On the Statistical Properties of Epidemics on Networks

On the Statistical Properties of Epidemics on Networks

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Abstract

One major aim of statistics is to systematically study outcomes of interest in a population by observing the properties of a sample of that population. Some outcomes, such as the total number of people infected in an epidemic, can depend on properties of the whole population, such as the structure of contacts among the individuals, or contact network. A network is a collection of individuals as well as the pairwise connections between them. This dissertation explores how the effects of network structure on infectious outcomes yield challenges for statistical analysis, and suggests strategies to address them.

In Section I, we consider an intervention to reduce the spread of an epidemic on a collection of individuals in partially-connected networks, and show how network structure and mixing across networks can reduce the probability of observing true intervention effects, or statistical power. In Section II, we show how accounting for estimated properties of an epidemic contact network can improve statistical power, and that this improvement depends on the properties of the whole network as well as the epidemic spreading through them. Finally, in Section III, we derive the conditions under which a particular kind of network — the Degree-Corrected Stochastic Blockmodel — is susceptible to extensive epidemic spread, enabling statistical analysts to estimate when and to what extent the challenges and corrections explored here require consideration. We will conclude with a discussion of how the estimates and derivations in the final two sections can be used as adjustment covariates when assessing the effect of treatment on epidemic spread.

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Section I: Challenges in Cluster Randomized Trials with Contact Network Structure

Whenever possible, the efficacy of a new treatment is investigated by randomly assigning some individuals to a treatment and others to control, and comparing the outcomes between the two groups. Often, when the treatment aims to slow an infectious disease, clusters of individuals are assigned to each treatment arm. The structure of interactions within and between clusters can reduce the power of the trial, i.e. the probability of correctly detecting a real treatment effect. We investigate the relationships among power, within-cluster structure, cross-contamination via between-cluster mixing, and infectivity by simulating an infectious process on a collection of clusters. We demonstrate that compared to simulation-based methods, current formula-based power calculations may be conservative for low levels of between-cluster mixing, but failing to account for moderate or high amounts can result in severely underpowered studies. Power also depends on within-cluster network structure for certain kinds of infectious spreading. Infections that spread opportunistically through highly connected individuals have unpredictable infectious breakouts, making it harder to distinguish between random variation and real treatment effects. This approach can be used before conducting a trial to assess power using network information, and we demonstrate how empirical data can inform the extent of between-cluster mixing.

Introduction

In order to determine how effective a treatment is, it is common to randomly assign test subjects to different treatment arms. In one arm, subjects receive the experimental treatment, and subjects in the other arm receive usual care or a placebo. Randomization helps to ensure that the treatment is the cause of any difference in outcomes between the subjects in the two treatment arms, as opposed to some pre-treatment characteristics of the individuals. If the treatment is effective, the probability that a trial will find a statistically significant difference attributed to the treatment is called the *power* of the trial[1]. Adequate power requires a sufficiently large number of subjects to be tested, which can be expensive or infeasible. Underpowered studies are not only less likely to find a true relationship if one exists, but they are also more likely to erroneously conclude that an effect exists when it does not.[2,3] In order to control the probability of these errors, it is important to be able to accurately assess power before conducting a study.

When designing a randomized trial, we may not want or be able to randomly assign individuals to treatment. Individuals may be members of a cluster with complex interactions, which makes it infeasible or unethical to assign some individuals within a cluster to treatment and others to control. For example, the spread of HIV from infected to uninfected individuals in a small village might be slowed by offering its members information about safer sexual practices. In this case, it may be difficult or unethical to keep treated individuals' sex partners from sharing information or resources. We may instead choose to randomly select villages to participate in this regime, where villages correspond to naturally occurring clusters, and to compare HIV infection rates between treatment and control villages. This type of experiment is called a *Cluster Randomized Trial* (CRT).[4,5,6,7] Several CRTs are underway to reduce the incidence of new cases of HIV in contact networks, including the BCPP[8], PopART[9], and SEARCH[10] trials.

The correlation in outcomes of individuals within a cluster (e.g. HIV infection statuses) is known to reduce the power of a trial[5]. This correlation is generally summarized by a single parameter, called the *Intracluster Correlation Coefficient* (ICC)[4], which is the average pairwise correlation of outcomes within clusters. This measure assumes that the correlation in outcomes for any two individuals within a cluster is identical. However, the structure of relationships within a cluster can be heterogeneous, and power may depend on that structure, which is not captured by the ICC. Usually, this structure is either ignored[11] or analysis is performed using methods that allow it to be left unspecified[12]. Furthermore, individuals are often likely to interact with others not only in the same cluster but also in other clusters.

Cross-contamination[13] or *interference*[14] occurs when subjects' outcomes depend not only on the treatment to which they are assigned, but on the treatment assignments of other subjects as well. This can reduce the difference in outcomes between treated and untreated clusters, thereby decreasing power[15]. For example, economic ties may exist between villages, the residents of which might then share information related to the treatment. In the context of infectious spread through clusters, cross-contamination would occur if infectious contact takes place across clusters. If the treatment succeeds in slowing the infection rate in the treatment cluster, mixing between clusters will decrease the difference between outcomes across clusters, so the power to detect a treatment effect will decrease and the probability of a false discovery will increase. This must be addressed either by adding more clusters to the trial or increasing cluster sizes, both of which could be difficult and costly. This issue is also often left unaddressed.[16][17]

The effect of within-cluster structure and between-cluster mixing may depend on the type of infection spreading through each cluster. For example, a highly contagious infectious disease like the flu can spread more efficiently through more highly connected individuals[18]. Other infectious diseases, such as a sexually transmitted disease, can only be transmitted to one person at a time, no matter how many partners one has. The number of individuals whom an infected person may infect at a given time is the person's *infectivity*. This quantity likely differs from person to person, and it depends crucially on the transmission dynamics of the disease.

In this section, we study, via simulation, the effect of within-cluster structure, the extent of between-cluster mixing, and infectivity on statistical power in CRTs. We simulate the spread of an infectious process and investigate how power is affected by features of the process. Specifically, we consider two infections with different infectivities spreading through a collection of clusters. We use a *matched-pairs design*, wherein clusters in the study are paired, and each pair has one cluster assigned to treatment one to control[7]. We model the complex within-cluster correlation structure as a network in which edges represent possible transmission pathways between two individuals, comparing results across three different well-known network models. To model one type of cross-contamination, we introduce a single parameter γ that summarizes the extent of mixing between the two clusters comprising each cluster pair. This approach departs from standard power calculations for CRTs, in which the researcher applies a formula that determines the required sample size as a function of the number and size of clusters, the ICC, and the effect size[19]. Figure 1 depicts the different assumptions behind these two approaches. We show that our measure of mixing between clusters can have a strong effect on experimental *power*, or the probability of correctly detecting a real treatment effect. We also show that within-cluster structure can affect power for certain kinds of infectivity. We contrast this method to standard power calculations. We end by demonstrating how to assess between-cluster mixing before designing a hypothetical

CRT, using a network dataset of inter-regional cell phone calls.

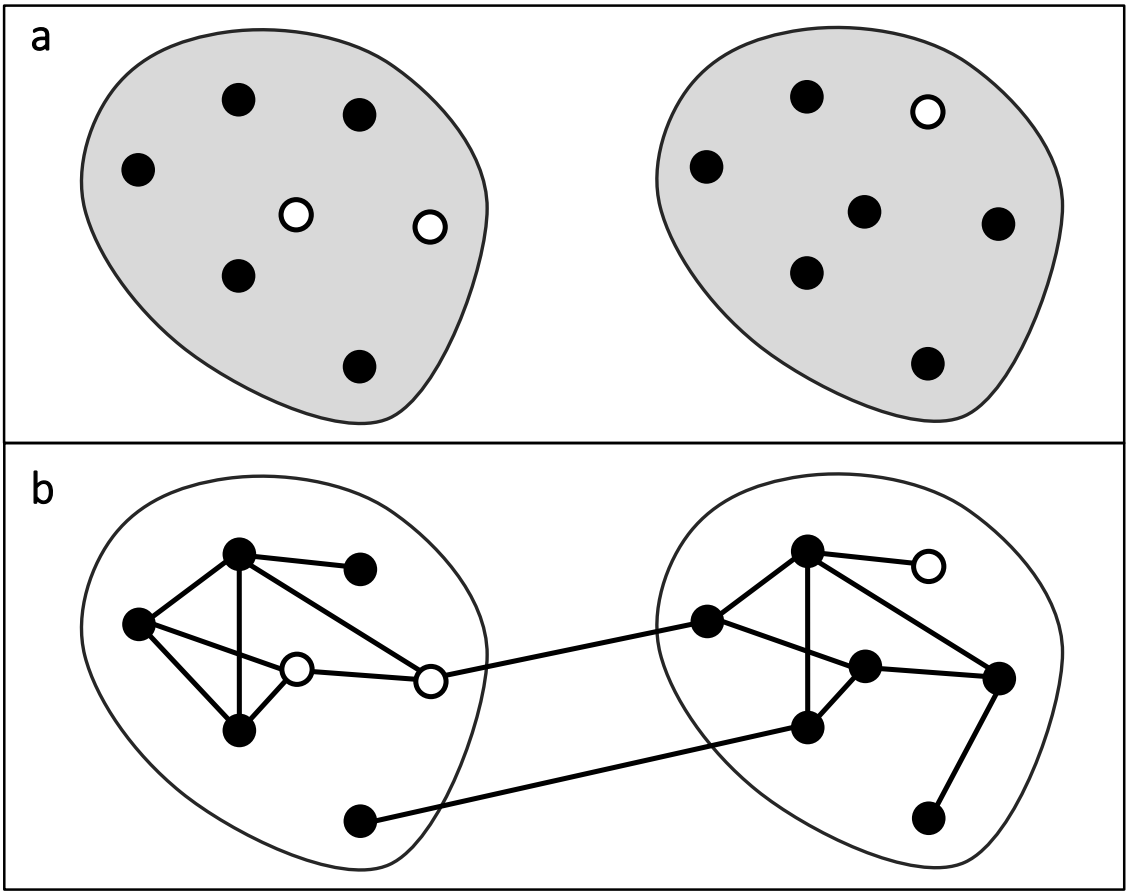

Figure 1: A schematic comparing the Intracluster Correlation Coefficient (ICC) approach to the design of this study. Each panel shows a cluster pair, and each enclosure represents a cluster. Panel **a** depicts cluster pair outcomes (circle colors) which are correlated (gray shading) within each cluster according to the ICC. In contrast, Panel **b** shows specific relationships (contact network ties) among individuals both within and between the two clusters, and outcomes among them will depend on an infection spreading only through these ties. We show that modeling both contact network structure and the spreading process explicitly rather than modeling correlations across outcomes results in new findings about power in CRTs.

Methods

Simulation of Cluster Randomized Trials

We simulate both within-cluster structure and between-cluster mixing using network models. We simulate pairs of clusters with each cluster in each pair initially generated as a stand-alone network. We examine the Erdös-Rényi (ER)[20], Barabási-Albert (BA)[21], and stochastic blockmodel (SBM)[22] random networks, and we simulate $2C$ clusters comprised of n nodes each. In order to explicitly allow for between-cluster mixing, we define a between-cluster mixing parameter γ as the number of network

edges between the treatment cluster and the control cluster, divided by the total number of edges in the cluster pair. To ensure that proportion γ of the edges are shared across clusters, we perform degree-preserving rewiring[23] within each of the C cluster-pairs until proportion γ edges are shared between clusters. We then use a compartmental model to simulate the spread of an infection across each cluster pair[24]. All nodes are either susceptible (S) or infected (I), and nodes may only transition from S to I. The number of neighbors each node can potentially infect at any given time is called its *infectivity*. We consider both unit and degree infectivity, for which infected nodes may contact one or all of their neighbors at a given time, respectively. Treated and control clusters infect their neighbors with equal probability under the null hypothesis, and infected individuals in treatment clusters infect with reduced probability under the alternative hypothesis. Finally, we analyze the resulting trial under two different analysis scenarios, and we juxtapose our findings with a standard power calculation[19].

Networks

Infectious disease dynamics have been studied extensively using deterministic ordinary differential equations[25] as well as network simulations[26]. Using networks to simulate the spread of infection allows rich epidemic detail, and this added complexity facilitates exploration of the effect of cluster structure on power in CRTs. A brief treatment of these features using differential equations is in the Additional Details subsection.

A simple *network* $\mathcal{G}$ consists of a set of n *nodes* (individuals) and a set of binary pairwise *edges* (relationships) between the nodes. This structure can be compactly expressed by a symmetric *adjacency matrix* $\mathbf{A}_{n\times n}$. If an edge exists between individuals i and j then $A_{ij} = A_{ji} = 1$, and 0 otherwise. The *degree* of node i, denoted by k_i, is the number of edges connecting node i to other nodes in the network. Networks can be used to describe complex systems like social communities, the structure of metabolic pathways, and the World Wide Web; many reviews of this work are available.[27,28,29,30]

A *random network ensemble* is a collection of all possible networks specified either by a probability model or a mechanistic model[28]. The simplest and most studied random network is the Erdös-Rényi (ER) model[20], which assumes that each potential edge between any pair of nodes in a network occurs independently with unit probability. Nodes in an ER network tend to have degrees close to their shared expected value, while in real-world social and contact networks, the distribution of node degrees is typically *heavy-tailed*: a few nodes are very highly connected ("hubs"), but most have small degree. To capture degree heterogeneity, we also simulate networks from the Barabási-Albert (BA) model.[31,21] These

networks are generated beginning with a small group of connected nodes and successively adding nodes one at a time, connecting them to the nodes in the existing network with probability proportional to the degree of each existing node. This mechanism has been shown to yield a power-law degree distribution:[21] $P(k) \sim k^{-\alpha}$ with $\alpha = 3$. This distribution is heavy-tailed, so the probability that some individuals are highly connected is more likely than in other network models like the ER. While it can be difficult to assess whether an observed network has a power-law degree distribution[32], the BA model comes closer to capturing the heavy-tailed degree distributions observed in social networks than the ER model. Another hallmark of real-world social networks is that individuals tend to cluster together into *communities*, or groups of individuals who share more edges with each other than between them[33]. We use *stochastic blockmodels* (SBMs)[22] to model within-cluster communities by assuming that each node is a member of a one block in a partition of blocks $\mathcal{B}$ comprising all nodes in the network, and that the probability of an edge between two nodes depends only on block membership (see Additional Details). Other popular families of random networks include Exponential Random Graphs (ERGMs)[34] and Small-World network of Watts and Strogatz, among others[35]. We leave their implications for CRTs for future research. Network instances generated using Python's `networkx` library. Each node within each cluster has the same expected number of edges $\langle k \rangle = 4$. For Figures 4 and 5, we chose $C = 20$ and $n = 300$, because for $\gamma = 0$ these parameters yield empirical power within $0.8 - 0.9$, which is a typical range used in cluster randomized trials.

Network Mixing

In each cluster pair, one cluster is randomly assigned to treatment and the other is not. The mixing parameter γ can be expressed in terms of the entries in the adjacency matrix, $\mathbf{A}$, and the treatment assignment of clusters:

$$\gamma := \frac{\sum_{ij} A_{ij} \left(1 - \delta(r_i, r_j)\right)}{\sum_{ij} A_{ij}} \tag{1}$$

$$= 1 - \frac{1}{2m} \sum_{ij} A_{ij} \delta(r_i, r_j). \tag{2}$$

Here, $m := \sum_{i<j} A_{ij}$ is the total number of edges in the study, $r_i = 1$ if node i is in the treatment arm and $r_i = 0$ otherwise, and $\delta(a, b)$ is equal to 1 when $a = b$ and 0 otherwise. This definition of between-cluster mixing is closely related to the concept of *modularity*, used extensively in network community detection

(see Additional Details). If $\gamma = 0$, the two clusters share no edges with each other. If $\gamma = 1/2$, there are as many edges reaching across two clusters as exist within them. Finally, if $\gamma = 1$, edges are only found between clusters, and the cluster pair network is said to be *bipartite*. A schematic of network mixing is shown in Figure 2.

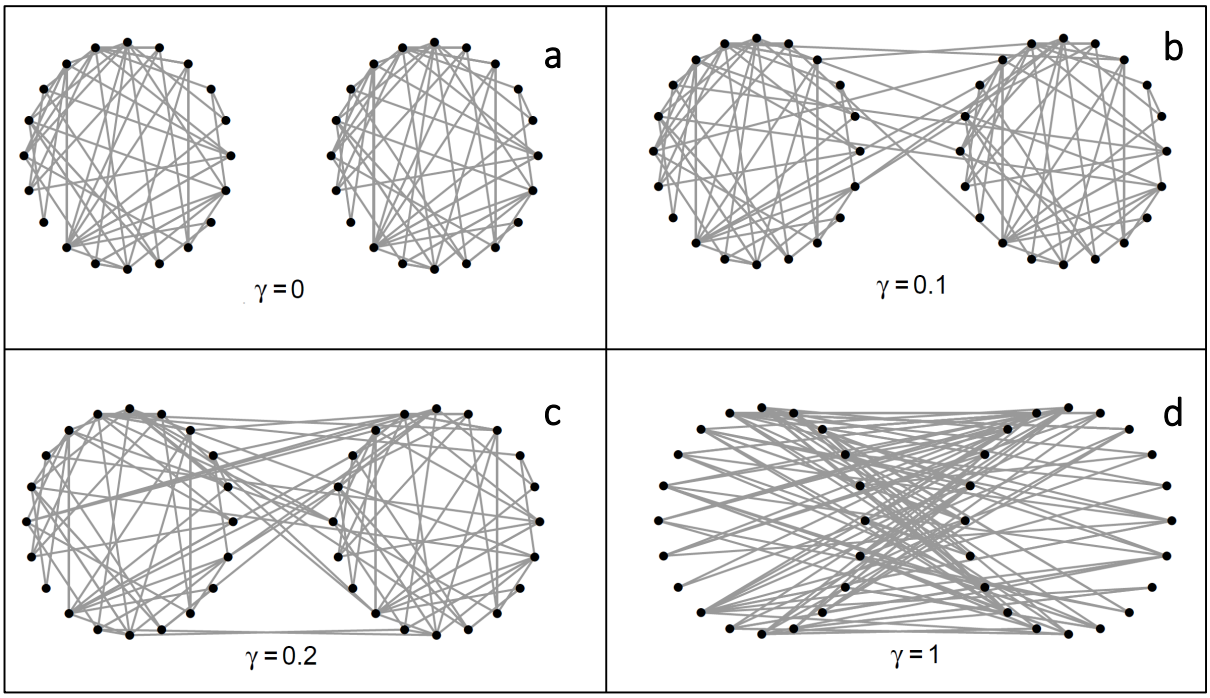

Figure 2: A diagram showing two clusters with various proportions of mixing.

Network Rewiring

We first simulate two random networks from the same network model and with the same number of edges, each corresponding to a cluster in a pair of clusters. Then, we randomly select one edge from each cluster in the pair and remove these two edges. Finally we create two new edges among the four nodes such that the two edges reach across the cluster pair. This process is called *degree-preserving rewiring*[23] because it preserves the degrees of all the nodes involved. The process is depicted in Figure 3. We repeat the rewiring process until proportion γ of the total edges are rewired. The result is a single cluster pair in our simulated CRT, and the pair-generating process is repeated until we have generated our target number of cluster pairs.

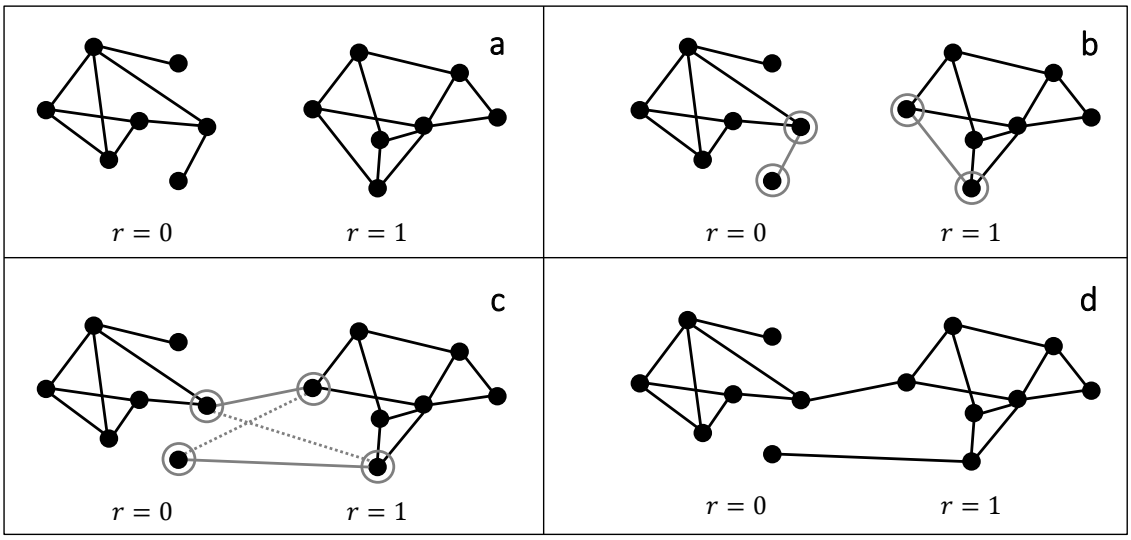

Figure 3: Degree-preserving rewiring is performed by selecting an edge within each cluster, and swapping them to reach across the cluster pair. The dashed gray lines represent another way the edges could have been rewired while still preserving degree; either rewiring is chosen with equal probability.

Infectious Spread

Compartmental models assume that each node in a population is in one of a few possible states, or compartments, and that individuals switch between these compartments according to some rules. Although more realistic models include more states[36], we will assume for simplicity that nodes are in only one of two states: uninfected but susceptible (S), and infected and contagious (I). We assume that the network structure of each cluster pair represents the possible transmission paths from infected nodes to susceptible ones.

Let I_{irct} represent the infectious status for node i in treatment arm $r = \{0,1\}$ and cluster pair $c = 1,...,C$ at discrete time $t = 1,...,T_c$, with $I_{irct} = 1$ if the node is infected and 0 otherwise. We define $r = 0$ if node i is in the control arm, and $r = 1$ if i is in the treatment arm. Let $I_{rct} := \langle I_{irct} \rangle$ represent the proportion of infected nodes in cluster pair c at discrete time t. At the beginning of the study, 1% of individuals in each cluster is infected, i.e. $I_{rc0} = 0.01$. For each time step t, each node i selects q_i network neighbors at random, and infects each one with probability p_i. Because different infectious diseases have different infectivity behavior, we study both unit and degree infectivity, or $q_i = 1$ and $q_i = k_i$, respectively. We assume that the infection probability depends only on the treatment arm membership of each node r_i, thus $p_i = p_{r_i}$. Treatment reduces the probability p_{r_i} of infection. If two clusters in a pair have the same infection rate, the treatment has no effect and $p_{r_i} = p$. This is the *null hypothesis* under examination in our hypothetical study. When we simulate trials under the null hypothesis we set $p = 0.30$ in every

cluster. The *alternative hypothesis* holds if the treatment succeeds in reducing the infection rate, $p_1 < p_0$. When we simulate under the alternative hypothesis, $p_0 = 0.30$ and $p_1 = 0.25$. The trial ends when the cumulative incidence of infection grows to 10% of the population, i.e., when the cluster pair infection rate $\langle I_{ircT_c} \rangle = 0.1$ for some time T_c.

Analysis

At the end of the simulation, we test whether the treatment was effective by comparing the number of infections between treated and control clusters according to two analysis scenarios. In real-world CRTs, the most efficient and robust way to compare the two groups depends on what information about the infection can feasibly be gathered from the trial. In some trials, surveying the infectious status of individuals is difficult, and therefore this information is only available for the beginning and end time points of the trial. In others, the times to infection for each node are available. In addition to what information is available, the researcher must choose a statistical test according to which assumptions they find suitable to their study. A *model-based test* assumes that the data are generated according to a particular model, which can be more powerful than other tests if the model is true[37]. Alternatively, a *permutation test*[38] does not make any assumptions about how the data were generated. To show how to conduct an analysis suited to different scenarios based on available data, we analyzed our simulated trial using two different sets of assumptions. In Scenario 1, we assume that outcomes are only known at the end of the trial, and perform a model-based test. In Scenario 2, we assume that the time to each infection is known, and perform a permutation test. We show that the results of the simulation are qualitatively similar under both scenarios. (Note that it is possible to use a permutation test for Scenario 1 or a model-based test for Scenario 2, which would create two new analyses.) For both scenarios, pseudo-code for carrying out a simulation-based power calculation for a CRT studying an infectious spread through networks is as follows:

1) For all clusters in the study:

  a) Ascertain or conjecture within-cluster network structure and between-cluster mixing for clusters.

2) Repeat several times:

  a) Simulate a collection of networks consistent with cluster structure and mixing properties.

  b) Simulate an infectious spread through networks.

3) Assess the empirical power of the simulation using the outcomes from the spreading process. Power calculations for two study scenarios are detailed below.

Table 1: Our simulation algorithm used to assess the effect of within-cluster structure, between-cluster mixing and infectivity on statistical power.

Scenario 1: The *log risk ratio* is the logarithmic ratio of infected individuals in the treatment clusters to the control clusters at the end of study. For simulation m, let $I_m^{(0)} := \langle \log \frac{I_{0cT_c}}{I_{1cT_c}} \rangle = \langle \log I_{0cT_c} - \log I_{1cT_c} \rangle$ be the difference in the number of infections between two clusters in a pair averaged over each of the C cluster pairs at the trial end T_c. The simulation was repeated 20,000 times under the null hypothesis and cutoff values $I_{2.5}^*$ and $I_{97.5}^*$ were established such that $P(I_{2.5}^* < I_m^{(0)} < I_{97.5}^*) = \alpha$ for significance level $\alpha = .05$. We repeated this process under the alternative 20,000 times, and the proportion of these trials with statistics $I_m^{(A)}$ more extreme than $(I_{2.5}^*, I_{97.5}^*)$ is the simulated power or empirical power.

Scenario 2: We pool the individual infection times for the treatment arm and the control arm, and summarize the difference between the two arms' infection times using an appropriate statistic (e.g. the logrank statistic[39]). The permutation test is performed by comparing the observed logrank statistic to the distribution of log-rank statistics when the treatment labels are permuted, or switched, for each cluster pair. The p-value for this analysis is the proportion of times the log-rank statistic with the real labels is more extreme than the permuted log-rank statistics. Because the permutation test is computationally expensive, this entire process is repeated 2,000 times, and we calculate the proportion of permutation p-values below 0.05, which is the empirical or simulated power.

We also compare this formulation to traditional methods. From Hayes and Bennett[19], the number of clusters required for power β in a CRT with binary outcomes is:

$$C = 2 + (z_{\alpha/2} + z_{\beta})^2 \times \left[\frac{\pi_0(1-\pi_0)}{n} + \frac{\pi_1(1-\pi_1)}{n} + k^2(\pi_0^2 + \pi_1^2) \right] \Big/ (\pi_0 - \pi_1)^2 \quad (3)$$

To calculate power, we fix $n = 300, C = 20$, and $\alpha = 0.05$, and solve for power β. In this formula, π_0 and π_1 are the mean proportion of outcomes within control and treated clusters, and k is the coefficient of variation, which is directly related to the ICC ρ [6 40] :

$$k = \sqrt{\rho \times \frac{1-\widehat{\pi}}{\widehat{\pi}}} \quad (4)$$

Where $\widehat{\pi}$ is the overall prevalence by study end. This calculation assumes that the log risk ratio by study end $\log\left(\frac{\pi_0}{\pi_1}\right)$ takes on the values observed in our simulation setting 0.135 for no between-cluster mixing $\gamma = 0$, and the overall prevalence is 10%, both assumed to be accurately estimated from a small pilot study. The value from the ICC must also be assumed beforehand or estimated in a small pilot study. To compare this approach with our simulation design, we assumed that the ICC took on a range of plausible empirical values $0.0 - 0.1$ reported in the literature.[7 40 41] For more details, see the Additional Details subsection.

Results

We begin by showing the effect of the mixing parameter γ on the infection risk ratios between treated and untreated clusters. The means and standard deviations of simulated risk ratios observed under Scenario 1 are presented in Figure 4.

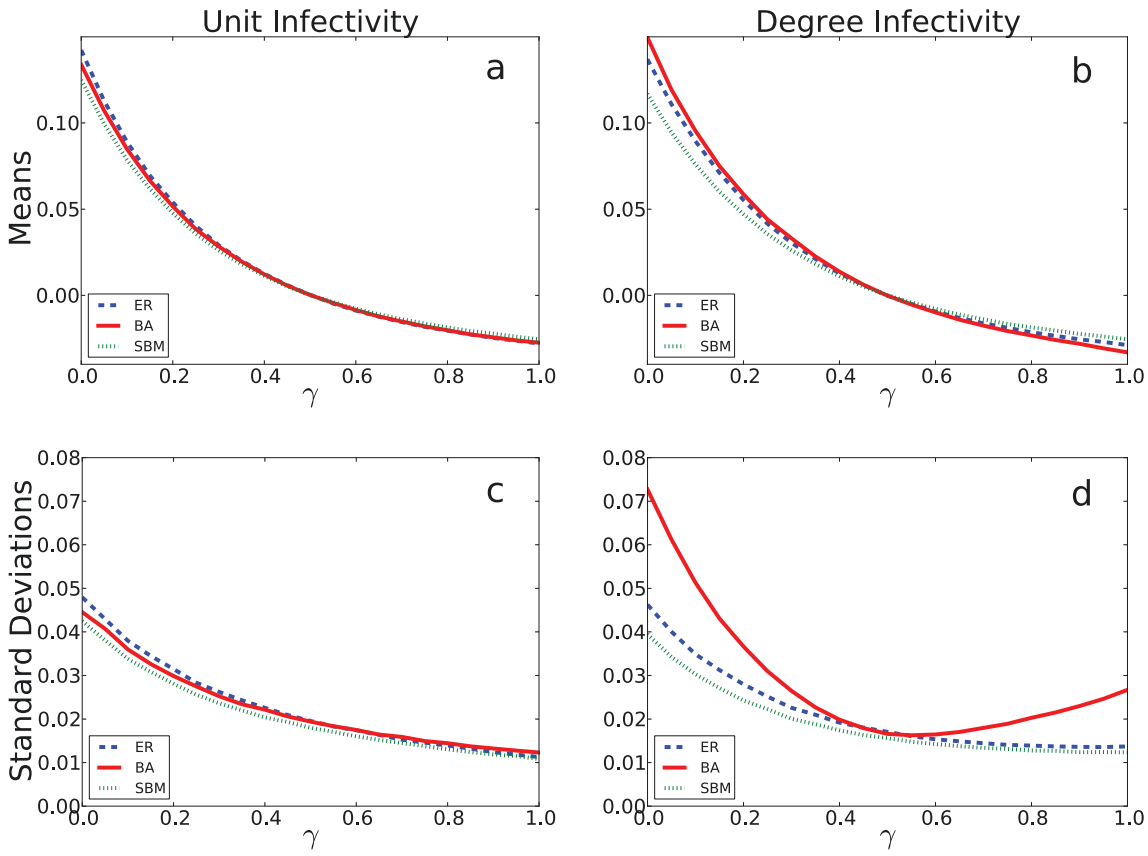

Figure 4: The log risk ratio means and standard deviations under Scenario 1. The rows correspond to the means (Panels **a** and **b**) and standard deviations (Panels **c** and **d**), shown on the y axis. The x-axis is the value of the mixing parameter γ, and each curve represents the three within-cluster network structures. The left column shows the spread of an infection in which an infected node may only infect one neighbor per time step (unit infectivity), whereas the right column assumes one may spread an infection to each of their neighbors (degree infectivity). We see that network topology has an effect on the variation of the log rate ratio only in the latter case.

For both kinds of infectivity, neither the heavy-tailed degree distribution of the BA network nor the within-cluster community structure of the SBM network dramatically impacts the differences between the proportion of infections in the treated and controlled clusters in each pair (top row) compared to the ER network. The differences between the risk of infections in the treated and untreated cluster pairs decreases as mixing increases, and reverses direction when $\gamma > 1/2$. This is expected because for this range of between-cluster mixing, infected individuals in the treatment cluster are more likely to contact members of the untreated cluster and vice versa, which is unlikely in practice but is included here for completeness. In almost all cases, the variation in the simulated studies' average log risk ratio decreases uniformly as γ increases, which suggests that increasing the amount of mixing across communities results in less variation in the average rate of infections. However, the BA network is an exception. Under degree infectivity, when individuals can infect everyone to whom they are connected in a single time step, an infected node with large degree may spread its infection to each of its contacts at a single

time point, which can cause a very fast outbreak. However, highly-connected individuals are rare, so in this case outbreaks are large but infrequent, increasing the variation in observed differences between treated and untreated clusters. This variation means that more clusters are required to estimate the average treatment effect with any precision. In other words, rare outbreaks make it harder to distinguish whether differences between the treatment arm and control arm are due to treatment or to a chance outbreak occurring in either arm. Therefore, under degree infectivity, the BA network results in less power than the SBM or ER networks, which shows that within-cluster network structure can impact the power to detect treatment effects in CRTs for certain kinds of infections.

For the two analysis scenarios described in Methods, we can directly estimate empirical power as the proportion of simulations resulting in the rejection of the null hypothesis at the $\alpha = 0.05$ level under the alternative for a range of mixing values γ. Our results, as well as a comparison with the standard approach, are summarized in Figure 5.

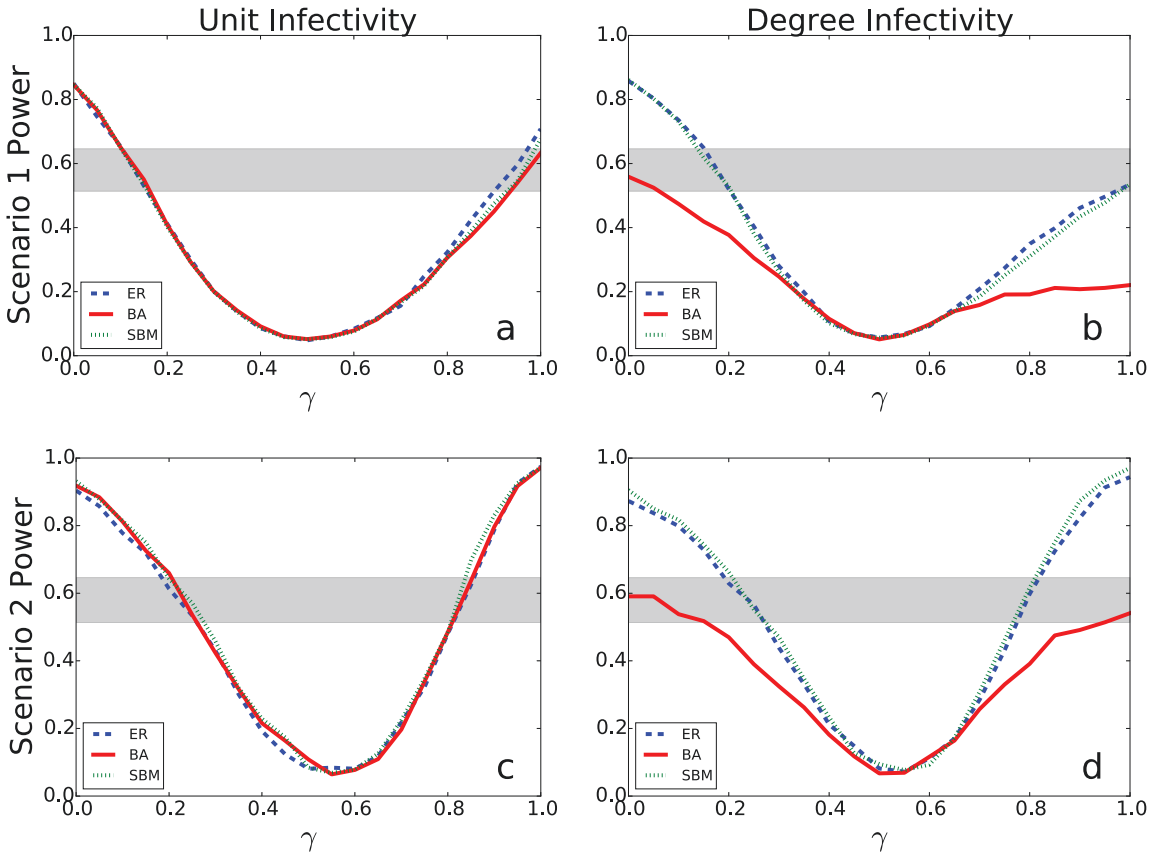

Figure 5: Estimated power for each scenario. The blue, red, and green lines represent the ER, BA, and SBM network models, respectively. The top row shows results for Scenario 1, and the bottom row shows results for Scenario 2. The left column shows unit infectivity, and the right column shows degree infectivity. The horizontal gray bars represent the expected power using the standard approach for a range of plausible values for the ICC.

In all settings, power is lowest when $\gamma \approx 1/2$, with approximately the same number of edges between clusters as within them. Scenarios 1 and 2 (the top and bottom rows, respectively) show few differences from one another, which suggests that the two strategies for significance testing tend to give qualitatively similar results. Unit infectivity (lefthand column) shows no differences in power among network types. This is not the case for degree infectivity (righthand column), in which the BA network shows less power than the other networks, for the reasons discussed above. Finally, the gray bars indicate that when no mixing is present, standard power calculations are conservative for all network types we studied, and no sample size adjustment may be needed. However, moderate to severe between-cluster mixing can greatly overestimate expected power. In the case of the BA network and degree infectivity, the standard approach always overestimates trial power.

Size and Number of Study Clusters

Our results so far have shown how power in CRTs is affected by between-cluster mixing, within-cluster structure, and infectivity. Next, we show how power relates to other trial features, namely the size and number of clusters, n and C, respectively. The results are qualitatively similar for Scenarios 1 and 2, and the results shown in Table 6 are for Scenario 1. The table shows results for each combination of a range of cluster sizes $n = \{100, 300, 1000\}$ and numbers $C = \{5, 10, 20\}$ as a 3×3 grid of pairs of cells. Each cell pair is a side-by-side comparison of results for unit infectivity (lefthand cell) and degree infectivity (righthand cell). Each cell shows simulated results for within-cluster structure (columns) as well as amount of between-cluster mixing (rows). Considering the case of $C = 10, n = 300$ (the middle-most cell pair), we notice a few trends. We see that increasing mixing (looking down each column) decreases power in all cases. We can directly compare the two types of infectivity (comparing cells in the pair), and see that all the entries are similar except for the BA network (middle column). For BA networks, power is much lower for degree infectivity spreading compared to unit infectivity. This suggests that CRTs with network structure similar to BA networks can have substantially less power when the infection spreads in proportion to how connected each node is. Finally, we may compare studies of differing cluster numbers and sizes (comparing cell pairs), and see qualitatively similar results: in each case, more or larger clusters in the study (cell pairs further down or right) result in more power overall. When power is very high (bottom-right cell pair), within-cluster structure affects results less. Therefore, careful consideration of expected power is most important when trial resources are limited, which is often the case in practice.

	$C = 5$						$C = 10$						$C = 20$						
	Unit			*Degree*			*Unit*			*Degree*			*Unit*			*Degree*			
$n = 100$	0.13	0.14	0.14	0.12	0.10	0.12	0.22	0.22	0.23	0.19	0.16	0.20	0.39	0.39	0.38	0.34	0.28	0.37	$\gamma = 0.0$
	0.10	0.10	0.10	0.11	0.09	0.10	0.15	0.17	0.15	0.18	0.12	0.16	0.27	0.27	0.24	0.26	0.21	0.26	$\gamma = 0.1$
	0.08	0.08	0.07	0.09	0.07	0.09	0.09	0.13	0.11	0.11	0.11	0.13	0.15	0.15	0.15	0.22	0.15	0.18	$\gamma = 0.2$
	0.07	0.06	0.06	0.07	0.06	0.07	0.08	0.09	0.06	0.08	0.08	0.08	0.10	0.09	0.10	0.11	0.11	0.11	$\gamma = 0.3$
$n = 300$	0.34	0.33	0.32	0.33	0.20	0.33	0.57	0.55	0.57	0.59	0.34	0.56	0.85	0.86	0.86	0.87	0.57	0.87	$\gamma = 0.0$
	0.21	0.22	0.21	0.25	0.13	0.27	0.39	0.39	0.39	0.46	0.28	0.46	0.63	0.65	0.65	0.71	0.44	0.70	$\gamma = 0.1$
	0.16	0.15	0.15	0.17	0.14	0.19	0.23	0.22	0.22	0.28	0.19	0.30	0.41	0.43	0.40	0.52	0.38	0.44	$\gamma = 0.2$
	0.08	0.08	0.08	0.12	0.10	0.10	0.13	0.14	0.13	0.14	0.13	0.17	0.21	0.21	0.19	0.28	0.24	0.27	$\gamma = 0.3$
$n = 1000$	0.78	0.80	0.76	0.84	0.39	0.81	0.97	0.97	0.97	0.98	0.75	0.98	1.00	1.00	1.00	1.00	0.95	1.00	$\gamma = 0.0$
	0.61	0.57	0.59	0.69	0.38	0.67	0.85	0.86	0.85	0.93	0.61	0.91	0.99	0.99	0.99	1.00	0.91	1.00	$\gamma = 0.1$
	0.39	0.37	0.36	0.47	0.31	0.51	0.62	0.60	0.59	0.76	0.52	0.76	0.89	0.90	0.87	0.97	0.83	0.96	$\gamma = 0.2$
	0.15	0.19	0.16	0.30	0.21	0.28	0.31	0.33	0.36	0.49	0.36	0.45	0.58	0.56	0.57	0.74	0.62	0.73	$\gamma = 0.3$
																			ER BA SBM

Figure 6: Experimental power in our simulation framework for different sizes and numbers of cluster pairs, n and C, respectively, for Scenario 1. Each cell shows output for 3,000 simulations of each combination of n and C, all three within-cluster structures, various values of mixing parameter γ, and both unit and degree infectivity. The results are similar for Scenario 2.

Empirical Estimation of the Extent of Mixing

Finally, we show how our mixing parameter can be estimated using data in the planning stages of a hypothetical CRT. Sometimes the entire network structure between individuals in a prospective trial is known beforehand, such as the sexual contact network on Likoma Island[42]. In this case, between-cluster mixing can be estimated using Equation 2. In other trials, perhaps only partial information is known, like the degree distribution[21] and/or the proportion of ties between clusters. In this case, clusters can be generated that preserve partial network information such as degree distribution,[43,44] and degree-preserving rewiring can be performed until proportion γ of ties between clusters is observed, where this quantity is estimated from the network data, if possible.

The structure of calls between cell phones is often persistent over time[45] and indicative of actual social relationships[46]. We use a network of cell phone calls as a proxy for a contact network, we use our definition of between-cluster mixing to estimate the amount of mixing between hypothetical clusters. The dataset consists of all the calls made between cellphones of a large mobile carrier within a quarter year. Individual phone numbers were anonymized, and we only report results for the number of individuals and calls within or between zip codes.

The dataset contains phone calls originating from $Z = 3806$ different zip codes, and we define a cluster as a collection of zip codes that are spatially close to one another. Because zip codes are numerically assigned according to spatial location, we assume that zip codes that are numerically contiguous to each

other are also close to each other spatially. Therefore, zip code $z = 1, ..., Z$ assigned to cluster $c_z = 1, ..., 2C$ is

$$c_z := \left\lceil \frac{z}{Z} 2C \right\rceil \tag{5}$$

where $2C$ is the total number of clusters in the trial, and $\lceil \cdot \rceil$ is the ceiling function. Once the number of clusters $2C$ is specified, clusters may be paired, with one cluster in each pair randomized to a hypothetical treatment, and the other to the control condition.

For this dataset, we consider two definitions for the number of edges shared between individuals, one in which they are unweighted and one in which they are weighted by the number of calls between them. That is, we consider two definitions for an edge A_{ij} between individuals i and j, belonging to clusters c_i and c_j respectively. The number of calls between i and j over the period of investigation is defined as d_{ij}. For Definition 1, we assume and edge exists between the two individuals if they have called each other at least once, $A_{ij} = \mathbb{I}(d_{ij} \geq 1)$, and otherwise no edge exists between them $A_{ij} = 0$. For Definition 2, we assume an edge between them may be weighted by the number of total calls made between them, $A_{ij} = d_{ij}$. Using both definitions, we found the degree distribution of each cell phone to be heavy-tailed (see Additional Details).

Next, we estimate mixing parameter γ for this dataset. For a range of numbers of cluster pairs C, we cluster all Z zip codes into $2C$ clusters, and randomize one cluster in each pair to a hypothetical treatment, and the other to a control. For 200 randomizations, we calculate the between-cluster mixing parameter γ according to Equation 2. We examine the relationship between γ and the number of clusters C. The mean and $(2.5, 97.5)$ percentiles of these estimates as a function of the number of clusters number C are shown in Figure 7.

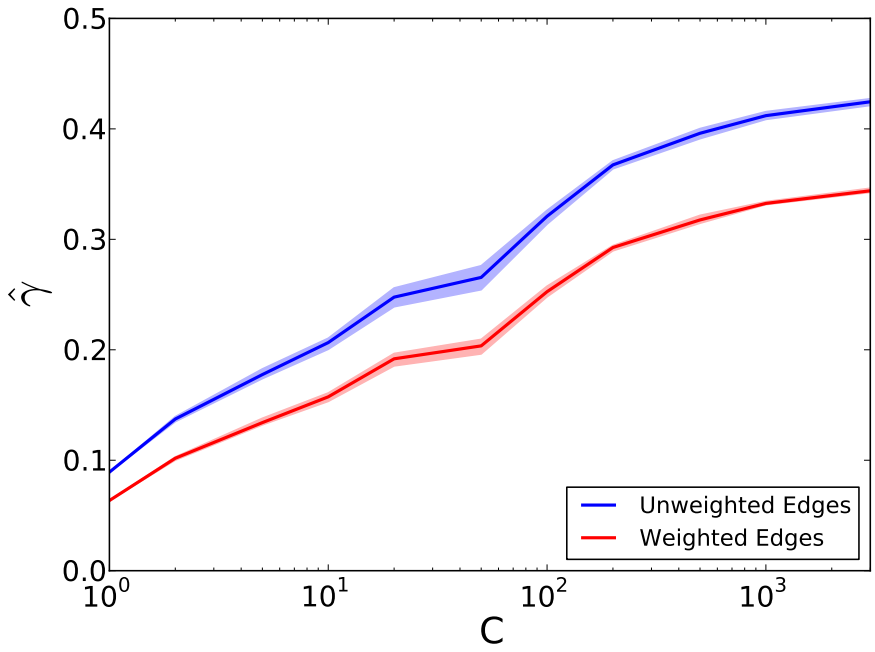

Figure 7: A log-linear plot displaying empirical values of mixing parameter γ. The y axis shows the mean and $(2.5, 97.5)$ quantiles of these estimates. The x axis in each panel corresponds to a range of cluster numbers C.

Figure 7 displays a number of distinct trends. As the number of clusters increases, fewer of the total zip codes are included in each cluster, and the number of calls between clusters increases. This means that individuals are more likely to call others in zip codes geographically closer to them, which has been confirmed in other phone communication networks[47]. Between-cluster mixing unweighted by the number of calls (blue) results in higher estimates of γ than weighted (red), which means that when individuals call others outside their cluster, they tend to call those people less than others they call within their cluster. There is significant between-cluster mixing for all values of C, implying that between-cluster mixing would significantly decrease the power of a trial that assumes each cluster to be independent ($\gamma = 0$). Furthermore, as the number of clusters increases, the average cluster size decreases, and mixing reaches a maximum of $\gamma = 0.45$. Extrapolating from our simulation framework, power could be reduced dramatically in this case.

Discussion

Before conducting a trial, it is important to have an estimate of statistical power in order to assess the risks of failing to find true effects and of spurious results. If individuals belong to interrelated clusters, randomly assigning them to treatment or control may not be a palatable option, and CRTs can be used

to test for treatment effects. Power in CRTs is known to depend on the number and size of clusters, as well as the amount of correlation within each cluster. However, within-cluster correlation structure is often measured by a single number and clusters are usually assumed to be independent of one another. Unfortunately, these assumptions can produce misleading estimates of power.

To investigate this problem, we studied the effects of complex within-cluster structure, a measure of between-cluster mixing strength, and infectivity on power by simulating a matched-pairs CRT for an infectious process. We simulated a collection of cluster pairs as a network, controlling the proportion of edges shared across each pair. We then simulated an SI infectious process on each cluster pair, with one cluster assigned to treatment and the other assigned to control. The effect of treatment in this simulation lowered the probability that an infected individual succeeds at infecting a susceptible neighbor. We also considered two types of infectivity: unit and degree.

We found that between-cluster mixing had a profound effect on statistical power, no matter what network or infectious process was simulated. As the number of edges shared across clusters in different treatment groups increased to $1/2$, on average the two clusters were nearly indistinguishable, and thus power fell to nearly zero. This is not surprising, but most power calculations assume clusters are independent, and this issue is usually left unaddressed. We compared these findings to the ICC approach, and found it will significantly underestimate expected power if the extent of between-cluster mixing is moderate to severe.

The effect of within-cluster structure was more nuanced. For degree infectivity, the spread of infection was less predictable if the network contained some highly-connected nodes, due to the variation in and strong effects of these hubs becoming infected. We did not observe this level of variability for networks without highly-connected hub nodes. We also did not observe this level of variability for unit infectivity, regardless of how many hubs were present in the network. Taken together, we found that for the network structures we studied, within-cluster structure had a significant impact on power only when the infectious process exhibited degree infectivity. The effect of within-cluster structure and between-cluster mixing on statistical power are qualitatively similar for a range of cluster sizes and numbers, although (as is well known) an increase in either results in more power overall.

Our simulation framework, outlined in the pseudo-algorithm in Methods, can be used to estimate power before an actual trial. If partial or full network information is available, it can be used to simulate an infectious processes using a compartmental model, and analyze the resulting outcomes as we have described. We demonstrated how to estimate between-cluster mixing using a dataset composed

of cellphone calls from a large mobile carrier, which are taken to represent a contact network. For a hypothetical prospective trial on the individuals in this dataset, we defined a cluster as a group of individuals within a collection of contiguous zip codes. We then grouped clusters into pairs, randomly assigned one cluster in each pair to a hypothetical treatment condition and the other to a control, and estimated mixing parameter γ for each simulation. We found substantial between-cluster mixing for all choices of cluster numbers, and mixing increased when clusters were chosen to be more numerous but smaller. Estimates of between-cluster mixing ranged from moderate to severe, regardless of whether the estimation adjusted for the frequency of calls or not.

We have shown that our simulation-based method of calculating power can differ quantitatively from the formula-based method (see Figure 5). The two differ qualitatively as well. Traditional formula-based power calculations have been developed outside the context of network theory and consequently they do not take either within-cluster structure or between-cluster mixing into account. Furthermore, although we selected a restrictively simple simulation for clarity of demonstration, simulations for an actual prospective trial could include a much higher level of study-specific realistic detail, making a simulation-based power calculation more appropriate to the given study. The methods that we propose are most appropriate for studies in which the outcome is infectious, spreading through the population via person-to-person contacts. We leave it to subject matter experts to recognize when this condition is satisfied.

Our study invites several investigations and extensions. First, we have employed restrictively simple network models and infectious spreading process, and more nuanced generalizations are available. While our work shows how infectious spreading and complex structure can affect expected results in CRTs, more specific circumstances require extensions with more tailored network designs and infection types for power to be properly estimated. Second, we have focused our attention on matched-pair CRTs, and our framework should be extended to other CRT designs used in practice[7]. Third, these findings should be replicated in data for which both network structure and infectious spread are available.

Additional Details

Here, we provide additional details for a few topics discussed in the main body of this section. We first demonstrate a simple approach to modeling infectious spread with between-cluster mixing using ordinary differential equations, and compares this result to the simulation approach used earlier. We then describe the ordinary stochastic blockmodel and provides details for the specific spatial version we used above. The next subsection connects our definition of between-mixing parameter γ with a common metric used in applications of network science. We also describe how the Intracluster Correlation Coefficient is defined, and we show estimates of this quantity for our simulations. The final subsection shows the degree distribution for the empirical cell phone network, with discussion.

