

Estimating Peer Effects Using Partial Network Data

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Abstract

We study the estimation of peer effects through social networks when researchers do not observe the entire network structure. Special cases include sampled networks, censored networks, misclassified links, and aggregated relational data. We assume that researchers can obtain a consistent estimator of the distribution of the network. We show that this assumption is sufficient for estimating peer effects using a linear-in-means model. We provide an empirical application to the study of peer effects on students academic achievement using the widely used Add Health database and show that network data errors have a first-order downward bias on estimated peer effects.

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1 Introduction

There is a large and growing literature on the impact of peer effects in social networks.¹ However, since eliciting network data is expensive (Breza et al., 2020), relatively few data sets contain comprehensive network information, and existing ones are prone to data errors. Despite some recent contributions, existing methodologies for the estimation of peer effects with incomplete or erroneous network data either focus on a specific kind of sampling or errors, or they are highly computationally demanding.

In this paper, we propose a unifying framework that allows for the estimation of peer effects under the widely used linear-in-means model (e.g. Manski (1993); Bramoullé et al. (2009)) when the researcher does not observe the entire network structure. Our methodology is computationally attractive and flexible enough to cover cases in which, for example, network data are sampled (Chandrasekhar and Lewis, 2011; Liu, 2013), censored (Griffith, 2019), missclassified (Hardy et al., 2019; Lewbel et al., 2019), or summarized by aggregated relational data (ARD; Breza et al. (2020); Alidaee et al. (2020)). Our central assumption is that the researcher is able to estimate a network formation model using some partial information about the network structure. Leveraging recent contributions on the estimation of network formation models, we show that this assumption is sufficient to identify and estimate peer effects.

We propose two estimators. First, we present a simple, yet widely applicable, instrumental variable (IV) strategy based on the assumption that contextual peer variables (e.g. the average age of one's peers) are observed.² The computational cost for our IV estimator is minimal and can be applied even to massive data sets. We study the finite sample properties of our IV estimator in the context of ARD using Monte Carlo simulations. Second, we present a flexible Bayesian estimator that is valid even when contextual peer variables are not observed. Although the computational cost is greater, we exploit recent computational advances in the literature (e.g. Mele (2017); Hsieh et al. (2019)) and show that the estimator can be successfully implemented on common-sized data sets. In particular, we

¹For recent reviews, see Boucher and Fortin (2016), Bramoullé et al. (2020), Breza (2016), and De Paula (2017).

²These can easily be elicited from survey data using questions such as, “On average, how old are your friends?”

use our estimator to study peer effects on academic achievement using the widely used Add Health database. We find that data errors have first-order downward bias on the estimated endogenous effect.

Our instrumental variable estimator is inspired by the literature on error-in-variable models with repeated observations.³ Using a network formation model, we obtain a consistent estimator of the distribution of the true network. We then use this estimated distribution to obtain two different draws from the distribution of the network. One draw is used to approximate the endogenous peer variable (e.g. the average behavior of my friends), while the other is used to construct instruments based on higher-order contextual peer variables (e.g. the average age of the friends of my friends), as proposed by [Bramoullé et al. \(2009\)](#).

We show that since the true networks and the two approximations are asymptotically drawn from the same distribution, the instruments are uncorrelated with the approximation error and are therefore valid. Importantly, our instrumental strategy requires only the (partial) observation of a *single* network, as opposed to, for example, the approach of [Zhang \(2020\)](#). This feature is due to two main properties of the model. First, we can consistently estimate the distribution of the mismeasured variable (i.e. the network) using a single (partial) observation of the variable. Second, in the absence of measurement error, valid instruments for the endogenous peer variable are available ([Bramoullé et al., 2009](#)).

We explore the finite sample properties of our instrumental variable estimator using Monte Carlo simulations. We consider the case in which the researcher only has access to aggregated relational data (ARD). In particular, we show that our IV estimator can be successfully combined with the network formation estimators proposed by [Breza et al. \(2020\)](#) and [Alidaee et al. \(2020\)](#). As long as ARD are sufficiently informative in regard to the linking probabilities, our IV estimator successfully recovers the model's parameters.

Our Bayesian estimator does not require the observation of contextual peer variables and is therefore complementary to the IV estimator. The estimated distribution for the network acts as a prior distribution, and the inferred network structure is updated through a Markov chain Monte Carlo (MCMC) algorithm. Our approach relies on data augmentation ([Tanner and Wong, 1987](#)), which treats the network as an additional set of parameters to

³See [Bound et al. \(2001\)](#) for a review and [Chen et al. \(2011\)](#) for a review focused on nonlinear models.

be estimated. This approach saves us from integrating over the $2^{N(N-1)}$ potential networks compatible with the data, which would create an important computational issue, as faced by [Chandrasekhar and Lewis \(2011\)](#).⁴ In particular, our MCMC builds on recent developments from the empirical literature on network formation (e.g. [Mele \(2017\)](#); [Hsieh et al. \(2019, 2020\)](#)). We show that the computational cost of our estimator is reasonable and that it can easily be applied to standard data sets.

We study the impact of errors in adolescents' friendship network data for the estimation of peer effects in education ([Calvó-Armengol et al., 2009](#)). We show that the widely used Add Health database features many missing links—around 30% of the within-school friendship nominations are coded with error—and that these data errors strongly bias the estimated peer effects. Specifically, we estimate a model of peer effects on students' academic achievement. Our Bayesian estimator probabilistically reconstructs the missing links, and we obtain a consistent estimator of peer effects. The bias due to data errors is qualitatively important. Our estimated endogenous peer effect coefficient is 1.6 times larger than the one obtained by assuming that the data contains no errors.

Related Literature

This paper contributes to the recent literature on the estimation of peer effects when the network is either not entirely observed or is observed with noise. In particular, our framework is valid when network data are either sampled, censored, misclassified, or consist of aggregate relational data.⁵ We unify these strands in the literature and provide a flexible and computationally tractable framework for estimating peer effects with incomplete or erroneous network data.

Sampled networks and censoring: [Chandrasekhar and Lewis \(2011\)](#) show that models estimated using sampled networks are generally biased. They propose an analytical correction as well as a two-step general method of moment (GMM) estimator. [Liu \(2013\)](#) shows that when the interaction matrix is not row-normalized, instrumental variable estimators based

⁴Here N is the number of individuals in a given network. As discussed below, [Chandrasekhar and Lewis \(2011\)](#) only had to integrate over the $2^{N(N-1)-M}$ networks, where M is the number of sampled links.

⁵For related literature that studies the estimation of peer effects when researchers have no network data, see [Manresa \(2016\)](#); [De Paula et al. \(2018a\)](#); [Souza \(2014\)](#); [Lewbel et al. \(2019\)](#).

on an out-degree distribution are valid, even with sampled networks. [Hsieh et al. \(2018\)](#) focus on a regression model that depends on global network statistics. They propose analytical corrections to account for nonrandom sampling of the network (see also [Chen et al. \(2013\)](#)). [Thirkettle \(2019\)](#) also focuses on global network statistics, assuming that the researcher only observes a random sample of links. Using a structural network formation model, he derives bounds on the identified set for both the network formation model and the network statistic of interest. Finally, [Zhang \(2020\)](#) studies program evaluation in a context in which networks are locally sampled and affected by a single type measurement error (either false positives or false negatives, but not both). Assuming that the researcher has access to two measurements of the network for each sampled unit, she presents a nonparametric estimator of the treatment and spillover effects.

Relatedly, [Griffith \(2019\)](#) explores the impact of imposing an upper bound to the number of links when eliciting network data, e.g. “Name your five best friends.” He shows, analytically and through simulations, that these bounds may bias the estimates significantly. He presents a bias-correction method and explores the impact of censoring using two empirical applications. He finds that censoring underestimates peer effects.

We contribute to this literature by proposing two simple and flexible estimators for the estimation of peer effects based on the linear-in-means model (as opposed to network statistics as in [Hsieh and Lee \(2016\)](#) and [Thirkettle \(2019\)](#)). Our estimators do not require many observations of the sampled network (contrary to [Zhang \(2020\)](#)). Similar to [Griffith \(2019\)](#), we find—using the Add Health database—that sampling leads to an underestimation of peer effects, although we find that censoring has negligible impact in the context of peer effects on academic achievement.

Our Bayesian estimator is similar in spirit to the two-stage GMM estimator proposed by [Chandrasekhar and Lewis \(2011\)](#), but it is computationally advantageous. Indeed, their GMM estimator is based on an unconditional moment condition, which requires integrating over the entire set of networks that are compatible in the data. In [Chandrasekhar and Lewis \(2011\)](#), there are $2^{N(N-1)-M}$ such networks, where M is the number of sampled pairs of individuals. Even for small networks, the computational cost is substantial whenever sampling is nontrivial. Our Bayesian approach allows us to exploit recent developments

from the empirical literature on network formation (e.g. [Mele \(2017\)](#); [Hsieh et al. \(2019\)](#)) and is computationally tractable, even when no link is sampled (e.g. with ARD), which would otherwise require integrating over the $2^{N(N-1)}$ networks compatible with the data.

Misclassification: [Hardy et al. \(2019\)](#) look at the estimation of (discrete) treatment effects when the network is observed noisily. Specifically, they assume that observed links are affected by iid errors and present an expectation maximization (EM) algorithm that allows for a consistent estimator of the treatment effect. [Lewbel et al. \(2019\)](#) show that the estimation of the linear-in-means model is consistent and that inference is valid if the expected number of misclassified links grows at a rate slower than $O(\sqrt{N})$.

Our model allows for misclassification of all links with positive probability. As in [Hardy et al. \(2019\)](#), we use a network formation model to estimate the probability of false positives and false negatives. However, our two-stage strategy—estimating the network formation model and then the peer effect model—allows for greater flexibility. In particular, our network formation model is allowed to flexibly depend on covariates. This is empirically important, as networks typically feature homophily on observed characteristics (e.g. [Currarini et al. \(2010\)](#); [Bramoullé et al. \(2012\)](#)).

Aggregate relational data: [Breza et al. \(2020\)](#) propose to estimate network effects using aggregate relation data (ARD). These are obtained from such survey questions as, “How many of your friends have trait X?” They present a network formation model that can be estimated using only ARD. They show the validity of their methodology using two empirical applications in which the outcome of interest depends on the summary statistics of the network. [Alidaee et al. \(2020\)](#) present an alternative estimator allowing to recover nonparametrically the linking probability through ARD. Using a low-rank assumption, they present a simple penalized regression.

We show that these recent methodologies can also be applied to the study of peer effects using the linear-in-means model, which significantly expands the scope of the potential applications of these approaches. In particular, we study the finite sample performance of our IV estimator using Monte Carlo simulations and show that we can successfully recover the simulated parameters when combined with the network formation estimators proposed by [Breza et al. \(2020\)](#) or by [Alidaee et al. \(2020\)](#).

A main contribution of this paper is that our estimators can be applied to each of the previously mentioned data issues or to their combination. Our two-step approach—first estimating the network formation and then the peer effects—is flexible and computationally attractive. To reduce the implementation costs, we also present an easy-to-use R package—named `PartialNetwork`—for applying our estimators. The package allows replicating all simulations and empirical applications in the paper, including the estimator proposed by Breza et al. (2020). The package is available online at: <https://github.com/ahoundetoungan/PartialNetwork>. Additional implementation examples are provided in the online Appendix. For example, we show that the implementation of our Bayesian estimator, combined with the estimator for ARD proposed by Breza et al. (2020), is straightforward and computationally tractable.

The remainder of the paper is organized as follows. In Section 2, we present the econometric model as well as the main assumptions. In Section 3, we present our instrumental variable estimator and study its performance when combined with the estimators for ARD proposed by Breza et al. (2020) and Alidaee et al. (2020). In Section 4, we present our Bayesian estimation strategy. In Section 5, we present our application to peer effects on academic achievement. Section 6 concludes with a discussion of the main results, limits, and challenges for future research.

2 The Model

We now formally present our model. We first describe the *linear-in-means* model (Manski, 1993; Bramoullé et al., 2009), arguably the most widely used model for studying peer effects in networks (see Bramoullé et al. (2020) for a recent review). We then introduce our main assumption, characterizing what is known about the structure of the network.

2.1 The Linear-in-Means Model

Let \mathbf{A} represent the $N \times N$ *adjacency matrix* of the network. We assume a directed network: $a_{ij} \in \{0, 1\}$, where $a_{ij} = 1$ if i is linked to j . We normalize $a_{ii} = 0$ for all i and let

$n_i = \sum_j a_{ij}$ denote the number of links of i . Let $\mathbf{G} = f(\mathbf{A})$, the $N \times N$ *interaction matrix* for some function f . Unless otherwise stated, we assume that \mathbf{G} is a row-normalization of the adjacency matrix \mathbf{A} .⁶ Our results extend to alternative specifications of f .

We focus on the following model:

$$\mathbf{y} = c\mathbf{1} + \mathbf{X}\boldsymbol{\beta} + \alpha\mathbf{G}\mathbf{y} + \mathbf{G}\mathbf{X}\boldsymbol{\gamma} + \boldsymbol{\varepsilon}, \quad (1)$$

where \mathbf{y} is a vector of an outcome of interest (e.g. academic achievement), c is a constant, \mathbf{X} is a matrix of observable characteristics (e.g. age, gender...), and $\boldsymbol{\varepsilon}$ is a vector of errors.⁷ The parameter α therefore captures the impact of the average outcome of one's peers on their behavior (the endogenous peer effect). The parameter $\boldsymbol{\beta}$ captures the impact of one's characteristics on their behavior (the individual effects). The parameter $\boldsymbol{\gamma}$ captures the impact of the average characteristics of one's peers on their behavior (the contextual peer effects).

The following set of assumptions summarizes our setup.

Assumption 1. $|\alpha| < 1/\|\mathbf{G}\|$ for some submultiplicative norm $\|\cdot\|$.

Assumption 2. *The population is partitioned into $M > 1$ groups, where the size N_r of each group $r = 1, \dots, M$ is bounded. The probability of a link between individuals of different groups is equal to 0.*

Assumption 3. *For each group, the outcome and individual characteristics are observed, i.e. $(\mathbf{y}_r, \mathbf{X}_r)$, $r = 1, \dots, M$, are observed.*

Assumption 4. *The network is exogenous in the sense that $\mathbb{E}[\boldsymbol{\varepsilon} | \mathbf{X}, \mathbf{G}] = \mathbf{0}$.*

Assumption 1 ensures that the model is coherent and that there exists a unique vector \mathbf{y} compatible with (1). When \mathbf{G} is row-normalized, $|\alpha| < 1$ is sufficient. Assumption 2 is introduced for exposition purposes; for example, the data could consist of a collection of small

⁶In such a case, $g_{ij} = a_{ij}/n_i$ whenever $n_i > 0$, whereas $g_{ij} = 0$ otherwise.

⁷Note that [Boucher and Bramoullé \(2020\)](#) recently showed that (1) is valid (coherent, complete, and microfounded), even when y_i is binary.

villages (Banerjee et al., 2013) or schools (Calvó-Armengol et al., 2009). Our methods extend to alternative assumptions such as those proposed by Lee (2004) and Lee et al. (2010).⁸

Assumption 3 implies that the data is composed of a subset of fully sampled groups.⁹ A similar assumption is made by Breza et al. (2020). Note that we assume that the network is exogenous (Assumption 4), mostly to clarify the presentation of the estimators. In Section 6.1, we discuss how recent advances for the estimation of peer effects in endogenous networks can be adapted to our context.

