Leveraging Contact Network Information in Clustered Observational Studies of Contagion Processes

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Abstract

In an observational study, obtaining unbiased estimates of an exposure effect requires adjusting for all potential confounders. When this condition is met, leveraging additional covariates related to the outcome may produce less variable estimates of the effect of exposure. For contagion processes operating on a contact network, transmission can only occur through ties that connect exposed and unexposed individuals; the outcome of such a process is known to depend intimately on the structure of the network. In this paper, we investigate the use of contact network features as both confounders and efficiency covariates in exposure effect estimation. Using doubly-robust augmented generalized estimating equations (GEE), we estimate how gains in efficiency depend on the network structure and spread of the contagious agent or behavior. We apply this approach to estimate the effects of two distinct exposures, the proportion of leaders in a village and the proportion of households participating in a self-help program, for the spread of a microfinance program in a collection of villages in Karnataka, India. We compare these results to simulated observational trials using a stochastic compartmental contagion model on a collection of model-based contact networks and compare the bias and variance of the estimated exposure effects using an assortment of network covariate adjustment strategies.

1 Introduction

Contact networks capture the structure of possible pairwise transmissions (represented by network edges or ties) in a population of actors (represented by network nodes) for various types of contagion processes, which may describe the spread of

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pathogens, behaviors, or ideas of scientific or societal interest. Transmission on the network can only occur through ties that connect exposed and unexposed individuals and given that the structure of the network constrains pairwise transmissions, the outcome of such a process must depend on the structure of the network. In general, the relationship between network structure and contagion processes can be highly complex and it is not known which network properties are likely confounding factors or useful for improving efficiency of estimation. This paper investigates the question of whether incorporating information about contact network structure, and summaries of contagion process outcomes at baseline, can be used to improve the accuracy of estimating exposure effects of outcomes that are the result of a contagion process operating on a network, in our case the spread of a novel microfinance program in a collection of villages in India. To address the issues of correlation of the outcome (uptake of microfinancing) within villages and the potential for confounding (including that related to the social network in these villages), we develop and apply methods that treat the data as resulting from a contagion process within villages. Confounding may arise at both the individual and cluster level and the methods we present below can accommodate either or both of these possibilities. Regardless of whether a study is observational or randomized, as long as individual outcomes are correlated only within discrete and independent clusters but not across them, estimates of the treatment or exposure effect that ignore correlation may still be unbiased. Consistent estimation of the variance must adjust for within-cluster outcome correlation. Of note, even in randomized studies, contact network information can improve statistical efficiency of estimation.

To accommodate the microfinance outcomes that are correlated within clusters, we make use of generalized estimating equations (GEEs) that provide estimates of the average marginal treatment effect across all clusters in cluster randomized trials or in settings characterized by a strong correlation across groups of individuals. In particular, we consider the doubly-robust (DR) augmented GEE, which allows for use of baseline variables to adjust for confounding and improve efficiency. This estimator includes two user-specified models, an outcome model and an exposure model (i.e., propensity score or PS model). If either model is correctly specified, the estimate of the average exposure effect will be unbiased in expectation. Furthermore, the variance of this estimate decreases asymptotically if covariates are included in the outcome model that are related to the outcome even when they are not confounders. Other semiparametric, doubly-robust approaches with potential efficiency gains have been developed recently, such as targeted maximum likelihood estimation (TMLE) for clustered data. Although our investigation focuses on bias and efficiency using the doubly-robust augmented GEE, the issues we discuss are relevant for the TMLE approach as well.

The paper is structured as follows. Section 2 provides some background on networks and presents the details of the estimation procedure, including how to incorporate contact network structure in the estimation process. Section 3 applies this approach to an analysis of the spread of a microfinance program within a collection of villages in India. Section 4 demonstrates the ability of our methods to adjust for confounding and to evaluate the potential gains in efficiency under different conditions in a simulation study that considers a range of settings some of which resemble that of the study in India. Section 5 provides our
2 Methods

2.1 Networks

This section provides some necessary background on network concepts and the notation used throughout this paper. We assume that the true data generating mechanism is a contagion process spreading through a network. We identify a network as an independent cluster, such that outcomes within a network are correlated whereas those across networks (across clusters) are independent. A simple network $G$ consists of set of nodes $\mathcal{N} = \{1, ..., n\}$ and edges $\mathcal{E} \subseteq \mathcal{N} \times \mathcal{N}$. The placement of edges may be described by an $n \times n$ adjacency matrix $e$, where element $e_{jj'} = e_{j',j}$ has value 1 if an edge exists between nodes $j$ and $j'$ and is 0 otherwise. Complete network and contagion processes are not generally observable; but even when they are not, it may nevertheless be possible to characterize certain features of networks. Let $e_i$ represent the $n_i \times n_i$ adjacency matrix for the network in cluster $i$ consisting of $n_i$ nodes. The degree of a node is the number of edges that are adjacent to it: $k_{ij} = \sum_{j'} e_{ijj'}$. Mean neighbor degree $\sum_{j'} \frac{e_{ijj'}}{k_{ij}}$ is the unweighted average of a node’s neighbors’ degrees. Degree assortativity is a composite measure of mean neighbor degree across the entire network, defined as the Pearson correlation coefficient of degrees of adjacent nodes taken over all network edges, which can be calculated for a given network using a weighted and normalized sum across all degree pairs as $\sum_{jk} \frac{jk(e_{jk} - q_jq_k)}{\sigma^2_q}$, where $j$ and $k$ are given node degrees, $e_{jk}$ is the probability of a randomly-selected edge connecting a node with degree $j + 1$ and a node with degree $k + 1$ (known as excess degree), $q_j$ (and $q_k$) is the probability mass of the excess degree distribution, and $\sigma^2_q$ is the variance of the excess degree distribution. A connected component is a maximal subset of nodes for which a path exists between each pair of nodes. A path exists between two node $j$ and $j'$ if and only if there exists a subset of edges $\mathcal{E}_{jj'} \subseteq \mathcal{E}_i$ in the network that connect nodes $j$ and $j'$. The components of the network $c \in 1, ..., C_i$ are assumed to be ordered from largest to smallest, and node $j$ in network $i$ is belongs to connected component $c_{ij}$. The largest component in the network contains $\sum_j \mathbb{I}(c_{ij} = 1)$ nodes. The mean component size is $n_i/C_i$, and the size of the component node $j$ in network $i$ belongs to is $\sum_{j'} \mathbb{I}(c_{ij} = c_{ij'})$.

The contagion status of each node or that of the node’s network neighbors might also be observed at baseline. We describe a person who has been impacted by the contagion process as affected (e.g., infected if the process is infectious or impacted if the process alters behavior), and we use $I_{ij}(t)$ to denote the binary process outcome for node $j$ in network $i$ at time $t$. One simple metric of contagion status is the number of affected neighbors at baseline for each node $\sum_{j'} e_{ijj'}I_{ij'}(0)$, or the number of affected individuals at baseline belonging to the same component as a given node $\sum_{j'} \mathbb{I}(c_{ij} = c_{ij'})I_{ij'}(0)$. Another metric is the length of the shortest path between each node $j$ and each infected individual $j'$ in the network at baseline. The shortest
Path length between nodes $j$ and $j'$ is $d_{jj'}$, where $d_{jj'} := \infty$ when no path exists between the two nodes. The shortest path length from the closest node affected at baseline is $\min_{j'} d_{jj'}$, with inverse $(\min_{j'} d_{jj'})^{-1}$. The sum of the inverse path lengths to node $j$ is $\sum_{j'} (d_{jj'})^{-1}$. While some of these metrics would be difficult to determine in practice given limited knowledge about a network or process outcomes, we examine whether their inclusion in the analysis yields strong enough improvements to warrant the efforts necessary to gather the required data. Table 1 summarizes these network features.

| Table 1: A collection of summaries of the contact network and contagion status at baseline. |

| None: No adjustment term | $k_{ij}$ |
|--------------------------|---------|
| $X^{(1)}$: Degree | $\sum_{j'} A_{ij'j} k_{ij}$ |
| $X^{(2)}$: Mean neighbor degree | See Text (Page 4) |
| $X^{(3)}$: Assortativity | $\mathbb{I}(b_{ij} \in \{1, 5\})$ |
| $X^{(4)}$: Member of connected block | $\sum_{j'} \mathbb{I}(c_{ij} = 1)$ |
| $X^{(5)}$: Size of largest component | $n_{i}/C_{i}$ |
| $X^{(6)}$: Mean component size | $C_{i}$ |
| $X^{(7)}$: Number of components | $\sum_{j'} \mathbb{I}(c_{ij} = c_{ij'})$ |
| $X^{(8)}$: Size of node’s component | $\sum_{j'} A_{ij'j} I_{jj'}(0)$ |
| $X^{(9)}$: Total neighbor infections at baseline | $\sum_{j'} I(c_{ij} = c_{ij'}) I_{jj'}(0)$ |
| $X^{(10)}$: Total node’s component infections at baseline | $(\min_{j'} d_{jj'})^{-1}$ |
| $X^{(11)}$: 1/nearest affected path length at baseline | $\sum_{j'} (d_{jj'})^{-1}$ |
| $X^{(12)}$: $\sum_{j'} 1$/path length to affected $j$ at baseline | |

2.2 GEE-based estimation of the effect of an exposure on an outcome

The generalized estimating equations (GEE) approach provides a general approach for analyzing correlated outcomes that: i) is more robust to variance structure misspecification, ii) relies less on parametric assumptions than the standard likelihood methods, and iii) provides population level conclusions on the effect of an exposure on an outcome. This section reviews a modified version of the doubly-robust augmented GEE described in and describes incorporation of contact network structure in the estimation process.