Ordinary Differential Equation Approach to Between-Cluster Mixing

One of the most common approaches to investigating the spread of an epidemic on networks is Ordinary Differential Equations (ODEs)[24 26]. ODEs are functions of a variable in terms of its derivatives. Compartmental models for epidemic spread can use ODEs to specify the rate of change for individuals in terms of others. A common assumption used to specify ODEs for epidemic spread is *mass action*, in which the spread of an infection depends only on the proportion of individuals in each compartment. For example, an SI compartmental model assumes that individual i is either infected ($I_i(t) = 1$) or not infected but susceptible ($S_i(t) = 1$) at any time t. These two statuses are mutually exclusive, and $S_i(t) = 1 - I_i(t)$. An ordinary differential equation that assumes mass action would specify the change in the total proportion of infected individuals $I(t) := \langle I_i(t) \rangle$ in terms of the infected proportion $I(t)$ at time t. If we assume mass action, we may model the rate of infectious growth in an SI compartmental model as proportional to the proportion of infected individuals multiplied by the proportion of susceptible individuals:

$$\frac{dI(t)}{dt} = pS(t)I(t) = p(1 - I(t))I(t) \tag{6}$$

In this section, we consider a collection of $c = 1, ..., C$ cluster pairs, with one cluster in each pair assigned to the treatment condition $r = 1$ and the other to control $r = 0$. Furthermore, we assume that clusters are mixed according to mixing parameter γ, For the SI compartmental model, $I_{irc}(t) = 1$ if individual i

is infected and 0 otherwise. We may assume that the spread of an infection across the network pair is a mass action ODE as above, with a simple modification. Let $I_{rc}(t) = \langle I_{irc}(t) \rangle$ represent the proportion of infected nodes in cluster pair c at discrete time t. Individual i may contact an individual j in the opposing cluster with probability γ. In this case, the probability of a successful infection requires that i is susceptible and j is infectious. Mass action dictates that the rate of change for each cluster depends only on the proportion of individuals in each infectious status for either cluster, which is now sum of ODEs weighted by mixing parameter γ:

$$\frac{\partial I_{0c}(t)}{\partial t} = \left[(1-\gamma) I_{0c}(t) p_0 + \gamma I_{1c}(t) p_1\right] (1 - I_{0c}(t)) \tag{7}$$

$$\frac{\partial I_{1c}(t)}{\partial t} = \left[(1-\gamma) I_{1c}(t) p_1 + \gamma I_{0c}(t) p_0\right] (1 - I_{1c}(t)) \tag{8}$$

According to Equations 7 and 8, if $\gamma = 0$, the rate of infection in each cluster is identical to Equation 6. As γ approaches $1/2$, the difference in the proportion of infected individuals in the two treatment arms decreases to no difference.

The ODE approach is quite comparable to the stochastic approach we used in this section. To show this, we created network clusters with every node connected to each other in the cluster, performed degree-corrected rewiring, simulated an infectious processes with unit infectivity on the pair, and averaged the proportion of infections at each time step. Figure 8 shows the infection rates over time for a range of mixing values $\gamma = \{0.0, 0.1, 0.2, 1\}$. The solid lines shows the average of the network simulations. The dashed lines show the a numerical solution to Equations 7 and 8. The two are comparable, suggesting that differential equations and network simulations can approximately interchangeably describe the same infectious process.

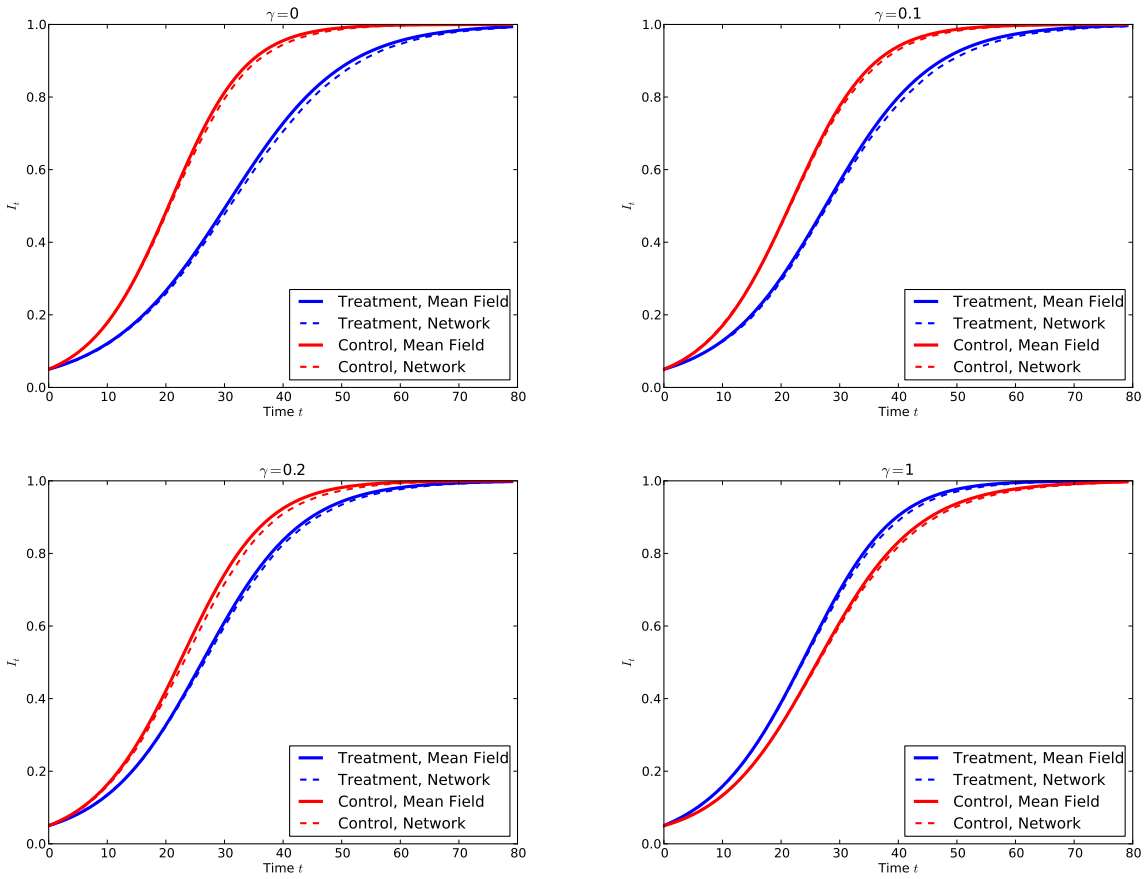

Figure 8: The proportion of infections over time. The solid line is the mass action rate equation, and the dashed lines are the mean of simulations of an infectious process on a complete (fully-connected) network. The infectious process was simulated for $\gamma = \{0.0, 0.1, 0.2, 1\}$, matching Figure 5. As γ approaches $1/2$, the difference in infection rates in two clusters in a pair decreases, demonstrated by the red and blue curves approaching each other. When $\gamma = 1$, the relative rates of infections switch.

Where the differential equation approach assumes individuals contact everyone in the population, infections spreading through fixed networks only allow contact through existing edges. This *redundant contact effect*[18] causes infections through networks to be slightly slower, also observable in Figure 8.

Modularity and Between-Mixing Parameter γ

Our definition of between-mixing parameter γ (Equation 2) has a convenient interpretation in terms of findings in network science. Modularity Q is a measure of how well the individuals in a network and their relationships fit into mutually exclusive groups[48]. For CRTs, we assume the natural groupings to be the two treatment arms. If $Q = 1$, all edges exist within treatment arms. If $Q = -1$, all edges are between the two treatment arms. The definition of modularity is written in the same terms as γ:

$$Q := \frac{1}{2m} \sum_{ij} \left(A_{ij} - \frac{k_i k_j}{2m} \right) \delta(r_i, r_j) \tag{9}$$

If the individuals between the two treatment arms have equal numbers of edges, $\sum_{ij} \frac{k_i k_j}{(2m)^2} \delta(r_i, r_j) = 1/2$, and $\gamma = 1/2 - Q$. Therefore, if modularity can be computed, so can the mixing between the two treatment arms. More generally, γ is entirely a function of cluster structure matrix $\mathbf{A}$ and treatment assignments, so if an experimenter knows the structure of relationships among individuals in the study, they may calculate the estimate the amount of mixing between the two treatment arms.

Details on the Stochastic Blockmodel

A stochastic blockmodel (SBM) is a probabilistic network model, which means that the probability of an edge existing between nodes i and j is specified by probability $p_{i,j}$. SBM assumes that each network node is a member of a exactly one block in a partition of b blocks $\mathcal{B} = B_1, ..., B_b$, and the probability $p_{i,j}$ of a connection between nodes i and j depends only on each node's block membership. Denote the block membership of node i as B_i. A probability matrix $P_{b \times b}$ describes all edge probabilities for a network, with $p_{i,j} = P_{B_i, B_j}$. We will return to the stochastic blockmodel in later sections.

In this section, we imitate within-cluster community structure using a SBM. We assume each cluster is comprised of blocks arranged in a triangular lattice structure. Blocks of nodes may be thought of near each other in geographic location, and while most edges are contained within each block, blocks share a few edges according to a triangular spatial pattern. We organized clusters into 10 equally-sized blocks, and individuals within each block are connected to others within their block such that average within-block degree is $\frac{9}{10}\langle k \rangle$. For between-block connections, we also assume that each edge between members of blocks share a total between-block degree of $\frac{1}{10}\langle k \rangle$ with adjacent blocks according to the lattice structure, and no edges with all other blocks. A diagram of this network ensemble is shown in Figure 9.

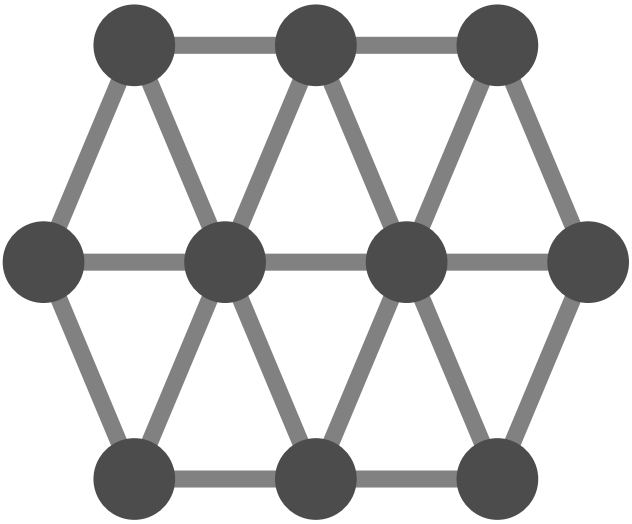

Figure 9: 10 communities or blocks within clusters were created according to the stochastic blockmodel, with a small probability of community ties in a triangular lattice. Edge probabilities were selected to preserve the average degree of a random network.

The ICC

The Intracluster Correlation Coefficient (ICC) is a measure of the average correlation between individual outcomes within a cluster. The ICC assumes that the correlation is identical for all pairs of individuals within a cluster, and is constant across clusters. The ICC can also be expressed as the ratio of between-cluster variance to the total outcome variance in the study[49]. We calculated this value for each network ensemble and value of γ in our simulations. These results are shown in Figure 10.

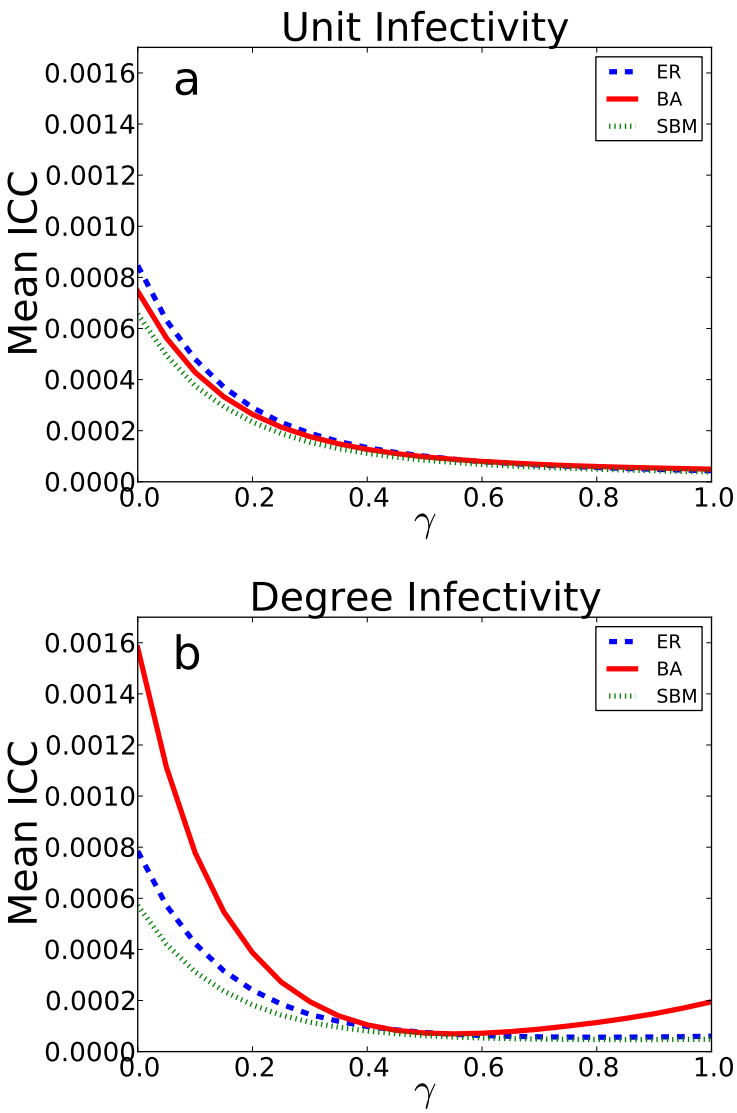

Figure 10: ICCs from Scenario 1, averaged over all simulations. ICC values are shown for unit infectivity (Panel **a**) and degree infectivity (Panel **b**), as well as each within-cluster structure and extent of between-cluster mixing specified in our simulations.

These values are quite low, but not very far from typical values[41] and lower values have been reported in actual trials[7]. These values for the ICC are low because in our design, the data is collected for each cluster pair when the average proportion of infections within each pair is 10%, which results in relatively low variation in infection proportions for each cluster.

Like power, the relative value of the ICC depends on within-cluster structure, the amount of between-cluster mixing, and infectivity. In the case of unit infectivity, the ICC shrinks as between-cluster mixing increases for all within-cluster structures. However, in many power calculation formulas[19], lower values of ICC indicate increased power, not less. This shows that even if sample size calculations account

for within-cluster correlations as measured by the ICC, power can be reduced by other trial features, such as the extent of between-cluster mixing.

Degree Distribution for an Empirical Cell Phone Network

This section specified two definitions for an edge between callers in the cell phone network, which are, respectively, unweighted or weighted by the number of total number of calls made between each pair of callers. The empirical degree distribution for both definitions are found in Figure 11.

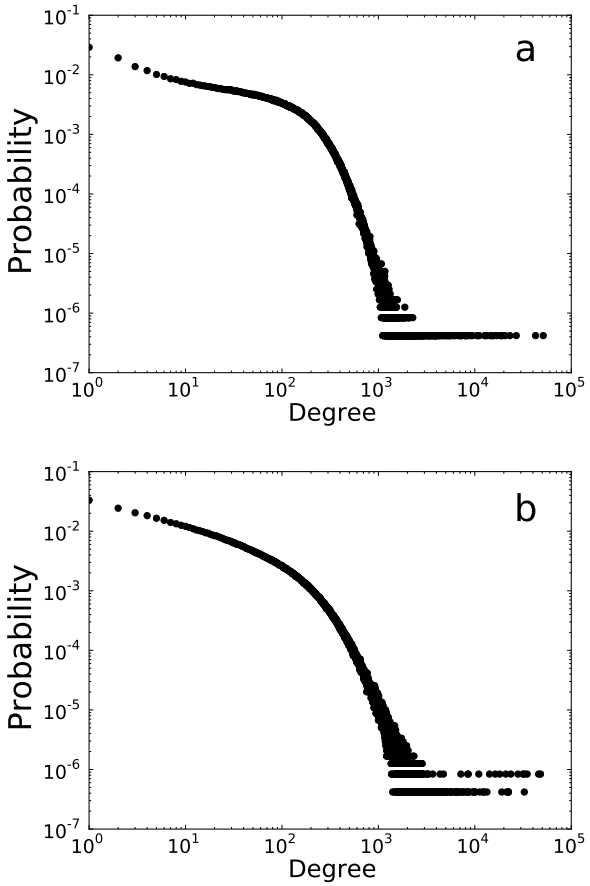

Figure 11: The empirical degree distribution for the calling network dataset. Panel **a** corresponds to Definition 1 (unweighted), and Panel **b** corresponds to Definition 2 (weighted).

Focusing on Panel **a**, we notice three distinct regimes. The vast majority of callers make calls with $1 - 100$ others. The distribution of those who call a large number $(100 - 1000)$ of others follows a nearly straight line on these log-log plots, which is indicative of a power-law for this segment. Finally, a few singular callers are found to call a very large number (> 1000) of callers within the quarter. The general shape is similar for both the unweighted and weighted definitions. This degree distribution is

in accordance to similar datasets analyzed in the literature[47].

Section II: Utilizing Network Properties to Improve Trial Power

In the previous section, we saw how mixing between treated and control contact networks in an epidemic process leads to reduced statistical power, or probability to observe a true reduction in spreading rate. We also observed that the size of this reduction depends on the type of epidemic, the extent of mixing and kind of network observed, and that these conditions may be met in empirical networks. In this section, we will describe how to improve statistical power when studying treatment effects to reduce epidemic spread in contact networks. We will again consider the cluster randomized trial, and utilize an estimator of treatment effect — Augmented Generalized Estimating Equations — that reduces treatment estimate variation by accounting for differences between the distribution of covariates in treated and control clusters. By simulating cluster randomized trials without between cluster mixing, we will estimate the size of the improvements to statistical power gained by measuring and including various features of each network and pre-trial epidemic outcomes in the analysis. Finally, we will estimate how much these gains are affected by a variety of network and epidemic characteristics.

Introduction

Infectious diseases such as HIV spreads through specific ties between individuals. For any fixed time, these transmission routes constitute a network[34 20 21 35 28]. For a deleterious infection, a treatment aims to reduce the probability of transmission from one node to another. In the context of HIV, one strategy to reduce the overall rate of transmission is to test and treat all infected individuals, which is the goal of several ongoing clinical trials[8 9 10].

In order to determine if the treatment is effective, we may randomly assign some individuals to treatment, and others to receive standard care or a placebo. This helps to ensure that average differences between individuals in different treatment groups is caused by the treatment assignment, rather than other characteristics of individuals belonging to the groups. *Interference* occurs when an individual's outcome depends on the outcomes of other individuals in addition to treatment assignment[50]. This can be avoided by randomly assigning independent clusters of individuals to treatment and control, and comparing the outcomes between clusters assigned to each treatment arm. This type of experiment is called a *Cluster Randomized Trial* (CRT)[4 7].

Generalized Estimating Equations (GEEs)[51] are a semi-parametric approach for estimating treatment effects when data are correlated[4], and can be applied to CRTs. This approach has the advantage of providing unbiased estimates of the average marginal treatment effect within the population, whereas mixed effect models only provide an estimated intervention effect conditional on adjustment covariates[52]. Despite randomizing clusters to either treatment arm, baseline covariates may be imbalanced between treatment groups. Furthermore, most CRTs studying infectious processes do not use contact network information to balance randomization (yet not all[10]), and more imbalance between treatment arms may be related to how the infectious outcome depends on baseline contact network features. In both cases, accounting for this covariate imbalance can improve the efficiency of treatment effect estimates[53], which could mean a reduction in treatment effect bias, standard error, or both.

In this section, we investigate the degree to which effect estimates are improved by adjusting for covariate imbalance in several simulated cluster randomized trials of epidemic processes in networks. We first describe the network generation framework as well as the infectious process on them. Next, we detail how these may be used as clusters in a CRT, and we describe the estimation of the intervention effect while adjusting for network features using augmented GEE. We then describe the simulation of each trial scenario, as well as various statistical properties of using each network feature adjustment.

We then show and discuss the main results of our approach, and conclude with discussion.

Network Generation and Epidemic Spread

In this section, we will describe a generative and flexible contact network model. Then, we will detail the epidemic dynamics used to simulate an infectious process.

Block Structure and Node Degree

Consider a network $\mathcal{G}$ with nodes $\mathcal{N} = \{1, ..., n\}$ and edges $\mathcal{E} \subset \mathcal{N} \times \mathcal{N}$. The edges may be described in an *adjacency matrix* $\mathbf{E}_{n \times n}$, which has value 1 if an edge exists between nodes i and j, and a 0 otherwise. The stochastic blockmodel of Anderson, Wasserman, Faust[22] assumes that each node i belongs to only one block b_i in a partition of nodes $\mathcal{B} = \{1, ..., B\}$. The complete set of node memberships may be represented compactly as a vector $\boldsymbol{b} = \{b_1, ..., b_n\}$. In this model, the probability of an edge existing between two nodes i and j depends only on block membership, thus $P(E_{ij} = 1) = p_{b_i b_j}$. Karrer and Newman[54] extend this model to the *Degree-Corrected Stochastic Blockmodel*, which allows each node to have an arbitrary expected degree $\theta_i = \mathbb{E}\left(\sum_j E_{ij}\right)$. The probability of an edge existing between two nodes i and j depends only on their expected degrees and the probability of edges existing between nodes of each block ω_{b_i, b_j}. The probability of an edge existing between members of any two blocks may be written compactly as a matrix $\boldsymbol{\omega}_{B \times B}$. The likelihood of this model assumes that the number of edges between any two nodes i and j is independent and Poisson distributed with mean count b_{ij}, where b_{ij} is the product of the expected degree of nodes i and j (θ_i and θ_j, respectively), multiplied by the expected amount of mixing between the blocks of which i and j belong ω_{b_i, b_j}. Karrer and Newman define the likelihood of the Degree-Corrected Stochastic Blockmodel using the Poisson distribution for mathematical convenience, but it implies that each pair of nodes may have more than one edge (a *multi-edge*), but we do not expect many of these to occur. We will prove this directly in Section III, but this for now we will give an intuitive argument. There are $\binom{n}{2}$ node pairs and only a finite expected number of edges for each node, and therefore means the number of edges between any two nodes approaches zero as the number of nodes in the network n increases. Therefore, while we expect single edges to exist between node pairs, each pairing is very unlikely, so we do not expect many more edges to occur between the same two nodes very often by chance. Finally, edges may also exist between a node and itself (a *self-edge*). These appear twice in the adjacency matrix, so they are given a half amount of likelihood each. Combining these, we can write the full likelihood as:

$$P(\mathbf{E}|\boldsymbol{\theta},\boldsymbol{\omega},\mathbf{b}) = \prod_{i<j} \frac{b_{ij}^{E_{ij}}}{E_{ij}!} \exp\left(-b_{ij}\right) \times \prod_{i} \frac{\left(\frac{1}{2}b_{ii}\right)^{E_{ij}/2}}{(E_{ij}/2)!} \exp\left(-\frac{1}{2}b_{ii}\right) \tag{10}$$

$$b_{ii} = \theta_i \theta_j \omega_{b_i,b_j} \tag{11}$$

This model has several attractive features. It allows for arbitrary degree for each node, as well as arbitrarily complex interaction between blocks, provided they are symmetric. (The number of edges existing between blocks must be the same, regardless of which block we identify first.) Second, it is *estimable*, meaning the parameters can be estimated from an empirical network. It is also *generative*, meaning one can generate networks that are consistent with the specified model parameters[54] (For more notes on generating networks from this model, see Section III.)

We will consider two types of block structure, both of which are special cases of *bipartite* networks. A bipartite network is one in which each node belongs to exactly one of two groups, and edges only exist between members of opposite groups. We consider eight blocks (four in each bipartite group), and two types of block structure: random, and heterogeneous (see Section 4). A diagram of these structures is shown in Figure 12.

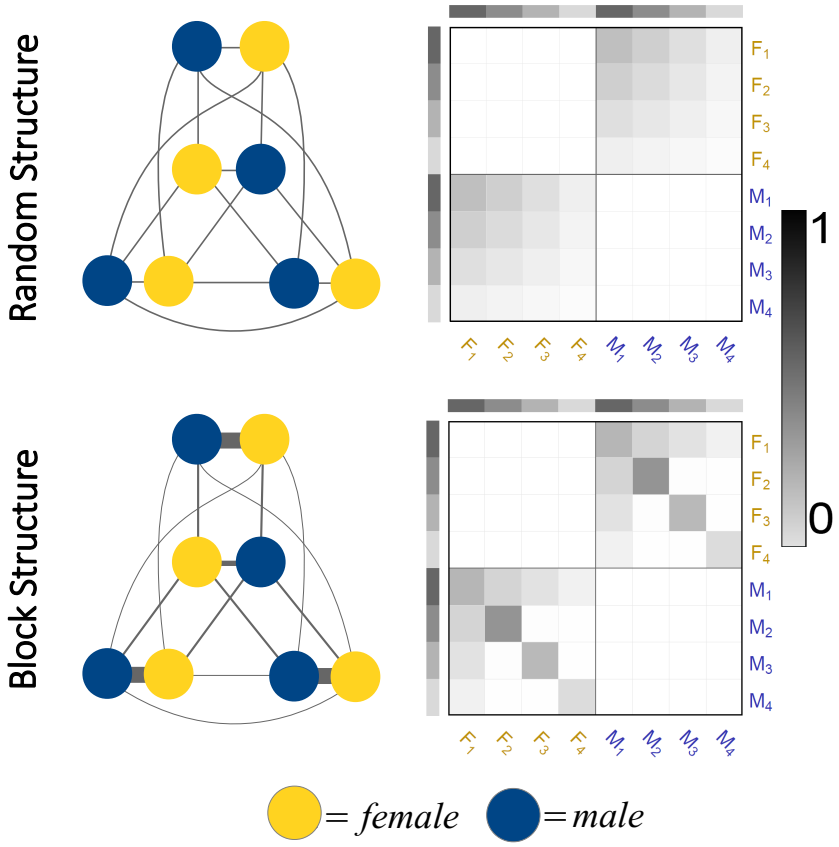

Figure 12: The left panel shows random bipartite mixing, in which males and females share edges independent of their block memberships. The right panels shows strong bipartite community structure, in which the edges in the network only exist in four bipartite communities, one of which also mixes significantly with the others. In both figures, the strength of mixing is shown by the thickness of each tie. Both of these block structures are bipartite, meaning edges only exist between nodes in Blocks 1-4 and nodes in Blocks 5-8.

Degree Assortative Rewiring

Finally, in addition to block structure and node degree, networks may vary in the extent to which having a high degree is correlated to sharing edges with other nodes with high degree[55]. One metric for this feature is *degree assortativity*, which is the Pearson correlation coefficient comparing the degree of the two nodes associated with every edge in the network[56]. We can vary this measure by performing *degree assortative rewiring*, which increases or decreases the assortativity in the network while preserving block structure and each node's degree[57]. This is performed by randomly selecting two edges within a block pair and rewiring them, as follows.

1 Select two blocks b_1 and b_2 at random.

2 Select two edges (n_1, n_2) and (n_3, n_4) at random between blocks b_1 and b_2.

3 Iff $|k_1 - k_2| + |k_3 - k_4| > |k_1 - k_4| + |k_2 - k_3|$:

Remove edges (n_1, n_2) and (n_3, n_4)

Add edges (n_1, n_4) and (n_2, n_3)

Table 2: Our algorithm used to rewire network edges in order to increase the assortativity of each network. To decrease assortativity, perform Step 3 if and only if the inequality is reversed.

A diagram of this process is shown in Figure 13.

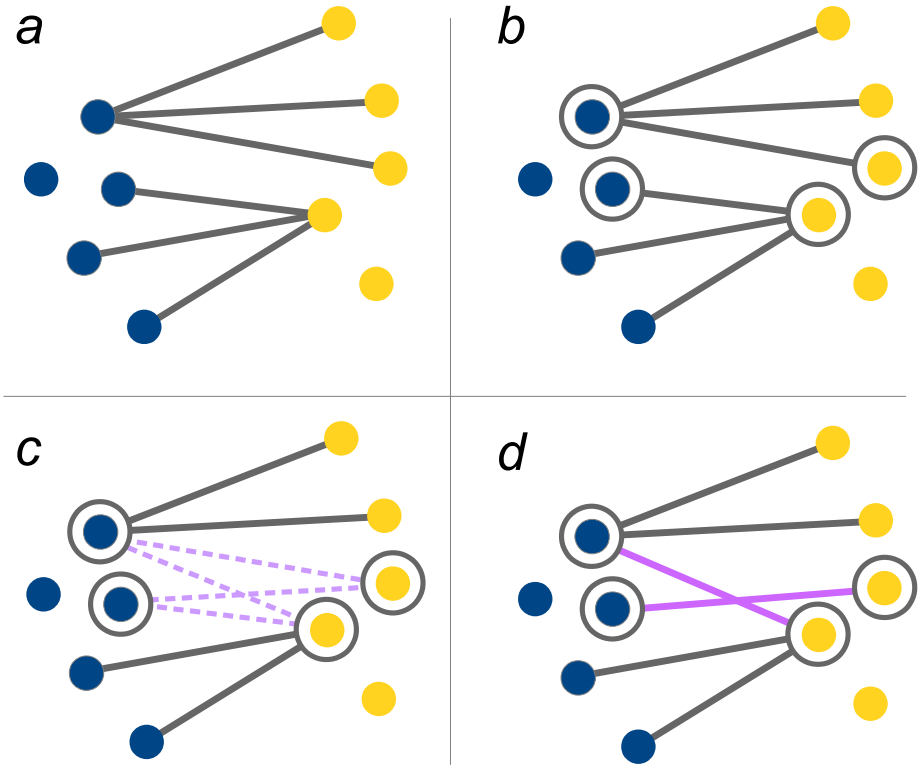

Figure 13: A schematic of degree assortative rewiring. Panel **a** displays a network. Panel **b** highlights two edges selected within the same block pair. Panel **c** shows a potential rewiring, which will only occur if rewiring will increase assortativity. In this case, rewiring does increase assortativity, and Panel **d** displays the successful rewiring.

We consider networks with both assortative and disassortative rewiring, further described in Section 4.

Infectious Spread

After creating a network, we simulate an infectious spread on a collection of networks[26], using Algorithm 3. Upon establishing an initial subset of nodes that are infected, each node with degree k_i may infect a subset of their neighbors q_i at each time step. This process is continued for a finite number of time steps. A diagram of the infectious process over time is shown in Figure 14.

1 1% of all nodes are selected at random to be initially infected.

2 Until B% population incidence:

For each infected node i (in random order):

a Successively select q_i neighbors.

b If neighbor j is already infected, do nothing. If not, infect with probability 0.3.

3 Repeat five times:

For each infected node i (in random order):

a Successively select q_i neighbors.

b If neighbor j is already infected, do nothing. If not, infect with probability:
$p = 0.3$ for those in control clusters,
$p = 0.1$ for those in treated clusters.

Table 3: Our simulation algorithm used to propagate an infectious spread through each network. Among other parameters, we consider all combinations of a range of values for q_i and B.

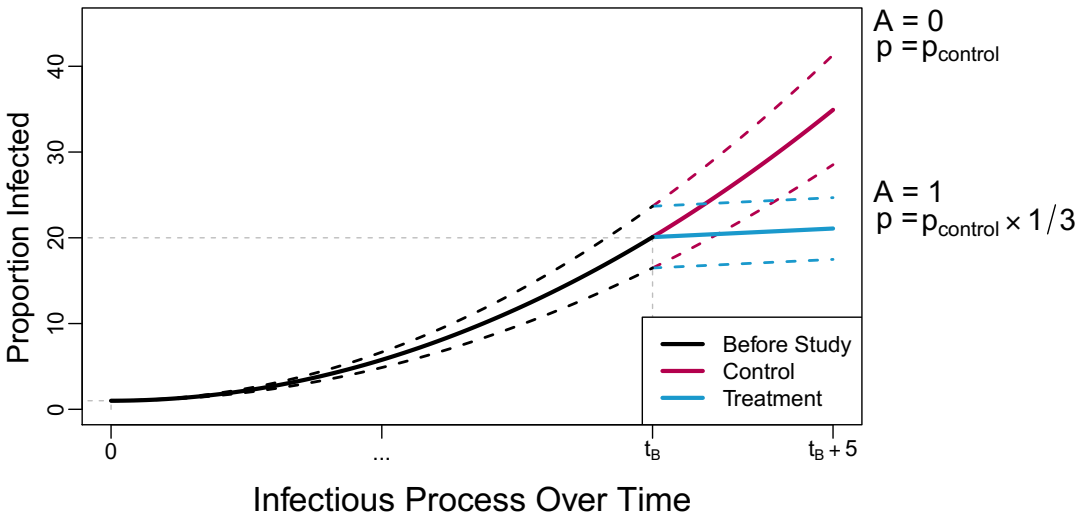

Figure 14: 1% of nodes are randomly selected as initially infected, and an infectious process spreads until B% overall baseline prevalence is reached (time t_B). Individuals are infected according to Algorithm 3. Then, each cluster is randomized to treatment ($A = 1$) or control ($A = 0$), wherein infected nodes in treated clusters have their infection probability reduced by 70%. The process continues for another 5 time steps.

In this process, infectivity q_i is the number of individuals one may infect at a given time, which may vary from none to the degree an individual has. Zhou et al.[18] showed that the properties of network spread can depend strongly on infectivity, which may differ between actual infectious processes. We will consider both unit infectivity and degree infectivity, in which an individual infects either one partner (selected at random) or each partner, respectively. A schematic of this infectious process is shown in Figure 15.

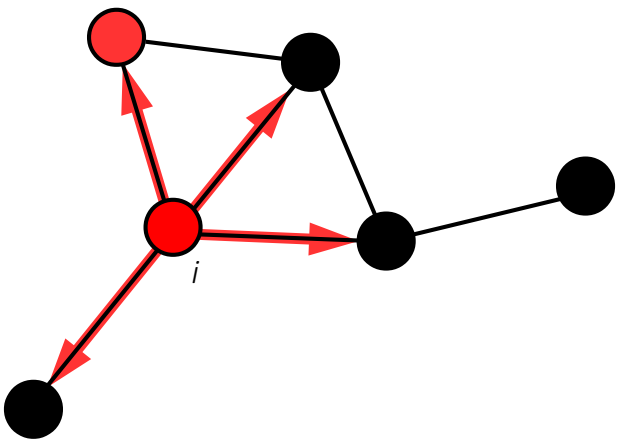

Figure 15: A schema of the stochastic agent-based infectious process. In general, $0 \leq q_i \leq k_i$ individuals may be selected at each time step. We will use infectivity $q_i = 1$ (unit) or $q_i = k_i$ (degree).

Treatment Effect Estimation and Adjustment

Now that we have detailed the simulation of networks and infectious spread through them, we will describe the augmented GEE, which will estimate the effect of treatment on clusters within the trial. Then, we will describe how network features may improve the estimate of treatment effect.

Consider a trial that consists of $i = 1, ..., m$ clusters with $j = 1, ..., n_i$ individuals per cluster, with $\sum_i n_i = N$ total individuals in the study. For each individual, Y_{ij} is 1 if the individual is infected by the end of the trial, and 0 otherwise. The vector $\mathbf{Y}_i = (Y_{i1}, ..., Y_{in_i})^\top$ is the related vector of outcomes in cluster i. In addition, each individual has a set of P covariates $\mathbf{X}_{ij} = (X_{ij}^1, ..., X_{ij}^P)^\top$, with all covariates represented compactly as $\mathbf{X}_i = (\mathbf{X}_{i1}, ..., \mathbf{X}_{in_i})^\top$. Individuals in cluster i are all assigned to the same treatment, and we assume two levels of treatment: $A_i = 0$ for controls, and $A_i = 1$ for communities receiving the intervention. Each individual belongs to a cluster specific contact network with corresponding adjacency matrix $\mathbf{E}_i$. Unlike Section I, in this section we assume there is no mixing across clusters.

In a trial, the data-generating mechanism is not directly observed, and the treatment effect must be estimated from observed outcomes. GEE evaluates the marginal treatment effect in the population, averaged over all individual characteristics. This type of analysis is unbiased if the data come from a random sample. This means that all possible confounding variables have the same expected distribution among the treated ($A_i = 1$) and control ($A_i = 0$) populations, and no differences in missingness across communities. The marginal treatment effect is $\beta_A = \mathbb{E}(\mathbb{E}(Y_{ij}|A_i = 1, \mathbf{X}_{ij}, \mathbf{E}_i)) - \mathbb{E}(\mathbb{E}(Y_{ij}|A_i = 0, \mathbf{X}_{ij}, \mathbf{E}_i))$ estimated by using the marginal regression model $\mathbb{E}(Y_{ij}|A_i) = \mu_i(\beta, A_i) = g(\beta_0 + \beta_A A_i)$. In this section, g will be the identity function, and β_A is the *risk difference* between outcomes averaged within clusters in the intervention compared to control.

The GEE-based approach gives estimates that are consistent and asymptotically normal[51]. However, we will consider a method to improve the efficiency with which this estimate is made. Although we expect the treated and control clusters to be similar due to randomization, chance imbalance can cause the two groups to differ. In the case that measured covariates are related to both treatment assignment as well as the outcome, Tsiatis et al.[53] proposed a way to add a term (*augment*) estimators to account for this imbalance, which decreases estimate variance and increases statistical efficiency. In the context of the GEE, Stephens et al.[58] propose the following estimating equations with an extra augmentation term:

$$0 = \sum_{i=1}^{m} \Bigg[\underbrace{\mathbf{D}_i^\top \mathbf{V}_i^{-1} (\mathbf{Y}_i - \boldsymbol{\mu}_i(\beta, A_i))}_{\text{classic GEE term}} \tag{12}$$

$$+ \underbrace{\sum_{a=0,1} \pi^a (1-\pi)^{1-a} \mathbf{D}_i^\top \mathbf{V}_i^{-1} \Big(\mathbf{B}(\mathbf{X}_i, \mathbf{E}_i, a) - \boldsymbol{\mu}_i(\beta, a) \Big)}_{\text{augmentation term}} \Bigg]. \tag{13}$$

Here, $\mathbf{D}_i^\top = \frac{\partial \mu_i(\beta, A_i)}{\partial \beta}$, V_i^{-1} is the covariance structure, and $\pi = \frac{1}{2}$ is the fixed probability of treatment attribution. The inverse variance covariance matrix is $V_i^{-1} = \phi \mathbf{U}_i^{1/2} \mathbf{R}(\alpha) \mathbf{U}_i^{1/2}$ where $\mathbf{U}_i = \text{diag}(\text{Var}(y_{ij}))$, ϕ is the scale parameter and $\mathbf{R}(\alpha)$ is the working correlation, specified by the analyst. The augmented GEE improves efficiency optimally if the outcome model is[59,60]:

$$\mathbf{B}(\mathbf{X}_{ij}, \mathbf{E}_i, A_i) = \mathbb{E}(Y_{ij} | \mathbf{X}_{ij}, \mathbf{E}_i, A_i). \tag{14}$$

To compute these quantities, we fit a generalized linear model regression for each treatment group ($a = 0, 1$), such as $\mathbf{B}(\mathbf{X}_{ij}, \mathbf{E}_i, A_i) = \mathbf{X}_{ij}^\top \boldsymbol{\Xi}_{\mathbf{i}}^{(\mathbf{X})} + \tilde{\mathbf{E}}_{ij}^\top \boldsymbol{\Xi}_{\mathbf{i}}^{(\mathbf{E})}$, where $\tilde{\mathbf{E}}_{ij}$ is a vector of covariates for individual j in cluster i derived from its cluster's adjacency matrix $\mathbf{E}_i$, and $\Xi_i^{(\mathbf{X})}$ and $\Xi_i^{(\mathbf{E})}$ are fitted covariates for demographic and network data, respectively. In this section, we will consider network features $\tilde{\mathbf{E}}_{i;j}$ only for the augmentation term, and absorb these two terms into the single, conventional notation $\mathbf{X}_{ij}$.

Next, we give the exact specification of the trials we performed, including fixed and variable aspects of the network generation process and the epidemic spread. Then, we describe which features are measured from the resulting trial, which are used as adjustment covariates in the augmented GEE. Finally, we specify a range of statistics that reflect the quality of the effect estimates from each trial.

Scenario Aspects

Each trial consists of an infectious process propagating on $m = 48$ clusters (networks) of sizes ranging from $n = 120$ to 280, with an average size of size 200. In addition, we also consider each possible combination of six trial aspects:

$\boldsymbol{a_1}$: Mean degree of each node:	$\{2,10\}$
$\boldsymbol{a_2}$: Node Degree Distribution:	$\in \{\text{Poisson}, \text{Powerlaw}\}$
$\boldsymbol{a_3}$: Assortativity	$\{-0.3, 0.3\}$
$\boldsymbol{a_4}$: Mixing structure	$(\mu, \lambda) \in \{(0,0), (0.8, 0.1)\}$
$\boldsymbol{a_5}$: Infectivity:	$\{\text{Unit}, \text{Degree}\}$
$\boldsymbol{a_6}$: Baseline Prevalence =	$B \in \{2\%, 25\%\}$

Table 4: A summary of the scenario aspects investigated. We consider each combination of these.

Finally, for each combination of trial aspect, we perform $R = 1000$ stochastic trials, and retain effect estimate statistics for each trial.

Network Features

While a network consists of pairwise connections between individuals i and j, the GEE augmentation term assumes imbalance can be modeled by a vector network features for each individual $\mathbf{X}_{ij}$. We assume this vector is composed of a small number of functions of the network in which they belong. Some of these are constant per network, and some are different for every individual. They fall into four broad classes: those involving degree, mesoscopic structure, baseline infections, and combinations of these.

Each node i has *degree* $k_i = \sum_j E_{ij}$, the total number of individuals that share an edge with that node. Mean neighbor degree $m_i = \frac{\sum_j E_{ij} k_j}{k_i}$ is the unweighted average of a node's neighbors' degrees. *Assortativity* is a composite measure of mean neighbor degree across the entire network, the Pearson correlation between both nodes' degrees across each edge in the network.

Network features may also capture *mesoscopic* network structure, or structure existing between local and global scope of the network. For example, the networks we consider contain block structure, and we consider $\mathbb{I}(B_i = 1 \text{ or } B_i = 5)$, an indicator if a node belongs to the two blocks that are highly connected with other blocks. We may also consider *components*, or subsets of the network in which each individual are in the same component if and only if they share a path. A *path* exists between two node i and j iff there exists a subset of edges $\mathcal{E}_{ij} \subset \mathcal{E}$ in the network that connect nodes i and j. Note that in this section, a cluster refers to a single network randomized to an intervention arm, whereas components are

distinct from clusters in that several components comprise a single cluster. The components of a cluster $c \in 1,...,C$ are assumed to be ordered from largest to smallest in size, where size is defined as the number of nodes in each component. We consider the size of the largest component in the network $\sum_i \mathbb{I}(C_i = 1)$, the mean component size n/C, the number of components C, and the size of the component each node belongs to, $\sum_j \mathbb{I}(C_i = C_j)$.

Another potential feature available for adjustment at baseline is the infectious status of each node in the network at baseline. One simple metric is the number of infected neighbors at baseline for each node $\sum_j E_{ij} I_j(0)$, or the number of infected individuals belonging to the same component as a node $\sum_j \mathbb{I}(C_i = C_j) I_j(0)$. We may also consider the length of the path between each node i and each infected individual j at baseline. We consider the inverse of the shortest path length from the closest node infected at baseline $\left(\min_j d_{ij}\right)^{-1}$, as well as the sum of the inverse path lengths $\sum_j d_{ij}^{-1}$.

We also consider any collection of these covariates. That is, we consider an outcome model including all these (12) covariates, as well as a stepwise selection of variables[61]. Finally, we also consider a few non-linear fits for the probability of infection for each covariate. Specifically, we consider a spline term, and a power-law fit for the *degree* covariate.

In Table 5, we summarize the network features we use for the augmentation term:

Unadj: No adjustment term	
1: Degree	k_i
2: Mean Neighbor Degree	$m_i := \frac{\sum_j A_{ij} k_j}{k_i}$
3: Assortativity	$\rho_{\mathbf{k},\mathbf{m}}$
4: Member of Connected Block	$\mathbb{I}(B_i = 1)$
5: Size of Largest Component	$\sum_i \mathrm{I}(C_i = 1)$
6: Mean Component Size	n/C
7: Number of Components	C
8: Size of Node's Component	$\sum_j \mathbb{I}(C_i = C_j)$
9: Total Neighbor Infections at baseline	$\sum_j A_{ij} I_j(0)$
10: Total Node's Component Infections at baseline	$\sum_j \mathbb{I}(C_i = C_j) I_j(0)$
11: 1/nearest infected path length at baseline	$\left(\min_j d_{ij}\right)^{-1}$
12: $\sum_i$ 1/path length to Infected Node i at baseline	$\sum_j \left(d_{ij}^{-1}\right)$
13: Complete inclusion of the above	
14: Stepwise regression of the above	
Spl: Spline(Degree)	$\mathrm{spline}_3(k_i)$
Pow: Powerlaw(Degree)	$C \cdot k_i^a$

Table 5: A summary of the network feature sets used in the augmentation term of the augmented GEE.

Statistics Measured

We now describe the statistics we will use to compare the unadjusted GEE to the augmented GEE with network features. For $r = 1, ..., R$ trials, we compute the augmented GEE estimates of treatment effect size $\widehat{\beta}_r$ and estimate standard deviation $\widehat{\mathrm{sd}}_r(\widehat{\beta}_r)$. In addition, we use trial outcomes $Y_{ij;r}$ to compute the true treatment effect by calculating the average risk difference across all trials:

$$\beta^* := \frac{\sum_{ijr} Y_{ij;r} \cdot \mathbb{I}(A_i = 1)}{\sum_{ijr} \mathbb{I}(A_i = 1)} - \frac{\sum_{ijr} Y_{ij;r} \cdot \mathbb{I}(A_i = 0)}{\sum_{ijr} \mathbb{I}(A_i = 0)} \tag{15}$$

From this value, obtain the estimated empirical bias and empirical variance of the treatment effect estimate:

$$\widehat{\text{Bias}}_r(\widehat{\beta}_r) = \beta^* - \widehat{\beta}_r \tag{16}$$

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:

$$\widehat{\text{RMSE}} := \sqrt{\frac{1}{R}\sum_r \widehat{\text{Bias}}_r(\widehat{\beta}_r)^2 + \widehat{\text{Var}}(\widehat{\beta})} \tag{17}$$

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 $\widehat{\text{RMSE}}_{\text{adj}}$ to that of the unadjusted GEE ($\widehat{\text{RMSE}}_{\text{GEE}}$:

$$\widehat{\text{Gain}} := 100 \times \left(1 - \frac{\widehat{\text{RMSE}}_{\text{adj}}}{\widehat{\text{RMSE}}_{\text{GEE}}}\right) \tag{18}$$

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

$$P(\beta_A^* \in CI(\hat{\beta}^*)) \tag{19}$$

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 treatment effect is not zero:

$$P(0 \notin CI(\hat{\beta}_A^*) | \beta_A \neq 0) \tag{20}$$

These measures are summarized in Table 6.

Bias	$\overline{\widehat{\beta_0}} - \beta$
SE_{model}	$\widehat{\text{se}}\left(\widehat{\beta}\right)$
$\text{SE}_{\text{empirical}}$	$\widehat{\text{se}}\left(\widehat{\beta_m}\right)$
$\text{RMSE}_{\text{model}}$	$\sqrt{\text{Bias}^2 + \text{SE}^2_{\text{mod}}}$
$\text{RMSE}_{\text{empirical}}$	$\sqrt{\text{Bias}^2 + \text{SE}^2_{\text{emp}}}$
%Reduction $\text{RMSE}_{\text{model}}$	$\frac{\widehat{\text{RMSE}}^{(\text{mod})}_{\text{adj}}}{\widehat{\text{RMSE}}^{(\text{mod})}_{\text{GEE}}}$
%Reduction $\text{RMSE}_{\text{empirical}}$	$\frac{\widehat{\text{RMSE}}^{(\text{emp})}_{\text{adj}}}{\widehat{\text{RMSE}}^{(\text{emp})}_{\text{GEE}}}$
$\text{Coverage}_{\text{model}}$	$\sum_m \text{I}\left(\beta \in \widehat{CI}\left(\widehat{\beta_m}\right)\right) / M$
$\text{Power}_{\text{model}}$	$\sum_m \text{I}\left(0 \notin \widehat{CI}\left(\widehat{\beta_m}\right)\right) / M$

Table 6: The result statistics we evaluate for each trial scenario and adjustment covariate set.

Results

Descriptive Statistics

Adjusting for covariates increases efficiency when the covariate is related to outcomes (on average) as well as to treatment effects that occur from chance imbalance. Figure 16 shows the correlation in our generated trials between the outcome and each covariate, as well as with the treatment.

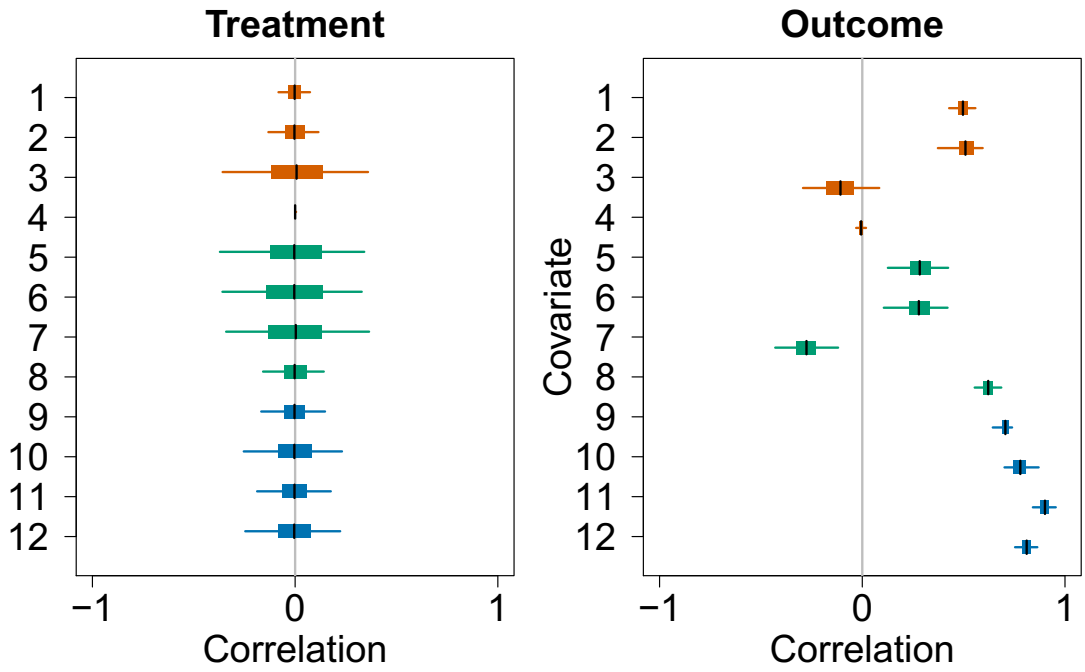

Figure 16: A plot of the distribution of univariate correlations between single covariates and indicators for either treatment or outcome. The left shows correlations with variation around zero, suggesting imperfect randomization due to finite sample sizes, and the right panel shows that some network or baseline epidemic covariates are correlated with the outcome. Nonzero covariate correlations in both panels suggests gains in efficiency when estimating the effect of treatment.

Because Figure 16 shows that the adjustment covariates are correlated with both treatment and outcome, we expect gains, or reductions in the RMSE.

Main Results

In this section, we will show results for each adjustment strategy and statistic. First, we show the improvements (percent reductions) in RMSE in Figure 17.