2.2 Partial Network Information

In this paper, we relax the costly assumption that the adjacency matrix \mathbf{A} is observed. We assume instead that sufficient information about the network is observed so that a network formation model can be estimated.

More formally, we let \mathcal{A} denote the observed information about the true network structure. That is, \mathcal{A} is a function of the true network \mathbf{A} and potentially of individuals' characteristics (see Example 4). We impose no particular structure on \mathcal{A} but discuss important examples below (see Examples 1–4).

We assume that links are generated as follows:

$$P(a_{ij}) \equiv P(a_{ij}|\boldsymbol{\rho}_0) \propto \exp\{a_{ij}Q(\boldsymbol{\rho}_0, \mathbf{w}_{ij})\}, \quad (2)$$

where Q is some known continuous function, \mathbf{w}_{ij} is a vector of observed characteristics for the pair ij , and $\boldsymbol{\rho}_0$ is the true value of $\boldsymbol{\rho}$, a vector of parameters to be estimated. Note that we omit the dependence of $P(a_{ij})$ on \mathbf{w}_{ij} to simplify the notation.

As will be made clear, our estimation strategy requires that the econometrician be able to draw samples from (a consistent estimator) $P(\mathbf{A})$. Thus, and for the sake of simplicity, we focus on distributions that are conditionally independent across links (i.e. $P(a_{ij}|\mathbf{A}_{-ij}) = P(a_{ij})$), as in (2), although this is not formally required.¹⁰

⁸The authors assume that the adjacency matrix \mathbf{A} is bounded in row- and column-sums.

⁹Contrary to Liu et al. (2017) or Wang and Lee (2013), for example.

¹⁰A prime example of a network distribution that is not conditionally independent is the distribution for an exponential random graph model (ERGM), e.g. Mele (2017).

We now present our main assumption.

Assumption 5 (Partial Network Information). *Given network information \mathcal{A} and the parametric model (2), there exists an estimator $\hat{\rho}_N$, such that $\hat{\rho}_N \rightarrow_p \rho_0$ as $N \rightarrow \infty$.*

Assumption 5 implies that, using (5), the researcher has access to “sufficient information” about the network structure to obtain a consistent estimator of the distribution of the true network $P(\mathbf{A})$. We denote such a consistent estimator by $\hat{P}(\mathbf{A}) \equiv P(\mathbf{A}|\hat{\rho}, \mathcal{A})$. We omit the dependence on \mathcal{A} to simplify the notation when this does not create confusion. Note that we can use $\hat{P}(\mathbf{A})$ to obtain the consistent estimator $\hat{P}(\mathbf{G})$, since $\mathbf{G} = f(\mathbf{A})$ for some known function f .¹¹

Importantly, it should be noted that even if the econometrician has access to a consistent estimator of the distribution of the true network, it *does not* imply that they could simply proxy \mathbf{G} in (1) using a draw $\tilde{\mathbf{G}}$ from the distribution $\hat{P}(\mathbf{G})$. The reason is that for any vector \mathbf{z} , $\tilde{\mathbf{G}}\mathbf{z}$ generally does not converge to $\mathbf{G}\mathbf{z}$ as the number of individuals N goes to infinity. In other words, knowledge of $\hat{P}(\mathbf{G})$ and \mathbf{z} is not sufficient to obtain a consistent estimator of $\mathbf{G}\mathbf{z}$. To see why, note that $(\mathbf{G}\mathbf{z})_i = \sum_{j=1}^N g_{ij}z_j$. Under Assumption 2, the set of j such that $g_{ij} \neq 0$ is bounded, so a consistent estimator of $P(\mathbf{G})$ is not sufficient to obtain a consistent estimator of $\mathbf{G}\mathbf{X}$. This is also true under the alternative assumptions in Lee (2004) and De Paula et al. (2018b).¹²

Assumption 5 covers a large range of cases in which networks are partially observed. We specifically discuss four leading examples in which Assumption 5 holds: *sampled networks* (Example 1), *censored networks* (Example 2), *misclassified network links* (Example 3), and *aggregated relational data* (Example 4).

Example 1 (Sampled Networks). *Suppose that we observe the realizations of a_{ij} for a random sample of m pairs (e.g. Chandrasekhar and Lewis (2011)). Here \mathcal{A} can be represented by an $N \times N$ binary matrix \mathbf{A}^{obs} . Conley and Udry (2010) present such a sampling scheme*

¹¹Since \mathbf{A} takes a finite number of values, so does \mathbf{G} , and $P(\mathbf{G})$ is a multinomial distribution.

¹²Lee (2004) requires that \mathbf{G} be bounded in row- and column-sums (in absolute value), whereas De Paula et al. (2018b) assume that \mathbf{A} is bounded in row-sums. An exception is the graphon games approach proposed by Parise and Ozdaglar (2019), although their method has yet to be implemented to the estimation of network formation games.

and ask individuals about their relationship with a random sample of other individuals, for example, “Do you know person X ? ”

Such a setup is sufficient to consistently estimate flexible network formation models such as the one in [Graham \(2017\)](#). A simpler example would be to assume that the network formation model (2) is equal to $P(a_{ij} = 1) \propto \exp\{\mathbf{w}_{ij}\boldsymbol{\rho}\}$. In this case, a simple logistic regression provides a consistent estimator of $\boldsymbol{\rho}$.

Given this consistent estimator for $\boldsymbol{\rho}$ and the assumed parametric model, we can compute an estimator for the distribution of the true network $\hat{P}(\mathbf{A}) = P(\mathbf{A}|\hat{\boldsymbol{\rho}}, \mathcal{A})$. Here, $\hat{P}(a_{ij}) = a_{ij}^{obs}$ for any sampled link ij , while $\hat{P}(a_{ij}) \propto \exp\{a_{ij}\mathbf{w}_{ij}\hat{\boldsymbol{\rho}}\}$ for the remaining unsampled links.

Example 2 (Censored Network Data). As discussed in [Griffith \(2019\)](#), network data is often censored. This typically arises when surveyed individuals are asked to name only $T > 1$ links (among the N possible links they may have). Here, \mathcal{A} can be represented by an $N \times N$ binary matrix \mathbf{A}^{obs} . We can use censored network data to estimate a network formation model such as $P(a_{ij} = 1) \propto \exp\{\mathbf{w}_{ij}\boldsymbol{\rho}\}$, for example.

For simplicity, let us assume as in [Griffith \(2019\)](#) that each link has the same probability of being censored. Then, the parameters in $\boldsymbol{\rho}$ (other than the constant) are identified from the observed ratios $\sum_{ij} a_{ij} w_{ij}^k / \sum_{ij} w_{ij}^k$ (for observable characteristic k), as these sufficient statistics are not biased by censoring. To identify the constant, note that we can easily compute the likelihood of the censored degree distribution (i.e. $n_i = \sum_j a_{ij}$). That is $P(n_i = t|\mathbf{W}; \boldsymbol{\rho})$ for observed $t < T$ and $P(n_i \geq T|\mathbf{W}; \boldsymbol{\rho})$ for observed $t = T$, which allows identifying the constant.¹³

Once such estimator of $\boldsymbol{\rho}$ is obtained, we can compute an estimator for the distribution of the true network $\hat{P}(\mathbf{A}) = P(\mathbf{A}|\hat{\boldsymbol{\rho}}, \mathcal{A})$. In particular, $P(a_{ij}|\hat{\boldsymbol{\rho}}, a_{ij}^{obs} = 1) = 1$ because observed links necessarily exist. Also note that for all individuals i , such that $n_i < T$, we have $P(a_{ij}|\hat{\boldsymbol{\rho}}, a_{ij}^{obs}) = a_{ij}^{obs}$ for all j , as their network data are not censored. Here, the structural model is only used to obtain the probability of links that are not observed for individuals whose links are potentially censored, i.e. $P(a_{ij}|\hat{\boldsymbol{\rho}}, a_{ij}^{obs} = 0) \propto \exp\{a_{ij}\mathbf{w}_{ij}\hat{\boldsymbol{\rho}}\}$ for all ij , such that $n_i \geq T$.

¹³A simple alternative, when the data of only a few individuals is censored, is to estimate the model only for individuals for whom $n_i < T$. We follow this strategy in Section 5.

Example 3 (Misclassification). *Hardy et al. (2019)* study cases in which networks are observed but may include misclassified links (i.e. false positives and false negatives). Here, \mathcal{A} can be represented by an $N \times N$ binary matrix \mathbf{A}^{mis} . The (consistent) estimation of (2) in such a context follows directly from the existing literature on misclassification in binary outcome models, e.g. *Hausman et al. (1998)*.

Let q_1 be the probability of false positives and q_0 be the probability of false negatives (both being elements of $\boldsymbol{\rho}$). The estimator for the distribution of the true network is given by $P(a_{ij} = 1 | \hat{\boldsymbol{\rho}}, a_{ij}^{mis}) = a_{ij}^{mis}(1 - \hat{q}_1) + (1 - a_{ij}^{mis})\hat{q}_0$.

Example 4 (Aggregated Relational Data). Aggregated relational data (ARD) are obtained from survey questions such as, “How many friends with trait ‘X’ do you have?” Here, \mathcal{A} can be represented by an $N \times K$ matrix of integer values, where K is the number of traits that individuals were asked about.

Building on *McCormick and Zheng (2015)*, *Breza et al. (2020)* proposed a novel approach for the estimation of network formation models using only ARD. They assume:

$$P(a_{ij} = 1) \propto \exp\{\nu_i + \nu_j + \zeta \mathbf{z}'_i \mathbf{z}_j\}, \quad (3)$$

where ν_i , ν_j , ζ , \mathbf{z}_i , and \mathbf{z}_j are not observed by the econometrician but follow parametric distributions. Here, parameters ν_i and ν_j can be interpreted as i and j ’s propensities to create links, irrespective of the identity of the other individual involved. The other component, $\zeta \mathbf{z}'_i \mathbf{z}_j$, is meant to capture homophily (like attracts like) on an abstract latent space (e.g. *Hoff et al. (2002)*).

Breza et al. (2020) show that it is possible to use aggregate relational data (ARD) to recover the values of the variables in (3). In particular, letting $\boldsymbol{\rho} = [\{\nu_i\}_i, \{\mathbf{z}_i\}_i, \zeta]$, *Breza et al. (2019)* provide sufficient conditions for the consistent estimation of $\boldsymbol{\rho}$.

Contrary to Examples 1–3, ARD does not provide information on any specific links;¹⁴ therefore, the predicted distribution of the true network is $P(a_{ij} | \hat{\boldsymbol{\rho}}, \mathcal{A}) = P(a_{ij} | \hat{\boldsymbol{\rho}})$, which is given by Equation (3).

¹⁴That is, unless ARD include the degree distribution with some individuals reporting having no links at all.

3 Estimation Using Instrumental Variables

We now present our instrumental variable strategy. To understand the underlying intuition, note that it is not necessary to observe the complete network structure to observe \mathbf{y} , \mathbf{X} , \mathbf{GX} , and \mathbf{Gy} . For example, one could simply obtain \mathbf{Gy} from survey data, “What is the average value of your friends’ y ?”

However, even observing \mathbf{y} , \mathbf{X} , \mathbf{GX} , and \mathbf{Gy} , the model (1) cannot be simply estimated using simple linear regression. The reason is that \mathbf{Gy} is endogenous; thus, a linear regression would produce biased estimates (e.g. [Manski \(1993\)](#), [Bramoullé et al. \(2009\)](#)).

The typical instrumental approach to deal with this endogeneity is to use instruments based on the structural model, i.e. instruments constructed using second-degree peers (e.g. $\mathbf{G}^2\mathbf{X}$, see [Bramoullé et al. \(2009\)](#)). These are less likely to be found in survey data. Indeed, we could doubt the informativeness of questions such as, “What is the average value of your friends’ average value of their friends’ x ?”

[Propositions 1](#) and [2](#) describe how to construct valid instruments when the researcher observes \mathbf{y} , \mathbf{X} , and \mathbf{GX} . To clearly expose the argument, we first start by discussing the special case where there are no contextual effects: $\boldsymbol{\gamma} = \mathbf{0}$. The model in (1) can therefore be rewritten as:

$$\mathbf{y} = c\mathbf{1} + \mathbf{X}\boldsymbol{\beta} + \alpha\mathbf{Gy} + \boldsymbol{\varepsilon}.$$

The following proposition holds.¹⁵

Proposition 1. *Assume that $\boldsymbol{\gamma} = \mathbf{0}$. There are two cases:*

1. *Suppose that \mathbf{Gy} is observed and let \mathbf{H} be an interaction matrix, correlated with \mathbf{G} , and such that $\mathbb{E}[\boldsymbol{\varepsilon}|\mathbf{X}, \mathbf{H}] = \mathbf{0}$. Then, $\mathbf{HX}, \mathbf{H}^2\mathbf{X}, \dots$ are valid instruments.*
2. *Suppose that \mathbf{Gy} is not observed and let $\dot{\mathbf{G}}$ and $\ddot{\mathbf{G}}$ be two independent draws from the distribution $\hat{P}(\mathbf{G})$. Then, $\dot{\mathbf{G}}\mathbf{X}, \dot{\mathbf{G}}^2\mathbf{X}, \dots$ are valid instruments when $\ddot{\mathbf{G}}\mathbf{y}$ is used as a proxy for \mathbf{Gy} , as $N \rightarrow \infty$.*

First, suppose that \mathbf{Gy} is observed directly from the data. Then, any instrument correlated with the usual instruments $\mathbf{GX}, \mathbf{G}^2\mathbf{X}, \dots$, while being exogenous, are valid. Note that

¹⁵Proofs of [Propositions 1](#) and [2](#) can be found in [Appendix A](#).

a special case of the first part of Proposition 1 is when \mathbf{H} is drawn from $\hat{P}(\mathbf{G})$. However, the instrument remains valid if the researcher uses a *mispecified* estimator of the distribution $P(\mathbf{G})$.¹⁶ A similar strategy is used by Kelejian and Piras (2014) and Lee et al. (2020) in a different context. Of course, the specification error on $P(\mathbf{G})$ must be independent of $\boldsymbol{\varepsilon}$. In Section 3.1, we discuss the importance of this robustness feature in a context in which the network formation process could be misspecified or subject to small sample biases.¹⁷

When \mathbf{Gy} is *not* observed directly, however, specification errors typically produce invalid instruments. As stated in Part 2 of Proposition 1, the estimation also requires two independent draws from $\hat{P}(\mathbf{G})$ instead of just one. To see why, let us rewrite the model as:

$$\mathbf{y} = c\mathbf{1} + \mathbf{X}\boldsymbol{\beta} + \alpha\ddot{\mathbf{G}}\mathbf{y} + [\boldsymbol{\eta} + \boldsymbol{\varepsilon}],$$

where $\boldsymbol{\eta} = \alpha[\mathbf{Gy} - \ddot{\mathbf{G}}\mathbf{y}]$ is the error due to the approximation of \mathbf{Gy} . Suppose also that $\dot{\mathbf{G}}\mathbf{X}$ is used as an instrument for \mathbf{Gy} .

The validity of the instrument therefore requires $\mathbb{E}[\boldsymbol{\eta} + \boldsymbol{\varepsilon} | \mathbf{X}, \dot{\mathbf{G}}\mathbf{X}] = 0$, and in particular:

$$\mathbb{E}[\mathbf{Gy} | \mathbf{X}, \dot{\mathbf{G}}\mathbf{X}] = \mathbb{E}[\ddot{\mathbf{G}}\mathbf{y} | \mathbf{X}, \dot{\mathbf{G}}\mathbf{X}],$$

which is true since \mathbf{G} and $\ddot{\mathbf{G}}$ are drawn from the same asymptotic distribution.