Consider an observational study of a contagion process that consists of $i = 1, \ldots, m$ clusters (each cluster can be represented by one large network or a collection of smaller networks) with $j = 1, \ldots, n_{i}$ individuals per cluster, and $\sum_{i} n_{i} = N$ is the total number of individuals in the study. The binary outcome for individual $j$ in cluster $i$, $Y_{ij}$, is 1 if the individual is affected by the process by the end of the study, otherwise $Y_{ij} = 0$. $Y_{i} = (Y_{i1}, \ldots, Y_{in_{i}})^{T}$ denotes the associated vector of outcomes in cluster $i$. We assume there is no mixing across clusters and assume the clusters to be independent. We consider a setting where some of the clusters are exposed to a specific treatment, intervention or exposure while others are not; and we use $A_{i} = a$ to denote an exposure indicator such that $a = 1$ for the exposed clusters and $a = 0$ for the unexposed (control)
clusters. The outcome can be modeled as a function of exposure such that \( Y_i = \mu_i(\beta, A_i) = h(\beta_0 + \beta_A A_i) \), with \( h \) a link function. The general form of a classical GEE is \( U(\beta) = \sum_{i=1}^{m} D_i^T V_i^{-1} \{ Y_i - \mu_i(\beta, A_i) \} \), where \( D_i = \frac{\partial \mu_i(\beta_A A_i)}{\partial \beta} \) is the design matrix, \( V_i \) is the covariance matrix equal to \( \phi R_i^{1/2} C(\alpha) R_i^{1/2} \), \( R_i \) a diagonal matrix with elements \( \text{var}(Y_{ij}) \), \( \phi \) is the dispersion parameter, and \( C(\alpha) \) is the “working” correlation structure with non-diagonal terms \( \alpha \). Parameters are estimated by setting \( U(\beta) \) to 0. Because our goal is to estimate the effect of exposure, our causal parameter of interest \( \beta_A \) is the difference in average probability of being affected by the contagion process between the exposed and unexposed clusters: \( \mathbb{E}(Y|A = 1) - \mathbb{E}(Y|A = 0) \).

We assume each individual to have a set of \( P \) cluster-level and individual-level covariates \( X_{ij} = (X_{ij}^{(1)}, ..., X_{ij}^{(P)})^\top \), with all covariates represented compactly as \( X_i = (X_{i1}, ..., X_{in_i})^\top \). Some of the covariates may relate to the network in which the individual is embedded and are described in the previous subsection. Accounting for this information is important in the estimation process. To account for non-randomized exposure \( A \), it is possible to account for a different probability of exposure between clusters using a propensity score (PS) and to use classical inverse-probability weighting approaches for estimation of exposure effects. The propensity score is an arbitrary function \( g_i(X_i, \eta_G) \). The estimation procedure is unbiased when it exactly models \( P(A_i = a|X_i) \). It is often fit using a logistic regression model if the cluster exposure status is binary and \( \eta_G \) are nuisance parameters resulting from this estimation. To reduce confounding bias and improve efficiency of estimation, it is possible to introduce covariate adjustment to the standard GEE framework by augmenting the GEE itself. This requires specification of an outcome model (OM) \( B_i(X_i, A_i = a, \eta_B) = [B_{ij}(X_i, A_i = a, \eta_B)]_{j=1,...,n_i} \), which is an arbitrary function of \( X_i \) given for each exposure level, where \( \eta_B \) are nuisance parameters to be estimated. The estimation is unbiased and most efficient if the OM models the probability of the outcome of interest given baseline covariates \( \mathbb{E}(Y_{ij}|X_i, A_i = a) \). The estimation is said doubly robust as either the OM or the PS (but not both) need to be set to a specific quantity to ensure unbiased estimation. In this case, we will call the OM or the PS “correctly specified” as it corresponds to the true data generation process. Equation (1) incorporates these additional terms in the estimating function.

\[
0 = \sum_{i=1}^{m} \left[ D_i^T V_i^{-1} G_i(X_i, A_i, \eta_G) (Y_i - B_i(X_i, A_i, \eta_B)) 
- \sum_{a=0,1} D_i^T(a) V_i^{-1}(a) (B_i(X_i, A_i = a, \eta_B) - \mu_i(\beta, A_i = a)) \right]
\]  

(1)

The \( n_i \times n_i \) matrix \( G_i(X_i, A_i, \eta_G) = \text{diag} \left[ \frac{A_i}{g_i(X_i, \eta_G)} + \frac{1-A_i}{1-g_i(X_i, \eta_G)} \right]_{j=1,...,n_i} \) is an inverse probability weighting matrix specific to each cluster. The variance of \( \beta \) is estimated by using an empirical or “sandwich” estimator, which is also robust in the sense that it provides valid standard errors even when the assumed covariance structure is not correct. Given the OM and PS, the exposure effect is represented by the vector of coefficients \( \beta \).
In practice, we estimate the OM as $E(Y_{ij}|X_i, A_i = a)$ and the PS as $E(A_i = a|X_i)$ using regression approaches. More specifically, we use a stepwise selection of relevant network and sociodemographic covariates $X_i$. Because $P$ is small, we assume that over-fitting is unlikely, although cross-validation could be used to fit OM and PS models if needed.

3 Analysis of Microfinance Diffusion in Indian Villages

We used the methods described above to estimate exposure effects in the adoption of microfinance loans in a collection of villages in Karnataka, India based on information for 49,707 individuals located in 49 villages. In our approach, we consider each village as its own network and we assume the villages to be independent of one another. Six months before a microfinance institution entered the villages and began offering microfinance loans to villagers, investigators used surveys to collect detailed social network data about social, familial and economic ties. The microfinance institution began by inviting “leaders” (e.g., teachers and shopkeepers) to informational meetings and asked them to spread information about the loans to villagers. The leaders constituted 14.7% of the total population. Data was also collected on participation in savings self-help groups. Household membership and sociodemographic information, such as age and sex, was collected for 12,122 individuals.

The outcome of interest, both in the original study and in our re-analyses of data, is household participation in the microfinance program by the end of the study. We describe two exposures as follows: a village (network) experiences Exposure 1, high proportion of leaders, if the fraction of its households containing leaders is in the top quartile compared to all other villages; a village experiences Exposure 2, high proportion of savers, if the fraction of its households that participate in the savings self-help groups is in the top quartile compared to all other villages. Exposures 1 and 2 allow investigation of whether villages with more leaders and with higher participation rates in the self-help have greater participation rates in the microfinance program. We calculate and compare the average difference in microfinance uptake between village exposure groups. A crude estimate of this quantity is obtained as the difference between exposed and unexposed villages in average household uptake of microfinance. The standard GEE accounts for the correlation of outcomes within each village. We fit two doubly-robust GEEs: (1) using only network covariates in the outcome model ($X^{(1)}$ through $X^{(10)}$), and (2) using also the proportion of men in the village and the age of the villagers as covariates. PS and OM were found using stepwise variable selection. Using the model described in the previous section, the estimated uptake of microfinance in the control group is $\beta_0$ and the change in its uptake associated with both exposures is $\beta_A$. Results are given in Table.
| Exp. | β₀ | Crude Estimate | Unadjusted GEE Estimate | Network Covariates Only | Network & Sociodemographic |
|------|----|----------------|-------------------------|------------------------|---------------------------|
| 1    | β₀ | 0.209          | 0.249                   | 0.214                  | 0.215                     |
|      | S.E. | 0.019          | 0.043                   | 0.019                  | 0.019                     |
|      | Wald-score | 11.207          | 5.761                   | 11.12                  | 11.11                     |
|      | p-value | <0.001         | <0.001                  | <0.001                 | <0.001                    |
|      | β₁ | -0.002         | -0.069                  | -0.138                 | -0.137                    |
|      | S.E. | 0.039          | 0.058                   | 0.031                  | 0.031                     |
|      | Wald-score | -0.055          | -1.191                  | -4.49                  | -4.45                     |
|      | p-value | 0.478          | 0.120                   | 0.001                  | <0.001                    |
| 2    | β₀ | 0.203          | 0.201                   | 0.208                  | 0.208                     |
|      | S.E. | 0.018          | 0.018                   | 0.018                  | 0.018                     |
|      | Wald-score | 11.15           | 11.05                   | 11.37                  | 11.38                     |
|      | p-value | <0.001         | <0.001                  | <0.001                 | <0.001                    |
|      | β₁ | 0.018          | 0.03              | 0.045                  | 0.045                     |
|      | S.E. | 0.04           | 0.038                   | 0.041                  | 0.041                     |
|      | Wald-score | 0.44           | 0.79                    | 1.08                   | 1.08                      |
|      | p-value | 0.332          | 0.216                   | 0.143                  | 0.143                     |

Table 2: Estimates of the exposure effect on microfinance uptake for different adjustment strategies. Exposure 1 refers to a village having a high fraction of village leaders, and Exposure 2 refers to a village having a high fraction of savings self-help group participants. β₀ is the estimated uptake of microfinance in unexposed villages and β₁ is the average mean difference in uptake comparing exposed to unexposed villages.

