Misspecification, Sparsity, and Superpopulation Inference for Sparse Social Networks*

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Abstract

Generative network models are popular tools for understanding network data. However, because they are models of complex phenomena, they are inevitably misspecified. These misspecified models can still be scientifically useful, but only if they are well-matched to the specific inference problem at hand. In this paper, we focus on the a class of problems we call network superpopulation inference problems, in which the goal is to understand dynamics that are shared across distinct social networks composed of different sets of actors. We present a theoretical framework for evaluating models in the context of network superpopulation inference problems, and specify an invariance criterion for determining whether a misspecified model and its corresponding estimation procedure are well-matched to a network superpopulation inference problem. We show that this criterion is not met if a model is *sparsity misspecified*, meaning that the model does not faithfully represent how the sparsity of network samples drawn from the same network population changes with sample size. Motivated by this result, we propose a modeling approach that satisfies our invariance criterion without explicitly explaining the sparse scaling of a social network process. The corresponding sparsity-robust estimator satisfies our stability criterion and has the added advantage of computational efficiency. We demonstrate both the theory and methodology on simulated and real data.

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Contents

1 Introduction

In recent years, social network data have become available in a wide range of contexts. These data record social interactions between actors, from co-authorship to personal relationships to email correspondence. Social network data have inspired investigations about network structure in a variety of fields including organizational behavior, marketing, political science, and sociology. In response, the statistical and machine learning communities have offered a variety of modeling approaches that give intuitive quantitative summaries of networks in terms of generative parameters (for an overview, see von Luxburg, 2010). Unfortunately, because of the sheer complexity of social processes, these models are inevitably misspecified. This fact raises a key question: in which cases is a misspecified model for social interaction data useful for scientific inquiry? In this paper, we develop some formalism to answer this question, and propose a new family of models that, according to our standard, can be applied to a wider range of scientific questions than many existing models for social interaction data.

We consider data with the following form. Let V be a set of actors of size $|V|$, and let $\binom{V}{2}$ represent the set of pairs of actors in V.[1] Let ij index each pair in $\binom{V}{2}$. Let Y_V be the set of outcomes associated with each pair of actors in $\binom{V}{2}$. In a dataset of this type, the measured outcomes for each pair, $Y_{ij} \in Y_V$ for $ij \in \binom{V}{2}$, summarize social activity between the actors in the pair; for example, Y_{ij} could represent the number of emails sent between individuals i and j. Each summary Y_{ij} may live in an arbitrary probability space. For example, we may consider binary interaction networks that represent the presence or absence of interactions, count-valued interaction networks that record the number of observed interactions, or point-process valued interaction networks that record the timestamps of repeated interactions. In this paper, we call Y_V a random graph, although it is technically a generalization of the standard notion of an undirected random graph. We call a particular instantiation of a random graph Y_V defined with respect to an actor-set V a network sample. In addition to outcomes, there is often a corresponding covariate collection X_V, containing covariate information X_{ij} for each pair of actors ij.

These data can be used to make a wide variety of scientific inferences. We consider two categories of scientific inference problems concerning network processes: single-sample inference problems and superpopulation inference problems. When making single-sample inferences, investigators wish to characterize social interactions among a fixed, finite set of actors V. For example, investigators may wish to predict future interactions among the actors in V, or infer the presence or absence of links that are missing from the current dataset Y_V. Statistically, single-sample inferences are claims about the distribution of a particular random graph Y_V under replications of Y_V; we call this the *replication distribution*. When making superpopulation inferences, investigators wish to characterize dynamics that are shared between social network samples defined on different actor sets, say V and V'. For example, investigators may wish to test whether two network samples Y_V

[1] The notation $\binom{V}{2}$ is meant to be analogous to the notation for the power set 2^V.

and $Y_{V'}$ were generated by the same stochastic process, or define a hierarchical model to borrow strength between network samples. Statistically, superpopulation inferences are claims about the over-arching stochastic process that characterizes the non-identical random graphs Y_V and $Y_{V'}$.

In this paper, we develop a theoretical framework for evaluating a network model's suitability for making superpopulation inferences. The major tool in our framework is an infinite stochastic process representation of a network superpopulation. In our framing, the random graph Y_V is defined as a finite-dimensional distribution of a superpopulation stochastic process indexed by the actor set V. Under this framing, we argue that an analysis based on a network model is suitable for making superpopulation inferences only if the procedure summarizes aspects of the data-generating process that do not depend on the index V. Importantly, this condition requires that certain aspects of the model, which are irrelevant for single sample problems, be correctly specified in order to answer superpopulation questions. We illustrate this dynamic in Section 1.1.

1.1 A running example: inventor collaboration network

Throughout the paper, we use the data analysis problem that motivated this work as a running example. We use an inventor-disambiguated version of the US patent record (Li et al., 2014) to build a collaboration network among inventors who filed for patents in the United States between 1975 and 2010. In the collaboration network, inventors are represented as vertices, and the pairwise outcomes Y_{ij} record pairwise patent co-authorships between each pair of inventors ij. The dataset contains the date of each patent application, and we often see repeated co-authorships between pairs of inventors. Thus, for each pair of inventors ij, the co-authorship record Y_{ij} is a sequence of co-authorship times, and has a point-process structure.

The inventor data also contain side information that can be used to construct covariates to model collaboration behavior, including each inventor's firm and zip code. In examples throughout this paper, we consider three simple binary covariates that are available for each inventor pair at each time: whether the inventors live in the same zip code (`Zip`), whether the inventors work for the same firm or "assignee" at the time of the patent application (`Asg`), and whether the inventors had a previous patent collaboration before the current patent application (`Prev`). Thus, in this example we define X_{ij} to be a 3-component time-dependent binary vector for each ij.

Suppose the investigator is interested in how inventors select their collaborators at certain points in their careers, and particularly in how these decisions vary in different regions of the country. A natural model here is a point-process regression model, in the style of (Perry and Wolfe, 2013), where we specify a model for the waiting time between collaboration events for each inventor-pair ij. In particular, we specify the log-hazard of a collaboration event between a pair of inventors ij as a linear combination of the covariates `Zip`, `Asg`, and `Prev` described above. We describe this specification in full detail in Section 7.1. We apply this model to regional collaboration networks

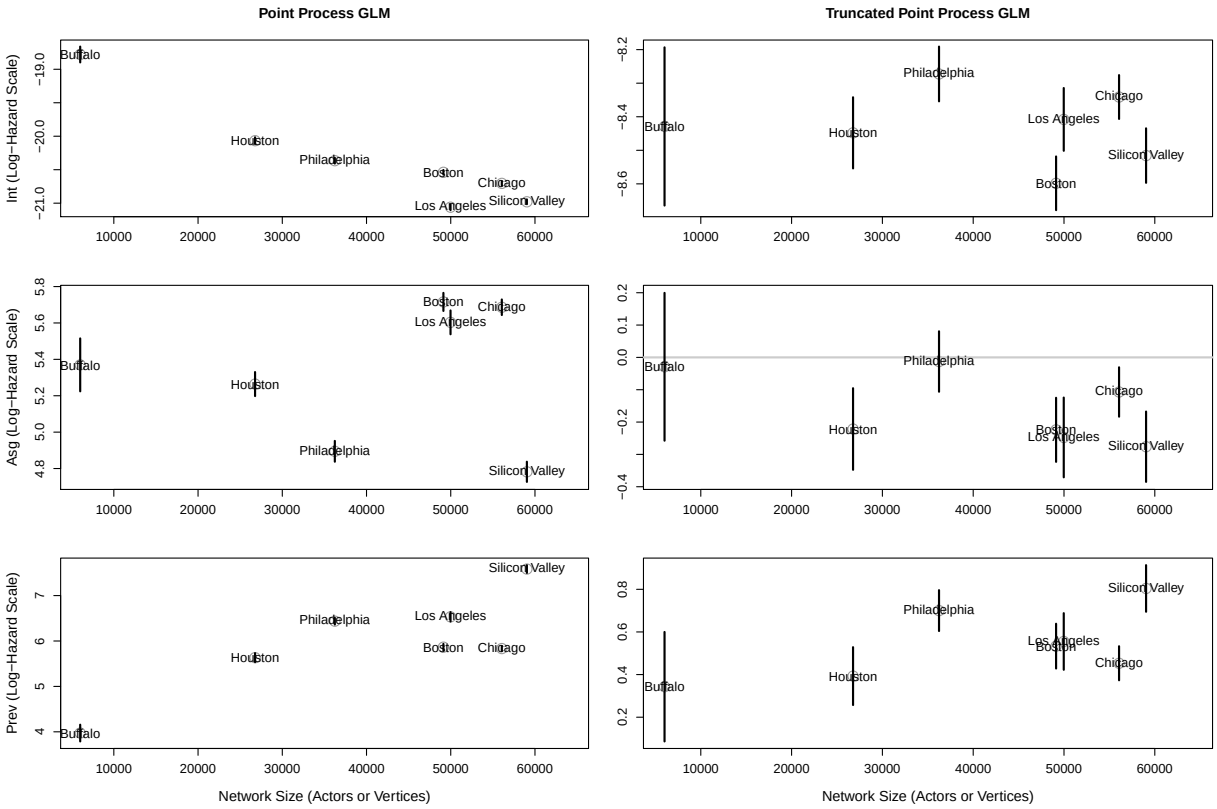

Figure 1: Estimated parameter values and asymptotic intervals from a simple point process regression model explaining patent collaboration events occurring in different regional inventor networks in the United States. (Left) parameter estimates from this standard conditionally independent dyad (see Section 4.3) model show strong dependence on sample size, extremely large effect estimates, and very small error estimates. (Right) parameter estimates from our truncated methodology (see Section 6.1) show stability across regions with more realistic effect and error estimates.

constructed from a 6-year window of interaction data beginning in 1983, defining V for each model fit to be the set of inventors residing in a particular Census Bureau Statistical Area (CBSA) during the observation window. The maximum-likelihood estimates and asymptotic confidence intervals for the coefficients of `Zip`, `Asg`, and `Prev` for several CBSAs are shown on the left of Figure 1, all on the log-hazard scale.

The effect estimates are highly variable between regions. Clearly, the model fit summarizes properties of each region's social network that are completely distinct. However, it is also clear that these properties are strongly related to the number of actors in each sample. Thus, despite specifying a model in terms of local information that a pair of individuals might use to make a decision, the parameter estimates appear to capture some global structure (namely, the total number of actors) that is not directly relevant.

If the investigator were interested in each region in isolation, these extreme parameter estimates

would not be surprising or troubling. For example, when collaboration events are relatively rare compared to the total number of inventor-pairs, we would expect collaboration events between inventors who have already generated a patent together to be orders of magnitude more common than events occurring between any arbitrary pair of inventors. However, if the investigator were interested in comparing common pairwise decision processes in social networks of different size, these parameter estimates would be difficult to interpret. Some variation should be expected between regions, but it would be difficult to separate the apparent sample size effect from true differences in the decision processes of interest. This difficulty—and methods to avoid it—are the main focus of this paper.

The problem here is that, despite specifying a model for collaboration decisions that appears to rely on only pairwise information, this model is sparsity-misspecified (a notion we defined below), and the corresponding estimation procedure targets different parameters when applied to network samples of different size, even if these samples were drawn from the same network population. We make this idea precise in Section 3. The plots on the right display parameter estimates and confidence intervals for the effect of each covariate on a slightly different aspect of the collaboration decision, using the model and methodology laid out in Section 6. This model is not sparsity misspecified—in fact, it makes no attempt to describe the part of the data-generating process that induces sparsity—and the estimation procedure appears to target a parameter that is comparable across these network samples of differing size. We will return to a simulated version of this example in Section 7.2.

1.2 Contributions

This paper has two main components: a theoretical component characterizing how a particular type of misspecification, which we call sparsity misspecification, makes many network models inappropriate for network superpopulation inference; and a methodological component in which we propose a class of models and inferential procedures that are robust to this type of misspecification.

The theoretical contributions in the first half of the paper lay the groundwork for the main negative result presented in Section 5. This result requires three building blocks. First, in Section 2 we introduce formalism that defines superpopulation inference in the context of social network analysis. Second, in Section 3, we state an invariance criterion for valid superpopulation inference. Third, in Section 4 we describe network sparsity in a superpopulation context. This section includes a result showing that many popular network models are "sparsity-misspecified", or fail to correctly model sparsity in a superpopulation sense. Finally, we use these building blocks in Section 5 to establish the main negative result: under mild conditions, sparsity-misspecified models violate our invariance criterion because the estimators they imply target different parameters depending on the size of the observed network sample.

In the second half of the paper, we propose methods based on a novel modeling framework that defines and estimates invariant parameters of network generating processes that are conserved across samples, even when the generating process is sparse. In Section 6, we present a "Conditionally Independent Relationship" (CIR) class of graph processes that have a sparsity-independent component, and in Section 6.1 we present sparsity-robust methodology for estimating properties of this sparsity-independent subprocess. Finally, we present simulated and real data examples in Section 7, and conclude with a discussion in Section 8.

1.3 Related work

Recently, there has been a growing interest in characterizing and addressing difficulties resulting from the limitations of popular network modeling frameworks. Sparsity misspecification in particular has received attention, as authors have pointed out that modeling principles built around vertex exchangeability in network generating processes are incompatible with the empirically observed sparsity property of network data (Bickel and Chen, 2009; Orbanz and Roy, 2013; Crane and Dempsey, 2015). To date, authors have taken one of two approaches to resolve this conflict: either focus on single-sample problems (Choi et al., 2012; Bickel et al., 2013), or seek to develop novel stochastic processes and corresponding model families that can simultaneously exhibit some form of exchangeability and the sparsity property (Caron and Fox, 2014; Veitch and Roy, 2015; Crane and Dempsey, 2015; Cai et al., 2016).

Our approach is conceptually distinct from the single-sample literature because we are concerned with fundamentally different inference problems. We highlight these differences throughout the paper. In particular, we discuss differences between single-sample and superpopulation criteria for valid inference in Section 3.2, and we discuss difference between single-sample and superpopulation notions of sparsity in Section 4. These differences motivate the novel asymptotic arguments we make in the main result, Theorem 2.

Our approach is more similar to work in the sparse exchangeable modeling literature. We seek to address the same incompatibility between population network models and sparsity, but we take different approaches. The sparse exchangeable modeling literature is primarily concerned with specifying probabilistic models that can represent some version of the sparsity property. On the other hand, we take a more practical view and focus on whether a model-derived estimation procedure has an invariant target of estimation across distinct samples drawn from a sparse superpopulation. Our approach is useful in determining exactly which aspects of a generating process needs to be well-represented by a model, and to what degree of accuracy, in order to answer superpopulation questions effectively. In particular, our main result shows that specifying a model that generates a sparse population process is not sufficient to satisfy our stability criterion; the sparsity rate of the model must also match the true sparsity rate of the generating process.

In this vein, the criteria we use are more similar to notions of stability (Yu, 2013). In general, an estimation procedure is stable if nominally similar samples yield similar estimates, where the definition of "nominally similar" depends on the application and the investigator's goals. In network analysis, (Schweinberger, 2011) investigated this idea in identifying instability in ERGM models that have particular degeneracies in their supports on the space of sufficient statistics, and a number of papers followed in a similar vein in the ERGM literature, e.g., (Krivitsky and Handcock, 2011). These studies have focused on a definition of stability that is necessary for answering single-sample questions: specifically, the requirement that small perturbations in the data only cause small changes in the resulting estimates. On the other hand, we are interested in a broader notion of stability, where we require that an estimation procedure return similar results for data generated by the same stochastic process, regardless of the index of the finite dimensional distribution that generated the data. We approach this stability question using formalism developed in D'Amour and Airoldi (2016).

In addition to the sparse exchangeable modeling literature, there have been other proposals to adjust network models to achieve inferential stability across sample size. (Krivitsky and Handcock, 2011) proposed an offset term that stabilizes change statistics in ERGMs, but did not attempt to justify this as a likelihood-based approach. (Hoff et al., 2013) proposed generative models for the true observation in fixed rank nomination networks that the effect of removing sample-size dependent artifacts that appeared in previous naïve modeling approaches.

The methodology we propose lies between these approaches. Instead of constructing a model family that explains the sparse structure of social network data, as the sparse exchangeable modeling literature does, we specify a class of models for which a subset of the parameters describe properties of the network superpopulation that are unrelated to the sparsity of the superpopulation process, then describe an estimation procedure that does not require specification of the sparsity-explaining portion of the model at all. However, as opposed to procedures that incorporate explicit size adjustments, our procedure corresponds to the maximum likelihood estimator of a zero-truncated data model that only treats non-zero pairwise outcomes as having been observed. Our procedure can be characterized as a partial likelihood method (Cox, 1975; Wong, 1986), or a marginal likelihood method, where we have chosen to ignore the actual sample size of the data and to marginalize over it instead (Gelman, 2004). This approach was inspired by (Perry and Wolfe, 2013), in which the authors introduced the notion of a "risk set" to the networks literature. This approach partitions dyads into dyads "at risk" of producing observable interactions, and dyads that will deterministically produce zeros.

Procedures similar to zero-truncation, including dyad subsampling and zero-inflation, have also been proposed in the literature before, but, rather than invariance to sparsity in superpopulation inference, these proposals have focused on single-sample fit (Braun and Bonfrer, 2010), novel network representations (Soufiani and Airoldi, 2012), or approximate likelihood inference for com-

putational efficiency (Gopalan and Blei, 2013). Notably, our proposed procedure is able to achieve similar computational efficiency using an exact likelihood function.

Over all, our theoretical approach was inspired by Shalizi and Rinaldo (2013) and their representation of network samples as being generated by finite-dimensional distributions of stochastic processes. As such, our approach is similar to work such as Crane and Dempsey (2015), which was also heavily influenced by Shalizi and Rinaldo (2013).