Of course, Proposition 1 assumes that there are no contextual effects. We show that a similar result holds when $\boldsymbol{\gamma} \neq \mathbf{0}$. To estimate (1) using an instrumental variable approach, however, we must assume that \mathbf{GX} are *observed*. The reason is that there are no natural, strong instruments for \mathbf{GX} .¹⁸ In Section 4, we present an alternative estimation strategy that does not require the observation of \mathbf{GX} .

¹⁶We would like to thank Chih-Sheng Hsieh and Arthur Lewbel for discussions on this important point.

¹⁷Note, however, that if the specification error is too large, the correlation between \mathbf{Gy} and \mathbf{HX} will likely be small, leading to a problem of weak instruments. It is also worth noting that the first part of Proposition 1 does not depend on the assumption that groups are entirely sampled (i.e. Assumption 3).

¹⁸Indeed, the strengths of the instruments in Proposition 1 come from the fact that \mathbf{GX} are strong instruments for \mathbf{Gy} when \mathbf{G} is observed. Proxying \mathbf{GX} with $\dot{\mathbf{G}}\mathbf{X}$ and instrumenting with $\dot{\mathbf{G}}\mathbf{X}$ would be valid. However, the explanatory power of $\dot{\mathbf{G}}\mathbf{X}$, conditional on $\ddot{\mathbf{G}}\mathbf{X}$, would be much too weak to be of any practical use.

Proposition 2. Assume that $\mathbf{G}\mathbf{X}$ are observed. There are two cases:

1. Suppose that $\mathbf{G}\mathbf{y}$ is observed and let \mathbf{H} be an interaction matrix, correlated with \mathbf{G} , and such that $\mathbb{E}[\boldsymbol{\varepsilon}|\mathbf{X}, \mathbf{H}] = \mathbf{0}$. Then, $\mathbf{H}^2\mathbf{X}, \mathbf{H}^3\mathbf{X}, \dots$ are valid instruments.
2. Suppose that $\mathbf{G}\mathbf{y}$ is not observed and let $\dot{\mathbf{G}}$ and $\ddot{\mathbf{G}}$ be two independent draws from the distribution $\hat{P}(\mathbf{G})$. Then, $\dot{\mathbf{G}}^2\mathbf{X}, \dot{\mathbf{G}}^3\mathbf{X}, \dots$ are valid instruments when $\dot{\mathbf{G}}\mathbf{y}$ is used as a proxy for $\mathbf{G}\mathbf{y}$, if $\dot{\mathbf{G}}\mathbf{X}$ are added as additional explanatory variables and as $N \rightarrow \infty$.

The first part of Proposition 2 is a simple extension of the first part of Proposition 1. The second part of Proposition 2 requires more discussion. Essentially, it states that $\dot{\mathbf{G}}^2\mathbf{X}, \dot{\mathbf{G}}^3\mathbf{X}, \dots$ are valid instruments when the following *expanded model* is estimated:

$$\mathbf{y} = c\mathbf{1} + \mathbf{X}\boldsymbol{\beta} + \alpha\ddot{\mathbf{G}}\mathbf{y} + \mathbf{G}\mathbf{X}\boldsymbol{\gamma} + \ddot{\mathbf{G}}\mathbf{X}\check{\boldsymbol{\gamma}} + \boldsymbol{\eta} + \boldsymbol{\varepsilon}, \quad (4)$$

where the true value of $\check{\boldsymbol{\gamma}}$ is $\mathbf{0}$.

To understand why the introduction of $\mathbf{G}\mathbf{X}\check{\boldsymbol{\gamma}}$ is needed, recall that the constructed instrument must be uncorrelated with the approximation error $\boldsymbol{\eta}$. This correlation is conditional on the explanatory variables, which contain \mathbf{G} . In particular, it implies that generically,

$$\mathbb{E}[\mathbf{G}\mathbf{y}|\mathbf{X}, \mathbf{G}\mathbf{X}, \dot{\mathbf{G}}^2\mathbf{X}] \neq \mathbb{E}[\ddot{\mathbf{G}}\mathbf{y}|\mathbf{X}, \mathbf{G}\mathbf{X}, \dot{\mathbf{G}}^2\mathbf{X}].$$

However, adding the auxiliary variable $\dot{\mathbf{G}}\mathbf{X}$ as a covariate is sufficient to restore the result, i.e. as $N \rightarrow \infty$:

$$\mathbb{E}[\mathbf{G}\mathbf{y}|\mathbf{X}, \mathbf{G}\mathbf{X}, \dot{\mathbf{G}}^2\mathbf{X}, \dot{\mathbf{G}}\mathbf{X}] = \mathbb{E}[\ddot{\mathbf{G}}\mathbf{y}|\mathbf{X}, \mathbf{G}\mathbf{X}, \dot{\mathbf{G}}^2\mathbf{X}, \dot{\mathbf{G}}\mathbf{X}].$$

Proposition 1 and Proposition 2 therefore show that the estimation of (1) is possible, even with very limited information about the network structure. Note, however, that the validity of the constructed instruments only holds asymptotically. In Section 3.1, we study the finite sample properties of our approach using network formation models estimated on aggregated relational data (Breza et al. (2020); see Example 4). Before, however, we briefly discuss how one can adapt this estimation strategy while allowing for group-level unobservables.

Indeed, a common assumption is that each group in the population is affected by a common shock, unobserved by the econometrician (e.g. [Bramoullé et al. \(2009\)](#)). As such, for each group $r = 1, \dots, M$, we have: $\mathbf{y}_r = c_r \mathbf{1}_r + \mathbf{X}_r \boldsymbol{\beta} + \alpha \mathbf{G}_r \mathbf{y}_r + \mathbf{G}_r \mathbf{X}_r \boldsymbol{\gamma} + \boldsymbol{\varepsilon}_r$, where c_r is not observed, $\mathbf{1}_r$ is an N_r -dimensional vector of ones, N_r is the size of the group r , \mathbf{G}_r is the subinteraction matrix in the group r , and $\boldsymbol{\varepsilon}_r$ is the vector of error terms in the group r .

Under Assumption 2, it is not possible to obtain a consistent estimator of $\{c_r\}_{r=1}^m$ because the number of observations used to estimate each c_r is bounded. This is known as the *incidental parameter problem*.¹⁹ A common strategy is to use deviations from the group average and estimate the model in deviations (e.g. [Bramoullé et al. \(2009\)](#)).

Let $\mathbf{J} = \text{diag}\{\mathbf{I}_{N_r} - \frac{1}{N_r} \mathbf{1}_r \mathbf{1}'_r\}$ be the group-differentiating matrix, where \mathbf{I}_{N_r} is the identified matrix of dimension N_r . The operator *diag* generates a block-diagonal matrix in which each group is a block.²⁰ We can rewrite: $\mathbf{Jy} = \mathbf{JX}\boldsymbol{\beta} + \alpha \mathbf{JGy} + \mathbf{JGX}\boldsymbol{\gamma} + \mathbf{J}\boldsymbol{\varepsilon}$. Note that the results of Propositions 1 and 2 extend directly, using instruments in deviation with the group average.

3.1 Finite Sample Performance Using ARD

In this section, we study the small sample performance of the estimator presented in Section 3 when the researcher only has access to ARD (as in Example 4). First, we simulate network data using the model proposed by [Breza et al. \(2020\)](#) and simulate outcomes using the linear in means model (1) conditional on the simulated networks. Second, we estimate the network formation model using the Bayesian estimator proposed by [Breza et al. \(2020\)](#) (yielding $\hat{\rho}_B$), as well as using the classical estimator proposed by [Alidaee et al. \(2020\)](#) (yielding $\hat{\rho}_A$). Third, we estimate the linear-in-means model, using our IV estimator based on $\hat{\rho}_A$ and $\hat{\rho}_B$.

Recall that

$$P(a_{ij} = 1) \propto \exp\{\nu_i + \nu_j + \zeta \mathbf{z}'_i \mathbf{z}_j\}, \quad (5)$$

where ν_i , ν_j , ζ , \mathbf{z}_i , and \mathbf{z}_j are not observed by the econometrician but follow parametric distributions. We refer the interested reader to [McCormick and Zheng \(2015\)](#), [Breza et al. \(2020\)](#), and [Breza et al. \(2019\)](#) for a formal discussion of the model, including its identification

¹⁹See [Lancaster \(2000\)](#) for a review.

²⁰Then, \mathbf{Jw} gives \mathbf{w} minus the group average of \mathbf{w} .

and consistent estimation. Here, we discuss the intuition using a simple analogy.

Suppose that individuals are located according to their geographical position on Earth. Suppose also that there are a fixed number of cities on Earth in which individuals can live. The econometrician does not know the individuals' locations on Earth nor do they know the location of the cities. In model (5), \mathbf{z}_i represent i 's position on Earth. However, the econometrician has access to ARD for a subset of the population, i.e. answers to questions such as, "How many of your friends live in city A ?"

To understand the intuition behind the identification of the model, consider the following example: suppose that individual i has many friends living in city A . Then, city A is likely located close to i 's location. Similarly, if many individuals have many friends living in city A , then city A is likely a large city. Finally, if i has many friends from many cities, i likely has a large ν_i .

To study the finite sample performance of our instrumental strategy in this context, we simulate 20 groups of 250 individuals each. Within each subpopulation, we simulate the ARD responses as well as a series of observable characteristics (e.g. cities). The details of the Monte Carlo simulations can be found in Appendix B.

Importantly, the model in (5) is based on a single population framework. Thus, the network formation model must be estimated separately for each of the 20 groups. With only 250 individuals in each group, we therefore expect significant small-sample bias.

We contrast the estimator proposed by Breza et al. (2020) with the one proposed by Alidaee et al. (2020). Whereas Breza et al. (2020) present a parametric Bayesian estimator, Alidaee et al. (2020) propose a (nonparametric) penalized regression based on a low-rank assumption. One main advantage of their estimator is that it allows for a wider class of model and ensures that the estimation is fast and easily implementable.²¹ Note, however, that their method only yields a consistent estimator of $\hat{P}(\mathbf{A})$ if the true network is effectively low rank.

Very intuitively, the low-rank assumption implies that linking probabilities were generated from a small number of parameters; for example, in the example above, knowing individuals' gregariousness parameters ν_i and city in which they live would allow a predic-

²¹The authors developed user-friendly packages in R and Python. See their paper for links and details.

tion of the linking probabilities.

Importantly, the model (5) is not necessarily low rank; for example, if the individuals' locations on Earth (i.e. the \mathbf{z}_i 's) are uniformly distributed and there are only very few large cities, then the model produced is not low rank and the method proposed by Alidaee et al. (2020) performs poorly. Intuitively, in such a case, the fact that individual i lives in city A poorly explains the linking probabilities.

We compare the performance of both estimators as we vary the concentration parameter for the individuals' locations on Earth (that is, κ , see Appendix B for details). This has the effect of changing the *effective rank* of the linking probabilities: increasing κ decreases the effective rank.²² We therefore expect the estimator proposed by Alidaee et al. (2020) to perform better for larger values of κ .

Results are presented in Tables 1 and 2. When \mathbf{Gy} is observed, both estimators perform extremely well. In light of Propositions 1 and 2, this is expected, as the IV estimator is valid even under misspecification. When \mathbf{Gy} is not observed, results are more nuanced. First, note that for all specifications, the introduction of the non-pertinent variables $\ddot{\mathbf{G}}\mathbf{X}$ contaminates the estimation of $\boldsymbol{\gamma}$. This occurs because \mathbf{GX} and $\ddot{\mathbf{G}}\mathbf{X}$ are highly correlated.²³ Note, however, that the estimated values for $\boldsymbol{\gamma} + \dot{\boldsymbol{\gamma}}$ are centered on the true value. Second, the bias of the estimated endogenous peer effect (i.e. α) goes to zero when the linking probabilities are of lower rank, with an advantage for the estimator proposed by Breza et al. (2020). This is expected because the model is correctly specified and the estimator is parametric.

Overall, our IV estimator can be successfully implemented in small samples, using either the estimator proposed by Breza et al. (2020) or by Alidaee et al. (2020), both of which only rely on the observation of ARD.

²²We refer the interested reader to Alidaee et al. (2020) for a formal discussion of the effective rank and of its importance for their estimator.

²³This issue is not because of the assumed network formation model and would arise even if the linking probabilities were known (instead of being estimated).

Table 1: Simulation results with ARD - network distribution estimated following Breza et al. (2020)

Statistic	Mean	Std. Dev.	Pctl(25)	Median	Pctl(75)
$\kappa = 0, N = 250, M = 20$					
\mathbf{Gy} is observed					
$\alpha = 0.4$	0.400	0.007	0.395	0.400	0.405
$\gamma_1 = 5$	5.000	0.021	4.986	5.000	5.014
$\gamma_2 = -3$	-3.001	0.031	-3.021	-3.000	-2.980
\mathbf{Gy} is not observed					
$\alpha = 0.4$	0.371	0.013	0.363	0.372	0.380
$\gamma_1 = 5$	5.396	0.021	5.383	5.397	5.410
$\gamma_2 = -3$	-2.400	0.041	-2.428	-2.400	-2.371
$\hat{\gamma}_1 = 0$	-0.380	0.028	-0.400	-0.382	-0.362
$\hat{\gamma}_2 = 0$	-0.553	0.044	-0.584	-0.551	-0.525
$\kappa = 10, N = 250, M = 20$					
\mathbf{Gy} is observed					
$\alpha = 0.4$	0.400	0.006	0.396	0.400	0.404
$\gamma_1 = 5$	5.001	0.019	4.988	5.001	5.014
$\gamma_2 = -3$	-3.000	0.031	-3.020	-3.000	-2.978
\mathbf{Gy} is not observed					
$\alpha = 0.4$	0.400	0.007	0.395	0.400	0.405
$\gamma_1 = 5$	5.392	0.019	5.379	5.393	5.405
$\gamma_2 = -3$	-2.397	0.037	-2.421	-2.398	-2.373
$\hat{\gamma}_1 = 0$	-0.391	0.022	-0.405	-0.390	-0.375
$\hat{\gamma}_2 = 0$	-0.604	0.038	-0.630	-0.605	-0.579
$\kappa = 20, N = 250, M = 20$					
\mathbf{Gy} is observed					
$\alpha = 0.4$	0.400	0.006	0.396	0.400	0.404
$\gamma_1 = 5$	5.000	0.020	4.986	4.999	5.013
$\gamma_2 = -3$	-3.001	0.031	-3.021	-3.001	-2.981
\mathbf{Gy} is not observed					
$\alpha = 0.4$	0.400	0.007	0.396	0.400	0.405
$\gamma_1 = 5$	5.390	0.019	5.377	5.390	5.403
$\gamma_2 = -3$	-2.398	0.036	-2.422	-2.398	-2.375
$\hat{\gamma}_1 = 0$	-0.390	0.022	-0.405	-0.390	-0.376
$\hat{\gamma}_2 = 0$	-0.604	0.036	-0.628	-0.604	-0.579

Note: In each subnetwork, the spherical coordinates of individuals are generated from a von Mises–Fisher distribution with a location parameter $(1, 0, 0)$ and intensity parameter κ . Details of the simulation exercise can be found in Appendix B. Predicted probabilities are computed using the mean of the posterior distribution. We do not report the estimated values for c and β to keep the table readable, but they are available upon request. Instruments are build using only second-degree peers, i.e. $\mathbf{G}^2\mathbf{X}$.

