Structure and bias in the network autocorrelation model

Eric J. Neuman a,∗, Mark S. Mizruchi b

a Department of Business Administration, University of Illinois, 350A Wohlers Hall, 1206 South Sixth Street, Champaign, IL 61820, United States

b Department of Sociology, University of Michigan, United States

ARTICLE INFO

Keywords:
Network autocorrelation model
Density
Simulation

ABSTRACT

In a recent paper (Mizruchi and Neuman, 2008), we showed that estimates of \( \rho \) in the network autocorrelation model exhibited a systematic negative bias and that the magnitude of this bias increased monotonically with increases in network density. We showed that this bias held regardless of the size of the network, the number of exogenous variables in the model, and whether the matrix \( W \) was normalized or in raw form. The networks in our simulations were random, however, which raises the question of the extent to which the negative bias holds in various structured networks. In this paper, we reproduce the simulations from our earlier paper on a series of networks drawn to represent well-known structures, including star, caveman, and small-world structures. Results from these simulations indicate that the pattern of negative bias in \( \rho \) continues to hold in all of these structures and that the negative bias continues to increase at increasing levels of density. Interestingly, the negative bias in \( \rho \) is especially pronounced at extremely low-density levels in the star network. We conclude by discussing the implications of these findings.

1. Introduction

One of the most central issues in social network analysis is the identification of network effects: to what extent is an actor’s behavior affected by those to whom he or she is connected? Finding ways to specify the role of network effects has been a persistent problem for network analysts, and several approaches have been tried. In recent years, however, one technique has come to predominate: the network autocorrelation model (Cliff and Ord, 1981; Ord, 1975). Maximum likelihood remains the dominant procedure for estimating the parameters of this model (Anselin, 1988; Doreian, 1981; Ord, 1975).

Network autocorrelation models have been widely adopted, in part, because unlike other techniques such as ego-centric analysis or dyadic analysis, they allow investigators to model simultaneously both individual-level and network-level effects. Yet issues remain surrounding the network autocorrelation model. Principal among these issues are concerns about the accuracy of estimating the network parameter. Past work in the geography literature considered the implications of model misspecification (see, for example, Florax and Rey, 1995; Stetzer, 1982). More recent research now suggests that estimation bias may appear even in a properly specified model. In a recent paper (Mizruchi and Neuman, 2008), we used simulations to demonstrate that the maximum likelihood solution to the network autocorrelation model exhibits a systematic negative bias in estimating the network parameter and that the magnitude of this bias increases monotonically with increases in network density and the size of the parameter itself. We showed that this bias held regardless of the size of the network, the number of exogenous variables in the model, and whether the matrix representing the network was row-normalized or in raw form. Our finding of negative bias has been replicated by other network scholars (Phillip Bonacich and Carter Butts, in separate private communications). Other scholars also have found a bias in the estimation of the network parameter using different means (Farber et al., 2009; Páez et al., 2008; Smith, 2009). This negative bias is a potentially serious problem. It suggests that in some cases in which network effects exist they will not be identified; in other cases, even if network effects are identified, the size of the effect is likely to be underestimated.

The networks on which our simulations were conducted were random, however (Mizruchi and Neuman, 2008). That is, the networks were drawn from Bernoulli distributions such that every pair of actors had an equal probability of being connected. Networks such as these, which are based on random graph theory (Erdős and Rényi, 1959), tend to bear little resemblance to actual social networks. In the latter, people tend to develop relationships with those to whom they are geographically proximate (Festinger et al., 1950), with whom they interact (Brass, 1981; Lincoln and Miller, 1979),
and with similar backgrounds (McPherson et al., 2001). A legitimate question to ask is, do the findings from our previous study hold under conditions that are more similar to actual social networks? Or, to put it differently, does the negative bias exhibited in the estimation of the network parameter persist when the network autocorrelation model is applied to networks with a non-random structure?

In this paper, we address this question by applying the network autocorrelation model to three well-known network structures: star, caveman, and small-world. We compare findings from these simulations with those resulting from random networks. We show that the negative bias in the estimate of the network parameter holds for each of the network types regardless of structure. However, in one of these structures—the star—the negative bias exhibits a curvilinear effect. For the star network, the estimate of the network parameter is negatively biased at extremely low levels of density and becomes less biased as density increases before the bias once again appears at higher levels of density. We conduct additional analysis on low-density networks to explicate this finding. We conclude by discussing the implications of these findings.