Social scientific questions about the organizational behavior of inventors holding patents in the United States in, e.g., (Marx et al., 2009), were the original motivation of this work.

2 Framework and Preliminaries

2.1 Network superpopulation problems

Here, we formally define network superpopulation problems. In network superpopulation problems, the object of inference is a stochastic process that encodes properties that are shared between non-identical random graphs. We define this object as an infinite random graph process. Specifically, let $\mathbb{V}$ be a countably infinite set of actors, and let $V \subset \mathbb{V}$ be a finite subset of actors. A random graph process corresponding to this actor population is defined as follows.

Definition 1 (Random Graph Process)**.** A random graph process $Y_{\mathbb{V}}$ is a stochastic process indexed by a countably infinite vertex set $\mathbb{V}$ whose finite-dimensional distribution for any finite subset $V \subset \mathbb{V}$ defines a random graph Y_V with vertex set V.

For a given random graph process $Y_{\mathbb{V}}$, we will write the distribution of the entire process as $\mathbb{P}_{\mathbb{V}}$, and the distribution of any finite-dimensional projection Y_V as $\mathbb{P}_V$. To emphasize that $\mathbb{P}_V$ only describes the variation in outcomes Y_V between replicated observations on the same actor-set V, we call $\mathbb{P}_V$ the *replication distribution* of Y_V. This is in contrast to the superpopulation distribution, which also summarizes variation between outcomes, say, Y_V and $Y_{V'}$ corresponding to non-identical actor-sets $V \neq V'$; this variation includes both fundamental randomness from replications and systematic variation due to the differences in the composition of V and V'.

With this formalism, we define the statistical problem. Let the network superpopulation $Y_{\mathbb{V}}$ be a random graph process and let Y_V be a network sample corresponding to a particular actor-set $V \subset \mathbb{V}$. Y_V is a finite-dimensional projection of the network superpopulation $Y_{\mathbb{V}}$. Let $\mathbb{P}_{0,\mathbb{V}}$ be the distribution of the superpopulation process, and let $\mathbb{P}_{0,V}$ be the finite-dimensional replication distribution for the random graph Y_V; we use the subscript 0 to indicate a "true" distribution. The goal is to make inferences about some parameter of the superpopulation distribution, which we write as $\Phi(\mathbb{P}_{0,\mathbb{V}})$, where $\Phi(\cdot)$ maps the distribution $\mathbb{P}_{0,\mathbb{V}}$ to a finite- or infinite-dimensional vector

of real numbers.

2.2 Model-based estimation and inference

In this paper, we will examine the behavior of estimation and inference procedures that are derived from generative network models. We establish formalism for describing these procedures in this section.

Let $\mathcal{P}_{\Theta,\mathbb{V}} \equiv \{\mathbb{P}_{\theta,\mathbb{V}}\}_{\theta\in\Theta}$ be a model family, or a set of probability distributions on $Y_{\mathbb{V}}$ indexed by the finite- or infinite-dimensional parameter $\theta \in \Theta$. For each θ, $\mathbb{P}_{\theta,\mathbb{V}}$ is a candidate population distribution. We call $\mathcal{P}_{\Theta,\mathbb{V}}$ the *inferential model*. In most cases, the investigator specifies the particular model family because the parameter vector of the true superpopulation process is the parameter of interest; that is, $\Phi(\mathbb{P}_{0,\mathbb{V}}) \equiv \theta_0 \in \Theta$, such that $\mathbb{P}_{\theta_0,\mathbb{V}} = \mathbb{P}_{0,\mathbb{V}}$. When such a true parameter θ_0 exists, we say the inferential model is *well-specified*; otherwise, we say the inferential model is *misspecified*. Because θ_0 may not exist, despite being the object of the investigator's interest, we call it the *nominal estimand*.

For any finite actor set $V \subset \mathbb{V}$, the superpopulation model family $\mathcal{P}_{\Theta,\mathbb{V}}$ implies a corresponding finite-dimensional model family composed of distributions on the network sample Y_V. Let $\mathcal{P}_{\Theta,V} \equiv \{\mathbb{P}_{\theta,V}\}_{\theta\in\Theta}$ be the projected model family, where for each $\theta \in \Theta$, $\mathbb{P}_{\theta,V}$ is a finite-dimensional distribution of $\mathbb{P}_{\theta,\mathbb{V}}$. The parametric specification implies that, for any θ, the projected distribution $\mathbb{P}_{\theta,V}$ inherits the parameter θ from the superpopulation distribution $\mathbb{P}_{\theta,\mathbb{V}}$, regardless of the choice of V. Thus, within the inferential model, there is coherence between projected distributions; for any two finite actor-sets V and V', the projection of $\mathbb{P}_{\theta,\mathbb{V}}$ onto these actor sets will have the same parameter θ.

We assume that the investigator uses maximum likelihood estimation to estimate θ_0. Given Y_V, the investigator estimates θ_0 by computing the maximum likelihood estimator (MLE) $\hat{\theta}_V$, which satisfies

$$\hat{\theta}_V = \arg\max_{\theta\in\Theta} \log \mathbb{P}_{\theta,V}(Y_V). \tag{1}$$

For inference, we assume the investigator uses asymptotic Wald intervals for the MLE constructed from the inverse observed Fisher information matrix.

2.3 Misspecification and the effective estimand

We will pay special attention to model-based estimation in the case where the inferential model is misspecified. Because of the complexity of social network processes, misspecification is likely in most if not all model-based analyses. In this section, we introduce the effective estimand, which is

a formal tool useful for characterizing model-based estimators from misspecified inferential models (D'Amour and Airoldi, 2016).

When the inferential model is misspecified, the nominal estimand θ_0 does not exist because the true superpopulation distribution $\mathbb{P}_{0,\mathbb{V}}$ is not contained in the model family $\mathcal{P}_{\Theta,\mathbb{V}}$. However, it can be argued that the estimation procedure in (1) implies its own well-defined estimand (D'Amour and Airoldi, 2016). In particular, the MLE can be understood as an estimate of the index of the best approximation to the replication distribution $\mathbb{P}_{0,V}$ in the finite-dimensional model family $\mathcal{P}_{\Theta,V}$. Following D'Amour and Airoldi (2016), we call this target of estimation the *effective estimand*.

Definition 2 (Effective Estimand of the MLE)**.** Let $\hat{\theta}_V$ be the maximum likelihood estimator, defined with respect to a particular model family $\mathcal{P}_{\Theta,V}$. The effective estimand of $\hat{\theta}_V$ is

$$\bar{\theta}_V = \arg\max_{\theta\in\Theta} \mathbb{E}_{\mathbb{P}_{0,V}}[\log \mathbb{P}_{\theta,V}(Y_V)]. \tag{2}$$

The effective estimand of the MLE $\bar{\theta}_V$ is a deterministic quantity that indexes the best approximation to $\mathbb{P}_{0,V}$ in the following sense: the optimization in (2) is equivalent to minimizing the Kullback-Leibler (KL) divergence $KL(\mathbb{P}_{0,V}||\mathbb{P}_{\theta,V})$ among all models $\mathbb{P}_{\theta,V} \in \mathcal{P}_{\Theta,V}$. Thus, $\bar{\theta}_V$ indexes a specific projection of the true distribution of Y_V into the finite-dimensional model family $\mathcal{P}_{\Theta,V}$. Because of this property, Sawa (1978) called the parameter value satisfying (2) the "pseudo-true parameter".

The effective estimand of the MLE has several important properties. First, it is well-defined whether or not the inferential model is misspecified. In the case where the inferential model is well-specified, the effective estimand reduces to the nominal estimand, so $\bar{\theta}_V = \theta_0$. Secondly, when the log-likelihood $\log \mathbb{P}_{\theta,V}(Y_V)$ satisfies certain regularity conditions, the MLE $\hat{\theta}_V$ concentrates about the effective estimand $\bar{\theta}_V$ across replications of Y_V (Spokoiny, 2012a). Finally, the effective estimand can be represented as a parameter of the replication distribution $\mathbb{P}_{0,V}$, in the sense that $\bar{\theta}_V \equiv \Phi_\Theta(\mathbb{P}_{0,V})$ for a particular operator $\Phi_\Theta(\cdot)$, and the MLE $\hat{\theta}_V$ can be represented as a plug-in estimator of $\bar{\theta}_V$ (D'Amour and Airoldi, 2016).

In the context of a network superpopulation problem, the inferential model $\mathcal{P}_{\Theta,\mathbb{V}}$ implicitly specifies an effective estimand $\bar{\theta}_V$ for each actor-set $V \subset \mathbb{V}$. Thus, for a given inferential model, we can understand $\bar{\theta}_V$ as a function of V. We will analyze this function to determine whether an inferential model is appropriate for solving a superpopulation problem.

Remark 1. *It is possible that $\bar{\theta}_V$ is not a unique quantity, if the maxmizer of Equation 2 is not unique. In this case, we may also consider $\bar{\theta}_V$ to be set-valued. This does not change our results that characterize the effective estimand, although all of our examples will involve cases where the effective estimand is unique.*

3 An Invariance Criterion for Valid Superpopulation Inference

3.1 Statement of criterion

In a network superpopulation problem, the central aim is to estimate properties of the network superpopulation $\mathbb{P}_{0,\mathbb{V}}$ from a single network sample Y_V. This goal necessarily requires extrapolation from sample to superpopulation. Thus, when model-based estimation is used in network superpopulation problems, it is natural to require that the estimand of the model-based procedure not depend on the specific actor-set V. We formally state this requirement below.

Criterion 1 (Invariance Criterion)**.** *For any finite actor-set $V \subset \mathbb{V}$ the effective estimand $\bar{\theta}_V$ of the MLE $\hat{\theta}_V$ derived from the inferential model $\mathcal{P}_{\Theta,\mathbb{V}}$ is invariant to the indexing set V.*

Criterion 1 requires $\bar{\theta}_V$ be a constant function in V. This is a common-sense, minimal bar to set for methods used in superpopulation inquiries. In particular superpopulation parameters do not depend on the choice of finite-sample projection V, so estimates computed from different samples drawn from the same source should be interpretable as measurements of the same superpopulation quantities. Logically, this invariance justifies generalization from one network sample Y_V to another $Y_{V'}$; at the very least the data summaries $\hat{\theta}_V$ and $\hat{\theta}_{V'}$ will approximate each other.

Criterion 1 is not always directly verifiable, because computing the effective estimand $\bar{\theta}_V$ requires computing an expectation over the true distribution $\mathbb{P}_{0,V}$. However, in social network modeling, investigators are often aware of properties of the true social process that they are unable to encode directly in the model specification. In this case, if we assume that $\mathbb{P}_{0,\mathbb{V}}$ has some of these unmodeled properties, we can deduce whether the effective estimand $\bar{\theta}_V$ appears to vary with V. In the sections below, we demonstrate this approach, and derive some properties of the effective estimand when the proposed model does not match the sparsity of the true data-generating process. In particular, we show that when the sparsity property of social networks is not modeled appropriately, the effective estimand $\bar{\theta}_V$ must depend on the sample size $|V|$, implying that sparsity misspecified models violate Criterion 1.

3.2 Comparison to single-sample criteria

Before we proceed to our discussion of sparsity misspecification, we briefly discuss how Criterion 1 differs from criteria that are used to evaluate model-based estimators in single-sample problems.

In our notation, for single-sample problems, the investigator is only interested in estimating a parameter of the replication distribution $\mathbb{P}_{0,V}$, so the parameter of interest can be written as $\Phi(\mathbb{P}_{0,V})$ for some parameter map $\Phi(\cdot)$. In the model-based approach, the investigator only specifies a finite-dimensional inferential model $\mathcal{P}_{\Theta,V}$. Estimation proceeds in the same way as in the superpopulation

case, with the MLE $\hat{\theta}_V$ defined according to (1), and the effective estimand $\bar{\theta}_V$ defined according to (2).

Importantly, the validity of claims made in single sample problems does not depend on Criterion 1, because the goal is restricted to characterizing the specific replication distribution $\mathbb{P}_{0,V}$; whether the inferences can generalize to other actor-sets is irrelevant. Instead, the primary concern in single-sample problems is whether the estimator $\hat{\theta}_V$ is stable between replications of Y_V if V is large enough. Thus, single-sample estimators are evaluated in according to asymptotic arguments involving sequences of random graphs, with the limiting behavior of the estimator $\hat{\theta}_V$ serving as an approximation for the behavior of $\hat{\theta}_V$ in a large but finite sample. For example, in Bickel et al. (2013), the authors define a sequence of ever-larger exchangeable random graphs whose expected degree, ρ_n, decreases with n so that the limit of the sequence has a vanishing network density, and show that their estimator converges in this sparse limit. Importantly, in these arguments, there is no requirement that the random graphs in the sequence be stochastically consistent with one another, so that they could be represented as finite dimensional projections from a common stochastic process. Thus, in the example of Bickel et al. (2013), the fact that the sequence cannot define a consistent stochastic process, because no non-trivial exchangeable random graph process has a sparse limit (Orbanz and Roy, 2013; Crane and Dempsey, 2015), does not invalidate the argument.

On the other hand, in superpopulation problems, the object of inference is a random graph process. When we analyze superpopulation estimators in Section 5, we will also use sequences of random graphs, but we will require each of these graphs to be a finite-dimensional projection of the network superpopulation. In this approach, we will not only examine the limit of the sequence; we will also to compare the effective estimand defined by each element of the sequence.

4 Sparsity

Sparsity is one of the most salient features of social networks, but is also difficult to represent in generative models. As such, sparsity is one of the primary sources of model misspecification in the analysis of social network data. In this section, we will formally define sparsity in the context of network superpopulation problems.

Heuristically, the word "sparsity" is used to describe the the phenomenon that in large network samples, an overwhelming proportion of actor-pairs engage in no interactions, and further, the larger the network sample, the larger this proportion of non-interactions. This phenomenological description has been translated into mathematical formalism in a number of ways. In the theory of sparse graph limits, sparsity is defined in terms of the limit of a sequence of random graphs of increasing size (Bollobás and Riordan, 2011). This formalism has been applied to the analysis of

estimators in single-sample problems, where the limit of these sequences has been used as analogy for large but finite network samples in which the proportion of non-zero social interactions is relatively small (Bickel and Chen, 2009; Airoldi et al., 2013; Bickel et al., 2013).

Here, we define sparsity as a property of a random graph process, in line with Crane and Dempsey (2015). For ease of discussion, we define a density operator, which corresponds to the proportion of dyads in an random graph with corresponding nonzero interactions.

Definition 3 (Density Operator)**.** Let Y_V be a random graph with vertex set V. The density operator D is

$$D(Y_V) = \frac{\sum_{ij} A_{ij}}{\binom{|V|}{2}},$$

and returns the proportion of pairwise outcomes in Y_V that are nonzero.

We say a random graph process $Y_{\mathbb{V}}$ is sparse if larger network samples Y_V drawn from the process tend to have smaller network densities. Formally, for a random graph process $Y_{\mathbb{V}}$, let $\binom{\mathbb{V}}{n}$ be the set of all subsets of $\mathbb{V}$ of size n, and define $D_n \equiv \max_{V \in \binom{\mathbb{V}}{n}} \mathbb{E}(D(Y_V))$ to be the maximum expected density of any finite projection Y_V.

Definition 4 (Sparse Graph Process)**.** The random graph process $Y_{\mathbb{V}}$ is *sparse* if and only if $\lim_{n\to\infty} D_n = 0$.

It is also useful to define the *sparsity rate* of a process, which characterizes how quickly the upper bound on network densities of growing samples drawn from a given population process converge to zero.

Definition 5 (Sparsity Rate)**.** Let D_n be defined as in Definition 4. We say a random graph process $Y_{\mathbb{V}}$ has sparsity rate $\epsilon(n)$ iff there exists some finite positive constant C such that

$$\lim_{n\to\infty} \frac{D_n}{\epsilon(n)} = C.$$

Similarly, we say two random graph processes defined on the same index set $\mathbb{V}$, $Y_{\mathbb{V}}$ and $Y'_{\mathbb{V}}$, have the same sparsity rate iff there exists some finite positive constant C such that,

$$\frac{D_n}{D'_n} \to C$$

where $D'_n \equiv \max_{V \in \binom{\mathbb{V}}{n}} \mathbb{E}(D(Y'_V))$.

Remark 2. *A sparse graph process can be used to produce sparse graph sequences in the sense of Bollobás and Riordan (2011). In fact, any increasing subgraph sequence defined with respect to a sparse random graph process has a sparse limit, i.e., for any increasing sequence of vertex sets $(V_n)_{n>0}$ ordered by subset inclusion, $D(Y_{V_n}) \to 0$ as n grows large. This property is invariant to*

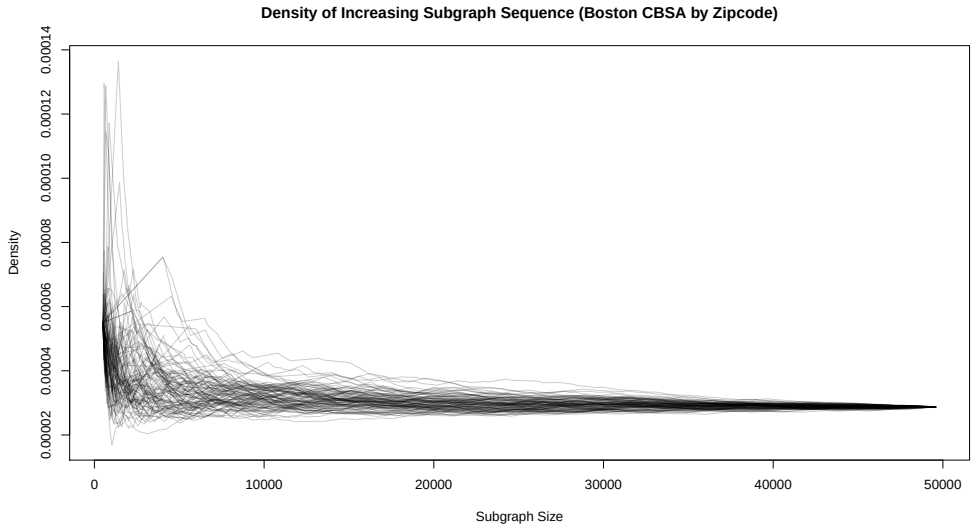

Figure 2: Sequences of random subgraphs drawn from the Boston-area inventor collaboration network observed over a 6-year time interval beginning in 1983. Each line is a randomly generated subgraph sequence, generated by building up a subgraph zip code-by-zip code in a random order. A clear relationship between network size and density is visible here. This is the phenomenon meant that we model in Definition 4.

the scheme used to construct the subgraph sequence. A sparse graph sequence constructed in this way is Kolmogorov consistent.