Table 2: Simulation results with ARD - network distribution estimated following [Alidaee et al. \(2020\)](#)

Statistic	Mean	Std. Dev.	Pctl(25)	Median	Pctl(75)
$\kappa = 0, N = 250, M = 20$					
Gy is observed					
$\alpha = 0.4$	0.400	0.012	0.393	0.400	0.407
$\gamma_1 = 5$	5.000	0.029	4.980	4.999	5.019
$\gamma_2 = -3$	-3.000	0.032	-3.021	-3.000	-2.978
Gy is not observed					
$\alpha = 0.4$	0.371	0.024	0.357	0.373	0.387
$\gamma_1 = 5$	5.504	0.036	5.479	5.503	5.528
$\gamma_2 = -3$	-2.480	0.057	-2.517	-2.480	-2.441
$\hat{\gamma}_1 = 0$	-0.364	0.031	-0.385	-0.363	-0.344
$\hat{\gamma}_2 = 0$	-0.302	0.070	-0.349	-0.304	-0.254
$\kappa = 10, N = 250, M = 20$					
Gy is observed					
$\alpha = 0.4$	0.400	0.009	0.395	0.400	0.405
$\gamma_1 = 5$	4.999	0.022	4.985	4.999	5.014
$\gamma_2 = -3$	-3.000	0.032	-3.022	-3.001	-2.978
Gy is not observed					
$\alpha = 0.4$	0.395	0.021	0.388	0.397	0.405
$\gamma_1 = 5$	5.396	0.027	5.378	5.394	5.412
$\gamma_2 = -3$	-2.412	0.045	-2.439	-2.410	-2.383
$\hat{\gamma}_1 = 0$	-0.385	0.032	-0.404	-0.387	-0.370
$\hat{\gamma}_2 = 0$	-0.462	0.117	-0.534	-0.483	-0.414
$\kappa = 20, N = 250, M = 20$					
Gy is observed					
$\alpha = 0.4$	0.400	0.008	0.395	0.400	0.405
$\gamma_1 = 5$	5.000	0.021	4.985	5.000	5.013
$\gamma_2 = -3$	-2.999	0.032	-3.020	-2.999	-2.979
Gy is not observed					
$\alpha = 0.4$	0.399	0.010	0.393	0.400	0.406
$\gamma_1 = 5$	5.391	0.020	5.378	5.391	5.404
$\gamma_2 = -3$	-2.400	0.039	-2.425	-2.400	-2.374
$\hat{\gamma}_1 = 0$	-0.391	0.022	-0.406	-0.391	-0.376
$\hat{\gamma}_2 = 0$	-0.573	0.047	-0.605	-0.575	-0.544

Note: In each subnetwork, the spherical coordinates of individuals are generated from a von Mises–Fisher distribution with location parameter $(1, 0, 0)$ and intensity parameter κ . Details of the simulation exercise can be found in Appendix B. We chose the weight associated with the nuclear norm penalty to minimize the RMSE through cross-validation. This value of $\lambda = 600$ is smaller than the recommended value in [Alidaee et al. \(2020\)](#). We do not report the estimated values for c and β to keep the table readable, but they are available upon request. Instruments are build using only second-degree peers, i.e. $\mathbf{G}^2\mathbf{X}$.¹⁹

4 Estimation Using Bayesian Inference

The approach developed in the previous section assumes that \mathbf{GX} are observed. When they are not, the instrumental variable estimators fail. We therefore present a likelihood-based estimator. Accordingly, greater structure must be imposed on the errors $\boldsymbol{\varepsilon}$.²⁴

To clarify the exposition, we will focus on the network adjacency matrix \mathbf{A} rather than the interaction matrix \mathbf{G} . Of course, this is without any loss of generality. Given parametric assumptions for $\boldsymbol{\varepsilon}$, one can write the log-likelihood of the outcome as:²⁵

$$\ln \mathcal{P}(\mathbf{y}|\mathbf{A}, \boldsymbol{\theta}), \quad (6)$$

where $\boldsymbol{\theta} = [\alpha, \boldsymbol{\beta}', \boldsymbol{\gamma}', \boldsymbol{\sigma}']'$, $\boldsymbol{\sigma}$ are unknown parameters from the distribution of $\boldsymbol{\varepsilon}$. Note that $\mathbf{y} = (\mathbf{I}_N - \alpha\mathbf{G})^{-1}(c\mathbf{1} + \mathbf{X}\boldsymbol{\beta} + \mathbf{GX}\boldsymbol{\gamma} + \boldsymbol{\varepsilon})$ and $(\mathbf{I}_N - \alpha\mathbf{G})^{-1}$ exist under our Assumption 1.

If the adjacency matrix \mathbf{A} was observed, then $(\boldsymbol{\theta})$ could be estimated using a simple maximum likelihood estimator (as in [Lee et al. \(2010\)](#)) or using Bayesian inference (as in [Goldsmith-Pinkham and Imbens \(2013\)](#)).

Since \mathbf{A} is not observed, an alternative would be to focus on the unconditional likelihood, i.e.

$$\ln \mathcal{P}(\mathbf{y}|\boldsymbol{\theta}) = \ln \sum_{\mathbf{A}} \mathcal{P}(\mathbf{y}|\mathbf{A}, \boldsymbol{\theta}) P(\mathbf{A}).$$

A similar strategy is proposed by [Chandrasekhar and Lewis \(2011\)](#) using a GMM estimator.

One particular issue with estimating $\ln \mathcal{P}(\mathbf{y}|\boldsymbol{\theta})$ is that the summation is not tractable. Indeed, the sum is over the set of possible adjacency matrices, which contain $2^{N(N-1)}$ elements. Then, simply simulating networks from $P(\mathbf{A})$ (or rather from $\hat{P}(\mathbf{A})$) as proposed by [Chandrasekhar and Lewis \(2011\)](#), and taking the average likely lead to poor approximations. A classical way to address this issue is to use an EM algorithm ([Dempster et al., 1977](#)). Although valid, we found that the Bayesian estimator proposed in this section is less restrictive and numerically outperforms its classical counterpart.

²⁴One could also use our estimator to solve a classical estimator such as a GMM estimator, like that proposed by [Chandrasekhar and Lewis \(2011\)](#), using either the approach proposed by [Chernozhukov and Hong \(2003\)](#), or the Bayesian empirical likelihood approach by [Chib et al. \(2018\)](#).

²⁵Note that under Assumption 2, the likelihood can be factorized across groups.

For concreteness, we will assume that $\boldsymbol{\varepsilon} \sim \mathcal{N}(0, \sigma^2 \mathbf{I}_N)$; however, it should be noted that our approach is valid for a number of alternative assumptions. We have for $\mathbf{G} = f(\mathbf{A})$,

$$\begin{aligned}\ln \mathcal{P}(\mathbf{y}|\mathbf{A}, \boldsymbol{\theta}) &= -N \ln(\sigma) + \ln |\mathbf{I}_N - \alpha \mathbf{G}| - \frac{N}{2} \ln(\pi) \\ &\quad - \frac{1}{2\sigma^2} [(\mathbf{I}_N - \alpha \mathbf{G})\mathbf{y} - c\mathbf{1}_N - \mathbf{X}\boldsymbol{\beta} - \mathbf{G}\mathbf{X}\boldsymbol{\gamma}]' \cdot \\ &\quad [(\mathbf{I}_N - \alpha \mathbf{G})\mathbf{y} - c\mathbf{1}_N - \mathbf{X}\boldsymbol{\beta} - \mathbf{G}\mathbf{X}\boldsymbol{\gamma}].\end{aligned}$$

Since \mathbf{A} is not observed, we follow [Tanner and Wong \(1987\)](#) and [Albert and Chib \(1993\)](#), and we use data augmentation to evaluate the posterior distribution of $\boldsymbol{\theta}$. That is, instead of focusing on the posterior $p(\boldsymbol{\theta}|\mathbf{y}, \mathbf{A})$, we focus on the posterior $p(\boldsymbol{\theta}, \mathbf{A}|\mathbf{y}, \mathcal{A})$, treating \mathbf{A} as another set of unknown parameters. Note that we now make the dependence on \mathcal{A} explicit for clarity.

Indeed, the identification of the model rests on the a priori information of \mathbf{A} . A sensible prior for \mathbf{A} is the consistent estimator of its distribution, i.e. $\hat{P}(\mathbf{A}|\mathcal{A}) \equiv P(\mathbf{A}|\hat{\boldsymbol{\rho}}, \mathcal{A})$. One may wish, however, to also use the information regarding the sampling uncertainty around $\hat{P}(\mathbf{A}|\mathcal{A})$. This is very similar to inference for two-step estimators in a classical setting: estimation uncertainty in the first stage must be accounted for to provide valid inference in the second stage (see [Cameron and Trivedi \(2005\)](#), Section 6.6, for a discussion).

Let $\pi(\boldsymbol{\rho}|\mathcal{A})$ be the prior density on $\boldsymbol{\rho}$. How to obtain $\pi(\boldsymbol{\rho}|\mathcal{A})$, depending on whether $\hat{\boldsymbol{\rho}}$ is obtained using a Bayesian or classical setting, is discussed in Examples 5 and 6 below. Given $\pi(\boldsymbol{\rho}|\mathcal{A})$, it is possible to obtain draws from the posterior distribution $p(\boldsymbol{\rho}, \mathbf{A}|\mathbf{y}, \mathcal{A})$ using the following MCMC:

Algorithm 1. *The MCMC goes as follows for $t = 1, \dots, T$, starting from any $\mathbf{A}_0, \boldsymbol{\theta}_0$, and $\boldsymbol{\rho}_0$.*

1. Draw $\boldsymbol{\rho}^*$ from the proposal distribution $q_{\boldsymbol{\rho}}(\boldsymbol{\rho}^*|\boldsymbol{\rho}_{t-1})$ and accept $\boldsymbol{\rho}^*$ with probability

$$\min \left\{ 1, \frac{P(\mathbf{A}_{t-1}|\boldsymbol{\rho}^*, \mathcal{A}) q_{\boldsymbol{\rho}}(\boldsymbol{\rho}_{t-1}|\boldsymbol{\rho}^*) \pi(\boldsymbol{\rho}^*|\mathcal{A})}{P(\mathbf{A}_{t-1}|\boldsymbol{\rho}_{t-1}, \mathcal{A}) q_{\boldsymbol{\rho}}(\boldsymbol{\rho}^*|\boldsymbol{\rho}_{t-1}) \pi(\boldsymbol{\rho}_{t-1}|\mathcal{A})} \right\}.$$

2. Propose \mathbf{A}^* from the proposal distribution $q_A(\mathbf{A}^* | \mathbf{A}_{t-1})$ and accept \mathbf{A}^* with probability

$$\min \left\{ 1, \frac{\mathcal{P}(\mathbf{y} | \boldsymbol{\theta}_{t-1}, \mathbf{A}^*) q_A(\mathbf{A}_{t-1} | \mathbf{A}^*) P(\mathbf{A}^* | \boldsymbol{\rho}_{t-1}, \mathcal{A})}{\mathcal{P}(\mathbf{y} | \boldsymbol{\theta}_{t-1}, \mathbf{A}_{t-1}) q_A(\mathbf{A}^* | \mathbf{A}_{t-1}) P(\mathbf{A}_{t-1} | \boldsymbol{\rho}_{t-1}, \mathcal{A})} \right\}.$$

3. Draw α^* from the proposal $q_\alpha(\cdot | \alpha_{t-1})$ and accept α^* with probability

$$\min \left\{ 1, \frac{\mathcal{P}(\mathbf{y} | \mathbf{A}_t; \boldsymbol{\beta}_{t-1}, \boldsymbol{\gamma}_{t-1}, \alpha^*) q_\alpha(\alpha_{t-1} | \alpha^*) \pi(\alpha^*)}{\mathcal{P}(\mathbf{y} | \mathbf{A}_t; \boldsymbol{\theta}_{t-1}) q_\alpha(\alpha^* | \alpha_{t-1}) \pi(\alpha_{t-1})} \right\}.$$

4. Draw $[\boldsymbol{\beta}, \boldsymbol{\gamma}, \sigma]$ from their conditional distributions.

As discussed, Step 1 accounts for the sampling uncertainty around the true value of $\boldsymbol{\rho}$. If the true value of $\boldsymbol{\rho}$ was known (instead of being estimated) Step 1 would not be required. Step 1 shows that the flexibility of the network formation model comes at a cost. For example, [Graham \(2017\)](#) and [Breza et al. \(2020\)](#) propose network formation models for which the number of parameters is $O(N)$. In turn, this large number of parameters increases the computational cost of Step 1.

Example 5 (Priors from the Asymptotic Distribution of $\boldsymbol{\rho}$). *In a classical setting, and under the usual assumptions, the estimation of (2) produces a estimator $\hat{\boldsymbol{\rho}}$ of $\boldsymbol{\rho}_0$ as well as an estimator of the asymptotic variance of $\hat{\boldsymbol{\rho}}$, i.e. $\hat{\mathbf{V}}(\hat{\boldsymbol{\rho}})$. In this case, we define the prior density $\pi(\boldsymbol{\rho})$ as the density of a multivariate normal distribution with mean $\hat{\boldsymbol{\rho}}$ and variance-covariance matrix $\hat{\mathbf{V}}(\hat{\boldsymbol{\rho}})$.*

Example 6 (Priors from the Posterior Distribution of $\boldsymbol{\rho}$). *In a Bayesian setting, the estimation of $\boldsymbol{\rho}$ from the network formation model (2) results in draws from the posterior distribution of $\boldsymbol{\rho}$. It is therefore natural to use such a posterior distribution as the prior distribution of \mathbf{A} for the estimation based on (6). Performing such a sequential Bayesian updating approach comes with a well-known numerical issue.²⁶*

Indeed, the evaluation of the acceptance ratio in Step 1 of Algorithm 1 below requires the evaluation of the density of $\boldsymbol{\rho}$ at different values. Ideally, one would use the draws from the posterior distribution of $\boldsymbol{\rho}$ from the first step (network formation model) and perform

²⁶See [Thijssen and Wessels \(2020\)](#) for a recent discussion.

a nonparametric kernel density estimation of the posterior distribution. However, when the dimension of ρ is large, the kernel density estimation may be infeasible in practice.

This is especially true for very flexible network formation models, such as the one proposed by Breza et al. (2020), for which the number of parameters to estimate is $O(N)$. In such a case, it might be more reasonable to use a more parametric approach or to impose additional restrictions on the dependence structure of ρ across dimensions.²⁷

Detailed distributions for Steps 3 and 4 can be found in Appendix C.1. Step 2, however, involves requires some discussion. Indeed, the idea is the following: given the prior information $P(\mathbf{A}|\rho_{t-1}, \mathcal{A})$, one must be able to draw samples from the posterior distribution of \mathbf{A} , given \mathbf{y} . This is not a trivial task.

In particular, there is no general rule for selecting the network proposal distribution $q_A(\cdot|\cdot)$. A natural candidate is a Gibbs sampling algorithm for each link, i.e. change only one link ij at every step t and propose a_{ij} according to its marginal distribution, i.e. $a_{ij} \sim P(\cdot|\mathbf{A}_{-ij}, \mathbf{y}, \mathcal{A})$, where $\mathbf{A}_{-ij} = \{a_{kl}; k \neq i, l \neq j\}$. In this case, the proposal is always accepted.

However, it has been argued that Gibbs sampling could lead to slow convergence (e.g. Snijders (2002), Chatterjee et al. (2013)), especially when the network is *sparse* or exhibits a high level of *clustering*. For example, Mele (2017) and Bhamidi et al. (2008) propose different blocking techniques that are meant to improve convergence.