2. Bias in the network autocorrelation model

In ordinary least-squares analysis with $N$ observations, the model $Y = X\beta + \epsilon$ assumes that the error terms $\epsilon$ are normally distributed around 0, and that the $N$ observations are statistically independent. Yet this assumption is often violated. If one is examining rates of violent crime across the United States, for example, it seems likely that the unexplained outcomes in Montana and Wyoming are more likely to be a result of similar forces than are those of Montana and New Jersey. This likelihood of spatial dependence is what led geographers to develop models to account for spatial autocorrelation. Geographers were interested in removing correlated residuals across cases in order to render the observations statistically independent (Cliff and Ord, 1981). That is, they decomposed the error term, $\epsilon$, into $\epsilon = \rho W \epsilon + \upsilon$, where $W$ is an $N \times N$ distance matrix of the observations; $\rho$ is the parameter representing the degree of autocorrelation among elements in $\epsilon$; and $\upsilon$ is a vector of residuals that, with the removal of $\rho W \epsilon$, are uncorrelated with $X$. With this transformation, the system of equations $Y = X\beta + \epsilon$ and $\epsilon = \rho W \epsilon + \upsilon$ can be solved to yield unbiased estimates for $\beta$.

Doreian (1980) refers to this as the spatial disturbances model, while Anselin and Hudak (1992) call this the spatial lag model.

Modeling the spatial dependence in the error terms treats the autocorrelation across units as a nuisance to be removed. Researchers could also include the autocorrelation as a substantive effect to be measured and tested, however (Doreian, 1980). Thus a second way of modeling the autocorrelation is in the behavioral outcomes: $Y = \rho W Y + X\beta + \epsilon$, where $W$ remains an $N \times N$ distance matrix of the observations; $\rho$ is now the parameter representing the degree of autocorrelation among observations; $\epsilon$ is now uncorrelated with $X$. Doreian (1980) refers to this as the spatial effects model, while Anselin and Hudak (1992) call this the spatial lag model.

There is nothing that requires the distances in $W$ to represent geographic distance, however. Network scholars, therefore, soon picked up on these methods and began implementing them with the elements of $W$ representing social, rather than physical, proximity between observations (White et al., 1981). The term network autocorrelation model soon came to represent both types of autocorrelation models when $W$ represented a social network. Our focus in this paper will be on modeling autocorrelation in the dependent variable (that is, the spatial effects/spatial lag model). When we refer to the network autocorrelation model, it is this particular autocorrelation model that we have in mind.

In our previous research (Mizruchi and Neuman, 2008), we used simulations to examine the network autocorrelation model and made a rather disturbing discovery: the maximum likelihood estimates of the network parameter $\rho$ are systematically biased in a negative direction. The bias increased as the density of $W$ increased and became more pronounced at higher values of target $\rho$. Despite numerous robustness tests on network size, number of exogenous variables, model noise, and normalization of the network matrix $W$, we never completely eliminated the bias.

The discovery of this underestimation bias is disturbing because the bias can lead to incorrect conclusions about the test of a hypothesis. Either type of error can occur. Consistent underestimation of $\rho$ can lead to Type I error—concluding that there is a network effect when in fact there is none. When no network effect is present (that is, the population $\rho$ is 0), the underestimation bias increases the probability that the estimate for $\rho$ will suggest a significant negative network effect, especially in dense networks. A more important issue, though, and one that is more likely to occur, is that the consistent underestimation of $\rho$ can lead to Type II error—failing to detect a network effect when such an effect is present. This issue stems from the fact that the bias increases as the population value of $\rho$ increases. It therefore becomes more difficult to detect network effects in the very conditions that we care most about them—when there is strong autocorrelation.