4.1 Example: Empirically observed sparsity in patent collaboration network

In Figure 2 we show an example of an empirically observed "sparsity" phenomenon that maps cleanly onto the mathematical formalism presented in the previous section. From the dataset described in Section 1.1, we explore subsamples of the set of all patent co-authorships in the Boston area in a 6-year time interval beginning in 1983.We then obtain sequences of increasing, nested subgraphs from this regional collaboration network by randomly drawing a sequence of zip codes and incrementally adding the batches of inventors who live in these zip codes to the network subsample. In Figure 2, each line corresponds to one of these subgraph sequences, with the x-axis showing the number of inventors included in the subgraph and the y-axis showing the network density of that subgraph.

Even in this finite example, we see that the maximal density of the network clearly decreases with sample size. This justifies the "limiting to 0" notion presented in the Definition 4, despite the fact that the "limiting" network density in finite real-world networks is a positive constant. To obtain an empirical analogue of the sparsity rate $\epsilon_0(n)$, the figure would need to include all possible subgraph sequences (V_n).

4.2 Sparsity misspecification

Sparsity is an attribute of real-world social networks that is often not well-represented by generative network models. When the sparsity of the real process $\mathbb{P}_{0,\mathbb{V}}$ is not correctly represented by the inferential model $\mathcal{P}_{\Theta,\mathbb{V}}$, we say that the model is *sparsity misspecified*. Intuitively, sparsity misspecification occurs when there is no member of the inferential model family with the same sparsity rate as the true superpopulation process. Formally,

Definition 6 (Sparsity Misspecification)**.** For an inferential family $\mathcal{P}_{\Theta,\mathbb{V}}$ and true population process $\mathbb{P}_{0,\mathbb{V}}$, we say that the inferential family is sparsity misspecified if and only if there exists no $\theta \in \Theta$ such that $\mathbb{P}_{\theta,\mathbb{V}}$ has the same sparsity rate as $\mathbb{P}_{0,\mathbb{V}}$.

4.3 Example: Sparsity misspecification in infinitely exchangeable random graph models

Sparsity misspecification is particularly prominent in model families that are built on local assumptions about how individual actors make decisions to interact. Infinitely vertex-exchangeable random graph models are the most popular class of such generative network models. These models assume that the likelihood for any network sample Y_V drawn from a superpopulation process $Y_{\mathbb{V}}$ is invariant to permutations of the actor-set V – this translates to joint exchangeability of the rows and columns of any finite adjacency matrix. We consider the extension of these models to the case where actors are exchangeable up to observed covariates. These models are appealing for several reasons. Under the assumption of correct specification, they imply that within an observed network sample Y_V, the pairwise outcomes can be treated as a set of $\binom{|V|}{2}$ conditionally independent replications, given observed and potentially unobserved covariates. They also justify ignoring the mechanism by which the actor-set V was chosen from $\mathbb{V}$, because the observed outcomes are conditionally independent of the unobserved outcomes in $\binom{\mathbb{V}}{2} \backslash \binom{V}{2}$. Finally, these models generate simple predictions at the dyad level based only on local information. We describe several different classes of these models in turn.

The simplest subclass of these exchangeable random graph models treats all pairwise outcomes in the network as conditionally independent given *observed* pairwise covariates. These models reduce parameter estimation to a regression problem on the vectorized adjacency matrix. These models tend to be specified as a generalized linear model, and have been proposed with binary, count-valued, and point process-valued outcomes (Perry and Wolfe, 2013; Vu and Asuncion, 2011; Handcock et al., 2007; von Luxburg, 2010)). These models assign a particular observed network sample Y_V with covariates X_V a likelihood of the form:

$$\mathbb{P}(Y_V \mid X_V) = \prod_{ij} \mathbb{P}(Y_{ij} \mid X_{ij}). \tag{3}$$

We call models in this subclass *conditionally independent dyad* or CID models. This model class subsumes models that incorporate node-level covariates, as these can be encoded as dyad-level covariates.

More general exchangeable random graph models include specifications that assume conditional independence between the dyads given unobserved covariates. These models have seen an explosion of interest with a wide variety of structures proposed for the latent covariate structure including latent single- and mixed-membership classes, latent positions, latent eigenspaces, and their infinite-dimensional counterparts (Lloyd et al., 2013). This class of models has been unified under an array-exchangeability representation by Aldous and Hoover that, up to isomorphism, maps these latent covariate processes to a single probability surface W on the unit square. Given this surface, a network sample Y_V is generated by randomly assigning each actor in V a position C_V^i so that the pairwise covariate X_{ij} is generated by querying $W(C_V^i, C_V^j)$. Several recent works have been dedicated to estimating this latent surface, called the graphon, directly (Wolfe and Olhede, 2013; Airoldi et al., 2013). Models with this structure induce the following likelihood on network samples

$$\mathbb{P}(Y_V \mid X_V) = \int_{\mathcal{C}_V} \prod_{ij} P(Y_{ij} \mid W(C_i, C_j)) d\mathbb{P}(C_V). \tag{4}$$

Model specifications that mix latent and observed covariates have also been proposed in several places, e.g., Handcock et al. (2007).

Several authors have noted that infinitely vertex-exchangeable graph models without covariates cannot be extended to form non-trivial sparse graph processes; in particular, any infinitely vertex-exchangeable random graph process that is sparse can only generate empty network samples Y_V for any V. Orbanz and Roy (2013) show this explicitly, using a law of large numbers argument to show that any graph sequence constructed from an exchangeable random graph process would have a limiting network density $\lim_{n\to\infty} D(Y_{V_n}) = \frac{1}{2}\int_{[0,1]^2} W(x,y)dxdy$, which is 0 only if $W(\cdot,\cdot)$ is zero almost everywhere. Crane and Dempsey (2015) provide a similar proof.

In our current terminology, this result indicates that infinitely vertex-exchangeable random graph models are sparsity misspecified when they are applied to study sparse social networks. With appropriate conditions on observed covariates $X_{\mathbb{V}}$, we can extend this result to exchangeable random graph models with covariates, including CID models.

Theorem 1. *Let $\mathcal{P}_{\Theta,\mathbb{V}}$ be a family of infinitely vertex-exchangeable random graph processes. Let $X_{\mathbb{V}}$ be the set of covariates corresponding to each pair of actors in $\binom{\mathbb{V}}{2}$, and denote by $\mathcal{N}_\theta \subset \mathcal{X}$ the set of covariate vectors that, for a given $\theta \in \Theta$, satisfy $\mathbb{P}_\theta(Y_{ij} \neq 0 \mid X_{ij} \in \mathcal{N}_\theta) = 0$. If, for each $\theta \in \text{int}\Theta$, some positive proportion of covariate vectors does not fall into $\mathcal{N}_\theta$, so that $|\mathcal{N}_\theta| \Big/ \binom{|\mathbb{V}|}{2} < 1$, then the model is sparsity misspecified.*

The argument here is straightforward. The covariate vectors X_{ij} parameterize the surface W

described by Aldous and Hoover, so that every X_{ij} defines a corresponding surface $W_{X_{ij}}$. For each $ij \in \binom{\mathbb{V}}{2}$, the marginal probability $\mathbb{P}(Y_{ij} \neq 0 \mid X_{ij}) = \int_{\mathcal{C}_\mathbb{V}} W_{X_{ij}}(C_i, C_j) d\mathbb{P}(C_\mathbb{V})$. Thus, if a positive proportion of covariate vectors in the population define a latent surface $W_{X_{ij}}$ whose integral is not zero, there will be a positive proportion of dyads in the population for which $\mathbb{P}(Y_{ij} \neq 0 \mid X_{ij}) > 0$ resulting in a limiting positive network density by the law of large numbers.

Intuitively, unless the model family contains distributions that set an arbitrarily high proportion of dyads to have deterministically zero outcomes on the basis of the observed covariates X_{ij}, the model will be sparsity misspecified. In most social network analysis applications, such a highly informative set of covariates is not available. In fact, regression and latent variable modeling schemes are often proposed precisely because so little is known about the network's structure.

We can confirm that infinitely vertex-exchangeable random graph models are sparsity misspecified for social processes *a priori* because they do not contain non-trivial sparse graph processes. Other model families, for example the edge exchangeable models of Veitch and Roy (2015), Crane and Dempsey (2015), and Cai et al. (2016), do include sparse graph processes, and in these cases it is not possible to judge sparsity misspecification *a priori*. However, many families that include sparse graph processes impose a particular functional form on the sparsity rate. In these cases, sparsity misspecification is still possible, but generally we do not have enough prior knowledge of the true generating process' sparsity rate to judge this misspecification until after the data have been examined.

5 Main Result: Moving Target Theorem

In the last few sections, we have established a statistical framework for representing superpopulation problems, discussed a criterion for valid model-based superpopulation inference, and identified sparsity misspecification as a common issue in the study of sparse social networks. In this section, we bring these ideas together, and show that many MLE's derived from a sparsity-misspecified models violate Criterion 1, making these models inappropriate for superpopulation problems.

We introduce one final definition before we proceed to the theorem.

Definition 7 (Responsiveness)**.** Let (V_n) be an arbitrary increasing sequence of vertex sets from $\mathbb{V}$, ordered by subset inclusion. We say an estimator is *responsive* to a statistic $T(Y_V)$ under a true generating process $\mathbb{P}_{0,V}$ if and only if, for any (V_n),

$$|\mathbb{E}_{\bar{\theta}}(T(Y_{V_n})) - \mathbb{E}_0(T(Y_{V_n}))| = o_p(1). \tag{5}$$

Responsiveness can be interpreted as a goodness-of-fit condition, and is a minimal requirement for many estimators. It implies that the distribution indexed by the effective estimand gives an

asymptotically unbiased prediction for the statistic $T(Y_{V_n})$.

In Theorem 2, we show that if the estimator of a sparsity misspecified model is responsive to the network density of a sample $D(Y_V)$, the effective estimand varies as a function of the size of V. The theorem is set up as follows: suppose we fit a sparsity misspecified model to some data Y_{V_0}, for which the effective estimand is $\bar{\theta}_{V_0}$. For any such V_0, there is a sequence of sufficiently large actor sets (V_n) for which $\bar{\theta}_{V_n} \neq \bar{\theta}_{V_0}$.

Theorem 2 (Moving target theorem)**.** *Let $Y_{0,\mathbb{V}}$ be a sparse graph process with sparsity rate $\epsilon_0(n)$. Let $\mathcal{P}_{\Theta,\mathbb{V}}$ be a model family.*

Suppose that there exists at least one $V_0 \subset \mathbb{V}$ such that $\mathbb{E}_{\bar{\theta}_{V_0}}(D(Y_{V_0})) > 0$. Fix one such V_0, can call the effective estimand for this actor-set $\bar{\theta}_{V_0}$.

In addition, suppose that the following hold:

(M1) The model family $\mathcal{P}_{\Theta,\mathbb{V}}$ is sparsity misspecified for the true population process $\mathbb{P}_{0,\mathbb{V}}$.

(M2) The distribution implied by the actor-set V_0, $\mathbb{P}_{\bar{\theta},\mathbb{V}}$ has sparsity rate $\epsilon_{\bar{\theta}_{V_0}}(n)$.

(M3) The model is responsive to the sample density $D(Y_{V_n})$ under the true population process.

(M4) The rate of the effective estimand's prediction bias $|\mathbb{E}_{\bar{\theta}_{V_n}}(D(Y_{V_n})) - \mathbb{E}_0(D(Y_{V_n}))|$ is of lower order than $\epsilon_0(n)$ and $\epsilon_{\bar{\theta}}(n)$.

Then, there exists a minimum size n' and a sequence of actor sets (V_n) with $n > n'$, for which $\bar{\theta}_{V_n} \neq \bar{\theta}_{V_0}$.

Proof. Because the model family is sparsity-misspecified, there are two cases to consider: either the target distribution is too sparse or too dense.

Case 1: Target distribution is too sparse, so that $\epsilon_{\bar{\theta}_{V_0}}(n) = o(\epsilon_0(n))$. Let (V_n^0) be a vertex sequence so that, for each n, $D(Y_{V_n^0}) = \max_{V \in \binom{\mathbb{V}}{n}} \mathbb{E}_0(D(Y_V))$. By the definition of the sparsity rate, for all n, $\mathbb{E}_{\bar{\theta}_{V_0}}(D(Y_{V_n^0})) \leq \epsilon_{\bar{\theta}}(n)$. By construction of (V_n^0), the responsiveness assumption (M3), and rate assumption (M4), $\mathbb{E}_{\bar{\theta}_{V_n^0}}(D(Y_{V_n^0})) = O(\epsilon_0(n))$. Thus, $\mathbb{E}_{\bar{\theta}_{V_0}}(D(Y_{V_n^0})) = o(\mathbb{E}_{\bar{\theta}_{V_n^0}}(D(Y_{V_n^0})))$. Thus there exists an n' such that for each $n > n'$, $\bar{\theta} \neq \bar{\theta}_{V_n^0}$.

Case 2: Target distribution is too dense, so that $\epsilon_0(n) = o(\epsilon_{\bar{\theta}}(n))$. Let $(V_n^{\bar{\theta}})$ be a vertex sequence so that, for each n, $D(Y_{V_n^{\bar{\theta}}}) = \max_{V \in \binom{\mathbb{V}}{n}} \mathbb{E}_{\bar{\theta}}(D(Y_V))$. By definition of sparsity rate, for all n, $\mathbb{E}_0(D(Y_{V_n^{\bar{\theta}}})) \leq \epsilon_0(n)$. Combined with the responsiveness assumption (M3) and the rate assumption (M4), $\mathbb{E}_{\bar{\theta}_{V_n^{\bar{\theta}}}}(D(Y_{V_n^{\bar{\theta}}})) < O(\epsilon_0(n))$. By construction of $(V_n^{\bar{\theta}})$, $\mathbb{E}_{\bar{\theta}_{V_n^{\bar{\theta}}}}(D(Y_{V_n^{\bar{\theta}}})) = O(\epsilon_{\bar{\theta}}(n)$. Thus, $\mathbb{E}_{\bar{\theta}_{V_n^0}}(D(Y_{V_n^{\bar{\theta}}})) = o(\mathbb{E}_{\bar{\theta}_V}(D(Y_{V_n^{\bar{\theta}}})))$. Thus there exists an n' such that for each $n > n'$, $\bar{\theta} \neq \bar{\theta}_{V_n^{\bar{\theta}}}$. □

Remark 3. *The sequences of actor-sets (V_n) in the proof were chosen in order to maximize expected network density of the outcomes Y_{V_n}. This may seem like an edge case, but it is in fact realistic. In practice investigators usually choose V, or procedures to sample V, so that the chosen actor-sets have a network density that is close to the upper bound D_n, for example, by specifying their samples in terms of cohesive sets of individuals who live in the same region.*

Theorem 2 is a general result that applies to all types of misspecified model families, and is sufficient to show that Criterion 1 is violated, but it is a weaker statement than we can make in the case of some common model families. In particular, for dense model families that contain no sparse distributions like those discussed in Section 4.3 we can make the following stronger statement.

Theorem 3 (Moving Target for Dense Models)**.** *In the same set-up as Theorem 2 suppose that the following hold:*

(M1) The model family $\mathcal{P}_{\Theta,\mathbb{V}}$ is dense, so that for each θ, $\lim \max_{V \in \binom{\mathbb{V}}{2}} E_\theta(D(Y_V)) > 0$.

(M2) The model is responsive to the sample density $D(Y_{V_n})$ under the true population process.

(M3) The rate of the effective estimand's prediction bias $|\mathbb{E}_{\bar{\theta}}(D(Y_{V_n})) - \mathbb{E}_0(D(Y_{V_n}))|$ is of lower order than $\epsilon_0(n)$.

Then, there exists a minimum size n' such that for all actor sets actor sets V with $|V| > n'$, $\bar{\theta}_{V_n} \neq \bar{\theta}_{V_0}$.

These results establish a fundamental tension between single-sample and superpopulation inference when a model is sparsity misspecified. In particular, if a sparsity misspecified model $\mathcal{P}_{\Theta,\mathbb{V}}$ fits individual network samples well, so that the distribution of best fit $\mathbb{P}_{\bar{\theta},V}$ accurately approximates the network density of the network sample $E_{\mathbb{P}_{0,V}}(D(Y_V))$, then the model family cannot also be used for superpopulation inference. This resolves the seemingly paradoxical observation that popular sparsity misspecified models like CID models or vertex-exchangeable random graph models (described in Section 4.3) tend to give nonsensical results in superpopulation contexts despite having strong theoretical support for performance in single-sample inference. Given that they are sparsity misspecified, these models fail as tools for superpopulation inference *precisely because* they are effective tools for single-sample inference.