Here, however, achieving Step 2 involves an additional computational issue because evaluating the likelihood ratio in Step 1 requires comparing the determinants $|\mathbf{I} - \alpha f(\mathbf{A}^*)|$ for each proposed \mathbf{A}^* , which is computationally intensive. In particular, taking $\mathbf{G}^* = f(\mathbf{A}^*)$ to be a row-normalization of \mathbf{A}^* , changing a single element of \mathbf{A}^* results in a change in the entire corresponding row of \mathbf{G}^* . Still, comparing the determinant of two matrices that differ only in a single row is relatively fast. Moreover, when $\mathbf{G} = \mathbf{A}$, Hsieh et al. (2019) propose a blocking technique that facilitates the computation of the determinant.

In any case, note that the computational complexity of Step 2 depends strongly on $P(\mathbf{A}|\rho_{t-1}, \mathcal{A})$, which is a function of the assumed network formation model (2) and of

²⁷For example, if we assume that the posterior distribution of ρ is jointly normal, the estimation of the mean and variance-covariance matrix is straightforward, even in a high-dimensional setting. Simulations reported in the online Appendix suggest that this approach performs well in practice.

the observed information about the network structure \mathcal{A} . For censored network data, for example, most of the network structure is observed (see Example 2). This implies that $P(a_{ij}|\boldsymbol{\rho}_{t-1}, \mathcal{A}) \in \{0, 1\}$ for most pairs ij . As such, few entries of \mathbf{A} must be updated in Step 2. The opposite is true for ARD (see Example 4) for which all entries of \mathbf{A} must be updated.

Then, the appropriate blocking technique depends strongly on $P(\mathbf{A}|\boldsymbol{\rho}_{t-1}, \mathcal{A})$ as well as on the assumed distribution for $\boldsymbol{\varepsilon}$. For the simulations and estimations presented in this paper, we use the Gibbs sampling algorithm for each link, adapting the strategy proposed by Hsieh et al. (2019) to our setting (see Proposition 3 in Appendix C.2). This can be viewed as a *worse-case* scenario. Nonetheless, we show in the online Appendix, using simulations, that the Gibbs sampler performs reasonably well in practice, even for ARD; however, we encourage researchers to try other updating schemes if Gibbs sampling performs poorly in their specific contexts. In particular, we present a blocking technique in Appendix C.2 that is also implemented in our R package `PartialNetwork`.²⁸

It is important to note that the complexity of Step 2 is not limited to our Bayesian approach. Classical estimators, such as GMM estimators, face a similar challenge in requiring the integration over the entire set of networks. The strategy used here is to rely on a Metropolis–Hastings algorithm, a strategy that has also been successfully implemented in the related literature on ERGMs (e.g. Snijders (2002); Mele (2017, 2020); Badev (2018); Hsieh et al. (2019, 2020)).

Finally, note that for simple network formation models, it is possible to estimate $\boldsymbol{\rho}$ and $\boldsymbol{\theta}$ within the same MCMC instead of using the two-step procedure described above. In that case, Step 1 can simply be replaced by:

- 1'. Draw $\boldsymbol{\rho}^*$ from the proposal distribution $q_\rho(\boldsymbol{\rho}^*|\boldsymbol{\rho}_{t-1})$ and accept $\boldsymbol{\rho}^*$ with probability

$$\min \left\{ 1, \frac{P(\mathbf{A}_{t-1}|\boldsymbol{\rho}^*, \mathcal{A})P(\mathcal{A}|\boldsymbol{\rho}^*)q_\rho(\boldsymbol{\rho}_{t-1}|\boldsymbol{\rho}^*)\pi(\boldsymbol{\rho}^*)}{P(\mathbf{A}_{t-1}|\boldsymbol{\rho}_{t-1}, \mathcal{A})P(\mathcal{A}|\boldsymbol{\rho}_{t-1})q_\rho(\boldsymbol{\rho}^*|\boldsymbol{\rho}_{t-1})\pi(\boldsymbol{\rho}_{t-1})} \right\}.$$

Here, $P(\mathcal{A}|\boldsymbol{\rho}^*)$ is the likelihood of the network information \mathcal{A} assuming the network formation model in (2). Note that $\pi(\boldsymbol{\rho})$, the prior density on $\boldsymbol{\rho}$, no longer depends on \mathcal{A} and can be chosen arbitrarily (e.g. uniform).

²⁸ Available at: <https://github.com/ahoundetouungan/PartialNetwork>

This approach would work well for simple models, such as the ones discussed in Examples 1 and 3. It is impractical, however, for more involved models, such as the one proposed by Breza et al. (2020).

5 Imperfectly Measured Networks

In this section, we assume that the econometrician has access to network data but that the data may contain errors. To show how our method can be used to address these issues, we consider a simple example where we are interested in estimating peer effects on adolescents' academic achievements.

We use the widely used AddHealth database and show that network data errors have a first-order impact on the estimated peer effects. Specifically, we focus on a subset of schools from the "In School" sample that each have less than 200 students. Table 3 displays the summary statistics.

Most of the papers estimating peer effects that use this particular database have taken the network structure as given. One notable exception is Griffith (2019), looking at censoring: students can only report up to five male and five female friends. We also allow for censoring but show that censoring is not the most important issue with the Add Health data. To understand why, we discuss the organization of the data.

Each adolescent is assigned a unique identifier. The data includes ten variables for the ten potential friendships (maximum of five male and five female friends). These variables can contain missing values (no friendship was reported), an error code (the named friend could not be found in the database), or an identifier for the reported friends. This data is then used to generate the network's adjacency matrix \mathbf{A} .

Of course, error codes cannot be matched to any particular adolescent; as well, even in the case where the friendship variable refers to a valid identifier, the referred adolescent may still be absent from the database. A prime example is when the referred adolescent has been removed from the database by the researcher, perhaps due to other missing variables for these particular individuals. These missing links are quantitatively important as they account for roughly 30% of the total number of links (7,830 missing for 17,993 observed

Table 3: Summary statistics.

Statistic	Mean	Std. Dev.	Pctl(25)	Pctl(75)
Female	0.540	0.498	0	1
Hispanic	0.157	0.364	0	0
Race				
White	0.612	0.487	0	1
Black	0.246	0.431	0	0
Asian	0.022	0.147	0	0
Other	0.088	0.283	0	0
Mother's education				
High	0.310	0.462	0	1
<High	0.193	0.395	0	0
>High	0.358	0.480	0	1
Missing	0.139	0.346	0	0
Mother's job				
Stay-at-home	0.225	0.417	0	0
Professional	0.175	0.380	0	0
Other	0.401	0.490	0	1
Missing	0.199	0.399	0	0
Age	13.620	1.526	13	14
GPA	2.088	0.794	1.5	2.667

Note: We only keep the 33 schools having less than 200 students from the In-School sample. The variable GPA is computed by taking the average grade for English, Mathematics, History, and Science, letting $A = 1$, $B = 2$, $C = 3$, and $D = 4$. Thus, lower scores indicate better academic achievement.

links). Figure 1 displays the distribution of the number of “unmatched named friends.”²⁹

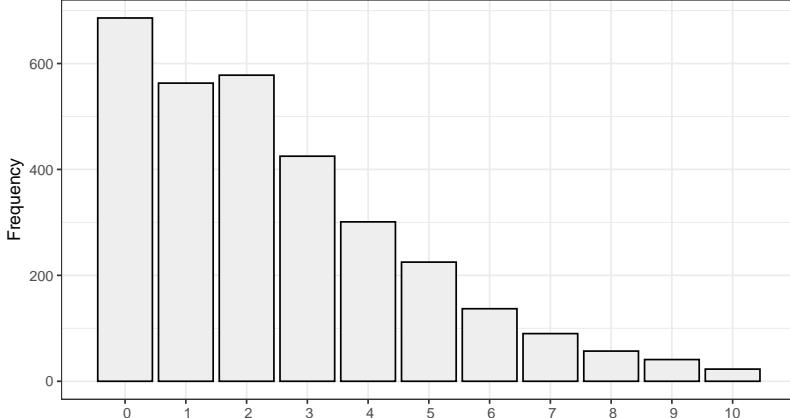


Figure 1: Frequencies of the number of missing links per adolescent.

To use the methodology developed in Section 4, we first need to estimate a network formation model using the observed network data. In this section, we assume that links are generated using a simple logistic framework, i.e.

$$P(a_{ij} = 1) \propto \exp\{\mathbf{w}_{ij}\boldsymbol{\rho}\},$$

where \mathbf{w}_{ij} is built to capture homophily on the observed characteristics of i and j (see Table 4). We estimate the network formation model on the set of individuals who nominate strictly less than five male and five female friends and for which we observe no “unmatched friends.” For these students, we know for sure that their friendship data is complete. Under a missing at random assumption, the estimation is consistent.

Table 4 presents the estimation results for the network formation model (panel *Network Formation*), as well as for the peer effect model (panel *Peer Effect Model*, column *Reconstructed Network*).³⁰ We also present the results for the (inconsistent) estimation of the peer effect model under the assumption that the observed network is the true one (panel *Peer Effect Model*, column *Observed Network*).

We find evidence of homophily on all observed covariates, which is coherent with the

²⁹We focus on within-school friendships; thus, nominations outside of school are not treated as “unmatched friends.”

³⁰Trace plots and posterior distributions are presented in Figures D.1, D.2, and D.3 of Appendix D.

literature (e.g. [Currarini et al. \(2010\)](#); [Boucher and Mourifié \(2017\)](#); [Mele \(2020\)](#)). The bias on the peer effects' coefficients (endogenous and contextual) is qualitatively important (and statistically significant). The estimated endogenous peer effect using the reconstructed network is 1.6 times larger than the one estimated assuming that the observed network is the true network. The reconstructed network also allows capturing a positive effect of having a high proportion of Hispanic friends on academic achievement.

The contribution of censoring to these biases is insignificant. In Table D.1 of Appendix D, we report estimates for two alternative cases: one in which we disregard censoring and another in which censoring is the only data issue. The impact of controlling for censoring is almost null, coherent with the fact that only about 5% of the observations are potentially censored.

Our exercise shows that data errors are a first-order concern when using the Add Health database. We do not argue, however, that our estimated coefficients in Table 4 are necessarily causal because the friendship network is likely endogenous (e.g. [Goldsmith-Pinkham and Imbens \(2013\)](#); [Hsieh and Van Kippersluis \(2018\)](#); [Hsieh et al. \(2020\)](#)). The estimation of peer effects with partial endogenous network data is left for future research but is discussed in the next section.

6 Discussion

In this paper, we proposed two types of estimators of peer effects given that the researcher only has access to partial network information. In this section, we discuss how these proposed estimators can be adapted if the underlying network is endogenous and discuss the implications of our results for survey design.

6.1 Endogenous Networks

In this paper, we assumed away any endogeneity of the network structure (Assumption 4). As discussed in Section 2, this is done for the purposes of presentation. Indeed, there are multiple ways to introduce, and correct for, endogenous networks, which lead to many possible models and estimators. In this section, we discuss how existing endogenous network

Table 4: Posterior distribution.

Statistic	Observed network			Reconstructed network		
	Mean	Std. Dev.	t-stat	Mean	Std. Dev.	t-stat
Peer effect model						
Peer effects	0.350***	(0.024)	14.809	0.564***	(0.044)	12.842
Own effects						
Female	-0.144***	(0.029)	-5.018	-0.120***	(0.031)	-3.822
Hispanic	0.083**	(0.042)	1.980	0.145**	(0.047)	3.090
Race (White)						
Black	0.230***	(0.045)	5.070	0.210***	(0.055)	3.787
Asian	0.091	(0.089)	1.024	0.115	(0.089)	1.286
Other	-0.055	(0.051)	-1.064	-0.036	(0.052)	-0.686
Mother's education (High)						
<high	0.122**	(0.039)	3.147	0.126**	(0.039)	3.201
>high	-0.140***	(0.034)	-4.131	-0.109**	(0.034)	-3.208
missing	0.060	(0.050)	1.182	0.065	(0.051)	1.277
Mother's job (Stay-at-home)						
Professional	-0.080*	(0.045)	-1.793	-0.078*	(0.044)	-1.759
Other	-0.003	(0.035)	-0.078	0.006	(0.035)	0.168
Missing	0.066	(0.047)	1.400	0.068	(0.048)	1.427
Age	0.073***	(0.010)	7.606	0.078***	(0.011)	7.168
Contextual effects						
Female	-0.011	(0.049)	-0.221	-0.072	(0.092)	-0.779
Hispanic	-0.060	(0.069)	-0.868	-0.353**	(0.115)	-3.081
Race (White)						
Black	-0.050	(0.058)	-0.865	-0.058	(0.075)	-0.769
Asian	-0.209	(0.186)	-1.126	-0.518	(0.579)	-0.895
Other	0.137	(0.089)	1.537	0.230	(0.185)	1.241
Mother's education (High)						
<High	0.269***	(0.070)	3.841	0.363**	(0.158)	2.290
>High	-0.072	(0.059)	-1.213	-0.062	(0.114)	-0.540
Missing	0.077	(0.093)	0.835	0.025	(0.197)	0.128
Mother's job (Stay-at-home)						
Professional	0.110	(0.080)	1.373	-0.032	(0.157)	-0.204
Other	0.101*	(0.060)	1.686	0.051	(0.114)	0.451
Missing	0.093	(0.085)	1.086	0.006	(0.188)	0.029
Age	-0.066***	(0.006)	-11.323	-0.091***	(0.010)	-9.228
SE ²	0.523			0.515		
Network formation model						
Same sex				0.456***	(0.016)	28.208
Both Hispanic				0.343***	(0.023)	14.739
Both White				0.320***	(0.022)	14.741
Both Black				1.167***	(0.032)	36.121
Both Asian				0.278***	(0.043)	6.502
Mothers education <High				0.178***	(0.018)	10.063
Mothers education >High				0.075***	(0.016)	4.756
Mothers job Professional				-0.130***	(0.017)	-7.544
Age absolute difference				-0.648***	(0.010)	-64.105

Note: $N = 3,126$. Observed links = 17,993. Proportion of inferred network data = 77.7%. Significance levels: *** = 1%, ** = 5%, * = 10%. The explained variable is computed by taking the average grade for English, Mathematics, History, and Science, letting $A = 1$, $B = 2$, $C = 3$, and $D = 4$. Thus, lower scores indicate better academic achievement.

corrections can be adapted to our setting. Specifically, we assume that there exists some unobserved variable correlated with both the network \mathbf{A} and the outcome \mathbf{y} . This violates Assumption 4.

A first remark is that our ability to accommodate such an unobserved variable depends on the flexibility of the used network formation model. Indeed, some models can obtain estimates of the unobserved heterogeneity (e.g. Breza et al. (2020) or Graham (2017)). In such cases, one could simply include the estimated unobserved variables as additional explanatory variables. In particular, the approach followed by Houndetoungan (2020) could be adapted to our context. Johnsson and Moon (2015) discuss this approach as well as other control-function approaches in detail. Since their instrumental variable estimator is based on the higher-order link relations (i.e. $\mathbf{G}^2\mathbf{X}, \mathbf{G}^3\mathbf{X}, \dots$), it is also valid for the instrumental variable estimator proposed in Section 3.

However, these approaches may not be entirely satisfactory because they assume that the network formation is estimated consistently, independent of the peer-effect model.³¹ The Bayesian estimator presented in Section 4 allows for more flexibility. Indeed, one could expand Algorithm 1 and include unobserved latent variables, as has been done, for instance, by Goldsmith-Pinkham and Imbens (2013), Hsieh and Van Kippersluis (2018), and Hsieh et al. (2020)) in contexts where the network is observed. The exploration of such models, in particular their identification and computational complexity, goes far beyond the scope of the current paper and is left for future (exciting) research.