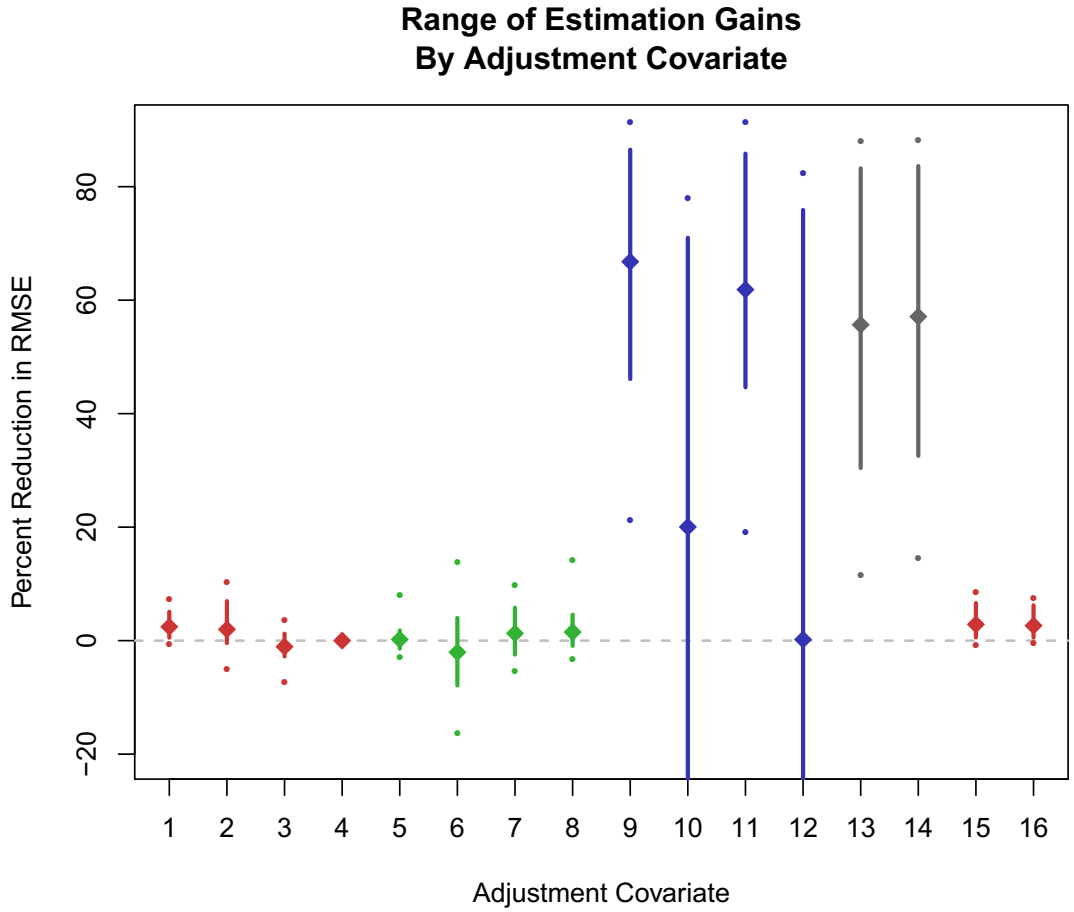

Figure 17: Improvements, or percent reductions, in RMSE for each covariate set. Means are shown with diamonds, each line shows the 80% quartile range, and outer dots show the extrema.

.

We see that each covariate displays very different behavior. Degree-related covariates (red) are modest, but consistent in displaying gains. Component covariates (green) are also modest, and not reliably positive. In contrast, covariates involving other infections at baseline (blue) can be very informative, with some covariates showing a very wide range of effects, including an inflation of RMSE. Finally, fitted non-linear covariates for degree did not result in larger improvements overall, which suggests that a linear fit takes advantage of much of the potential gains in reducing estimate RMSE.

We also consider several other statistics, averaged across of the 2^6 treatment scenarios (with standard deviations across scenarios in parentheses). These results are shown in Table 7.

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
Bias	0	0	0	0	0	0	0	0	0	-0.02	-0.05	0	-0.05	-0.02	-0.01	0	0
RobSE	3.02	2.94	2.91	2.96	3.02	2.92	2.87	2.89	2.98	0.88	1.62	1.02	1.78	0.76	0.75	2.92	2.94
EmpSE	2.92	2.83	2.82	2.93	2.92	2.89	2.89	2.85	2.84	0.73	1.56	0.93	1.84	0.86	0.85	2.81	2.82
Gains	0(0)	2(2)	2(3)	-1(2)	0(0)	0(2)	-2(5)	1(3)	2(3)	67(15)	20(39)	62(16)	0(60)	56(22)	57(21)	3(2)	3(2)
Power	30.6	30.8	31.2	31.7	30.6	32.4	32.2	32.6	30.4	81.1	45.6	74.4	38.1	82.7	83.7	31	31
Coverage	95(2)	95(2)	95(2)	94(2)	95(2)	94(2)	94(2)	94(2)	95(2)	94(6)	96(3)	94(6)	94(3)	89(7)	90(7)	95(2)	95(2)

Table 7: A table of treatment effect statistics averaged across each trial aspects. Each row displays a statistic, and each column displays an adjustment feature or strategy. Standard deviations across trial aspects are shown in parentheses. Positive numbers indicate the percent improvement in RMSE.

We see that the improvements shown in Figure 17 translate to very significant gains in power. In addition, coverage is adequate for most scenarios, ensuring a valid interpretation of power for those scenarios. This is owed to low bias, and broadly accurate (albeit somewhat conservative) estimates of standard error.

For brevity, the statistics of each trial conditional on each trial aspect combination are given in the Appendix. In addition to results averages across each trial aspect, we may consider the effect each aspect has on each trial statistic. To accomplish this, we used a simple linear regression, modelling each trial scenario with a statistic as the outcome and trial aspect as a binary covariate. The coefficients resulting from this model represent the percent improvement what results from changing one trial aspect from 0 to 1, holding all other trial aspects constant. The results for each statistic is found in the Appendix, but we focus on the percent improvement in RMSE, shown in Table 8. To provide guidance on how to interpret coefficients, we provide an example of a description of a coefficient of improvement modification by singling out the row corresponding to `Deg_Infect` and column F_9. Holding constant average degree, degree distribution, network assortativity, community structure, and baseline prevalence, an epidemic process exhibiting degree infectivity shows an additional improvement of 12 percentage points in RMSE compared to an epidemic process exhibiting unit infectivity. Therefore, in this case, using adjustment variable F_9 (total number of infected neighbors at baseline) is more important if the epidemic process has degree infectivity compared to unit infectivity.

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
(Intercept)	-0	1	-1	-2	-0	-1	-5	0	-1	57	-27	56	-46	30	34	1	1
High Degree	0	-1	-1	-1	0	-1	-1	-2	-2	-9	11	-14	-33	-3	-4	-1	-1
Powerlaw	0	3	2	2	0	1	0	4	3	-8	-4	-8	-7	-1	-1	3	3
Assortative	0	1	-0	-1	0	0	-1	-0	-1	4	2	6	3	4	4	-0	0
Communities	-0	-1	-1	-0	-0	-0	-1	-2	-1	0	-3	-0	-7	-1	-1	-2	-1
Deg. Infect	0	1	4	1	0	2	4	1	2	12	32	14	52	14	12	1	1
High Base.	0	1	2	1	0	1	6	2	2	19	55	14	84	38	36	1	1

Table 8: A table of percent estimate improvement modification in RMSE modified by each trial aspect. Each row displays a trial aspect, and each column displays an adjustment feature or strategy.

In trials in which clusters of individuals have a heavy-tailed (powerlaw) distribution, we observe modest positive improvements in RMSE reductions when adjusting for Features $1-8$ (covariates related to degree and component sizes). However, this change also results in diminished gains when adjusting for baseline infection-related covariates. In contrast, much the opposite holds when adjusting for either degree infectivity, high baseline, or both: the benefits of adjusting for Features 1-8 are positive but diminished, whereas the improvements for adjusting for baseline infections (Features 9-12) are much larger. This suggests that a node's local network of partners and their infectious status can be quite predictive of the risk acquire the infection, which has also been reported by Ghani et al.[62] However, these infectious covariates can show a wide range of possible effects on RMSE, including significant inflations for some scenarios. Care should therefore be taken to ensure that the epidemic context is sufficiently similar to the cases described here in which they are beneficial before measuring and using these covariate of interest for adjustment. In addition, while we have considered a range of simulation variants, several additional modeling assumptions are likely incongruent with an empirical study, including being well-characterized by an SI process propagating on a fixed network.

Full statistics for each simulation scenario and adjustment strategy are shown in the tables, both marginal across scenarios as well as conditional on each scenario (see Appendix). In addition, the effect of modifying any specific scenario aspect (holding the others constant) is shown in the modification results.

Auxiliary Analyses

We also considered the analysis detailed above for two variants: increasing the size of the networks, and including covariates in the classic GEE covariate adjustment set.

First, we consider the analysis with networks considerably larger (six-fold) than those considered above.

This yields networks with an average size of $n = 1200$ (ranging from size 720 to 1680). These results can be found in the second segment of the appendix at the end of this section.

We first observe that the expected treatment effect is larger: incidence is reduced by 3.43% in the treatment arm compared to the control arm, which is greater than the 2.64% observed in the trials with smaller networks. Because the baseline incidence and followup time is held constant for the two, this means that the 70% reduction in infection probability for each individual more effectively reduces the overall incidence throughout the trial for larger networks. We also observe that for each adjustment covariate set, the bias is very low (0-0.02), and coverage is higher (94-100%) compared to than that observed for smaller networks. In addition to larger treatment effect sizes, the empirical and robust standard errors are generally attenuated compared to the smaller networks, which yields greater power for all scenarios.

For the larger network case, we also observe gains in efficiency when incorporating an adjustment set, and the gains differ in several ways. The gains obtained from using degree-based covariates (Features 1-2) are greater both in expectation as well as the maximum. However, the variation in gains is also increased. The incorporation of assortativity (Feature 3) is generally less helpful, again with a wide range of potential gain percentage points. Block and component Features (4-8) also display a wide range of variability, with no substantial differences in expected gains in efficiency. In contrast, variables involving baseline infections (Features 9-11) are somewhat attenuated and highly variable, but still display the greatest expected and maximum gains. Somewhat surprisingly, Feature 12 (the sum of inverse path lengths to an infected individual) becomes unhelpful on balance. Including all variables or a stepwise selection of the above variables shows generally substantial gains. Note that with larger network sizes, these composite adjustment sets display low bias and high coverage compared to the smaller networks. Finally, we consider non-linear functions of Feature 9 (number of infected neighbors at baseline), including fitted powerlaw curves as well as polynomial splines with degree 3. These both show slightly attenuated and more variable gains compared to the linear fit, which suggest that these expansions do not generally improve the utility of the adjustment covariate.

Finally, we consider using each covariate or covariate set as adjustment terms in the classic GEE, compared to the augmented GEE. For equal comparison with the main results, we include the analysis for the smaller size of networks only. Recall that the classic GEE consists only of Equation 12, whereas the augmented GEE includes a second set of terms adjusting for covariate imbalance across treatment strata (Equation 13). Both of these approaches incorporate a vector of covariates for each cluster, and potentially each individual. In the classic GEE, variation in the treatment effect estimate is reduced by

accounting for the correlation of the covariate set to the observed outcome for each individual. This contrasts with the augmentation term of the augmented GEE, in which the covariate set is used in the second term to estimate the outcome for each individual, conditional on that individual belonging to each treatment stratum. Both adjustment strategies are expected to yield improvements in efficiency when estimating the treatment effect[58 63]. These results can be found in the final segment of the appendix at the end of this section.

The result of including the adjustment in the unaugmented GEE is very similar to the augmentation term, with a few differences we explore here. We observe that the overall treatment effect estimate is slightly larger. However, the standard error estimates have also increased on balance. Combined, these have a negligible effect on bias (low) and coverage (91-95%), which are substantially similar. The differences in standard error estimates are reflected in the percent improvements in RMSE: substantially equivalent for covariates related to degree, block, and component membership (Features 1-8), but some variation in covariates related to infections at baseline (Features 9-12). The gains from features related to local measures of infected nodes at baseline are somewhat attenuated: the number of infected neighbors at baseline (Feature 9) and inverse minimum path length to an infected individual at baseline (Feature 11) are both lower for the classic GEE analysis. In contrast, more global measures of infections at baseline, including total component infections at baseline (Feature 10) and sum of inverse path lengths to infected individuals at baseline (Feature 12), both show increased gains. These differences are reflected in gains in power, which are lower for the first two covariates and higher for the second two, respectively. Because the gains from each of these features is highly variable but generally high, it is not clear if these reflect qualitatively significant differences between these two analyses, which otherwise comparable in improvement of the efficiency in effect estimation.

Discussion

In an epidemic process, infectious outcomes depend on network structure and spreading process dynamics. When assessing the marginal effect of treatment on the infectious process, one strategy to improve the estimation of the treatment effect is to adjust for covariate imbalance in the clusters randomized to each treatment arm. Several contact network features and characteristics of epidemic spread can be included to adjust this analysis. In this section, we have used the augmented GEE to estimate the magnitude of these gains, as well as how these gains are modified by aspects of each network and epidemic dynamics. We found that adjusting for baseline infections yields robust gains across each

scenario, and that the improvement size depends on the specific aspects of the epidemic process.

We consider including augmentation terms that reduce network properties to a single covariate for each node. These covariates differ in the gains they provide in our simulation scenarios, but also in their robustness to scenario specification, interpretability, and feasibility of gathering in practice. For example, the sum of all inverse path lengths to an infected individual shows both wide variation in RMSE improvements across each setting. It would also be difficult to assess this covariate for each person unless one obtains the full network and the infectious state of each individual at baseline. In contrast, each individuals' degree may be feasible to obtain, but the gains we observe from this covariate are modest. The number of neighbors infected at baseline is an excellent covariate in each of these respects. When analysing a spreading process through a network, we recommend assessing and incorporating this information for each member of each cluster.

This work also invites several extensions. We assume that each collection of networks is known with perfect accuracy, an assumption that is not realistic. Information may be missing or misreported for individual outcomes, network data, or both, a phenomenon that may lead to bias or low power in estimating the treatment effect. In addition, binary data is amenable to using other measures of treatment effect such as the log odds ratio, the analysis of which would require a suitable adjustment in the definition of the true treatment effect across all trials (Equation 15). Finally, we consider a restrictively simple epidemic process and treatment regime, an assumption that does not capture realistic dynamics of most epidemics.

Section III: Derivation of Epidemic Properties of the Degree-Corrected Stochastic Blockmodel

We have explored a range of challenges and remedies in the study of epidemic processes on networks. We have also determined how these effects depend on properties of each network and epidemic propagating on them. However, all of our examples so far assume that the network has a sufficient network structure to sustain an epidemic. When a network is not sufficient to sustain an epidemic, we may not expect network effects like those considered in Section I, and the remedies of Section II may not be needed. It is therefore important to know when this condition is met. In this section, we will examine a specific type of network model — the Degree-Corrected Stochastic Blockmodel, a generative model which allows nodes of the network to belong to blocks that differ in their degree distribution, as well as their mixing patterns with other blocks, each of which may be estimated from an empirical network. This model is valuable to investigate because it allows the flexibility to account for both block structure and a variety of degree distributions, both of which are observed in real networks. We will derive conditions for the existence of a giant component, as well as the size of an epidemic propagating on it. We will also find the proportion of the epidemic size contained in each block. Using these results, a researcher can assess whether a network with a given degree sequence and block structure can sustain an epidemic, as well as the extent of that epidemic for network nodes with a particular degree and block membership.

Introduction and Relevant Work

The study of networks, or network science, has become a very active research field in recent decades, and many exact and probabilistic results for networks have been derived. In addition to theoretical insight, the practical advantage of these results is to predict properties and behaviors of networks when data or simulations are not available. Paul Erdös and Alfréd Renyí proved the size of the giant component (largest connected subnetwork) for the random graph[20], in which edges are distributed randomly through the network. This work was expanded by Molloy and Reed[44] and later by Bèla Bollobas[64] to include random networks with arbitrary degree distributions. Mark Newman found several properties of the configuration model using probability generating functions[65]. Dimitris Achlioptas discussed the conditions for an extensive epidemic in the stochastic blockmodel using techniques developed for multi-type Galton-Watson branching processes[66]. However, many network properties such as the size of the giant component, have not been derived directly for the stochastic blockmodel, with or without correcting for degree. The existence of a giant component is particularly important, as it indicates that a substantial portion of the nodes in a network are connected to one another, which is a precondition for an epidemic to spread through the network, which we turn to next.

The SIR process is an epidemic compartmental model[24] that assumes that individuals are either susceptible to a disease (state S), infected and contagious (state I), or recovered with no chance of again changing state (state R). Scalia-Tomba derived the asymptotic final size distribution of a multitype SIR processes for fully-mixed populations[67]. Peter Neal derived a central limit theorem for the size of multitype SIR epidemics on random graphs[68]. Newman derived exact properties of an SIR epidemic propagating through networks with arbitrary degree distribution, again using generating functions[69]. In this Section, we apply this final approach to a more general network model to derive the size of the giant component and final size of an SIR epidemic propagating on this network.

Generative Specification for the Degree-Corrected Stochastic Blockmodel

The Degree-Corrected Stochastic Blockmodel (DegSBM) was first defined by Brian Karrer and Mark Newman[54]. They define the likelihood for the DegSBM using the observed degree sequence (see Equation 10), and show that community-detection methods that use this likelihood find block structure while

accounting for the observed degree sequence of the whole network. However, the likelihood in that paper only specifies the expected number of edges for each node, and generating new networks consistent with its likelihood yields a different expected degree distribution in expectation. In this section, we give a specification of the DegSBM that is written in a way that allows for the generation of new networks that are *consistent*, meaning that the empirical estimates of parameters from the generated network converge to the specified parameters in the limit of large networks. We then show a number of exact properties of the network in the infinite limit of large sizes, as well as infectious properties of infinite-time SIR process propagating on the network. We conclude by demonstrating that these theoretical properties match simulation studies of empirical networks.

We begin by describing our formulation of the DegSBM. As noted in Section II, a network[28] is a collection of individuals (*nodes*) as well as the pairwise connections between them. These relationships can be described using an *adjacency matrix* $\mathbf{A}_{n\times n} = \{0,1\}^{n\times n}$, where $A_{ij} = 1$ iff an edge exists between nodes i and j. Each node i has a *degree* $d_i = \sum_j A_{ij}$, the total number of edges in which node i is a member.

Assume that for any given number of nodes n, each node i belongs to block $k \in 1,...,K$ ($b_i = k$) according to a multinomial distribution Π with one draw and block probabilities $\{\pi_1,...,\pi_K\}^\top = \boldsymbol{\pi}$ with $\boldsymbol{\pi}^\top \mathbf{1} = 1$. The members of block k are assumed to share a common degree distribution belonging to X_k, an arbitrary non-negative integer-valued random variable. The Probability Generating Function[70] (PGF) for a distribution is defined as

$$g_{X_k}(t) := \mathbb{E}\left(t^{X_k}\right) \tag{21}$$

The PGF exhibits several useful properties. First, as the name suggests, we may use the function to generate the probabilities of each value of the random variable:

$$P_{X_k}(d) = P(X_k = d) = \frac{1}{d!}\left.\frac{\mathrm{d}^d g_{X_k}(t)}{\mathrm{d}t^d}\right|_{t=0} \tag{22}$$

PGFs also allow us to quickly derive the moments of the distribution:

$$\left.\frac{\mathrm{d}^r g_{X_k}(t)}{dt^r}\right|_{t=1} = \mathbb{E}\left(\frac{X_k!}{(X_k-r)!}\right) \tag{23}$$

This can be a major advantage, because moments are derived in terms of the derivatives of the PGF, rather than by integrating over functions of the probability mass function (PMF), which can be prohibitively difficult. Note that g_{X_k} also specifies the expected degree for nodes belonging to block k, $g'_{X_k}(0) = \mathbb{E}(X_k) := \langle d_k \rangle$. In this section, we assume that the PGF exists for each block, implying that each moment for each degree distribution exists. Let $\boldsymbol{g}(t) := [g_{X_1}(t), ..., g_{X_K}(t)]$ be the vector of PGFs for each block k.

With classes and class degrees defined, it remains to specify how the probabilities of edges depend on block membership. For node i with block membership $b_i = k$ and degree $d_{(i)} \sim X_k$, the membership of each node with which node i shares an edge is again a multinomial distribution with $d_{(i)}$ draws and block membership probabilities $\Theta_{k\cdot} := \{\theta_{k1}, ..., \theta_{kK}\}$ subject to $\Theta_{k\cdot}\mathbf{1} = 1$. The edge mixing probabilities for nodes of all block memberships can be compactly written as a matrix $\Theta_{K\times K} := \{\Theta_{1\cdot}^\top, ..., \Theta_{K\cdot}^\top\}^\top$, subject to $\Theta\mathbf{1} = \mathbf{1}$. We also define the expected number of edges between any member of block k to members of block l, $\langle d_{kl} \rangle := \langle d_k \rangle \Theta_{kl}$. Therefore, the expected total number of edges with one node in block k and another in block l is $m_{kl} := n\pi_k \langle d_k \rangle \Theta_{kl}$. Because this relationship is symmetric, the DegSBM requires one final constraint that $m_{kl} = m_{lk}$ for all block pairs k, l.

Having defined all necessary parameters for our specification of the DegSBM, we now describe how to sample a network consistent with these parameters. To ensure that block memberships, edge counts by block pair, and degree distributions are correctly represented by $\boldsymbol{\pi}$, Θ, and $\boldsymbol{g}$ respectively, consider the following sampling scheme. First, for nodes $i = 1, ..., n$, sample node memberships $b_i = 1, ..., K$ such that $[n\pi_k]$ nodes belong to each block (where $[\cdot]$ indicates rounding to the nearest integer). Then, for each node i, sample its degree according to the random variable X_{b_i} specified by PGF $g_{X_k}(t)$, subject to the constraint that the sum of each blocks' total degree sums to $[n\langle d_k \rangle]$. The degree of each node can be thought of as a stub, or edge end whose destination node has not yet been defined. Then, for each block pair $1 \leq k \leq l \leq K$, select $[m_{kl}]$ stubs in each block (or twice this number if $k = l$), select two stubs (one from each block) at random, and connect them.

Together, $\boldsymbol{\pi}$, Θ, and $\boldsymbol{g}(t)$ specify the probabilistic version of the DegSBM. For intuition, the model may be viewed as a composition of configuration models within each block, summed with random bipar-

tite networks between each block, where members of either block share the degree distribution of the block's configuration portion. A schematic example of a DegSBM network is shown in Figure 18.

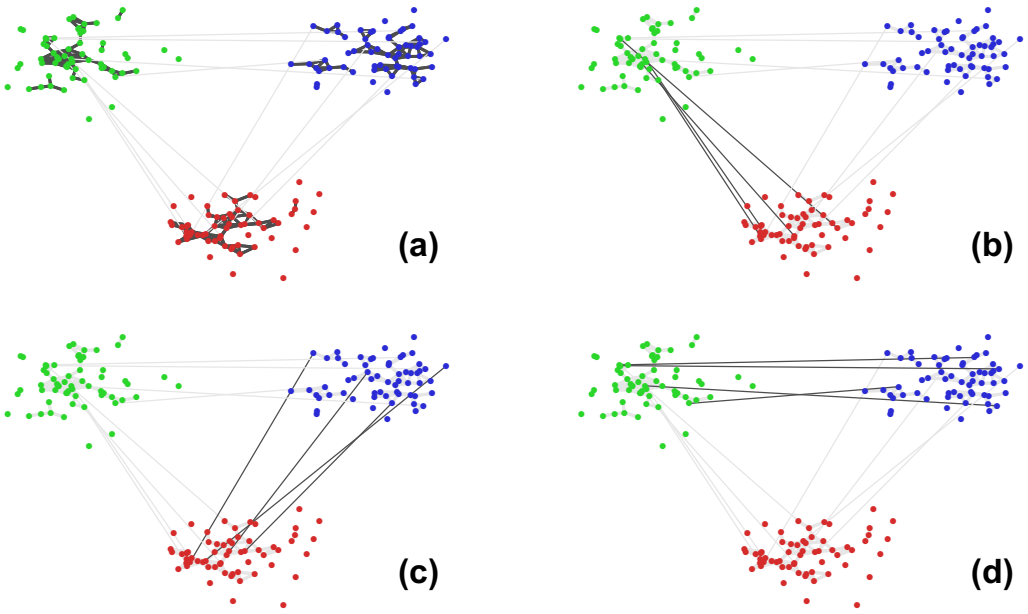

Figure 18: A schematic for the Degree-Corrected Stochastic Blockmodel. In this diagram, the model is shown as a mixture of K configuration models (subplot **a**) and $\binom{K}{2}$ random bipartite networks (subplots **b** $-$ **d**).

Derivation of Network Properties

In this section, we show the derivation of several properties of the DegSBM, including the number of self-edges and multiedges, the clustering coefficient, the number of second neighbors for members of each block, the size of the giant component, and the final epidemic size of an SIR epidemic process. We also find the proportion of nodes belonging to each block in the giant component, or recovered nodes at the end of an SIR process. We use techniques and definitions similar to those found in Newman[28], as well as papers by Newman, Strogatz and Watts[65,69].

Number of Self-Edges and Multi-Edges

We begin by finding the number of Self-Edges and Multi-Edges for the DegSBM. In particular, we show that these values are negligible for large n.

A *self-edge* is an edge between a node and itself. Because edges residing within each block are selected at random, this probability is the inverse of the number of edges within the block. The expected number of edges for all individuals in block k is $n\pi_k\langle d_k\rangle$, of which Θ_{kk} remain within that block. Consider that node i with $d_{(i)}$ edges remaining within its block may connect to itself $\binom{d_{(i)}}{2} = \frac{d_{(i)}(d_{(i)}-1)}{2}$ different ways, where $\mathbb{E}\left[\binom{d_{(i)}}{2}\right] = \frac{\langle d_{kk}^2\rangle - \langle d_{kk}\rangle}{2}$. For all K blocks and $n\pi_k$ nodes within each block, the total number of expected self-edges is

$$\sum_{k=1}^{K} \frac{n\pi_k\left[\langle d_{kk}^2\rangle - \langle d_{kk}\rangle\right]}{2m_{kk}} = \sum_{k=1}^{K} \frac{\langle d_{kk}^2\rangle - \langle d_{kk}\rangle}{2\langle d_{kk}\rangle} \cdot \mathbb{I}\left(\Theta_{kk} > 0\right) \tag{24}$$

Because this value does not depend on n and the expected number of edges in the graph is $\frac{n}{2}\sum_{i=1}^{K}\pi_k\langle d_k\rangle = \mathcal{O}(n)$, the ratio of self-edges tend to zero as $n \to \infty$.

Similarly, a *multi-edge* is an additional edge between two nodes that already share an edge. Let nodes i and j belong to blocks k and l, with degrees $d_{(i)}$ and $d_{(j)}$, respectively. There are $d_{(i)} \times d_{(i)}$ ways this can occur. With a total expected number of m_{kl} edges existing between blocks k and l, the probability that i and j share an edge is therefore $\frac{d_{(i)}d_{(j)}}{m_{kl}}$. The probability that nodes i and j share at least two edges follows similarly: given they are already connected, $d_{(i)} - 1$ and $d_{(j)} - 1$ edges from node i and j remain respectively, so the probability of another edge is $\frac{(d_{(i)}-1)(d_{(j)}-1)}{m_{kl}-1}$. The total probability of a multiedge between nodes i and j is therefore

$$\frac{d_{(i)}d_{(j)}}{m_{kl}} \frac{(d_{(i)}-1)(d_{(j)}-1)}{m_{kl}-1} \tag{25}$$

For $i \neq j$, $\mathbb{E}(d_{(i)}d_{(j)}) = \mathbb{E}(d_{(i)})\mathbb{E}(d_{(j)}) = \langle d_{b_j b_i}\rangle$, and the expected probability of a multiedge between nodes i and j is therefore

$$\frac{\left[\langle d_{kl}^2\rangle - \langle d_{kl}\rangle\right]\left[\langle d_{lk}^2\rangle - \langle d_{lk}\rangle\right]}{m_{kl}(m_{kl}-1)} \tag{26}$$

Recall that there are $n\pi_k$ and $n\pi_l$ expected number of nodes in blocks k and l, respectively. Summing the probability of a multiedge for all nodes per block and for all unique pairs of blocks k and l (and dividing by 2 to avoid double-counting), the total expected number of multiedges is

$$\sum_{k=1}^{K}\sum_{l=k}^{K}\frac{n^2\pi_k\pi_l\left[\langle d_{kl}^2\rangle-\langle d_{kl}\rangle\right]\left[\langle d_{lk}^2\rangle-\langle d_{lk}\rangle\right]}{2m_{kl}(m_{kl}-1)} \tag{27}$$

$$\xrightarrow[n\to\infty]{}\sum_{k=1}^{K}\sum_{l=k}^{K}\frac{\pi_k\pi_l}{2\pi_k\langle d_{kl}\rangle(\pi_l\langle d_{lk}\rangle)}\left[\langle d_{kl}^2\rangle-\langle d_{kl}\rangle\right]\left[\langle d_{lk}^2\rangle-\langle d_{lk}\rangle\right] \tag{28}$$

$$=\sum_{k=1}^{K}\sum_{l=k}^{K}\frac{1}{2}\left(\frac{\langle d_k^2\rangle}{\langle d_k\rangle}-1\right)\left(\frac{\langle d_l^2\rangle}{\langle d_l\rangle}-1\right)\cdot 1\left(\Theta_{lk}>0\right) \tag{29}$$

Note again that this term is or order $\mathcal{O}(1)$, whereas the total number of edges in the DegSBM is $\mathcal{O}(n)$, making this term negligible as the network size tends to infinity.

Clustering Coefficient

Next, we find the clustering coefficient for the DegSBM. There are several ways to define the clustering coefficient for a network. In this section, we use a commonly-used definition: the probability that any two nodes i and j having at least one common neighbor also share an edge directly, meaning an edge exists between them. The probability that nodes i and j connected to common node c share a direct edge depends on their degrees. However, the degree distribution of a node selected by randomly selecting the node at either end of a randomly selected edge is not the same as the probability specified by the degree distribution of each node. We first describe the *excess degree distribution* for nodes i and j, and then find the probability that they are directly connected to one another.

The probability that a node selected at random within block k has degree d is $P_{X_k}(d)$. In contrast, if you select an edge at random with at least one stub belonging to block k, that stub will belong to a node with degree e proportional to $e \times P_{X_k}(e)$, since there are e edges or e ways to choose that node by randomly selecting an edge with a node in block k. Similarly, the probability that this node has degree in excess of e edges is $(e+1)P_{X_k}(e+1)$. The probability of the excess degree distribution X_k^* is therefore

$$P_{X_k^*}(e) = \frac{(e+1)P_{X_k}(e+1)}{\sum_{d=0}^{\infty}(e+1)P_{X_k}(e+1)} \tag{30}$$

$$= \frac{(e+1)P_{X_k}(e+1)}{\sum_{d=1}^{\infty}(e)P_{X_k}(e)} \tag{31}$$

$$= \frac{(e+1)P_{X_k}(e+1)}{\sum_{d=0}^{\infty}(e)P_{X_k}(e)} \tag{32}$$

$$= \frac{(e+1)P_{X_k}(e+1)}{\langle d_k \rangle} \tag{33}$$

Note that Equation holds because the first term in the sum is $0 \cdot P_{X_k}(0) = 0$.

Given that nodes i and j belong to blocks k and l respectively and share common neighbor c, the probability that they share a direct edge, *i.e.* are connected to one another, is $\frac{(d_{(i)}-1)\Theta_{kl}(d_{(j)}-1)}{m_{kl}} = \frac{(d_{(i)}-1)(d_{(j)}-1)}{n\pi_k\langle d_k \rangle}$. The probability that nodes i and j have their respective excess degrees is $P_{X_k^*}(d_{(i)}-1)$ and $P_{X_l^*}(d_{(j)}-1)$, respectively. Thus, given they share a common neighbor, the total probability of members of block k and block l sharing a direct edge is

$$\sum_{d_{(i)}=1}^{\infty}\sum_{d_{(j)}=1}^{\infty} P_{X_k^*}(d_{(i)}-1)P_{X_l^*}(d_{(j)}-1)\frac{(d_{(i)}-1)(d_{(j)}-1)}{n\pi_k\langle d_k \rangle} \tag{34}$$

$$= \sum_{d_{(i)}=0}^{\infty}\sum_{d_{(j)}=0}^{\infty} P_{X_k^*}(d_{(i)})P_{X_l^*}(d_{(j)})\frac{d_{(i)}d_{(j)}}{n\pi_k\langle d_k \rangle} \tag{35}$$

$$= \frac{1}{n\pi_k\langle d_k \rangle}\sum_{d_{(i)}=0}^{\infty} P_{X_k^*}(d_{(i)})d_{(i)}\sum_{d_{(j)}=0}^{\infty} P_{X_l^*}(d_{(j)})d_{(j)} \tag{36}$$

$$= \frac{1}{n\pi_k\langle d_k \rangle}\left[\sum_{d_{(i)}=0}^{\infty}\frac{(d_{(i)}+1)P_{X_k}(d_{(i)}+1)}{\langle d_k \rangle}d_{(i)}\right]\left[\sum_{d_{(j)}=0}^{\infty}\frac{(d_{(j)}+1)P_{X_l}(d_{(j)}+1)}{\langle d_l \rangle}d_{(j)}\right] \tag{37}$$

$$= \frac{1}{n\pi_k\langle d_k \rangle\langle d_k \rangle\langle d_l \rangle}\left[\sum_{d_{(i)}=0}^{\infty} d_{(i)}(d_{(i)}-1)P_{X_k}(d_{(i)})\right]\left[\sum_{d_{(j)}=0}^{\infty} d_{(j)}(d_{(j)}-1)P_{X_l}d_{(j)}\right] \tag{38}$$

$$= \frac{\left[\langle d_k^2 \rangle - \langle d_k \rangle\right]\left[\langle d_l^2 \rangle - \langle d_l \rangle\right]}{n\pi_k\langle d_k \rangle^2\langle d_l \rangle} \tag{39}$$

Finally, the probabilities that nodes i and j belong to blocks k and l , and the probability that node c is in block m, is π_k. Putting these together, the clustering coefficient for the whole network is:

$$\sum_{m=1}^{K}\sum_{k=1}^{K}\sum_{l=1}^{K}\frac{\pi_m\theta_{mk}\theta_{ml}}{n\pi_k\pi_l}\frac{\left[\langle d_k^2\rangle-\langle d_k\rangle\right]\left[\langle d_l^2\rangle-\langle d_l\rangle\right]}{\langle d_k\rangle^2\langle d_l\rangle} \tag{40}$$

Because this term is $\mathcal{O}\left(\frac{1}{n}\right)$, the clustering coefficient vanishes for large n for the DegSBM. This may seem like a surprising result: the purpose using block structure is to allow for network structures that are *mesoscopic*, (medium-sized), which is often assumed to include clustering as we have defined it, but does not exist in the limit of large DegSBM networks. However, when $\Theta \to \text{diag}_K(1)$, nodes can be made to connect only to members of their own block, which is one way to conceptualize network community structure, an example of a mesoscopic structure that the DegSBM may exhibit.

Number of Second Neighbors

In this section, we derive the distribution for the number of *second neighbors* for nodes in block k. A second neighbor of *parent node* i is a neighbor k of a node j with whom i shares an edge, provided nodes i and k do not also share a direct edge. Simply described, the distribution of second neighbors is the distribution of the number of first neighbors of nodes who are themselves first neighbors of a node. The distribution of neighbors' degrees depends both on the block membership of node i, as well as the block membership of their first neighbors. We proceed by using PGFs to describe the distribution of excess degree conditional on the block membership of each neighbor of the parent node, and find the marginal distribution over this profile.

First, we describe the probability generating function of the excess degree distribution. For node i in block k, the PGF for the excess degree of node depends on the block membership of the node reached by selecting a random edge. Given the node membership of this node is block l, the PGF of excess degree is:

$$g_{X_l^*}(t) = \frac{\sum_{d=0}^{\infty}(d+1)P_{X_l}(d+1)t^d}{\sum_{d=0}^{\infty}(d+1)P_{X_l}(d+1)} \tag{41}$$

$$= \frac{\sum_{d=1}^{\infty} dP_{X_l}(d)t^{d-1}}{\sum_{d=1}^{\infty} dP_{X_l}(d)} \tag{42}$$

$$= \frac{\sum_{d=0}^{\infty} dP_{X_l}(d)t^{d-1}}{\sum_{d=0}^{\infty} dP_{X_l}(d)} \tag{43}$$

$$= \frac{g'_{X_l}(t)}{\mathbb{E}(X_l)} \tag{44}$$

$$= \frac{g'_{X_l}(t)}{g'_l(1)} \tag{45}$$

Given node i is in block k, the probability that each of its neighbors have membership l is Θ_{kl}. The unconditional PGF for excess degree is:

$$g_{X_{k;1}}(t) = \mathbb{E}_l\left[g_{X_l^*}(t)\right] \tag{46}$$

$$= \sum_{l=1}^{K} \Theta_{kl} \cdot g_{X_l^*}(t) \tag{47}$$

$$= \sum_{l=1}^{K} \Theta_{kl} \frac{g'_{X_l}(t)}{g'_{X_l}(1)} \tag{48}$$

$$= \Theta_{k\cdot}^{\top}\left[\frac{\boldsymbol{g}'(t)}{\boldsymbol{g}'(1)}\right] \tag{49}$$

We use the sum of excess degrees to second neighbor PGF, which requires we derive the PGF of the sum of independent draws from a distribution. Consider the distribution of the sum of D draws from an arbitrary random variable X:

$$g_{\sum_{d=1}^{D} X}(t) = \mathbb{E}\left[t^{\sum_{d=1}^{D} X}\right] \tag{50}$$

$$= \mathbb{E}\left[\prod_{d=1}^{D} t^{X}\right] \tag{51}$$

$$= \prod_{d=1}^{D} \mathbb{E}\left[t^{X}\right] \tag{52}$$

$$= \left(\mathbb{E}\left[t^{X}\right]\right)^{D} \tag{53}$$

$$= g_{X}^{D}(t) \tag{54}$$

This mathematical convenience is a known property of PGFs, sometimes called the "power property"[70]. Let's consider a parent node i belonging to block k, which shares $d^{(l)}$ edges with members of block $l = 1,...,K$, summing to d edges total. The PGF for the degree of each node connected to node i is distributed according to PGF $g_{x_l;1}(t)$. Because the block membership of each neighbor is independent, their sum has PGF $g_{X_l;1}^{d^{(l)}}(t)$. Adding across all blocks, the PGF for second nearest neighbors of node i conditional on their edge profile $\boldsymbol{d} := d^{(1)},...,d^{(K)}$ is

$$g_{X_k;2}(t|\boldsymbol{d}) = \prod_{l=1}^{K} g_{X_l;1}^{d^{(l)}}(t) \tag{55}$$

For the DegSBM, each block membership of each neighbor of a node belonging to block k is identically and independently distributed according to a multinomial distribution with probabilities $\Theta_{k\cdot}$, with PMF

$$P_{\Pi}(\boldsymbol{d}) \frac{\left(\sum_{l=1}^{K} d^{(l)}\right)!}{\prod_{l=1}^{K} d^{(l)}!} \prod_{l=1}^{K} \left[\Theta_{kl}^{d^{(l)}}\right] \tag{56}$$

By the law of iterated expectation, the PGF for second neighbors for node i in block k with d total neighbors is

$$g_{X_k;2}(t|d) = \sum_{\boldsymbol{d}:\boldsymbol{d}^\top \mathbf{1}=d} \left\{ \left[P_\Pi(\boldsymbol{d}) \frac{\left(\sum_{l=1}^K d^{(l)}\right)!}{\prod_{l=1}^K d^{(l)}!} \prod_{l=1}^K \left[\Theta_{kl}^{d^{(l)}}\right] \right] \prod_{l=1}^K g_{X_l;1}^{d^{(l)}}(t) \right\} \tag{57}$$

$$\tag{58}$$

While exact, this does not appear to simplify any further, and marginalizing over the distribution of first edges X_k does not appear useful. We may alternatively consider marginalizing over degree directly. Consider the expected number of d neighbors belonging to block $l = 1, ..., K$. The PGF of the *expected* excess degree is $g_{X_k;1}(t)$. Summing over each block, the PGF of for the second nearest neighbors for a node in block k with degree d is

$$g_{X_k;2}(t|d) = g_{X_k;1}(t)^d \tag{59}$$

Finally, let's write for the PMF as $P_{X_k;2(e|d)}$ be the probability of having e second neighbors given d first neighbors, corresponding to PGF $g_{X_k;2}(t|d)$. The probability of node i in block k having degree d has probability $P_{X_k}(d)$, so the PGF of second neighbors for node i is

$$\begin{aligned}
g_{x_k;2}(t) &= \sum_{e=0}^{\infty} P_{X_k;2}(e) t^e && (60)\\
&= \sum_{e=0}^{\infty} \sum_{d=0}^{\infty} P_{X_k}(d) P_{X_k;2}(e|d)\ t^e && (61)\\
&= \sum_{d=0}^{\infty} P_{X_k}(d) \underbrace{\sum_{e=0}^{\infty} P_{X_k;2}(e|d)\ t^e}_{g_{X_k;2}(t|d)} && (62)\\
&= \sum_{d=0}^{\infty} P_{X_k}(d) g_{X_k;1}(t)^d && (63)\\
&= \boxed{g_{X_k}\left(g_{X_k;1}(t)\right)} && (64)
\end{aligned}$$

With this in hand, we may calculate the average number of second neighbors for nodes in block k as $\frac{dg_{X_k;2}(t)}{dt} = g'_{X_k}\left(g_{X_k;1}(t)\right) \cdot g'_{X_k;1}(t)$. Evaluating each part of this expression:

$$g_{X_k}(1) = 1 \tag{65}$$

$$g'_{X_k}(1) = \langle d_k \rangle \tag{66}$$

$$g_{X_k;1}(1) = \Theta_{k\cdot}^{\top} \left[\frac{\boldsymbol{g}'(1)}{\boldsymbol{g}'(1)} \right] = \Theta_{k\cdot}^{\top} \mathbf{1} = 1 \tag{67}$$

$$g'_{X_k;1}(1) = \Theta_{k\cdot}^{\top} \left[\frac{\boldsymbol{g}'(t)}{\boldsymbol{g}'(1)} \right]' \Bigg|_{t=1} \tag{68}$$

$$= \sum_{l=1}^{K} \frac{\Theta_{kl}}{\langle d_l \rangle} g''_{X_l}(1) \tag{69}$$

$$= \sum_{l=1}^{K} \frac{\Theta_{kl}}{\langle d_l \rangle} \mathbb{E}\left(d_l^2 - d_l \right) \tag{70}$$

$$= \sum_{l=1}^{K} \frac{\Theta_{kl}}{\langle d_l \rangle} \left(\langle d_l^2 \rangle - \langle d_l \rangle \right) \tag{71}$$

$$= \sum_{l=1}^{K} \Theta_{kl} \left(\frac{\langle d_l^2 \rangle}{\langle d_l \rangle} - 1 \right) \tag{72}$$

$$= \left(\sum_{l=1}^{K} \Theta_{kl} \frac{\langle d_l^2 \rangle}{\langle d_l \rangle} \right) - 1 \tag{73}$$

Putting these together, we obtain the mean number of second neighbors for members of block k:

$$\frac{d g_{X_k;2}(t)}{dt}\Big|_{t=1} = \boxed{\langle d_k \rangle \left[\left(\sum_{l=1}^{K} \Theta_{kl} \frac{\langle d_l^2 \rangle}{\langle d_l \rangle} \right) - 1 \right]}$$

It is possible to consider further network neighbors[n2], but unfortunately this does not appear to simplify as neatly.

Degree Distribution With Block Members

To find the size of the giant component in the DegSBM, we consider the degree distribution for connected components of members belonging to each block k, and sum across all blocks. Consider two nodes i and j in block k. If they are members of the same component, a path exists between the two. This may occur in several ways. One obvious route is to share an edge directly. Another is for both nodes to share a common neighbor c in block l (where l may equal k). More circuitous paths may exist,

but for analytical tractability we only consider these two routes. If we assume the former is a special case of the latter[n2], the number of edges shared by members of block k through a connecting node in block l is generated by the degree distribution of edges in block pair (k,l), and the degree distribution of a node reached by randomly selecting an edge emanating from block k. Using the same arguments for the number of second neighbors and summing over each block l, this is distributed according to the PGF:

$$G_{X_k}(t) = g_{X_k}\left(\sum_{l=1}^{K}\Theta_{kl}\frac{g'_{X_l}(t)}{g'_{X_l}(1)}\right) \tag{74}$$

$$= g_{X_k}\left(\Theta_{k\cdot}^{\top}\boldsymbol{g}'_{\cdot 1}(t)\right) \tag{75}$$

$$= \boxed{g_{X_k}\left(g_{X_k;1}(t)\right)} \tag{76}$$

Similarly, we may describe the degree distribution for a connected block being reach by selecting an edge at random among the nodes belonging to members of block k:

$$G_{X_k;1}(t) = \sum_{l=1}^{K}\Theta_{kl}\frac{g'_{X_l}\left(\sum_{m=1}^{K}\Theta_{lm}g'_{X_l}\left(\frac{g'_{X_m}(t)}{g_{X_m}(1)}\right)\right)}{g'_{X_l}(1)} \tag{77}$$

$$= \sum_{l=1}^{K}\Theta_{kl}\frac{g'_{X_l}\left(\frac{\Theta_{l\cdot}^{\top}g_{\cdot 1(t)}}{g_{X_l}(t)}\right)}{g'_{X_l}(1)} \tag{78}$$

$$= \sum_{l=1}^{K}\Theta_{kl}\left(\frac{g'_{X_l}(g_{X_l;1}(t))}{g'_{X_l}(1)}\right) \tag{79}$$

$$= \boxed{\Theta_{k\cdot}^{\top}\left[\frac{\boldsymbol{g}'(\boldsymbol{g}_{\cdot 1}(t))}{\boldsymbol{g}'(1)}\right]} \tag{80}$$

In the following section, we describe how to use these PGFs to find the distribution of finite component sizes and the size of the giant component.

Finite Component Size Distribution

Consider the distribution of sizes of components that are reached by randomly selected member of block k. Let $h_0^{(k)}(t) = \sum_{s=0}^{\infty} \sigma_s^{(k)} t^s$ be the PGF for this distribution for each block k. Similarly, let $h_1^{(k)}(t) = \sum_{s=0}^{\infty} \rho_s^{(k)} t^s$ be the PGF for the distribution of sizes of components found when following an edge selected at random with one of its nodes (also selected at random) belonging to block k. We find these probabilities by first considering the degree of the removed node, and integrate over all degrees. Let $P^c_{X_k}$ and $P^c_{X_k;1}$ be the degree distributions corresponding to PGFs G_{X_k} and $G_{X_k;1}$ from the previous section. Additionally, let $P^{(k)}(s|d)$ represent the probability that node i belonging to block k and component size of s (excluding itself) has degree d. Then:

$$\sigma_s^{(k)} = \sum_{d=0}^{\infty} P^c_{X_k}(d) P^{(k)}(s-1|d) \tag{81}$$

Substituting this into $h_0^{(k)}$, we obtain

$$\begin{aligned}
h_0^{(k)}(t) &= \sum_{s=1}^{\infty} \sum_{d=0}^{\infty} P^c_{X_k}(d) P^{(k)}(s-1|d) t^s && (82)\\
&= t \sum_{d=0}^{\infty} P^c_{X_k}(d) \sum_{s=1}^{\infty} P^{(k)}(s-1|d) t^{s-1} && (83)\\
&= t \sum_{d=0}^{\infty} P^c_{X_k}(d) \underbrace{\sum_{s=0}^{\infty} P^{(k)}(s|d) t^s}_{\left[h_1^{(k)}(t)\right]^d} && (84)\\
&= \boxed{t G_{X_k}(h_1^{(k)}(t))} && (85)
\end{aligned}$$

The final sum follows because $P^{(k)}(s|d)$ describes probability of the component size found by following a random member of block k, which may occur d independent ways, and recalling the "power property" of PGFs, this sum yields a multiplication for its PGF, as described in the previous section. Similarly, we may find the probability of finding a component of size s after the removal of node i belonging to block k with degree d:

$$\rho_s^{(k)} = \sum_{d=0}^{\infty} P^c_{X_k;1}(d) P(s-1|d) \tag{86}$$

Substituting into $h_1^{(k)}$, we obtain:

$$\begin{aligned}
h_1^{(k)}(t) &= \sum_{s=1}^{\infty} \sum_{d=0}^{\infty} P^c_{X_k;1}(d) P^{(k)}(s-1|d) t^s && (87)\\
&= t \sum_{d=0}^{\infty} P^c_{X_k;1}(d) \sum_{s=1}^{\infty} P^{(k)}(s-1|d) t^{s-1} && (88)\\
&= t \sum_{d=0}^{\infty} P^c_{X_k;1}(d) \underbrace{\sum_{s=0}^{\infty} P^{(k)}(s|d) t^s}_{\left[h_1^{(k)}(t)\right]^d} && (89)\\
&= \boxed{t G_{X_k;1}(h_1^{(k)}(t))} && (90)
\end{aligned}$$

We may therefore evaluate $h_0^{(k)}(t)$ by first finding $u^{(k)}(t)$ such that $u^{(k)}(t) = tG_{X_k;1}(u^{(k)}(t))$, substitute these function into $h_0(t)$, and take its derivatives to find the fraction of nodes belonging to components of size s. However, because $h_0(t)$ is not evaluated directly, taking its explicit derivatives is prohibitive.

Size of the Giant Component

Note that $\sum_{s=0}^{\infty} \sigma_s^{(k)}$ need not sum to 1 for any k. Failure to sum to 1 occurs only if there is a component that is a substantial (non-zero) fraction of the total number of nodes n as $n \to \infty$, called a *giant component* S. This component must therefore have the size described by the remainder of nodes after each finite component is considered. This can be found for each block k, and summed across each block:

$$S = 1 - \sum_{k=1}^{K} \pi_k \sum_{s=0}^{\infty} \sigma_s^{(k)} \tag{91}$$

$$= 1 - \sum_{k=1}^{K} \pi_k h_0^{(k)}(1) \tag{92}$$

$$= 1 - \sum_{k=1}^{K} \pi_k G_{X_k}(h_1^{(k)}(1)) \tag{93}$$

We may thus find the size of the giant component by solving:

$$S = 1 - \sum_{k=1}^{K} \pi_k G_{X_k}(u^k) \tag{94}$$

$$\forall k \big(u^{(k)} = G_{X_k}(u^{(k)}) \big) \tag{95}$$

This may be written compactly:

$$\boldsymbol{u} = \boxed{\boldsymbol{G}_{\cdot 1}(\boldsymbol{u})} \tag{96}$$

$$S = \boxed{1 - \boldsymbol{\pi}^\top \boldsymbol{G}(\boldsymbol{u})} \tag{97}$$

Note that this also yields a formulation for the fraction of nodes in the giant component and also a member of block k:

$$1 - \boldsymbol{\pi}^\top \boldsymbol{G}(\boldsymbol{u}) = \boldsymbol{\pi}^\top [\mathbf{1} - \boldsymbol{G}(\boldsymbol{u})] \tag{98}$$

$$\Rightarrow S_k = \boxed{\pi_k \left(1 - G(u^{(k)}) \right)} \tag{99}$$

Infectious Spread

So far, we have considered how the full set of parameters specifying the DegSBM allow for probabilistic estimates of other properties, such as the number of multi-edges, self-edges, clustering coefficient, number of second neighbors, number of finite component sizes, and the size of the giant component. In this section, we extend the methods used previously in this section to find properties or epidemic processes occurring on the DegSBM. Specifically, we consider the properties of an infinite-time SIR process on the DegSBM in the limit of network size, most of which have analogs of the statistics we have already derived. Alternatively, it is also possible to study the finite-time behavior of compartmental epidemic network processes on networks[26], which we save for future work.

SIR Processes on Networks

An SIR process is a compartmental model[24] describing the spread of an infectious disease. The model specifies a number of individuals, and assumes that each has one of three infectious states: susceptible (S), infected and contagious (I), and recovered and no longer susceptible (R). Specifically, susceptible nodes in contact with infected neighbors may become infected themselves, and infectious nodes may recover (and lose susceptibility) at a fixed time in the future. The *fully-mixed* assumption states that each individual is equally likely to come in contact with any other. These conditions are the underpinnings of the Reed-Frost model[71], which simplifies the description of the infection to the proportion of individuals in each state compartment over time.

Epidemic processes on networks are different. A natural way to consider the role of a network in epidemics is as the specific contacts each node has, or could have, with other nodes. On this view, an SIR process on a network consists of a stochastic process, in which each node is one of three infectious states. At any time, a suspectable neighbor may be infected by an infected network node with probability β, and infected individuals may recover (independent of others' states) at any time with independent probability γ.