The "moving target" problem identified here manifests in several ways in applied investigations. Because the model's MLE is effectively estimating distinct quantities from network samples of different size, even if they are drawn from the same network superpopulation, downstream analyses such as hypothesis tests, prediction procedures, and shrinkage schemes do not behave as expected. Even in cases where the desire is to simply interpret the parameter estimates for theoretical context, this inhomogeneity of interpretation with respect to size presents challenges when applying models that were developed for analysis of small networks (e.g., Sampson's monastery) to large-scale

social networks. Depending on the application, establishing a meaningful scale for such parameter estimates may not be possible.

5.1 Example: Poisson regression with binary covariate

We demonstrate some of the difficulties that result from the Theorem 2 in a simple example based on a hypothetical analysis of the patent collaboration network data presented in Section 1.1.

Let $\mathbb{V}$ be a superpopulation of inventors, from which we have sampled a set of individuals V of size n. Let Y_V be a matrix recording the number of pairwise patent collaborations that have taken place between the n sampled inventors, so that Y_{ij} is the number of times inventor i and inventor j appeared together on the same patent application. Denote the true distribution of Y_V as $\mathbb{P}_{0,V}$. For each pair ij, let X_{ij} be a binary covariate that indicates whether inventors i and j work for the same firm. The investigator is interested in summarizing network samples Y_V so that they may be compared, e.g., to make statements about whether within-firm collaborations are more prominent in one industry than another.

The investigator also knows the following facts about the collaboration-generating process:

(A1) The true collaboration-generating process $Y_{0,\mathbb{V}}$ is sparse in the sense of Definition 4 with an unknown rate $\epsilon_0(n)$.

(A2) All firms have finite size.

(A3) A non-vanishing fraction of firms have a positive number of expected within-firm interactions.

However, the investigator is unable to encode all of these assumptions into a tractable modeling framework for network samples Y_V. Because it is intuitive and computationally convenient, the investigator proposes a model family $\mathcal{P}_{\Theta,\mathbb{V}}$ whose finite-dimensional distributions have the form of a Poisson regression model:

$$Y_{ij} \overset{\perp\!\!\!\perp}{\sim} \text{Pois}(\exp(\theta^{(1)} + X_{ij}\theta^{(2)})), \tag{6}$$

where the parameter vector $\theta \equiv (\theta^{(1)}, \theta^{(2)})$ can take values in $\Theta \equiv \mathbb{R}^2$. According to standard interpretations of GLM coefficients (McCullagh and Nelder, 1989), $\theta^{(1)}$ is the log of the interaction rate of any "between-firm" inventor pair, while $\theta^{(2)}$ is the log ratio of interaction rates between any "within-firm" and any "between-firm" inventor pair. For a given sample Y_V, the investigator uses maximum likelihood estimation to obtain estimates $\hat{\theta}_V$, which will be used to compare different network samples.

We can now ask whether the analysis satisfies Criterion 1, which is a necessary condition for estimates $\hat{\theta}_V$ obtained from different samples to be comparable in general. We will show that

under some simple conditions, Criterion 1 is indeed violated because the model's effective estimand depends on the size of the indexing set V.

We make the following assumptions to ensure that the analysis is identifiable

(B1) $\mathbb{E}_0(Y_{ij})$ is finite for all $ij \in \binom{V}{2}$.

(B2) For some finite n', for every V such that $|V| > n'$, the expected number of within-firm and between-firm interactions are nonzero:

$$\sum_{ij} \mathbb{E}_0(Y_{ij})(1 - X_{ij}) > 0 \quad \text{and} \quad \sum_{ij} \mathbb{E}_0(Y_{ij}) X_{ij} > 0$$

(B3) The variance of the total number of collaborations is proportional to its expectation, so that for all V, there exists a $d < \infty$ such that

$$\mathbb{V}\text{ar} \sum Y_{ij} \leq d \cdot \mathbb{E}_0 \sum Y_{ij}.$$

Because the model proposed in Equation 6 is an exponential family, the effective estimand has a simple analytical form that mimics the form of the MLE with expectations of sufficient statistics plugged in:

$$\bar{\theta}_V^{(1)} = \log \left(\frac{\sum_{ij} \mathbb{E}_0(Y_{ij} \mid X_{ij} = 0)(1 - X_{ij})}{\sum_{ij}(1 - X_{ij})} \right) \tag{7}$$

$$\bar{\theta}_V^{(2)} = \log \left(\frac{\sum_{ij} \mathbb{E}_0(Y_{ij} \mid X_{ij} = 1) X_{ij}}{\sum_{ij} X_{ij}} \Bigg/ \frac{\sum_{ij} \mathbb{E}_0(Y_{ij} \mid X_{ij} = 0)(1 - X_{ij})}{\sum_{ij}(1 - X_{ij})} \right). \tag{8}$$

Given this functional form, we can establish the following proposition

Proposition 1. *Fix a sequence of sets of actors (V_n), such that $|V_n| = n$. Under assumptions (A1), (A2), (B1), and (B2), the effective estimand implied by the CID Poisson model in Equation 6 varies with n when applied to data generated by $Y_{0,\mathbb{V}}$.*

Proof. Given (A1), the true generating process $Y_{0,\mathbb{V}}$ is sparse, so by Theorem 1, the CID Poisson model in Equation 6 is sparsity misspecified. Given (B1), all samples Y_{V_n} with $n > n'$ are expected to be non-empty. Now, we check that the model is responsive with respect to network density.

Taking $g(x) = 1 - \exp(-\exp(x))$, or the c-log-log transformation, we can write

$$\begin{aligned}
\mathbb{E}_{\bar{\theta}_{V_n}}(D(Y_{V_n})) &= \binom{n}{2}^{-1}\left[g(\bar{\theta}^{(1)}_{V_n} + \bar{\theta}^{(2)}_{V_n})\sum_{ij} X_{ij} + g(\bar{\theta}^{(1)}_{V_n})\sum_{ij}(1 - X_{ij})\right] \\
&< \binom{n}{2}^{-1}\left[\exp(\bar{\theta}^{(1)}_{V_n} + \bar{\theta}^{(2)}_{V_n})\sum_{ij} X_{ij} + \exp(\bar{\theta}^{(1)}_{V_n})\sum_{ij}(1 - X_{ij})\right] \\
&= \binom{n}{2}^{-1}\sum_{ij}\mathbb{E}_0(Y_{ij}) \\
&\sim O(\epsilon_o(n)),
\end{aligned}$$

where the second step follows from (A2) and the inequality $1 - e^{-x} < x$ for $x > 0$, the third step follows from Equations 7 and 8, and the final step follows from assumptions (A1) and (B1). Thus, the model is responsive with respect to network density and the plug-in prediction bias decreases at the appropriate rate, so by Theorem 2, the model violates Criterion 1. □

In this particular investigation, Proposition 1 would manifest in a number of ways. We can show this directly by establishing that the MLE $\hat{\theta}_V$ concentrates around the effective estimand $\bar{\theta}_V$ for all finite samples Y_V, and then showing that the effective estimand can be manipulated arbitrarily by the choice of V.

Lemma 1. *The distribution of the MLE for the parameters of the model in Equation 6 concentrates around its effective estimand for all finite samples V, with probability bounds given by*

$$\begin{aligned}
\mathbb{P}(|\hat{\theta}^{(2)}_V - \bar{\theta}^{(1)}_V| \leq \log(1+\delta)) &\geq 1 - \frac{d}{\delta^2\mathbb{E}_0\sum Y_i(1 - X_i)} \\
\mathbb{P}(|\hat{\theta}^{(2)}_V - \bar{\theta}^{(2)}_V| \leq \log(1+\delta)) &\geq 1 - \frac{4d}{\delta^2\mathbb{E}_0\sum Y_i(1 - X_i)} - \frac{4d}{\delta^2\mathbb{E}_0\sum Y_i X_i}
\end{aligned}$$

The proof is included in the appendix.

Given this result, we can characterize the behavior of the MLE in terms of the effective estimands. First, we characterize the behavior of the effective estimand vector $\bar{\theta}_V$.

Proposition 2. *$\bar{\theta}^{(1)}_V$ can be made arbitrarily negative by selecting a large actor-set V.*

Proof. Given (A2), the proportion of between-firm dyads $\sum(1 - X_{ij})/\binom{|V|}{2} \to c > 0$. Combined with the sparsity condition (A1) and the finite expectation condition (B1), the ratio in Equation 7 must fall to zero as $|V| \to \infty$. □

Proposition 3. *The effective estimand $\bar{\theta}^{(2)}_V$ can be made arbitrarily positive and large by incorporating a larger number of firms in the study.*

Proof. Because of (A2), the ratio of within-firm to between-firm dyads falls to zero as $n \to \infty$,

$$\frac{\sum_{V_n} X_{ij}}{\sum_{V_n} (1 - X_{ij})} \to 0.$$

Given the sparsity of the overall process (A1), and the scaling of between-firm dyads (B1), the denominator ratio in Equation 8 goes to zero as $n \to \infty$. Meanwhile, given (A2) and (A3), the numerator ratio in Equation 8 converges to a constant as $n \to \infty$. □

Combining Lemma 1 with these propositions, we have shown that the estimates $\hat{\theta}_V$ are strongly sensitive to the sizes and firm compositions of the samples that the investigator collects. As such, these estimates cannot be interpreted as descriptions of an underlying social process that each of these samples have in common.

6 Conditionally Independent Relationship Processes

So far, we have established that sparsity misspecification is difficult to avoid and that sparsity misspecified models are poor tools for obtaining scientifically meaningful answers for superpopulation inquiries. This difficulty highlights a mismatch between the modeling tools that are currently available for describing social network generating processes, and the properties of real social network processes that we hope to summarize in superpopulation investigations. This motivates us to seek out aspects of network superpopulations that we can describe stably with the modeling tools that are currently available.

As a solution to this problem, we describe a class of random graph processes that admit a particular factorization in their generating process that separates the sparsity-generating component of the process from a more easily-modeled conditionally independent component. For this class of processes, it is possible to make stable inferences about sparsity-invariant superpopulation properties, regardless of the sparsity rate of the process as a whole. We call this class of processes *conditionally independent relationship*, or CIR processes. We give a formal definition of CIR processes below.

In CIR processes, dyad-level observations Y_{ij} are drawn from a zero-inflated process in which only certain pairs of actors are capable of generating non-zero outcomes. We say these pairs of actors have a "relationship". This corresponds to the generative intuition that in order to generate an observable interaction where $Y_{ij} \neq 0$ (e.g., collaborate on a patent applications), two actors must first have an unobservable social relationship R_{ij}; for example, they must have been introduced to each other). Furthermore, conditional on these relationships and covariates X_V, pairwise outcomes Y_{ij} are independent; hence, the outcomes corresponding to each relationship in the actor-set are conditionally independent. Figure 3 provides a graphical description of this process.

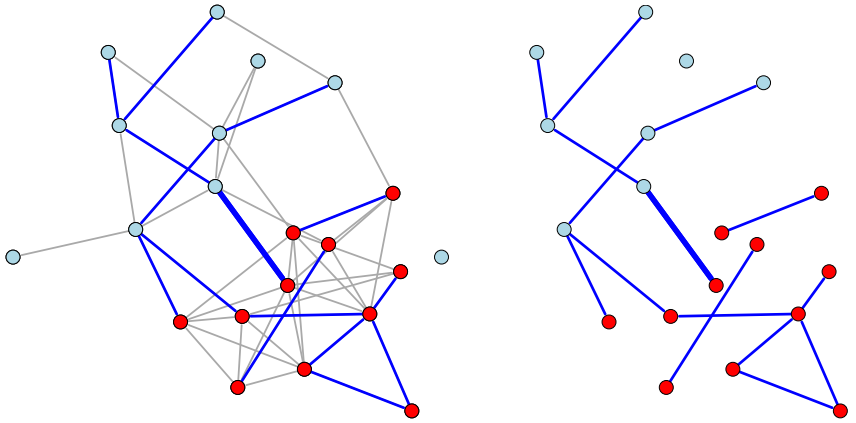

Figure 3: (Left) CIR generation process, where gray ties are "relationships" and blue ties are observed interactions. To generate an observable interaction, a pair of actors much first have a relationship, or in the language of the diagram, blue ties can only appear on top of gray ties. (Right) The observed network sample, where relationships with no observed interactions are indistinguishable from dyads with no relationship.

Formally, for any actor-set index $V \subset \mathbb{V}$, let Y_V be the observed random graph sample and R_V be the unobservable *relationship graph*. R_V is a binary random graph, and similarly to the observable outcome graph Y_V, we assume that the relationship graph is a subgraph from a superpopulation relationship process $R_{\mathbb{V}}$.

Definition 8. Let $Y_{\mathbb{V}}$ be a random graph process on $\mathbb{V}$. We say $Y_{\mathbb{V}}$ is a Conditionally Independent Relationship, or CIR, process if and only if for each finite index set $V \subset \mathbb{V}$, the distribution of Y_V can be written generically as

$$\mathbb{P}_0(Y_V \mid X_V) = \sum_{R \in \mathcal{G}_V} \left[\mathbb{P}_0(R_V \mid X_V) \prod_{ij} \mathbf{1}_{\{Y_{ij}=0\}}^{1-R_{ij}} \mathbb{P}_0(Y_{ij} \mid X_{ij}, R_{ij} = 1)^{R_{ij}} \right]. \tag{9}$$

where $\mathcal{G}_V$ is the set of all undirected binary graphs on V.

If a random graph process $Y_{\mathbb{V}}$ satisfies the factorization in Equation 9, we can make the following statement about the sparsity rate of a CIR process.

Proposition 4. *Let $Y_{\mathbb{V}}$ and $R_{\mathbb{V}}$ be the observable and unobservable components of a random graph process, whose finite dimensional distributions can be factorized according to Equation 9. Let $X_{\mathbb{V}}$ be the population set of covariates, and denote by $\mathcal{N}_\theta \subset \mathcal{X}$ the set of covariate vectors so that for a given $\theta \in \Theta$, $\mathbb{P}_{\mathbb{V}}(Y_{\mathbb{V}}^{ij} \neq 0 \mid R_{\mathbb{V}}^{ij} = 1, X_{\mathbb{V}}^{ij} \in \mathcal{N}_\theta) = 0$. Assume that for each $\theta \in \text{int}\Theta$, the population proportion of covariate vectors $X_{ij} \in \mathcal{N}_\theta < 1$. Then the sparsity rate of the marginal process $Y_{\mathbb{V}}$ is equal to the sparsity rate of the marginal process $R_{\mathbb{V}}$.*

This proposition can be shown using the same law of large numbers argument as in Theorem 1. The independence structure of the observable process $Y_{\mathbb{V}}$ conditional on the relationship process

$R_{\mathbb{V}}$ ensures that the marginal sparsity rates of $Y_{\mathbb{V}}$ and $R_{\mathbb{V}}$ can only differ by a constant factor. Thus the sparsity rate $\epsilon_0(n)$ of the observable process $Y_{\mathbb{V}}$ is not a function of the conditional distribution $\mathbb{P}_{0,V}(Y_V \mid X_V, R_V)$.

If a social process is in the CIR class, the conditional finite dimensional distributions $\mathbb{P}_{0,V}(Y_V \mid R_V, X_V)$ do not have the same sparsity-related inhomogeneities that characterize the marginal finite-dimensional distributions $\mathbb{P}_{0,V}(Y_V \mid X_V)$ and drive the result in Theorem 2. In practical terms, if the true social process is sparse but allows a CIR factorization as in Equation 9, the answer to the general question "How does *any pair* of actors generate social interactions?" must explain why the social process is sparse, but the answer to the specific question "How do pairs of actors with an existing relationship generate social interactions?" does not require such an explanation. Thus, if our modeling tools are ill-equipped to correctly model sparsity, it is reasonable to switch focus to the latter question. We discuss a procedure for estimating the properties of the sparsity-invariant conditional outcome process in the next section.

6.1 Truncated estimator for CIR processes

To model the observable process $Y_{\mathbb{V}}$, we propose a model family $\mathcal{P}_{\Theta,\mathbb{V}}$ that is composed of CIR processes. For this model family, we divide the parameter space Θ into two components, so that $\theta = (\beta, \gamma)$ for $\beta \in B$ and $\gamma \in \Gamma$ and $\Theta \equiv B \times \Gamma$. We specify the processes contained in $\mathcal{P}_{\Theta,\mathbb{V}}$ to have finite dimensional distributions for each V of the form

$$\mathbb{P}_\theta(Y_V \mid X_V) = \sum_{R \in \mathcal{G}_V} \left[\mathbb{P}_\theta(R_V \mid X_V) \prod_{ij} \mathbf{1}_{\{Y_{ij}=0\}}^{1-R_{ij}} \mathbb{P}_0(Y_{ij} \mid X_{ij}, R_{ij} = 1)^{R_{ij}} \right]. \tag{10}$$

where $\mathcal{G}_V$ is the set of all undirected binary graphs on V. The parameters β represent sparsity-invariant properties of a CIR process; we define these as the parameters of interest. We treat γ as nuisance parameters. While the conditional distribution $\mathbb{P}_\beta(Y_V \mid R_V, X_V)$ is free of γ, the marginal distribution $\mathbb{P}_\theta(R_V \mid X_V)$ may depend on components of β.

Direct maximum likelihood estimation using Equation 10 would be the most straightforward option, but such an approach runs into the same sparsity misspecification problems described in Section 5. Because the relationship graph R_V is unobserved, the investigator would still need to specify a functional form for the marginal distribution $\mathbb{P}_{V,\theta}(R_V \mid X_V)$. If this portion of the model is sparsity misspecified, then the resulting estimator for $\hat{\beta}$ may still violate Criterion 1. In particular, the following corollary to Theorem 2 gives an additional condition under which sparsity misspecification invalidates estimators for the parameter of interest β.

Corollary 1 (Moving Target with Nuisance)**.** *In the setting of Theorem 2, assume in addition to (M1)–(M3) that*

(M5) The inferential family is specified such that parameters of interest β are identified by the binarized process A_{V_n}.