These results show a sizable effect of adjusting for baseline covariates, including network features by fitting the OM and PS models. Details of these model fits are provided in the supplementary material; in general, degree as well as number and size of components were selected in the OM for both exposures, as was age for models in which demographic variables were included. For the PS models, only degree assortativity was selected for Exposure 2, but degree and component features were also included for Exposure 1. For Exposure 1, using the doubly-robust approach leads to a doubling of the point estimate compared to that of the unadjusted GEE and suggests that a greater number of leaders is negatively associated with microfinance uptake. The DR analyses detect the presence of an exposure effect not detected by the unadjusted analysis. For Exposure 2, the DR approach leads to a 50% increase in the point estimates of its effect, although the latter is associated with a p-value of 0.14. These differences suggest the presence of confounding. In addition, adjusting for both network and sociodemographic covariates reduces estimated standard error for Exposure 1 (by about 50%) but not for Exposure 2. None of the estimates of the Exposure 2 effects reach statistical significance at the 0.05 level. Taken together, these results imply that the presence of a high proportion of leaders reduces microfinance uptake—perhaps reflecting the greater influence of leaders when there are fewer of them—but do not demonstrate an effect of participation in savings self-help groups.
4 Simulation

In this section we describe simulation of a contagion process on a network in an observational study setting to estimate the effect of an intervention on that process. We use this simulation study to investigate the usefulness of our method to adjust for baseline confounding factors in order to reduce both bias and variance of estimates of effects of exposure. As before, we assume that individuals are nested within a collection of independent clusters, each with its own contact network structure, and that the outcome of interest arises from a contagion process propagating through network ties. We also assume that the intervention will reduce the rate of the contagion by varying amounts.

We first describe the network generation and the contagious spreading processes as well as the effect of the exposure (or intervention) on the latter. We also describe the process by which individuals would be sampled for an observational study. To estimate the average exposure effect, we apply the doubly-robust augmented GEE described above and compare results to a standard GEE and the effect of the simulation conditions on them.

The structure of our simulation is very general and could apply to many settings, including that of the microfinance intervention study. It can also apply to observational studies of interventions, such as vaccines for control of infectious diseases. Among the settings that we consider is one that closely matches the characteristics of the microfinance study. At the end of this section, we describe the simulation results for this specific setting.

Simulated Contact Networks

The network generation model in our simulation study is the degree-corrected stochastic block model with degree correlation. Because of the complexity of this model, it is not possible to analytically obtain an estimate of the improvement in efficiency resulting from incorporation of network information in analyses. The original stochastic block model\(^\text{13}\) assumes that, in a given network, each node \(j\) belongs to only one block \(b_j\) in a partition of nodes \(B = \{1, \ldots, B\}\); the set of node memberships is given by the vector \(b = \{b_1, \ldots, b_n\}\). In this model, the probability of an edge between nodes \(j\) and \(j'\) depends only on their block membership \(P(e_{jj'} = 1) = p_{b_jb_j'}\). An extension of this model, the so-called degree-corrected stochastic block model, allows each node \(j\) to have arbitrary expected degree \(\theta_j := E(k_j)\), where \(k_j\) is the observed degree \(\sum_{j'} e_{jj'}\) for node \(j\).\(^\text{13}\) The likelihood associated with this model assumes that the mean number of edges \(n_{jj'}\) between any two nodes \(j\) and \(j'\) is the product of the expected degrees of nodes \(j\) and \(j'\) (\(\theta_j\) and \(\theta_{j'}\), respectively), multiplied by the expected amount of mixing.
between the blocks to which nodes \( j \) and \( j' \) belong. The full likelihood of this model is

\[
P(e | \theta, \omega, b) = \prod_{j < j'} \nu_{jj'}^e \exp \left( -\nu_{jj'} \right) \times \prod_j \frac{\left( \frac{1}{2} \nu_{jj} e_{jj} / 2 \right)!}{\left( e_{jj} / 2 \right)!} \exp \left( -\frac{1}{2} \nu_{jj} \right),
\]

(2)

where \( \nu_{jj'} = \theta_j \theta_{j'} \omega_{b_j, b_{j'}} \). The model assumes that \( e_{jj} \) is Poisson distributed (allowing for multiple edges between pairs of nodes), which converges to a simple Bernoulli network for sparse networks in the limit \( n_i \to \infty \). The 1/2 terms in the second half of the likelihood account for the fact that self-edges (edges from one node to itself) are counted twice by this indexing.

In addition to block structure and node degree, networks may vary in the extent to which degrees of adjacent nodes are correlated. One metric for quantifying this property is degree assortativity, which was defined above. Degree assortativity can be varied in the network generating process by performing degree assortative rewiring, which increases or decreases the assortativity in the network while preserving block structure and each node’s degree. The details of this algorithm are given in the Appendix.

Contagion Process

We simulate a contagion process operating on the collection of networks by employing a stochastic compartmental SI (susceptible-infectious) model, shown in Algorithm 1. \( S\% \) of all nodes are initially selected to be affected by the contagion process (capable of transmitting) at random across all study networks \( i = 1, \ldots, m \). After initiation, affected node \( j \) in network \( i \) selects \( q_{ij} \) of their \( k_{ij} \) neighbors at random and transmit to them with probability \( p_0 \), where \( q_{ij} \) is the node’s affectivity, which may vary between 0 and \( k_{ij} \). Zhou et al. showed that the properties of spreading processes on networks can depend strongly on affectivity. Unit affectivity and degree affectivity occur when an individual attempts to affect either one partner (selected at random) or all partners, respectively. (Illustrative diagrams of the contagion process over time are given in Section 1 of supplementary material.) This process is repeated until \( B\% \) of the population is affected by contagion, which defines the baseline, or earliest time an infection is assumed to be observed, and can be included in the estimation procedure without risk of bias in the exposure effect estimate. Half of the clusters are exposed \((A_i = 1)\) and half unexposed \((A_i = 0)\) and the probability of assignment depends on a single confounder. The contagion process continues for \( T \) time steps with a probability to infect \( p_0 \) for unexposed clusters and \( p_1 \) for exposed clusters. The contagion process ends at time \( T \).
Algorithm 2: Stochastic Compartmental Contagion Process

1 \( S\% \) of all nodes are selected at random to be initially affected.

2 Until \( B\% \) population incidence:
   
   For each affected node \( j \) (in random order):
   
   a Successively select \( q_{ij} \) neighbors.
   
   b If neighbor \( j' \) is already affected, do nothing. If not, affect with probability \( p_0 \).

3 Repeat \( T \) times:
   
   For each affected node \( j \) (in random order):
   
   a Successively select \( q_{ij} \) neighbors.
   
   b If neighbor \( j' \) is already affected, do nothing. If not, affect with probability:

   \( p_0 \) for those in unexposed clusters.

   \( p_1 \) for those in exposed clusters.

Simulation Setting Parameters

To match the approximate size of the empirical dataset used in the microfinance application, each simulated study consists of a contagion process propagating on \( m = 48 \) clusters (networks) of sizes ranging from \( n = 120 \) to 280, with an average size of size 200, totaling 9600 individuals.

Block Structure

Each network in our simulation comprises eight blocks. We simulate networks using two types of block structure, random and heterogeneous. For a complete description of the block structures used, see Section 2 in supplementary material. A diagram of these structures is shown in Figure 1.
Figure 1: The top and bottom rows show the two kinds of mixing used, and the left and right panels show the block mixing structure and block mixing matrices, respectively. In all diagrams, the eight blocks represent the eight groups of nodes that partition each network. Panel a shows the random block structure, with lines connecting blocks that share edges. Panel b shows the corresponding mixing matrix, where the rows and columns represent each block, and color shade (see the color bar) represents the fraction of edges shared between members of each block. Panels c and d show the block mixing structure and matrices for the heterogeneous structure, respectively.

Contagion Process

The contagion process continues for $T = 5$ time steps. For simplicity, we assume a strong exposure effect that reduces contagious spread: the probability each affected node affects a selected neighbor is $p_0 = 0.3$ in unexposed clusters and $p_1 = 0.1$ in exposed clusters.