A classic way to proceed with this specification was first described by Denis Mollison[72] and Peter Grassberger[73]. Consider a single infected individual, who may infect some of their neighbors before recovering from the disease. The edges between the original node and the subset of its neighbors who are ultimately infected by it is a subset of the network. These newly-infected nodes go on to infect other

nodes, and the subset of edges along which the infection progresses together constitute an increasingly larger subset of the network. This is very similar to a percolation process[74,75], which we introduce next.

A percolation process considers a network or lattice, and assumes that *sites* (nodes) or *bonds* (edges) are "occupied" according to a set of rules. The simplest rule is a random selection for each entity. With these rules in place, does the lattice contain an unbroken path of occupied sites or bonds that spans the lattice? This and related questions are key research topics in percolation theory. Returning to SIR processes on networks, the lattice is a given DegSBM network, and the percolation process rule is the sequential infection and recovery of individual nodes, beginning with a single infected ("occupied") node. The result of this process is a subset of the network edges along which individuals have become infected, which may have properties like the ones we have already derived. In the next subsection, we will argue that the addition of a single term for transmissibility T allows us to then derive results for these properties for the final size of an edge percolation process on the DegSBM model, whose constituent nodes comprise those infected in an epidemic on these networks.

Transmissibility

Assume that the time to infection for the susceptible neighbor is a Poisson process[76] with rate β, and the probability of the infected individual recovering is also a Poisson process with a rate of recovery γ. If each individual in a population contacts all others with equal probability, this is called *mass action*, and epidemics with this property have been studied extensively, neatly reviewed by Anderson and May[24]. However, we may also consider contacts existing within a fixed network structure, which has been considered by Newman[69], whose treatment we will review for the remainder of this subsection.

Consider a susceptible individual j who is connected to only one infected individual i. We presently assume that the rate of transmission is the same for each node. If node j is exposed to infectious node i for a total period of time with length t_i, the probability of not being infected during a short moment of time with length dt is $1 - \beta \cdot dt$. It is often assumed that this process is continuous, wherefore simulations may use a discrete representation for time. Here we consider the continuous case. For Poisson processes, the probability of infection for each infinitesimal moment is independent. Thus, if the total probability of node i being infected for a period of susceptibility of length t_i is T_i, the total probability of no infection is

$$1 - T_i = (1 - \beta dt)^{t_i/dt} \tag{100}$$

$$\underset{dt \to 0}{\longrightarrow} T_i = 1 - e^{-\beta t_i} \tag{101}$$

For the recovery Poisson process, $t_i \overset{\text{iid}}{\sim} \exp(\gamma)$, so the average probability of infection between nodes i and j is

$$\langle T_i \rangle = \int_0^\infty \left[1 - e^{-\beta t}\right] \gamma e^{-\gamma t} dt \tag{102}$$

$$= \left[\int_0^\infty \gamma e^{-\gamma t} dt\right] - \left[\gamma e^{-(\gamma+\beta)t} dt\right] \tag{103}$$

$$= 1 - \frac{1}{1 + \beta\gamma^{-1}} \tag{104}$$

For use in simulations, we now turn to the discrete case, $dt_i = 1$. Here, β represents the probability of an infection at each time step, and γ represents the probability of recovery for an infected node at each time step. In this setting, the probability of not being infected is $1 - T_i = (1 - \beta)^{t_i}$, where $t_i \overset{\text{iid}}{\sim} \text{geo}(\gamma)$. Then:

$$\langle 1 - T_i \rangle = 1 - \langle T_i \rangle \tag{105}$$

$$= \sum_{t=1}^{\infty} \gamma (1 - \gamma)^t \cdot (1 - \beta)^t \tag{106}$$

$$= \gamma \sum_{t=1}^{\infty} \left[(1 - \gamma)(1 - \beta)\right]^t \tag{107}$$

$$= \frac{\gamma}{1 - (1 - \gamma)(1 - \beta)} \tag{108}$$

$$\langle T_i \rangle = 1 - \frac{1}{1 + \beta(\gamma^{-1} - 1)} \tag{109}$$

Note that for $\beta \to 0$ and $\beta\gamma^{-1} \to \lambda$, the discrete case converges to a Poisson process.

Consider that this average transmissibility is in fact the probability that any node (belonging to the

same compartment of the initial infected node) ever becomes infected. Then the probability of a node in block k with degree d having e infected neighbors is generated by the PGF

$$g_{X_k}(t;T) = \sum_{e=0}^{\infty}\sum_{d=0}^{\infty}\left[\binom{d}{e}T^e(1-T)^{d-e}\right]P_{X_k}(d)t^e \tag{110}$$

$$= \sum_{d=0}^{\infty}P_{X_k}(d)\sum_{d=0}^{d}\left[\binom{d}{e}T^e(1-T)^{d-e}\right]t^e \tag{111}$$

$$= \sum_{d=0}^{\infty}P_{X_k}(d)\left[\binom{d}{e}(Tt)^e(1-T)^{d-e}\right] \tag{112}$$

$$= \sum_{d=0}^{\infty}P_{X_k}(d)\left(1-T+Tt\right)^d \tag{113}$$

$$= \boxed{g_{X_k}(1+(t-1)\cdot T)} \tag{114}$$

This form for the PGF of infected nodes is very similar to the block-specific PGFs used to derive network statistics for the DegSBM. Indeed, in the special case that $T = 1$, bond percolation is guaranteed to proliferate throughout the network component, reducing to the results we have shown so far. In the general case $T \in [0,1]$, we may derive new statistics for the percolation subnetwork corresponding to the final size of an SIR epidemic. Let's consider these in turn.

Final Size of the Epidemic

We now apply the discussion of transmissibility and bond percolation to find the final epidemic size of the DegSBM. Just as before, we may define the PGF for infected nodes belonging to connected components of block k:

$$G_{X_k}(t;T) = G_{X_k}(1+(t-1)\cdot T) \tag{115}$$

$$G_{X_k;1}(t;T) = G_{X_k;1}(1+(t-1)\cdot T) \tag{116}$$

The arguments used before to derive the final size of the epidemic follow exactly as those for the giant component, yielding:

$$\boldsymbol{u} = \boldsymbol{G}_{\cdot 1}(\boldsymbol{u};\, T) \tag{117}$$

$$S = 1 - \boldsymbol{\pi}^{\top} \boldsymbol{G}(\boldsymbol{u};\, T) \tag{118}$$

Note that this also yields a formulation for the fraction of nodes in the giant component and also a member of block k:

$$1 - \boldsymbol{\pi}^{\top} \boldsymbol{G}(\boldsymbol{u};\, T) = \boldsymbol{\pi}^{\top} \left[\mathbf{1} - \boldsymbol{G}(\boldsymbol{u};\, T)\right] \tag{119}$$

$$\Rightarrow S_k = \boxed{\pi_k \left(1 - G(u^{(k)};\, T)\right)} \tag{120}$$

Node Risk of Infection

The quantity $u^{(k)}$ may be interpreted as the probability that the node in block k at the end of a randomly chosen edge in the network remains uninfected during an epidemic[69]. Therefore, the probability that the infection propagates along any given edge to a member of block k is $T \cdot (1 - u^{(k)})$. If this node also has degree d, the total probability that a node does not become infected through any of its edges is then $\left[1 - T \cdot (1 - u^{(k)})\right]^d$. We may therefore write the probability or risk of becoming infected $R_d^{(k)}$ for a given node with degree d in block k as:

$$\boxed{R_d^{(k)} = 1 - \left[1 - T \cdot \left(1 - u^{(k)}\right)\right]^d} \tag{121}$$

Results

In this section, we describe a simulation study to validate our results. For several specific choices using the full range of DegSBM parameters, we simulated 100 DegSBMs for each specification. We also carried out a single SIR infectious process on each one, beginning with a single infected node selected at random with transmissibility $T = 0.9$, and proceeded until no remaining nodes were infected (all had either recovered or were never infected). For each specification, we also varied a single parameter (usually the degree for some or all blocks), and plotted each statistic while varying this parameter. Although smaller networks also perform well, in each case we simulated networks of size $n = 48{,}000$.

In plots 19-73, we show several theoretical and simulated values for important statistics derived in this section. The first plot shows the average number of second neighbors for members of each block. That is, we show the average number of neighbors of the neighbors for members of each block k. We also plot the total *size of the giant component*, or the fraction of all nodes that belong to the giant component, ranging from $0 - 1$. In addition, we show the fraction of all nodes that belong to both the giant component as well as each block k, showing the relative contribution of members of each block to the giant component. Similarly, we show the final *epidemic size* of the single SIR process conducted on each simulation, which is the fraction of nodes that are recovered from being infected at the end of the infectious process. We also show the epidemic size for members of each block: that is, the fraction of nodes that are both members of block k as well as ever became infected throughout the SIR process. Because all infected individuals eventually recover, this fraction is the same and all those who are recovered by the end of the epidemic process.

Here, we discuss each of the figures. For all of the following, the theoretical value is shown as a line, and each dot shows a simulation. All results fit our theory well, with a few exceptions we will discuss in turn. We begin by discussing base cases. The configuration model is a network where only the degree distribution is specified, and edges are otherwise uncorrelated. Within our framework, this corresponds to a single mixing and allocation block, where $\boldsymbol{\pi}$ and Θ to 1. We consider a series of configuration models, for which each simulation increases in its mean degree. Figure 24 shows the average number of second neighbors for each node. Figure 25 shows the size of the giant component. We observe that a giant component only exists when the mean degree is greater than 1, and increases quickly thereafter. Figure 26 shows the fraction of nodes that belong to both the giant component and a particular block. (In the case of a single block, these are the same.) Figure 27 shows the final size of an SIR epidemic, or the fraction of nodes that were infected (and recovered, which all eventually do). This shows similar

behavior to that of Figure 21: only when the mean degree has reached a sufficient number of nodes does an epidemic of substantial size occur. Similarly, 28 shows the fraction of nodes that were both infected and belonged to each block, which in this case is the same.

Not all simulated infections lead to a significant fraction of infected nodes. Note that for the epidemic to spread through a non-zero fraction of the network, the single infected node must meet two conditions: first, it must be connected to a significant fraction of the network (that is, it must be a member of the giant component if one exists); second, it must successfully transmit the infection to at least some of its neighbors, who in turn transmit the disease (that is, the infection does not die out prematurely). Because we select a node at random, we expect the first condition to only be met with a probability equal to the size of the giant component, which we discussed above. The second condition is a function of transmissibility parameter T as well as the first infected node's specific degree, as well as some chance that the infection dies out by chance. While it would be possible to only keep simulations that meet these two conditions, we show these results to show the qualitative dichotomy of outcomes, as well as their frequency as a function of these conditions.

Figures 19-23 show an alternative specification for the configuration model: each of three blocks share the same degree distribution as well as expected degree, and the mixing structure is equal across all three blocks. These results show that using blocks that are similar to each other does not result in different behavior from the classic configuration model. However, we note that Figures 21 and 23 show that each block contributes an equal third of its nodes to form the giant component, as well as the final size of the epidemic.

Next, we show that the DegSBM is also able to recover similar results for the random bipartite network as well. Recall that a bipartite network is one in which each node belongs to exactly one of two groups, and edges only exist between members of opposite groups. This is easily represented as a two-block DegSBM, with mixing matrix values of 0 belonging to the diagonals. We show results for which one group is half the size of the other, but has twice the number of edges. Figure 29 shows that the two blocks (groups) have the same number of second neighbors. This may first seem surprising because the two have differing degree distributions. However, in the case of bipartite networks, each second neighbor is reached by first selecting a neighbor in the opposite group, who can in turn only be connected to a member of the second group, which remains true regardless of which is a symmetric relationship. Figure 30, show again that a giant component only occurs with a sufficient density of edges. However, Figure 31 shows that this giant component is not equally comprised of nodes belonging to both blocks, as one is larger than the other. This critical behavior and asymmetric contribution of each block is

similar in the final epidemic size, shown in Figures 32 and 33.

Turning to more exotic cases, we consider cases for which blocks are arranged to form distinct shapes using the mixing matrix. We first consider four blocks arranged to form a square. (That is, each block have edges with exactly two other blocks, and not themselves.) Figure 34 shows that the number of second neighbors remains equal for each. Figures 35 and 36 shows again that only a sufficient number of edges will cause a giant component to appear, and in this case each corner of the square contributes to the size of the giant component equally. This is also the case for the final epidemic size, shown in Figures 37 and 38. We also consider four blocks arranged in a tube, meaning two inner blocks are connected to exactly two other blocks (and not within either block), and two outer blocks are each connected only to one inner block. This results in non-equivalent values for the number of second neighbors (Figure 39) as well as contributions to the giant component and final epidemic size (Figures 41 and 43), respectively.

We next consider two cases in which half of the nodes have a fixed degree distribution and mean degree, and the other half of the nodes have a sequentially increasing expected degree, and consider what happens to the existence of a giant component and epidemic size (and the relative contributions of either block to these). In the first case, we hold the constant degree block to have an average degree of 1, which is the threshold for the existence of a giant component[20]. In this case, we see that the number of second neighbors increases for member of both blocks (Figure 44). We also observe that a giant component begins to exist when both blocks have degree greater than 1 (45), but that the non-constant block always contributes more to the giant component (Figure 46). We observe similar behavior for the final epidemic size (Figures 47 and 48). We also consider the case where the constant block has an insufficient degree distribution and mean degree to cause a giant component to exist. Again, Figure 49 shows that the number of second neighbors increases for both blocks. However, Figures 50 and 51 show that while nodes in the changing block are part of a giant component to an equal degree as those in Figure 46, the constant block only exhibits half the number of nodes to the giant component, decreasing its overall size (Figure 50) compared to Figure 45. This is also similar in Figures 52 and 53.

Next, we consider a large number of blocks, each with different mean degree, and very little mixing between them. In the limit, each of these blocks can be considered independence configuration models, but it is not known if a slight amount of mixing causes different behavior than treating them separately. Figure 54 shows that the number of second neighbors grows multiplicatively faster for each block according to their own mean degree. Figure 55 shows that for these parameter values, a giant component appears rapidly, but the contribution of each block (Figure 56) does not rise quickly from zero at the same time for all blocks. Although some mixing exists between each of the blocks, it is insufficient to

cause a significant number of nodes to be a part of the giant component unless that block itself has a sufficient number of edges to cause a giant component to appear of its own accord. We note that the simulation results for Figure 56 show an underestimation of the number of nodes in the giant component for the smallest block. This is due to our only considering two of the major ways nodes can be a part of a larger component, (discussed in the subsection *Degree Distribution With Block Members*). These patterns are also similar when considering the final epidemic size (see Figures 57 and 58).

What will happen if we hold the degree distribution and mean degree to be the same in the previous case, but increase the mixing somewhat among these blocks? Figure 59 shows substantially the same number of second neighbors for each block, although the blocks containing the fewest edges increase in the number of their second neighbors somewhat. Figures 60 and 57 also show similar behavior, albeit with more members overall belonging to the giant component and final epidemic size, respectively. In contrast, Figures 61 and 63 show that with a sufficient amount of mixing between the blocks, each block begins to significantly contribute to the giant component and final epidemic size (albeit differing amounts), even though some do not have a sufficient number of edges to create these of their own accord. This shows that connections with other blocks can significantly alter the epidemic behavior when either considering blocks alone, or as a single random block.

Finally, we show two examples of block structure designed to have no easy interpretation, besides shuffling each of the parameters in order to assess whether the in these cases. We shows these results for three blocks (Figures 64-68) and four blocks (Figures 69-73). In both cases, we still see a close fit for each statistic. This suggests that the simulation of most structures specifiable by the model fit our theoretical predictions well.

Configuration (One Block)

$$\boldsymbol{\pi} = [1]$$

$$\boldsymbol{g} = [\text{Poi}(a)]$$

$$\Theta = [1]$$

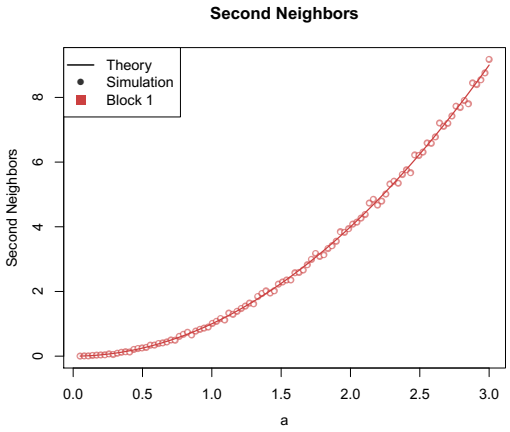

Figure 19: The number of second neighbors for members of each block, for a range of values a.

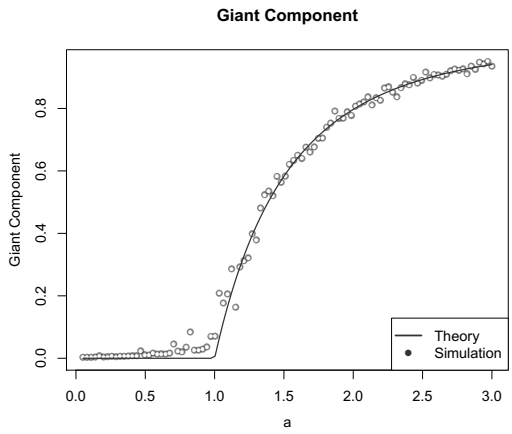

Figure 20: The size of the giant component for a range of values a.

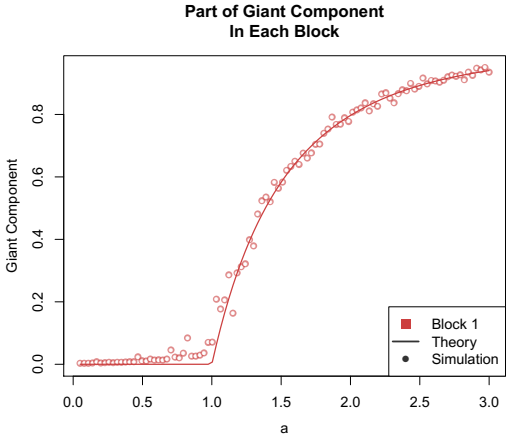

Figure 21: The fraction of members in a block and the giant component, for a range of values a.

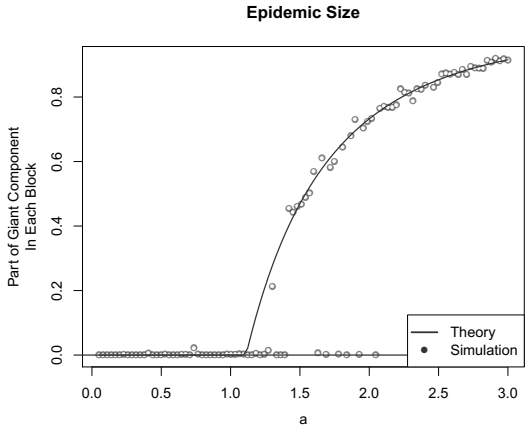

Figure 22: The size of an epidemic for a range of values a.

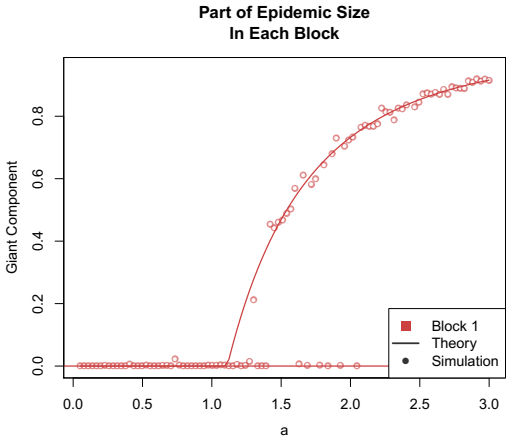

Figure 23: The fraction of members in a block and infected in the epidemic, for a range of values a.

Configuration (Many Blocks)

$$\boldsymbol{\pi} = \left[\frac{1}{3}, \frac{1}{3}, \frac{1}{3}\right]$$

$$\boldsymbol{g} = [\text{Poi}(a), \text{Poi}(a), \text{Poi}(a)]$$

$$\Theta = \begin{bmatrix} \frac{1}{3} & \frac{1}{3} & \frac{1}{3} \\ \frac{1}{3} & \frac{1}{3} & \frac{1}{3} \\ \frac{1}{3} & \frac{1}{3} & \frac{1}{3} \end{bmatrix}$$

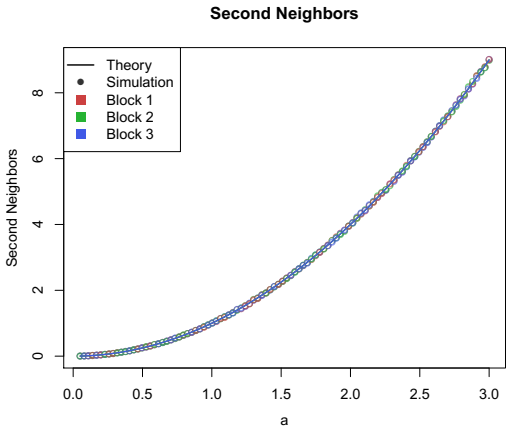

Figure 24: The number of second neighbors for members of each block, for a range of values a.

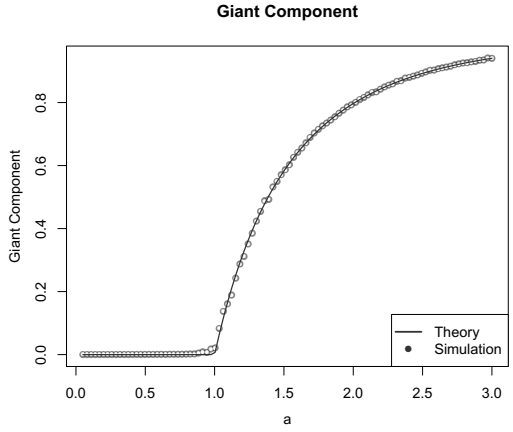

Figure 25: The size of the giant component for a range of values a.

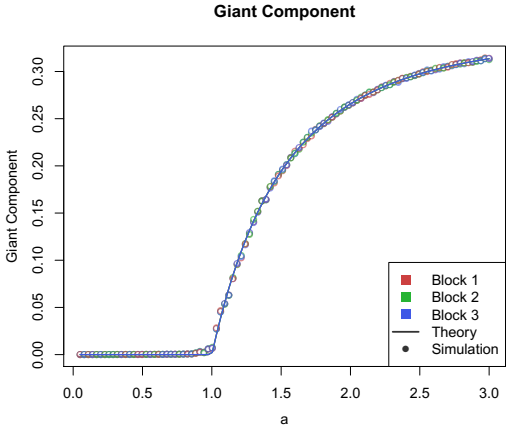

Figure 26: The fraction of members in a block and the giant component, for a range of values a.

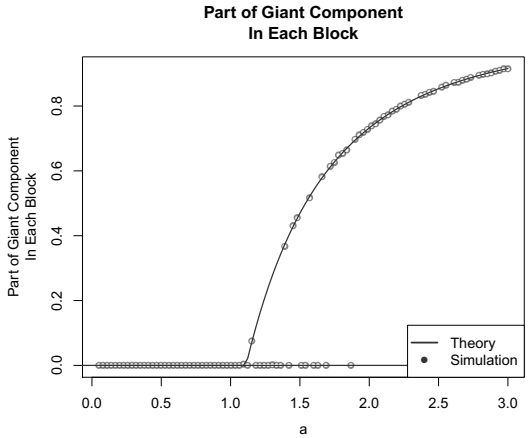

Figure 27: The size of an epidemic for a range of values a.

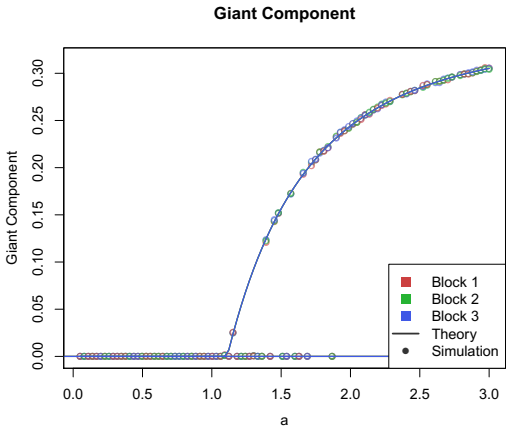

Figure 28: The fraction of members in a block and infected in the epidemic, for a range of values a.

Bipartite

$$a \in [0.05, 1.5]$$

$$\boldsymbol{\pi} = \left[\frac{1}{3}, \frac{2}{3}\right]$$

$$\boldsymbol{g} = [\text{Poi}(2a), \text{Poi}(a)]$$

$$\Theta = \begin{bmatrix} 0 & 1 \\ 1 & 0 \end{bmatrix}$$

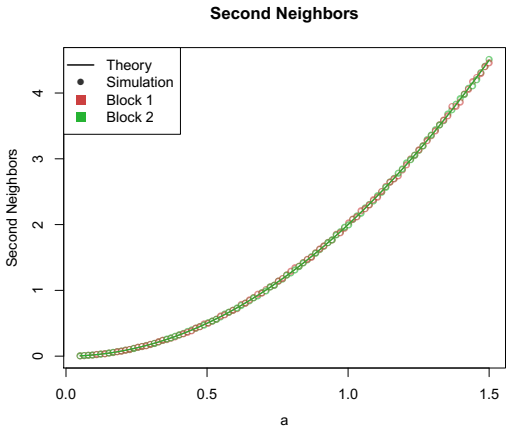

Figure 29: The number of second neighbors for members of each block, for a range of values a.

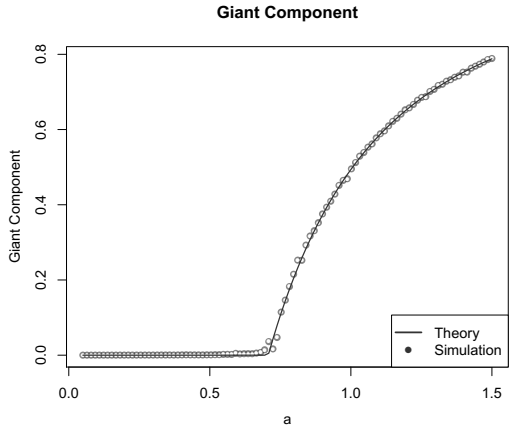

Figure 30: The size of the giant component for a range of values a.

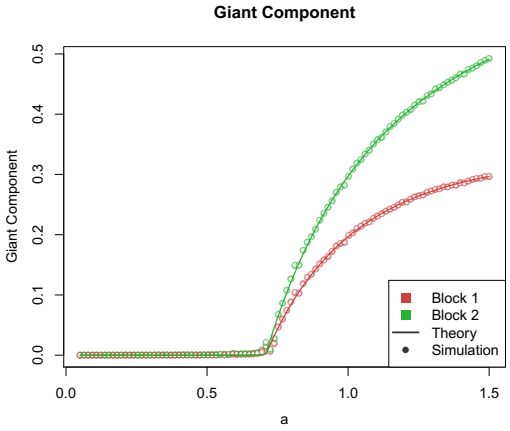

Figure 31: The fraction of members in a block and the giant component, for a range of values a.

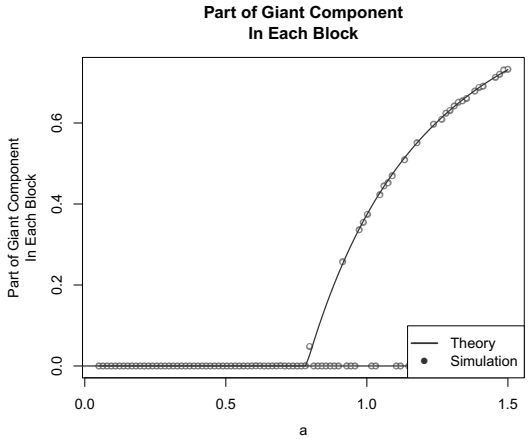

Figure 32: The size of an epidemic for a range of values a.

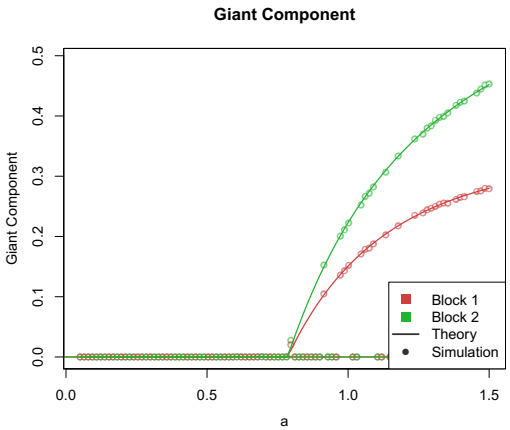

Figure 33: The fraction of members in a block and infected in the epidemic, for a range of values a.

Square

$$a \in [0.6, 5]$$

$$\boldsymbol{\pi} = \left[\frac{1}{4}, \frac{1}{4}, \frac{1}{4}, \frac{1}{4}\right]$$

$$\boldsymbol{g} = [\text{Poi}(a), \text{Poi}(a), \text{Poi}(a), \text{Poi}(a)]$$

$$\Theta = \begin{bmatrix} 0 & \frac{1}{2} & \frac{1}{2} & 0 \\ \frac{1}{2} & 0 & 0 & \frac{1}{2} \\ \frac{1}{2} & 0 & 0 & \frac{1}{2} \\ 0 & \frac{1}{2} & \frac{1}{2} & 0 \end{bmatrix}$$

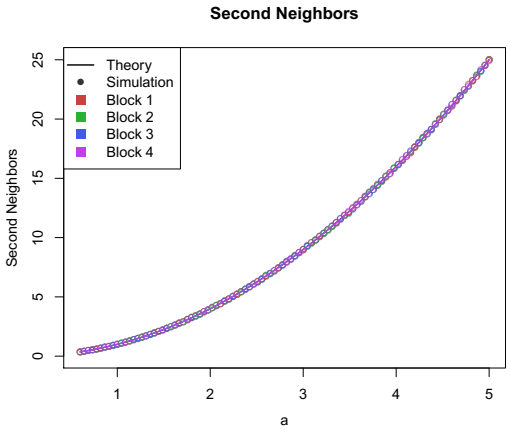

Figure 34: The number of second neighbors for members of each block, for a range of values a.

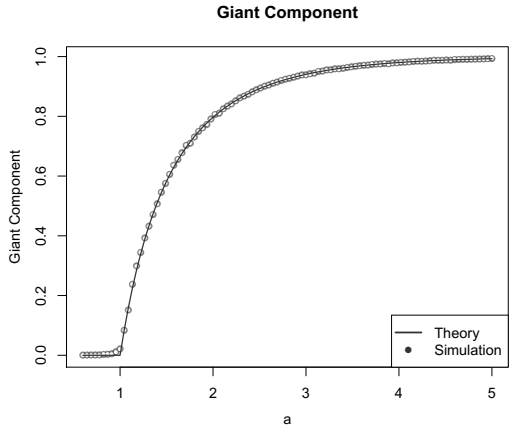

Figure 35: The size of the giant component for a range of values a.

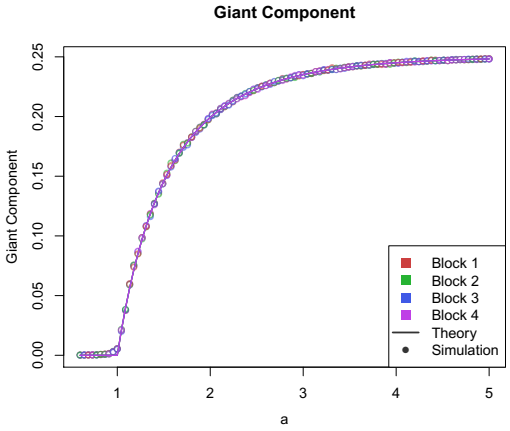

Figure 36: The fraction of members in a block and the giant component, for a range of values a.

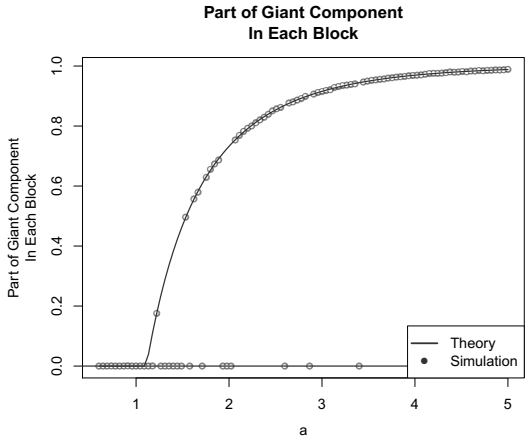

Figure 37: The size of an epidemic for a range of values a.

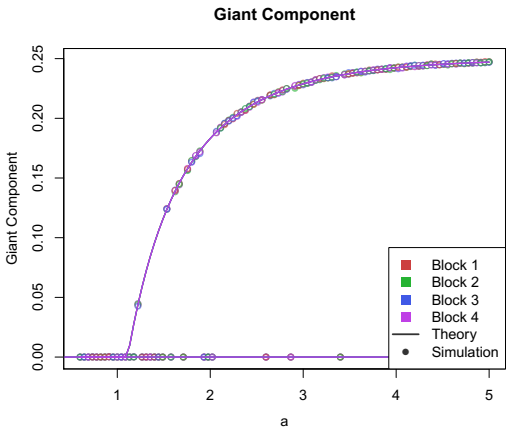

Figure 38: The fraction of members in a block and infected in the epidemic, for a range of values a.

Tube

$$a \in [0.6, 5]$$

$$\boldsymbol{\pi} = \left[\frac{1}{4}, \frac{1}{4}, \frac{1}{4}, \frac{1}{4}\right]$$

$$\boldsymbol{g} = [\text{Poi}(a), \text{Poi}(a), \text{Poi}(a/2), \text{Poi}(a/2)]$$

$$\Theta = \begin{bmatrix} 0 & \frac{1}{2} & \frac{1}{2} & 0 \\ \frac{1}{2} & 0 & 0 & \frac{1}{2} \\ 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \end{bmatrix}$$

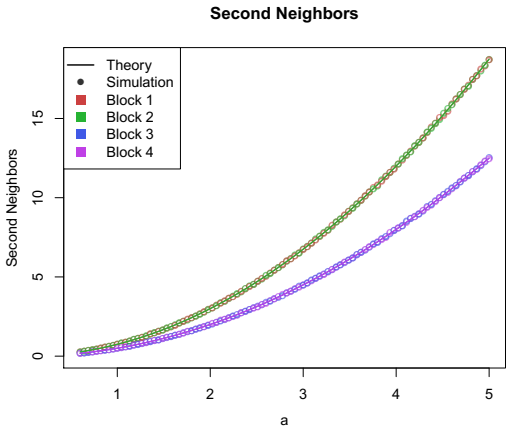

Figure 39: The number of second neighbors for members of each block, for a range of values a.

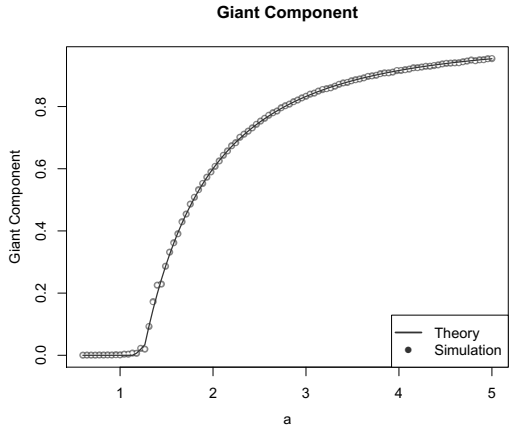

Figure 40: The size of the giant component for a range of values a.

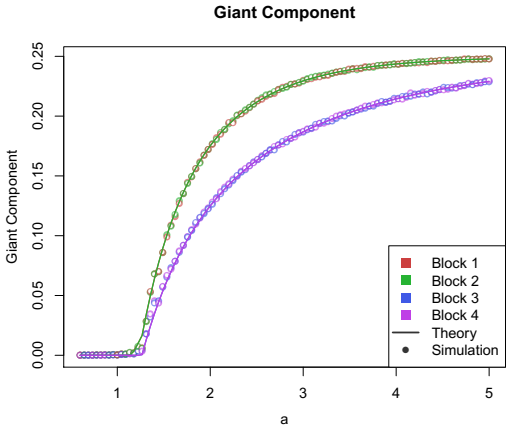

Figure 41: The fraction of members in a block and the giant component, for a range of values a.

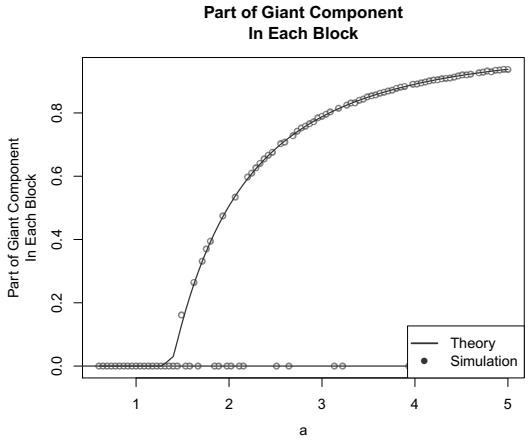

Figure 42: The size of an epidemic for a range of values a.

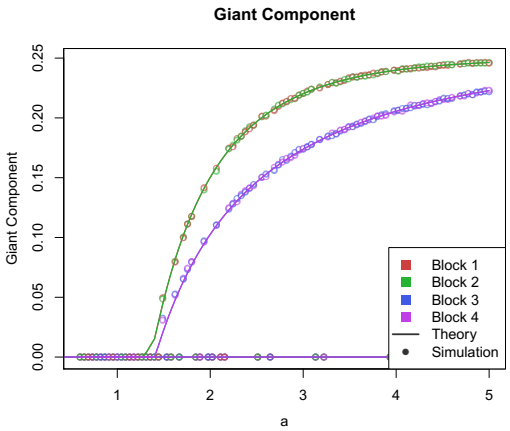

Figure 43: The fraction of members in a block and infected in the epidemic, for a range of values a.

Core with Saturated Periphery

$$a \in [.6, 3]$$

$$\boldsymbol{\pi} = \left[\frac{1}{2}, \frac{1}{2}\right]$$

$$\boldsymbol{g} = [\text{Poi}(a), \text{Poi}(1)]$$

$$\Theta = \begin{bmatrix} 1 - \frac{1}{2\langle d_1 \rangle} & \frac{1}{2\langle d_1 \rangle} \\ \frac{1}{2} & \frac{1}{2} \end{bmatrix}$$

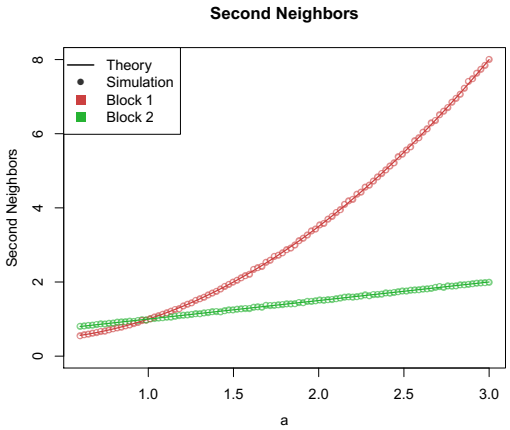

Figure 44: The number of second neighbors for members of each block, for a range of values a.

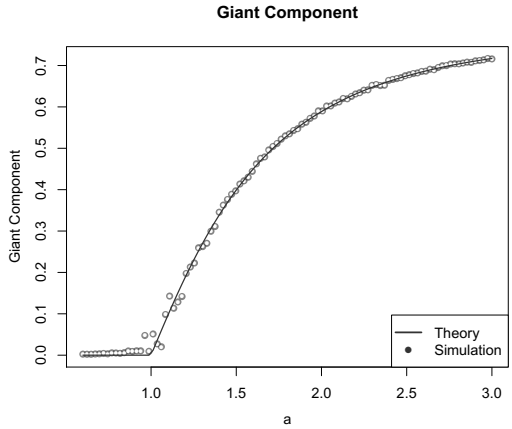

Figure 45: The size of the giant component for a range of values a.

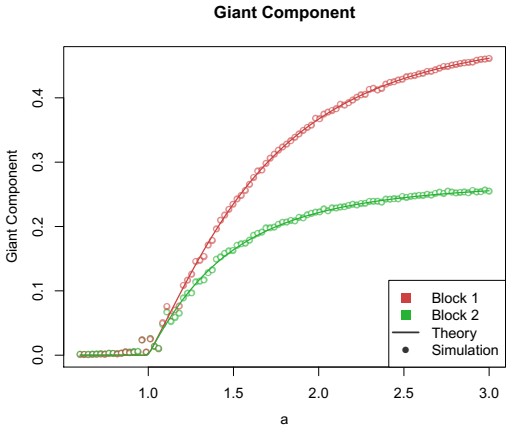

Figure 46: The fraction of members in a block and the giant component, for a range of values a.

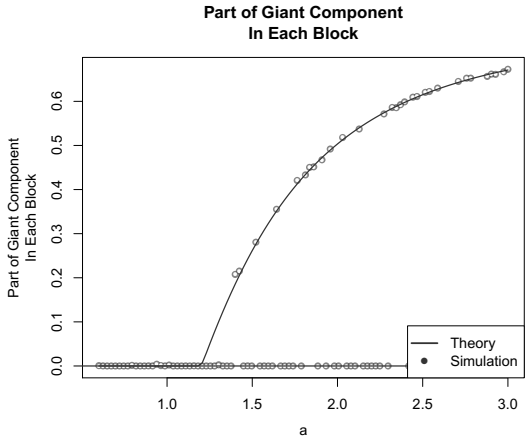

Figure 47: The size of an epidemic for a range of values a.

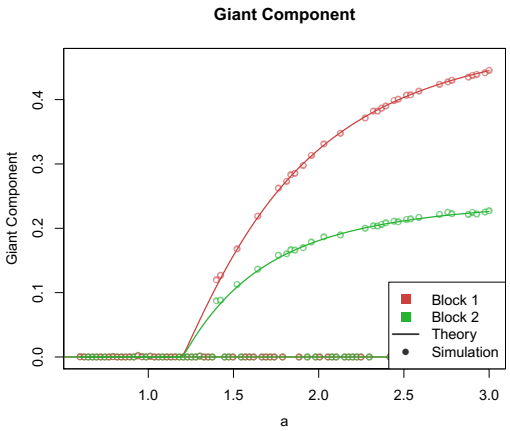

Figure 48: The fraction of members in a block and infected in the epidemic, for a range of values a.

Core with Unsaturated Periphery

$$a \in [.6, 3]$$

$$\boldsymbol{\pi} = \left[\frac{1}{2}, \frac{1}{2}\right]$$

$$\boldsymbol{g} = [\text{Poi}(a), \text{Poi}(1/2)]$$

$$\Theta = \begin{bmatrix} 1 - \frac{1}{4a} & \frac{1}{4a} \\ \frac{1}{2} & \frac{1}{2} \end{bmatrix}$$

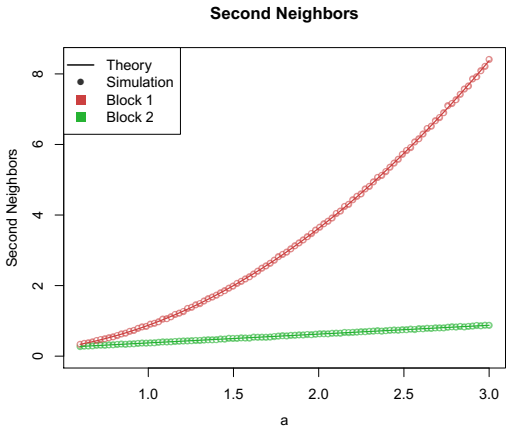

Figure 49: The number of second neighbors for members of each block, for a range of values a.

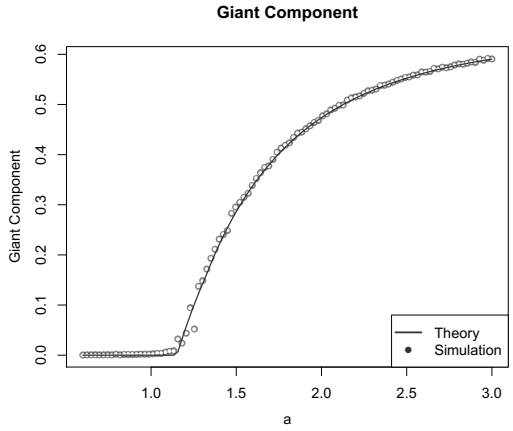

Figure 50: The size of the giant component for a range of values a.

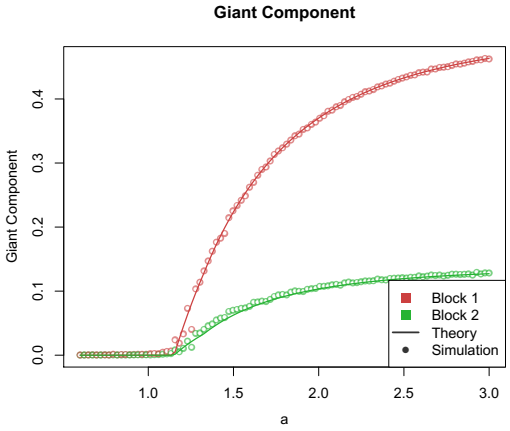

Figure 51: The fraction of members in a block and the giant component, for a range of values a.

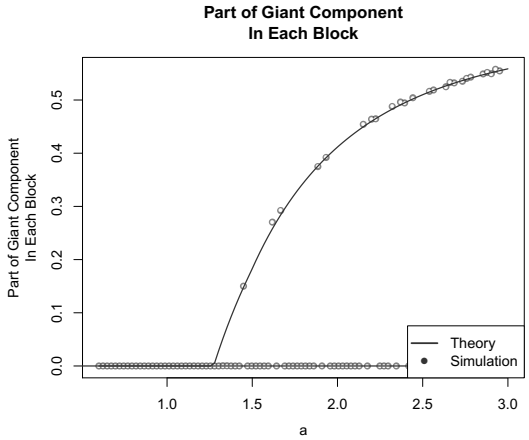

Figure 52: The size of an epidemic for a range of values a.

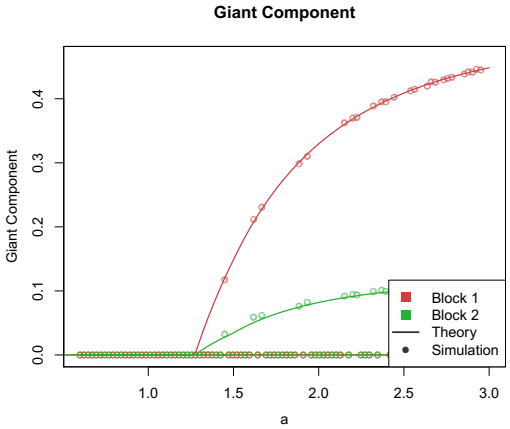

Figure 53: The fraction of members in a block and infected in the epidemic, for a range of values a.

Isolated Communities

For $K = 6, \boldsymbol{K} = [K, ..., 1]$,

$$a \in (0.01, 2.5)$$

$$\boldsymbol{\pi} = \mathbf{1}/K$$

$$\boldsymbol{g} = [\text{Poi}(\boldsymbol{K} \cdot a)]$$

$$\Theta = \left[\text{diag}(\boldsymbol{K} - 0.05) + \mathbf{1}\mathbf{1}^\top \cdot 0.01\right] \odot \boldsymbol{K}^{-1}\mathbf{1}^\top$$

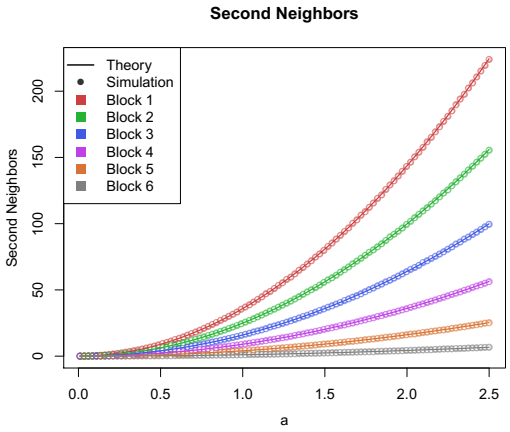

Figure 54: The number of second neighbors for members of each block, for a range of values a.

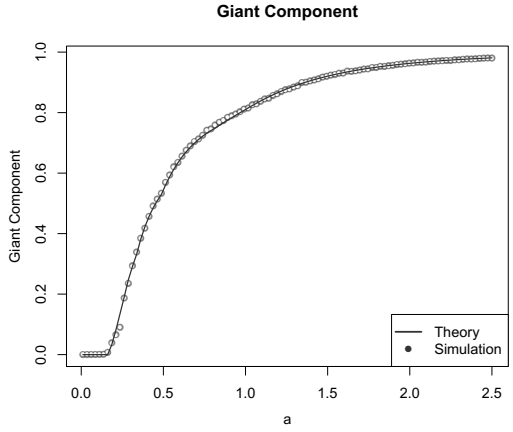

Figure 55: The size of the giant component for a range of values a.

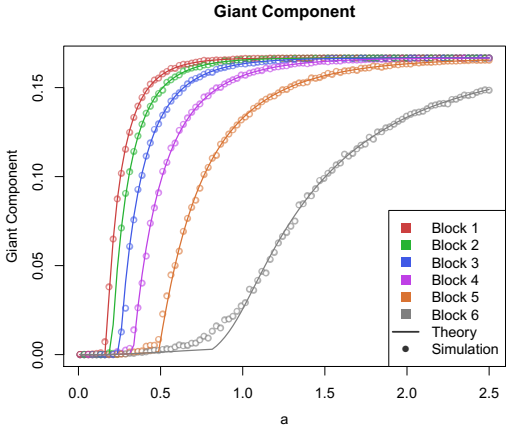

Figure 56: The fraction of members in a block and the giant component, for a range of values a.

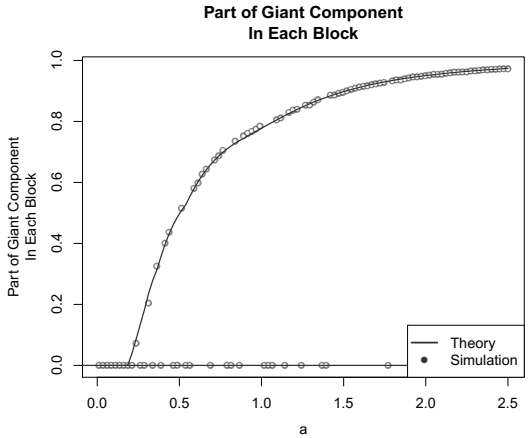

Figure 57: The size of an epidemic for a range of values a.

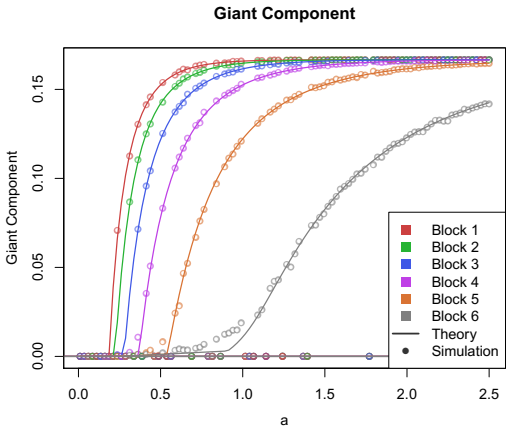

Figure 58: The fraction of members in a block and infected in the epidemic, for a range of values a.

Connected Communities

For $K = 6, \boldsymbol{K} = [K, ..., 1]$,

$$a \in [0.01, 2.5]$$

$$\boldsymbol{\pi} = \mathbf{1}/K$$

$$\boldsymbol{g} = [\text{Poi}(\boldsymbol{K} \cdot a)]$$

$$\Theta = \left[\text{diag}(\boldsymbol{K} - 0.5) + \mathbf{1}\mathbf{1}^\top \cdot 0.1\right] \odot \boldsymbol{K}^{-1}\mathbf{1}^\top$$

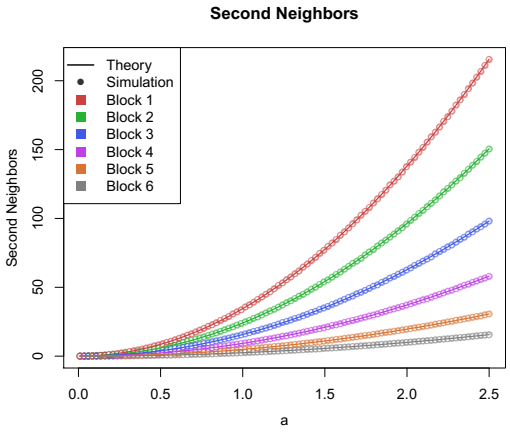

Figure 59: The number of second neighbors for members of each block, for a range of values a.