One lingering question about our simulations is how we constructed $W$. The networks in our simulation were random. Pairs of nodes in our $W$’s were independent from one another and each had an equal probability of being tied (Erdős and Rényi, 1959). Ties in most social networks, however, seldom follow this pattern. Social networks tend to have some semblance of structure. Each node may have the potential to be connected to only a small subset of nodes, for example, or certain nodes may have a higher likelihood of forming ties than other nodes. Because the structural properties that emerge in actual social networks may overcome the bias associated with high density or with strong network effects in random networks, it is important to ask whether our findings hold under conditions that are more similar to actually existing networks. We investigate this question in the following analysis.

3. Testing procedure

To examine whether the negative bias in the estimation of $\rho$ persists when $W$ has a non-random structure, we conducted four sets of simulations. Each set of simulations used a different representation for $W$. One of these sets was random in order to provide us with a baseline for comparison (and also to ensure that we could replicate our previous work). The remaining three sets use well-known network structures: star, caveman, and small-world. Graphical depictions of each network appear in Fig. 1.

We attempted to construct $W$’s with target densities as close as possible to .005, .01, .02, .05, .10, .15, .20, .30, .40, and .50. We did not examine networks with densities higher than .50 because we assumed that at that point it becomes difficult to differentiate a non-random network from a random network. In order to achieve network densities as close as possible to our targets, we increased the size of the networks in our simulation to $N = 400$. Random and star networks use exactly 400 nodes, though cave-

---

1. We briefly introduce the network autocorrelation model in this section. Detailed descriptions of the model appear elsewhere (Cliff and Ord, 1981; Doreian, 1980; Leenders, 2002).

Fig. 1. Stylized representations of four network types. Each network has exactly 36 nodes, and the networks within each column have approximately the same number of ties. The networks in the left column have about 70 ties (density \( \approx .05 \)) and the networks in the right column have about 200 ties (density \( \approx .15 \)). All ties are reciprocal and are displayed with a single connection. Small-world networks are shown without random rewiring.

Man and small-world networks use a slightly different number in order to come closer to matching the target densities. These minor differences in network size should have no impact on our ability to compare results across network type. Our earlier study (Mizruchi and Neuman, 2008) revealed virtually no differences between networks of sizes 50 and 100.

The four types of networks were constructed as follows:

1. Random \((N=400)\): Every pair of nodes in \(W_{\text{random}}\) is connected with the same probability. By letting the probability equal the target density, \(d\), the expected value of density of \(W_{\text{random}} = d\). This is the same type of \(W\) that we used in our previous examination (Mizruchi and Neuman, 2008), although there we set \(N=50\).

2. Star \((N=400)\): In a true star network, one node is connected to all other nodes and no other connections exist. In this minimal star configuration, the number of ties is \(N-1\) and the density of \(W_{\text{star}} = ((N - 1)/(N(N - 1)/2)) = (2/N)\). For \(N=400\), the density of \(W_{\text{star}} = 2/N = 2/400 = .005\), which is our lowest target density. For target densities greater than this, we added ties at...
random such that the expected density of the total network \( W_{\text{small}} \)—the minimal star plus these “random” ties—equals the target density.\(^3\)

3. Caveman \((N = 360)\): In caveman networks, \(N\) nodes are clustered into \(m\) groups, and each group is fully connected among its \(N/m\) nodes. One node from each group serves as a connector to two other groups, and all groups are connected to exactly two other groups.\(^4\) As a function of \(N\) and \(m\), the density of \( W_{\text{caveman}} = (m(m - 1) + 2)/m(N - 1) \).\(^5\) We set \( N = 360 \) for our caveman network simulations because it allowed us to achieve densities of \(0.0056\) (\(m = 2\)), \(0.0097\) (\(m = 4\)), \(0.0202\) (\(m = 8\)), \(0.0477\) (\(m = 18\)), \(0.0976\) (\(m = 36\)), \(0.1644\) (\(m = 60\)), \(0.1978\) (\(m = 72\)), \(0.2480\) (\(m = 90\)), \(0.3315\) (\(m = 120\)), and \(0.4986\) (\(m = 180\)). Setting \( N = 400 \) does not yield this many densities because \(400\) does not factor into as many distinct integers as does \(360\).