Probability of Cluster Exposure

The true simulation propensity score, the probability that a given cluster is exposed, is generated by a simple logistic function of a single cluster-level covariate, the number of affected neighbors at baseline summed for all nodes in each cluster (see Equation 3). For each scenario, $\psi_0$ and $\psi_A$ are selected such that this probability is between 0.1 and 0.9 for all clusters. In the estimation procedure, the regression used for the exposure propensity model includes this covariate, ensuring asymptotically unbiased estimation of the exposure effect.
\[ \mathbb{P}(A_i = 1 | X^C_i) = \expit \left( \psi_0 + \psi_A \sum_j X^{(9)}_{ij} \right) = \expit \left( \psi_0 + \psi_A \sum_j \sum_{j'} e_{ijj'} I_{ij}(0) \right) \] (3)

**Estimation Performance Metrics**

In principle, our doubly-robust approach to estimation should remove bias as well as reduce variance in the estimation of \( \beta_A \).

Based on the simulation specifications, we define estimation metrics for the average exposure effect \( \beta_A \). For \( r = 1, \ldots, R \) replicates, the estimate of exposure effect is denoted \( \hat{\beta}_r \) and the estimated standard deviation \( \hat{sd}(\hat{\beta}_r) \). These standard deviation estimates are compared with the empirical bootstrap estimates evaluated as the standard deviations of all the estimates \( \hat{\beta}_r \) in the R replicates. Empirical power and coverage are derived from these simulation study point estimates and confidence intervals.

Although the contagious spreading rates in unexposed and exposed groups are specified as \( p_0 \) and \( p_1 \), the true value for the average exposure effect must be determined through simulation\(^{20}\). Because the doubly-robust GEE yields consistent exposure effect estimates\(^{21}\) under appropriate assumptions, the true value for \( \beta^* \) is estimated as the average of all exposure effect estimates calculated with correctly specified models (known in simulation), \( \beta^*_A := \frac{1}{R} \sum_{r=1}^{R} \hat{\beta}^*_r \). We define improvement in estimation efficiency as the percent reduction in root mean squared error (RMSE) for each covariate set in the outcome model, comparing the augmentation adjustment \( \hat{\text{RMSE}}_{\text{adj}} \) to that of the unadjusted GEE (\( \hat{\text{RMSE}}_{\text{GEE}} \)):

\[ \text{Improvement} := 100 \times \left( 1 - \frac{\hat{\text{RMSE}}_{\text{adj}}}{\hat{\text{RMSE}}_{\text{GEE}}} \right). \] (4)

**Sensitivity Analysis**

To estimate the sensitivity of estimation performance on simulation features, we vary six aspects of the simulation in two ways each: mean degree (values 2 and 10), degree distribution (Poisson or power law distribution), assortativity (values -0.3 and 0.3), block mixing structure (random or heterogenous), infectivity (unit or degree), and infection prevalence at baseline (values (S,B) are low (1,2)% or high (10, 25)%). It leads to a total of \( 2^6 = 64 \) scenarios.
Simulation Results

In our setup, the covariates included in the outcome model are correlated with both the outcome and exposure; hence adjustment for these confounding factors can reduce bias and RMSE. Bias in estimation, average model standard error, empirical standard error, RMSE reduction, power, and coverage are provided in Table 3; full simulation results are given in Section 3 in supplementary material. Results are averaged across all 64 observational scenarios with standard deviations across scenarios in parentheses. Averaged across all simulation replications and variants, inclusion of covariates in outcome and propensity score models led to reduction in bias and gains in efficiency. We also find that a single covariate, the node’s number of affected neighbors at baseline ($X^{(9)}$), provides a reduction in RMSE comparable to variable selection approach. As an additional sensitivity analysis, we repeated these simulations for larger networks, each larger than those specified here by six-fold, and obtained similar results.

|                        | None | $X^{(9)}$ | $X^{(1)}, \ldots, X^{(10)}$ | Stepwise |
|------------------------|------|-----------|-----------------------------|----------|
| Bias                   | 0.007 | -0.024    | -0.032                      | -0.034   |
| Estimated SE           | 1.82  | 1.09      | 0.86                        | 0.86     |
| Empirical Bootstrap SE | 1.5   | 0.95      | 0.86                        | 0.86     |
| Improvement            | 0(0)  | 34(25)    | 39(22)                      | 39(23)   |
| Power                  | 59.6  | 87.1      | 90.2                        | 90.6     |
| Coverage               | 96(2) | 97(2)     | 95(2)                       | 95(2)    |

Table 3: Exposure effect statistics averaged across each simulation characteristic, adjusted for all confounding factors. Each row displays a metric, and each column displays an adjustment feature or strategy for the outcome model. Standard deviations across scenarios are shown in parentheses.

Covariate Selection

The covariates selected in a stepwise procedure for inclusion in the outcome model vary across the different simulated datasets. To assess which covariates are most useful for adjustment in the outcome model, we measure the frequency of covariate inclusion and its variability by simulation scenario (see Figure 3). Degree ($X^{(1)}$) and covariates related to contagion at baseline (covariates $X^{(9)} - X^{(12)}$) are included most often; others are selected in a range of frequencies. The outcomes models for the two exposure groups are similar.
Figure 2: The distribution of the proportion of occasions each covariate is included in the outcome model. The covariates along the x-axis are described in Table 1. Blue bars show results for the exposed group, and red bars show results for the unexposed group. The middle values represent medians, the bars represent the (25, 75)% quartiles across scenarios, and endpoints indicate minima and maxima.

Sensitivity Analysis Results

Features of the simulated contagion process affect performance metrics such as bias and improvement in RMSE. To evaluate the sizes of these effects, we used simple linear regression treating the RMSE as the outcome and simulation features (i.e., mean degree, degree distribution, assortativity, block mixing structure, Infectivity mode, and infection prevalence at baseline) as covariates, coded as binary variables. The fitted coefficients represent the metric change when changing simulation features, holding all other simulation features constant. The percent improvement in RMSE is shown in Table 4. For example, holding all other simulation features constant, a contagion process exhibiting high baseline prevalence shows an additional RMSE reduction of 29-33 percentage points compared to a contagion process exhibiting low baseline prevalence. Therefore, using covariate $X^{(9)}$ (total number of affected neighbors at baseline) yields larger reductions in RMSE if the contagion begins with high compared to low prevalence at baseline. This suggests that a node’s local network contacts and whether they are contagious, i.e. can cause a process to spread on the network, can be quite predictive of the risk of the node becoming affected — a finding also reported by Ghani et al. [2]
Table 4: Change in percentage point RMSE reduction when changing simulation assumptions. Rows display a simulation assumption, and columns display an adjustment feature or strategy.

|                     | All  | Step |
|---------------------|------|------|
| (Intercept)         | 27   | 36   |
| High vs. Low Degree | -1   | -5   |
| Powerlaw vs. Poisson| -19  | -10  |
| Assortative vs. Disassortative | 4   | 3    |
| Communities vs. No Communities | 2   | 0    |
| Degree vs. Unit Infectivity | -4  | -18  |
| High vs. Low Baseline       | 29   | 34   |

Comparison to Microfinance Study Analysis

As mentioned above, we set up the simulation study so that one of the settings closely matched the characteristics observed in the microfinance study. In that dataset, the average degree of participants is high ($\bar{k} = 16.0$, averaged across all villages), and the degree distribution is not strongly right skewed; further details are provided in Section 5 of supplementary material. Mean degree assortativity is positive and moderately strong (0.346). Leaders were encouraged to inform all individuals they knew about the microfinance loan program, which would be expected to induce degree affectivity. Finally, individuals who both were leaders and participated in the microfinance program total 3.1% of the study population, suggesting a low exposure at baseline. Section 4 of the supplementary material (scenario $a=(111110)$) shows the simulation performance metrics for these observations. This simulation configuration exhibits good statistical coverage of interval estimates and a substantial improvement in the RMSE for each adjustment strategy, especially when using a stepwise selection of covariates in the outcome model. The outcome model in the microfinance data analysis included network and sociodemographic covariates for Exposure 1 and led to a 46% reduction in estimated standard error, which is fairly similar to the 53% reduction in the closest-matching simulation setting.

5 Discussion

In a spreading process, contagion outcomes depend on contact network structure and spreading process dynamics. To estimate the marginal effect of exposure on the contagion process, one strategy to adjust for confounding and reduce the variation of the exposure effect estimate is to make use of the doubly-robust augmented GEE methods described here. We investigated the extent to which bias and RMSE reduction in exposure effect estimates depend on network and contagion properties. Adjusting for contact network features and baseline contagion reduced bias and yielded a considerable reduction in RMSE across a range
of simulation settings; such adjustment also reduced RMSE in the analysis of the spread of microfinance.

In our models, covariates derived from network features differed in their usefulness in reducing exposure estimate variance. They also differed in how feasible their estimation is in practice. Obtaining the degree of an individual may be quite feasible using a simple survey, yet the gains we observed from using this covariate were modest. We found that the number of neighbors affected at baseline yielded the largest reduction in variance and may be feasible to estimate in some practical settings.