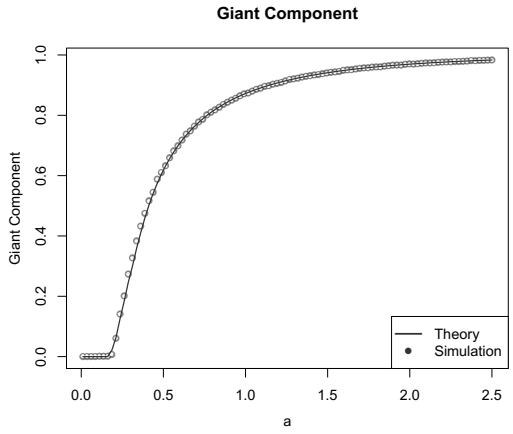

Figure 60: The size of the giant component for a range of values a.

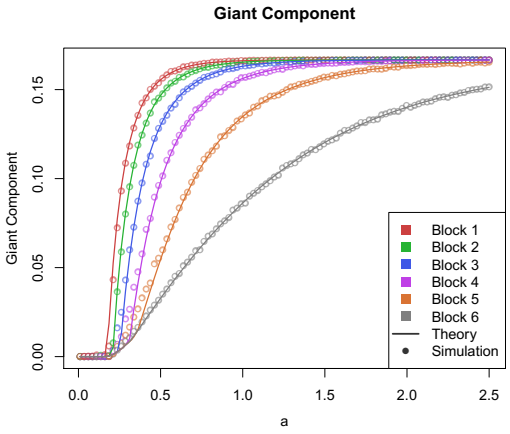

Figure 61: The fraction of members in a block and the giant component, for a range of values a.

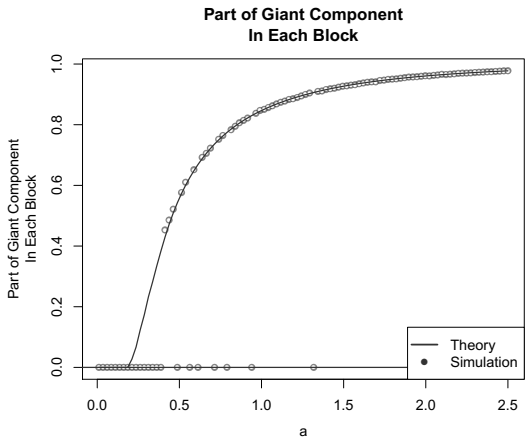

Figure 62: The size of an epidemic for a range of values a.

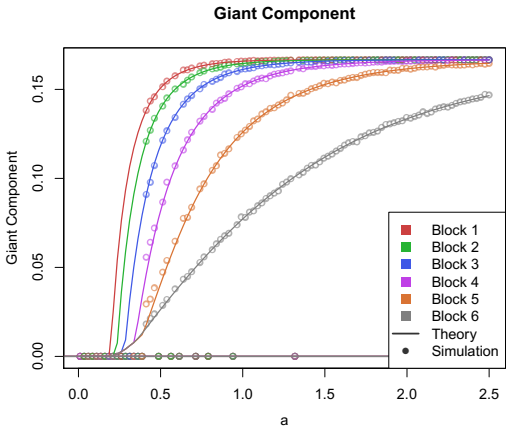

Figure 63: The fraction of members in a block and infected in the epidemic, for a range of values a.

Three Shuffled Blocks

$$a \in (0.6, 7)$$

$$\boldsymbol{\pi} = \left[\frac{1}{3}, \frac{1}{3}, \frac{1}{3}\right]$$

$$\boldsymbol{g} = [\text{Poi}(a), \text{Poi}(1), \text{Poi}(3/4)]$$

$$\Theta = \begin{bmatrix} 1 - \frac{1}{2a} & \frac{1}{4a} & \frac{1}{2a} \\ \frac{1}{4} & \frac{1}{2} & \frac{1}{4} \\ \frac{1}{3} & \frac{1}{3} & \frac{1}{3} \end{bmatrix}$$

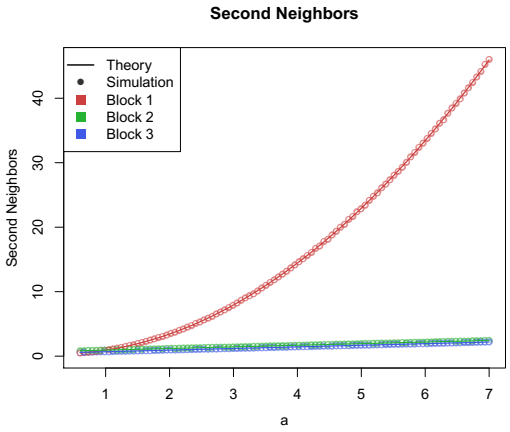

Figure 64: The number of second neighbors for members of each block, for a range of values a.

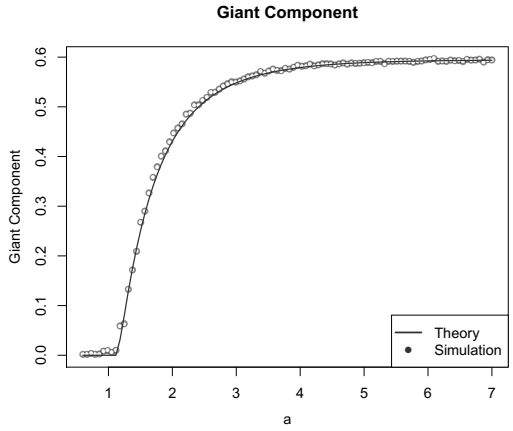

Figure 65: The size of the giant component for a range of values a.

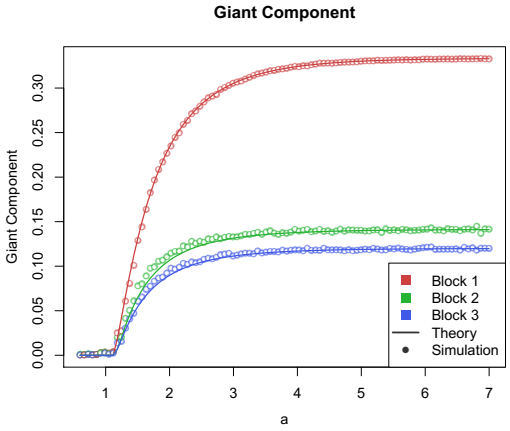

Figure 66: The fraction of members in a block and the giant component, for a range of values a.

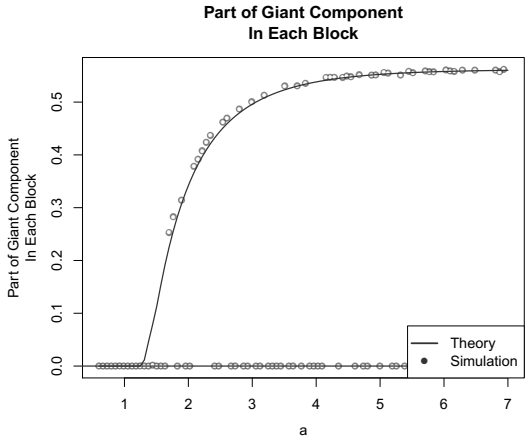

Figure 67: The size of an epidemic for a range of values a.

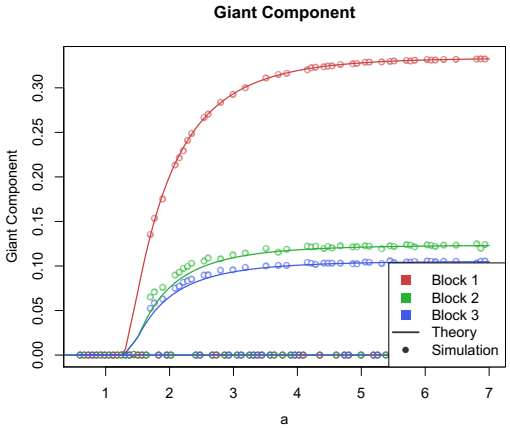

Figure 68: The fraction of members in a block and infected in the epidemic, for a range of values a.

Four Shuffled Blocks

$$a \in [1.1, 5]$$

$$\boldsymbol{\pi} = \left[\frac{1}{4}, \frac{1}{4}, \frac{1}{4}, \frac{1}{4}\right]$$

$$\boldsymbol{g} = [\text{Poi}(a), \text{Poi}(3/4), \text{Poi}(2/4), \text{Poi}(1/4)]$$

$$\Theta = \begin{bmatrix} 1 - \frac{5}{8a} & \frac{1}{2a} & \frac{1}{8a} & 0 \\ \frac{2}{3} & 0 & \frac{1}{3} & 0 \\ \frac{1}{4} & \frac{1}{2} & 0 & \frac{1}{4} \\ 0 & 0 & \frac{1}{2} & \frac{1}{2} \end{bmatrix}$$

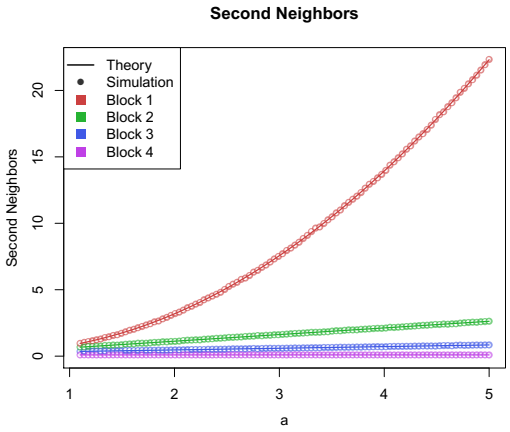

Figure 69: The number of second neighbors for members of each block, for a range of values a.

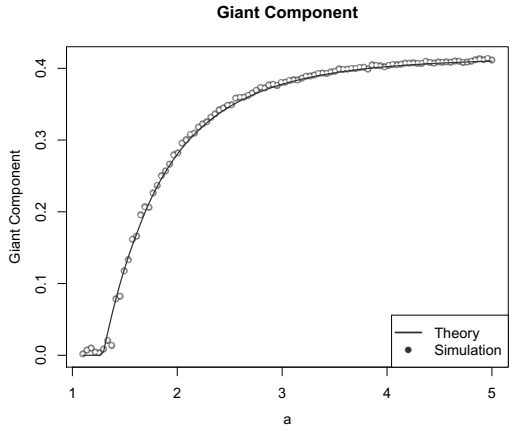

Figure 70: The size of the giant component for a range of values a.

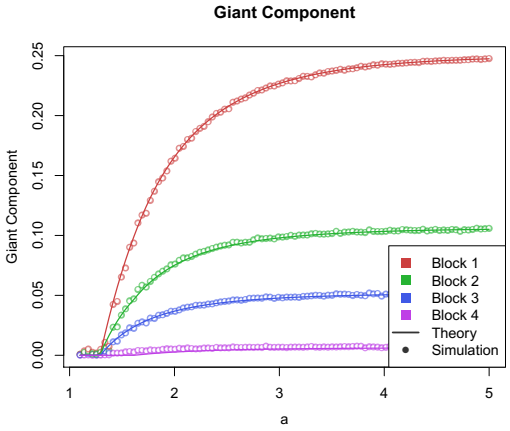

Figure 71: The fraction of members in a block and the giant component, for a range of values a.

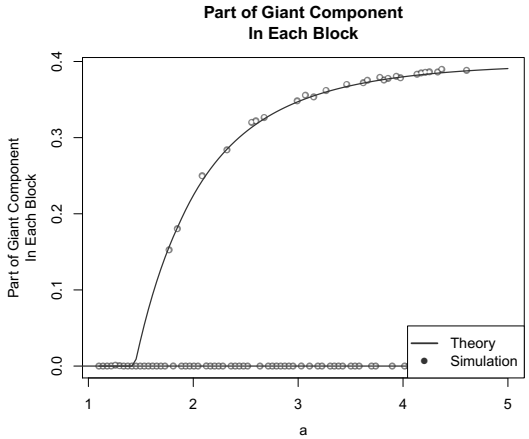

Figure 72: The size of an epidemic for a range of values a.

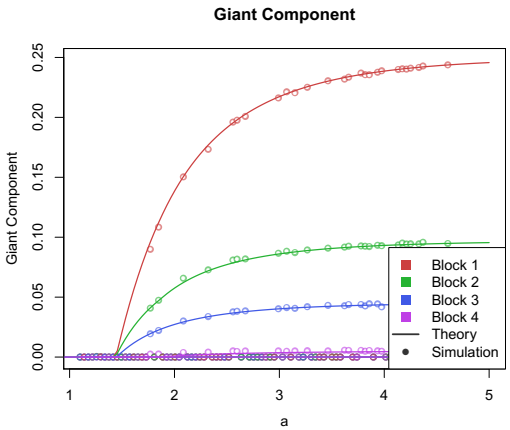

Figure 73: The fraction of members in a block and infected in the epidemic, for a range of values a.

Discussion

Degree-Corrected Stochastic Blockmodel is a network model that allows for each node to have an arbitrary degree, and for members to belong to a finite number of discrete blocks, between which the members of each block may share an arbitrary number of its edges, subject to an equal number of edges shared between each pair. In this section, we detailed a procedure that generates networks whose properties are consistent with its specification as the size of the network grows.

We then derived several asymptotic statistics for this model. We find that the number of self edges and multiedges for this model are constants as the network grows, so we may ignore these for large networks. We also found that the clustering coefficient decreases as the size of the network increases, so the clustering coefficient for the Degree-Corrected Stochastic Blockmodel is negligible in the limit of $n \to \infty$. This is unlike many empirical networks which exhibit significant clustering, making this a drawback for the realism of this model. We also derived the size of the giant component as a function of node membership, degree distribution, and mixing structure. We also found the fraction of nodes each block contributes to the network. We then described an infinite-time SIR process propagating on the network, and found the final size of the epidemic in similar terms to that of the giant component.

Finally, we simulated several kinds of networks specifiable as a DegSBM. We find that our theoretical results match simulation well. These results could be used in practice by applying community detection methods to an empirical network, finding the empirical mixing distribution and degree distribution, and using these results to detect the size of a giant component or epidemic, as well as the relative contributions of each block.

Several extensions of the Degree-Corrected Stochastic Blockmodel may be useful. Our results do not require any bound on the complexity of the mixing matrix of degree distributions, but in each case the results only hold asymptotically. It is desirable to consider the case where block structure increases in complexity along with network size n. A particularly interesting case would be when most all block structure is contained on or near the diagonal of the mixing matrix, such as those with strong community or lattice structure. Finally, it is possible to incorporate a term for clustering in many networks[65 77], which would be a welcome addition to this model.

Concluding Remarks

In this dissertation, we have investigated the statistical properties of epidemic spread on networks. We also find how to use these properties to improve the efficiency of statistical analysis. We review each of these in turn.

In Section I, we found that for trials of infectious processes in networks, network structure can reduce the probability of correctly detecting a real treatment effect, or statistical power. We show this by considering a simulated cluster randomized trial in which individuals become infected through network neighbors. These networks consisted of within-cluster network structure, as well as network edges across clusters belonging to different intervention arms, and found that empirical power depends on both of these. We also showed that a common way to estimate power before a study does not capture these dependencies. This presents a challenge and opportunity to develop and apply statistical adjustments to recover power by accounting for the dependence of the infectious process on these network properties.

In Section II, we consider one strategy for improving statistical power. We again consider the cluster randomized setting, wherein isolated networks are randomized to two treatment arms. Upon simulating each trial, we obtain several covariates for each node and cluster based on each network and baseline infection, and consider their use in statistical methods designed to more efficiently estimate the treatment effect. To this end, we used the recently developed Augmented Generalized Estimating Equations, which account for the relationship between these covariates and the outcome for both treatment arms. We show that under a wide range of simulation parameters, network-related covariates show modest gains in statistical efficiency, and covariates relates to baseline infections show substantial gains. We also show that these gains depend on specific assumptions about the network and epidemic process. However, not each collection of relationships implies that an infectious epidemic is possible or likely, or how that infection depends on the properties of each individual in the network. This prompts the development of analytical derivations that link network structure to global and individual risk of infection.

In Section III, we consider an analytical approach to understand these relationships for the Degree-Corrected Stochastic Blockmodel, which is sufficiently flexible to consider the degree of each network node as well as mixing structure between discrete blocks of nodes. For this model, we derive a range of network properties, such as a global measure of connectivity (the size of the giant component) and the

risk and extent of potential epidemic spread. We also show that this is related to a measure of risk for individual nodes in the network. To return to the context of cluster randomized trials, these estimates of network and node properties can also be used as adjustment covariates in adjustment methods that aim to increase statistical efficiency.

Taken together, Section I shows that properties of the network and infectious spread can reduce the efficiency with which treatment effects reduce the incidence of infectious outcomes. We have also shown how this reduction can be remedied by incorporating network features in the estimation procedure. When properties of networks can be assessed directly, Section II suggests which covariates would be efficient for a range of epidemic scenarios. When network structure can only be partially estimated, such as degree distribution and mixing structure, we derive in Section III the extent of risk of an epidemic, and derive several other network and node properties. When estimating the effect of a treatment on reducing the epidemic spread on networks, the methods of these latter two sections can both be used to produce network-related covariates that can be used in adjustment techniques to recover statistical power.

References

[1] Mark W Lipsey. *Design sensitivity: Statistical power for experimental research*, volume 19. Sage, 1990.

[2] Katherine S Button, John PA Ioannidis, Claire Mokrysz, Brian A Nosek, Jonathan Flint, Emma SJ Robinson, and Marcus R Munafò. Power failure: why small sample size undermines the reliability of neuroscience. *Nature Reviews Neuroscience*, 14(5):365–376, 2013.

[3] John PA Ioannidis. Why most published research findings are false. *PLoS medicine*, 2(8):e124, 2005.

[4] David M Murray. *Design and analysis of group-randomized trials*, volume 29. Oxford University Press, 1998.

[5] Allan Donner and Neil Klar. *Design and analysis of cluster randomization trials in health research*, volume 220. London Arnold Publishers, 2000.

[6] Richard Hayes and L Moulton. *Cluster randomised trials*. Chapman & Hall/CRC, 2009.

[7] Sandra Eldridge and Sally Kerry. *A practical guide to cluster randomised trials in health services research*, volume 120. John Wiley & Sons, 2012.

[8] Tendani Gaolathe, Kathleen E Wirth, Molly Pretorius Holme, Joseph Makhema, Sikhulile Moyo, Unoda Chakalisa, Etienne Kadima Yankinda, Quanhong Lei, Mompati Mmalane, Vlad Novitsky, et al. Botswana's progress toward achieving the 2020 unaids 90-90-90 antiretroviral therapy and virological suppression goals: a population-based survey. *The Lancet HIV*, 2016.

[9] Richard Hayes, Helen Ayles, Nulda Beyers, Kalpana Sabapathy, Sian Floyd, Kwame Shanaube, Peter Bock, Sam Griffith, Ayana Moore, Deborah Watson-Jones, et al. Hptn 071 (popart): rationale and design of a cluster-randomised trial of the population impact of an hiv combination prevention intervention including universal testing and treatment-a study protocol for a cluster randomised trial. *Trials*, 15(1):57, 2014.

[10] G Chemie et al. Uptake of community-based hiv testing during a multi-disease health campaign in rural uganda. *PLoS One*, 9(1):e84317, 2014.

[11] Catherine M Crespi, Weng Kee Wong, and Shiraz I Mishra. Using second-order generalized estimating equations to model heterogeneous intraclass correlation in cluster-randomized trials. *Statistics in medicine*, 28(5):814–827, 2009.

[12] Rui Wang, Ravi Goyal, Quanhong Lei, Max Essex, and Victor De Gruttola. Sample size considerations in the design of cluster randomized trials of combination hiv prevention. *Clinical Trials*, page 1740774514523351, 2014.

[13] Simon Gilbody, Peter Bower, David Torgerson, and David Richards. Cluster randomized trials produced similar results to individually randomized trials in a meta-analysis of enhanced care for depression. *Journal of clinical epidemiology*, 61(2):160–168, 2008.

[14] Michael E Sobel. What do randomized studies of housing mobility demonstrate? causal inference in the face of interference. *Journal of the American Statistical Association*, 101(476):1398–1407, 2006.

[15] Karla Hemming, Alan J Girling, Alice J Sitch, Jennifer Marsh, and Richard J Lilford. Sample size calculations for cluster randomised controlled trials with a fixed number of clusters. *BMC Medical Research Methodology*, 11:1471–2288, 2011.

[16] Obioha C Ukoumunne, Martin C Gulliford, Susan Chinn, Jonathan AC Sterne, Peter GJ Burney, and Allan Donner. Methods in health service research: evaluation of health interventions at area and organisation level. *BMJ: British Medical Journal*, 319(7206):376, 1999.

[17] RJ Hayes, N DE Alexander, S Bennett, and SN Cousens. Design and analysis issues in cluster-randomized

trials of interventions against infectious diseases. *Statistical Methods in Medical Research*, 9(2):95–116, 2000.

[18] Tao Zhou, Jian-Guo Liu, Wen-Jie Bai, Guanrong Chen, and Bing-Hong Wang. Behaviors of susceptible-infected epidemics on scale-free networks with identical infectivity. *Physical Review E*, 74(5):056109, 2006.

[19] RJ Hayes and S Bennett. Simple sample size calculation for cluster-randomized trials. *International journal of epidemiology*, 28(2):319–326, 1999.

[20] P. Erdös and Alfréd. Rényi. The evolution of random graphs. *Publ. Math. Inst. Hung. Acad. Sci.*, 5:17–61, 1960.

[21] Albert-László Barabási and Réka Albert. Emergence of scaling in random networks. *Science*, 286:509–512, 1999.

[22] Carolyn J Anderson, Stanley Wasserman, and Katherine Faust. Building stochastic blockmodels. *Social Networks*, 14(1–2):137–161, 1992. Special Issue on Blockmodels.

[23] M. E. J. Newman. Mixing patterns in networks. *Phys. Rev. E*, 67:026126, Feb 2003.

[24] Roy M. Anderson and Robert M. May. *Infectious Diseases of Humans*. Oxford University Press, Oxford, U.K., 1991.

[25] Matt J Keeling and Pejman Rohani. *Modeling infectious diseases in humans and animals*. Princeton University Press, 2008.

[26] Romualdo Pastor-Satorras, Claudio Castellano, Piet Van Mieghem, and Alessandro Vespignani. Epidemic processes in complex networks. *Rev. Mod. Phys.*, 87:925–979, Aug 2015.

[27] M. E. J. Newman. The structure and function of complex networks. *SIAM Review*, 45(2):167–256, 2003.

[28] M. E. J. Newman. *Networks: An Introduction*. Oxford University Press, Inc., New York, NY, USA, 2010.

[29] Eric D Kolaczyk. *Statistical analysis of network data: methods and models*. Springer Science & Business Media, 2009.

[30] Piet Van Miegham. *Performance Analysis of Complex Networks and Systems*. Cambridge University Press, 2014.

[31] Derek J. de Solla Price. Networks of scientific papers. *Science*, 149(3683):510–515, 1965.

[32] Aaron Clauset, Cosma Rohilla Shalizi, and M. E. J. Newman. Power-law distributions in empirical data. *SIAM Review*, 51(4):661–703, February 2009.

[33] Mason A Porter, Jukka-Pekka Onnela, and Peter J Mucha. Communities in networks. *Notices of the AMS*, 56(9):1082–1097, 2009.

[34] Ove Frank and David Strauss. Markov graphs. *Journal of the American Statistical Association*, 81(395):832–842, 1986.

[35] Duncan J. Watts and Steven H. Strogatz. Collective dynamics of 'small-world' networks. *Nature*, 393:440–442, 1998.

[36] Esther van Kleef, Julie V Robotham, Mark Jit, Sarah R Deeny, and William J Edmunds. Modelling the transmission of healthcare associated infections: a systematic review. *BMC infectious diseases*, 13(1):294, 2013.

[37] David M Murray, Sherri P Varnell, and Jonathan L Blitstein. Design and analysis of group-randomized trials: a review of recent methodological developments. *American Journal of Public Health*, 94(3):423–432, 2004.

[38] Phillip I Good. *Resampling methods*. Springer, 2001.

[39] David Harrington. Linear rank tests in survival analysis. *Encyclopedia of biostatistics*, 2005.

[40] Christina Pagel, Audrey Prost, Sonia Lewycka, Sushmita Das, Tim Colbourn, Rajendra Mahapatra, Kishwar Azad, Anthony Costello, and David Osrin. Intracluster correlation coefficients and coefficients of variation for perinatal outcomes from five cluster-randomised controlled trials in low and middle-income countries: results and methodological implications. *Trials*, 12(1):151, 2011.

[41] Rebecca M Turner, Simon G Thompson, and David J Spiegelhalter. Prior distributions for the intracluster correlation coefficient, based on multiple previous estimates, and their application in cluster randomized trials. *Clinical Trials*, 2(2):108–118, 2005.

[42] Stephane Helleringer and Hans-Peter Kohler. Sexual network structure and the spread of hiv in africa: evidence from likoma island, malawi. *Aids*, 21(17):2323–2332, 2007.

[43] Ravi Goyal, Joseph Blitzstein, and Victor De Gruttola. Sampling networks from their posterior predictive distribution. *Network Science*, 2:107–131, 4 2014.

[44] Michael Molloy and Bruce Reed. A critical point for random graphs with a given degree sequence. *Random structures & algorithms*, 6(2-3):161–180, 1995.

[45] Cesar A Hidalgo and C Rodriguez-Sickert. The dynamics of a mobile phone network. *Physica A: Statistical Mechanics and its Applications*, 387(12):3017–3024, 2008.

[46] Nathan Eagle, Alex Sandy Pentland, and David Lazer. Inferring friendship network structure by using mobile phone data. *Proceedings of the National Academy of Sciences*, 106(36):15274–15278, 2009.

[47] Jukka-Pekka Onnela, Samuel Arbesman, Marta C González, Albert-László Barabási, and Nicholas A Christakis. Geographic constraints on social network groups. *PLoS one*, 6(4):e16939, 2011.

[48] Brian Karrer and M. E. J. Newman. Stochastic blockmodels and community structure in networks. *Phys. Rev. E*, 83:016107, Jan 2011.

[49] Sally M Kerry and J Martin Bland. The intracluster correlation coefficient in cluster randomisation. *Bmj*, 316(7142):1455–1460, 1998.

[50] Michael G Hudgens and M Elizabeth Halloran. Toward causal inference with interference. *Journal of the American Statistical Association*, 2012.

[51] Scott L Zeger and Kung-Yee Liang. Longitudinal data analysis for discrete and continuous outcomes. *Biometrics*, pages 121–130, 1986.

[52] Alan E Hubbard, Jennifer Ahern, Nancy L Fleischer, Mark Van der Laan, Sheri A Lippman, Nicholas Jewell, Tim Bruckner, and William A Satariano. To gee or not to gee: comparing population average and mixed models for estimating the associations between neighborhood risk factors and health. *Epidemiology*, 21(4):467–474, 2010.

[53] Anastasios A Tsiatis et al. Covariate adjustment for two-sample treatment comparisons in randomized clinical trials: A principled yet flexible approach. *Statistics in medicine*, 27(23):4658–4677, 2008.

[54] Brian Karrer and Mark EJ Newman. Stochastic blockmodels and community structure in networks. *Physical Review E*, 83(1):016107, 2011.

[55] Mark EJ Newman. Assortative mixing in networks. *Physical review letters*, 89(20):208701, 2002.

[56] Duncan S Callaway, John E Hopcroft, Jon M Kleinberg, Mark EJ Newman, and Steven H Strogatz. Are randomly grown graphs really random? *Physical Review E*, 64(4):041902, 2001.

[57] R Xulvi-Brunet and IM Sokolov. Reshuffling scale-free networks: From random to assortative. *Physical Review*

E, 70(6):066102, 2004.

[58] Alisa J Stephens, Eric J Tchetgen Tchetgen, and Victor De Gruttola. Augmented gee for improving efficiency and validity of estimation in cluster randomized trials by leveraging cluster-and individual-level covariates. *Statistics in medicine*, 31(10):915, 2012.

[59] James M Robins, Andrea Rotnitzky, and Lue Ping Zhao. Estimation of regression coefficients when some regressors are not always observed. *Journal of the American statistical Association*, 89(427):846–866, 1994.

[60] Min Zhang, Anastasios A Tsiatis, and Marie Davidian. Improving efficiency of inferences in randomized clinical trials using auxiliary covariates. *Biometrics*, 64(3):707–715, 2008.

[61] RI Jennrich and PF Sampson. Application of stepwise regression to non-linear estimation. *Technometrics*, 10(1):63–72, 1968.

[62] Azra C Ghani and Geoffrey P Garnett. Risks of acquiring and transmitting sexually transmitted diseases in sexual partner networks. *Sexually transmitted diseases*, 27(10):579–587, 2000.

[63] Stuart J Pocock, Susan E Assmann, Laura E Enos, and Linda E Kasten. Subgroup analysis, covariate adjustment and baseline comparisons in clinical trial reporting: current practiceand problems. *Statistics in medicine*, 21(19):2917–2930, 2002.

[64] Béla Bollobás, Svante Janson, and Oliver Riordan. The phase transition in inhomogeneous random graphs. *Random Structures & Algorithms*, 31(1):3–122, 2007.

[65] Mark EJ Newman, Steven H Strogatz, and Duncan J Watts. Random graphs with arbitrary degree distributions and their applications. *Physical review E*, 64(2):026118, 2001.

[66] Dimitris Achlioptas and Paris Siminelakis. Symmetric graph properties have independent edges. In *Automata, Languages, and Programming*, pages 467–478. Springer, 2015.

[67] Gianpaolo Scalia-Tomba. Asymptotic final size distribution of the multitype reed-frost process. *Journal of applied probability*, pages 563–584, 1986.

[68] Peter Neal et al. Multitype randomized reed–frost epidemics and epidemics upon random graphs. *The Annals of Applied Probability*, 16(3):1166–1189, 2006.

[69] Mark EJ Newman. Spread of epidemic disease on networks. *Physical review E*, 66(1):016128, 2002.

[70] Herbert S Wilf. *generatingfunctionology*. Elsevier, 2013.

[71] Helen Abbey. An examination of the reed-frost theory of epidemics. *Human biology*, 24(3):201, 1952.

[72] Denis Mollison. Spatial contact models for ecological and epidemic spread. *Journal of the Royal Statistical Society. Series B (Methodological)*, pages 283–326, 1977.

[73] Peter Grassberger. On the critical behavior of the general epidemic process and dynamical percolation. *Mathematical Biosciences*, 63(2):157–172, 1983.

[74] Dietrich Stauffer and Ammon Aharony. *Introduction to percolation theory*. CRC press, 1994.

[75] Geoffrey Grimmett. *What is Percolation?* Springer, 1999.

[76] Thomas R Fleming and David P Harrington. *Counting processes and survival analysis*, volume 169. John Wiley & Sons, 2011.

[77] Mark EJ Newman. Random graphs with clustering. *Physical review letters*, 103(5):058701, 2009.

Appendix: Augmented GEE on Smaller Networks

Statistics Marginal Across All Scenarios

Treatment Effect $\overline{\beta}$: -2.64

	None	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
Bias	0	0	0	0	0	0	0	0	0	-0.02	-0.05	0	-0.05	-0.02	-0.01	0	0
RobSE	3.02	2.94	2.91	2.96	3.02	2.92	2.87	2.89	2.98	0.88	1.62	1.02	1.78	0.76	0.75	2.92	2.94
EmpSE	2.92	2.83	2.82	2.93	2.92	2.89	2.89	2.85	2.84	0.73	1.56	0.93	1.84	0.86	0.85	2.81	2.82
Gains	0(0)	2(2)	2(3)	-1(2)	0(0)	0(2)	-2(5)	1(3)	2(3)	67(15)	20(39)	62(16)	0(60)	56(22)	57(21)	3(2)	3(2)
Power	30.6	30.8	31.2	31.7	30.6	32.4	32.2	32.6	30.4	81.1	45.6	74.4	38.1	82.7	83.7	31	31
Coverage	95(2)	95(2)	95(2)	94(2)	95(2)	94(2)	94(2)	94(2)	95(2)	94(6)	96(3)	94(6)	94(3)	89(7)	90(7)	95(2)	95(2)

Unadj: No adjustment term
F_1: Degree
F_2: Mean Neighbor Degree
F_3: Assortativity
F_4: Member of Connected Block
F_5: Size of Largest Component
F_6: Mean Component Size
F_7: Number of Components
F_8: Size of Node's Component
F_9: Total Neighbor Infections at baseline
F_{10}: Total Node's Component Infections at baseline
F_{11}: 1/nearest infected path length at baseline
F_{12}: $\sum_i$ 1/path length to Infected Node i at baseline
All: Complete inclusion of the above
Step: Stepwise regression of the above
Pow: Powerlaw(Degree)
Spl: Spline(Degree)

$\boldsymbol{a} =$ [𝕀(High Degree),
𝕀(Powerlaw),
𝕀(Assortativity),
𝕀(Blocks),
𝕀(Degree Infectivity),
𝕀(High Baseline)]

Statistics Modification By Scenario Aspect

a	γ_a
(Intercept)	0.33
High Degree	-0.00
Powerlaw	-2.27
Assortative	0.01
Communities	-0.16
Deg. Infect.	-3.00
High Base	-0.52

Bias

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
(Intercept)	-0.00	0.00	0.01	0.01	-0.00	-0.00	-0.00	-0.00	0.00	0.06	0.02	0.06	0.01	0.05	0.05	0.00	0.00
High Degree	0.00	0.00	0.01	0.00	0.00	-0.00	0.02	-0.01	-0.00	-0.03	0.02	-0.01	-0.01	-0.00	0.00	-0.00	0.00
Powerlaw	0.00	-0.00	-0.01	-0.01	0.00	-0.00	0.01	-0.00	-0.00	-0.01	-0.02	0.00	-0.02	0.00	0.01	-0.01	-0.00
Assortative	0.00	-0.00	0.01	-0.00	0.00	0.00	0.02	0.01	0.00	0.02	0.04	0.01	0.06	0.03	0.02	0.01	0.00
Communities	-0.00	0.00	-0.00	0.00	-0.00	0.01	0.00	0.00	-0.00	-0.05	-0.03	-0.05	-0.01	-0.04	-0.04	-0.00	-0.00
Deg. Infect.	0.00	-0.00	-0.01	-0.01	0.00	-0.00	-0.01	0.00	0.00	-0.03	-0.08	-0.01	-0.06	-0.03	-0.01	0.00	-0.00
High Base.	0.00	-0.00	-0.02	-0.02	0.00	0.00	-0.03	-0.01	-0.00	-0.05	-0.06	-0.07	-0.07	-0.09	-0.11	-0.01	-0.00

Robust S.E.

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
(Intercept)	-0.47	-0.37	-0.36	-0.45	-0.47	-0.48	-0.35	-0.43	-0.44	0.07	0.33	-0.10	0.39	0.15	0.13	-0.37	-0.38
High Degree	0.67	0.70	0.73	0.69	0.67	0.68	0.75	0.62	0.73	0.60	0.66	0.90	1.12	0.45	0.46	0.69	0.65
Powerlaw	0.91	0.77	0.71	0.83	0.91	0.86	0.68	0.75	0.84	0.32	0.33	0.25	0.35	0.17	0.16	0.74	0.79
Assortative	0.00	-0.04	-0.01	0.01	0.00	-0.01	-0.00	0.00	-0.01	-0.09	-0.04	-0.13	-0.02	-0.06	-0.06	-0.02	-0.03
Communities	-0.20	-0.15	-0.14	-0.14	-0.20	-0.18	-0.12	-0.12	-0.16	-0.06	-0.04	-0.05	0.05	-0.02	-0.01	-0.14	-0.15
Deg. Infect.	2.66	2.53	2.45	2.58	2.66	2.59	2.40	2.58	2.56	0.63	0.80	0.65	0.54	0.57	0.58	2.51	2.55
High Base.	2.93	2.82	2.79	2.86	2.93	2.84	2.73	2.80	2.90	0.23	0.86	0.61	0.73	0.12	0.11	2.80	2.83

Empirical S.E.

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
(Intercept)	-0.53	-0.46	-0.43	-0.51	-0.53	-0.50	-0.38	-0.47	-0.48	0.12	0.75	-0.11	0.80	0.36	0.36	-0.46	-0.47
High Degree	0.52	0.52	0.56	0.55	0.52	0.59	0.59	0.56	0.61	0.39	0.27	0.76	0.95	0.30	0.31	0.53	0.52
Powerlaw	0.87	0.76	0.71	0.81	0.87	0.80	0.72	0.70	0.71	0.27	0.39	0.23	0.43	0.17	0.17	0.72	0.74
Assortative	0.02	0.01	0.03	0.05	0.02	0.03	0.07	0.04	0.05	-0.09	-0.02	-0.08	-0.01	-0.05	-0.07	0.03	0.02
Communities	-0.16	-0.11	-0.11	-0.14	-0.16	-0.14	-0.12	-0.08	-0.11	-0.06	-0.05	-0.06	0.02	-0.05	-0.05	-0.09	-0.10
Deg. Infect.	2.48	2.35	2.27	2.44	2.48	2.37	2.30	2.36	2.33	0.32	0.61	0.46	0.38	0.47	0.47	2.33	2.35
High Base.	3.17	3.06	3.03	3.16	3.17	3.12	2.98	3.07	3.03	0.40	0.42	0.79	0.30	0.16	0.15	3.03	3.04

Unadj: No adjustment term
F_1: Degree
F_2: Mean Neighbor Degree
F_3: Assortativity
F_4: Member of Connected Block
F_5: Size of Largest Component
F_6: Mean Component Size
F_7: Number of Components
F_8: Size of Node's Component
F_9: Total Neighbor Infections at baseline
F_{10}: Total Node's Component Infections at baseline
F_{11}: 1/nearest infected path length at baseline
F_{12}: $\sum_i$ 1/path length to Infected Node i at baseline
All: Complete inclusion of the above
Step: Stepwise regression of the above

Improvement

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
(Intercept)	-0	1	-1	-2	-0	-1	-5	0	-1	57	-27	56	-46	30	34	1	1
High Degree	0	-1	-1	-1	0	-1	-1	-2	-2	-9	11	-14	-33	-3	-4	-1	-1
Powerlaw	0	3	2	2	0	1	0	4	3	-8	-4	-8	-7	-1	-1	3	3
Assortative	0	1	-0	-1	0	0	-1	-0	-1	4	2	6	3	4	4	-0	0
Communities	-0	-1	-1	-0	-0	-0	-1	-2	-1	0	-3	-0	-7	-1	-1	-2	-1
Deg. Infect.	0	1	4	1	0	2	4	1	2	12	32	14	52	14	12	1	1
High Base.	0	1	2	1	0	1	6	2	2	19	55	14	84	38	36	1	1

Power

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
(Intercept)	28	28	28	29	28	31	30	30	28	75	37	69	28	70	72	28	28
High Degree	35	34	34	34	35	36	34	36	35	6	46	9	27	11	10	34	35
Powerlaw	-4	-3	-3	-3	-4	-5	-3	-3	-5	2	3	2	1	9	9	-3	-3
Assortative	1	1	1	1	1	0	1	0	1	6	1	6	-1	3	3	1	1
Communities	5	4	4	4	5	5	4	4	4	4	3	3	0	3	2	4	4
Deg. Infect.	-4	-3	-3	-4	-4	-5	-3	-5	-3	4	-8	9	9	5	4	-3	-3
High Base.	-26	-26	-27	-26	-26	-27	-27	-27	-27	-10	-27	-17	-16	-5	-5	-26	-26

Coverage

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
(Intercept)	95	95	95	94	95	94	94	94	96	92	94	94	93	87	88	95	95
High Degree	2	2	2	2	2	1	2	1	1	7	3	6	3	8	8	2	2
Powerlaw	-0	-0	-0	-0	-0	-0	-0	0	0	1	0	1	0	1	1	-0	0
Assortative	-0	-0	-0	-0	-0	-0	-1	-0	-0	-0	-1	-0	-0	0	0	-0	-0
Communities	-0	-0	-0	-0	-0	-0	-0	-0	-0	0	0	-0	0	0	0	-0	-0
Deg. Infect.	1	1	1	1	1	2	1	2	1	-1	-2	-1	-2	0	0	1	1
High Base.	-2	-2	-2	-2	-2	-2	-2	-2	-1	-4	2	-5	2	-4	-5	-2	-2

Unadj: No adjustment term
F_1: Degree
F_2: Mean Neighbor Degree
F_3: Assortativity
F_4: Member of Connected Block
F_5: Size of Largest Component
F_6: Mean Component Size
F_7: Number of Components
F_8: Size of Node's Component
F_9: Total Neighbor Infections at baseline
F_{10}: Total Node's Component Infections at baseline
F_{11}: 1/nearest infected path length at baseline
F_{12}: $\sum_i$ 1/path length to Infected Node i at baseline
All: Complete inclusion of the above
Step: Stepwise regression of the above

Statistics Conditional On Each Scenario

a	β_a
000000	-0.34
000001	-0.43
000010	-1.37
000011	-0.82
000100	-0.43
000101	-0.47
000110	-1.62
000111	-2.03
001000	-0.32
001001	-0.54
001010	-1.39
001011	-0.94
001100	-0.42
001101	-0.49
001110	-1.46
001111	-0.93
010000	-0.77
010001	-1.24
010010	-5.00
010011	-2.51
010100	-0.72
010101	-1.20
010110	-5.13
010111	-3.72
011000	-0.86
011001	-1.38
011010	-4.80
011011	-1.76
011100	-0.81
011101	-1.32
011110	-4.77
011111	-3.09
100000	-2.01
100001	-8.51
100010	-5.61
100011	-3.58
100100	-2.07
100101	-8.89
100110	-5.54
100111	-3.37
101000	-1.99
101001	-8.37
101010	-5.59
101011	-3.48
101100	-1.97
101101	-8.37
101110	-5.59
101111	-3.47
110000	-1.64
110001	-5.03
110010	-5.17
110011	-3.64
110100	-1.67
110101	-5.31
110110	-5.32
110111	-3.54
111000	-1.71
111001	-5.69
111010	-5.42
111011	-3.36
111100	-1.65
111101	-5.74
111110	-5.59
111111	-3.18

$$\boldsymbol{a} = [\mathbb{I}(\text{High Degree}),\ \mathbb{I}(\text{Powerlaw}),\ \mathbb{I}(\text{Assortativity}),\ \mathbb{I}(\text{Blocks}),\ \mathbb{I}(\text{Degree Infectivity}),\ \mathbb{I}(\text{High Baseline})]$$

Bias

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
000000	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
000001	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.10	0.00	0.10	0.00	0.10	0.10	0.00	0.00
000010	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
000011	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.40	0.40	0.40	0.40	0.40	0.40	0.00	0.00
000100	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	-0.10	-0.10	-0.10	-0.10	0.00	0.00	0.00	0.00
000101	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
000110	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	-0.10	0.00	-0.10	-0.10	-0.10	0.00	0.00
000111	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	-0.50	-0.60	-0.60	-0.60	-0.60	-0.60	0.00	0.00
001000	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.10	0.10	0.00	0.10	0.10	0.10	0.00	0.00
001001	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
001010	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	-0.10	0.10	0.00	0.00	0.00	0.00	0.00
001011	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.10	-0.20	-0.20	-0.20	-0.20	-0.20	-0.20	0.00	0.00
001100	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
001101	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	-0.10	0.00	0.00	0.00	0.00	0.00	0.00
001110	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	-0.10	0.00	-0.10	-0.10	0.00	0.00	0.00
001111	0	0.00	0.00	0.00	0	0.00	-0.10	0.00	0.00	0.10	0.00	0.10	0.10	0.00	0.00	0.00	0.00
010000	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.10	-0.10	-0.10	0.00	0.00
010001	0	0.00	0.00	0.00	0	0.00	-0.10	0.00	0.00	0.00	0.00	0.00	-0.10	0.00	0.00	0.00	0.00
010010	0	0.00	0.10	0.10	0	0.00	0.10	0.00	0.10	0.10	-0.30	0.20	-0.20	0.10	0.20	0.00	0.00
010011	0	0.00	-0.10	-0.10	0	0.00	-0.10	0.00	0.00	0.20	0.10	0.20	0.10	0.10	0.10	0.00	0.00
010100	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.10	0.00	0.10	0.00	0.00	0.00	0.00
010101	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
010110	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.10	-0.20	0.20	-0.10	0.20	0.20	0.00	0.00
010111	0	0.00	-0.10	0.00	0	0.00	-0.20	0.00	-0.10	-0.50	-0.60	-0.50	-0.60	-0.60	-0.60	-0.10	-0.10
011000	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.10	0.00	0.00	0.00	0.00
011001	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.10	0.10	0.10	0.10	0.10	0.10	0.00	0.00
011010	0	0.00	0.00	0.00	0	0.00	0.10	0.00	0.00	0.10	-0.10	0.20	0.00	0.20	0.20	0.00	0.00
011011	0	-0.10	-0.10	-0.10	0	-0.10	-0.20	0.00	-0.10	0.00	0.10	0.00	0.10	0.00	0.00	0.00	0.00
011100	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.10	0.00	0.10	0.00	0.00	0.00	0.00
011101	0	0.00	0.00	0.00	0	0.00	0.10	0.00	0.00	0.10	0.00	0.10	0.00	0.10	0.10	0.00	0.00
011110	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	-0.10	0.10	0.00	0.10	0.10	0.00	0.00
011111	0	0.00	0.00	-0.10	0	0.10	0.00	0.00	0.10	-0.20	-0.30	-0.20	-0.20	-0.30	-0.30	0.00	0.00
100000	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
100001	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	-0.10	0.10	-0.20	0.10	0.10	0.00	0.00
100010	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.10	0.10	0.10	0.10	0.10	0.10	0.00	0.00
100011	0	0.00	0.00	0.00	0	0.00	-0.10	-0.10	0.00	-0.10	-0.10	-0.10	-0.10	-0.20	-0.20	0.00	0.00
100100	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
100101	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	-0.20	-0.30	-0.10	-0.40	-0.20	-0.20	0.00	0.00
100110	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.10	0.10	0.10	0.10	0.10	0.00	0.00
100111	0	0.00	0.00	0.00	0	0.00	-0.10	-0.10	0.00	0.00	0.00	0.10	0.00	0.00	0.00	0.00	0.00
101000	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
101001	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.10	0.00	0.10	0.00	0.10	0.00	0.00	0.00
101010	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	-0.10	0.00	-0.20	0.00	0.00	0.00	0.00
101011	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	-0.20	-0.10	-0.20	-0.10	-0.20	-0.20	0.00	0.00
101100	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.00	0.00	0.00	0.00
101101	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.10	0.10	0.10	0.10	0.10	0.10	0.00	0.00
101110	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.10	0.00	0.10	0.10	0.10	0.00	0.00
101111	0	0.00	0.00	0.00	0	0.00	0.10	0.10	0.00	-0.10	-0.10	0.00	-0.20	-0.10	-0.10	0.00	0.00
110000	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.10	0.10	0.10	0.00	0.00	0.00	0.00
110001	0	0.00	0.00	0.00	0	0.00	0.00	-0.10	0.00	-0.10	-0.10	-0.10	-0.20	-0.10	-0.10	-0.10	0.00
110010	0	0.00	0.00	0.00	0	0.00	0.10	0.00	0.00	0.10	0.00	0.10	0.00	0.10	0.20	0.00	0.00
110011	0	0.00	-0.10	-0.10	0	0.00	0.00	0.00	0.00	-0.20	-0.40	-0.20	-0.40	-0.40	-0.30	0.00	0.00
110100	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.10	0.00	0.10	0.00	0.00	0.00	0.00
110101	0	0.00	0.00	0.00	0	0.00	0.10	0.00	0.00	-0.10	-0.10	-0.10	-0.10	-0.10	-0.10	0.00	0.00
110110	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.10	-0.10	0.20	0.20	0.00	0.00
110111	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	-0.10	-0.20	-0.10	-0.10	-0.10	-0.10	0.00	0.00
111000	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
111001	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	-0.10	-0.10	0.00	-0.10	-0.10	-0.10	0.00	0.00
111010	0	0.00	0.10	0.00	0	0.00	0.10	0.00	0.00	-0.10	-0.20	-0.10	-0.30	0.00	0.00	0.00	0.00
111011	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	-0.10	-0.10	-0.10	-0.10	0.00	0.00	0.00	0.00
111100	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.10	0.00	0.10	0.00	0.00	0.00	0.00
111101	0	0.00	0.00	0.00	0	0.00	0.00	-0.10	0.00	-0.10	-0.10	-0.10	-0.20	-0.10	-0.10	0.00	0.00
111110	0	0.00	0.00	0.00	0	0.00	0.10	0.00	0.00	-0.10	0.00	0.00	-0.10	0.00	0.10	0.00	0.00
111111	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.20	0.30	0.20	0.30	0.20	0.20	0.00	0.00

Percent Relative Bias

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
000000	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
000001	-0	-0	-0	-0	-0	-0	-0	-0	-0	-23	-0	-23	-0	-23	-23	-0	-0
000010	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
000011	-0	-0	-0	-0	-0	-0	-0	-0	-0	-49	-49	-49	-49	-49	-49	-0	-0
000100	-0	-0	-0	-0	-0	-0	-0	-0	-0	23	23	23	23	-0	-0	-0	-0
000101	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
000110	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	6	-0	6	6	6	-0	-0
000111	-0	-0	-0	-0	-0	-0	-0	-0	-0	25	29	29	29	29	29	-0	-0
001000	-0	-0	-0	-0	-0	-0	-0	-0	-0	-31	-31	-0	-31	-31	-31	-0	-0
001001	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
001010	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	7	-7	-0	-0	-0	-0	-0
001011	-0	-0	-0	-0	-0	-0	-0	-0	-11	21	21	21	21	21	21	-0	-0
001100	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
001101	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	20	-0	-0	-0	-0	-0	-0
001110	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	7	-0	7	7	-0	-0	-0
001111	-0	-0	-0	-0	-0	-0	11	-0	-0	-11	-0	-11	-11	-0	-0	-0	-0
010000	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	13	13	13	-0	-0
010001	-0	-0	-0	-0	-0	-0	8	-0	-0	-0	-0	-0	8	-0	-0	-0	-0
010010	-0	-0	-2	-2	-0	-0	-2	-0	-2	-2	6	-4	4	-2	-4	-0	-0
010011	-0	-0	4	4	-0	-0	4	-0	-0	-8	-4	-8	-4	-4	-4	-0	-0
010100	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-14	-0	-14	-0	-0	-0	-0
010101	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
010110	-0	-0	-0	-0	-0	-0	-0	-0	-0	-2	4	-4	2	-4	-4	-0	-0
010111	-0	-0	3	-0	-0	-0	5	-0	3	13	16	13	16	16	16	3	3
011000	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	12	-0	-0	-0	-0
011001	-0	-0	-0	-0	-0	-0	-0	-0	-0	-7	-7	-7	-7	-7	-7	-0	-0
011010	-0	-0	-0	-0	-0	-0	-2	-0	-0	-2	2	-4	-0	-4	-4	-0	-0
011011	-0	6	6	6	-0	6	11	-0	6	-0	-6	-0	-6	-0	-0	-0	-0
011100	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-12	-0	-12	-0	-0	-0	-0
011101	-0	-0	-0	-0	-0	-0	-8	-0	-0	-8	-0	-8	-0	-8	-8	-0	-0
011110	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	2	-2	-0	-2	-2	-0	-0
011111	-0	-0	-0	3	-0	-3	-0	-0	-3	6	10	6	6	10	10	-0	-0
100000	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
100001	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	1	-1	2	-1	-1	-0	-0
100010	-0	-0	-0	-0	-0	-0	-0	-0	-0	-2	-2	-2	-2	-2	-2	-0	-0
100011	-0	-0	-0	-0	-0	-0	3	3	-0	3	3	3	3	6	6	-0	-0
100100	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
100101	-0	-0	-0	-0	-0	-0	-0	-0	-0	2	3	1	4	2	2	-0	-0
100110	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-2	-2	-2	-2	-2	-0	-0
100111	-0	-0	-0	-0	-0	-0	3	3	-0	-0	-0	-3	-0	-0	-0	-0	-0
101000	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
101001	-0	-0	-0	-0	-0	-0	-0	-0	-0	-1	-0	-1	-0	-1	-0	-0	-0
101010	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	2	-0	4	-0	-0	-0	-0
101011	-0	-0	-0	-0	-0	-0	-0	-0	-0	6	3	6	3	6	6	-0	-0
101100	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-5	-0	-0	-0	-0
101101	-0	-0	-0	-0	-0	-0	-0	-0	-0	-1	-1	-1	-1	-1	-1	-0	-0
101110	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-2	-0	-2	-2	-2	-0	-0
101111	-0	-0	-0	-0	-0	-0	-3	-3	-0	3	3	-0	6	3	3	-0	-0
110000	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-6	-6	-6	-0	-0	-0	-0
110001	-0	-0	-0	-0	-0	-0	-0	2	-0	2	2	2	4	2	2	2	-0
110010	-0	-0	-0	-0	-0	-0	-2	-0	-0	-2	-0	-2	-0	-2	-4	-0	-0
110011	-0	-0	3	3	-0	-0	-0	-0	-0	5	11	5	11	11	8	-0	-0
110100	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-6	-0	-6	-0	-0	-0	-0
110101	-0	-0	-0	-0	-0	-0	-2	-0	-0	2	2	2	2	2	2	-0	-0
110110	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-2	2	-4	-4	-0	-0
110111	-0	-0	-0	-0	-0	-0	-0	-0	-0	3	6	3	3	3	3	-0	-0
111000	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
111001	-0	-0	-0	-0	-0	-0	-0	-0	-0	2	2	-0	2	2	2	-0	-0
111010	-0	-0	-2	-0	-0	-0	-2	-0	-0	2	4	2	6	-0	-0	-0	-0
111011	-0	-0	-0	-0	-0	-0	-0	-0	-0	3	3	3	3	-0	-0	-0	-0
111100	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-6	-0	-6	-0	-0	-0	-0
111101	-0	-0	-0	-0	-0	-0	-0	2	-0	2	2	2	3	2	2	-0	-0
111110	-0	-0	-0	-0	-0	-0	-2	-0	-0	2	-0	-0	2	-0	-2	-0	-0
111111	-0	-0	-0	-0	-0	-0	-0	-0	-0	-6	-9	-6	-9	-6	-6	-0	-0