4. Small-World \((N = 401)\): We follow Watts and Strogatz’s (1998) method for constructing small-world networks. We begin with a ring lattice of \(N\) nodes with \(k\) edges per node. By definition, this creates high clustering in the network. With probability \(p\), each tie is randomly ‘rewired’. For \(p\) that is neither too small nor too large, this process does not fully disrupt the high clustering in \(W\) but greatly reduces the average length between any two nodes in \(W\). Through experimentation, we found that \(p > 0.10\) achieves the goals of high clustering and low average path length for most values of \(k\) in our simulations. For the parameters \(N\) and \(k\), the density of \( W_{\text{smallworld}} = k/((N − 1)N) \). By setting \(N = 401\) and letting \(k\) range across the set \(\{2, 4, 8, 20, 40, 60, 80, 120, 160, 200\}\) we achieved densities of \( W_{\text{smallworld}} \) that are exact matches for our target densities.\(^6\)

For each of these network types, we ran a set of simulations. Each of the four sets of simulations involved a combination of different values for \(\rho\) and different target densities for \(W\). In each set we tested the estimation procedure at three values of \(p\): 0.02, and 0.5.\(^7\) For each value of \(\rho\), we ran 100 replications of our model at each of the different target densities. Each of the four sets of simulations included 10 different target densities. This yielded \(3 \times 10 \times 100\) (replications), or 3000, individual replications in each of these sets, and therefore \(4 \times 3000\), or 12,000, replications in all.

The procedure we followed to run our simulations was similar to that of our previous study (Mizruchi and Neuman, 2008). Our models consisted of three \(X\) variables and a constant. We drew values of \(X\), \(\beta\), and \(\epsilon\) from standard normal distributions. \(W\) was set according to the type of network and target density being tested. As in our previous study, ties in \(W\) were reciprocated (that is, for node \(i\) and \(j\), \(W_{ij} = W_{ji}\) and \(W\) was row-normalized. We computed “observed” values of \(Y\) as \((1 - \rho W)^{-1}(X\beta + \epsilon)\) and used this \(Y\) along with \(X\) and \(W\) to estimate the model parameters \(\rho\) and \(\beta\).\(^8\)

4. Results

Fig. 2 (panels a–l) presents scatterplots of the estimated \(\rho\) for each replication as a function of the actual density of \(W\). Each panel consists of replications for a specific network type at one of the three population values of \(\rho\). Table 1 (panels a–l) presents the 95% confidence intervals around the sample mean of \(\rho\) for a given target density. Again, each panel consists of replications for a specific network type at one of the three population values of \(\rho\).

The graphs in Fig. 2 reveal that the overall pattern of underestimation of \(\rho\) is present even when \(W\) is not random. Except in one instance that we will address below, estimates for \(\rho\) remain close to the population parameter at very low densities but decrease with increasing density. As in our previous work, the effect appears slightly more pronounced with increasing \(\rho\) (moving from left to right in the columns of the graphs).

As noted above, Table 1 displays the extent to which the sample means fall below the population parameters by reporting sample means and their surrounding 95% confidence intervals. If the estimate for \(\rho\) were unbiased, we would expect about half of the sample means to be above the population \(\rho\) and about half to be below the population \(\rho\). For each of the four network types, we have 30 sample means—one sample mean for each of the 10 target densities at each of the 3 target \(\rho\)’s. Even if as many as 20 of the 30 sample means were above or below the population \(\rho\), we could still consider the 1—breakdown to be statistically equal.\(^9\) Examining the sample means shows, however, that the vast majority of them fall below their respective population \(\rho\). For the random networks, only two of the sample means are higher than their respective population parameter while 28 are lower (\(\chi^2 = 22.53\), with 1 d.f., \(p < .001\)). Small-world networks have three sample means that are greater than the population parameter and 27 that are lower (\(\chi^2 = 19.20\), with 1 d.f., \(p < .001\)). All 30 sample means are lower than the population value of \(\rho\) in both the star networks\(^10\) and the caveman networks.

Of course, just because a sample mean is lower than the population parameter does not imply that the sample mean is significantly different from that population value. To address this question, we compare the number of times that the lower bound of the confidence interval was above the population parameter (statistically significant overestimation) with the number of times that the upper bound of the confidence interval was below the population parameter (statistically significant underestimation). Once again, if the estimate for \(\rho\) were unbiased, these counts should be roughly equal. Furthermore, the number of times that the population parameter did not fall within the confidence interval should be small (that is, about 5% of the time, or about six total times here).