6.2 Survey Design

As discussed in Section 3, instrumental variable estimators are only valid if the researcher observes \mathbf{GX} . Also, as discussed in Section 3.1, Breza et al. (2020) and Alidaee et al. (2020) propose using ARD to estimate network formation models. Importantly, although ARD responses and \mathbf{GX} are similar, they are not equivalent. For example, consider a binary variable (e.g. gender). One can obtain \mathbf{GX} by asking questions such as, “What fraction of your friends are female?” For ARD, the question would be, “How many of your friends are female?” This suggests asking two questions: one related to the number of female friends

³¹See, for example, Assumption 1 and Assumptions 6–11 in Johnsson and Moon (2015).

and another related to the number of friends.³²

For continuous variables (e.g. age), this creates additional issues. One can obtain \mathbf{GX} by asking about the average age of one's friends, but ARD questions must be discrete: "How many of your friends are in the same age group as you?" Then, in practice, an approach could be to ask individuals about the number of friends they have and the number of friends they have from multiple age groups: "How many of your friends are between X and Y years old?" Using this strategy allows construction of both the ARD and \mathbf{GX} .

Recall that an implication of Propositions 1 and 2 is that asking directly for \mathbf{Gy} in the survey leads to a more robust estimation strategy. Indeed, the constructed instruments are valid even if the network formation model is misspecified. We therefore encourage researchers to design their survey questions to elicit ARD as well as \mathbf{Gy} and \mathbf{GX} .

6.3 Next Steps

In this paper, we proposed two estimators where peer effects can be estimated without having knowledge of the entire network structure. We found that, perhaps surprisingly, even very partial information on network structure is sufficient. Nonetheless, many important challenges remain, in particular with respect to the study of compatible models of network formation, which can be estimated under nonrandom sampling, for example.

³²Breza et al. (2020) do not require information on the number of friends, although this significantly helps the estimation.

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A Appendix – Proofs

A.1 Proof of Proposition 1

The model can be written as:

$$\mathbf{y} = [\mathbf{I} - \alpha \mathbf{G}]^{-1} [\mathbf{X}\boldsymbol{\beta} + \boldsymbol{\varepsilon}].$$

Or, using the geometric expansion:

$$\mathbf{y} = \sum_{k=0}^{\infty} \alpha^k \mathbf{G}^k \mathbf{X} \boldsymbol{\beta} + \sum_{k=0}^{\infty} \alpha^k \mathbf{G}^k \boldsymbol{\varepsilon}$$

or

$$\mathbf{Gy} = \sum_{k=0}^{\infty} \alpha^k \mathbf{G}^{k+1} \mathbf{X} \boldsymbol{\beta} + \sum_{k=0}^{\infty} \alpha^k \mathbf{G}^{k+1} \boldsymbol{\varepsilon}.$$

As such, any variable correlated with \mathbf{GX} , $\mathbf{G}^2\mathbf{X}, \dots$ is also correlated with \mathbf{Gy} , conditional on \mathbf{X} . It remains to show that such variables are valid. For the first part of Proposition 1, we need:

$$\mathbb{E}[\boldsymbol{\varepsilon} | \mathbf{X}, \mathbf{HX}, \mathbf{H}^2\mathbf{X}, \dots] = 0,$$

which is true by assumption. For the second part of Proposition 1, we need:

$$\mathbb{E}[\boldsymbol{\varepsilon} + \boldsymbol{\eta} | \mathbf{X}, \dot{\mathbf{G}}\mathbf{X}, \dot{\mathbf{G}}^2\mathbf{X}, \dots] = 0.$$

By Assumption 4, this is equivalent to:

$$\mathbb{E}[\boldsymbol{\eta} | \mathbf{X}, \dot{\mathbf{G}}\mathbf{X}, \dot{\mathbf{G}}^2\mathbf{X}, \dots] = 0,$$

which is equivalent to:

$$\mathbb{E}[\mathbf{Gy} | \mathbf{X}, \dot{\mathbf{G}}\mathbf{X}, \dot{\mathbf{G}}^2\mathbf{X}, \dots] = \mathbb{E}[\ddot{\mathbf{Gy}} | \mathbf{X}, \dot{\mathbf{G}}\mathbf{X}, \dot{\mathbf{G}}^2\mathbf{X}, \dots].$$

Using iterated expectations, $\mathbb{E}[\mathbf{G}\mathbf{y}|\mathbf{X}, \dot{\mathbf{G}}\mathbf{X}, \dot{\mathbf{G}}^2\mathbf{X}, \dots]$ can be written as:

$$\mathbb{E}_{\mathbf{y}} \mathbb{E}[\mathbf{G}\mathbf{y}|\mathbf{X}, \dot{\mathbf{G}}\mathbf{X}, \dot{\mathbf{G}}^2\mathbf{X}, \dots, \mathbf{y}]|\mathbf{X}, \dot{\mathbf{G}}\mathbf{X}, \dot{\mathbf{G}}^2\mathbf{X}, \dots = \mathbb{E}[\mathbf{G}|\mathbf{X}, \dot{\mathbf{G}}\mathbf{X}, \dot{\mathbf{G}}^2\mathbf{X}, \dots] \mathbb{E}[\mathbf{y}|\mathbf{X}, \dot{\mathbf{G}}\mathbf{X}, \dot{\mathbf{G}}^2\mathbf{X}, \dots],$$

and similarly for $\mathbb{E}[\ddot{\mathbf{G}}\mathbf{y}|\mathbf{X}, \dot{\mathbf{G}}\mathbf{X}, \dot{\mathbf{G}}^2\mathbf{X}, \dots]$. It is therefore sufficient to show that:

$$\mathbb{E}[\mathbf{G}|\mathbf{X}, \dot{\mathbf{G}}\mathbf{X}, \dot{\mathbf{G}}^2\mathbf{X}, \dots] = \mathbb{E}[\ddot{\mathbf{G}}|\mathbf{X}, \dot{\mathbf{G}}\mathbf{X}, \dot{\mathbf{G}}^2\mathbf{X}, \dots].$$

Recall that $\mathbf{G} = f(\mathbf{A})$, $\ddot{\mathbf{G}} = f(\ddot{\mathbf{A}})$, and $\dot{\mathbf{G}} = f(\dot{\mathbf{A}})$, where \mathbf{A} is drawn from $P(\mathbf{A}|\boldsymbol{\rho})$, whereas $\dot{\mathbf{A}}$ and $\ddot{\mathbf{A}}$ are drawn from $P(\mathbf{A}|\hat{\boldsymbol{\rho}})$. As $m \rightarrow \infty$, $P(\mathbf{A}|\hat{\boldsymbol{\rho}}) \rightarrow P(\mathbf{A}|\boldsymbol{\rho})$ and \mathbf{A} , $\dot{\mathbf{A}}$, and $\ddot{\mathbf{A}}$ are independently drawn from the same distribution. This property also applies to \mathbf{G} , $\dot{\mathbf{G}}$, and $\ddot{\mathbf{G}}$; thus,

$$\lim_{m \rightarrow \infty} \mathbb{E}_m[\mathbf{G}|\mathbf{X}, \dot{\mathbf{G}}\mathbf{X}, \dot{\mathbf{G}}^2\mathbf{X}, \dots] = \lim_{m \rightarrow \infty} \mathbb{E}_m[\ddot{\mathbf{G}}|\mathbf{X}, \dot{\mathbf{G}}\mathbf{X}, \dot{\mathbf{G}}^2\mathbf{X}, \dots].$$

A.2 Proof of Proposition 2

The model can be written as:

$$\mathbf{y} = [\mathbf{I} - \alpha \mathbf{G}]^{-1} [\mathbf{X}\boldsymbol{\beta} + \mathbf{G}\mathbf{X}\boldsymbol{\gamma} + \boldsymbol{\varepsilon}].$$

Or, using the geometric expansion:

$$\mathbf{y} = \sum_{k=0}^{\infty} \alpha^k \mathbf{G}^k \mathbf{X} \boldsymbol{\beta} + \sum_{k=0}^{\infty} \alpha^k \mathbf{G}^k + \mathbf{G}\mathbf{X}\boldsymbol{\gamma} \sum_{k=0}^{\infty} \alpha^k \mathbf{G}^k \boldsymbol{\varepsilon}$$

or

$$\mathbf{G}\mathbf{y} = \sum_{k=0}^{\infty} \alpha^k \mathbf{G}^{k+1} \mathbf{X} \boldsymbol{\beta} + \sum_{k=0}^{\infty} \alpha^k \mathbf{G}^{k+2} \mathbf{X} \boldsymbol{\gamma} + \sum_{k=0}^{\infty} \alpha^k \mathbf{G}^{k+1} \boldsymbol{\varepsilon}.$$

As such, any variable correlated with $\mathbf{G}^2\mathbf{X}$, $\mathbf{G}^3\mathbf{X}, \dots$ is also correlated with $\mathbf{G}\mathbf{y}$, conditional on \mathbf{X} and $\mathbf{G}\mathbf{X}$. It remains to show that such variables are valid. For the first part of Proposition 2, we need:

$$\mathbb{E}[\boldsymbol{\varepsilon}|\mathbf{X}, \mathbf{G}\mathbf{X}, \mathbf{H}^2\mathbf{X}, \mathbf{H}^3\mathbf{X}, \dots] = 0,$$

which is true by assumption. For the second part of Proposition 1, we need:

$$\mathbb{E}[\varepsilon + \eta | \mathbf{X}, \mathbf{GX}, \ddot{\mathbf{GX}}, \dot{\mathbf{G}}^2\mathbf{X}, \dot{\mathbf{G}}^3\mathbf{X}, \dots] = 0.$$

By Assumption 4, this is equivalent to:

$$\mathbb{E}[\eta | \mathbf{X}, \mathbf{GX}, \ddot{\mathbf{GX}}, \dot{\mathbf{G}}^2\mathbf{X}, \dot{\mathbf{G}}^3\mathbf{X}, \dots] = 0,$$

which is equivalent to:

$$\mathbb{E}[\mathbf{Gy} | \mathbf{X}, \mathbf{GX}, \ddot{\mathbf{GX}}, \dot{\mathbf{G}}^2\mathbf{X}, \dot{\mathbf{G}}^3\mathbf{X}, \dots] = \mathbb{E}[\ddot{\mathbf{Gy}} | \mathbf{X}, \mathbf{GX}, \ddot{\mathbf{GX}}, \dot{\mathbf{G}}^2\mathbf{X}, \dot{\mathbf{G}}^3\mathbf{X}, \dots].$$

Using iterated expectations, $\mathbb{E}[\mathbf{Gy} | \mathbf{X}, \mathbf{GX}, \ddot{\mathbf{GX}}, \dot{\mathbf{G}}^2\mathbf{X}, \dot{\mathbf{G}}^3\mathbf{X}, \dots]$ can be written as:

$$\begin{aligned} & \mathbb{E}_y \mathbb{E}[\mathbf{Gy} | \mathbf{X}, \mathbf{GX}, \ddot{\mathbf{GX}}, \dot{\mathbf{G}}^2\mathbf{X}, \dot{\mathbf{G}}^3\mathbf{X}, \dots, y] | \mathbf{X}, \mathbf{GX}, \ddot{\mathbf{GX}}, \dot{\mathbf{G}}^2\mathbf{X}, \dot{\mathbf{G}}^3\mathbf{X}, \dots \\ &= \mathbb{E}[\mathbf{G} | \mathbf{X}, \mathbf{GX}, \ddot{\mathbf{GX}}, \dot{\mathbf{G}}^2\mathbf{X}, \dot{\mathbf{G}}^3\mathbf{X}, \dots] \mathbb{E}[y | \mathbf{X}, \mathbf{GX}, \ddot{\mathbf{GX}}, \dot{\mathbf{G}}^2\mathbf{X}, \dot{\mathbf{G}}^3\mathbf{X}, \dots], \end{aligned}$$

and similarly for $\mathbb{E}[\ddot{\mathbf{Gy}} | \mathbf{X}, \mathbf{GX}, \ddot{\mathbf{GX}}, \dot{\mathbf{G}}^2\mathbf{X}, \dot{\mathbf{G}}^3\mathbf{X}, \dots]$.

It is therefore sufficient to show that:

$$\mathbb{E}[\mathbf{G} | \mathbf{X}, \mathbf{GX}, \ddot{\mathbf{GX}}, \dot{\mathbf{G}}^2\mathbf{X}, \dot{\mathbf{G}}^3\mathbf{X}, \dots] = \mathbb{E}[\ddot{\mathbf{G}} | \mathbf{X}, \mathbf{GX}, \ddot{\mathbf{GX}}, \dot{\mathbf{G}}^2\mathbf{X}, \dot{\mathbf{G}}^3\mathbf{X}, \dots].$$

Recall that $\mathbf{G} = f(\mathbf{A})$, $\ddot{\mathbf{G}} = f(\ddot{\mathbf{A}})$, and $\dot{\mathbf{G}} = f(\dot{\mathbf{A}})$, where \mathbf{A} is drawn from $P(\mathbf{A} | \boldsymbol{\rho})$, whereas $\dot{\mathbf{A}}$ and $\ddot{\mathbf{A}}$ are drawn from $P(\mathbf{A} | \hat{\boldsymbol{\rho}})$. As $m \rightarrow \infty$, $P(\mathbf{A} | \hat{\boldsymbol{\rho}}) \rightarrow P(\mathbf{A} | \boldsymbol{\rho})$ and \mathbf{A} , $\dot{\mathbf{A}}$, and $\ddot{\mathbf{A}}$ are independently drawn from the same distribution. This property also applies to \mathbf{G} , $\dot{\mathbf{G}}$, and $\ddot{\mathbf{G}}$.

$$\lim_{m \rightarrow \infty} \mathbb{E}_m[\mathbf{G} | \mathbf{X}, \mathbf{GX}, \ddot{\mathbf{GX}}, \dot{\mathbf{G}}^2\mathbf{X}, \dot{\mathbf{G}}^3\mathbf{X}, \dots] = \lim_{m \rightarrow \infty} \mathbb{E}_m[\ddot{\mathbf{G}} | \mathbf{X}, \mathbf{GX}, \ddot{\mathbf{GX}}, \dot{\mathbf{G}}^2\mathbf{X}, \dot{\mathbf{G}}^3\mathbf{X}, \dots].$$

B Appendix – ARD Details

This section provides details about ARD simulation and model estimation using a MCMC method. We simulate the network for a population of 5000 individuals divided into $m = 20$ groups of $n = 250$ individuals. Within each group, the probability of a link is:

$$P(a_{ij} = 1) \propto \exp\{\nu_i + \nu_j + \zeta \mathbf{z}'_i \mathbf{z}_j\}. \quad (7)$$

Since there is no connection between the groups, the networks are simulated and estimated independently. We first present how we simulate the data following the model (5).

B.1 ARD Simulation

The parameters are defined as follows: $\zeta = 1.5$, $\nu_i \sim \mathcal{N}(-1.25, 0.37)$, and \mathbf{z}_i are distributed uniformly according to a von Mises–Fisher distribution. We use a hypersphere of dimension 3. We set the same values for the parameter for the 20 groups. We generate the probabilities of links in each network following [Breza et al. \(2020\)](#).

$$P(a_{ij} = 1 | \nu_i, \nu_j, \zeta, \mathbf{z}_i, \mathbf{z}_j) = \frac{\exp\{\nu_i + \nu_j + \zeta \mathbf{z}'_i \mathbf{z}_j\} \sum_{i=1}^N d_i}{\sum_{ij} \exp\{\nu_i + \nu_j + \zeta \mathbf{z}'_i \mathbf{z}_j\}}, \quad (8)$$

where d_i is the degree defined by $d_i \approx \frac{C_p(0)}{C_p(\zeta)} \exp(\nu_i) \sum_{i=1}^N \exp(\nu_i)$, and the function $C_p(\cdot)$ is the normalization constant in the von Mises–Fisher distribution density function. After computing the probability of a link for any pair in the population, we sample the entries of the adjacency matrix using a Bernoulli distribution with probability (8).