Robust Standard Error

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
000000	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.20	0.80	0.20	0.70	0.30	0.30	0.80	0.80
000001	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.20	0.80	0.30	0.80	0.30	0.20	1.00	1.00
000010	1.60	1.60	1.60	1.60	1.60	1.60	1.50	1.60	1.60	0.50	1.00	0.50	0.90	0.50	0.50	1.60	1.60
000011	4.50	4.40	4.40	4.40	4.50	4.40	4.30	4.40	4.60	0.40	1.30	0.40	0.90	0.40	0.40	4.40	4.40
000100	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.20	0.80	0.20	0.70	0.30	0.30	0.80	0.80
000101	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.90	1.00	0.20	0.90	0.30	0.80	0.30	0.20	1.00	1.00
000110	1.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50	0.50	1.10	0.50	1.00	0.50	0.50	1.50	1.50
000111	4.50	4.50	4.40	4.50	4.50	4.40	4.40	4.50	4.60	0.40	1.50	0.40	1.00	0.40	0.40	4.50	4.50
001000	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.20	0.80	0.20	0.70	0.30	0.30	0.90	0.90
001001	1.10	1.10	1.10	1.10	1.10	1.10	1.10	1.10	1.20	0.20	0.90	0.30	0.80	0.30	0.30	1.10	1.10
001010	1.70	1.70	1.70	1.70	1.70	1.70	1.70	1.70	1.70	0.60	1.00	0.50	0.90	0.50	0.50	1.70	1.70
001011	4.20	4.10	4.10	4.10	4.20	4.10	4.00	4.10	4.20	0.30	1.00	0.30	0.70	0.40	0.40	4.10	4.10
001100	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.90	0.20	0.80	0.20	0.70	0.30	0.30	0.80	0.80
001101	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.10	0.20	0.90	0.30	0.80	0.30	0.30	1.00	1.00
001110	1.60	1.60	1.60	1.60	1.60	1.50	1.50	1.60	1.60	0.50	1.00	0.50	0.90	0.50	0.50	1.60	1.60
001111	4.20	4.10	4.10	4.20	4.20	4.10	4.10	4.20	4.20	0.40	1.20	0.30	0.90	0.40	0.40	4.10	4.10
010000	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.70	0.80	0.50	0.90	0.60	1.10	0.40	0.40	0.80	0.80
010001	1.70	1.60	1.60	1.60	1.70	1.60	1.60	1.50	1.70	0.70	1.40	0.80	1.60	0.50	0.50	1.60	1.60
010010	3.40	3.30	3.10	3.20	3.40	3.20	3.00	3.10	3.20	1.70	2.20	1.40	2.10	1.40	1.40	3.20	3.30
010011	8.40	7.90	7.50	7.90	8.40	7.80	7.20	7.80	7.70	0.80	2.00	0.80	1.70	0.70	0.70	7.70	8.20
010100	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.40	0.80	0.50	1.10	0.40	0.40	0.70	0.70
010101	1.50	1.50	1.50	1.50	1.50	1.50	1.50	1.40	1.60	0.60	1.30	0.70	1.60	0.40	0.40	1.50	1.50
010110	3.00	2.90	2.80	2.90	3.00	2.90	2.70	2.90	2.90	1.60	2.10	1.30	2.00	1.30	1.30	2.90	2.90
010111	8.00	7.80	7.50	7.80	8.00	7.70	7.30	7.80	7.70	0.80	2.30	0.90	2.00	0.70	0.70	7.70	7.90
011000	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.80	0.90	0.40	1.00	0.40	1.10	0.40	0.30	0.90	0.90
011001	2.00	1.90	1.90	1.90	2.00	2.00	1.90	1.90	2.00	0.50	1.50	0.70	1.70	0.40	0.40	1.90	1.90
011010	3.10	2.90	2.80	2.90	3.10	2.90	2.80	2.90	2.90	1.70	2.00	1.30	1.90	1.30	1.30	2.90	2.90
011011	8.10	7.40	7.10	7.70	8.10	7.40	6.90	7.50	7.30	0.60	1.70	0.50	1.30	0.60	0.50	7.30	7.60
011100	0.80	0.80	0.80	0.70	0.80	0.70	0.80	0.70	0.80	0.30	0.90	0.40	1.10	0.30	0.30	0.70	0.80
011101	1.80	1.70	1.80	1.80	1.80	1.80	1.80	1.70	1.80	0.50	1.40	0.60	1.70	0.40	0.40	1.70	1.70
011110	2.60	2.50	2.40	2.60	2.60	2.50	2.40	2.50	2.50	1.50	1.80	1.20	1.90	1.20	1.20	2.50	2.50
011111	7.90	7.50	7.30	7.80	7.90	7.50	7.10	7.80	7.50	0.70	2.20	0.70	1.80	0.70	0.70	7.50	7.60
100000	0.80	0.80	0.80	0.80	0.80	0.70	0.80	0.80	0.80	0.40	0.60	0.40	1.20	0.40	0.40	0.80	0.80
100001	4.10	4.10	4.10	4.10	4.10	3.90	4.10	3.90	4.00	1.00	2.40	1.60	2.70	0.80	0.80	4.10	4.10
100010	2.00	2.00	2.00	2.00	2.00	1.90	2.00	2.00	2.00	1.10	1.50	1.00	2.00	1.00	1.00	2.00	2.00
100011	6.00	5.90	5.90	5.90	6.00	5.80	5.90	5.80	6.00	2.00	3.30	2.90	3.40	1.70	1.70	5.90	5.90
100100	0.80	0.80	0.80	0.80	0.80	0.70	0.80	0.70	0.70	0.40	0.60	0.40	1.20	0.40	0.40	0.80	0.80
100101	3.90	4.00	3.90	3.90	3.90	3.70	3.90	3.80	3.80	1.00	2.30	1.60	2.90	0.80	0.80	3.90	3.90
100110	1.90	1.90	1.90	1.90	1.90	1.80	1.90	1.90	1.90	1.00	1.40	1.00	2.00	1.00	1.00	1.90	1.90
100111	5.60	5.60	5.60	5.50	5.60	5.50	5.50	5.50	5.60	2.00	3.20	2.80	3.50	1.80	1.80	5.60	5.60
101000	0.80	0.80	0.80	0.80	0.80	0.70	0.80	0.80	0.80	0.40	0.60	0.40	1.20	0.40	0.40	0.80	0.80
101001	4.20	4.20	4.20	4.10	4.20	3.90	4.10	4.00	4.10	1.10	2.40	1.60	2.80	0.80	0.80	4.20	4.10
101010	2.10	2.10	2.10	2.10	2.10	2.10	2.10	2.10	2.10	1.10	1.60	1.10	2.00	1.00	1.00	2.10	2.10
101011	6.20	6.20	6.20	6.20	6.20	6.10	6.10	6.10	6.20	1.90	3.30	2.80	3.50	1.70	1.70	6.20	6.10
101100	0.80	0.80	0.80	0.80	0.80	0.70	0.80	0.70	0.70	0.40	0.60	0.40	1.20	0.40	0.40	0.80	0.80
101101	4.00	4.00	4.10	3.90	4.00	3.80	3.90	3.90	3.90	1.00	2.30	1.50	2.90	0.80	0.80	4.00	4.00
101110	1.90	1.90	1.90	1.90	1.90	1.90	1.90	1.90	1.90	1.10	1.50	1.00	2.10	1.00	1.00	1.90	1.90
101111	5.80	5.80	5.80	5.80	5.80	5.80	5.80	5.70	5.80	1.90	3.10	2.70	3.40	1.70	1.70	5.80	5.80
110000	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.60	0.70	0.60	1.10	0.50	0.50	0.80	0.80
110001	3.30	3.20	3.30	3.30	3.30	3.30	3.20	3.00	3.50	1.40	2.10	1.60	2.50	0.80	0.80	3.20	3.20
110010	2.90	2.90	2.80	2.80	2.90	2.90	2.80	2.80	2.90	1.60	2.20	1.50	2.30	1.50	1.50	2.80	2.80
110011	7.70	7.30	7.10	7.30	7.70	7.60	6.90	7.10	7.60	2.30	3.30	3.20	3.20	1.60	1.60	7.10	7.20
110100	0.80	0.80	0.80	0.80	0.80	0.70	0.80	0.70	0.80	0.50	0.70	0.60	1.10	0.50	0.40	0.80	0.80
110101	3.20	3.10	3.10	3.10	3.20	3.00	3.10	3.00	3.30	1.20	2.00	1.40	2.60	0.80	0.80	3.10	3.10
110110	2.60	2.60	2.50	2.60	2.60	2.60	2.50	2.50	2.60	1.30	1.90	1.30	2.20	1.30	1.30	2.50	2.50
110111	7.10	6.90	6.80	7.00	7.10	7.00	6.70	6.80	7.10	2.10	3.10	3.00	3.20	1.60	1.60	6.80	6.80
111000	0.90	0.90	0.90	0.80	0.90	0.80	0.90	0.80	0.90	0.50	0.70	0.50	1.20	0.40	0.40	0.90	0.90
111001	3.90	3.70	3.80	3.80	3.90	3.80	3.70	3.60	4.00	1.20	2.30	1.40	2.70	0.80	0.80	3.70	3.70
111010	2.60	2.50	2.50	2.50	2.60	2.50	2.50	2.40	2.50	1.30	1.90	1.20	2.10	1.20	1.20	2.50	2.50
111011	7.40	6.80	6.70	7.10	7.40	7.30	6.60	6.70	7.30	1.70	3.20	2.50	3.20	1.30	1.30	6.80	6.80
111100	0.80	0.80	0.80	0.80	0.80	0.70	0.80	0.70	0.80	0.40	0.70	0.40	1.20	0.40	0.40	0.80	0.80
111101	3.50	3.50	3.50	3.50	3.50	3.40	3.40	3.30	3.60	1.00	2.10	1.20	2.70	0.70	0.70	3.40	3.40
111110	2.30	2.20	2.20	2.30	2.30	2.30	2.20	2.20	2.30	1.30	1.80	1.20	2.20	1.20	1.20	2.20	2.20
111111	6.80	6.40	6.30	6.70	6.80	6.70	6.40	6.50	6.80	1.50	2.90	2.30	3.20	1.30	1.30	6.40	6.50

Empirical Standard Error

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
000000	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.20	1.00	0.20	0.90	0.50	0.50	0.80	0.80
000001	1.00	1.00	1.00	1.10	1.00	1.10	1.10	1.00	1.00	0.20	1.00	0.30	0.90	0.40	0.40	1.00	1.00
000010	1.70	1.60	1.60	1.70	1.70	1.60	1.70	1.60	1.70	0.50	1.20	0.40	1.00	0.70	0.70	1.60	1.60
000011	4.60	4.50	4.50	4.60	4.60	4.50	4.50	4.60	4.40	0.40	1.20	0.40	0.90	0.60	0.60	4.50	4.50
000100	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.20	1.10	0.30	0.80	0.50	0.50	0.80	0.80
000101	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.20	1.10	0.30	0.90	0.40	0.40	1.00	1.00
000110	1.50	1.50	1.50	1.60	1.50	1.50	1.60	1.50	1.50	0.50	1.30	0.40	1.10	0.70	0.70	1.50	1.50
000111	4.60	4.50	4.50	4.60	4.60	4.50	4.50	4.60	4.50	0.50	1.40	0.40	1.00	0.50	0.50	4.50	4.50
001000	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.20	1.00	0.30	0.90	0.60	0.50	0.90	0.90
001001	1.10	1.10	1.10	1.20	1.10	1.20	1.20	1.10	1.20	0.20	1.10	0.30	0.90	0.50	0.50	1.10	1.10
001010	1.70	1.70	1.70	1.80	1.70	1.70	1.80	1.70	1.80	0.60	1.10	0.50	1.00	0.70	0.70	1.70	1.70
001011	4.30	4.20	4.20	4.30	4.30	4.30	4.30	4.30	4.30	0.30	1.00	0.30	0.70	0.70	0.60	4.20	4.20
001100	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.20	1.20	0.30	0.90	0.60	0.60	0.90	0.90
001101	1.00	1.00	1.00	1.00	1.00	1.00	1.10	1.00	1.00	0.20	1.10	0.30	0.90	0.50	0.50	1.00	1.00
001110	1.60	1.60	1.60	1.60	1.60	1.60	1.70	1.60	1.60	0.50	1.30	0.50	1.10	0.80	0.80	1.60	1.60
001111	4.40	4.30	4.30	4.40	4.40	4.30	4.40	4.40	4.30	0.40	1.20	0.40	0.90	0.60	0.60	4.30	4.30
010000	0.80	0.80	0.80	0.80	0.80	0.80	0.90	0.80	0.80	0.60	1.20	0.70	1.50	0.70	0.70	0.80	0.80
010001	1.60	1.60	1.60	1.60	1.60	1.70	1.70	1.60	1.60	0.80	1.70	0.90	2.00	0.70	0.70	1.50	1.50
010010	2.90	2.80	2.60	2.80	2.90	2.80	2.90	2.70	2.70	1.00	2.20	0.80	2.20	1.40	1.40	2.70	2.80
010011	8.50	8.00	7.60	8.20	8.50	7.80	7.30	7.70	7.30	1.00	1.90	1.10	1.70	1.00	1.00	7.80	7.90
010100	0.70	0.70	0.70	0.70	0.70	0.70	0.80	0.70	0.70	0.40	1.00	0.50	1.30	0.60	0.60	0.70	0.70
010101	1.60	1.50	1.60	1.60	1.60	1.60	1.60	1.50	1.50	0.60	1.50	0.70	1.90	0.60	0.50	1.50	1.50
010110	2.50	2.40	2.30	2.50	2.50	2.40	2.50	2.40	2.40	1.00	2.30	0.80	2.30	1.30	1.30	2.40	2.40
010111	8.10	7.90	7.60	8.10	8.10	7.90	7.40	7.80	7.50	0.80	1.90	1.00	1.80	0.80	0.80	7.70	7.80
011000	0.90	0.80	0.90	0.90	0.90	0.90	1.00	0.80	0.90	0.40	1.30	0.50	1.40	0.60	0.60	0.80	0.80
011001	2.10	2.00	2.10	2.10	2.10	2.10	2.10	2.00	2.00	0.60	1.80	0.70	2.00	0.60	0.50	2.00	2.00
011010	2.70	2.50	2.50	2.60	2.70	2.60	2.70	2.50	2.50	1.10	2.00	0.90	2.00	1.20	1.20	2.50	2.50
011011	7.90	7.30	7.00	7.70	7.90	7.20	7.10	7.30	7.00	0.90	1.70	0.90	1.50	1.00	0.90	7.20	7.30
011100	0.70	0.70	0.80	0.70	0.70	0.80	0.90	0.70	0.70	0.30	1.10	0.40	1.30	0.50	0.40	0.70	0.70
011101	1.90	1.90	1.90	2.00	1.90	1.90	2.00	1.90	1.90	0.50	1.80	0.60	2.10	0.50	0.50	1.90	1.90
011110	2.40	2.30	2.20	2.40	2.40	2.30	2.40	2.30	2.30	1.20	2.00	0.90	2.00	1.10	1.10	2.30	2.30
011111	8.00	7.60	7.50	8.00	8.00	7.70	7.50	7.80	7.50	0.70	1.90	0.80	1.70	0.90	0.90	7.60	7.60
100000	0.70	0.70	0.70	0.70	0.70	0.70	0.80	0.70	0.70	0.40	0.60	0.40	1.50	0.50	0.50	0.70	0.70
100001	4.10	4.00	4.10	4.20	4.10	4.10	4.20	4.10	4.10	1.00	1.80	1.60	2.50	0.90	0.90	4.00	4.00
100010	1.40	1.40	1.40	1.40	1.40	1.40	1.50	1.40	1.40	0.50	1.60	0.60	2.40	0.90	0.90	1.40	1.40
100011	5.60	5.40	5.50	5.60	5.60	5.60	5.60	5.60	5.60	1.60	2.40	2.60	2.70	1.70	1.70	5.40	5.50
100100	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.40	0.60	0.40	1.40	0.50	0.40	0.70	0.70
100101	3.90	3.90	3.90	4.00	3.90	3.90	4.00	4.00	3.90	1.00	1.60	1.50	2.50	0.90	0.90	3.90	3.90
100110	1.40	1.40	1.40	1.40	1.40	1.40	1.50	1.40	1.40	0.50	1.70	0.50	2.60	0.90	0.90	1.40	1.40
100111	5.50	5.40	5.40	5.50	5.50	5.50	5.50	5.50	5.50	1.60	2.20	2.60	2.70	1.70	1.70	5.40	5.40
101000	0.70	0.70	0.70	0.80	0.70	0.70	0.80	0.80	0.70	0.40	0.70	0.40	1.50	0.40	0.40	0.70	0.70
101001	4.20	4.20	4.20	4.30	4.20	4.30	4.30	4.30	4.20	1.10	1.90	1.60	2.50	0.90	0.90	4.20	4.20
101010	1.50	1.40	1.40	1.60	1.50	1.50	1.50	1.50	1.50	0.50	1.80	0.60	2.60	0.90	0.90	1.40	1.40
101011	6.20	6.10	6.10	6.20	6.20	6.20	6.30	6.20	6.20	1.50	2.30	2.70	2.80	1.60	1.60	6.10	6.10
101100	0.70	0.70	0.70	0.80	0.70	0.70	0.80	0.80	0.70	0.40	0.60	0.40	1.50	0.40	0.40	0.70	0.70
101101	3.90	3.90	3.90	4.00	3.90	3.90	3.90	3.90	3.90	1.00	1.70	1.50	2.60	0.90	0.90	3.90	3.90
101110	1.40	1.30	1.40	1.40	1.40	1.40	1.40	1.40	1.40	0.50	1.60	0.60	2.60	0.90	0.90	1.30	1.30
101111	5.80	5.80	5.80	5.90	5.80	5.80	5.90	5.90	5.80	1.50	2.30	2.60	2.70	1.60	1.50	5.80	5.80
110000	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.60	0.90	0.60	1.50	0.70	0.70	0.80	0.80
110001	3.20	3.10	3.20	3.30	3.20	3.30	3.20	3.10	3.10	1.40	1.90	1.50	2.40	0.90	0.90	3.00	3.00
110010	2.30	2.20	2.20	2.30	2.30	2.30	2.40	2.20	2.20	0.80	2.30	0.90	2.60	1.40	1.40	2.20	2.20
110011	7.70	7.30	7.20	7.50	7.70	7.60	7.10	7.10	7.40	2.00	2.50	3.20	2.70	1.70	1.70	7.10	7.20
110100	0.70	0.70	0.70	0.70	0.70	0.70	0.80	0.70	0.70	0.50	0.70	0.50	1.40	0.60	0.60	0.70	0.70
110101	3.30	3.20	3.30	3.30	3.30	3.30	3.30	3.30	3.30	1.20	1.80	1.40	2.60	0.90	0.90	3.20	3.20
110110	2.00	1.90	1.90	2.00	2.00	2.00	2.10	2.00	2.00	0.60	2.20	0.70	2.60	1.20	1.10	1.90	1.90
110111	7.10	6.90	6.70	7.10	7.10	7.10	6.80	6.90	7.00	1.90	2.40	3.00	2.60	1.70	1.70	6.80	6.90
111000	0.80	0.80	0.90	0.80	0.80	0.80	0.90	0.80	0.80	0.50	0.90	0.50	1.50	0.60	0.60	0.80	0.80
111001	3.90	3.70	3.80	3.90	3.90	3.90	3.90	3.70	3.80	1.20	2.00	1.40	2.60	0.90	0.90	3.70	3.70
111010	1.90	1.80	1.90	2.00	1.90	1.90	2.10	1.90	1.90	0.60	2.20	0.70	2.60	1.10	1.10	1.80	1.80
111011	7.60	7.00	6.90	7.50	7.60	7.50	7.00	6.90	7.20	1.40	2.50	2.40	2.60	1.40	1.40	7.00	7.00
111100	0.70	0.70	0.70	0.70	0.70	0.70	0.80	0.70	0.70	0.40	0.70	0.40	1.40	0.50	0.50	0.70	0.70
111101	3.70	3.60	3.60	3.70	3.70	3.70	3.70	3.60	3.60	1.00	1.80	1.20	2.70	0.90	0.80	3.60	3.60
111110	1.60	1.60	1.60	1.60	1.60	1.60	1.70	1.60	1.60	0.60	1.90	0.70	2.60	1.10	1.10	1.60	1.60
111111	6.80	6.50	6.40	6.90	6.80	6.80	6.60	6.60	6.70	1.20	2.20	2.30	2.50	1.30	1.30	6.50	6.50

Improvement

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
000000	0	2	1	-3	0	-1	-0	1	-2	76	-28	69	-5	39	42	2	2
000001	0	1	0	-1	0	-1	-2	1	-0	78	0	73	10	59	62	1	1
000010	0	2	3	-2	0	0	-2	1	0	68	26	73	37	57	59	2	2
000011	0	2	3	-1	0	1	3	0	4	87	73	87	78	85	85	2	2
000100	0	1	-0	-1	0	-1	-2	0	-1	76	-41	68	-5	37	40	1	1
000101	0	1	1	-1	0	-1	-0	1	0	78	-7	72	10	56	59	1	1
000110	0	1	1	-1	0	-0	-1	0	-0	67	15	72	29	55	57	1	1
000111	0	2	2	-1	0	1	1	-0	2	84	67	84	74	82	83	2	1
001000	0	1	1	-1	0	-0	-2	1	-2	75	-15	69	1	34	42	2	2
001001	0	1	0	-2	0	-0	-2	0	-2	79	6	74	19	58	60	1	1
001010	0	2	2	-2	0	0	-3	0	-3	66	37	71	44	58	60	2	2
001011	0	2	2	-1	0	0	0	-0	0	91	76	91	82	84	84	2	1
001100	0	1	-0	-1	0	-1	-2	1	-2	77	-33	70	-5	29	33	1	1
001101	0	1	-0	-1	0	-1	-3	0	-1	78	-9	72	8	52	54	1	1
001110	0	1	1	-1	0	0	-2	-0	-1	67	22	72	35	51	54	1	1
001111	0	2	2	-1	0	1	-2	-0	1	91	74	91	80	87	87	1	1
010000	0	4	-2	-1	0	-2	-9	6	3	31	-49	19	-84	12	15	6	5
010001	0	5	2	2	0	-0	-5	6	4	53	-5	46	-24	60	60	7	6
010010	0	4	9	2	0	4	0	8	6	67	24	70	23	51	52	6	5
010011	0	5	10	4	0	8	14	10	14	89	78	87	79	88	88	9	7
010100	0	1	-1	-1	0	-2	-13	1	0	37	-47	24	-84	13	17	2	1
010101	0	3	1	-0	0	-1	-2	3	3	59	2	53	-24	64	66	4	4
010110	0	2	6	-1	0	2	-2	4	4	61	8	65	7	45	46	3	3
010111	0	3	7	0	0	3	9	4	8	89	75	86	77	88	88	5	4
011000	0	4	-4	-2	0	-0	-12	3	1	57	-53	46	-59	32	34	5	4
011001	0	6	3	1	0	1	-1	6	4	72	12	68	6	73	74	7	7
011010	0	7	10	3	0	5	-0	8	6	59	27	68	26	54	55	7	7
011011	0	7	10	2	0	8	10	8	11	89	78	89	81	87	88	8	7
011100	0	2	-3	-0	0	-2	-16	2	1	59	-52	47	-73	33	40	3	2
011101	0	4	2	-1	0	0	-4	2	3	75	8	70	-8	73	75	4	4
011110	0	5	6	-0	0	2	-2	4	4	52	17	63	16	53	54	4	4
011111	0	5	6	-1	0	4	6	2	7	90	76	90	79	88	88	5	5
100000	0	-0	-0	-2	0	-0	-4	-2	-0	51	12	50	-101	28	30	0	0
100001	0	1	1	-2	0	-0	-2	-1	-0	75	56	62	40	78	78	1	1
100010	0	1	1	-3	0	-0	-5	-4	0	63	-16	58	-74	34	35	1	1
100011	0	2	2	-1	0	-0	-1	-1	-0	72	57	53	52	69	69	2	2
100100	0	0	0	-1	0	-0	-3	-4	-0	46	16	45	-98	34	36	-0	0
100101	0	1	0	-1	0	-0	-3	-2	-0	75	58	62	35	76	77	1	0
100110	0	0	0	-2	0	-0	-5	-3	-0	64	-20	62	-91	35	36	0	0
100111	0	1	1	-1	0	-0	-1	-1	0	71	59	53	50	68	68	1	1
101000	0	1	0	-4	0	-0	-3	-4	-0	46	5	47	-103	39	41	1	0
101001	0	2	2	-1	0	-0	-1	-1	-0	74	56	63	40	78	78	2	2
101010	0	1	1	-7	0	-0	-6	-3	-0	64	-21	59	-74	36	36	1	1
101011	0	2	2	-1	0	-0	-1	0	-0	76	62	56	55	73	74	2	2
101100	0	-1	-0	-6	0	0	-5	-5	0	46	14	45	-102	37	38	-1	-1
101101	0	0	0	-2	0	-0	-1	-1	-0	74	56	63	33	76	77	0	1
101110	0	1	0	-4	0	-0	-6	-3	-0	62	-17	58	-90	33	33	1	1
101111	0	1	1	-1	0	0	-1	-1	0	75	60	56	53	73	74	1	1
110000	0	2	-0	-2	0	-3	-6	1	0	21	-14	21	-90	16	18	2	2
110001	0	5	1	-3	0	-2	1	4	3	57	42	52	27	71	71	6	6
110010	0	3	3	-1	0	-1	-6	3	1	65	-3	61	-14	38	39	5	4
110011	0	5	7	3	0	1	8	8	4	73	67	59	65	78	78	8	6
110100	0	1	-0	-0	0	-1	-7	-1	0	29	0	25	-96	14	18	1	1
110101	0	3	0	-1	0	-1	-1	1	0	64	46	59	21	72	73	3	3
110110	0	2	2	-2	0	-0	-8	-0	0	67	-9	62	-30	41	42	2	2
110111	0	3	5	-0	0	0	4	3	2	73	66	58	63	76	76	4	3
111000	0	1	-5	-1	0	-2	-7	-2	0	41	-7	42	-79	32	32	1	1
111001	0	5	3	-1	0	-1	1	4	3	69	47	64	34	77	78	6	6
111010	0	5	1	-2	0	-1	-9	3	2	66	-14	63	-38	44	45	5	5
111011	0	7	9	1	0	1	7	9	5	81	67	69	65	81	82	8	7
111100	0	1	-1	-4	0	-1	-7	-1	-0	44	-1	41	-101	31	33	2	1
111101	0	3	3	-0	0	-0	-1	1	1	72	50	68	27	77	77	3	3
111110	0	2	2	-0	0	-0	-9	-1	0	61	-20	58	-63	30	31	2	2
111111	0	5	7	-2	0	0	4	4	2	81	67	66	63	80	80	5	5

Power

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
000000	7	7	7	8	7	8	7	7	6	45	6	29	6	37	39	7	7
000001	7	7	8	8	7	8	9	8	7	66	9	45	10	59	62	7	7
000010	12	12	12	12	12	13	14	12	11	91	29	97	35	85	87	12	12
000011	6	6	7	7	6	6	7	6	5	97	13	96	26	94	94	6	6
000100	9	9	9	10	9	10	11	10	7	53	7	34	6	44	47	9	9
000101	7	7	8	8	7	8	8	9	6	67	8	46	9	60	62	7	7
000110	18	18	18	19	18	19	19	19	16	97	33	99	40	92	93	18	18
000111	8	8	7	8	8	8	8	8	6	99	15	99	28	96	97	7	8
001000	6	6	6	6	6	6	7	6	5	51	8	30	8	43	46	6	6
001001	7	7	8	9	7	8	8	8	6	68	10	46	10	62	64	7	7
001010	10	11	12	12	10	12	13	11	12	87	28	98	36	86	88	11	11
001011	7	7	6	7	7	8	8	7	6	87	10	85	16	71	75	7	6
001100	8	8	8	9	8	9	9	9	7	54	7	32	6	44	48	8	8
001101	6	6	6	7	6	7	8	7	6	65	7	44	8	56	60	6	6
001110	14	14	14	14	14	15	16	14	13	91	26	98	32	87	89	14	14
001111	8	8	8	8	8	8	9	8	7	94	10	93	18	87	88	8	8
010000	15	16	16	16	15	16	17	20	13	36	14	25	8	51	53	16	15
010001	10	10	10	11	10	12	11	12	8	46	18	34	13	73	74	10	10
010010	29	31	38	36	29	32	39	35	34	96	65	100	68	97	97	33	31
010011	7	7	7	7	7	7	7	6	6	97	21	92	30	93	94	7	7
010100	18	18	18	19	18	20	19	21	15	48	17	31	10	59	58	18	18
010101	12	13	13	14	12	14	14	14	11	56	16	38	11	79	80	13	13
010110	38	40	44	41	38	40	46	42	40	99	69	100	73	98	98	41	40
010111	9	9	9	9	9	9	9	8	8	99	22	96	30	99	99	9	8
011000	13	14	14	14	13	14	16	16	12	68	18	54	11	72	75	14	14
011001	10	10	10	11	9	10	11	11	9	79	18	64	15	93	95	10	9
011010	33	38	40	37	33	37	42	38	37	95	71	100	76	98	99	37	37
011011	6	6	6	7	6	7	7	6	6	94	15	94	23	88	90	6	6
011100	18	17	17	18	18	19	20	20	15	82	19	64	11	78	80	18	17
011101	13	13	14	14	13	13	15	14	11	90	18	77	12	94	96	13	13
011110	45	48	50	46	45	47	51	47	47	99	76	100	77	99	99	48	48
011111	8	9	9	8	8	8	10	8	8	100	21	100	32	98	98	9	8
100000	73	72	73	73	73	79	74	76	76	100	92	100	48	98	99	72	72
100001	55	54	54	55	55	58	55	58	55	100	98	100	88	100	100	54	54
100010	88	89	88	88	88	90	88	89	89	100	96	100	85	100	100	89	89
100011	8	8	8	8	8	9	8	9	8	38	10	20	11	49	49	8	8
100100	78	76	78	78	78	84	78	80	82	100	95	100	52	99	99	76	77
100101	61	60	61	63	61	64	62	64	62	100	99	100	88	100	100	60	60
100110	90	89	89	90	90	92	90	90	91	100	95	100	83	99	99	89	89
100111	11	10	10	11	11	12	11	11	10	37	11	23	11	49	49	10	10
101000	73	71	71	73	73	79	72	75	76	100	91	100	48	99	99	72	72
101001	51	51	51	52	51	54	52	55	52	100	96	100	88	100	100	52	52
101010	82	83	83	83	82	85	83	84	83	100	93	100	81	100	100	83	83
101011	9	9	8	9	9	10	10	10	8	37	9	17	12	50	50	9	9
101100	75	72	73	76	75	82	75	78	79	100	95	100	45	98	98	72	74
101101	56	55	54	57	56	59	56	58	56	100	98	100	86	100	100	55	56
101110	90	90	89	90	90	91	90	91	90	100	97	100	81	100	100	90	90
101111	10	10	10	10	10	10	10	10	10	42	13	25	10	53	52	10	10
110000	48	49	49	50	48	54	52	55	48	82	79	78	45	90	90	50	50
110001	32	33	32	33	32	34	33	37	29	95	70	88	50	100	100	33	33
110010	41	42	44	45	41	42	46	46	41	100	72	100	68	98	98	43	44
110011	9	9	9	10	9	9	9	10	8	31	12	20	14	56	56	9	9
110100	59	57	58	60	59	65	58	65	58	91	83	86	41	91	92	59	58
110101	39	40	40	40	39	42	41	44	36	100	80	96	56	100	100	41	41
110110	57	58	59	59	57	58	60	61	57	100	83	100	74	99	100	58	58
110111	9	8	8	9	9	9	9	9	8	35	14	20	13	59	60	9	8
111000	51	52	52	53	51	54	53	56	50	94	76	95	38	95	96	52	52
111001	30	32	31	31	30	31	32	35	27	100	75	99	58	100	100	33	33
111010	61	64	65	62	61	62	64	66	61	100	81	100	73	100	100	65	65
111011	9	10	10	10	9	9	11	9	8	53	11	28	14	71	72	9	10
111100	58	55	57	60	58	62	58	62	57	99	83	97	35	97	98	56	56
111101	37	37	37	39	37	38	39	41	35	100	83	100	58	100	100	38	38
111110	76	78	78	77	76	76	78	78	75	100	89	100	77	100	100	78	78
111111	10	10	10	10	10	10	10	10	9	64	16	31	14	75	76	10	10

Coverage

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
000000	94	95	95	93	94	94	94	94	95	94	95	94	95	88	90	95	95
000001	93	94	94	92	93	93	92	92	95	94	95	94	95	88	88	94	94
000010	92	93	93	92	92	92	92	92	93	91	90	94	90	86	88	93	93
000011	94	94	94	93	94	94	93	94	95	88	95	88	92	83	83	94	94
000100	94	94	94	93	94	93	94	93	95	90	94	92	94	85	85	94	93
000101	94	94	94	93	94	94	93	93	95	92	95	93	95	87	87	94	94
000110	93	94	94	93	93	93	93	93	94	91	91	93	91	88	89	94	94
000111	95	94	94	95	95	95	95	95	96	68	91	66	87	61	61	95	95
001000	95	96	96	95	95	95	94	94	96	92	94	93	94	87	88	95	95
001001	94	94	94	93	94	94	94	93	95	90	92	92	92	85	86	94	94
001010	94	94	94	93	94	93	92	94	93	90	90	92	90	86	88	94	94
001011	95	95	94	94	95	94	93	95	95	77	92	80	88	71	72	95	95
001100	93	93	93	92	93	92	92	92	94	92	95	92	96	83	84	93	93
001101	94	95	95	93	94	94	93	94	96	91	95	92	96	85	87	95	95
001110	92	92	91	92	92	92	91	92	92	90	89	93	90	86	87	92	92
001111	93	93	93	93	93	92	92	93	93	91	94	91	94	86	86	93	93
010000	94	95	94	94	94	93	94	94	96	94	97	95	96	88	88	96	95
010001	95	95	95	94	95	94	93	94	95	92	95	93	94	86	85	94	94
010010	97	97	97	97	97	97	95	97	97	98	91	99	91	95	95	97	97
010011	94	94	94	93	94	94	95	95	96	84	94	84	91	80	81	95	96
010100	95	95	94	94	95	93	93	93	96	95	97	94	96	89	89	95	95
010101	94	95	95	93	94	94	93	93	96	92	96	94	96	88	88	95	95
010110	98	98	98	97	98	98	96	98	98	98	92	99	91	94	95	98	98
010111	93	93	94	92	93	93	93	93	94	89	97	87	95	82	82	93	94
011000	95	95	94	94	95	94	94	94	95	93	96	95	96	88	88	95	95
011001	92	93	92	92	92	92	92	92	94	93	95	94	94	91	92	93	94
011010	96	96	96	96	96	96	95	96	96	97	93	99	93	94	95	96	96
011011	94	94	94	94	94	94	93	95	95	71	94	72	91	67	68	94	94
011100	95	95	95	94	95	94	94	94	96	95	98	94	96	90	90	95	95
011101	92	92	92	91	92	92	91	92	94	94	94	94	94	88	89	92	92
011110	94	94	94	94	94	94	92	94	95	95	92	96	92	94	94	94	94
011111	94	94	94	93	94	94	93	94	95	88	96	86	94	83	83	94	94
100000	97	97	97	96	97	94	96	96	96	97	98	96	96	93	94	97	97
100001	94	94	94	93	94	92	93	92	94	95	99	95	97	92	93	94	94
100010	99	100	100	99	99	99	99	99	99	100	96	100	93	98	98	100	100
100011	96	96	96	96	96	96	96	95	96	98	99	97	99	95	95	96	96
100100	97	97	97	96	97	96	96	95	96	95	98	96	95	91	92	97	97
100101	94	95	95	94	94	93	94	93	94	94	99	95	97	90	92	95	95
100110	99	99	99	99	99	99	99	99	99	100	95	100	92	97	97	99	99
100111	94	94	95	94	94	94	94	94	94	98	100	96	99	96	95	95	94
101000	96	97	97	96	96	95	95	95	96	96	96	97	95	93	94	97	97
101001	93	94	94	93	93	92	92	92	93	93	99	94	97	91	92	94	94
101010	99	99	99	99	99	99	99	99	99	100	95	100	92	98	98	99	99
101011	95	95	95	94	95	94	94	94	94	98	99	95	98	95	95	95	95
101100	96	97	96	95	96	94	96	94	95	96	97	95	96	93	94	97	96
101101	96	96	96	94	96	95	95	95	95	96	99	96	98	92	93	96	96
101110	100	100	100	99	100	99	99	99	99	100	95	100	93	98	98	100	100
101111	95	95	95	95	95	95	94	93	95	98	98	96	98	96	96	95	95
110000	95	96	95	95	95	94	95	94	96	95	97	95	96	90	90	96	96
110001	95	95	95	94	95	94	95	93	97	95	98	96	97	90	90	95	95
110010	98	98	98	98	98	98	97	98	98	100	94	100	93	96	96	99	99
110011	94	94	94	94	94	94	92	93	95	97	99	95	98	92	92	94	94
110100	96	96	95	95	96	94	95	94	96	95	97	96	95	89	91	96	96
110101	93	92	92	93	93	92	93	91	94	94	97	95	96	89	89	93	93
110110	98	98	98	98	98	98	98	98	98	100	94	100	93	97	98	98	98
110111	93	94	94	93	93	93	94	94	94	97	99	95	98	94	94	94	94
111000	95	95	95	95	95	93	95	94	96	94	95	96	96	91	92	96	95
111001	95	94	94	93	95	94	94	92	96	94	97	94	96	90	91	95	94
111010	99	99	99	98	99	99	98	98	99	100	92	99	90	96	97	99	99
111011	94	93	93	92	94	94	92	93	94	97	99	95	98	93	93	93	93
111100	95	96	96	94	95	94	94	94	95	96	97	96	96	93	92	96	96
111101	92	93	94	92	92	92	91	92	94	94	98	95	96	91	90	93	93
111110	99	99	99	99	99	99	98	99	99	100	95	100	92	97	97	99	99
111111	93	93	94	93	93	93	93	93	94	98	99	94	98	93	93	93	93

Appendix: Augmented GEE on Larger Networks

Statistics Marginal Across All Scenarios

Treatment Effect $\overline{\beta}$: -3.43

	None	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
Bias	0	0	0	0	0	0	0	0	0	0.01	0.02	0	0	0.02	0.02	0.01	0.01
RobSE	1.61	1.54	1.53	1.52	1.61	1.43	1.5	1.38	1.81	0.79	1.47	0.96	1.75	0.62	0.62	0.9	1
EmpSE	1.33	1.24	1.22	1.31	1.33	1.34	1.25	1.29	1.25	0.6	0.86	0.74	1.37	0.58	0.57	0.62	0.63
Gains	0(0)	4(5)	3(9)	-4(9)	0(0)	-3(6)	0(9)	-1(10)	3(6)	38(45)	19(31)	30(46)	-57(75)	44(30)	44(30)	33(55)	34(51)
Power	67	68.4	67.9	68.8	67	73.5	69.2	75	58	89.3	62.9	86.5	54.5	92.2	92.2	88.2	84.1
Coverage	98(2)	98(2)	98(2)	98(2)	98(2)	95(2)	98(2)	95(2)	99(1)	98(2)	99(1)	98(2)	98(2)	94(4)	95(4)	99(2)	98(2)

Unadj: No adjustment term
F_1: Degree
F_2: Mean Neighbor Degree
F_3: Assortativity
F_4: Member of Connected Block
F_5: Size of Largest Component
F_6: Mean Component Size
F_7: Number of Components
F_8: Size of Node's Component
F_9: Total Neighbor Infections at baseline
F_{10}: Total Node's Component Infections at baseline
F_{11}: 1/nearest infected path length at baseline
F_{12}: $\sum_i$ 1/path length to Infected Node i at baseline
All: Complete inclusion of the above
Step: Stepwise regression of the above
Pow: Powerlaw(Degree)
Spl: Spline(Degree)

$\boldsymbol{a} =$ [𝕀(High Degree),
𝕀(Powerlaw),
𝕀(Assortativity),
𝕀(Blocks),
𝕀(Degree Infectivity),
𝕀(High Baseline)]

Statistics Modification By Scenario Aspect

a	γ_a
(Intercept)	-1.40
High Degree	-1.18
Powerlaw	-0.68
Assortative	-0.13
Communities	-0.17
Deg. Infect.	-1.66
High Base.	-0.23

Bias

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
(Intercept)	-0.00	-0.00	0.01	0.01	-0.00	-0.00	-0.01	0.00	-0.00	-0.03	-0.03	-0.03	-0.04	-0.00	-0.00	-0.03	-0.03
High Degree	0.00	-0.01	-0.01	-0.02	0.00	0.00	-0.01	-0.00	-0.00	0.01	0.00	0.00	0.01	0.01	0.00	0.00	0.01
Powerlaw	0.00	-0.00	-0.01	-0.00	0.00	0.00	-0.01	-0.00	0.01	0.01	0.02	0.01	-0.00	0.03	0.03	0.01	0.01
Assortative	0.00	0.01	0.01	0.00	0.00	0.00	0.01	0.00	-0.00	0.02	0.03	0.02	0.04	0.02	0.02	0.02	0.02
Communities	-0.00	0.00	0.01	0.00	-0.00	-0.00	0.01	0.00	-0.00	0.01	0.02	0.01	0.03	0.00	0.00	0.02	0.02
Deg. Infect.	0.00	0.00	-0.01	-0.00	0.00	0.00	0.00	-0.00	0.00	0.01	0.01	0.02	-0.02	0.02	0.03	0.00	0.00
High Base.	0.00	-0.00	-0.01	-0.00	0.00	0.00	-0.00	-0.00	0.00	0.02	0.02	0.00	0.02	-0.02	-0.03	0.02	0.02

Robust S.E.

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
(Intercept)	-0.32	-0.28	-0.28	-0.28	-0.32	-0.43	-0.27	-0.41	-0.23	-0.28	-0.05	-0.42	-0.00	-0.25	-0.25	-0.06	-0.54
High Degree	0.68	0.72	0.77	0.64	0.68	0.48	0.74	0.53	0.32	0.60	0.48	0.82	0.70	0.53	0.53	0.53	0.57
Powerlaw	0.34	0.24	0.22	0.29	0.34	0.43	0.19	0.28	0.43	0.39	0.20	0.38	0.34	0.19	0.19	0.31	0.81
Assortative	-0.01	-0.03	0.04	-0.02	-0.01	-0.01	0.00	-0.00	0.02	-0.03	0.02	-0.02	0.05	-0.02	-0.02	-0.02	-0.11
Communities	-0.01	0.04	0.06	0.01	-0.01	-0.04	0.08	0.04	0.04	0.02	0.04	0.06	0.08	0.04	0.04	0.02	-0.02
Deg. Infect.	1.32	1.24	1.14	1.27	1.32	1.49	1.15	1.44	1.41	0.72	0.92	0.70	0.81	0.75	0.75	0.76	1.04
High Base.	1.53	1.43	1.41	1.43	1.53	1.37	1.37	1.28	1.84	0.44	1.38	0.81	1.53	0.26	0.26	0.33	0.79

Empirical S.E.

