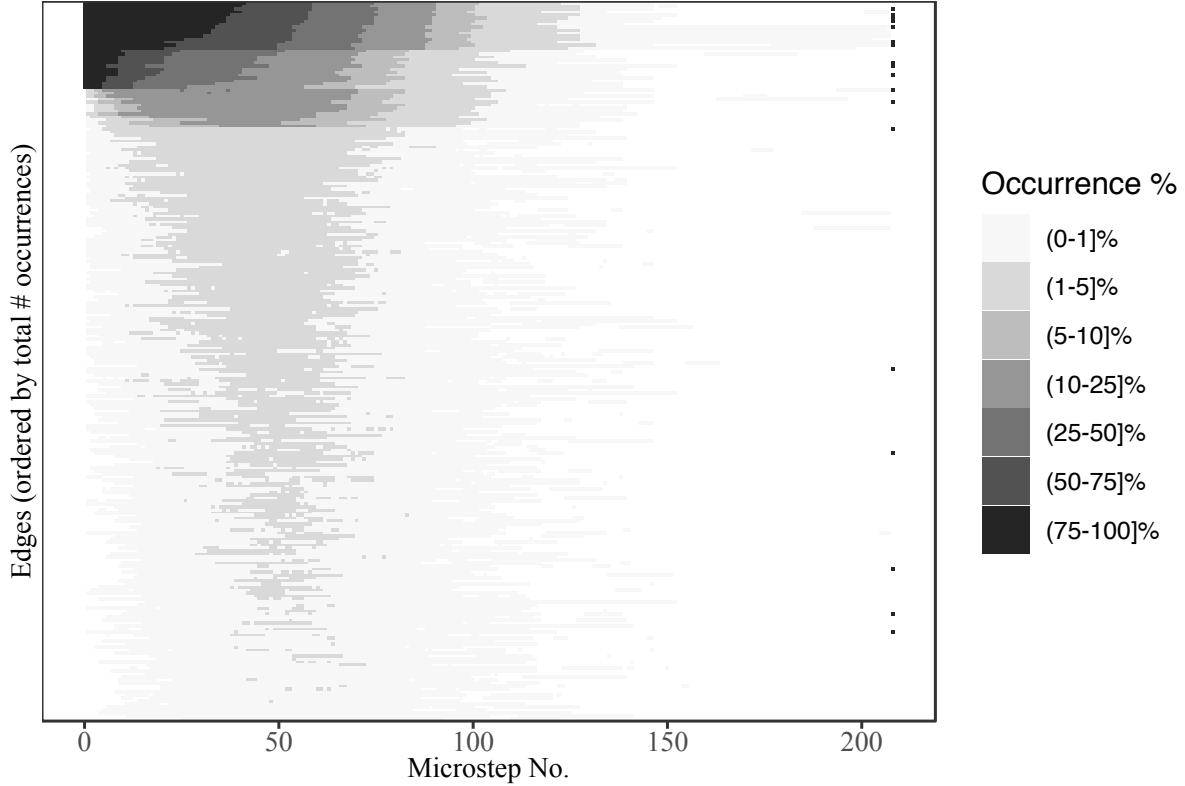
Figure 17: Visualizing all microsteps taken in 1,000 simulations from the model M1. The occurrence percent is split up into groups to correspond with its distribution: only about 10% of the possible edges appear more than 10% of the time in the 1,000 simulations, while about 60% appear less than 1% of the time. The first wave network is shown at microstep 0, and the second wave of the network is shown as the last microstep for comparison. We see that it is rare for a microstep process to last longer than 150 steps, and also that the edges that appear past the 150th step tend to be in either the first wave or the second wave.

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