This work invites several extensions. Information may be missing or misreported for individual outcomes, contact network data, or both, which may lead to bias or increased variation in estimating the exposure effect. We also did not estimate the effect of unmeasured confounding—an important consideration in observational studies. Although we carried out extensive simulations, they are neither intended to be, nor can they be, comprehensive. Simulation of other settings would be useful to help guide research studies in which network features may confound results of observational studies or may help improve efficiency of estimation in both randomized and observational studies.

6 Appendix

Degree assortative rewiring. This is performed by randomly selecting two edges within a block pair and rewiring them, as described in Algorithm 2. A diagram of this process is shown in Figure 3. To decrease assortativity, the inequality in Step 3 must be reversed.
Algorithm 1: Edge Rewiring to Adjust Assortativity

1. Select two blocks \( b_l \) and \( b_{l'} \) at random.

2. Select two edges \((N_1, N_2)\) and \((N_3, N_4)\) at random between blocks \( b_l \) and \( b_{l'} \).

3. If \(|k_{N_1} - k_{N_2}| + |k_{N_3} - k_{N_4}| > |k_{N_1} - k_{N_4}| + |k_{N_2} - k_{N_3}|\):

   Remove edges \((N_1, N_2)\) and \((N_3, N_4)\)

   Add edges \((N_1, N_4)\) and \((N_2, N_3)\)

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Figure 3: A schematic of degree assortative rewiring. Panel a displays a network, containing nodes \( N_1, ..., N_4 \). Panel b highlights two edges selected within the same block pair. Panel c shows a potential rewiring, which will only occur if rewiring will increase assortativity. In this case, rewiring would increase degree assortativity, and panel d displays the rewiring.

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Supplementary Material

In this supplement, we provide additional details from the main paper. In Section 1, we provide two figures that illustrate the contagion/spreading process. In Section 2, we provide details regarding the empirical degree distribution and outcome models employed in Section 3 of the main paper. In Section 3, we formally specify the block structure used in the simulated contagion process in Section 4 of the main paper. In Section 4, we provide an expanded set of simulation results from Section 4 of the main paper.

1 Figures of the Contagious Process

Figure 1 shows a schematic of the contagion process for a specific node in a given network. Figure 2 shows the contagion process from its onset until study end.

Figure 1: A schematic of the stochastic agent-based contagion process. Node $j$ is shown in network (cluster) $i$. In this figure, red nodes are affected by the contagion, and black nodes are susceptible. Individual $j$ is connected to $k_{ij} = 4$ other nodes. The arrows represent the neighbors that might receive the contagion from an infected individual; the total number of arrows is the contagion affectivity of node $j$. 
Figure 2: A diagram of the contagion process over time. At the beginning of the contagious spread, S% of nodes are randomly selected as initially affected, and the network contagion process spreads until B% overall baseline prevalence (across all clusters) is reached (time \( t_B \)). In this figure, \( S = 1 \) and \( B = 20 \). Individuals are affected according to Algorithm 2 in the paper. Then, each cluster is randomly assigned to be exposed \( (A = 1) \) or unexposed \( (A = 0) \). The probability of transmission from an affected node in an exposed cluster is \( 1/3 \) that on a node in an unexposed cluster. The process continues for another \( T = 5 \) time steps.
2 Estimates Outcome and Propensity Score Model Parameters

In this section, the distribution for the degree of all individuals in the Karnataka dataset is displayed. We also provide details on the outcome and propensity score models used in Section 3 of the main paper.

2.1 Karnataka Degree Distribution

Figure 3 shows the empirical log-log distribution of degree for the Karnataka dataset.

Figure 3: The empirical degree distribution for the Karnataka dataset. The $x$-axis shows the log degree, and the $y$-axis shows the log proportion of individuals with degree exceeding the corresponding degree.

2.2 Exposure 1: Fraction of Households Reported As Containing Leaders

In this subsection, we report on the outcome models (OM) and propensity score (PS) models that were fit using a stepwise procedure for inclusion in the doubly-robust (DR) estimation procedure in Section 3 of the main paper. Tables 1, 2 and 3 provide the results of fitting these models; the exposure of interest was the fraction of households that include village leaders.
Separate outcome models are used for exposed and unexposed villages.

| Parameter                        | Estimate | Standard Error | t-value | p-value |
|----------------------------------|----------|----------------|---------|---------|
| Intercept                        | 0.1936   | 0.0326         | 5.9415  | < 0.001 |
| Degree $X^{(1)}$                 | 0.0077   | 0.0014         | 5.6074  | < 0.001 |
| LCC Size $X^{(5)}$              | -0.0006  | 0.0001         | -7.6842 | < 0.001 |
| Mean Component Size $X^{(6)}$   | -0.0005  | 0.0001         | -5.5891 | < 0.001 |
| Total Cluster Seeds $X^{(10)}$  | 0.0030   | 0.0004         | 6.9553  | < 0.001 |

Using network covariates and sociodemographics

| Parameter                        | Estimate | Standard Error | t-value | p-value |
|----------------------------------|----------|----------------|---------|---------|
| Intercept                        | 0.2362   | 0.0385         | 6.1321  | < 0.001 |
| Age                              | -0.0013  | 0.0006         | -2.0704 | 0.0385  |
| Degree $X^{(1)}$                 | 0.0082   | 0.0014         | 5.8544  | < 0.001 |
| LCC Size $X^{(5)}$              | -0.0006  | 0.0001         | -7.6616 | < 0.001 |
| Mean Component Size $X^{(6)}$   | -0.0005  | 0.0001         | -5.6084 | < 0.001 |
| Total Cluster Seeds $X^{(10)}$  | 0.0030   | 0.0004         | 6.9282  | < 0.001 |

Table 1: Outcome model coefficient estimates for exposed villages for the exposure: fraction of leaders in each village.

| Parameter                        | Estimate | Standard Error | t-value | p-value |
|----------------------------------|----------|----------------|---------|---------|
| Intercept                        | 0.3951   | 0.0225         | 17.5977 | < 0.001 |
| Mean Neighbor Degree $X^{(2)}$   | -0.0081  | 0.0012         | -6.8472 | < 0.001 |
| LCC Size $X^{(5)}$               | -0.0001  | 0.0000         | -8.3894 | < 0.001 |
| Mean Component Size $X^{(6)}$   | 0.0003   | 0.0001         | 3.8005  | < 0.001 |
| Total Neighbor Seeds $X^{(9)}$  | 0.0039   | 0.0014         | 2.9035  | 0.0037  |

Using network covariates and sociodemographics

| Parameter                        | Estimate | Standard Error | t-value | p-value |
|----------------------------------|----------|----------------|---------|---------|
| Intercept                        | 0.4344   | 0.0249         | 17.4641 | < 0.001 |
| Sex                              | 0.0162   | 0.0085         | 1.9094  | 0.0562  |
| Age                              | -0.0013  | 0.0003         | -3.8254 | < 0.001 |
| Mean Neighbor Degree $X^{(2)}$   | -0.0078  | 0.0012         | -6.4798 | < 0.001 |
| LCC Size $X^{(5)}$               | -0.0001  | 0.0000         | -8.4663 | < 0.001 |
| Mean Component Size $X^{(6)}$   | 0.0003   | 0.0001         | 3.7191  | < 0.001 |
| Total Neighbor Seeds $X^{(9)}$  | 0.0039   | 0.0014         | 2.8641  | 0.0042  |

Table 2: Outcome model coefficient estimates for unexposed villages for the exposure: fraction of leaders in each village.
| Parameter                        | Estimate | Standard Error | t-value | p-value |
|---------------------------------|----------|----------------|---------|---------|
| **Using only network covariates** |          |                |         |         |
| Intercept                       | 7.4663   | 4.4971         | 1.6603  | 0.0969  |
| Degree $X^{(1)}$                | -2.0346  | 1.0254         | -1.9841 | 0.0472  |
| Mean Neighbor Degree $X^{(2)}$  | 1.6106   | 1.0198         | 1.5792  | 0.1142  |
| Assortativity $X^{(3)}$         | 7.9825   | 5.6278         | 1.4184  | 0.1560  |
| LCC Size $X^{(5)}$              | -0.0029  | 0.0016         | -1.8172 | 0.0691  |
| Mean Component Size $X^{(6)}$   | 0.0109   | 0.0060         | 1.8136  | 0.0697  |
| **Using network covariates and sociodemographics** |          |                |         |         |
| Intercept                       | 7.4663   | 4.4971         | 1.6603  | 0.0969  |
| Degree $X^{(1)}$                | -0.4444  | 0.3101         | -1.4327 | 0.1519  |
| Mean Neighbor Degree $X^{(2)}$  | 1.6106   | 1.0198         | 1.5793  | 0.1143  |
| Assortativity $X^{(3)}$         | 12.0840  | 6.3294         | 1.9091  | 0.0562  |
| LCC Size $X^{(5)}$              | -0.0030  | 0.0016         | -1.8173 | 0.0692  |
| Mean Component Size $X^{(6)}$   | 0.0109   | 0.0060         | 1.8137  | 0.0697  |

Table 3: Propensity score model coefficient estimates for exposure: the fraction of leaders in each village.