Then, for any n, there exists an $n' > n$ such that $\bar{\beta}_{V_n} \neq \bar{\beta}_{V_{n'}}$.

When the true process distribution $\mathbb{P}_{0,\mathbb{V}}$ is a CIR process, this corollary can apply even when the conditional process $\mathbb{P}_{\beta,\mathbb{V}}(Y_{\mathbb{V}} \mid R_{\mathbb{V}}, X_{\mathbb{V}})$ is well-specified. We discuss this further in Section 6.2.

To avoid misspecification issues, we develop a likelihood-based procedure that only relies on a model a subset of the available data. Recall that we defined the indicators $A_{ij} = \mathbf{1}\{Y_{ij} > 0\}$. For an actor-set V, let $\mathcal{A} \equiv \{ij : A_{ij} = 1\}$ be the set of indices of nonzero outcomes, and let $Y_V^{\mathcal{A}} \equiv \{Y_{ij} : ij \in \mathcal{A}\}$ and $X_V^{\mathcal{A}} \equiv \{X_{ij} : ij \in \mathcal{A}\}$ be the outcomes and covariates corresponding to these indices. We define the *truncated likelihood* as the conditional distribution

$$\mathbb{P}^{tr}_{\beta,V}(Y_V \mid X_V) \equiv \mathbb{P}_{\beta,V}(Y_V^{\mathcal{A}} \mid X_V^{\mathcal{A}}) \tag{11}$$

$$= \prod_{ij \in \mathcal{A}} \mathbb{P}_{\beta}(Y_{ij} \mid X_{ij}, A_{ij} = 1). \tag{12}$$

The key property of the truncated likelihood is that it is completely free of the nuisance parameter γ. Intuitively, this is because for each pair ij that generates a nonzero outcome Y_{ij} and is included in $\mathcal{A}$, we can deduce that there is an underlying relationship such that $R_{ij} = 1$. Given this fact, the distribution $\mathbb{P}_{\theta,V}(R_V \mid X_V)$ is irrelevant to the distribution of $Y_V^{\mathcal{A}}$. Because the factors in Equation 12 are the zero-truncated probabilities of the outcomes Y_{ij} in $Y^{\mathcal{A}}$, we call $\mathbb{P}^{tr}_{\beta,V}(Y_V \mid X_V)$ the *truncated likelihood*. To estimate β, we calculate the maximizer of the truncated likelihood with respect to β, which we write as $\hat{\beta}^{tr}_V$, and call this the *maximum truncated likelihood estimator*, or MTLE.

This estimation procedure is a simple application of partial likelihood estimation (Cox, 1972, 1975; Wong, 1986). The MTLE $\hat{\beta}^{tr}_V$ is also the MLE for β under a slightly modified data model. In the original observation model, the investigator chooses an actor-set V and observes all pairwise outcomes Y_V among those actors; in the alternative data model the investigator only observes the non-zero outcomes in $Y_V^{\mathcal{A}}$, and does not observe the rest of the actor pairs, including the total number of actor pairs $\binom{|V|}{2}$. We define the effective estimand of the MTLE $\bar{\beta}^{tr}_V$ in the same way that we did for the MLE of the full data model. Formally, the maximum truncated likelihood estimator of $\hat{\beta}^{tr}_V$ and its effective estimand $\bar{\beta}^{tr}_V$ are

$$\hat{\beta}^{tr}_V = \arg\max_\beta \log \mathbb{P}^{tr}_{\beta,V}(Y_V \mid A_V) \qquad \text{and } \bar{\beta}^{tr}_V = \arg\max_\beta \mathbb{E}_0 \log \mathbb{P}^{tr}_{\beta,V}(Y_V \mid A_V). \tag{13}$$

6.2 Invariance of the truncated estimator

Here we show that the MTLE $\hat{\beta}_V^{tr}$ has an effective estimand that does not in general depend on the sparsity of the process $Y_{\mathbb{V}}$, making it a promising candidate for answering superpopulation inquiries about sparse social processes in the CIR class. In fact, when the model family $\mathcal{P}_{\Theta,\mathbb{V}}$ includes a correct specification for the the conditional process $\mathbb{P}_\beta(Y_{\mathbb{V}} \mid X_{\mathbb{V}}, R_{\mathbb{V}})$, the MTLE $\hat{\beta}_V^{tr}$ satisfies Criterion 1.

Theorem 4 (Invariance of Truncated Estimator)**.** *Let $Y_{\mathbb{V}}$ is a random graph process, $\mathbb{P}_{0,\mathbb{V}}$ be the true distribution of the process, and $\mathcal{P}_{\Theta,\mathbb{V}}$ be a model family proposed by the investigator. Assume the following*

(T1) The finite-dimensional distributions of $Y_{\mathbb{V}}$ can be factorized as in Equation 9 for all sample indices V.

(T2) The model family $\mathcal{P}_{\Theta,\mathbb{V}}$ correctly specifies the conditional process $\mathbb{P}_{0,\mathbb{V}}(Y_{\mathbb{V}} \mid X_{\mathbb{V}}, R_{\mathbb{V}})$, so that there exists a $\beta_0 \in B$ such that for all ij, $\mathbb{P}_{\beta_0,\mathbb{V}}(Y_{ij} \mid X_{ij}, R_{ij}) = \mathbb{P}_{0,\mathbb{V}}(Y_{ij} \mid X_{ij}, R_{ij})$.

(T3) The model family $\mathcal{P}_{\Theta,\mathbb{V}}$ is specified so that β is identified by the truncated data $(Y_V^{\mathcal{A}}, X_V^{\mathcal{A}})$.

Then the effective estimand of the MTLE does not depend on V and, in particular, $\bar{\beta}_V^{tr} = \beta_0$ for all V.

Proof. Applying the law of total expectation, we split Equation 13,

$$\bar{\beta}_V^{tr} = \arg\max_\beta \mathbb{E}_0 \sum_{ij \in \mathcal{A}} [\log \mathbb{P}_\beta(Y_{ij} \mid X_{ij}, A_{ij} = 1)] \tag{14}$$

$$= \arg\max_\beta \mathbb{E}_0 \left[\mathbb{E}_0 \left[\sum_{ij \in \mathcal{A}} \log \mathbb{P}_\beta(Y_{ij} \mid X_{ij}, A_{ij} = 1) \,\middle|\, \mathcal{A} \right] \right]. \tag{15}$$

By the correct specification assumptions (T1) and (T2), the truncated likelihood derived $\mathcal{P}_{\Theta,\mathbb{V}}$ is correctly specified for $\mathbb{P}_{0,V}(Y_V \mid X_V, A_V)$. Thus, the inner conditional expectation in Equation 15 is maximized by the same value β_0 for all values of A_V, and the entire expression in Equation 15 is maximized by β_0. If this were not the case, so that Equation 15 were maximized by some other value $\tilde{\beta} \neq \beta_0$, by (T3), all terms of the implicit sum in the outer expectation could be increased by switching the argument of the maximization to β_0, yielding a contradiction. Thus, the effective estimand is equal to β_0 for all V. □

Remark 4. *The identification assumption (T3) excludes several cases where the truncated estimator $\hat{\beta}_V^{tr}$ would be meaningless, for example, cases where the outcomes in Y_V are binary such that $Y_{ij} = A_{ij}$ for all ij. In this case, all parameter values β would yield identical truncated likelihood*

functions for the data $(Y_V^{\mathcal{A}}, X_V^{\mathcal{A}})$ *because the zero-truncated distribution for each* $Y_{ij} \in Y_V^{\mathcal{A}}$ *would be degenerate.*

Although the correct specification conditions (T1) and (T2) in Theorem 4 are strong, this does not make the theorem trivial. The conditions isolate sparsity misspecification as a potential source of instability in the sense of Criterion 1. If we were to use the MLE of a sparsity misspecified CIR model, even if conditions (T1) and (T2), by Corollary 1, misspecification in the remaining components of the model would be sufficient to induce a violation of the invariance required by Criterion 1. On the other hand, Theorem 4 puts no requirements on the sparsity of Y_V or the range of sparsity rates that the model family $\mathcal{P}_{\Theta,\mathbb{V}}$ can represent. There may be other ways in which a truncated estimator $\hat{\beta}_V^{tr}$ could violate Criterion 1 – for example, the correct specification assumptions could be violated – an inadequate explanation for the sparsity of a social process Y_V is not one of them. We demonstrate the invariance of the truncated estimator in simulation studies and real data analysis in Section 7.

6.3 Statistical efficiency of the MTLE

The MTLE $\hat{\beta}_V^{tr}$ achieves robustness to the sparsity of the social process Y_V by modeling less of the data than the investigator has available. This choice necessarily comes at the cost of statistical efficiency. In this section, we examine the worst-case efficiency loss that could be incurred from using the truncated estimator $\hat{\beta}_V^{tr}$ instead of an idealized full-likelihood "oracle" estimator $\hat{\beta}_V^{or}$ that is provided full knowledge of the sample relationship graph R_V. We study the case where the correct specification and identification assumptions (T1)–(T3) hold and we compute the oracle estimator $\hat{\beta}_V^{or}$ using the true the relationship graph R_V for all V, so that the only relevant parameters in the estimation problem are the parameters of interest β that characterize the conditional process $\mathbb{P}_{\mathbb{V}}(Y_{\mathbb{V}} \mid R_{\mathbb{V}}, X_{\mathbb{V}})$.

In this section, we evaluate the efficiency of the estimators $\hat{\beta}_V^{or}$ and $\hat{\beta}_V^{tr}$ in terms of Fisher Information, making use of asymptotic arguments. We supplement these arguments with with finite-sample simulation studies in Section 7.2.

For convenience, we define the following quantities:

$$p_{\beta,V}^{ij} = \mathbb{P}_{\beta,V}(A_{ij} = 1 \mid X_{ij}, R_{ij} = 1) \tag{16}$$

$$l_{\beta,V}^{ij}(Y_V^{ij}) = \log \mathbb{P}_{\beta,V}(Y_{ij} \mid X_{ij}, R_{ij} = 1) \tag{17}$$

These are, respectively, the probability that a given dyad has an observed nonzero interaction value, and the log-likelihood of the outcome of a single dyad, given that the dyad has an underlying relationship.As with previous notation, we write the true superpopulation analogues of these quantities with a subscript 0 instead of β.

Under the assumption that the relationship graph R_V is fully available, all dyads ij for which $R_{ij} = 0$ (i.e., that have no relationship) are deterministically zero, and therefore contribute nothing to either the oracle or truncated likelihood. Letting $\mathcal{R} = \{ij : R_{ij} = 1\}$, we rewrite the oracle and truncated log-likelihoods for a whole sample Y_V:

$$\mathbb{P}^{tr}_{\beta,V}(Y_V \mid X_V) = \sum_{ij \in \mathcal{R}} A_{ij}(l^{ij}_{\beta,V}(Y^{ij}_V) - \log p^{ij}_{\beta,V}) \tag{18}$$

$$\mathbb{P}^{or}_{\beta,V}(Y_V \mid X_V, R_V) = \sum_{ij \in R} \left[A_{ij} \log p^{ij}_{\beta,V} + (1 - A_{ij}) \log(1 - p^{ij}_{\beta,V})\right] + \mathbb{P}^{tr}_{\beta,V}(Y_V \mid X_V). \tag{19}$$

The first equation follows from the identity $\mathbb{P}_\beta(Y_{ij} \mid X_{ij}, A_{ij} = 1) = \mathbb{P}_\beta(Y_{ij} \mid X_{ij}, R_{ij})/\mathbb{P}_\beta(A_{ij} = 1 \mid X_{ij})$, which holds for all $ij \in \mathcal{A}$.

The Fisher Information matrices for the truncated and oracle estimators are, respectively:

$$\mathcal{I}^{tr}_{\beta,V} = -\left[\sum_{ij \in \mathcal{R}} p^{ij}_{0,V} \left(\mathbb{E}_0(\nabla^2_\beta \, l^{ij}_{\beta,V}(Y_{ij}) \mid A_{ij} = 1) - \nabla^2_\beta \log p^{ij}_{\beta,V}\right)\right] \tag{20}$$

$$\mathcal{I}_{\beta,V} = -\left[\sum_{ij \in \mathcal{R}} p^{ij}_{0,V} \, \nabla^2_\beta \log p^{ij}_{\beta,V} + (1 - p^{ij}_{0,V}) \, \nabla^2_\beta \log(1 - p^{ij}_{\beta,V})\right] + \mathcal{I}^{tr}_{\beta,V}. \tag{21}$$

Quite intuitively, the truncated procedure ignores information from two sources: the sample size lost by reducing the observed outcomes from Y_V to $Y^{\mathcal{A}}_V$, and the identification lost by discarding the indicators $\{A_{ij} : R_{ij} = 1\}$ The ignored information expression in Equation 21 scales as the number of relationships in the sample $\sum_{ij} R_{ij}$, whereas the information from the truncated likelihood $\mathcal{I}^{tr}_{\beta,V}(Y_V)$ scales as $\sum_{ij} p^{ij}_{0,V} R_{ij}$, or the expected number of nonzero outcomes in the sample Y_V. Thus, we can establish the following statement about the asymptotic fraction of ignored information, and thus lost efficiency, when using the truncated estimator $\hat{\beta}^{tr}_V$ over the oracle estimator $\hat{\beta}^{or}_V$ in this setting.

Theorem 5 (Efficiency loss of the truncated estimator.)**.** *Assume the following conditions hold for all increasing sequences of actor-sets (V_n) from $\mathbb{V}$.*

(E1) For all V_n, $\left(\mathbb{E}_0(\nabla^2_\beta \, l^{ij}_{\beta_0,V}(Y_{ij}) \mid A_{ij} = 1) - \nabla^2_\beta \log p^{ij}_{\beta_0,V}\right) > C_{tr}$ for some constant positive definite matrix C_{tr} for all $ij \in \mathcal{R}$.

(E2) $\frac{\sum_{ij} R_{ij} p^{ij}_{0,V}}{\sum_{ij} R_{ij}} \to c_{size}$ for some constant scalar $c_{size} > 0$.

(E3) The model family $\mathcal{P}_{\Theta,\mathbb{V}}$ is specified such that for all ij in all V_n, $\mathbb{E}_0 \nabla^2_\beta \log p^{ij}_{\beta_0,V_n}$ and $\mathbb{E}_0 \nabla^2_\beta \log(1 - p^{ij}_{\beta_0,V_n})$ are both bounded from above by some finite constant positive definite matrix C_{bin}.

Then the truncated and oracle estimators accumulate information at the same rate but differ by a constant factor. Specifically, $\lim_{n\to\infty} \mathcal{I}^{tr}_{\beta_0,V_n} (\mathcal{I}_{\beta_0,V_n})^{-1} \geq \left(I + (c_{size} C_{tr})^{-1} C_{bin}\right)^{-1} > 0$.

Under conditions (E1)–(E3) the result is straightforward. (E1) requires that each dyad provide some information under the truncated likelihood if it generates a nonzero outcome. (E2) requires that the expected number of nonzero outcomes grow proportionally to the number of relationships in R_{V_n}, so that the effective sample sizes incorporated into each estimator remain proportional to each other. (E3) requires that the information provided by the indicators $\{A_{ij} : R_{ij} = 1\}$ not be too large. These conditions ensure that the information ignored by the truncated likelihood does not dominate the total information available to the oracle likelihood.

Theorem 5 establishes a worst case scenario for efficiency loss from the truncated estimator. However, in application, the sparsity of a social process only presents difficulties if the relationship graph R_V is not known. Thus, in cases where an investigator would have reason to use the truncated estimator $\hat{\beta}_V^{tr}$, the relative efficiency of the truncated estimator with respect to a full-likelihood alternative that sums over a distribution for R_V would be strictly better than the limit established in Theorem 5. Taken together, the instability of full-likelihood estimators shown in Corollary 1, the invariance of the truncated estimator shown in Theorem 4, and the constant relative efficiency bound of the truncated estimator shown in Theorem 5, make a compelling case for the robustness-efficiency tradeoff made by the MTLE in superpopulation investigations.

6.4 Other properties of the MTLE

6.4.1 Single-sample properties

For a superpopulation estimator to be useful, it should still have good single-sample properties as well. Several parts of the statistical literature are relevant to establishing single-sample properties of the truncated estimator, including the partial-likelihood literature (Cox, 1972, 1975; Wong, 1986), the conditional likelihood literature (Lindsay, 1980; Andersen, 1970; Godambe, 1976), and more specific discussion of truncated data models, e.g., (Gelman, 2004).

6.4.2 Computational properties

Computation of the MTLE is highly efficient, because computation of the truncated likelihood in Equation 12 only requires the nonzero outcomes $Y_V^{\mathcal{A}}$ as opposed to the full set of $\binom{|V|}{2}$ outcomes required by full likelihood methods. For sparse social processes, this implies that the computational cost of the truncated estimator grows at a slower rate than the computational cost of a full-likelihood estimator as we analyze larger and larger social network data – in fact, the ratio of computational cost rates here is upper-bounded by the sparsity rate $\epsilon_0(n)$ of the social process Y_V. This makes the truncated estimator a practical tool for analysis of modern massive social network data.

7 Simulated and Real Data Examples

In this section, we make the arguments of the paper concrete with real and simulated data. The examples here are meant to replicate aspects of the data analysis project that was the motivation for this work in the setting first described in Section 1.1. Originally, the goal of the project was the perform a comparative analysis of inventor collaboration networks across time periods and regions of the United States using data from the US patent record assembled by Li et al. (2014). Because the outcomes in Y_V in this dataset are recorded as sequences of timestamps, we chose the counting process regression model described in Perry and Wolfe (2013), which has strong theoretical support for use in single-sample investigations. However, because the model is a sparsity-misspecified member of the CID class described in Section 4.3, the estimates obtained showed strong signs of violating Criterion 1 that one would expect given Theorem 2.