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
(Intercept)	-0.44	-0.43	-0.40	-0.44	-0.44	-0.43	-0.40	-0.39	-0.44	-0.23	0.04	-0.37	0.34	-0.24	-0.24	-0.19	-0.18
High Degree	0.37	0.39	0.45	0.46	0.37	0.39	0.45	0.44	0.47	0.43	0.05	0.56	0.37	0.48	0.48	0.43	0.39
Powerlaw	0.35	0.26	0.23	0.26	0.35	0.36	0.23	0.22	0.24	0.33	0.31	0.36	0.37	0.26	0.26	0.37	0.39
Assortative	-0.02	-0.00	0.03	0.06	-0.02	0.00	0.01	-0.01	0.00	-0.04	0.01	-0.04	-0.02	-0.04	-0.04	-0.05	-0.07
Communities	-0.04	0.03	0.03	0.01	-0.04	-0.05	0.05	0.04	0.04	-0.00	-0.02	0.02	-0.02	0.03	0.02	-0.01	-0.02
Deg. Infect.	1.33	1.27	1.13	1.22	1.33	1.29	1.19	1.24	1.21	0.48	0.77	0.59	0.66	0.61	0.61	0.43	0.47
High Base.	1.54	1.40	1.37	1.49	1.54	1.54	1.36	1.45	1.40	0.47	0.50	0.73	0.70	0.31	0.31	0.45	0.46

Unadj: No adjustment term
F_1: Degree
F_2: Mean Neighbor Degree
F_3: Assortativity
F_4: Member of Connected Block
F_5: Size of Largest Component
F_6: Mean Component Size
F_7: Number of Components
F_8: Size of Node's Component
F_9: Total Neighbor Infections at baseline
F_{10}: Total Node's Component Infections at baseline
F_{11}: 1/nearest infected path length at baseline
F_{12}: $\sum_i$ 1/path length to Infected Node i at baseline
All: Complete inclusion of the above
Step: Stepwise regression of the above

Improvement

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
(Intercept)	-0	3	-1	-6	-0	-9	-5	-5	1	18	-13	17	-161	37	38	9	11
High Degree	0	-2	-3	-6	-0	3	-4	-9	-5	-14	25	-17	-2	-21	-21	-13	-11
Powerlaw	0	4	1	2	0	-3	3	8	4	-37	-5	-39	1	-20	-20	-46	-45
Assortative	0	0	-3	-6	0	-0	-2	-0	-1	7	-1	5	9	4	4	8	9
Communities	-0	-4	-2	-2	0	3	-4	-4	-3	2	1	1	2	-1	-1	4	4
Deg. Infect.	0	0	10	10	-0	6	7	7	4	33	3	38	89	7	6	42	38
High Base.	0	5	6	5	0	2	10	8	4	47	39	38	110	46	46	54	52

Power

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
(Intercept)	89	90	89	90	89	103	90	107	72	114	86	114	70	115	115	109	117
High Degree	4	2	2	4	4	3	1	-1	24	-14	6	-15	11	-15	-15	-13	-8
Powerlaw	13	14	13	11	13	3	14	6	14	-4	19	-5	8	-1	-1	-6	-15
Assortative	2	3	1	3	2	2	2	1	0	2	2	3	2	1	1	3	4
Communities	4	2	3	4	4	4	2	2	3	1	3	1	1	-1	-1	2	2
Deg. Infect.	-14	-13	-10	-15	-14	-25	-12	-26	-9	-16	-15	-18	0	-15	-15	-14	-24
High Base.	-52	-50	-51	-50	-52	-46	-49	-46	-61	-17	-61	-20	-53	-15	-15	-15	-25

Coverage

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
(Intercept)	100	100	100	100	100	95	100	95	100	98	99	98	95	94	94	100	97
High_Degree	1	1	1	1	1	1	1	1	-1	1	1	1	1	1	1	0	1
Powerlaw	-0	-0	-0	0	-0	0	-0	0	0	-1	-0	-0	1	-2	-2	-2	0
Assortative	-0	-0	-0	-1	-0	-0	-0	0	0	1	-0	1	0	0	0	0	1
Communities	-0	-0	-0	-0	-0	-0	-0	-0	-0	0	0	0	0	-0	0	0	0
Deg. Infect.	-2	-2	-2	-2	-2	2	-2	2	-1	0	-1	-1	-0	4	4	0	1
High Base.	-2	-2	-2	-3	-2	-2	-2	-2	-1	-1	1	-1	3	-2	-2	-1	-0

Unadj: No adjustment term
F_1: Degree
F_2: Mean Neighbor Degree
F_3: Assortativity
F_4: Member of Connected Block
F_5: Size of Largest Component
F_6: Mean Component Size
F_7: Number of Components
F_8: Size of Node's Component
F_9: Total Neighbor Infections at baseline
F_{10}: Total Node's Component Infections at baseline
F_{11}: 1/nearest infected path length at baseline
F_{12}: $\sum_i$ 1/path length to Infected Node i at baseline
All: Complete inclusion of the above
Step: Stepwise regression of the above

Statistics Conditional On Each Scenario

a	β_a
000000	-0.57
000001	-1.12
000010	-3.08
000011	-3.42
000100	-0.69
000101	-1.45
000110	-4.20
000111	-3.50
001000	-0.62
001001	-1.34
001010	-4.38
001011	-3.19
001100	-0.72
001101	-1.67
001110	-5.39
001111	-3.54
010000	-0.93
010001	-2.35
010010	-5.55
010011	-3.46
010100	-1.04
010101	-2.77
010110	-5.60
010111	-3.66
011000	-1.01
011001	-3.01
011010	-5.53
011011	-3.33
011100	-1.11
011101	-3.43
011110	-5.73
011111	-3.48
100000	-2.23
100001	-3.79
100010	-5.73
100011	-3.32
100100	-2.40
100101	-3.75
100110	-5.68
100111	-3.17
101000	-2.25
101001	-3.68
101010	-5.69
101011	-3.27
101100	-2.39
101101	-3.77
101110	-5.66
101111	-3.13
110000	-1.78
110001	-6.52
110010	-4.88
110011	-3.51
110100	-1.92
110101	-7.35
110110	-5.03
110111	-3.22
111000	-1.83
111001	-7.14
111010	-5.17
111011	-3.24
111100	-1.92
111101	-6.61
111110	-5.24
111111	-3.23

$$\boldsymbol{a} = [\mathbb{I}(\text{High Degree}),\ \mathbb{I}(\text{Powerlaw}),\ \mathbb{I}(\text{Assortativity}),\ \mathbb{I}(\text{Blocks}),\ \mathbb{I}(\text{Degree Infectivity}),\ \mathbb{I}(\text{High Baseline})]$$

Bias

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
000000	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
000001	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	-0.10	-0.20	-0.10	-0.30	-0.10	-0.10	-0.10	-0.10
000010	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
000011	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
000100	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
000101	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
000110	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
000111	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.10	0.00	0.10	0.00	0.00	0.00	0.00
001000	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
001001	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
001010	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	-0.10	0.00	0.00	0.00	0.00
001011	0	0.00	0.00	0.00	0	0	0.00	0.00	-0.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
001100	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
001101	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.10	0.00	0.10	0.00	0.00	0.00	0.00
001110	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	-0.10	0.00	0.00	0.00	0.00
001111	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	-0.10	-0.10	-0.10	-0.10	-0.10	-0.10	-0.10	-0.10
010000	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
010001	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	-0.10	0.00	-0.10	-0.10	0.00	0.00	-0.10	-0.10
010010	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	-0.10	-0.10	0.00	-0.20	0.10	0.10	-0.10	-0.10
010011	0	0.00	0.00	0.10	0	0	0.00	0.00	0.10	0.20	0.30	0.10	0.30	0.20	0.20	0.20	0.20
010100	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
010101	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.10	0.10	0.00	0.10	0.00	0.00	0.10	0.10
010110	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.10	0.00	0.00	0.10	0.20	0.00	0.00
010111	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	-0.10	0.00	-0.10	-0.10	-0.10	0.00	0.00
011000	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
011001	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
011010	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	-0.10	0.10	0.10	0.00	0.00
011011	0	0.10	0.10	0.10	0	0	0.10	0.00	0.10	0.20	0.20	0.20	0.30	0.20	0.20	0.20	0.10
011100	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
011101	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
011110	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	-0.10	0.10	0.10	0.00	0.00
011111	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10
100000	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.00	0.00	0.00	0.00
100001	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	-0.10	0.00	0.00	0.00	0.00
100010	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.10	0.10	0.00	0.00
100011	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	-0.10	0.00	0.00	0.00	0.00
100100	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
100101	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
100110	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.10	0.00	0.00
100111	0	0.00	0.00	0.00	0	0	0.10	0.00	0.00	0.10	0.10	0.10	0.20	0.10	0.10	0.10	0.10
101000	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
101001	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.10	0.10	0.00	0.20	0.10	0.10	0.10	0.10
101010	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
101011	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
101100	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
101101	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	-0.10	0.00	0.00	0.00	0.00
101110	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	-0.10	0.00	0.00	0.00	0.00
101111	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.10	0.20	0.10	0.20	0.10	0.10	0.10	0.10
110000	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
110001	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.10	0.10	0.00	0.10	0.10	0.10	0.10	0.10
110010	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	-0.10	0.10	0.10	0.00	0.00
110011	0	-0.10	-0.20	-0.20	0	0	-0.30	-0.10	0.00	-0.20	-0.40	-0.10	-0.60	-0.40	-0.40	-0.30	-0.20
110100	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
110101	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
110110	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.10	0.00	0.00	0.10	0.10	0.00	0.00
110111	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	-0.10	0.00	0.00	0.00	0.00
111000	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.00	0.00	0.00	0.00
111001	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.10	0.00	0.00	0.10	0.10	0.00	0.00
111010	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.10	0.00	0.00	0.10	0.10	0.00	0.00
111011	0	0.00	-0.10	-0.10	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
111100	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.00	0.00	0.00	0.00
111101	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.10	0.10	0.00	0.10	0.10	0.10	0.10	0.10
111110	0	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.10	0.10	0.10	0.10	0.20	0.20	0.10	0.10
111111	0	0.00	0.00	0.00	0	0	0.10	0.00	0.00	0.00	0.00	0.00	0.00	-0.10	-0.10	0.00	0.00

Percent Relative Bias

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
000000	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
000001	-0	-0	-0	-0	-0	-0	-0	-0	-0	9	18	9	27	9	9	9	9
000010	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
000011	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
000100	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
000101	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
000110	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
000111	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-3	-0	-3	-0	-0	-0	-0
001000	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
001001	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
001010	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	2	-0	-0	-0	-0
001011	-0	-0	-0	-0	-0	-0	-0	-0	3	-0	-0	-0	-0	-0	-0	-0	-0
001100	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
001101	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-6	-0	-6	-0	-0	-0	-0
001110	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	2	-0	-0	-0	-0
001111	-0	-0	-0	-0	-0	-0	-0	-0	-0	3	3	3	3	3	3	3	3
010000	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
010001	-0	-0	-0	-0	-0	-0	-0	-0	-0	4	-0	4	4	-0	-0	4	4
010010	-0	-0	-0	-0	-0	-0	-0	-0	-0	2	2	-0	4	-2	-2	2	2
010011	-0	-0	-0	-3	-0	-0	-0	-0	-3	-6	-9	-3	-9	-6	-6	-6	-6
010100	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
010101	-0	-0	-0	-0	-0	-0	-0	-0	-0	-4	-4	-0	-4	-0	-0	-4	-4
010110	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-2	-0	-0	-2	-4	-0	-0
010111	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	3	-0	3	3	3	-0	-0
011000	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
011001	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
011010	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	2	-2	-2	-0	-0
011011	-0	-3	-3	-3	-0	-0	-3	-0	-3	-6	-6	-6	-9	-6	-6	-6	-3
011100	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
011101	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
011110	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	2	-2	-2	-0	-0
011111	-0	-0	-0	-0	-0	-0	-0	-0	-0	-3	-3	-3	-3	-3	-3	-3	-3
100000	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-4	-0	-0	-0	-0
100001	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	3	-0	-0	-0	-0
100010	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-2	-2	-2	-0	-0
100011	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	3	-0	-0	-0	-0
100100	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
100101	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
100110	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-2	-2	-0	-0
100111	-0	-0	-0	-0	-0	-0	-3	-0	-0	-3	-3	-3	-6	-3	-3	-3	-3
101000	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
101001	-0	-0	-0	-0	-0	-0	-0	-0	-0	-3	-3	-0	-5	-3	-3	-3	-3
101010	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
101011	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
101100	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
101101	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	3	-0	-0	-0	-0
101110	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	2	-0	-0	-0	-0
101111	-0	-0	-0	-0	-0	-0	-0	-0	-0	-3	-6	-3	-6	-3	-3	-3	-3
110000	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
110001	-0	-0	-0	-0	-0	-0	-0	-0	-0	-2	-2	-0	-2	-2	-2	-2	-2
110010	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	2	-2	-2	-0	-0
110011	-0	3	6	6	-0	-0	9	3	-0	6	11	3	17	11	11	9	6
110100	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
110101	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
110110	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-2	-0	-0	-2	-2	-0	-0
110111	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	3	-0	-0	-0	-0
111000	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-5	-0	-0	-0	-0
111001	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-1	-0	-0	-1	-1	-0	-0
111010	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-2	-0	-0	-2	-2	-0	-0
111011	-0	-0	3	3	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
111100	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-5	-0	-0	-0	-0
111101	-0	-0	-0	-0	-0	-0	-0	-0	-0	-2	-2	-0	-2	-2	-2	-2	-2
111110	-0	-0	-0	-0	-0	-0	-0	-0	-0	-2	-2	-2	-2	-4	-4	-2	-2
111111	-0	-0	-0	-0	-0	-0	-3	-0	-0	-0	-0	-0	-0	3	3	-0	-0

Robust Standard Error

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
000000	0.30	0.30	0.30	0.30	0.30	0.20	0.30	0.20	0.40	0.10	0.30	0.10	0.50	0.10	0.10	0.20	0.10
000001	0.70	0.70	0.70	0.70	0.70	0.60	0.70	0.60	1.00	0.20	0.80	0.20	1.00	0.10	0.10	0.30	0.20
000010	0.70	0.70	0.70	0.70	0.70	0.60	0.70	0.60	0.90	0.40	0.70	0.30	0.90	0.30	0.30	0.70	0.40
000011	2.20	2.00	1.90	2.20	2.20	2.20	1.90	2.10	3.20	0.30	2.10	0.40	1.80	0.30	0.30	0.50	0.30
000100	0.30	0.30	0.30	0.30	0.30	0.20	0.30	0.20	0.40	0.10	0.30	0.10	0.50	0.10	0.10	0.20	0.10
000101	0.80	0.80	0.80	0.80	0.80	0.70	0.80	0.60	1.20	0.20	0.90	0.20	1.10	0.10	0.10	0.30	0.20
000110	0.80	0.80	0.80	0.80	0.80	0.70	0.80	0.70	1.00	0.50	0.80	0.40	1.00	0.40	0.40	0.90	0.50
000111	2.10	2.00	2.00	2.10	2.10	2.10	2.00	2.00	3.50	0.40	2.40	0.50	2.20	0.30	0.30	0.50	0.40
001000	0.30	0.30	0.30	0.30	0.30	0.20	0.30	0.20	0.40	0.10	0.30	0.10	0.40	0.10	0.10	0.20	0.10
001001	0.80	0.80	0.80	0.80	0.80	0.70	0.80	0.70	1.20	0.20	0.90	0.20	1.00	0.10	0.10	0.30	0.20
001010	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.80	1.10	0.60	0.90	0.40	1.00	0.40	0.40	1.00	0.60
001011	1.70	1.50	1.40	1.70	1.70	1.70	1.40	1.60	2.70	0.30	2.00	0.30	1.60	0.30	0.30	0.50	0.30
001100	0.30	0.30	0.30	0.30	0.30	0.20	0.30	0.20	0.40	0.10	0.30	0.10	0.50	0.10	0.10	0.20	0.10
001101	0.90	0.90	0.90	0.90	0.90	0.80	0.90	0.80	1.30	0.20	1.00	0.30	1.20	0.20	0.20	0.30	0.20
001110	1.00	0.90	1.00	0.90	1.00	0.90	0.90	0.90	1.20	0.60	1.00	0.50	1.10	0.50	0.50	1.10	0.60
001111	1.80	1.70	1.70	1.80	1.80	1.80	1.70	1.80	3.10	0.30	2.30	0.50	2.10	0.30	0.30	0.50	0.30
010000	0.30	0.30	0.30	0.30	0.30	0.20	0.30	0.20	0.40	0.40	0.30	0.40	0.50	0.20	0.20	0.50	0.40
010001	1.10	1.00	1.10	1.10	1.10	1.00	1.00	0.70	1.50	0.70	1.20	0.80	1.60	0.30	0.30	0.80	0.80
010010	1.70	1.70	1.50	1.50	1.70	1.70	1.50	1.60	1.70	0.90	1.60	0.90	1.70	0.90	0.90	1.20	1.10
010011	3.80	3.30	2.70	3.00	3.80	3.70	2.70	3.40	3.90	1.10	2.50	1.50	2.60	0.70	0.70	1.10	3.00
010100	0.30	0.30	0.30	0.30	0.30	0.20	0.30	0.20	0.40	0.40	0.30	0.40	0.50	0.20	0.20	0.40	0.40
010101	1.10	1.10	1.10	1.10	1.10	0.90	1.10	0.80	1.60	0.60	1.30	0.80	1.60	0.30	0.30	0.70	0.70
010110	1.50	1.50	1.40	1.40	1.50	1.50	1.40	1.40	1.60	0.90	1.40	0.80	1.70	0.80	0.80	1.10	1.00
010111	3.30	3.10	2.70	2.90	3.30	3.30	2.90	3.20	3.90	1.20	2.50	1.60	2.90	0.90	0.90	1.20	3.00
011000	0.30	0.30	0.40	0.30	0.30	0.30	0.30	0.20	0.40	0.40	0.30	0.40	0.50	0.20	0.20	0.40	0.40
011001	1.40	1.20	1.40	1.40	1.40	1.30	1.30	0.90	2.00	0.60	1.50	0.80	1.90	0.30	0.30	0.60	0.60
011010	1.50	1.40	1.40	1.40	1.50	1.50	1.30	1.40	1.60	0.90	1.40	0.80	1.60	0.80	0.80	1.20	1.00
011011	3.10	2.50	2.20	2.80	3.10	2.90	2.00	2.70	3.40	0.70	2.50	0.90	2.80	0.40	0.40	0.70	2.00
011100	0.30	0.40	0.40	0.30	0.30	0.20	0.40	0.20	0.40	0.30	0.30	0.30	0.50	0.20	0.20	0.40	0.30
011101	1.40	1.30	1.50	1.40	1.40	1.10	1.40	1.00	2.00	0.50	1.50	0.80	1.90	0.30	0.30	0.60	0.60
011110	1.40	1.30	1.30	1.30	1.40	1.30	1.30	1.30	1.50	0.80	1.30	0.80	1.60	0.80	0.80	1.20	0.90
011111	2.60	2.30	2.20	2.50	2.60	2.50	2.20	2.40	3.40	0.80	2.50	1.00	3.00	0.50	0.50	0.70	2.00
100000	0.40	0.40	0.40	0.40	0.40	0.20	0.40	0.30	0.30	0.20	0.40	0.20	0.70	0.20	0.20	0.30	0.20
100001	2.20	2.20	2.20	2.10	2.20	1.40	2.10	1.50	1.90	0.50	2.20	1.30	2.90	0.40	0.40	0.60	0.50
100010	1.20	1.20	1.20	1.20	1.20	1.00	1.20	1.00	1.10	0.70	1.00	0.70	1.10	0.70	0.70	1.00	0.70
100011	3.40	3.40	3.40	3.40	3.40	2.90	3.40	3.00	3.20	2.00	3.00	2.40	3.40	1.80	1.80	2.00	1.90
100100	0.40	0.40	0.40	0.40	0.40	0.20	0.40	0.30	0.30	0.20	0.40	0.20	0.70	0.20	0.20	0.30	0.20
100101	2.10	2.20	2.20	2.10	2.10	1.30	2.10	1.50	1.80	0.50	2.20	1.30	2.90	0.40	0.40	0.70	0.50
100110	1.40	1.40	1.40	1.40	1.40	1.30	1.40	1.30	1.30	1.00	1.10	1.00	1.30	0.90	0.90	1.10	1.00
100111	4.00	4.00	4.00	4.00	4.00	3.60	4.00	3.70	3.80	2.10	3.10	2.80	3.30	1.90	1.90	2.10	2.10
101000	0.40	0.40	0.40	0.30	0.40	0.20	0.40	0.30	0.30	0.20	0.40	0.20	0.60	0.20	0.20	0.30	0.20
101001	2.20	2.20	2.20	1.80	2.20	1.40	2.20	1.50	2.00	0.50	2.20	1.30	2.90	0.40	0.40	0.60	0.50
101010	1.20	1.20	1.20	1.20	1.20	1.10	1.20	1.10	1.20	0.80	1.00	0.80	1.20	0.80	0.80	1.00	0.80
101011	3.60	3.60	3.60	3.40	3.60	3.20	3.60	3.30	3.50	2.00	3.00	2.50	3.50	1.80	1.80	2.00	2.00
101100	0.40	0.40	0.40	0.30	0.40	0.20	0.40	0.30	0.30	0.20	0.40	0.20	0.60	0.20	0.20	0.30	0.20
101101	2.20	2.20	2.20	1.60	2.20	1.30	2.10	1.50	1.80	0.50	2.20	1.40	2.90	0.40	0.40	0.70	0.50
101110	1.40	1.40	1.40	1.30	1.40	1.30	1.40	1.30	1.30	1.00	1.20	1.00	1.30	0.90	0.90	1.20	1.00
101111	4.00	4.00	4.10	3.80	4.00	3.70	4.00	3.70	3.90	2.10	3.10	2.80	3.40	1.90	1.90	2.10	2.10
110000	0.40	0.40	0.40	0.40	0.40	0.30	0.40	0.30	0.40	0.40	0.40	0.50	0.50	0.20	0.20	0.50	0.50
110001	1.80	1.70	1.80	1.80	1.80	1.50	1.70	1.20	2.40	1.20	2.00	1.30	2.60	0.50	0.50	1.20	1.60
110010	1.70	1.60	1.60	1.60	1.70	1.60	1.60	1.50	1.70	1.10	1.50	1.10	1.80	1.10	1.10	1.20	1.20
110011	4.00	3.70	3.60	3.60	4.00	4.00	3.50	3.60	4.30	2.40	3.00	3.00	3.40	2.00	2.00	2.40	4.10
110100	0.40	0.40	0.40	0.40	0.40	0.20	0.40	0.30	0.40	0.40	0.40	0.40	0.60	0.20	0.20	0.50	0.40
110101	1.80	1.70	1.70	1.80	1.80	1.30	1.70	1.20	2.30	1.00	2.10	1.40	2.70	0.50	0.50	1.10	1.20
110110	1.70	1.60	1.60	1.60	1.70	1.60	1.60	1.60	1.70	1.20	1.50	1.20	1.80	1.20	1.20	1.30	1.30
110111	3.70	3.60	3.50	3.50	3.70	3.60	3.40	3.40	3.90	2.50	3.00	2.90	3.50	2.10	2.10	2.40	3.70
111000	0.40	0.40	0.40	0.40	0.40	0.30	0.40	0.30	0.40	0.40	0.40	0.50	0.60	0.20	0.20	0.50	0.50
111001	2.10	1.90	2.20	2.00	2.10	1.70	2.00	1.30	2.70	1.10	2.30	1.50	3.00	0.40	0.40	1.20	1.30
111010	1.70	1.70	1.70	1.70	1.70	1.70	1.60	1.60	1.70	1.30	1.50	1.30	1.80	1.30	1.30	1.40	1.30
111011	4.10	3.80	3.80	4.00	4.10	4.10	3.60	3.80	4.30	2.30	2.80	2.80	3.40	1.80	1.80	2.20	3.50
111100	0.40	0.40	0.40	0.40	0.40	0.20	0.40	0.30	0.40	0.40	0.40	0.40	0.60	0.20	0.20	0.40	0.40
111101	2.10	2.00	2.10	1.70	2.10	1.40	2.00	1.30	2.50	1.10	2.40	1.50	3.10	0.40	0.40	1.10	1.20
111110	1.60	1.60	1.60	1.60	1.60	1.60	1.60	1.60	1.70	1.30	1.40	1.30	1.80	1.20	1.20	1.40	1.30
111111	3.90	3.80	3.80	3.90	3.90	3.90	3.70	3.80	4.10	2.30	2.70	2.80	3.40	1.90	1.90	2.20	3.10

Empirical Standard Error

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
000000	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.10	0.20	0.10	0.50	0.10	0.10	0.10	0.10
000001	0.60	0.50	0.50	0.60	0.60	0.60	0.60	0.60	0.60	0.10	0.70	0.20	1.10	0.10	0.10	0.10	0.10
000010	0.60	0.60	0.60	0.60	0.60	0.60	0.60	0.60	0.60	0.30	0.60	0.30	0.90	0.30	0.30	0.30	0.30
000011	2.10	1.90	1.80	2.10	2.10	2.10	1.80	2.10	1.70	0.20	0.90	0.40	1.10	0.20	0.20	0.20	0.20
000100	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.10	0.20	0.10	0.50	0.10	0.10	0.10	0.10
000101	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.20	0.70	0.20	1.10	0.20	0.10	0.20	0.20
000110	0.70	0.60	0.60	0.70	0.70	0.70	0.70	0.70	0.70	0.40	0.70	0.30	1.10	0.30	0.30	0.40	0.40
000111	2.10	2.00	2.00	2.10	2.10	2.10	2.00	2.10	2.00	0.30	0.90	0.50	1.10	0.30	0.30	0.30	0.30
001000	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.10	0.20	0.10	0.50	0.10	0.10	0.10	0.10
001001	0.70	0.70	0.70	0.70	0.70	0.80	0.70	0.70	0.70	0.20	0.70	0.20	1.00	0.20	0.20	0.20	0.20
001010	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.50	0.80	0.30	1.00	0.30	0.30	0.40	0.50
001011	1.80	1.60	1.50	1.80	1.80	1.80	1.60	1.70	1.50	0.20	0.80	0.30	0.80	0.20	0.20	0.20	0.20
001100	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.10	0.20	0.10	0.50	0.10	0.10	0.10	0.10
001101	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.20	0.80	0.20	1.10	0.20	0.20	0.20	0.20
001110	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.50	0.90	0.40	1.20	0.40	0.40	0.50	0.50
001111	1.80	1.70	1.70	1.90	1.80	1.90	1.70	1.80	1.70	0.30	0.90	0.40	0.90	0.30	0.30	0.30	0.30
010000	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.40	0.20	0.40	0.50	0.20	0.20	0.50	0.50
010001	0.90	0.80	0.90	0.90	0.90	1.00	0.80	0.80	0.80	0.60	0.90	0.60	1.50	0.40	0.40	0.70	0.70
010010	1.30	1.20	1.00	1.10	1.30	1.20	1.20	1.10	1.10	0.50	1.70	0.50	2.00	0.80	0.80	0.50	0.70
010011	4.00	3.40	2.80	3.20	4.00	3.80	2.80	3.40	2.90	1.10	1.60	1.50	2.00	0.70	0.70	1.00	1.20
010100	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.30	0.20	0.40	0.50	0.20	0.20	0.40	0.40
010101	0.90	0.80	0.90	0.90	0.90	0.90	0.90	0.80	0.80	0.50	0.80	0.60	1.40	0.40	0.40	0.60	0.60
010110	1.10	1.00	0.90	1.00	1.10	1.10	1.00	1.00	1.00	0.40	1.50	0.50	2.00	0.70	0.70	0.50	0.60
010111	3.40	3.20	2.70	3.00	3.40	3.40	3.00	3.30	3.10	1.20	1.40	1.50	1.90	0.90	0.90	1.10	1.20
011000	0.20	0.20	0.30	0.20	0.20	0.30	0.20	0.20	0.20	0.30	0.20	0.40	0.60	0.20	0.20	0.40	0.40
011001	1.10	0.90	1.10	1.10	1.10	1.20	1.10	1.00	1.10	0.40	1.10	0.70	1.60	0.30	0.30	0.60	0.50
011010	1.00	1.00	1.00	1.00	1.00	1.00	1.10	0.90	1.00	0.40	1.50	0.50	1.80	0.70	0.70	0.40	0.50
011011	3.20	2.60	2.20	2.80	3.20	3.00	2.10	2.70	2.10	0.80	1.50	0.90	1.90	0.40	0.40	0.70	0.90
011100	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.30	0.20	0.30	0.50	0.20	0.20	0.30	0.30
011101	1.00	1.00	1.10	1.10	1.00	1.10	1.10	1.00	1.00	0.40	1.10	0.50	1.60	0.30	0.30	0.40	0.40
011110	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.40	1.40	0.40	1.90	0.60	0.60	0.40	0.40
011111	2.60	2.30	2.10	2.40	2.60	2.50	2.20	2.40	2.20	0.70	1.20	0.90	1.80	0.50	0.50	0.70	0.80
100000	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.30	0.20	0.20	0.20	0.20	0.70	0.20	0.20	0.20	0.20
100001	1.40	1.30	1.40	1.40	1.40	1.40	1.40	1.50	1.40	0.40	0.50	0.70	1.80	0.30	0.30	0.40	0.40
100010	0.70	0.60	0.60	0.70	0.70	0.70	0.70	0.70	0.70	0.30	0.60	0.30	1.20	0.50	0.50	0.30	0.30
100011	2.80	2.70	2.70	2.80	2.80	2.80	2.80	2.80	2.80	1.50	1.60	1.80	2.30	1.60	1.60	1.50	1.50
100100	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.30	0.20	0.20	0.20	0.20	0.70	0.20	0.20	0.20	0.20
100101	1.30	1.30	1.30	1.30	1.30	1.30	1.30	1.50	1.30	0.40	0.60	0.70	1.70	0.30	0.30	0.40	0.40
100110	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.50	0.60	0.50	1.10	0.60	0.60	0.50	0.50
100111	3.60	3.60	3.60	3.70	3.60	3.60	3.60	3.70	3.60	1.60	1.80	2.30	2.20	1.80	1.80	1.60	1.60
101000	0.20	0.20	0.20	0.30	0.20	0.20	0.20	0.30	0.20	0.20	0.20	0.20	0.60	0.20	0.20	0.20	0.20
101001	1.40	1.30	1.30	1.60	1.40	1.40	1.40	1.50	1.40	0.40	0.50	0.70	1.80	0.30	0.30	0.40	0.40
101010	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.40	0.60	0.40	1.10	0.50	0.50	0.40	0.40
101011	3.20	3.20	3.10	3.30	3.20	3.20	3.20	3.20	3.20	1.50	1.70	2.00	2.40	1.60	1.60	1.50	1.50
101100	0.20	0.20	0.20	0.30	0.20	0.20	0.20	0.30	0.20	0.20	0.20	0.20	0.70	0.20	0.20	0.20	0.20
101101	1.30	1.30	1.30	1.50	1.30	1.30	1.30	1.50	1.30	0.40	0.60	0.70	1.70	0.40	0.40	0.40	0.40
101110	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.40	0.60	0.50	1.10	0.60	0.60	0.40	0.40
101111	3.70	3.60	3.60	3.70	3.70	3.70	3.70	3.70	3.70	1.60	1.80	2.40	2.40	1.70	1.70	1.60	1.50
110000	0.20	0.20	0.20	0.20	0.20	0.30	0.20	0.30	0.20	0.40	0.20	0.40	0.50	0.30	0.30	0.50	0.50
110001	1.50	1.20	1.50	1.50	1.50	1.60	1.40	1.30	1.40	1.00	0.70	1.00	1.70	0.60	0.60	1.10	1.10
110010	1.10	1.10	1.10	1.20	1.10	1.20	1.20	1.10	1.10	0.80	1.30	0.80	1.90	1.00	1.00	0.80	0.80
110011	3.80	3.50	3.30	3.50	3.80	3.80	3.30	3.40	3.60	2.10	2.00	2.70	2.60	2.00	2.00	2.00	2.10
110100	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.30	0.20	0.40	0.20	0.40	0.60	0.20	0.20	0.40	0.40
110101	1.30	1.10	1.30	1.30	1.30	1.30	1.20	1.20	1.20	0.80	0.50	1.00	1.50	0.60	0.60	0.90	0.90
110110	1.10	1.10	1.10	1.10	1.10	1.10	1.10	1.10	1.10	0.70	1.20	0.70	1.80	1.10	1.00	0.80	0.80
110111	3.30	3.20	3.00	3.20	3.30	3.30	3.20	3.20	3.30	2.00	1.90	2.50	2.50	2.00	2.00	1.90	2.00
111000	0.20	0.20	0.20	0.30	0.20	0.30	0.30	0.30	0.20	0.40	0.20	0.40	0.50	0.30	0.30	0.50	0.40
111001	1.60	1.20	1.60	1.70	1.60	1.80	1.40	1.30	1.40	0.80	0.90	0.90	1.90	0.50	0.50	0.90	0.90
111010	1.10	1.10	1.10	1.10	1.10	1.10	1.10	1.10	1.10	0.70	1.20	0.70	1.80	1.10	1.10	0.80	0.70
111011	4.10	3.80	3.60	3.90	4.10	4.10	3.60	3.80	3.90	2.10	1.80	2.60	2.50	1.80	1.80	2.00	2.00
111100	0.20	0.20	0.20	0.30	0.20	0.20	0.30	0.30	0.20	0.30	0.20	0.30	0.50	0.20	0.20	0.30	0.30
111101	1.40	1.40	1.40	1.70	1.40	1.50	1.40	1.40	1.40	0.80	0.80	1.00	1.80	0.70	0.70	0.90	0.90
111110	1.00	1.00	1.00	1.10	1.00	1.00	1.10	1.00	1.00	0.70	1.10	0.70	1.70	1.00	1.00	0.70	0.70
111111	3.70	3.60	3.60	3.70	3.70	3.70	3.60	3.70	3.70	2.00	1.80	2.60	2.30	1.70	1.70	1.90	1.90

Improvement

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
000000	0	3	2	-1	0	-11	-2	2	1	53	-10	46	-140	44	44	53	53
000001	0	4	4	-2	0	-5	-3	1	-0	69	-24	66	-97	71	72	69	68
000010	0	5	5	-2	0	-6	4	2	4	44	-9	55	-58	53	53	45	44
000011	0	11	16	-1	0	-1	14	2	18	90	58	83	49	89	89	90	90
000100	0	0	0	-3	0	-4	-4	0	0	53	1	47	-133	45	46	52	52
000101	0	2	1	-2	0	-3	-2	1	0	77	-9	73	-68	77	78	77	77
000110	0	2	2	-2	0	-2	-2	1	1	42	-11	54	-63	55	55	43	42
000111	0	5	7	-1	0	-1	4	1	5	85	57	76	49	86	86	85	85
001000	0	1	1	-9	0	-8	-2	1	-1	53	-12	44	-122	51	51	51	52
001001	0	4	4	-4	0	-6	1	2	1	79	-4	75	-35	78	78	78	78
001010	0	3	4	-4	0	-3	1	1	1	42	-3	57	-24	56	56	43	42
001011	0	11	15	-1	0	-0	11	1	14	89	55	83	57	87	87	89	89
001100	0	-0	-0	-7	0	-3	-4	0	-1	52	-11	46	-127	48	49	51	51
001101	0	2	2	-5	0	-2	-1	1	-0	78	-5	75	-38	78	79	78	78
001110	0	1	2	-1	0	-1	-0	1	-0	40	-5	54	-35	54	54	41	40
001111	0	7	9	-0	0	-1	5	1	8	84	51	76	50	85	85	84	84
010000	0	5	-4	-5	0	-25	-5	-2	4	-118	5	-126	-166	-14	-15	-154	-140
010001	0	16	2	-3	0	-13	8	17	11	31	3	30	-64	56	56	23	23
010010	0	5	20	11	0	1	4	10	10	63	-35	59	-60	35	35	61	46
010011	0	14	30	19	0	5	30	13	25	73	59	62	48	82	82	73	69
010100	0	2	-1	-6	0	-9	-9	-3	2	-85	16	-95	-156	-11	-7	-115	-102
010101	0	7	-1	-3	0	-6	-1	5	4	36	7	29	-61	54	54	29	31
010110	0	3	12	1	0	-1	2	6	6	58	-45	53	-84	28	29	55	46
010111	0	5	21	13	0	0	12	4	10	66	60	56	44	74	74	67	65
011000	0	5	-39	-10	0	-27	-14	-1	1	-62	-4	-95	-165	10	11	-99	-91
011001	0	13	-3	-4	0	-15	-1	10	-4	60	-9	38	-55	70	70	48	53
011010	0	6	8	3	0	-0	-4	9	8	59	-44	53	-74	35	35	57	51
011011	0	19	31	10	0	6	34	16	33	75	51	71	39	85	85	77	71
011100	0	2	-13	-19	0	-11	-16	-3	2	-50	9	-65	-150	10	11	-69	-64
011101	0	6	-5	-8	0	-8	-3	4	2	63	-3	48	-53	70	70	57	60
011110	0	3	4	1	0	-1	-3	4	5	56	-51	54	-109	31	32	55	53
011111	0	9	17	5	0	0	14	5	14	71	51	64	31	81	81	73	69
100000	0	-1	-0	-5	0	0	-10	-33	1	19	15	22	-257	21	23	22	22
100001	0	3	2	-2	0	-0	-3	-7	-0	74	62	46	-31	77	77	73	73
100010	0	1	1	-5	-0	-0	-4	-5	-1	50	14	48	-85	30	29	49	50
100011	0	1	1	-2	0	-0	-3	-3	-0	47	40	35	15	41	41	47	47
100100	0	-0	-0	-7	0	0	-4	-24	0	25	20	25	-212	21	22	25	26
100101	0	1	1	-4	0	-0	-3	-12	-0	72	56	43	-32	73	73	71	71
100110	0	0	0	-4	0	0	-5	-6	-0	41	18	40	-42	23	23	41	41
100111	0	0	0	-3	0	-0	-1	-2	-0	56	49	35	37	51	51	55	56
101000	0	1	1	-25	0	-0	-6	-17	-0	22	22	25	-186	21	22	25	25
101001	0	1	1	-16	0	-0	-2	-10	-0	72	61	46	-31	74	74	71	72
101010	0	1	1	-8	0	-0	-6	-5	-0	44	16	42	-64	24	25	44	45
101011	0	1	1	-4	0	-0	-1	-1	-0	52	46	37	23	49	49	52	53
101100	0	0	0	-18	0	-0	-6	-25	-0	23	19	23	-192	21	22	24	25
101101	0	1	1	-15	0	-0	-4	-16	-0	71	57	42	-29	72	72	71	71
101110	0	0	0	-4	0	-0	-4	-4	-0	44	19	43	-40	23	23	44	44
101111	0	0	1	-1	0	-0	-2	-1	-0	57	51	36	35	54	54	57	58
110000	0	2	-2	-7	0	-10	-4	-15	0	-83	26	-83	-126	-21	-21	-120	-107
110001	0	20	-1	0	0	-9	9	17	10	32	54	33	-13	62	63	29	26
110010	0	3	6	-3	0	-1	-3	3	1	34	-17	34	-65	10	9	30	31
110011	0	7	14	7	0	-1	12	10	4	45	47	30	30	46	46	47	44
110100	0	0	-1	-11	0	-1	-5	-17	-0	-62	22	-69	-159	-11	-11	-94	-82
110101	0	10	1	-1	0	-3	2	3	3	34	58	24	-15	55	55	32	31
110110	0	1	2	-3	0	-0	-3	2	0	34	-12	32	-68	2	2	30	30
110111	0	3	9	3	0	-0	3	3	1	39	42	25	25	41	41	42	39
111000	0	3	-1	-23	0	-13	-9	-15	0	-65	20	-78	-138	-11	-11	-95	-86
111001	0	21	1	-11	0	-13	11	17	11	49	45	43	-24	70	70	44	46
111010	0	4	3	1	0	-1	-2	4	2	35	-8	33	-62	-4	-4	32	32
111011	0	8	12	5	0	-0	11	8	5	49	55	36	40	57	57	53	51
111100	0	1	-0	-33	0	-2	-28	-25	-0	-41	17	-46	-136	-9	-9	-58	-52
111101	0	6	-0	-16	0	-3	0	-0	2	41	43	32	-22	53	53	40	40
111110	0	2	2	-2	0	-0	-5	1	0	33	-3	32	-65	5	5	32	32
111111	0	2	4	0	0	-0	3	2	1	46	53	31	39	53	53	48	49

Power

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
000000	45	45	46	48	45	75	46	83	17	100	45	100	20	100	100	92	100
000001	33	32	32	35	33	49	34	54	6	100	20	100	18	100	100	100	100
000010	100	100	100	100	100	100	100	100	99	100	99	100	94	100	100	100	100
000011	34	42	47	36	34	35	46	38	6	100	20	100	45	100	100	100	100
000100	65	64	64	66	65	92	67	94	34	100	66	100	31	100	100	100	100
000101	39	40	40	42	39	57	40	60	9	100	33	100	24	100	100	100	100
000110	100	100	100	100	100	100	100	100	100	100	100	100	97	100	100	100	100
000111	39	42	44	39	39	41	42	42	6	100	12	100	24	100	100	100	100
001000	50	50	49	53	50	78	51	84	22	100	51	100	29	100	100	96	100
001001	34	36	36	36	34	46	36	51	10	100	29	100	28	100	100	100	100
001010	100	100	100	100	100	100	100	100	100	100	100	100	99	100	100	100	100
001011	49	60	63	50	49	50	62	51	9	100	20	100	55	100	100	100	100
001100	69	68	67	70	69	90	70	92	36	100	70	100	37	100	100	100	100
001101	43	43	42	45	43	55	44	60	13	100	42	100	33	100	100	100	100
001110	100	100	100	100	100	100	100	100	100	100	100	100	98	100	100	100	100
001111	54	58	59	54	54	55	57	55	6	100	12	100	26	100	100	100	100
010000	95	96	94	95	95	97	96	99	85	63	97	58	50	98	99	50	56
010001	57	66	57	58	57	62	68	86	22	92	49	89	30	100	100	86	86
010010	94	96	99	99	94	95	99	97	96	100	92	100	84	100	100	100	99
010011	17	20	27	24	17	17	27	19	9	90	25	68	24	100	100	92	20
010100	99	99	99	99	99	100	98	100	96	84	100	78	64	100	100	71	78
010101	75	79	74	76	75	87	78	93	34	99	70	98	44	100	100	98	98
010110	98	98	100	99	98	98	99	99	98	100	96	100	89	100	100	100	100
010111	20	22	27	26	20	21	25	22	10	84	18	65	15	98	98	85	18
011000	94	96	89	94	94	96	94	100	86	84	97	73	58	100	100	70	75
011001	62	75	57	63	62	67	67	90	23	100	58	98	36	100	100	100	99
011010	98	100	100	100	98	98	99	100	100	100	94	100	87	100	100	100	100
011011	21	32	37	25	21	22	41	27	8	99	19	96	15	100	100	100	47
011100	99	99	97	98	99	100	98	100	95	94	100	91	71	100	100	89	91
011101	73	79	67	75	73	88	75	94	28	100	71	100	46	100	100	100	100
011110	100	100	100	100	100	100	100	100	100	100	97	100	88	100	100	100	100
011111	29	33	35	31	29	30	37	31	10	100	15	96	10	100	100	100	49
100000	100	100	100	100	100	100	100	100	100	100	100	100	94	100	100	100	100
100001	39	38	39	42	39	78	40	72	51	100	14	95	12	100	100	100	100
100010	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
100011	12	12	11	13	12	19	13	19	13	36	6	23	7	42	42	34	35
100100	100	100	100	100	100	100	100	100	100	100	100	100	95	100	100	100	100
100101	36	35	35	38	36	81	38	69	59	100	17	93	10	100	100	100	100
100110	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
100111	9	9	9	11	9	14	10	13	11	31	6	18	8	37	36	29	31
101000	100	100	100	100	100	100	100	100	100	100	100	100	97	100	100	100	100
101001	33	34	33	53	33	76	36	65	45	100	13	95	11	100	100	100	100
101010	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
101011	13	12	12	16	13	17	13	17	14	34	6	23	8	44	44	33	34
101100	100	100	100	100	100	100	100	100	100	100	100	100	97	100	100	100	100
101101	37	36	32	64	37	80	39	69	58	100	17	93	10	100	100	100	100
101110	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
101111	11	10	10	14	11	14	12	14	12	29	6	16	8	38	38	27	29
110000	100	100	100	100	100	100	100	100	100	98	100	98	94	100	100	92	95
110001	97	100	97	97	97	98	98	100	91	100	100	100	83	100	100	100	94
110010	89	91	92	92	89	90	92	93	89	100	91	100	80	100	99	100	99
110011	13	13	12	13	13	13	15	14	8	26	7	19	7	37	37	24	11
110100	100	100	100	100	100	100	100	100	100	100	100	100	96	100	100	99	99
110101	100	100	100	100	100	100	100	100	99	100	100	100	91	100	100	100	99
110110	93	94	94	94	93	94	95	95	93	100	96	100	83	100	100	100	100
110111	13	14	13	14	13	14	14	15	9	21	8	18	6	30	30	22	11
111000	100	100	100	100	100	100	100	100	100	100	100	98	95	100	100	97	98
111001	95	100	95	96	95	97	98	100	89	100	99	100	76	100	100	100	98
111010	93	95	95	94	93	94	95	96	93	100	97	100	86	100	100	100	100
111011	13	14	13	12	13	14	15	15	10	28	13	22	10	43	42	31	16
111100	100	100	100	100	100	100	100	100	100	100	100	100	96	100	100	100	100
111101	96	98	96	97	96	99	97	100	89	100	99	100	65	100	100	100	99
111110	98	98	98	98	98	98	98	98	97	100	98	100	88	100	100	100	100
111111	13	13	14	13	13	13	16	13	11	26	12	19	8	39	40	27	17

Coverage

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
000000	100	100	100	99	100	94	99	93	100	99	100	98	97	92	92	100	99
000001	98	99	99	98	98	97	98	93	100	91	99	93	92	84	84	100	89
000010	98	98	98	98	98	95	98	95	100	98	98	98	96	96	96	100	98
000011	95	95	96	94	95	94	96	94	100	98	100	96	100	97	97	100	98
000100	100	100	100	100	100	94	99	94	100	99	100	98	96	92	93	100	99
000101	98	98	98	97	98	94	98	94	100	97	99	97	97	92	92	100	97
000110	98	98	98	98	98	95	98	95	100	98	98	99	96	98	98	100	98
000111	95	95	95	94	95	94	94	93	100	97	100	96	100	94	95	100	97
001000	100	100	100	99	100	95	100	95	100	99	100	98	97	94	95	100	98
001001	97	98	98	96	97	93	97	94	100	97	99	98	97	92	92	100	97
001010	98	98	98	96	98	95	97	96	99	98	97	98	96	98	98	100	98
001011	93	94	95	93	93	93	94	93	100	98	100	97	100	97	97	100	98
001100	100	100	100	98	100	95	99	94	100	99	100	99	96	94	94	100	99
001101	98	98	98	97	98	93	97	93	100	97	99	99	97	92	94	100	97
001110	95	95	96	94	95	92	95	93	100	97	97	97	93	95	95	100	97
001111	94	95	96	95	94	94	94	94	100	97	100	94	100	95	94	100	97
010000	100	100	100	100	100	95	100	95	100	96	100	96	97	91	90	96	96
010001	98	99	99	97	98	94	98	94	100	96	100	98	98	90	91	96	96
010010	99	99	100	98	99	99	99	99	99	100	96	100	94	98	98	100	98
010011	94	94	95	93	94	94	94	95	99	96	100	95	99	92	92	95	100
010100	100	100	100	100	100	95	100	95	100	97	100	97	98	93	93	96	97
010101	99	99	99	99	99	94	99	94	100	98	100	98	98	91	91	97	98
010110	99	99	99	98	99	98	99	99	100	100	98	99	96	98	98	100	99
010111	93	93	94	93	93	93	92	94	98	96	100	95	100	96	96	96	100
011000	100	100	100	100	100	95	100	96	100	98	100	97	98	92	92	98	97
011001	98	98	99	98	98	95	98	93	100	99	99	99	98	92	92	98	98
011010	99	99	99	100	99	99	99	99	100	100	97	99	95	98	98	100	100
011011	94	94	95	94	94	94	93	95	100	94	100	94	99	90	90	93	99
011100	100	100	100	99	100	94	100	95	100	96	100	96	98	92	92	97	95
011101	99	99	99	98	99	94	99	93	100	100	100	100	98	91	90	99	99
011110	100	100	100	100	100	99	99	99	100	100	97	100	95	99	99	100	100
011111	94	95	95	95	94	94	94	94	100	95	100	96	100	94	94	96	99
100000	100	100	100	100	100	97	100	96	99	98	100	99	97	97	97	100	99
100001	100	100	100	100	100	93	100	95	100	98	100	100	100	97	97	100	97
100010	100	100	100	100	100	99	100	99	99	100	100	100	94	100	100	100	100
100011	98	98	98	98	98	96	98	96	97	99	100	99	99	97	97	99	99
100100	100	100	100	100	100	96	100	96	99	99	100	98	95	95	96	100	98
100101	100	100	100	100	100	95	100	95	98	98	100	100	100	97	98	100	98
100110	100	100	100	100	100	100	100	100	100	100	100	100	98	100	100	100	100
100111	97	97	97	95	97	95	96	94	96	99	100	98	99	96	96	99	99
101000	100	100	100	99	100	97	100	96	100	98	100	99	97	96	96	100	98
101001	100	100	100	97	100	95	99	95	99	99	100	100	100	96	96	100	99
101010	100	100	100	100	100	100	100	100	100	100	100	100	97	100	100	100	100
101011	98	98	98	96	98	96	97	96	97	98	100	99	100	97	97	98	98
101100	100	100	100	98	100	97	100	95	100	98	100	99	95	96	95	100	99
101101	100	100	100	96	100	95	100	95	99	100	100	100	100	97	97	100	100
101110	100	100	100	100	100	100	100	100	100	100	100	100	97	99	99	100	100
101111	97	97	97	96	97	95	96	95	96	99	100	98	99	97	98	98	98
110000	100	100	100	100	100	95	100	97	100	96	100	97	97	91	91	96	96
110001	98	100	98	98	98	93	99	92	100	96	100	99	100	91	91	97	98
110010	98	98	98	98	98	98	98	98	99	97	98	98	96	96	96	98	97
110011	97	96	98	96	97	97	96	95	97	97	100	95	98	94	93	96	99
110100	100	100	100	100	100	95	100	95	100	97	100	97	97	93	94	96	96
110101	99	100	100	99	99	93	100	94	100	98	100	100	100	91	91	98	98
110110	99	100	99	99	99	99	99	99	99	98	98	98	97	97	97	98	98
110111	96	96	97	96	96	95	95	95	98	98	99	97	99	95	95	98	99
111000	100	100	100	99	100	96	100	98	100	98	100	98	98	93	93	98	97
111001	99	100	99	97	99	94	100	95	100	99	100	100	100	92	92	99	99
111010	99	99	99	99	99	99	99	99	100	99	99	99	97	98	98	100	99
111011	95	95	96	95	95	95	93	94	97	97	100	96	100	95	95	97	99
111100	100	100	100	99	100	96	100	96	100	99	100	100	99	92	94	100	99
111101	99	99	99	95	99	93	99	92	100	99	100	100	100	77	77	98	99
111110	99	99	99	99	99	99	100	100	99	100	99	100	97	98	98	100	100
111111	96	95	96	96	96	96	95	95	97	98	99	97	100	94	95	97	99

Appendix: Classic GEE on Smaller Networks

Statistics Marginal Across All Scenarios

Treatment Effect $\overline{\beta}$: -2.98

	None	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
Bias	0	0	0	0	0	0	-0.01	0	0	0.01	-0.01	0.02	-0.01	-0.05	-0.05	0.03	0.03
RobSE	3.02	2.94	2.91	2.98	3.02	2.92	2.87	2.91	2.95	1.33	1.36	1.47	1.54	0.9	0.9	0.91	0.91
EmpSE	2.93	2.83	2.82	2.93	2.93	2.89	2.82	2.87	2.83	1.18	1.07	1.45	1.44	0.95	0.95	0.74	0.76
Gains	0(0)	3(2)	3(3)	-1(1)	0(0)	0(2)	2(4)	1(3)	2(3)	59(15)	58(10)	34(30)	32(32)	57(18)	57(18)	66(17)	66(17)
Power	30.6	31.1	31.2	31	30.6	32.3	31.6	32.2	30.7	64	56.2	51.9	47.4	68.3	68.3	77.5	78.3
Coverage	95(2)	95(2)	95(2)	95(2)	95(2)	94(2)	95(2)	95(2)	95(2)	95(3)	96(3)	94(3)	93(4)	91(4)	91(4)	95(4)	94(4)

Unadj: No adjustment term
F_1: Degree
F_2: Mean Neighbor Degree
F_3: Assortativity
F_4: Member of Connected Block
F_5: Size of Largest Component
F_6: Mean Component Size
F_7: Number of Components
F_8: Size of Node's Component
F_9: Total Neighbor Infections at baseline
F_{10}: Total Node's Component Infections at baseline
F_{11}: 1/nearest infected path length at baseline
F_{12}: $\sum_i$ 1/path length to Infected Node i at baseline
All: Complete inclusion of the above
Step: Stepwise regression of the above
Pow: Powerlaw(Degree)
Spl: Spline(Degree)

$\boldsymbol{a} =$ [𝕀(High Degree),
𝕀(Powerlaw),
𝕀(Assortativity),
𝕀(Blocks),
𝕀(Degree Infectivity),
𝕀(High Baseline)]

Statistics Modification By Scenario Aspect

a	γ_a
(Intercept)	-0.80
High Degree	-2.71
Powerlaw	-0.28
Assortative	0.04
Communities	-0.12
Deg. Infect.	-0.88
High Base.	-0.43

Bias

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
(Intercept)	-0.00	0.00	-0.01	-0.00	-0.00	0.00	-0.01	0.00	0.00	-0.06	-0.10	-0.08	-0.13	-0.15	-0.15	-0.06	-0.05
High Degree	0.00	0.00	0.01	0.00	0.00	0.00	-0.01	-0.01	-0.00	0.04	0.08	0.06	0.08	0.11	0.11	0.05	0.05
Powerlaw	0.00	-0.00	0.01	0.01	0.00	-0.00	-0.01	0.01	0.00	0.02	0.02	0.05	0.02	0.00	0.00	0.05	0.05
Assortative	0.00	-0.00	-0.01	-0.00	0.00	-0.00	-0.00	0.01	-0.01	0.01	-0.00	0.03	0.02	0.01	0.01	0.01	0.02
Communities	-0.00	0.00	0.00	-0.01	-0.00	0.00	0.01	-0.01	0.01	0.01	0.00	-0.02	0.01	-0.02	-0.02	-0.01	-0.02
Deg. Infect.	0.00	-0.00	0.01	0.01	0.00	-0.00	-0.01	0.01	0.00	0.00	-0.03	0.03	-0.01	-0.05	-0.05	0.04	0.03
High Base.	0.00	-0.00	0.01	0.01	0.00	-0.00	0.01	-0.01	0.00	0.04	0.12	0.05	0.13	0.15	0.15	0.04	0.05

Robust S.E.

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
(Intercept)	-0.46	-0.38	-0.38	-0.45	-0.46	-0.47	-0.37	-0.44	-0.45	-0.18	-0.06	0.04	0.13	0.05	0.05	0.12	0.10
High Degree	0.68	0.70	0.74	0.70	0.68	0.67	0.78	0.67	0.77	0.20	0.55	1.12	0.68	0.51	0.51	0.55	0.45
Powerlaw	0.90	0.77	0.71	0.84	0.90	0.87	0.65	0.77	0.81	0.90	0.33	0.39	0.35	0.32	0.32	0.33	0.43
Assortative	0.02	-0.03	-0.01	0.00	0.02	-0.00	-0.00	0.01	0.01	-0.32	-0.04	-0.08	-0.02	-0.07	-0.07	-0.11	-0.15
Communities	-0.20	-0.17	-0.14	-0.15	-0.20	-0.18	-0.13	-0.14	-0.16	-0.18	-0.07	-0.05	0.03	-0.02	-0.02	-0.04	-0.10
Deg. Infect.	2.65	2.54	2.46	2.60	2.65	2.59	2.43	2.58	2.53	1.50	1.07	0.68	0.83	0.63	0.63	0.67	0.69
High Base.	2.92	2.83	2.81	2.88	2.92	2.83	2.76	2.80	2.84	0.92	1.02	0.80	0.96	0.33	0.33	0.17	0.29

Empirical S.E.