### 2.3 Exposure 2: Fraction of Households Using Self-Help

In this subsection, we report on the outcome and PS models for the exposure: fraction of households that included village leaders. Tables 3 and 4 provide the results of fitting these models using a stepwise procedure.

| Parameter                        | Estimate | Standard Error | t-value | p-value |
|---------------------------------|----------|----------------|---------|---------|
| **Using only network covariates** |          |                |         |         |
| Intercept                       | 0.0452   | 0.0530         | 0.8526  | 0.3939  |
| Degree $X^{(1)}$                | 0.0074   | 0.0015         | 4.9437  | < 0.001 |
| Mean Neighbor Degree $X^{(2)}$  | 0.0047   | 0.0029         | 1.6456  | 0.1021  |
| Assortativity $X^{(3)}$         | 0.8153   | 0.1031         | 7.9059  | < 0.001 |
| LCC Size $X^{(5)}$              | -0.0001  | 0.0000         | -1.5428 | 0.1220  |
| Mean Component Size $X^{(6)}$   | -0.0003  | 0.0001         | -3.8290 | < 0.001 |
| Sums of paths $X^{(12)}$        | -0.0033  | 0.0008         | -4.1623 | < 0.001 |
| **Using network covariates and sociodemographics** |          |                |         |         |
| Intercept                       | 0.0452   | 0.0530         | 0.8526  | 0.3939  |
| Degree $X^{(1)}$                | 0.0073   | 0.0015         | 4.9436  | < 0.001 |
| Mean Neighbor Degree $X^{(2)}$  | 0.0046   | 0.0028         | 1.6352  | 0.1021  |
| Assortativity $X^{(3)}$         | 0.8152   | 0.1031         | 7.9059  | < 0.001 |
| LCC Size $X^{(5)}$              | -0.0001  | 0.0000         | -1.5470 | 0.1220  |
| Mean Component Size $X^{(6)}$   | -0.0003  | 0.0001         | -3.8145 | < 0.001 |
| Sums of paths $X^{(12)}$        | -0.0034  | 0.0008         | -4.1704 | < 0.001 |

Table 4: Outcome model coefficient estimates for exposed villages for estimating the exposure: fraction of individuals concurrently participating in the self-help program in each village.
| Parameter                      | Estimate | Standard Error | t-value | p-value |
|-------------------------------|----------|----------------|---------|---------|
| **Using only network covariates** |          |                |         |         |
| Intercept                     | 0.3585   | 0.0224         | 16.0091 | < 0.001|
| Mean Neighbor Degree $X^{(2)}$ | -0.0077  | 0.0012         | -6.3968 | < 0.001|
| LCC Size $X^{(5)}$            | -0.0001  | 0.0000         | -7.8174 | < 0.001|
| Mean Component Size $X^{(6)}$ | 0.0004   | 0.0001         | 4.6739  | < 0.001|
| Total Neighbor Seeds $X^{(9)}$| 0.0042   | 0.0013         | 3.2388  | 0.0012  |
| **Using network covariates and sociodemographics** |          |                |         |         |
| Intercept                     | 0.4030   | 0.0247         | 16.3435 | < 0.001|
| Sex                           | 0.0178   | 0.0085         | 2.1068  | 0.0352  |
| Age                           | -0.0015  | 0.0003         | -4.4782 | < 0.001|
| Mean Neighbor Degree $X^{(2)}$| -0.0073  | 0.0012         | -5.9668 | < 0.001|
| LCC Size $X^{(5)}$            | -0.0001  | 0.0000         | -7.8681 | < 0.001|
| Mean Component Size $X^{(6)}$ | 0.0004   | 0.0001         | 4.6036  | < 0.001|
| Total Neighbor Seeds $X^{(9)}$| 0.0042   | 0.0013         | 3.1995  | 0.0014  |

Table 5: Outcome model coefficient estimates for unexposed villages for the exposure: fraction of individuals concurrently participating in the self-help program in each village.

| Parameter                      | Estimate | Standard Error | t-value | p-value |
|-------------------------------|----------|----------------|---------|---------|
| **Using only network covariates** |          |                |         |         |
| Intercept                     | 2.1783   | 1.8949         | 1.1495  | 0.2503  |
| Assortativity $X^{(3)}$       | -9.9629  | 5.8182         | -1.7123 | 0.0868  |
| **Using network covariates and sociodemographics** |          |                |         |         |
| Intercept                     | 2.1783   | 1.8949         | 1.1495  | 0.2503  |
| Assortativity $X^{(3)}$       | -9.9629  | 5.8182         | -1.7123 | 0.0868  |

Table 6: Propensity score model coefficient estimates for the exposure: fraction of individuals concurrently participating in the self-help program in each village.
3 Generation of Block Structure

In this section, we provide details on the block structure used in Section 4 of the main paper. The collection of networks are designed to mimic community structure and mixing patterns found in contact networks using the degree-corrected stochastic block model, which allows for an arbitrary degree distribution and block structure.

Let \( b_i \in \{1, ..., B\} \) be the block membership for node \( i \), with \( B = 8 \) blocks total. Define the total degree for members of each block \( j \) as \( \kappa_j := \sum_i k_i \mathbb{1}(b_i = j) \), and the total number of edges \( m = \frac{\sum_{j=1}^{B} \kappa_j}{2} \). The model specifies the amount of mixing between blocks by specifying mixing matrix \( \omega \in \mathbb{N}^{B \times B} \), which defines the total number of edges shared between members of pairs of blocks. This matrix requires a constraint to ensure all edges belong to some block pair: \( \omega \mathbf{1} \equiv \kappa \), where \( \mathbf{1} = \{1, ..., 1\}^T \) and \( \kappa = \{\kappa_1, ..., \kappa_B\}^T \).

Before specifying the chosen mixing structure, we define three valid mixing matrix specifications, which we combine for our final specification. Nodes might form ties exclusively with members of their same block, in which case \( \omega_{\text{community}} \) gives the mixing matrix corresponding to edges with this structure. Blocks may also mix preferentially with other blocks, forming a core. Mixing matrix \( \omega_{\text{core}} \) assumes block 1 mixes with other blocks with greater frequency than members of other blocks. Finally, all blocks may share their edges proportional to the total degree of each other block holding average block degree constant, which is detailed by \( \omega_{\text{random}} \). Each of these mixing matrices are detailed below.
The simulations in Section 4 of the main paper comprise a range of linear combinations of these matrices:

\[
\omega = \lambda \cdot \omega_{\text{community}} + \mu \cdot \omega_{\text{core}} + (1 - \lambda - \mu) \cdot \omega_{\text{random}}
\]  \hspace{1cm} (5)

To create a random community structure, we selected mixing matrix values \((\lambda = 0.0, \mu = 0.0)\). To create a block structure and establish block 1 as the network core, we selected mixing matrix values \((\lambda = 0.3, \mu = 0.3)\).
4 Extended Simulation Results

In this section, we present an expanded set of results from Section 4 of the main paper. Specifically, we provide tables for the exposure effect size, bias, estimated and robust standard errors, reduction in RMSE, statistical power, and statistical coverage.

For \( r = 1, \ldots, R \) trials, we compute the augmented GEE estimates of exposure effect size \( \hat{\beta}_r \) and estimate standard deviation \( \hat{\text{sd}}_r(\hat{\beta}_r) \). After calculating \( \beta \) as detailed in the paper, we obtain the estimated empirical bias and empirical variance of the exposure effect estimate, where

\[
\hat{\text{Bias}}(\hat{\beta}_r) = \beta - \hat{\beta}_r.
\] (6)

To combine the amount of bias and size of the standard error in a single composite measure, we compute the root mean squared error for each trial, defined as:

\[
\hat{\text{RMSE}} = \sqrt{\frac{1}{R} \sum_r \hat{\text{Bias}}_r(\hat{\beta}_r)^2 + \text{Var}(\hat{\beta})}.
\] (7)

Our metric for the gained improvement by the augmentation term is the percent reduction in RMSE for each adjustment covariate set, comparing the augmentation adjustment \( \hat{\text{RMSE}}_{\text{adj}} \) to that of the unadjusted GEE (\( \hat{\text{RMSE}}_{\text{GEE}} \)):

\[
\hat{\text{Gain}} := 100 \times \left( 1 - \frac{\hat{\text{RMSE}}_{\text{adj}}}{\hat{\text{RMSE}}_{\text{GEE}}} \right).
\] (8)

Statistical coverage is the probability that the estimated confidence intervals cover the true exposure effect, which must be 95% or greater for valid inference:

\[
\hat{\text{Coverage}} := P(\beta_A^* \in CI(\hat{\beta}^*)).
\] (9)