7.1 Model specification

Under the counting process regression model of Perry and Wolfe (2013), a set of actors V are observed for a time interval of length T. The individual pairwise outcomes $Y_{ij} \in Y_V$ are represented as counting processes $Y_{ij}(\cdot)$ with instantaneous hazard given by a GLM specification:

$$\log \lambda_{ij}(t) = \beta' X_{ij}(t). \tag{22}$$

In this case, $X_{ij}(t)$ represent covariates associated with each pair which may depend on time, and which may include aspects of the history of the counting process itself. Conditional on the relationship graph R_V, log-likelihood for β under this model is:

$$\mathbb{P}_{\beta,V}(Y_V \mid X_V, R_V) = \sum_{ij \in R_V} \left(- \int_0^T \lambda_{ij}(s \mid \mathcal{F}_s) ds \right) + \sum_{k=1}^{Y_{ij}(T)} \log \lambda_{ij} \left(t_{ij}^{(k)} \mid \mathcal{F}_{t_{ij}^{(k)}} \right), \tag{23}$$

where $t_{ij}^{(k)}$ is the time of the kth observed interaction between actors i and j. Likewise, the truncated log-likelihood for β has the form

$$\begin{aligned} \mathbb{P}^{tr}_{\beta,V}(Y_V^{\mathcal{A}} \mid X_V^{\mathcal{A}}) = \sum_{ij \in \mathcal{A}} & \left(- \int_0^T \lambda_{ij}(s \mid \mathcal{F}_s) ds \right) + \sum_{k=1}^{Y_{ij}(T)} \log \lambda_V^{ij} \left(t_{ij}^{(k)} \mid \mathcal{F}_{t_{ij}^{(k)}} \right), \\ & - \log \left(1 - \exp \left(- \int_0^T \lambda_V^{ij}(s \mid \mathcal{F}_s^0) ds \right) \right) \end{aligned} \tag{24}$$

where $\mathcal{F}_s^0$ is the history that would have been induced if no interactions had taken place between actors i and j before time s.

Recall that the patent database also includes inventor-specific information including the zip code of

their residence at the time of submitting a patent application, and the firm that they worked for at the time of the patent application (called an "assignee"). Using these attributes, we define binary covariate vectors for each pair of actors that report whether the actors live in the same zip code, or work for the same assignee. At each time t, we also keep track of whether the actors have had previous collaborations. We denote these pairwise covariates as `Zip`, `Asg`, and `prev`, respectively.

7.2 Simulated counting process examples

We begin with simulated data. The first purpose of this simulation is to demonstrate the moving target phenomenon from Theorem 2 under sparsity misspecification, by showing instability in the effective estimand, and the corresponding instability in the MLE. The second purpose is to demonstrate the robustness of the truncated estimator to sparsity misspecification, both in terms of the invariance of the effective estimand of the MTLE and the behavior of the MTLE itself. The final purpose is to explore the properties of the truncated estimator more generally, using a full factorial design to explore how the efficiency and coverage properties of the truncated estimator and its corresponding asymptotic confidence interval depend on the underlying generative parameters. The results of the factorial experiment speak to the applicability of the asymptotic results in Section 6.3 to finite sample data analysis problems.

We simulate from a sparse CIR process in which the non-zero outcomes follow the counting process model described above. We make the simulated CIR model sparse by introducing an ordering on all of the vertices in the actor population $\mathbb{V}$, and assuming that for any actor pair ij, the baseline probability of having a relationship ρ_{ij} is decreasing in the the population index of lower-indexed actor i. We denote dependence on this global population index by subscripting with the population $\mathbb{V}$.

For a given actor-set V, the formal specification of the data simulation process is as follows:

$$\begin{aligned} R_{ij} \mid X_{ij} &\sim \text{Bin}(\rho_{ij}) \\ \text{logit}\, \rho_{ij} &\equiv \gamma_0 \,\text{logit}(\alpha_{\mathbb{V}}(i)) + \gamma_1 \cdot \texttt{Zip}_{ij} + \gamma_2 \cdot \texttt{Asg}_{ij} \\ Y_{ij}(t) \mid R_{ij}, X_{ij}, \mathcal{F}(t) &\sim \begin{cases} CP(\lambda_{ij}(t)) & \text{if } R_{ij} = 1 \\ 0(t) & \text{if } R_{ij} = 0 \end{cases} \\ \log \lambda_{ij}(t) &\equiv \beta_0 + \beta_1 \cdot \texttt{Zip}_{ij} + \beta_2 \cdot \texttt{Asg}_{ij} + \beta_3 \cdot \texttt{prev}_{ij}(t). \end{aligned} \tag{25}$$

Recall that `Zip` and `Asg` are indicators for whether actors i and j live in the same zip code or work for the same firm, respectively, and `prev` is an indicator for previous collaboration, i.e., $Y_{ij}(t) > 0$. γ is a vector of relationship process coefficients, while $\alpha_{\mathbb{V}}(i)$ is a function of i that approaches 0 as the actor-population index $i \to \infty$, and controls the sparsity of the generating process by making the relationship graph ever sparser as individuals with higher actor-population indices are included

in the sample.

Both γ and $\alpha_{\mathbb{V}}(i)$ are considered nuisance parameters in this case. β is a vector of conditional interaction process coefficients, which are the parameters of interest. In these simulations, we test our ability to recover β using full-likelihood estimator that make various assumptions about the generating process, and thus the sparsity rate, of $R_{\mathbb{V}}$ and the truncated likelihood estimator $\hat{\beta}_V^{tr}$. For each of the competing estimators, we have a correctly specified conditional outcome process $\mathbb{P}_{\beta,V}(Y_V \mid R_V, X_V)$.

We generate a network of size $n = 2000$ in which we observe 2000 interactions. From this network, we generate a sequence of subsamples by randomly choosing an assignee, then adding all vertices with this assignee attribute to the sample. This is meant to simulate a cluster-sampling design where firms are drawn randomly from the set of all firms and all employees are added to the network sample. Fixing this sample sequence, we regenerate the network 100 times to create 100 replications.

7.2.1 Moving target sensitivity and robustness

To demonstrate the moving target behavior derived in Theorem 2, we focus on a single set of simulation parameters. Here, we set $\alpha_{\mathbb{V}}(i) = \log(i)/i$, $\gamma = (0.02, 1, 2)$, and $\beta = (1e-5, 0, 0.2, 3)$. Thus, the expected *relationship* degree for actor i in the population $\mathbb{V}$ goes as $\log(i)/i$, with relationships concentrated more heavily between individuals in the same zip code and working for the same assignee. Conditional on these relationships, we assume zip code has no effect on the frequency of interactions between individuals who have a relationship, while assignee has a small positive effect on this frequency and having at least one previous collaboration has a large positive effect on this frequency.

Meanwhile, we apply the MLE of a model family that assumes the risk process R_V is fully connected for all V, corresponding to the popular GLM approach of vectorizing the data Y_V and treating each pair ij as conditionally independent given the covariates X_V. This was the specification used in Perry and Wolfe (2013). For each subsample generated by the sequence above, we compute the effecive estimand of the misspecified model in addition to the MLE $\hat{\beta}_V$ and MTLE $\hat{\beta}_V^{tr}$. We repeat this for each of the 100 replications. We plot these against the true values of β in Figure 4.

The simulations highlight several results from the discussion above. The effective estimands of the misspecified models show the moving target behavior predicted in Theorem 2, and particularly in Theorem 3, as the variation in the effective estimand holds regardless of the sequence of actor-sets chosen. The sampling distributions of the estimators at each sample size also concentrate around their effective estimands. Finally, the effective estimand of the MTLE is the true value of β for all sample sizes, and the MTLE sampling distribution shows no sensitivity to the sparsity of the

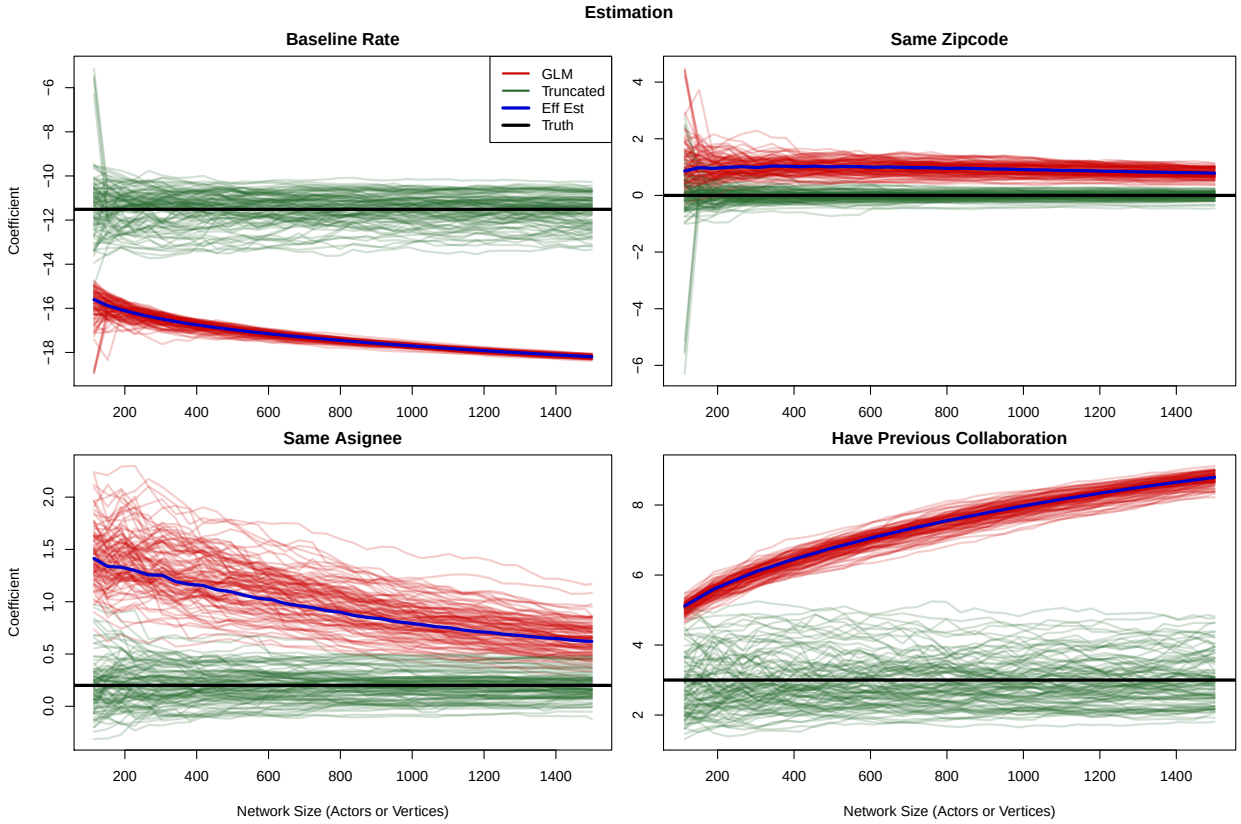

Figure 4: Plots of the sampling distribution of sequences the MLE $\hat{\beta}_V$ computed from the sparsity misspecified counting process model (red), and the MTLE $\hat{\beta}_V^{tr}$ computed from the truncated model (green) from samples of differing size. We also plot the effective estimand for the misspecified model (blue) and the true values of β (black).

population process, as predicted in Theorem 4.

7.2.2 Efficiency and coverage of truncated estimator

We also use this simulated example to demonstrate the efficiency and coverage properties of the truncated estimator and its corresponding asymptotic confidence interval in both the finite sample and large-sample limit. For this demonstration, we expand the above simulation to a full factorial design over the interaction parameter space B and the space of network sample sizes. Using the same simulation design as above, we fix each of the β coefficients corresponding `Zip`, `Asg`, and `prev` at one of four levels while keeping the intercept coefficient fixed across all runs, yielding 64 design points. We generate 100 replicated datasets at each design point, and within each experimental run, we obtain estimates from 8 nested samples of increasing sample size. We assess the efficiency and coverage properties of the MTLE and its corresponding asymptotic confidence interval for each of the four components of β (`Intercept`, `Zip`, `Asg`, `prev`).

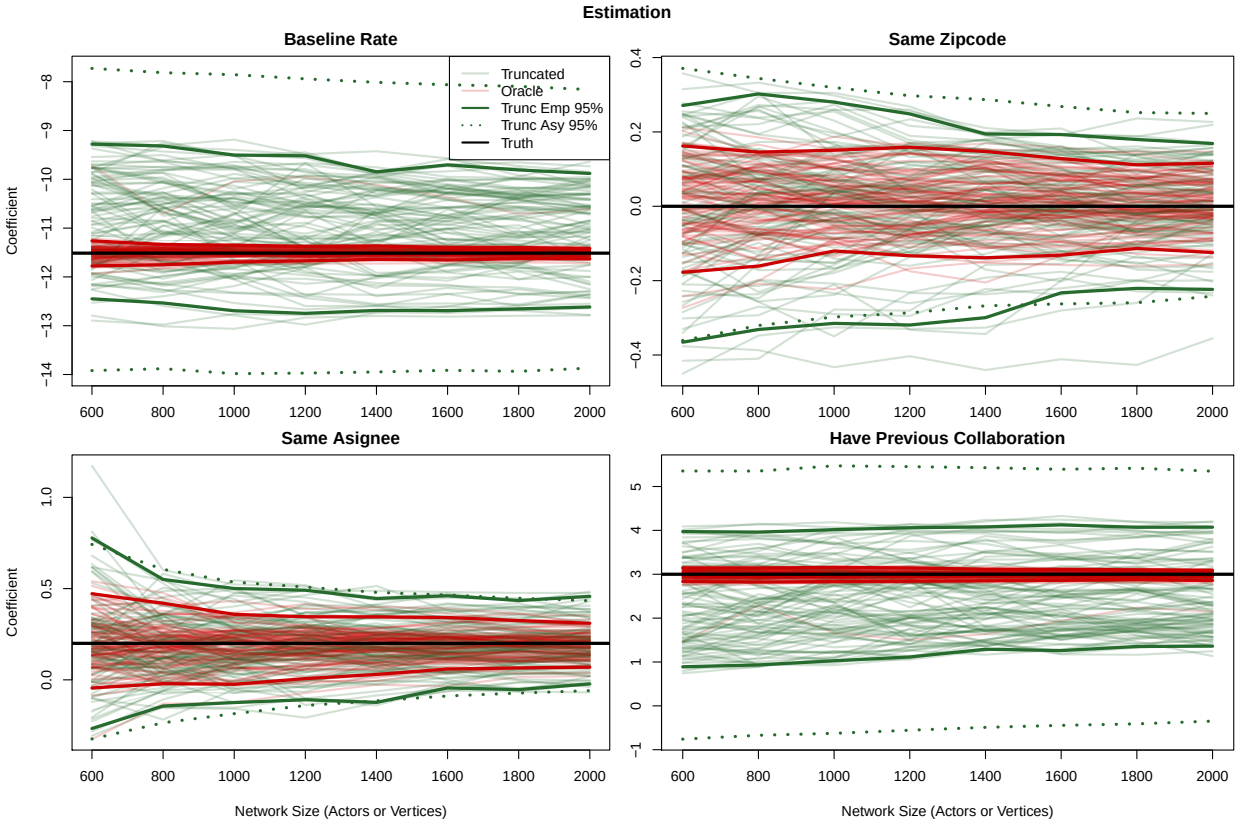

Figure 5: Plots of sampling distribution of sequences $\hat{\beta}_n$ computed from the truncated model (green) and the oracle model (red). The oracle model has full knowledge of the risk set R and is computed using the full likelihood on this subset of dyads.

Efficiency. Following Section 6.3, we compute the variance inflation factor of the MTLE with respect to an oracle estimator given by the MLE when the risk set is fully known. For finite sample sizes, we compute this inflation factor from the outputs of the factorial experiment. The simulation yields draws from the sampling distributions of the truncated and oracle estimators for each component of β at each design point and sample size. To compute the variance inflation factor, we take the ratio of the sampling distribution variances of the two estimators at each design point and sample size. The full output of the simulation at one design point, with coefficients for $(\texttt{Zip}, \texttt{Asg}, \texttt{prev})$ set to $(0, 0.2, 3)$, is shown in Figure 5 as an example. As expected, the sampling distributions of estimates from the oracle estimator are more concentrated than those of the truncated estimator at all sample sizes.