To generate the ARD, we require the “traits” (e.g. cities) for each individual. We set $K = 12$ traits on the hypersphere. Their location \mathbf{v}_k is distributed uniformly according to the von Mises–Fisher distribution. The individuals having the trait k are assumed to be generated by a von Mises–Fisher distribution with the location parameter \mathbf{v}_k and the intensity parameter $\eta_k \sim |\mathcal{N}(4, 1)|$, $k = 1, \dots, 12$.

We attribute traits to individuals given their spherical coordinates. We first define N_k ,

the number of individuals having the trait k :

$$N_k = \left\lfloor r_k \frac{\sum_{i=1}^N f_{\mathcal{M}}(\mathbf{z}_i | \mathbf{v}_k, \eta_k)}{\max_i f_{\mathcal{M}}(\mathbf{z}_i | \mathbf{v}_k, \eta_k)} \right\rfloor,$$

where $\lfloor x \rfloor$ represents the greatest integer less than or equal to x , r_k is a random number uniformly distributed over $(0.8; 0.95)$, and $f_{\mathcal{M}}(\mathbf{z}_i | \mathbf{v}_k, \eta_k)$ is the von Mises–Fisher distribution density function evaluated at \mathbf{z}_i with the location parameter \mathbf{v}_k and the intensity parameter η_k .

The intuition behind this definition for N_k is that when many \mathbf{z}_i are close to \mathbf{v}_k , many individuals should have the trait k .

We can finally attribute trait k to individual i by sampling a Bernoulli distribution with the probability f_{ik} given by:

$$f_{ik} = N_k \frac{f_{\mathcal{M}}(\mathbf{z}_i | \mathbf{v}_k, \eta_k)}{\sum_{i=1}^N f_{\mathcal{M}}(\mathbf{z}_i | \mathbf{v}_k, \eta_k)}.$$

The probability of having a trait depends on the proximity of the individuals to the trait's location on the hypersphere.

B.2 Model Estimation

In practice, we only have the ARD and the traits for each individual. [McCormick and Zheng \(2015\)](#) propose a MCMC approach to infer the parameters in model (7).

However, the spherical coordinates and the degrees in this model are not identified. The authors solve this issue by fixing some \mathbf{v}_k and use the fixed positions to rotate the latent surface back to a common orientation at each iteration of the MCMC using a Procrustes transformation. In addition, the total size of a subset b_k is constrained in the MCMC.

As discussed by [McCormick and Zheng \(2015\)](#), the numbers of \mathbf{v}_k and b_k to be set as fixed depend on the dimension of hypersphere. In our simulations, $\mathbf{v}_1, \mathbf{v}_2, \dots, \mathbf{v}_5$ are set as fixed to rotate back the latent space. When simulating the data, we let $\mathbf{v}_1 = (1, 0, 0)$, $\mathbf{v}_2 = (0, 1, 0)$, and $\mathbf{v}_3 = (0, 0, 1)$. This ensures that the fixed positions on the hypersphere are spaced, as suggested by the authors, to use as much of the space as possible, maximizing

the distance between the estimated positions. We also constrain b_3 to its true value. The results do not change when we constrain a larger set of b_k

Following Breza et al. (2020), we estimate the link probabilities using the parameters' posterior distributions. The gregariousness parameters are computed from the degrees d_i and the parameter ζ using the following equation:

$$\nu_i = \log(d_i) - \log \left(\sum_{i=1}^N d_i \right) + \frac{1}{2} \log \left(\frac{C_p(\zeta)}{C_p(0)} \right).$$

C Appendix – Bayesian Inference

C.1 Posterior Distributions for Algorithm 1.

To compute the posterior distributions, we set prior distributions on $\tilde{\alpha}$, Λ , and σ^2 , where $\tilde{\alpha} = \log(\frac{\alpha}{1-\alpha})$ and $\Lambda = [\beta, \gamma]$. In Algorithm 1, we therefore sample $\tilde{\alpha}$ and compute α , such that $\alpha = \frac{\exp(\tilde{\alpha})}{1 + \exp(\tilde{\alpha})}$. Using this functional form for computing α ensures that $\alpha \in (0, 1)$. The prior distributions are set as follows:

$$\begin{aligned}\tilde{\alpha} &\sim \mathcal{N}(\mu_{\tilde{\alpha}}, \sigma_{\tilde{\alpha}}^2), \\ \Lambda | \sigma^2 &\sim \mathcal{N}(\mu_{\Lambda}, \sigma^2 \Sigma_{\Lambda}), \\ \sigma^2 &\sim IG(\frac{a}{2}, \frac{b}{2}).\end{aligned}$$

For the simulations and estimations in this paper, we set $\mu_{\tilde{\alpha}} = -1$, $\sigma_{\tilde{\alpha}}^{-2} = 2$, $\mu_{\Lambda} = \mathbf{0}$, $\Sigma_{\Lambda}^{-1} = \frac{1}{100} \mathbf{I}_K$, $a = 4$, and $b = 4$, where \mathbf{I}_K is the identity matrix of dimension K and $K = \dim(\Lambda)$.

Following Algorithm 1, α is updated at each iteration t of the MCMC by drawing $\tilde{\alpha}^*$ from the proposal $\mathcal{N}(\tilde{\alpha}_{t-1}, \xi_t)$, where the jumping scale ξ_t is also updated at each t following Atchadé and Rosenthal (2005) for an acceptance rate of a^* targeted at 0.44. As the proposal is symmetrical, $\alpha^* = \frac{\exp(\tilde{\alpha}^*)}{1 + \exp(\tilde{\alpha}^*)}$ is accepted with the probability:

$$\min \left\{ 1, \frac{\mathcal{P}(\mathbf{y} | \mathbf{A}_t, \Lambda_{t-1}, \alpha^*) P(\tilde{\alpha}^*)}{\mathcal{P}(\mathbf{y} | \mathbf{A}_t, \theta_{t-1}) P(\tilde{\alpha}_t)} \right\}.$$

The parameters $\boldsymbol{\Lambda}_t = [\boldsymbol{\beta}_t, \boldsymbol{\gamma}_t]$ and σ_t^2 are drawn from their posterior conditional distributions, given as follows:

$$\begin{aligned}\boldsymbol{\Lambda}_t | \mathbf{y}, \mathbf{A}_t, \alpha_t, \sigma_{t-1}^2 &\sim \mathcal{N}(\hat{\boldsymbol{\mu}}_{\boldsymbol{\Lambda}_t}, \sigma_{t-1}^2 \hat{\Sigma}_{\boldsymbol{\Lambda}_t}), \\ \sigma_t^2 | \mathbf{y}, \mathbf{A}_t, \boldsymbol{\theta}_t &\sim IG\left(\frac{\hat{a}_t}{2}, \frac{\hat{b}_t}{2}\right),\end{aligned}$$

where,

$$\begin{aligned}\hat{\Sigma}_{\boldsymbol{\Lambda}_t}^{-1} &= \mathbf{V}'_t \mathbf{V}_t + \Sigma_{\boldsymbol{\Lambda}}^{-1}, \\ \hat{\boldsymbol{\mu}}_{\boldsymbol{\Lambda}_t} &= \hat{\Sigma}_{\boldsymbol{\Lambda}_t} (\mathbf{V}'_t (\mathbf{y} - \alpha_t \mathbf{G}_t \mathbf{y}) + \Sigma_{\boldsymbol{\Lambda}}^{-1} \boldsymbol{\mu}_{\boldsymbol{\Lambda}}), \\ \hat{a}_t &= a + N, \\ \hat{b}_t &= b + (\boldsymbol{\Lambda}_t - \boldsymbol{\mu}_{\boldsymbol{\Lambda}})' \Sigma_{\boldsymbol{\Lambda}}^{-1} (\boldsymbol{\Lambda}_t - \boldsymbol{\mu}_{\boldsymbol{\Lambda}}) + (\mathbf{y} - \alpha_t \mathbf{G}_t \mathbf{y} - \mathbf{V}_t \boldsymbol{\Lambda}_t)' (\mathbf{y} - \alpha_t \mathbf{G}_t \mathbf{y} - \mathbf{V}_t \boldsymbol{\Lambda}_t), \\ \mathbf{V}_t &= [\mathbf{1}, \mathbf{X}, \mathbf{G}_t \mathbf{X}].\end{aligned}$$

C.2 Network Sampling

This section explains how we sample the network in Algorithm 1 using Gibbs sampling. As discussed above, a natural solution is to update only one entry of the adjacency matrix at every step t of the MCMC. The entry (i, j) is updated according to its conditional posterior distribution. For each entry, however, we need to compute $\mathcal{P}(\mathbf{y}|0, \mathbf{A}_{-ij})$ and $\mathcal{P}(\mathbf{y}|1, \mathbf{A}_{-ij})$, which are the respective likelihoods of replacing a_{ij} by 0 or by 1. The likelihood computation requires the determinant of $(\mathbf{I} - \alpha \mathbf{G})$, which has a complexity $O(N^3)$ where N is the dimension of \mathbf{G} . This implies that we must compute $2N(N - 1)$ times $\det(\mathbf{I} - \alpha \mathbf{G})$ to update the adjacency matrix at each step of the MCMC. As \mathbf{G} is row-normalized, alternating any off-diagonal entry (i, j) in \mathbf{A} between 0 and 1 perturbs all off-diagonal entries of the row i in $(\mathbf{I} - \alpha \mathbf{G})$. We show that \mathbf{A}_{ij} and $\det(\mathbf{I} - \alpha \mathbf{G})$ can be updated by computing a determinant of an auxiliary matrix that requires only updating two entries.

Assume that we want to update the entry (i, j) . Let h be the function defined in \mathbb{N} such that $\forall x \in \mathbb{N}^*, h(x) = x$, and $h(0) = 1$. Let \mathbf{L} be an $N \times N$ diagonal matrix, where $\mathbf{L}_{ii} = h(n_i)$, and n_i stands for the degree of i , while $\mathbf{L}_{kk} = 1$ for all $k \neq i$, and \mathbf{W} is the

matrix \mathbf{G} where the row i of \mathbf{W} is replaced by the row i of \mathbf{A} . Then, as the determinant is linear in each row, we can obtain $\mathbf{I} - \alpha\mathbf{G}$ by dividing the row i of $\mathbf{L} - \alpha\mathbf{W}$ by $h(n_i)$. We get:

$$\det(\mathbf{I} - \alpha\mathbf{G}) = \frac{1}{h(n_i)} \det(\mathbf{L} - \alpha\mathbf{W}).$$

When a_{ij} changes (from 0 to 1, or 1 to 0), note that only the entries (i, i) and (i, j) change in $\mathbf{L} - \alpha\mathbf{W}$. Two cases can be distinguished.

- If $a_{ij} = 0$ before the update, then the new degree of i will be $n_i + 1$. Thus, the entry (i, i) in $\mathbf{L} - \alpha\mathbf{W}$ will change from $h(n_i)$ to $h(n_i + 1)$ (as the diagonal of \mathbf{W} equals 0) and the entry (i, j) will change from 0 to $-\alpha$. The new determinant is therefore given by:

$$\det(\mathbf{I} - \alpha\mathbf{G}^*) = \frac{1}{h(n_i + 1)} \det(\mathbf{L}^* - \alpha\mathbf{W}^*),$$

where \mathbf{G}^* , \mathbf{L}^* , and $\alpha\mathbf{W}^*$ are the new matrices, once a_{ij} has been updated.

- If $a_{ij} = 1$ before the update, then the new degree of k will be $n_i - 1$. Thus, the entry (i, i) in $\mathbf{L} - \alpha\mathbf{W}$ will change from $h(n_i)$ to $h(n_i - 1)$ and the entry (i, j) will change from $-\alpha$ to 0. The new determinant is therefore given by:

$$\det(\mathbf{I} - \alpha\mathbf{G}^*) = \frac{1}{h(n_i - 1)} \det(\mathbf{L}^* - \alpha\mathbf{W}^*).$$

Then, to update $\det(\mathbf{L} - \alpha\mathbf{W})$ when only the entries (i, i) and (i, j) change, we adapt the Lemma 1 in [Hsieh et al. \(2019\)](#) as follows:

Proposition 3. *Let \mathbf{e}_i be the i 'th unit basis vector in \mathbb{R}^N . Let \mathbf{M} denote an $N \times N$ matrix and $\mathbf{B}_{ij}(\mathbf{Q}, \epsilon)$ an $N \times N$ matrix as function of an $N \times N$ matrix \mathbf{Q} and a real value ϵ , such that:*

$$\mathbf{B}_{ij}(\mathbf{Q}, \epsilon) = \frac{\mathbf{Q}\mathbf{e}_i\mathbf{e}'_j\mathbf{Q}}{1 + \epsilon\mathbf{e}'_j\mathbf{Q}\mathbf{e}_i}. \quad (9)$$

Adding a perturbation ϵ_1 in the (i, i) th position and a perturbation ϵ_2 in the (i, j) th position to the matrix \mathbf{M} can be written as $\tilde{\mathbf{M}} = \mathbf{M} + \epsilon_1\mathbf{e}_i\mathbf{e}'_i + \epsilon_2\mathbf{e}_i\mathbf{e}'_j$.