Finally, in our setting with the null hypothesis \( \beta = 0 \), power is the probability that the confidence interval is significantly different from zero given that the exposure effect is not zero:

\[
\hat{\text{Power}} := P(0 \notin CI(\hat{\beta}^*_A) | \beta_A \neq 0)
\] (10)

The average values for these estimands are given in the main paper.
4.1 Sensitivity Analysis

In this subsection, we present the results in each statistical performance metric when changing various aspects of the simulation, holding all others constant. A total of 64 scenarios are described. Tables 7-12 present these coefficients for exposure effect size, bias, estimated effect estimate standard error, empirical effect estimate standard error, improvement in RMSE, power, and coverage. These estimates differ depending on which covariate set is used in the outcome models and propensity score model, which are presented as columns. The scenario of simulation is given by $a$ as described below:

$$a = \{I(\text{High Degree}),$$

$$I(\text{Powerlaw}),$$

$$I(\text{Assortativity}),$$

$$I(\text{Heterogeneous Block Structure}),$$

$$I(\text{Degree Affectivity}),$$

$$I(\text{High Baseline})\}$$
Bias
| None       | Only $X^{(0)}$ | All Step |
|------------|---------------|----------|
| 000000     | 0.008         | 0.10 0.30 0.30 |
| 000010     | 0.007         | 0.00 -0.10 -0.10 |
| 000100     | 0.005         | 0.10 0.30 0.30 |
| 000101     | 0.008         | -0.10 -0.20 -0.20 |
| 000110     | 0.007         | 0.20 0.40 0.40 |
| 000111     | 0.003         | -0.10 -0.10 0.00 |
| 001000     | 0.009         | 0.10 0.30 0.30 |
| 001001     | 0.007         | -0.10 -0.20 -0.20 |
| 001010     | 0.008         | 0.30 0.40 0.40 |
| 001011     | 0.000         | 0.10 0.10 0.10 |
| 001100     | 0.005         | 0.10 0.30 0.30 |
| 001101     | 0.004         | -0.10 -0.20 -0.20 |
| 001110     | 0.009         | 0.10 0.30 0.30 |
| 001111     | 0.008         | 0.20 0.30 0.30 |
| 010000     | 0.008         | 0.20 0.00 0.00 |
| 010001     | 0.009         | 0.10 -0.20 -0.20 |
| 010010     | 0.005         | 0.50 0.90 0.90 |
| 010011     | 0.006         | 0.00 0.00 0.00 |
| 010100     | 0.009         | 0.10 0.10 0.10 |
| 010101     | 0.006         | 0.20 0.10 0.10 |
| 010110     | 0.009         | 0.40 0.70 0.70 |
| 010111     | 0.010         | 0.30 0.30 0.30 |
| 011000     | 0.009         | 0.10 0.20 0.20 |
| 011001     | 0.009         | 0.00 -0.20 -0.20 |
| 011010     | 0.005         | 0.30 0.50 0.50 |
| 011011     | 0.011         | 0.00 -0.10 -0.10 |
| 011100     | 0.008         | 0.10 0.10 0.10 |
| 011101     | 0.010         | 0.20 0.10 0.10 |
| 011110     | 0.005         | 0.10 0.20 0.20 |
| 011111     | 0.006         | 0.20 0.20 0.20 |
| 100000     | 0.009         | 0.10 0.10 0.10 |
| 100001     | 0.006         | 0.10 0.10 0.10 |
| 100030     | 0.007         | 0.10 0.30 0.30 |
| 100111     | 0.008         | -0.10 -0.10 -0.10 |
| 100110     | 0.006         | 0.00 0.00 0.00 |
| 100101     | 0.006         | -0.20 -0.30 -0.30 |
| 100100     | 0.006         | 0.10 0.20 0.20 |
| 100111     | 0.005         | -0.20 -0.30 -0.30 |
| 101000     | 0.007         | 0.10 0.10 0.10 |
| 101001     | 0.012         | -0.30 -0.30 -0.30 |
| 101010     | 0.005         | 0.00 0.10 0.10 |
| 101011     | 0.004         | 0.00 0.00 0.00 |
| 101100     | 0.006         | 0.00 0.00 0.00 |
| 101101     | 0.010         | 0.10 0.00 0.00 |
| 101110     | 0.011         | 0.10 0.10 0.10 |
| 101111     | 0.008         | -0.20 -0.30 -0.30 |
| 110000     | 0.006         | 0.20 0.10 0.10 |
| 110001     | 0.007         | -0.20 -0.30 -0.30 |
| 110010     | 0.005         | 0.20 0.50 0.50 |
| 110011     | 0.009         | 0.30 0.30 0.30 |
| 110100     | 0.005         | 0.00 0.00 0.00 |
| 110101     | 0.007         | 0.00 0.00 0.00 |
| 110110     | 0.008         | 0.30 0.60 0.60 |
| 110111     | 0.009         | 0.10 0.10 0.10 |
| 111000     | 0.009         | 0.00 0.00 0.00 |
| 111001     | 0.004         | -0.30 -0.40 -0.50 |
| 111010     | 0.008         | 0.20 0.40 0.40 |
| 111011     | 0.008         | -0.10 -0.30 -0.30 |
| 111100     | 0.005         | 0.10 0.10 0.10 |
| 111101     | 0.008         | 0.20 0.20 0.20 |
| 111110     | 0.005         | 0.20 0.40 0.40 |
| 111111     | 0.004         | 0.00 0.00 0.00 |

Table 7: The average estimated bias in estimates for each exposure scenario, measured in percentage points of the estimated variance component.
Robust Standard Error

|       | None  | Only X[^9] | All Step |
|-------|-------|------------|----------|
| 000000| 0.70  | 0.20 0.20  | 0.20     |
| 000001| 1.60  | 0.60 0.30  | 0.30     |
| 000010| 1.40  | 0.50 0.40  | 0.40     |
| 000011| 1.90  | 0.50 0.40  | 0.40     |
| 000100| 0.70  | 0.20 0.20  | 0.20     |
| 000101| 1.60  | 0.60 0.30  | 0.30     |
| 000110| 1.20  | 0.40 0.40  | 0.40     |
| 000111| 1.80  | 0.50 0.40  | 0.40     |
| 001000| 0.80  | 0.20 0.20  | 0.20     |
| 001001| 1.50  | 0.60 0.30  | 0.30     |
| 001010| 1.30  | 0.40 0.40  | 0.40     |
| 001011| 1.60  | 0.50 0.30  | 0.30     |
| 001100| 0.80  | 0.40 0.30  | 0.30     |
| 001101| 1.90  | 1.20 0.60  | 0.60     |
| 001110| 2.80  | 1.40 1.10  | 1.10     |
| 001111| 2.90  | 0.80 0.50  | 0.50     |
| 010000| 0.60  | 0.40 0.30  | 0.30     |
| 010001| 1.70  | 1.10 0.50  | 0.50     |
| 010010| 2.40  | 1.30 1.00  | 1.00     |
| 010011| 2.20  | 0.80 0.50  | 0.50     |
| 010100| 0.80  | 0.40 0.30  | 0.30     |
| 010101| 2.10  | 0.90 0.50  | 0.50     |
| 010110| 2.60  | 1.50 0.90  | 0.90     |
| 010111| 2.70  | 0.70 0.50  | 0.50     |
| 011000| 0.60  | 0.20 0.20  | 0.20     |
| 011001| 1.80  | 0.90 0.40  | 0.40     |
| 011010| 1.90  | 1.10 0.80  | 0.80     |
| 011011| 2.10  | 0.70 0.40  | 0.40     |
| 011100| 0.70  | 0.30 0.30  | 0.30     |
| 011101| 1.80  | 0.80 0.50  | 0.50     |
| 011110| 1.90  | 1.10 0.90  | 0.90     |
| 011111| 2.60  | 1.60 1.40  | 1.40     |
| 100000| 0.70  | 0.30 0.30  | 0.30     |
| 100001| 1.80  | 0.80 0.50  | 0.50     |
| 100010| 1.80  | 1.00 0.80  | 0.80     |
| 100011| 2.70  | 1.60 1.40  | 1.40     |
| 100100| 0.70  | 0.40 0.30  | 0.30     |
| 100101| 1.90  | 0.80 0.50  | 0.50     |
| 100110| 2.10  | 1.10 0.90  | 0.90     |
| 100111| 2.50  | 1.50 1.30  | 1.30     |
| 101000| 0.70  | 0.30 0.30  | 0.30     |
| 101001| 1.90  | 0.90 0.50  | 0.50     |
| 101010| 1.80  | 1.10 0.80  | 0.80     |
| 101011| 2.50  | 1.60 1.40  | 1.40     |
| 101100| 0.70  | 0.40 0.30  | 0.30     |
| 101101| 1.90  | 1.30 0.60  | 0.60     |
| 101110| 2.20  | 1.10 0.90  | 0.90     |
| 101111| 2.40  | 1.70 1.40  | 1.40     |
| 110000| 0.70  | 0.50 0.40  | 0.40     |
| 110001| 1.80  | 1.50 0.60  | 0.60     |
| 110010| 2.40  | 1.20 1.10  | 1.10     |
| 110011| 2.70  | 1.70 1.40  | 1.40     |
| 110100| 0.60  | 0.50 0.30  | 0.30     |
| 110101| 1.70  | 1.30 0.60  | 0.60     |
| 110110| 2.20  | 1.10 0.90  | 0.90     |
| 111000| 0.70  | 0.30 0.30  | 0.30     |
| 111001| 1.80  | 1.10 0.50  | 0.50     |
| 111010| 2.60  | 1.60 1.30  | 1.30     |
| 111100| 0.70  | 0.30 0.30  | 0.30     |
| 111101| 1.90  | 1.10 0.90  | 0.90     |
| 111111| 2.30  | 1.50 1.20  | 1.20     |