Because this example is analytically tractable, we also compute the large-sample limiting variance inflation factor for each parameter combination by computing the limit of the inverse Fisher information matrix. We assume that zip code and assignee sizes remain fixed while the number of actors in the network grows to infinity, so dyads that match on neither zip code nor assignee (i.e. $\texttt{Zip}_{ij} = 0$ and $\texttt{Asg}_{ij} = 0$) dominate the limiting sample, yielding convenient simplifications. Details

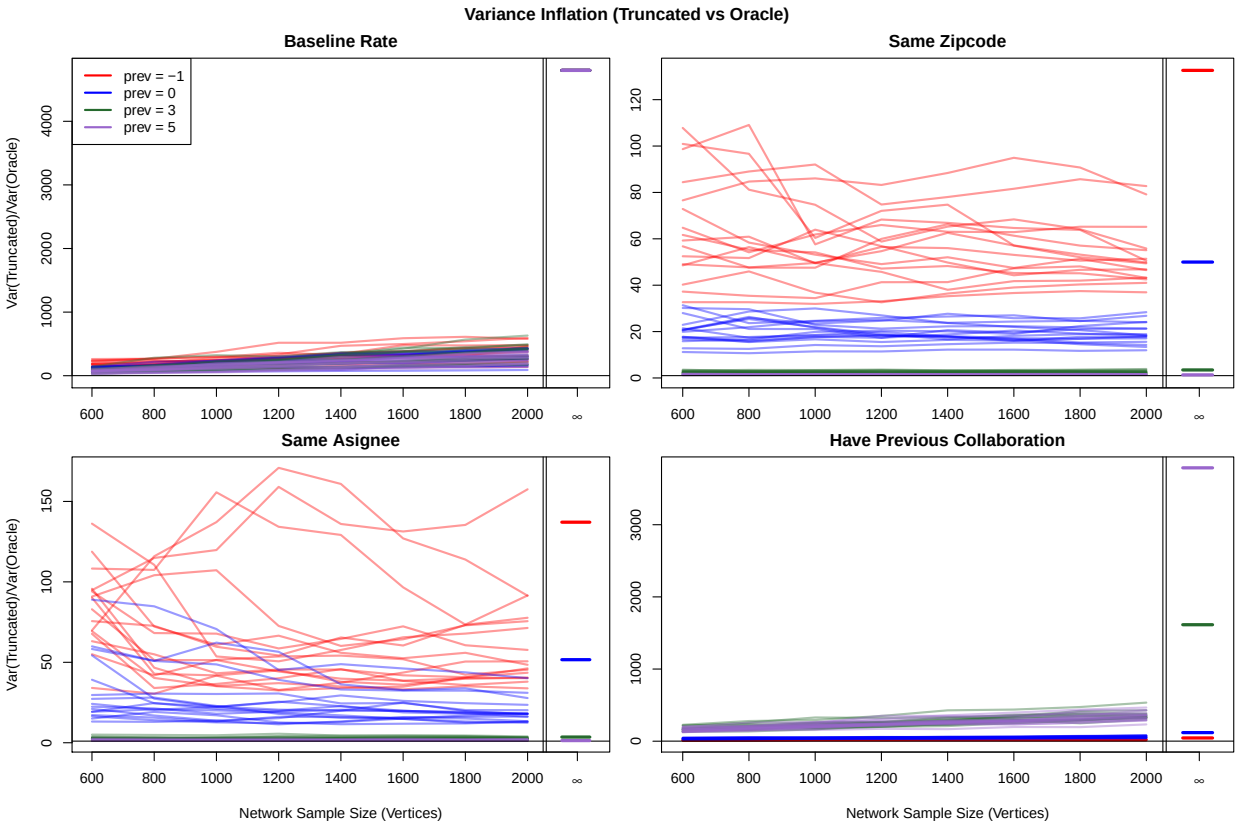

Figure 6: Variance inflation factors resulting from the comparison of the truncated estimator's sampling distribution to the oracle estimator. Lines are colored by the value of the `prev` coefficient, which shows the most influence on the efficiency of the non-intercept coefficients. For each value of `prev`, the largest limiting variance inflation factor among all remaining parameter configurations is shown on the right. These are computed from the limit of the inverse of the Fisher information matrix. Note that the variance inflation of the intercept is the same for all parameter combinations.

of this calculation, as well as a table of limiting variance inflation factors at each design point are given in the appendix.

The results in Figure 6 confirm the theory in Section 6.3. First, while in many cases the variance inflation factor is relatively large, it is finite in the large sample limit in all cases. Secondly, the scale of the variance inflation factors confirm that information is lost through both a loss of sample size and a loss of identification. In this particular case, the intercept, `Zip`, and `Asg` coefficients all lose efficiency because the truncated procedure drops all at-risk dyads with zero observed interactions. However, there is a greater loss of efficiency for the intercept and `prev` coefficients because all of the dyads dropped by the truncated procedure provide the oracle procedure with information about the intercept coefficient that is unconfounded with the `prev` coefficient. With the truncated procedure, these two coefficients are much more weakly identified by the time intervals before the first observed collaboration among the included dyads. This loss of identification is by far the larger effect, resulting in large variance inflation factors for the intercept and `prev` coefficients. Because

the intercept is affected by both forms of information loss, it has the largest variance inflation factor.

As noted in Section 6.3 the variance inflation factors computed with respect to the oracle estimator represent an upper bound on the variance inflation one would obtain from a realistic full likelihood estimator, which would require summation over the missing relationship indicators R_V using a model that is not sparsity misspecified. Assuming such a prior were available, the variance inflation of the truncated estimator with respect to the full-likelihood procedure would depend on the fraction of missing information implied by this model, with variance reduction coming at the cost of sensitivity to sparsity misspecification.

Coverage. Her we study the finite-sample coverage properties of the MTLE's asymptotic confidence interval, computed from the inverse of the observed Fisher information matrix $\mathcal{I}^{tr}_{\hat{\beta}^{tr}_V, V}$. This asymptotic interval is guaranteed to achieve nominal coverage in the large sample limit. For each of the 100 replications at each design point and sample size we check whether the asymptotic 95% intervals for each of the four parameters cover the true value and use logistic regression to quantify the sensitivity of the coverage rate to the true parameter values.

Table 1 shows the example output coverage table for the design point with coefficients for (`Zip`, `Asg`, `prev`) set to $(0, 0.2, 3)$. In the replications at this design point, the asymptotic confidence intervals show under-coverage for the baseline and `prev` coefficients, while the intervals for the `Zip` and `Asg` coefficients remain close to nominal coverage levels. We summarize the sensitivity of coverage rates to parameter values in analysis of deviance tables for each parameter estimator. These tables summarize how much of the deviance in the logistic regression fit can be explained by the levels of the underlying parameters and their interactions. We use these informally to highlight the relative magnitude of coverage variabilities across design points. The exact values in these tables, particularly the p-values, should not be taken at face value because the logistic regression analysis performed here did not account for the nesting of samples of different size into increasing sequences, and because the ordering of the covariates, which influences the deviance statistics associated with each parameter class, was chosen arbitrarily. We present the analysis of deviance table for the intercept coefficient estimator in Table 2 and reserve the remaining three tables for the appendix. In Table 2 the `prev` coefficient explains substantially more deviance than the other parameters or interactions. This pattern holds for the estimators for the remaining three coefficients.

The coverage rates associated with each value of the `prev` coefficient for each of the four estimators is shown in Figure 7. As suggested from the analysis of deviance table, the variability within each true `prev` value (boxplot length) is relatively small compared to the variability between these values (boxplot position). While the coefficient estimators for the `Zip` and `Asg` covariates show little sensitivity to the true value of the `prev` coefficient, the estimators for the intercept and `prev` coefficients show strong sensitivity, with coverage decreasing significantly when the true previous collaboration coefficient becomes large. This phenomenon is related to the discussion of efficiency above. Under

Table 1: Coverage rates using the 95% asymptotic confidence interval from the truncated procedure. Note that coefficients that are partially confounded under the truncation procedure show undercoverage.

	600	800	1000	1200	1400	1600	1800	2000
Base	0.74	0.76	0.77	0.83	0.79	0.84	0.85	0.87
Zip	0.96	0.96	0.97	0.95	0.95	0.95	0.94	0.93
Asg	0.99	0.93	0.95	0.95	0.97	0.96	0.98	0.97
Before	0.73	0.77	0.77	0.82	0.77	0.82	0.84	0.86

Table 2: Analysis of deviance table for intercept coefficient, summarizing deviance explained by the levels of parameter values and interactions when asymptotic confidence interval coverage was modeled using a logistic regression. The coverages rates show strong sensitivity to the level of the `prev` coefficient. This table is meant for informal analysis as the logistic regression model does not take into account the nested generation mechanism employed in the simulations and uses an arbitrary ordering of the covariates.

	Df	Deviance	Resid. Df	Resid. Dev	Pr(>Chi)
NULL			50039	34911.1	
asg	3	121.00	50036	34790.1	4.70E-26
zip	3	41.83	50033	34748.3	4.36E-09
prev	3	1740.57	50030	33007.7	0.00E+00
size	7	16.87	50023	32990.8	0.018
asg:zip	9	50.75	50014	32940.1	7.80E-08
asg:prev	9	55.12	50005	32885.0	1.15E-08
zip:prev	9	36.20	49996	32848.8	3.65E-05
asg:size	21	10.53	49975	32838.3	0.971
zip:size	21	4.36	49954	32833.9	1.000
prev:size	21	14.43	49933	32819.5	0.851
asg:zip:prev	27	77.30	49906	32742.2	9.62E-07
asg:zip:size	63	22.21	49843	32720.0	1.000
asg:prev:size	63	30.39	49780	32689.6	1.000
zip:prev:size	63	21.99	49717	32667.6	1.000
asg:zip:prev:size	189	73.31	49528	32594.3	1.000

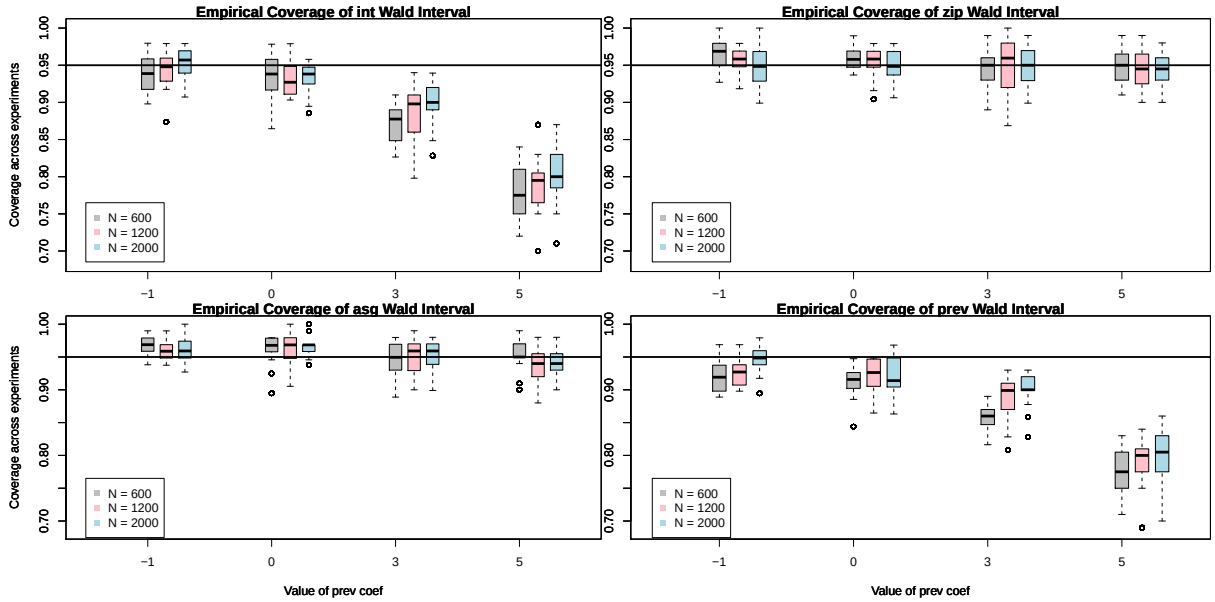

Figure 7: Coverage of 95% asymptotic confidence intervals computed using a full factorial design. Coverage was mostly sensitive to the level of the `prev` coefficient, which controls how much interaction frequency increases when a previous interaction has occurred. The truncation mechanism drops a portion of that data that uniquely informs the intercept coefficient without confounding this effect with the `prev` coefficient. For large values of `prev`, confounded information for the intercept and `prev` coefficients accumulates more quickly but the finite sample bias from the portion of the truncated estimator that separates the coefficients decreases at the same rate, resulting in under-coverage. As sample size increases, this under-coverage slowly dissipates as the finite sample bias decreases.

the truncated procedure, the information about the intercept and previous collaboration coefficients is largely confounded. The only information that separates these coefficients comes from the time intervals before collaborations are observed on each dyad in $Y_V^{\mathcal{A}}$. For larger values of the true `prev` coefficient, the confounded post-collaboration information accumulates more quickly, narrowing the intervals for both estimators, while the rate of information accumulation that separates the two coefficient accumulates at the same rate, keeping the finite sample bias the same. It is also possible to lose identification of `prev` and for the MTLE to break down for certain configurations of the data. We describe this breakdown point in the Appendix. See Figure 5 for an illustration of this confounding and finite sample bias. As the number of actors in the sample grows, this finite sample bias slowly dissipates and the asymptotic intervals approach nominal coverage in the limit. Figure 7 shows evidence of this slow dissipation as well.

7.3 Real data analysis

Finally, we return to the data analysis first presented in Section 1.1. The parameter estimates in Figure 1 show the results of fitting the Perry and Wolfe (2013) point process model (modified to include an intercept term) in a number of different metropolitan areas around the United States, using the real analogues of the `Asg` (indicator for i and j work for the same firm) and `prev` (indicator for i and j have collaborated before) covariates. As discussed in Section 1.1, the estimates from the naïve GLM show a strong dependence on the size of the sample that is confounded with any true differences between regions.

The results from using the truncated estimator $\hat{\beta}_V^{tr}$ obtained by maximizing Equation 24 are shown on the right of the figure. These estimates show no strong systematic dependence on the size of the sample. Put simply, the truncated estimator appears to be measuring an aspect of the patent collaboration process that is actually comparable across regions, and, as opposed to the highly sample-size-dependent, overconfident estimates on the left side of the figure, invite interpretation by social scientists.

8 Discussion

Data generated by social network processes have a number of idiosyncrasies that make the application of classical statistical frameworks difficult: there is dependence between outcomes, there is strong inhomogeneity in sample size, and accurate models are difficult to specify. Answering questions about these social processes with statistical approaches thus requires the investigator to wrestle with several foundational statistical issues at once. In this paper, we attempted to lay out several of these issues and follow their implications on an investigator's ability to make a scientifically coherent argument about the process of interest. In particular, we showed that if an investigator is interested in a network superpopulation, they should be extremely careful about sparsity misspecification, and that this problem that is not easily diagnosed using theoretical tools developed for single-sample problems. We also provided a simple methodology that allows investigators to avoid sparsity misspecification entirely, in exchange for answering a slightly different question about the superpopulation and a small hit in statistical efficiency.

Regarding the specific points of this paper, there are several loose ends that we wish to highlight. First, Although the theoretical results presented in this paper are specific to the MLE, they could be easily extended to more general model- or objective-function-based estimation procedures including GEE, M-estimation, and Bayesian approaches. D'Amour and Airoldi (2016) provides a more general construction of the effective estimand that could be applied to other types of estimation procedures. More general concentration results from Spokoiny (2012b) could also be helpful here.

Secondly, it may be the case that we took a methodological "coward's way out" in pivoting out of the sparsity misspecification problem by shifting the question to sparsity-invariant estimands rather than tackling the problem of modeling sparsity structure head-on. We do hope that in ongoing research such as Veitch and Roy (2015) and Crane and Dempsey (2015), more sophisticated probability models will be discovered that can address this need. However, even when these sparsity-compatible methodologies are applied, sensitivity to the specified sparsity rate still remains, and it seems that there is little information about this rate in individual samples Y_V. For this reason, we believe that the CIR class of models, the relationship-conditional estimand, and the MTLE that we have proposed give an attractive, and simple framework for summarizing an important aspect of network superpopulations. The computational properties of the MTLE make it an attractive option for investigating massive network data.

Finally, we also hope that our ultimate solution to use a partial likelihood approach for eliminating the sparsity process can serve as an example for work pertaining to estimation in the presence of high-dimensional nuisance parameters. Although this approach violates the likelihood principle, it provides an attractive way for statisticians and investigators who prefer parametric modeling approaches to investigate complex systems where not all parts of the data generating process is well-understood.

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Online supplementary material

A Proof of Lemma 1

Given Equation 7 and Equation 8, bounding the probability of events in terms of the the log proportional difference between observed and expected within- and between-firm collaboration counts, is especially convenient. We derive the probability bound for $\hat{\theta}_0$ explicitly, and the same formulation can be followed for $\hat{\theta}_1$.

$$\begin{aligned}
\mathbb{P}(|\hat{\theta}_0 - \bar{\theta}_0| \leq \log(1+\delta)) &\geq \mathbb{P}\left((1-\delta) \leq \left(\frac{\sum Y_i(1-X_i)}{\sum \mathbb{E}_0 Y_i(1-X_i)}\right) \leq (1+\delta)\right) \\
&= \mathbb{P}\left(\left|\sum Y_i(1-X_i) - \sum \mathbb{E}_0 Y_i(1-X_i)\right| \leq \delta \sum \mathbb{E}_0 Y_i(1-X_i)\right) \\
&\geq 1 - \frac{\mathbb{V}\mathrm{ar}_0\left(\sum Y_i(1-X_i)\right)}{\delta^2\left(\mathbb{E}_0 \sum Y_i(1-X_i)\right)^2} \\
&\geq 1 - \frac{d}{\delta^2 \mathbb{E}_0 \sum Y_i(1-X_i)},
\end{aligned}$$

where the penultimate step is an application of the Chebyshev inequality, and the final step applies assumption (B3) from Section 5.1.