1. The inverse of the perturbed matrix can be written as:

$$\tilde{\mathbf{M}}^{-1} = \mathbf{M}^{-1} - \epsilon_1 \mathbf{B}_{ii}(\mathbf{M}^{-1}, \epsilon_1) - \epsilon_2 \mathbf{B}_{ij} (\mathbf{M}^{-1} - \epsilon_1 \mathbf{B}_{ii}(\mathbf{M}^{-1}, \epsilon_1), \epsilon_2).$$

2. The determinant of the perturbed matrix can be written as:

$$\det(\tilde{\mathbf{M}}) = (1 + \epsilon_2 \mathbf{e}'_j (\mathbf{M}^{-1} - \epsilon_1 \mathbf{B}_{ii}(\mathbf{M}^{-1}, \epsilon_1) \mathbf{e}_i)) (1 + \epsilon_1 \mathbf{e}'_i \mathbf{M}^{-1} \mathbf{e}_i) \det(\mathbf{M}).$$

Proof. 1. By the Sherman–Morrison formula ([Mele, 2017](#)), we have:

$$(\mathbf{M} + \epsilon \mathbf{e}_i \mathbf{e}'_j)^{-1} = \mathbf{M}^{-1} - \epsilon \frac{\mathbf{M}^{-1} \mathbf{e}_i \mathbf{e}'_j \mathbf{M}^{-1}}{1 + \epsilon \mathbf{e}'_j \mathbf{M}^{-1} \mathbf{e}_i} = \mathbf{M}^{-1} - \epsilon \mathbf{B}_{ij}(\mathbf{M}, \epsilon).$$

Thus,

$$\begin{aligned} \tilde{\mathbf{M}}^{-1} &= ((\mathbf{M} + \epsilon_1 \mathbf{e}_i \mathbf{e}'_i) + \epsilon_2 \mathbf{e}_i \mathbf{e}'_j)^{-1}, \\ \tilde{\mathbf{M}}^{-1} &= (\mathbf{M} + \epsilon_1 \mathbf{e}_i \mathbf{e}'_i)^{-1} - \epsilon_2 \mathbf{B}_{ij}((\mathbf{M} + \epsilon_1 \mathbf{e}_i \mathbf{e}'_i)^{-1}, \epsilon_2), \\ \tilde{\mathbf{M}}^{-1} &= \mathbf{M}^{-1} - \epsilon_1 \mathbf{B}_{ii}(\mathbf{M}^{-1}, \epsilon_1) - \epsilon_2 \mathbf{B}_{ij} (\mathbf{M}^{-1} - \epsilon_1 \mathbf{B}_{ii}(\mathbf{M}^{-1}, \epsilon_1), \epsilon_2). \end{aligned}$$

2. By the matrix determinant lemma ([Johnson and Horn, 1985](#)), we have:

$$\det(\mathbf{M} + \epsilon \mathbf{e}_i \mathbf{e}'_j) = (1 + \epsilon \mathbf{e}'_j \mathbf{M}^{-1} \mathbf{e}_i) \det(\mathbf{M}).$$

It follows that:

$$\begin{aligned} \det(\tilde{\mathbf{M}}) &= \det((\mathbf{M} + \epsilon_1 \mathbf{e}_i \mathbf{e}'_i) + \epsilon_2 \mathbf{e}_i \mathbf{e}'_j), \\ \det(\tilde{\mathbf{M}}) &= (1 + \epsilon_2 \mathbf{e}'_j (\mathbf{M} + \epsilon_1 \mathbf{e}_i \mathbf{e}'_i)^{-1} \mathbf{e}_i) \det(\mathbf{M} + \epsilon_1 \mathbf{e}_i \mathbf{e}'_i), \\ \det(\tilde{\mathbf{M}}) &= (1 + \epsilon_2 \mathbf{e}'_j (\mathbf{M}^{-1} - \epsilon_1 \mathbf{B}_{ii}(\mathbf{M}^{-1}, \epsilon_1) \mathbf{e}_i)) (1 + \epsilon_1 \mathbf{e}'_i \mathbf{M}^{-1} \mathbf{e}_i) \det(\mathbf{M}). \end{aligned}$$

□

The method proposed above becomes computationally intensive when many entries must be

updated simultaneously. We also propose an alternative method that allows updating the block for entries in \mathbf{A} . Let $\mathbf{D} = (\mathbf{I} - \alpha\mathbf{G})$; we can write:

$$\det(\mathbf{D}) = \sum_{j=1}^N (-1)^{i+j} \mathbf{D}_{ij} \delta_{ij}, \quad (10)$$

where i denotes any row of \mathbf{D} and δ_{ij} the minor³³ associated with the entry (i, j) . The minors of row i do not depend on the values of entries in row i . To update any block in row i , we therefore compute the N minors associated with i and use this minor within the row. We can then update many entries simultaneously without increasing the number of times that we compute $\det(\mathbf{D})$.

One possibility is to update multiple links simultaneously by randomly choosing the number of entries to consider and their position in the row. As suggested by Chib and Ramamurthy (2010), this method would help the Gibbs to converge more quickly. We can summarize how we update the row i as follows:

1. Compute the N minors $\delta_{i1}, \dots, \delta_{in}$.
2. Let $\Omega_{\mathbf{G}}$ be the entries to update in the row i , and $n_{\mathbf{G}} = |\Omega_{\mathbf{G}}|$ the number of entries in $\Omega_{\mathbf{G}}$.
 - (a) Choose r , the size of the block to update, as a random integer number such that $1 \leq r \leq n_{\mathbf{G}}$. In practice, we choose $r \leq \min(5, n_{\mathbf{G}})$ because the number of possibilities of links to consider grows exponentially with r .
 - (b) Choose the r random entries from $\Omega_{\mathbf{G}}$. These entries define the block to update.
 - (c) Compute the posterior probabilities of all possibilities of links inside the block and update the block (there are 2^r possibilities). Use the minors calculated at 1 and the formula (10) to quickly compute $\det(\mathbf{D})$.
 - (d) Remove the r drawn positions from $\Omega_{\mathbf{G}}$ and let $n_{\mathbf{G}} = n_{\mathbf{G}} - r$. Replicate 2a, 2b, and 2c until $n_{\mathbf{G}} = 0$.

³³The determinant of the submatrix of \mathbf{M} by removing row i and column j .

D Appendix – Empirical Application

Figure D.1: Simulations from the posterior distribution of the outcome model's parameters

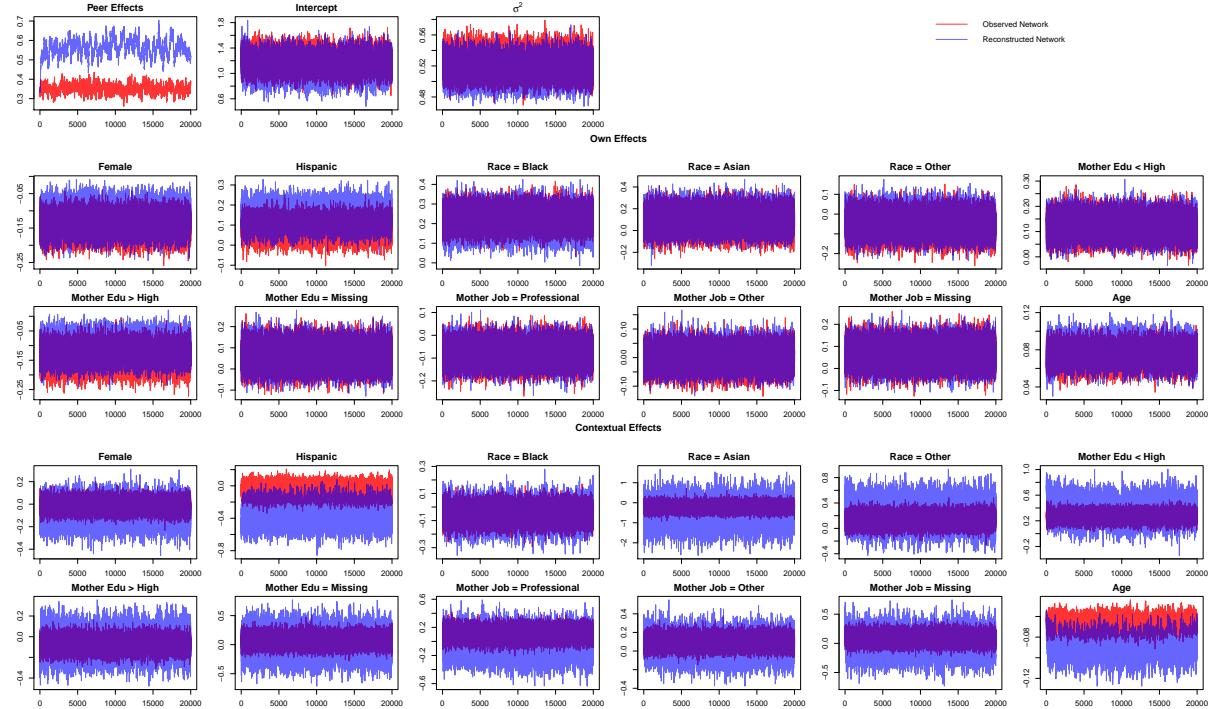


Figure D.2: Posterior density of the outcome model's parameters

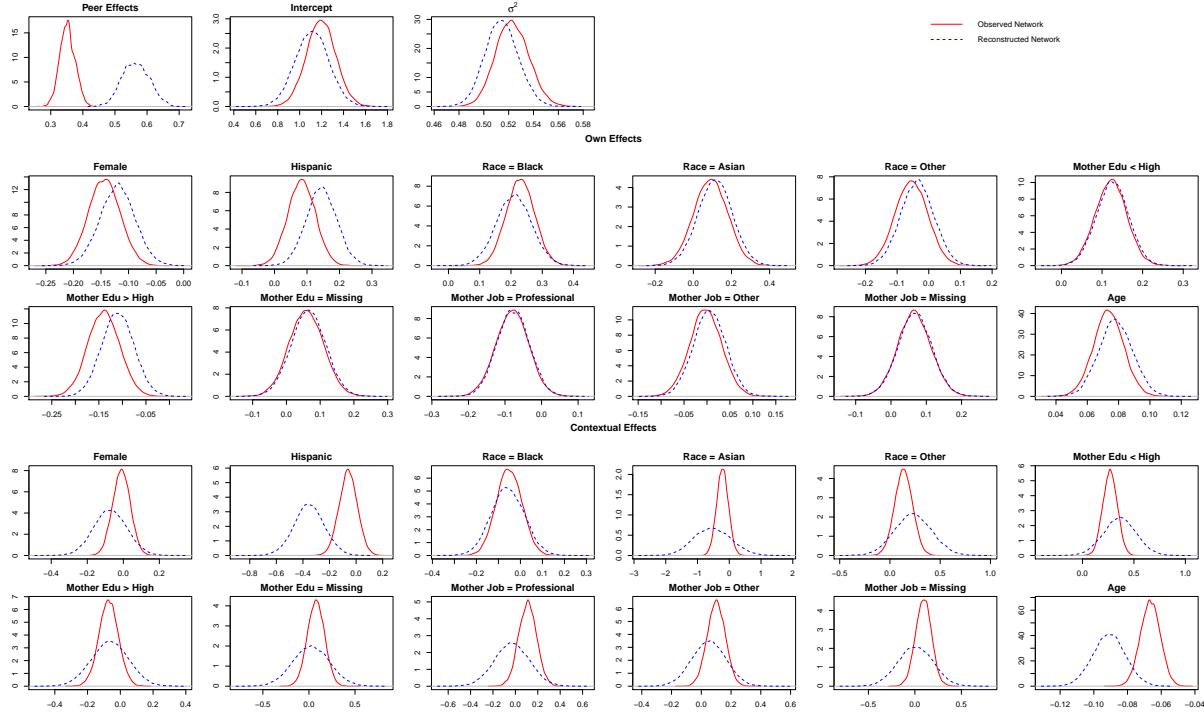


Figure D.3: Simulations from the posterior distribution of the network formation model's parameters

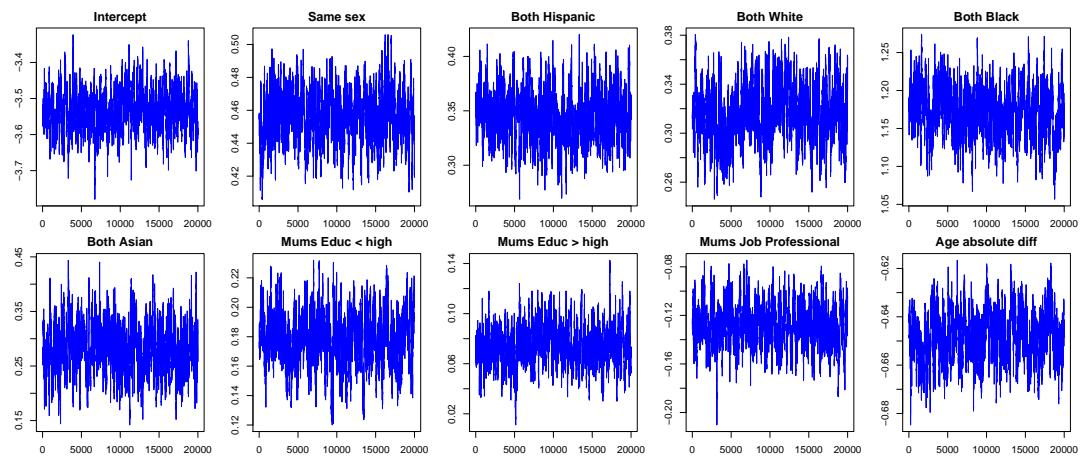


Table D.1: Posterior distribution by controlling for either censoring or missing links

Statistic	Censoring			Missing links		
	Mean	Std. Dev.	t-stat	Mean	Std. Dev.	t-stat
Peer effect model						
Peer effects	0.351***	(0.024)	14.718	0.565***	(0.041)	13.844
Own effects						
Female	-0.144***	(0.029)	-5.008	-0.125***	(0.031)	-4.050
Hispanic	0.083**	(0.042)	1.967	0.142**	(0.047)	3.046
Race (White)						
Black	0.232***	(0.046)	5.035	0.210***	(0.056)	3.778
Asian	0.090	(0.090)	0.999	0.119	(0.091)	1.308
Other	-0.053	(0.051)	-1.042	-0.038	(0.052)	-0.721
Mother's education. (High)						
<High	0.123**	(0.039)	3.182	0.123**	(0.040)	3.102
>High	-0.140***	(0.034)	-4.103	-0.110**	(0.034)	-3.216
Missing	0.061	(0.052)	1.172	0.064	(0.051)	1.235
Mother's job (Stay-at-home)						
Professional	-0.083*	(0.044)	-1.872	-0.074*	(0.044)	-1.686
Other	-0.004	(0.035)	-0.112	0.007	(0.035)	0.199
Missing	0.065	(0.047)	1.365	0.069	(0.047)	1.450
age	0.074***	(0.010)	7.745	0.079***	(0.011)	7.317
Contextual effects						
Female	-0.009	(0.049)	-0.177	-0.053	(0.094)	-0.569
Hispanic	-0.062	(0.068)	-0.905	-0.356**	(0.114)	-3.117
Race (White)						
Black	-0.053	(0.059)	-0.898	-0.057	(0.075)	-0.754
Asian	-0.233	(0.184)	-1.264	-0.505	(0.552)	-0.916
Other	0.138	(0.089)	1.538	0.240	(0.182)	1.317
Mother's education (High)						
<High	0.271***	(0.071)	3.833	0.373**	(0.157)	2.383
>High	-0.069	(0.060)	-1.154	-0.067	(0.111)	-0.606
Missing	0.078	(0.094)	0.833	0.024	(0.191)	0.127
Mother's job (Stay-at-home)						
Professional	0.117	(0.080)	1.474	-0.024	(0.150)	-0.157
Other	0.107*	(0.060)	1.767	0.038	(0.112)	0.345
Missing	0.103	(0.087)	1.190	-0.004	(0.184)	-0.024
Age	-0.067***	(0.006)	-11.441	-0.091***	(0.009)	-9.611
SE ²	0.523			0.513		
Network formation model						
Same sex	0.396***	(0.015)	27.043	0.383***	(0.015)	25.850
Both Hispanic	0.355***	(0.023)	15.245	0.301***	(0.024)	12.736
Both White	0.468***	(0.022)	21.537	0.289***	(0.024)	12.116
Both Black	0.859***	(0.032)	26.718	1.117***	(0.031)	36.066
Both Asian	0.164***	(0.045)	3.666	0.290***	(0.048)	6.039
Mothers education <High	0.212***	(0.016)	12.987	0.178***	(0.018)	9.936
Mothers education >High	0.037**	(0.015)	2.407	0.075***	(0.016)	4.668
Mothers job Professional	-0.077***	(0.017)	-4.592	-0.087***	(0.019)	-4.658
Age absolute diff	-0.616***	(0.010)	-64.156	-0.652***	(0.009)	-72.445

Note: $N = 3,126$. Observed links = 17,993.

Proportion of inferred network data: censoring = 4.8%, missing links = 76.2%. Significance levels:

*** = 1%, ** = 5%, * = 10%. The explained variable is computed by taking the average grade for English, Mathematics, History, and Science, letting $A = 1$, $B = 2$, $C = 3$, and $D = 4$. Thus, lower scores indicate better academic achievement.