Table 8: The average estimated robust standard error for each exposure scenario, measured in percentage points.
Empirical Standard Error
|     | None | Only $X^{(9)}$ | All Step |
|-----|------|----------------|----------|
| 000000 | 0.30 | 0.20 0.30 0.50 | 0.50     |
| 000001 | 1.30 | 0.40 0.40 0.40 | 0.40     |
| 000010 | 0.80 | 0.40 0.40 0.40 | 0.40     |
| 000011 | 1.60 | 0.50 0.30 0.30 | 0.30     |
| 000100 | 0.30 | 0.10 0.50 0.50 | 0.50     |
| 000101 | 1.50 | 0.50 0.30 0.30 | 0.30     |
| 000110 | 0.80 | 0.40 0.50 0.40 | 0.40     |
| 000111 | 1.40 | 0.50 0.40 0.30 | 0.30     |
| 001000 | 0.40 | 0.20 0.30 0.30 | 0.30     |
| 001001 | 1.40 | 0.50 0.30 0.30 | 0.30     |
| 001010 | 0.90 | 0.40 0.50 0.50 | 0.50     |
| 001011 | 1.50 | 0.50 0.40 0.40 | 0.40     |
| 001100 | 0.90 | 0.20 0.40 0.40 | 0.40     |
| 001101 | 1.50 | 0.50 0.30 0.30 | 0.30     |
| 001110 | 0.70 | 0.40 0.50 0.50 | 0.50     |
| 001111 | 1.60 | 0.40 0.30 0.30 | 0.30     |
| 010000 | 0.40 | 0.40 0.30 0.40 | 0.40     |
| 010001 | 1.80 | 0.90 0.60 0.60 | 0.60     |
| 010010 | 1.40 | 0.80 0.90 0.90 | 0.90     |
| 010011 | 2.50 | 0.80 0.60 0.60 | 0.60     |
| 010100 | 0.40 | 0.40 0.30 0.30 | 0.30     |
| 010101 | 1.70 | 0.70 0.60 0.60 | 0.60     |
| 010110 | 1.40 | 1.00 0.80 0.80 | 0.80     |
| 010111 | 2.10 | 0.70 0.60 0.60 | 0.60     |
| 011000 | 0.60 | 0.60 0.40 0.40 | 0.40     |
| 011001 | 1.80 | 0.70 0.50 0.50 | 0.50     |
| 011010 | 1.90 | 1.30 0.90 0.90 | 0.90     |
| 011011 | 1.90 | 0.60 0.50 0.50 | 0.50     |
| 011100 | 0.40 | 0.20 0.30 0.30 | 0.30     |
| 011101 | 1.60 | 0.60 0.50 0.50 | 0.50     |
| 011110 | 1.10 | 0.90 0.70 0.70 | 0.70     |
| 011111 | 1.60 | 0.70 0.50 0.50 | 0.50     |
| 100000 | 0.50 | 0.30 0.30 0.30 | 0.30     |
| 100001 | 1.90 | 0.60 0.50 0.50 | 0.50     |
| 100010 | 1.40 | 0.90 1.10 1.10 | 1.10     |
| 100011 | 2.50 | 1.30 1.20 1.20 | 1.20     |
| 100100 | 0.50 | 0.30 0.40 0.30 | 0.30     |
| 100101 | 1.90 | 0.60 0.60 0.60 | 0.60     |
| 100110 | 1.40 | 1.00 0.90 0.90 | 0.90     |
| 100111 | 2.70 | 1.30 1.20 1.20 | 1.20     |
| 101000 | 0.50 | 0.40 0.40 0.30 | 0.30     |
| 101001 | 2.00 | 0.60 0.60 0.50 | 0.50     |
| 101010 | 1.20 | 0.90 0.90 0.90 | 0.90     |
| 101011 | 2.20 | 1.20 1.20 1.20 | 1.20     |
| 101100 | 0.40 | 0.30 0.30 0.30 | 0.30     |
| 101101 | 1.70 | 0.60 0.50 0.50 | 0.50     |
| 101110 | 2.10 | 1.60 1.00 1.00 | 1.00     |
| 101111 | 2.30 | 1.30 1.10 1.10 | 1.10     |
| 110000 | 0.60 | 0.60 0.50 0.50 | 0.50     |
| 110001 | 1.80 | 0.90 0.70 0.60 | 0.60     |
| 110010 | 1.80 | 1.00 1.20 1.20 | 1.20     |
| 110011 | 2.20 | 1.50 1.60 1.60 | 1.60     |
| 110100 | 0.50 | 0.70 0.30 0.30 | 0.30     |
| 110101 | 1.70 | 0.90 0.60 0.60 | 0.60     |
| 110110 | 1.90 | 0.80 0.90 1.00 | 1.00     |
| 110111 | 1.90 | 1.30 1.30 1.30 | 1.30     |
| 111000 | 0.50 | 0.40 0.30 0.30 | 0.30     |
| 111001 | 2.20 | 0.90 0.50 0.50 | 0.50     |
| 111010 | 1.00 | 0.90 1.10 1.10 | 1.10     |
| 111011 | 2.30 | 1.30 1.10 1.10 | 1.10     |
| 111100 | 0.50 | 0.40 0.30 0.30 | 0.30     |
| 111101 | 1.90 | 0.70 0.60 0.60 | 0.60     |
| 111110 | 1.60 | 0.80 1.00 1.00 | 1.00     |
| 111111 | 2.30 | 1.20 1.20 1.20 | 1.20     |

**Table 9:** The average empirical standard error for each exposure scenario, measured in percentage points.
Improvement
Table 10: The average reduction in the RMSE using the adjusted GEE for each exposure scenario, measured in percentage points.
Table 11: The average statistical power for each exposure scenario, measured in percentage points.
Coverage
| None | Only $X^{(9)}$ | All Step |
|------|----------------|----------|
| 100  | 92  87  85     |          |
| 00001 | 99  100  88  89|          |
| 00010 | 98  94  88  88|          |
| 00011 | 99  95  96  95|          |
| 00100 | 100  95  80  81|          |
| 00101 | 97  96  95  95|          |
| 00110 | 98  97  87  87|          |
| 00111 | 100  97  96  98|          |
| 01000 | 99  91  83  83|          |
| 01001 | 95  96  93  93|          |
| 01010 | 100  98  81  83|          |
| 01011 | 95  95  92  93|          |
| 01100 | 99  98  89  91|          |
| 01101 | 96  98  92  93|          |
| 01110 | 99  94  85  87|          |
| 01111 | 96  93  91  92|          |
| 01000 | 99  95  93  92|          |
| 01010 | 100  92  92  93|          |
| 01011 | 100  93  92  92|          |
| 01100 | 99  93  92  92|          |
| 01110 | 99  94  93  93|          |
| 01111 | 98  94  93  93|          |
| 00000 | 98  97  95  95|          |
| 00011 | 95  98  97  97|          |
| 00100 | 100  98  95  95|          |
| 00110 | 100  98  98  98|          |
| 01000 | 99  96  92  92|          |
| 01010 | 100  99  95  95|          |
| 01011 | 100  99  95  94|          |
| 01100 | 99  95  93  93|          |
| 01101 | 97  96  92  92|          |
| 01110 | 99  94  92  92|          |
| 01111 | 93  97  98  98|          |
| 10000 | 98  95  97  97|          |
| 10001 | 96  98  97  97|          |
| 10010 | 99  98  92  92|          |
| 10011 | 93  97  98  98|          |
| 10100 | 99  98  98  98|          |
| 10101 | 96  97  98  98|          |
| 10110 | 99  97  98  98|          |
| 10111 | 93  97  98  98|          |
| 11000 | 98  95  97  97|          |
| 11001 | 98  95  97  97|          |
| 11010 | 99  98  92  92|          |
| 11011 | 97  99  90  90|          |
| 11100 | 99  98  98  98|          |
| 11101 | 96  100 96  97|          |
| 11110 | 99  98  93  93|          |
| 11111 | 95  95  95  94|          |

Table 12: The average statistical coverage for each exposure scenario, measured in percentage points.