For the other coefficient, we bound a similar deviation for the quantity

$$\widehat{(\theta_0 + \theta_1)} = \log\left(\frac{\sum \mathbb{E}_0 Y_i X_i}{\sum X_i}\right)$$

separately. This quantity has a rate related to the expected number of within-firm dyads:

$$\mathbb{P}(|(\widehat{(\theta_0+\theta_1)}) - (\bar{\theta}_0 + \bar{\theta}_1)| \leq \log(1+\delta)) \leq 1 - \frac{d}{\delta^2 \mathbb{E}_0 \sum Y_i X_i}$$

Combining these bounds, we obtain a deviation bound for $|\hat{\theta}_1 - \bar{\theta}_1|$

$$\begin{aligned}
\mathbb{P}(|\hat{\theta}_1 - \bar{\theta}_1| \leq \delta) \geq\ & 1 - \mathbb{P}(|\hat{\theta}_0 - \bar{\theta}_0| \geq \delta/2) \\
& - \mathbb{P}(|(\hat{\theta}_0 + \hat{\theta}_1) - (\bar{\theta}_0 + \bar{\theta}_1)| \geq \delta/2) \\
\geq\ & 1 - \frac{4C_1}{\delta^2 \mathbb{E}_0 \sum Y_i(1-X_i)} - \frac{4C_2}{\delta^2 \mathbb{E}_0 \sum Y_i X_i}.
\end{aligned}$$

B Breakdown point of truncated estimator for Point Process regression with "Previous Activity" covariate

The truncated point process regression model exhibits some fragility when it is fit using a previous activity" covariate (`prev`) that indicates whether a pair of actors have had at least one pairwise interaction in the past. This is because, for each pair of actors, at most one interaction can be observed in the $\texttt{prev} = 0$ state, but the truncated likelihood already conditions on the fact that one interaction will be observed during the observation period. Identification for this parameter comes from the waiting time until the first pairwise interaction is observed, specifically, the discrepancy between this waiting time distribution (which should be a uniform order statistic) and the uniform distribution over the observation period implied by the truncated model's conditioning. Heuristically, meaningful estimates can only be obtained if the expected waiting time in the $\texttt{prev} = 0$ state is substantially less than the expected waiting time under a uniform distribution; thus, the empirical expected waiting time in the $\texttt{prev} = 0$ must be less than half the length of the observation period $T/2$.

We can show this simply by examining the score equation from a single pair of actors in a simplified model where

$$\lambda_{ij}(t) = \beta_0 + \beta_1 \texttt{prev}. \tag{26}$$

Let T be the length of the total observation period, T_0 be the time spent in the $\texttt{prev} = 0$, and T_1 be the time spent in the $\texttt{prev} = 1$ state, so that $T = T_0 + T_1$. Let Y be the total number of observed interactions, constrained by the truncated observation mechanism to be greater than 0. We can show the following proposition about the breakdown point in the estimation of β_0 and β_1.

Proposition 5. *The MTLE $\hat{\beta}^{tr}$ diverges if $T_0 > T/2$. In addition, if $Y > 1$, the truncated estimator for β_1 diverges.*

Proof. We will reparameterize the problem so that $\lambda_0 = \exp(\beta_0)$ is the rate of interactions in the $\texttt{prev} = 0$ state and $\lambda_1 = \exp(\beta_0 + \beta_1)$ is the rate of interactions in the $\texttt{prev} = 1$ state.

In these terms, the truncated log-likelihood is

$$\mathbb{P}^{tr}_{\beta}(Y^{\mathcal{A}} \mid X^{\mathcal{A}}) = -(\lambda_0 T_0 + \lambda_1 T) + \log(\lambda_0) + (Y-1)\log(\lambda_1) - \log(1 - \exp(-\lambda_0(T_0 + T_1))) \tag{27}$$

The truncated likelihood factors such that the MTLE for λ_0 can be calculated independently of

the MTLE for λ_1. The score system for the MTLE $\hat{\lambda}_0$ is

$$\frac{1-(T\hat{\lambda}_0+1)\exp(-\hat{\lambda}_0 T)}{\hat{\lambda}_0(1-\exp(-\hat{\lambda}_0 T))} = T_0. \tag{28}$$

The expression on the left-hand side is positive everywhere and increases as λ_0 approaches 0. It behaves similarly to λ_0^{-1} when λ_0 is moderately sized, tracking closely to the intuition that the estimated rate $\hat{\lambda}$ should be close to the inverse of the observed waiting time T_0, but when λ_0 approaches zero this expression converges to a constant maximum instead of diverging. In particular, by two applications of L'Hopital's rule, we arrive at

$$\lim_{\hat{\lambda}_0 \to 0} \frac{1-(T\hat{\lambda}_0+1)\exp(-\hat{\lambda}_0 T)}{\hat{\lambda}_0(1-\exp(-\hat{\lambda}_0 T))} = \frac{T}{2}. \tag{29}$$

This indicates that if $T_0 > \frac{T}{2}$, the MTLE $\hat{\lambda}_0^{tr}$ satisfying Equation 28 is negative, meaning that in the original parameterization, the MTLE $\hat{\beta}_0^{tr}$ diverges to $-\infty$.

The second statement regarding $\hat{\beta}_1^{tr}$ follows by noting that if $Y > 1$, $\hat{\lambda}_1^{tr} = \exp(\hat{\beta}_0^{tr} + \hat{\beta}_1^{tr})$ is non-zero, so $\hat{\beta}_1^{tr}$ must diverge to ∞ to compensate for the divergence of $\hat{\beta}_0^{tr}$. □

In practical application, the MTLE becomes difficult to trust when T_0 is only slightly less than $\frac{T}{2}$, both due to high variability and to numerical errors. Thus, investigators should check that their data are well clear of this breakdown point before using a `prev` covariate.

The simulations in this paper are well clear of the breakdown point, but the patent data that we use in examples are not. For these, we use an alternative covariate `prev > 1`, which evaluates to 1 if there were more than one previous interactions between a pair of actors. Under this specification, the waiting times before the first two interactions between a pair of actors can inform the intercept term of the regression and there is no aliasing between the intercept and the truncated observation model.

C Limiting variance inflation calculation from Section 7.2.2

In this example, β is four-dimensional, composed of the coefficients for the intercept, Zip, Asg, and previous collaboration coefficients, respectively. Let $\mathcal{I}^s(\beta)$ be the 4×4 Fisher information matrix for estimator s, written $\hat{\beta}^s$. Let $\mathcal{V}^s(\beta) = \mathcal{I}^s(\beta)^{-1}$ be the asymptotic covariance matrix of $\hat{\beta}^s$. We wish to compute the asymptotic variance ratios for each parameter estimate, given by $\frac{V_{kk}^{trunc}(\beta)}{V_{kk}^{full}(\beta)}$ for $k = 1, \cdots, 4$.

The information matrix for estimator s can be represented as follows:

$$\mathcal{I}_n^s(\beta) = \sum_{ij \in \mathcal{R}_n} \mathbb{E}\left[t_{ij}^{(1)}\right] w_{ij}^{pre,s} X_{ij}^{pre} X_{ij}^{pre\top} + \left(T - \mathbb{E}\left[t_{ij}^{(1)}\right]\right) w_{ij}^{post} X_{ij}^{post} X_{ij}^{post\top} \tag{30}$$

Here, $\mathbb{E}\left[t_{ij}^{(1)}\right]$ is the expected time of the first interaction to be observed on dyad ij, and can be used the divide the information matrix into expected information obtained from dyads before their first interactions and expected information obtained afterward. This decomposition is useful because within these time intervals the covariate vector for a dyad remains fixed. We use the superscripts *pre* and *post* to label those quantities relevant to the pre- and post-interaction periods, respectively. As is customary for generalized linear models, we represent the information matrix contribution from each dyad ij as a weight w_{ij} and the outer product of the dyad's covariate vector X_{ij} with itself. Note that the oracle and truncated procedures only differ in the definition of w_{ij}^{pre}.

Note that because the covariates X_{ij} are discrete, the sums in Equation 30 can be collapsed into contributions by dyads with the same covariate values. In this case, because the intercept and `prev` covariates are fixed within the pre- and post-collaboration time intervals, there are only four unique covariate classes, corresponding to same/different zip code, and same/different assignee. WeLOG, we fix the definitions of the covariate classes as follows:

$$\begin{aligned}
X_1^{pre} &= (1,0,0,0)^\top & X_1^{post} &= (1,0,0,1)^\top \\
X_2^{pre} &= (1,0,1,0)^\top & X_2^{post} &= (1,0,1,1)^\top \\
X_3^{pre} &= (1,1,0,0)^\top & X_3^{post} &= (1,1,0,1)^\top \\
X_4^{pre} &= (1,1,1,0)^\top & X_4^{post} &= (1,1,1,1)^\top.
\end{aligned}$$

Using c to index these covariate classes, and letting N_c be the number of at-risk dyads in class c so that $\sum_c N_c = \sum_{ij} R_{ij}$,

$$\mathcal{I}_n^s(\beta) = \sum_c N_c \left(\mathbb{E}\left[t_c^{(1)}\right] w_c^{pre,s} X_c^{pre} X_c^{pre\top} + \left(T - \mathbb{E}\left[t_c^{(1)}\right]\right) w_c^{post} X_c^{post} X_c^{post\top}\right). \tag{31}$$

Here $\mathbb{E}\left[t_c^{(1)}\right]$ is a slight abuse of notation, but is meant to emphasize that all dyads within a given class share the same expected time of first observed interaction.

Using Equation 31, we take the limit of the analytical inverse of $\mathcal{I}_n^s(\beta)$ for the truncated and full estimators. These limits depend on the limiting composition of N_c. For these simulations, we assume that both zip codes and assignees have fixed size as the network size grows to infinity. Combined with the generative assumption in Equation 25, this implies that asymptotically class 1, corresponding pairs of inventors with different zip codes and different assignees, grows at a faster rate than the other three covariate classes. In particular, $N_1 \in O(N_k^2)$ for $k = 2, 3, 4$.

We compute the analytic inverses using Cramer's rule, which gives $V^s_{kk}(\beta) = \frac{C^s_n(k,k)}{\det(\mathcal{I}^s_n(\beta))}$, where $C^s_n(l,m)$ is the cofactor of element l,m in $\mathcal{I}^s_n(\beta)$. Thus, the variance inflation factor can be written

$$VI_k(\beta) = \lim_{n\to\infty} \frac{C^{tr}_n(k,k)}{C^{full}_n(k,k)} \frac{\det(\mathcal{I}^{full}_n)}{\det(\mathcal{I}^{tr}_n)}. \tag{32}$$

Beginning with the second factor of Equation 32, we note that these full determinants can be written as the difference of sums of four-way products of elements in $\mathcal{I}^s_n(\beta)$. The terms that grow fastest in this expression grow as N_1^2, so we can rewrite the determinant

$$\det(\mathcal{I}^s_n(\beta)) = (i^s_{n,22} i^s_{n,33} - (i^s_{n,23})^2)(i^s_{n,11} i^s_{n,44} - (i^s_{n,14})^2) + o(N_1^2). \tag{33}$$

Similarly, the cofactors can be written as the difference of sums of three-way products of elements in the corresponding information matrix. The relevant cofactors can also be written in terms of their fastest growing terms:

$$C^s_n(1,1) = (i^s_{n,22} i^s_{n,33} - (i^s_{n,23})^2) i^s_{n,44} + o(N_1) \tag{34}$$
$$C^s_n(2,2) = (i^s_{n,11} i^s_{n,44} - (i^s_{n,14})^2) i^s_{n,33} + o(N_1^2) \tag{35}$$
$$C^s_n(3,3) = (i^s_{n,11} i^s_{n,44} - (i^s_{n,14})^2) i^s_{n,22} + o(N_1^2) \tag{36}$$
$$C^s_n(4,4) = (i^s_{n,22} i^s_{n,33} - (i^s_{n,23})^2) i^s_{n,11} + o(N_1). \tag{37}$$

To write out the explicit forms of the elements of $\mathcal{I}^s_n(\beta)$, we define the following shorthand:

$$z^{pre,s}_c = \mathbb{E}\left[t^{(1)}_c\right] w^{pre,s}_c \qquad\qquad z^{post}_c = \left(T - \mathbb{E}\left[t^{(1)}_c\right]\right) w^{post}_c. \tag{38}$$

Evaluating Equation 31, the relevant elements of $\mathcal{I}^s_n(\beta)$ have the form

$$i^s_{n,11} = \sum_c N_c \left(z^{pre,s}_c + z^{post}_c\right) \tag{39}$$
$$i^s_{n,44} = i^s_{n,14} = \sum_c N_c z^{post}_c \tag{40}$$
$$i^s_{n,22} = N_3 \left(z^{pre,s}_3 + z^{post}_3\right) + N_4 \left(z^{pre,s}_4 + z^{post}_4\right) \tag{41}$$
$$i^s_{n,33} = N_2 \left(z^{pre,s}_2 + z^{post}_2\right) + N_4 \left(z^{pre,s}_4 + z^{post}_4\right) \tag{42}$$
$$i^s_{n,23} = N_4 \left(z^{pre,s}_4 + z^{post}_4\right). \tag{43}$$

We compute the variance inflation factors by substitution. After simplification, we have

$$VI_1(\beta) = \frac{\sum_c N_c z_c^{pre,full}}{\sum_c N_c z_c^{pre,tr}} \tag{44}$$

$$VI_2(\beta) = \frac{N_3\left(z_3^{pre,tr} + z_3^{post}\right) + N_4\left(z_4^{pre,tr} + z_4^{post}\right)}{N_3\left(z_3^{pre,full} + z_3^{post}\right) + N_4\left(z_4^{pre,full} + z_4^{post}\right)} \frac{K^{full}}{K^{tr}} \tag{45}$$

$$VI_3(\beta) = \frac{N_2\left(z_2^{pre,tr} + z_2^{post}\right) + N_4\left(z_4^{pre,tr} + z_4^{post}\right)}{N_2\left(z_2^{pre,full} + z_2^{post}\right) + N_4\left(z_4^{pre,full} + z_4^{post}\right)} \frac{K^{full}}{K^{tr}} \tag{46}$$

$$VI_4(\beta) = \frac{\sum_c N_c\left(z_c^{pre,tr} + z_c^{post}\right)}{\sum_c N_c\left(z_c^{pre,full} + z_c^{post}\right)} \frac{\sum_c N_c z_c^{pre,full}}{\sum_c N_c z_c^{pre,tr}} \tag{47}$$

where

$$\begin{aligned} K^s = {} & N_2\left(z_2^{pre,s} + z_2^{post}\right) N_3\left(z_3^{pre,s} + z_3^{post}\right) + \\ & N_2\left(z_2^{pre,s} + z_2^{post}\right) N_4\left(z_4^{pre,s} + z_4^{post}\right) + \\ & N_3\left(z_3^{pre,s} + z_3^{post}\right) N_4\left(z_4^{pre,s} + z_4^{post}\right) \end{aligned} \tag{48}$$

To fix constants and ensure identification in the limit for the example in Section 7.2.2, we make additional assumptions about the sizes and ordering of the assignees and zip codes. We assume that each assignee has 200 people while each zip code has 250 people, and that actors are assigned to these zip codes and assignees sequentially. In this way, the adjacency matrix can be partitioned into sets of 4 zip codes or 5 assignees such that there are no zip code or assignee matches across these partitions. This implies that in the limit, $N_2 = 2N_3 = 3N_4$.

D Analysis of deviance tables

Table 3: Analysis of Deviance for `Zip` coefficient.

	Df	Deviance	Resid. Df	Resid. Dev	Pr(>Chi)
NULL			50039	19873.3	
asg	3.000	42.44	50036	19830.9	3.24E-09
zip	3.000	21.82	50033	19809.0	7.12E-05
prev	3.000	20.25	50030	19788.8	1.51E-04
size	7.000	6.18	50023	19782.6	0.518
asg:zip	9.000	32.60	50014	19750.0	1.57E-04
asg:prev	9.000	73.40	50005	19676.6	3.27E-12
zip:prev	9.000	18.16	49996	19658.5	0.033
asg:size	21.000	9.78	49975	19648.7	0.982
zip:size	21.000	7.86	49954	19640.8	0.996
prev:size	21.000	10.93	49933	19629.9	0.964
asg:zip:prev	27.000	114.86	49906	19515.0	8.30E-13
asg:zip:size	63.000	32.35	49843	19482.7	1.000
asg:prev:size	63.000	39.51	49780	19443.2	0.991
zip:prev:size	63.000	24.56	49717	19418.6	1.000
asg:zip:prev:size	189.000	141.74	49528	19276.9	0.996

Table 4: Analysis of Deviance for `Asg` coefficient.

	Df	Deviance	Resid. Df	Resid. Dev	Pr(>Chi)
NULL			50039	18617.7	
asg	3.000	3.30	50036	18614.4	0.347
zip	3.000	3.68	50033	18610.8	0.298
prev	3.000	47.54	50030	18563.2	2.67E-10
size	7.000	7.72	50023	18555.5	0.358
asg:zip	9.000	26.48	50014	18529.0	0.002
asg:prev	9.000	27.33	50005	18501.7	0.001
zip:prev	9.000	41.19	49996	18460.5	4.62E-06
asg:size	21.000	24.46	49975	18436.0	0.271
zip:size	21.000	14.08	49954	18422.0	0.866
prev:size	21.000	24.02	49933	18398.0	0.292
asg:zip:prev	27.000	135.41	49906	18262.5	2.15E-16
asg:zip:size	63.000	30.46	49843	18232.1	1.000
asg:prev:size	63.000	35.38	49780	18196.7	0.998
zip:prev:size	63.000	60.39	49717	18136.3	0.570
asg:zip:prev:size	189.000	139.69	49528	17996.6	0.997

Table 5: Analysis of Deviance for `prev` coefficient.

	Df	Deviance	Resid. Df	Resid. Dev	Pr(>Chi)
NULL			50039	36518.9	
asg	3.000	67.19	50036	36451.7	1.70E-14
zip	3.000	22.12	50033	36429.6	6.16E-05
prev	3.000	1395.53	50030	35034.1	2.75E-302
size	7.000	46.68	50023	34987.4	6.44E-08
asg:zip	9.000	40.43	50014	34947.0	6.35E-06
asg:prev	9.000	26.53	50005	34920.4	0.002
zip:prev	9.000	20.05	49996	34900.4	0.018
asg:size	21.000	10.55	49975	34889.8	0.971
zip:size	21.000	6.42	49954	34883.4	0.999
prev:size	21.000	11.04	49933	34872.4	0.962
asg:zip:prev	27.000	101.10	49906	34771.3	1.70E-10
asg:zip:size	63.000	23.59	49843	34747.7	1.000
asg:prev:size	63.000	18.46	49780	34729.2	1.000
zip:prev:size	63.000	18.36	49717	34710.9	1.000
asg:zip:prev:size	189.000	71.78	49528	34639.1	1.000