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
(Intercept)	-0.53	-0.44	-0.43	-0.52	-0.53	-0.52	-0.44	-0.45	-0.49	-0.13	0.06	0.03	0.31	0.08	0.08	0.13	0.13
High Degree	0.47	0.46	0.50	0.49	0.47	0.55	0.57	0.51	0.59	-0.02	0.13	1.04	0.39	0.43	0.43	0.38	0.30
Powerlaw	0.86	0.75	0.71	0.84	0.86	0.81	0.65	0.71	0.70	0.85	0.33	0.38	0.38	0.37	0.37	0.30	0.35
Assortative	0.06	0.02	0.03	0.05	0.06	0.06	0.07	0.04	0.06	-0.33	0.01	-0.06	0.04	-0.07	-0.07	-0.09	-0.12
Communities	-0.18	-0.14	-0.14	-0.15	-0.18	-0.15	-0.13	-0.13	-0.12	-0.16	-0.09	-0.02	0.02	-0.01	-0.01	-0.07	-0.09
Deg. Infect.	2.51	2.39	2.33	2.50	2.51	2.43	2.33	2.41	2.35	1.19	0.87	0.62	0.74	0.57	0.57	0.31	0.38
High Base.	3.20	3.08	3.06	3.19	3.20	3.14	3.04	3.11	3.05	1.09	0.75	0.89	0.69	0.44	0.44	0.38	0.42

Unadj: No adjustment term
F_1: Degree
F_2: Mean Neighbor Degree
F_3: Assortativity
F_4: Member of Connected Block
F_5: Size of Largest Component
F_6: Mean Component Size
F_7: Number of Components
F_8: Size of Node's Component
F_9: Total Neighbor Infections at baseline
F_{10}: Total Node's Component Infections at baseline
F_{11}: 1/nearest infected path length at baseline
F_{12}: $\sum_i$ 1/path length to Infected Node i at baseline
All: Complete inclusion of the above
Step: Stepwise regression of the above

Improvement

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
(Intercept)	-0	1	1	-1	-0	-1	0	-0	2	58	50	17	11	47	47	54	55
High Degree	0	-1	-2	-1	0	-1	-3	-3	-3	-2	-2	-23	-16	-9	-9	-8	-7
Powerlaw	0	3	4	1	0	1	5	4	3	-16	-0	-8	2	-8	-8	-11	-11
Assortative	0	1	1	0	0	0	-0	0	0	8	1	2	-2	3	3	6	6
Communities	-0	-1	-1	-1	-0	-0	-1	-1	-1	2	-1	-4	-9	-2	-2	1	1
Deg. Infect.	0	1	3	1	0	2	2	1	2	-2	1	29	23	9	9	14	13
High Base.	0	1	0	1	0	1	1	2	1	13	18	37	46	27	27	21	20

Power

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
(Intercept)	29	29	30	29	29	31	30	31	30	70	52	39	41	52	52	64	72
High Degree	34	33	33	33	34	35	33	34	34	31	43	24	32	30	30	13	13
Powerlaw	-5	-4	-3	-4	-5	-5	-3	-3	-5	0	12	1	5	8	8	5	-2
Assortative	0	1	0	1	0	0	1	0	0	6	1	1	-1	3	3	6	8
Communities	4	3	4	4	4	4	3	3	4	6	2	1	-1	2	2	4	5
Deg. Infect.	-4	-3	-3	-4	-4	-6	-3	-5	-4	-28	-13	15	1	6	6	8	2
High Base.	-26	-27	-28	-26	-26	-27	-27	-27	-27	-27	-36	-16	-24	-17	-17	-9	-13

Coverage

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
(Intercept)	95	95	95	95	95	94	95	94	95	91	93	94	88	90	90	94	92
High Degree	2	2	2	2	2	1	2	2	1	4	5	3	5	5	5	4	5
Powerlaw	0	0	0	0	0	1	0	0	1	1	1	0	1	-0	-0	-1	2
Assortative	-0	-0	-0	-0	-0	-0	-0	-0	-0	0	-1	-1	-1	-1	-1	-1	-1
Communities	-0	-0	-0	-0	-0	-0	0	-0	-0	1	1	1	0	1	1	1	1
Deg. Infect.	1	0	0	1	1	1	1	1	0	3	-1	-0	1	0	0	0	1
High Base.	-2	-2	-2	-2	-2	-2	-2	-2	-2	-1	1	-2	3	-3	-3	-3	-2

Unadj: No adjustment term
F_1: Degree
F_2: Mean Neighbor Degree
F_3: Assortativity
F_4: Member of Connected Block
F_5: Size of Largest Component
F_6: Mean Component Size
F_7: Number of Components
F_8: Size of Node's Component
F_9: Total Neighbor Infections at baseline
F_{10}: Total Node's Component Infections at baseline
F_{11}: 1/nearest infected path length at baseline
F_{12}: $\sum_i$ 1/path length to Infected Node i at baseline
All: Complete inclusion of the above
Step: Stepwise regression of the above

Statistics Conditional On Each Scenario

a	β_a
000000	-0.32
000001	-0.50
000010	-1.45
000011	-1.28
000100	-0.35
000101	-0.50
000110	-1.65
000111	-1.33
001000	-0.45
001001	-0.58
001010	-1.38
001011	-0.84
001100	-0.38
001101	-0.46
001110	-1.50
001111	-1.12
010000	-0.78
010001	-1.19
010010	-4.84
010011	-2.13
010100	-0.74
010101	-1.21
010110	-5.21
010111	-3.29
011000	-0.86
011001	-1.46
011010	-4.72
011011	-1.81
011100	-0.80
011101	-1.36
011110	-4.84
011111	-2.79
100000	-1.97
100001	-8.49
100010	-5.62
100011	-3.36
100100	-2.02
100101	-8.55
100110	-5.60
100111	-3.48
101000	-1.98
101001	-8.34
101010	-5.48
101011	-2.83
101100	-2.03
101101	-8.36
101110	-5.54
101111	-3.29
110000	-1.69
110001	-4.96
110010	-5.22
110011	-3.01
110100	-1.68
110101	-5.05
110110	-5.28
110111	-3.37
111000	-1.76
111001	-5.65
111010	-5.24
111011	-3.39
111100	-1.67
111101	-5.22
111110	-5.58
111111	-3.14

$$\boldsymbol{a} = [\mathbb{I}(\text{High Degree}), \mathbb{I}(\text{Powerlaw}), \mathbb{I}(\text{Assortativity}), \mathbb{I}(\text{Blocks}), \mathbb{I}(\text{Degree Infectivity}), \mathbb{I}(\text{High Baseline})]$$

Bias

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
000000	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
000001	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	-0.10	-0.10	-0.10	-0.10	0.00	0.00
000010	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	-0.10	-0.20	-0.10	-0.20	-0.20	-0.20	-0.10	-0.10
000011	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	-0.10	-0.10	-0.10	-0.10	-0.20	-0.20	-0.10	-0.10
000100	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
000101	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	-0.10	-0.10	-0.10	-0.10	-0.10	0.00	0.00
000110	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	-0.10	-0.20	-0.10	-0.20	-0.20	-0.20	-0.10	-0.10
000111	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10
001000	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	-0.10	-0.10	-0.10	-0.10	-0.10	-0.10	-0.10	-0.10
001001	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	-0.10	-0.10	-0.10	-0.10	-0.10	-0.10	-0.10	-0.10
001010	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	-0.10	0.00	0.00	-0.10	-0.10	0.10	0.00
001011	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	-0.10	-0.10	-0.10	-0.10	-0.20	-0.20	-0.10	-0.10
001100	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	-0.10	0.00	-0.10	-0.10	0.00	0.00
001101	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
001110	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	-0.20	-0.10	-0.20	-0.20	-0.20	0.00	0.00
001111	0	0.00	0.00	0.00	0	0.00	0.10	0.00	0.00	-0.10	-0.20	-0.10	-0.10	-0.20	-0.20	-0.10	-0.10
010000	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.10	-0.10	-0.10	0.00	0.00
010001	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
010010	0	0.00	0.00	0.00	0	0.00	0.00	0.10	0.00	0.10	0.00	0.20	0.10	-0.20	-0.20	0.20	0.20
010011	0	0.00	0.00	0.10	0	0.00	0.00	0.00	0.00	0.20	0.30	0.50	0.30	0.50	0.50	0.50	0.40
010100	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
010101	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	-0.10	-0.10	-0.10	-0.10	-0.10	0.00	0.00
010110	0	0.00	0.00	0.00	0	0.00	-0.10	0.00	0.00	0.00	-0.20	0.00	-0.20	-0.40	-0.40	0.00	0.00
010111	0	0.00	0.10	0.00	0	0.00	0.20	0.10	0.10	0.00	0.10	-0.10	0.20	-0.10	-0.10	0.00	-0.10
011000	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	-0.10	-0.10	-0.10	-0.10	-0.10	0.00	0.00
011001	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.10	-0.10	-0.10	0.00	0.00
011010	0	0.00	0.00	0.00	0	0.00	-0.10	0.00	0.00	0.10	-0.10	0.10	-0.10	-0.30	-0.30	0.10	0.10
011011	0	-0.10	-0.10	0.00	0	-0.10	-0.10	0.00	-0.10	-0.10	-0.20	0.10	-0.20	0.00	0.00	0.00	0.10
011100	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.10	-0.10	0.00	0.00
011101	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.10	-0.10	0.00	0.00
011110	0	0.00	0.00	0.00	0	0.00	-0.10	0.00	0.00	0.00	-0.10	0.00	-0.10	-0.40	-0.40	0.00	0.00
011111	0	0.00	0.00	0.00	0	0.00	-0.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
100000	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
100001	0	0.00	0.00	0.00	0	0.00	-0.10	-0.10	0.00	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10
100010	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	-0.10	0.00	-0.10	-0.10	-0.10	0.00	0.00
100011	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.10	0.00	0.10	0.00	0.00	0.00	0.00
100100	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
100101	0	0.00	0.00	0.00	0	0.00	-0.10	0.00	0.00	0.10	0.10	0.20	0.20	0.10	0.10	0.10	0.10
100110	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	-0.10	0.00	-0.10	-0.10	-0.10	0.00	0.00
100111	0	0.00	0.00	0.00	0	0.00	-0.10	-0.10	0.00	-0.20	-0.20	-0.20	-0.30	-0.30	-0.30	-0.20	-0.20
101000	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
101001	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.00	0.00	0.00	0.00	0.00
101010	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.00	0.00	0.00	0.10	0.10
101011	0	0.00	0.00	0.00	0	0.00	0.00	0.10	0.00	0.40	0.40	0.40	0.60	0.50	0.50	0.50	0.50
101100	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.10	-0.10	-0.10	0.00	0.00
101101	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.10	0.10	0.00	0.10	0.10	0.10	0.10	0.10
101110	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.00	-0.10	-0.10	0.10	0.00
101111	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.10	0.10	-0.10	0.10	0.10	0.10	0.00	0.00
110000	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.10	0.00	0.00	0.00	0.00
110001	0	0.00	0.00	0.00	0	0.00	0.00	0.10	0.00	0.00	0.00	-0.10	0.00	-0.10	-0.10	0.00	0.00
110010	0	0.00	0.00	0.00	0	0.00	-0.10	0.00	0.00	-0.10	-0.30	0.00	-0.30	-0.30	-0.30	0.00	0.00
110011	0	0.00	0.10	0.10	0	0.00	0.00	-0.10	0.00	0.10	0.40	0.00	0.40	0.30	0.30	0.20	0.20
110100	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
110101	0	0.00	0.00	0.00	0	0.00	0.00	-0.10	0.00	0.00	0.10	0.00	0.00	0.10	0.10	0.00	0.00
110110	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.10	-0.10	0.00	-0.10	-0.20	-0.20	0.20	0.10
110111	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
111000	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	-0.10	-0.10	-0.10	-0.10	-0.10	-0.10	-0.10	-0.10
111001	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	-0.10	0.00	-0.10	0.00	0.00	0.00	0.00
111010	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	-0.10	0.10	-0.10	-0.10	-0.10	0.10	0.10
111011	0	0.00	0.10	0.10	0	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.00	0.00	0.00	0.00	0.00
111100	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
111101	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.40	0.40	0.50	0.60	0.40	0.40	0.40	0.40
111110	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	-0.10	-0.20	-0.10	-0.20	-0.30	-0.30	0.00	-0.10
111111	0	0.00	0.00	0.00	0	0.00	0.00	0.00	0.00	0.20	0.30	0.40	0.30	0.40	0.40	0.30	0.30

Percent Relative Bias

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
000000	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
000001	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	20	20	20	20	-0	-0
000010	-0	-0	-0	-0	-0	-0	-0	-0	-0	7	14	7	14	14	14	7	7
000011	-0	-0	-0	-0	-0	-0	-0	-0	-0	8	8	8	8	16	16	8	8
000100	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
000101	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	20	20	20	20	20	-0	-0
000110	-0	-0	-0	-0	-0	-0	-0	-0	-0	6	12	6	12	12	12	6	6
000111	-0	-0	-0	-0	-0	-0	-0	-0	-0	-8	-8	-8	-8	-8	-8	-8	-8
001000	-0	-0	-0	-0	-0	-0	-0	-0	-0	22	22	22	22	22	22	22	22
001001	-0	-0	-0	-0	-0	-0	-0	-0	-0	17	17	17	17	17	17	17	17
001010	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	7	-0	-0	7	7	-7	-0
001011	-0	-0	-0	-0	-0	-0	-0	-0	-0	12	12	12	12	24	24	12	12
001100	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	26	-0	26	26	-0	-0
001101	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
001110	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	13	7	13	13	13	-0	-0
001111	-0	-0	-0	-0	-0	-0	-9	-0	-0	9	18	9	9	18	18	9	9
010000	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	13	13	13	-0	-0
010001	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
010010	-0	-0	-0	-0	-0	-0	-0	-2	-0	-2	-0	-4	-2	4	4	-4	-4
010011	-0	-0	-0	-5	-0	-0	-0	-0	-0	-9	-14	-23	-14	-23	-23	-23	-19
010100	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
010101	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	8	8	8	8	8	-0	-0
010110	-0	-0	-0	-0	-0	-0	2	-0	-0	-0	4	-0	4	8	8	-0	-0
010111	-0	-0	-3	-0	-0	-0	-6	-3	-3	-0	-3	3	-6	3	3	-0	3
011000	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	12	12	12	12	12	-0	-0
011001	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	7	7	7	-0	-0
011010	-0	-0	-0	-0	-0	-0	2	-0	-0	-2	2	-2	2	6	6	-2	-2
011011	-0	6	6	-0	-0	6	6	-0	6	6	11	-6	11	-0	-0	-0	-6
011100	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	12	12	-0	-0
011101	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	7	7	-0	-0
011110	-0	-0	-0	-0	-0	-0	2	-0	-0	-0	2	-0	2	8	8	-0	-0
011111	-0	-0	-0	-0	-0	-0	4	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
100000	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
100001	-0	-0	-0	-0	-0	-0	1	1	-0	-1	-1	-1	-1	-1	-1	-1	-1
100010	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	2	-0	2	2	2	-0	-0
100011	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-3	-0	-3	-0	-0	-0	-0
100100	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
100101	-0	-0	-0	-0	-0	-0	1	-0	-0	-1	-1	-2	-2	-1	-1	-1	-1
100110	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	2	-0	2	2	2	-0	-0
100111	-0	-0	-0	-0	-0	-0	3	3	-0	6	6	6	9	9	9	6	6
101000	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
101001	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-1	-0	-0	-0	-0	-0
101010	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-2	-0	-0	-0	-2	-2
101011	-0	-0	-0	-0	-0	-0	-0	-4	-0	-14	-14	-14	-21	-18	-18	-18	-18
101100	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	5	5	5	-0	-0
101101	-0	-0	-0	-0	-0	-0	-0	-0	-0	-1	-1	-0	-1	-1	-1	-1	-1
101110	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-2	-0	2	2	-2	-0
101111	-0	-0	-0	-0	-0	-0	-0	-0	-0	-3	-3	3	-3	-3	-3	-0	-0
110000	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	6	-0	-0	-0	-0
110001	-0	-0	-0	-0	-0	-0	-0	-2	-0	-0	-0	2	-0	2	2	-0	-0
110010	-0	-0	-0	-0	-0	-0	2	-0	-0	2	6	-0	6	6	6	-0	-0
110011	-0	-0	-3	-3	-0	-0	-0	3	-0	-3	-13	-0	-13	-10	-10	-7	-7
110100	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
110101	-0	-0	-0	-0	-0	-0	-0	2	-0	-0	-2	-0	-0	-2	-2	-0	-0
110110	-0	-0	-0	-0	-0	-0	-0	-0	-0	-2	2	-0	2	4	4	-4	-2
110111	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
111000	-0	-0	-0	-0	-0	-0	-0	-0	-0	6	6	6	6	6	6	6	6
111001	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	2	-0	2	-0	-0	-0	-0
111010	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	2	-2	2	2	2	-2	-2
111011	-0	-0	-3	-3	-0	-0	-0	-0	-0	-0	-0	-3	-0	-0	-0	-0	-0
111100	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0	-0
111101	-0	-0	-0	-0	-0	-0	-0	-0	-0	-8	-8	-10	-11	-8	-8	-8	-8
111110	-0	-0	-0	-0	-0	-0	-0	-0	-0	2	4	2	4	5	5	-0	2
111111	-0	-0	-0	-0	-0	-0	-0	-0	-0	-6	-10	-13	-10	-13	-13	-10	-10

Robust Standard Error

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
000000	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.20	0.40	0.60	0.60	0.30	0.30	0.20	0.20
000001	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.20	0.40	0.60	0.60	0.30	0.30	0.20	0.20
000010	1.60	1.60	1.60	1.60	1.60	1.60	1.60	1.60	1.60	0.70	0.60	0.70	0.70	0.50	0.50	0.60	0.50
000011	4.50	4.40	4.40	4.50	4.50	4.40	4.30	4.40	4.40	1.40	1.40	0.60	1.20	0.50	0.50	0.40	0.40
000100	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.20	0.40	0.60	0.60	0.30	0.30	0.20	0.20
000101	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.90	1.00	0.20	0.40	0.60	0.70	0.30	0.30	0.20	0.20
000110	1.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50	0.70	0.70	0.70	0.80	0.60	0.60	0.60	0.50
000111	4.50	4.40	4.40	4.50	4.50	4.40	4.40	4.40	4.50	1.40	1.50	0.70	1.30	0.60	0.60	0.50	0.40
001000	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.20	0.40	0.50	0.50	0.30	0.30	0.20	0.20
001001	1.20	1.10	1.10	1.10	1.20	1.10	1.10	1.10	1.20	0.20	0.40	0.60	0.60	0.40	0.40	0.30	0.20
001010	1.70	1.70	1.70	1.70	1.70	1.70	1.70	1.70	1.70	0.80	0.70	0.60	0.70	0.50	0.50	0.60	0.60
001011	4.20	4.10	4.10	4.10	4.20	4.10	4.00	4.10	4.10	1.10	1.30	0.40	1.10	0.40	0.40	0.30	0.30
001100	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.20	0.40	0.60	0.60	0.30	0.30	0.20	0.20
001101	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.10	0.20	0.50	0.60	0.70	0.30	0.30	0.20	0.20
001110	1.60	1.60	1.60	1.60	1.60	1.60	1.50	1.60	1.60	0.70	0.70	0.70	0.70	0.50	0.50	0.60	0.50
001111	4.20	4.10	4.10	4.20	4.20	4.10	4.10	4.10	4.10	1.10	1.30	0.50	1.10	0.50	0.50	0.40	0.30
010000	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.50	0.40	0.80	0.70	0.50	0.50	0.60	0.60
010001	1.60	1.60	1.60	1.60	1.60	1.60	1.50	1.50	1.60	0.70	0.70	1.10	0.90	0.70	0.70	0.80	0.80
010010	3.40	3.30	3.00	3.20	3.40	3.30	3.00	3.20	3.20	2.40	1.90	1.80	1.80	1.50	1.50	1.80	1.70
010011	8.30	8.00	7.60	8.00	8.30	7.80	7.20	7.80	7.50	5.90	3.20	1.30	3.40	1.10	1.10	0.80	2.30
010100	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.40	0.40	0.80	0.70	0.50	0.50	0.50	0.50
010101	1.50	1.50	1.50	1.50	1.50	1.50	1.40	1.40	1.50	0.60	0.70	1.10	1.00	0.70	0.70	0.70	0.60
010110	3.00	2.90	2.80	3.00	3.00	2.90	2.70	2.90	2.90	2.10	1.70	1.70	1.70	1.40	1.40	1.80	1.60
010111	7.90	7.70	7.50	7.80	7.90	7.60	7.20	7.70	7.50	5.10	2.90	1.60	3.00	1.30	1.30	0.90	1.50
011000	0.90	0.90	0.90	0.90	0.90	0.90	0.80	0.80	0.90	0.40	0.50	0.90	0.70	0.50	0.50	0.40	0.40
011001	2.00	1.90	1.90	2.00	2.00	2.00	1.90	1.90	2.00	0.60	0.80	1.20	1.10	0.70	0.70	0.60	0.60
011010	3.10	2.90	2.80	3.00	3.10	3.00	2.70	2.90	2.90	2.10	1.60	1.60	1.60	1.30	1.30	1.80	1.70
011011	8.10	7.50	7.30	7.70	8.10	7.40	6.90	7.50	7.10	3.70	3.10	0.80	3.00	0.70	0.70	0.60	1.20
011100	0.80	0.70	0.70	0.70	0.80	0.70	0.70	0.70	0.80	0.30	0.40	0.90	0.80	0.40	0.40	0.30	0.30
011101	1.80	1.70	1.70	1.80	1.80	1.80	1.70	1.70	1.80	0.50	0.70	1.20	1.20	0.60	0.60	0.50	0.50
011110	2.60	2.50	2.40	2.60	2.60	2.50	2.40	2.50	2.50	1.70	1.40	1.50	1.50	1.20	1.20	1.70	1.50
011111	7.90	7.50	7.40	7.90	7.90	7.50	7.30	7.80	7.40	2.90	2.90	1.10	2.90	1.00	1.00	0.70	0.90
100000	0.80	0.80	0.80	0.80	0.80	0.70	0.80	0.80	0.80	0.40	0.50	0.70	0.90	0.40	0.40	0.40	0.40
100001	4.10	4.10	4.10	4.10	4.10	3.80	4.10	3.90	4.00	1.10	2.10	2.20	2.30	0.90	0.90	1.00	0.90
100010	2.00	2.00	2.00	2.00	2.00	1.90	2.00	2.00	2.00	1.10	1.20	1.40	1.50	1.00	1.00	1.20	1.10
100011	6.00	5.90	5.90	6.00	6.00	5.80	6.00	5.90	6.00	2.10	3.10	3.70	3.00	1.90	1.90	2.00	1.90
100100	0.80	0.80	0.80	0.80	0.80	0.70	0.80	0.80	0.70	0.40	0.50	0.70	0.90	0.40	0.40	0.40	0.40
100101	3.90	4.00	4.00	3.90	3.90	3.70	3.90	3.80	3.90	1.00	2.10	2.10	2.40	0.90	0.90	0.90	0.90
100110	1.90	1.90	1.90	1.90	1.90	1.80	1.90	1.90	1.90	1.10	1.10	1.30	1.50	1.00	1.00	1.10	1.00
100111	5.60	5.60	5.60	5.60	5.60	5.50	5.60	5.50	5.60	2.10	2.90	3.30	3.10	1.90	1.90	2.00	1.90
101000	0.80	0.80	0.80	0.80	0.80	0.70	0.80	0.80	0.80	0.40	0.50	0.80	0.90	0.40	0.40	0.40	0.40
101001	4.20	4.20	4.20	4.20	4.20	4.00	4.20	4.10	4.10	1.20	2.10	2.30	2.30	1.00	1.00	1.00	1.00
101010	2.10	2.10	2.10	2.10	2.10	2.00	2.10	2.10	2.10	1.20	1.30	1.50	1.50	1.10	1.10	1.20	1.10
101011	6.20	6.20	6.20	6.20	6.20	6.10	6.20	6.10	6.20	2.10	3.00	3.60	3.00	1.90	1.90	1.90	1.80
101100	0.80	0.80	0.80	0.80	0.80	0.70	0.80	0.80	0.70	0.40	0.50	0.80	1.00	0.40	0.40	0.40	0.40
101101	4.00	4.00	4.10	4.00	4.00	3.80	4.00	3.90	3.90	1.10	2.00	2.10	2.40	1.00	1.00	1.00	1.00
101110	1.90	1.90	1.90	1.90	1.90	1.90	1.90	1.90	1.90	1.10	1.20	1.30	1.60	1.00	1.00	1.20	1.00
101111	5.80	5.80	5.80	5.80	5.80	5.70	5.80	5.80	5.80	2.00	2.80	3.30	3.00	1.90	1.90	1.90	1.80
110000	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.60	0.50	0.80	0.70	0.50	0.50	0.60	0.60
110001	3.30	3.20	3.30	3.30	3.30	3.30	3.20	3.10	3.40	1.40	1.60	2.10	1.80	1.10	1.10	1.40	1.40
110010	2.90	2.80	2.80	2.90	2.90	2.90	2.80	2.80	2.90	1.80	1.70	2.00	1.70	1.50	1.50	1.60	1.50
110011	7.70	7.30	7.10	7.40	7.70	7.60	7.00	7.20	7.50	4.80	3.00	4.20	3.00	2.30	2.30	2.20	2.20
110100	0.80	0.80	0.80	0.80	0.80	0.70	0.80	0.70	0.80	0.50	0.50	0.80	0.80	0.50	0.50	0.60	0.50
110101	3.20	3.10	3.20	3.20	3.20	3.10	3.10	3.00	3.20	1.20	1.50	2.00	1.90	1.00	1.00	1.20	1.20
110110	2.60	2.50	2.50	2.60	2.60	2.60	2.50	2.50	2.60	1.50	1.50	1.70	1.60	1.30	1.30	1.40	1.30
110111	7.00	6.90	6.70	7.00	7.00	7.00	6.70	6.90	7.00	4.00	2.80	3.90	2.90	2.20	2.20	2.00	2.00
111000	0.90	0.90	0.90	0.90	0.90	0.80	0.90	0.80	0.90	0.50	0.50	0.90	0.80	0.50	0.50	0.50	0.50
111001	3.90	3.70	3.70	3.80	3.90	3.80	3.70	3.60	3.90	1.30	1.70	2.20	2.00	1.20	1.20	1.10	1.10
111010	2.60	2.50	2.50	2.50	2.60	2.50	2.40	2.50	2.60	1.50	1.40	1.80	1.50	1.30	1.30	1.40	1.30
111011	7.40	6.90	6.80	7.20	7.40	7.30	6.70	6.90	7.30	2.90	2.80	3.50	2.90	1.90	1.90	1.60	1.50
111100	0.80	0.80	0.80	0.80	0.80	0.70	0.80	0.70	0.80	0.40	0.50	0.90	0.90	0.40	0.40	0.40	0.40
111101	3.50	3.40	3.50	3.50	3.50	3.40	3.40	3.40	3.60	1.10	1.60	2.00	2.10	1.10	1.10	1.00	1.00
111110	2.30	2.20	2.20	2.30	2.30	2.30	2.20	2.20	2.30	1.40	1.40	1.70	1.60	1.20	1.20	1.40	1.30
111111	6.80	6.50	6.40	6.70	6.80	6.70	6.40	6.60	6.80	2.20	2.60	3.30	2.80	1.80	1.80	1.50	1.40

Empirical Standard Error

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
000000	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.20	0.40	0.60	0.60	0.30	0.30	0.20	0.20
000001	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.20	0.40	0.60	0.60	0.40	0.40	0.20	0.20
000010	1.70	1.60	1.60	1.70	1.70	1.70	1.60	1.70	1.60	0.70	0.60	0.60	0.70	0.60	0.60	0.50	0.50
000011	4.60	4.50	4.50	4.60	4.60	4.60	4.50	4.60	4.40	1.50	1.40	0.60	1.20	0.60	0.60	0.40	0.40
000100	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.20	0.40	0.60	0.70	0.40	0.40	0.20	0.20
000101	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.20	0.40	0.70	0.70	0.40	0.40	0.20	0.20
000110	1.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50	1.50	0.70	0.70	0.70	0.80	0.60	0.60	0.50	0.50
000111	4.70	4.60	4.60	4.70	4.70	4.60	4.60	4.70	4.60	1.50	1.30	0.70	1.30	0.70	0.70	0.40	0.40
001000	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.20	0.40	0.60	0.60	0.30	0.30	0.20	0.20
001001	1.20	1.20	1.20	1.20	1.20	1.20	1.20	1.20	1.20	0.30	0.40	0.60	0.60	0.40	0.40	0.30	0.30
001010	1.80	1.80	1.80	1.90	1.80	1.80	1.80	1.80	1.80	0.80	0.70	0.60	0.70	0.60	0.60	0.60	0.60
001011	4.50	4.40	4.40	4.50	4.50	4.40	4.40	4.50	4.30	1.20	1.30	0.50	1.10	0.50	0.50	0.30	0.30
001100	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.20	0.40	0.60	0.70	0.30	0.30	0.20	0.20
001101	1.10	1.10	1.10	1.10	1.10	1.10	1.10	1.10	1.10	0.20	0.40	0.60	0.70	0.40	0.40	0.20	0.20
001110	1.60	1.60	1.60	1.60	1.60	1.60	1.60	1.60	1.60	0.70	0.70	0.70	0.80	0.60	0.60	0.50	0.60
001111	4.30	4.20	4.20	4.30	4.30	4.20	4.20	4.30	4.20	1.10	1.30	0.60	1.20	0.50	0.50	0.40	0.40
010000	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.60	0.40	0.90	0.70	0.60	0.60	0.70	0.70
010001	1.70	1.60	1.60	1.60	1.70	1.60	1.50	1.60	1.60	0.70	0.60	1.20	1.00	0.80	0.80	0.90	0.80
010010	2.80	2.70	2.50	2.80	2.80	2.70	2.60	2.70	2.60	1.70	1.50	1.50	1.60	1.40	1.40	1.00	1.00
010011	8.60	8.30	7.90	8.40	8.60	8.00	7.60	8.00	7.60	6.00	3.10	1.60	3.60	1.40	1.40	1.00	2.00
010100	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.50	0.30	0.90	0.80	0.50	0.50	0.50	0.50
010101	1.50	1.40	1.50	1.50	1.50	1.50	1.40	1.40	1.40	0.60	0.60	1.20	1.10	0.80	0.80	0.70	0.70
010110	2.40	2.40	2.30	2.50	2.40	2.40	2.30	2.30	2.30	1.50	1.40	1.50	1.60	1.40	1.40	0.90	1.00
010111	8.20	7.90	7.70	8.30	8.20	7.90	7.30	7.90	7.50	5.20	2.40	1.80	2.90	1.60	1.60	0.70	1.20
011000	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.40	0.40	0.90	0.80	0.50	0.50	0.40	0.40
011001	2.00	1.90	1.90	2.00	2.00	2.00	1.90	1.90	1.90	0.60	0.80	1.20	1.20	0.80	0.80	0.70	0.60
011010	2.70	2.50	2.40	2.60	2.70	2.50	2.40	2.50	2.40	1.50	1.40	1.40	1.60	1.30	1.30	1.10	1.10
011011	8.40	7.80	7.70	8.20	8.40	7.70	7.40	7.80	7.30	3.80	3.10	1.10	3.30	1.10	1.10	0.90	1.30
011100	0.70	0.70	0.70	0.80	0.70	0.80	0.70	0.70	0.70	0.30	0.40	0.90	0.90	0.50	0.50	0.30	0.30
011101	1.90	1.80	1.80	1.90	1.90	1.90	1.80	1.80	1.80	0.50	0.60	1.20	1.30	0.70	0.70	0.50	0.50
011110	2.40	2.30	2.20	2.40	2.40	2.40	2.20	2.30	2.30	1.40	1.20	1.30	1.50	1.20	1.20	1.10	1.10
011111	8.30	7.90	7.80	8.30	8.30	8.00	7.80	8.20	7.70	3.00	2.60	1.30	2.90	1.20	1.20	0.70	0.80
100000	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.40	0.40	0.80	0.90	0.40	0.40	0.40	0.40
100001	4.20	4.20	4.20	4.30	4.20	4.20	4.30	4.30	4.20	1.10	1.30	2.20	1.80	1.00	1.00	0.90	0.90
100010	1.40	1.40	1.40	1.40	1.40	1.40	1.40	1.50	1.40	0.50	0.80	1.30	1.60	0.90	0.90	0.50	0.50
100011	5.60	5.50	5.50	5.70	5.60	5.60	5.70	5.70	5.60	1.70	1.90	3.50	2.20	1.80	1.80	1.60	1.50
100100	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.40	0.40	0.70	0.90	0.40	0.40	0.40	0.40
100101	3.90	3.80	3.80	3.90	3.90	3.90	3.90	4.00	3.90	1.00	1.20	2.10	1.90	1.00	1.00	0.90	0.90
100110	1.40	1.30	1.40	1.40	1.40	1.40	1.40	1.40	1.40	0.50	0.80	1.20	1.70	0.90	0.90	0.50	0.50
100111	5.40	5.40	5.40	5.50	5.40	5.40	5.50	5.50	5.40	1.60	1.90	3.30	2.20	1.80	1.80	1.60	1.50
101000	0.70	0.70	0.70	0.70	0.70	0.70	0.80	0.80	0.70	0.40	0.40	0.90	1.00	0.40	0.40	0.40	0.40
101001	3.90	3.90	3.90	4.00	3.90	3.90	4.00	4.00	3.90	1.10	1.30	2.20	1.80	1.20	1.20	1.00	1.00
101010	1.50	1.40	1.40	1.50	1.50	1.50	1.50	1.50	1.50	0.50	0.90	1.30	1.60	0.90	0.90	0.50	0.50
101011	6.30	6.10	6.10	6.30	6.30	6.30	6.20	6.20	6.30	1.60	2.00	3.50	2.30	1.80	1.80	1.50	1.40
101100	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.40	0.40	0.80	1.00	0.40	0.40	0.40	0.40
101101	4.10	4.00	4.00	4.10	4.10	4.10	4.10	4.20	4.10	1.10	1.30	2.10	2.00	1.10	1.10	0.90	0.90
101110	1.40	1.40	1.40	1.40	1.40	1.40	1.40	1.40	1.40	0.50	0.80	1.30	1.70	0.90	0.90	0.50	0.50
101111	5.80	5.70	5.70	5.80	5.80	5.80	5.80	5.70	5.80	1.50	1.90	3.20	2.30	1.80	1.80	1.50	1.50
110000	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.60	0.40	0.80	0.70	0.60	0.60	0.70	0.60
110001	3.20	3.00	3.20	3.20	3.20	3.30	3.10	3.10	3.10	1.40	1.10	2.00	1.60	1.30	1.30	1.40	1.40
110010	2.20	2.10	2.10	2.20	2.20	2.20	2.10	2.20	2.20	0.90	1.20	1.60	1.50	1.30	1.30	0.80	0.90
110011	7.60	7.30	7.10	7.50	7.60	7.60	7.00	7.20	7.30	4.60	2.20	4.10	2.40	2.30	2.30	2.00	2.00
110100	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.70	0.50	0.40	0.80	0.80	0.50	0.50	0.60	0.50
110101	3.20	3.10	3.10	3.20	3.20	3.20	3.10	3.10	3.10	1.20	1.00	1.90	1.50	1.20	1.20	1.20	1.20
110110	1.90	1.90	1.90	2.00	1.90	1.90	1.90	1.90	1.90	0.80	1.10	1.50	1.50	1.20	1.20	0.70	0.70
110111	7.10	6.90	6.80	7.20	7.10	7.10	6.90	7.00	7.00	3.80	2.00	3.90	2.30	2.30	2.30	1.80	1.70
111000	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.50	0.40	0.90	0.80	0.50	0.50	0.50	0.50
111001	4.00	3.70	3.80	4.00	4.00	4.00	3.80	3.80	3.90	1.20	1.30	2.10	1.80	1.30	1.30	1.10	1.10
111010	2.00	1.80	1.90	2.00	2.00	2.00	1.90	1.90	1.90	0.70	1.00	1.50	1.50	1.10	1.10	0.60	0.60
111011	7.40	6.90	6.90	7.30	7.40	7.40	7.00	6.90	7.10	2.70	2.10	3.60	2.40	2.00	2.00	1.40	1.40
111100	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.40	0.40	0.90	0.90	0.50	0.50	0.40	0.40
111101	3.50	3.40	3.40	3.50	3.50	3.50	3.50	3.50	3.50	1.10	1.20	2.00	1.80	1.20	1.20	1.00	1.00
111110	1.60	1.50	1.50	1.60	1.60	1.60	1.60	1.60	1.60	0.70	1.00	1.60	1.80	1.20	1.20	0.60	0.60
111111	6.80	6.40	6.30	6.80	6.80	6.80	6.40	6.50	6.60	2.00	1.80	3.40	2.10	1.90	1.90	1.40	1.30

Improvement

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
000000	0	3	3	-1	0	-1	3	2	4	79	53	28	25	59	59	75	75
000001	0	1	1	-2	0	-2	-0	1	2	79	61	38	38	60	60	77	78
000010	0	3	3	-1	0	0	2	1	4	57	59	61	54	64	64	69	69
000011	0	2	2	-1	0	0	1	0	4	68	70	86	73	87	87	91	91
000100	0	1	1	-1	0	-1	-0	1	0	77	51	22	16	55	55	74	74
000101	0	1	1	-2	0	-1	-0	0	0	79	59	33	30	60	60	78	78
000110	0	1	1	-1	0	-0	0	0	2	53	53	51	43	57	57	65	64
000111	0	1	1	-1	0	1	2	0	3	68	71	85	73	86	86	90	90
001000	0	2	2	-1	0	-0	0	1	2	78	58	39	38	61	61	75	75
001001	0	1	1	-1	0	-1	1	1	1	78	62	48	47	66	66	78	78
001010	0	2	2	-1	0	0	1	1	2	56	62	65	60	67	67	68	67
001011	0	2	2	-1	0	1	1	0	3	73	71	89	75	89	89	93	93
001100	0	1	1	-1	0	-1	1	1	2	78	51	29	19	58	58	76	76
001101	0	1	1	-1	0	-1	-0	0	1	80	61	40	35	64	64	79	79
001110	0	2	2	-1	0	0	2	0	3	56	56	56	49	60	60	66	65
001111	0	1	2	-1	0	1	1	-0	2	75	70	87	72	87	87	91	91
010000	0	5	3	-0	0	-1	6	4	5	26	55	-7	14	27	27	15	20
010001	0	6	4	2	0	0	7	4	6	57	61	30	40	51	51	47	49
010010	0	5	12	3	0	4	8	5	8	40	49	47	43	50	50	65	63
010011	0	4	8	2	0	6	12	7	11	30	64	81	58	83	83	87	77
010100	0	2	1	-2	0	-2	0	1	1	37	53	-23	-5	28	28	29	33
010101	0	4	2	-1	0	-1	5	4	3	60	61	22	28	47	47	52	54
010110	0	3	8	-2	0	1	7	4	5	40	44	39	35	43	43	61	59
010111	0	3	6	-1	0	4	10	3	9	37	71	78	65	81	81	91	85
011000	0	5	4	-0	0	-0	4	4	4	58	53	1	11	42	42	53	54
011001	0	7	6	2	0	1	6	5	6	70	60	40	41	61	61	67	68
011010	0	8	11	2	0	5	11	6	9	44	49	49	40	51	51	60	58
011011	0	7	8	2	0	8	12	7	12	54	63	87	60	87	87	89	84
011100	0	4	3	-0	0	-1	3	2	3	59	51	-21	-21	36	36	54	55
011101	0	5	5	-1	0	-0	6	4	4	74	67	39	33	63	63	73	73
011110	0	6	8	-0	0	2	8	4	5	43	50	45	36	50	50	55	54
011111	0	5	6	-0	0	4	6	2	7	64	69	84	65	85	85	92	90
100000	0	0	0	-3	0	-0	-1	-4	-0	49	46	-7	-21	45	45	49	49
100001	0	1	1	-1	0	-0	-0	-1	-0	75	70	47	58	75	75	77	78
100010	0	2	1	-2	0	-0	-1	-3	-0	64	40	10	-16	35	35	64	65
100011	0	2	2	-1	0	-0	-1	-1	0	70	65	37	61	68	68	71	73
100100	0	-0	-0	-3	0	-0	-1	-5	-0	48	46	-3	-27	43	43	47	47
100101	0	1	1	-1	0	-0	-1	-2	0	74	68	47	51	74	74	77	77
100110	0	1	1	-2	0	-0	-1	-2	-0	62	41	10	-24	35	35	64	64
100111	0	1	1	-1	0	-0	-2	-1	-0	70	65	39	60	66	66	70	72
101000	0	1	1	-1	0	-0	-3	-3	-0	46	44	-17	-30	42	42	46	45
101001	0	1	1	-1	0	-0	-2	-1	-0	71	68	43	53	70	70	75	75
101010	0	1	1	-3	0	-0	-2	-4	-0	63	42	11	-10	36	36	64	65
101011	0	2	2	-1	0	-0	1	1	0	73	67	44	62	71	71	75	76
101100	0	-0	-0	-0	0	-0	-3	-6	-0	46	45	-13	-43	41	41	46	45
101101	0	1	1	-1	0	-0	-1	-2	-0	73	68	48	51	73	73	77	77
101110	0	1	1	-2	0	0	-3	-4	0	61	41	9	-24	34	34	62	62
101111	0	2	2	-1	0	-0	0	1	0	74	67	45	61	70	70	73	74
110000	0	2	-0	-2	0	-3	1	-2	1	17	49	-9	12	24	24	15	17
110001	0	6	1	-2	0	-2	3	3	3	56	66	38	50	60	60	56	55
110010	0	4	5	2	0	-0	4	2	2	58	45	27	33	40	40	62	62
110011	0	4	7	2	0	1	8	6	4	39	71	46	68	69	69	74	74
110100	0	1	-0	-1	0	-1	-1	-2	0	23	49	-11	-10	29	29	22	24
110101	0	3	0	-0	0	-1	1	1	1	62	67	40	51	63	63	63	63
110110	0	3	4	-1	0	-0	2	-0	1	60	46	21	23	40	40	65	66
110111	0	3	5	-1	0	0	3	2	1	47	71	45	68	68	68	74	75
111000	0	1	2	-2	0	-3	-0	-2	1	41	48	-15	-4	35	35	40	39
111001	0	7	4	-0	0	-1	5	4	3	69	68	47	54	67	67	73	74
111010	0	6	6	-0	0	-0	3	1	3	62	51	21	21	42	42	69	69
111011	0	7	8	2	0	1	6	7	5	64	72	52	67	74	74	81	81
111100	0	1	1	-1	0	-1	-1	-3	0	47	53	-18	-22	40	40	47	46
111101	0	3	2	-0	0	-0	1	-0	1	67	65	41	46	64	64	70	70
111110	0	5	5	-1	0	-0	1	2	1	58	38	0	-11	25	25	62	62
111111	0	6	7	-1	0	0	6	4	2	71	73	49	68	72	72	80	81

Power

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
000000	7	7	7	7	7	8	7	8	6	49	12	12	17	21	21	31	43
000001	8	8	8	8	8	9	8	9	7	63	15	12	17	26	26	50	61
000010	14	14	15	13	14	14	15	14	14	47	50	50	44	65	65	83	90
000011	8	8	7	7	8	8	8	7	7	14	12	50	16	59	59	95	97
000100	8	8	8	8	8	9	8	9	7	62	11	11	16	24	24	43	55
000101	9	9	9	10	9	10	10	11	8	65	14	12	17	24	24	53	62
000110	17	18	18	18	17	18	18	18	17	64	56	53	46	73	73	91	96
000111	8	8	8	8	8	8	8	8	7	16	16	59	21	66	66	97	98
001000	7	8	8	8	7	8	8	9	7	48	13	14	18	25	25	37	46
001001	8	9	9	9	8	9	8	10	8	61	16	14	21	28	28	57	67
001010	12	12	12	12	12	13	13	13	12	43	50	57	52	67	67	79	87
001011	8	8	8	9	8	8	8	8	8	11	8	42	9	46	46	76	87
001100	7	7	7	7	7	8	7	7	6	52	12	9	15	20	20	39	48
001101	8	7	7	8	8	8	7	8	7	60	13	14	17	28	28	52	64
001110	14	15	15	15	14	16	16	15	14	54	55	55	44	69	69	83	90
001111	8	8	8	9	8	8	8	8	7	13	11	49	13	56	56	88	93
010000	15	16	16	15	15	16	16	18	14	36	39	19	24	33	33	30	33
010001	11	11	10	10	11	11	12	14	10	47	38	21	27	37	37	37	41
010010	28	31	37	31	28	31	36	33	32	59	84	87	85	92	92	96	94
010011	8	8	7	8	8	7	8	7	7	7	12	59	14	71	71	96	41
010100	17	17	18	19	18	20	18	20	15	43	43	16	22	36	36	37	42
010101	13	13	13	14	13	14	14	14	12	59	36	18	20	39	39	47	52
010110	42	43	46	42	42	43	46	43	43	79	95	91	93	94	94	98	98
010111	8	8	8	9	8	9	8	8	7	11	18	53	22	67	67	99	70
011000	16	17	17	17	16	16	17	19	16	66	40	17	25	42	42	59	63
011001	9	10	10	11	9	10	11	12	10	75	40	26	29	51	51	72	75
011010	32	37	40	35	32	36	40	36	36	70	92	92	90	95	95	93	95
011011	8	10	9	10	8	9	9	8	8	8	10	66	11	70	70	94	60
011100	17	17	17	18	17	18	18	20	16	78	41	16	21	43	43	74	76
011101	12	12	13	13	12	13	13	13	10	89	44	21	27	55	55	85	87
011110	46	48	49	45	46	47	51	47	47	89	99	92	92	97	97	99	99
011111	8	9	9	9	8	10	10	8	8	19	14	73	18	79	79	100	88
100000	73	72	73	72	73	79	72	74	78	100	100	74	63	100	100	100	100
100001	55	55	55	55	55	60	54	58	56	100	100	96	99	100	100	100	100
100010	89	89	89	88	89	90	88	89	89	100	100	99	95	100	100	100	100
100011	7	7	7	8	7	8	8	8	7	31	10	16	12	38	38	36	38
100100	77	75	76	76	77	83	77	78	81	100	100	78	57	100	100	100	100
100101	59	59	58	59	59	63	57	60	61	100	100	98	99	100	100	100	100
100110	92	92	92	91	92	93	92	92	93	100	100	98	92	100	100	100	100
100111	9	10	9	9	9	10	9	9	10	32	10	17	9	38	38	33	36
101000	70	70	70	71	70	78	70	73	75	100	100	69	59	100	100	100	100
101001	50	51	50	51	50	55	51	54	52	100	100	95	99	100	100	100	100
101010	82	83	82	82	82	84	80	82	83	100	100	98	94	100	100	100	100
101011	8	8	8	8	8	9	8	8	8	30	11	15	13	42	42	40	43
101100	79	78	78	78	79	84	78	80	82	100	100	72	52	100	100	100	100
101101	54	54	53	55	54	57	55	56	55	100	100	96	97	100	100	100	100
101110	89	89	88	89	89	90	89	89	90	100	100	99	93	100	100	100	100
101111	10	10	9	10	10	10	10	9	10	36	13	17	14	44	44	41	42
110000	54	55	54	54	54	56	56	59	54	75	98	53	67	86	86	76	80
110001	30	33	30	30	30	32	33	37	28	95	97	65	80	98	98	95	95
110010	40	42	44	43	40	42	45	44	40	94	96	80	91	96	96	100	99
110011	7	8	8	8	7	8	10	8	8	10	14	12	17	31	31	32	31
110100	59	57	59	58	59	66	57	61	60	86	99	50	57	92	92	87	89
110101	36	36	36	36	36	39	37	39	34	99	98	73	82	100	100	99	99
110110	58	59	60	58	58	60	60	60	58	98	99	90	95	98	98	100	100
110111	9	9	9	10	9	9	9	9	9	13	15	14	16	33	33	37	39
111000	53	53	54	54	53	56	54	57	52	95	98	45	52	93	93	94	94
111001	31	32	32	31	31	33	33	34	30	99	98	76	82	99	99	100	100
111010	55	60	60	57	55	56	61	59	55	99	100	89	92	100	100	100	100
111011	9	9	8	9	9	9	10	9	8	21	16	18	18	42	42	59	60
111100	58	56	57	59	58	63	58	61	57	98	98	46	44	95	95	98	98
111101	33	34	32	34	33	35	34	35	30	100	99	80	84	100	100	100	100
111110	74	76	77	75	74	76	77	77	74	100	100	92	89	100	100	100	100
111111	8	8	8	8	8	8	8	8	7	31	19	19	18	50	50	65	67

Coverage

	UnAdj	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}	F_{12}	All	Step	Pow	Spl
000000	94	94	94	93	94	94	94	94	95	94	94	94	88	92	92	97	94
000001	96	95	96	95	96	94	95	95	96	91	94	92	90	89	89	96	92
000010	93	93	93	92	93	93	93	93	94	90	86	94	85	87	87	91	87
000011	94	94	94	94	94	94	94	94	94	94	96	90	94	87	87	92	88
000100	95	96	95	95	95	94	95	95	96	94	96	94	91	90	90	96	94
000101	92	93	93	92	92	92	93	92	94	91	94	93	89	89	89	94	91
000110	93	93	93	93	93	93	93	93	94	91	90	93	87	88	88	92	89
000111	93	93	93	93	93	93	93	93	94	94	97	92	95	89	89	96	94
001000	94	94	94	94	94	94	94	93	94	88	90	92	86	88	88	91	88
001001	94	94	94	93	94	93	94	94	94	90	92	94	88	91	91	92	89
001010	93	93	93	92	93	92	92	93	92	91	89	93	87	87	87	92	90
001011	92	92	92	92	92	92	92	92	92	93	93	83	94	80	80	90	85
001100	94	95	95	94	94	93	94	94	96	92	95	93	88	88	88	95	92
001101	93	94	94	93	93	92	93	92	95	93	96	93	90	90	90	96	94
001110	94	94	94	94	94	94	94	94	94	91	88	94	86	86	86	92	89
001111	94	94	94	93	94	94	94	93	94	95	94	87	92	84	84	89	85
010000	95	95	95	94	95	94	95	94	96	90	97	93	90	88	88	93	93
010001	95	95	95	96	95	95	95	94	96	94	96	93	90	90	90	94	94
010010	97	98	97	97	97	97	97	97	98	98	96	97	93	95	95	99	98
010011	93	93	94	93	93	93	93	93	94	94	95	86	93	83	83	82	92
010100	94	94	94	94	94	94	94	93	95	93	98	93	91	92	92	96	96
010101	95	95	95	94	95	94	95	94	96	92	97	94	90	89	89	94	94
010110	97	97	98	97	97	97	97	97	98	98	94	96	92	93	93	99	98
010111	93	93	93	92	93	93	94	93	94	95	98	90	96	89	89	95	96
011000	94	94	93	93	94	93	93	93	95	92	95	93	89	90	90	94	94
011001	94	95	94	94	94	94	94	94	95	93	94	93	89	88	88	92	92
011010	97	96	96	96	97	96	96	97	97	97	93	97	90	92	92	98	97
011011	93	93	92	92	93	93	92	93	93	95	93	80	92	75	75	75	82
011100	95	94	94	94	95	94	95	93	95	95	97	94	90	92	92	96	95
011101	94	93	94	93	94	93	94	93	95	93	97	95	90	88	88	94	93
011110	94	95	95	95	94	94	95	94	96	96	94	96	91	93	93	97	96
011111	94	94	92	92	94	94	92	93	94	95	96	87	94	84	84	91	92
100000	97	97	97	97	97	95	96	95	96	96	99	94	96	95	95	97	96
100001	93	94	93	92	93	91	93	92	92	94	100	94	98	91	91	95	95
100010	99	99	99	99	99	99	100	100	99	100	99	98	94	96	96	100	100
100011	96	96	96	96	96	95	95	95	95	98	100	96	100	97	97	98	98
100100	97	97	97	96	97	94	96	95	95	96	99	95	96	93	93	96	96
100101	94	95	94	93	94	93	94	93	94	95	100	95	98	92	92	95	95
100110	99	99	99	99	99	98	98	98	99	100	98	97	91	97	97	100	100
100111	95	95	95	94	95	94	94	94	95	98	99	95	99	95	95	98	98
101000	96	96	96	96	96	94	96	95	95	95	99	92	93	94	94	96	95
101001	96	96	97	96	96	95	96	95	96	96	100	94	98	91	91	95	95
101010	99	99	99	99	99	99	99	99	99	100	98	97	93	97	97	100	100
101011	95	95	95	94	95	94	94	94	95	98	99	95	98	96	96	98	98
101100	97	97	97	96	97	95	97	95	96	96	98	95	95	94	94	97	96
101101	94	94	94	93	94	93	94	93	94	96	100	94	98	91	91	95	95
101110	99	99	99	98	99	99	99	99	99	100	98	96	92	95	95	100	100
101111	95	95	95	94	95	94	95	95	95	99	99	96	98	96	96	98	98
110000	96	96	96	96	96	95	96	94	97	93	98	94	94	92	92	95	95
110001	95	96	96	95	95	94	95	95	97	95	100	96	97	90	90	94	94
110010	99	99	99	99	99	98	98	98	99	100	97	98	94	95	95	100	100
110011	94	94	94	93	94	94	94	94	95	96	98	95	98	94	94	96	97
110100	96	97	96	96	96	95	96	95	96	94	98	95	94	93	93	95	95
110101	96	96	96	95	96	94	95	95	96	96	99	96	97	92	92	95	96
110110	98	99	99	98	98	98	99	98	99	100	98	97	94	96	96	100	100
110111	95	94	94	94	95	94	94	94	95	96	99	95	97	92	92	96	97
111000	97	97	97	96	97	96	96	95	97	94	98	95	94	93	93	95	95
111001	94	95	94	93	94	94	94	94	95	96	98	95	96	91	91	94	94
111010	98	99	99	98	98	98	98	98	98	100	98	97	92	96	96	100	100
111011	94	94	94	94	94	94	94	94	95	97	99	93	97	93	93	97	97
111100	94	95	95	94	94	92	94	93	95	96	99	95	94	93	93	96	96
111101	94	95	95	94	94	93	94	93	95	94	99	92	96	88	88	94	93
111110	99	99	99	99	99	99	99	99	99	100	97	96	91	93	93	100	100
111111	94	95	94	94	94	94	95	95	94	98	100	94	98	92	92	96	97