The results in Table 1 show that neither of these conditions holds. In the random networks, the population parameter falls outside the confidence interval 12 times, in the star networks 13 times, in the caveman networks 15 times, and in the small-world networks 10 times. Thus, out of 120 different trials, the population parameter fell outside the confidence interval a total of 50 times (41.7%). In every one of these cases the population value \(\rho\) was underestimated. Conversely, not once out of 120 trials was the sample mean of \(\rho\) significantly overestimated.

Our main purpose of this analysis was to determine whether the underestimation bias of \(\rho\) remains when \(W\) is not random. So far, we have been able to determine that the bias is still present in networks with a non-random structure. To compare the structured networks

---

\(^3\) See Appendix A for a derivation of the probability that any two non-central nodes are connected such that the expected total density of \(W\) will equal a given target density.

\(^4\) The lone exception to this is if \(m = 2\), in which case each group is connected to just one other group.

\(^5\) See Appendix B for the derivation.

\(^6\) According to Watts and Strogatz (1998), small world networks are those for which \(N \gg k \ln(N) \gg 1\). At \(N = 401\), \(\ln(N) \approx 5.99\). Clearly some of the \(W\)’s created here are not true small worlds because of the relationship between \(k\) and \(\ln(N)\). Yet the purpose of this exercise is to assess the effects of the network autocorrelation method on non-random \(W\)’s—that is, \(W\)’s with some structure. Our purpose here is therefore to provide a structure that approaches a small-world \(W\).

\(^7\) In our previous study we also examined negative values of \(\rho\). We decided not to include negative values of \(\rho\) in the present analyses for two reasons. First, such situations are unusual empirically. Second, our findings from the earlier study indicate that such simulations yield little additional information.

\(^8\) We estimated all models in this paper in R using the “inam” function in the sna package written by Butts (2007).

\(^9\) If the split were 20–10, \(\chi^2\) (with 1 d.f.) would equal 3.33, \(p = .07\).

\(^10\) Panel d (target \(\rho = 0\)) in Table 1 shows means of 0.000 for density targets of .02 and .10. At greater precision, these means are actually 0.0000377 (target density = .02) and 0.000375 (target density = .10).
Fig. 2. Scatterplot of the estimated network effect ($\rho$) against the actual density of $W$. Each point represents one replication of a trial at a combination of network type (Random, Star, Caveman, or Small-World), target $\rho$ (0, 0.2, or 0.5) and network density.

...with the random networks more thoroughly, we computed a multiple regression model with the estimated value for $\rho$ (which we term $RHOEST$) as our dependent variable. Our independent variables included the three selected values of the population $\rho$ (0, .2, and .5, which we term $RHOPOP$), and the observed density of $W$ (which we term $DENSITY$). We also included an interaction term between the population $\rho$ and the observed density ($RHOPOP \times DENSITY$) in order to examine our earlier finding of the tendency for the negative effect of density on the estimated $\rho$ to increase at higher levels of the true population $\rho$ (Mizruchi and Neuman, 2008). To facilitate the interpretation of the main effects in models with the interaction effect, we centered the population $\rho$ and the density of $W$ on their means before computing the interaction term (Aiken and West, 1991). To compare the bias across network types, we included three dummy variables representing the three non-random structures: star, caveman, and small-world. The random networks are the reference category.

11 Mean-centering has no effect on the size or significance of the interaction effect. Its primary benefit for our purposes is that the coefficients for the mean-centered main effects are identical to what they would be if the interaction term were absent from the model. This allows us to determine the precise estimates of the main effects for cases in which the interaction is not statistically significant.
We begin by examining the main effects for the population \( \rho \) and density in model 1 of Table 2. Before presenting these results, we should note the way that we tested the significance of RHOPOP. A 1-unit increase in RHOPOP should correspond to a 1-unit increase in RHODE, leading to a coefficient for RHOPOP of 1.000. We therefore performed significance tests for RHOPOP with respect to 1 rather than with respect to 0, as is conventionally done in regression analysis. Although the coefficient for RHOPOP in model 1 is clearly statistically different from 0, it is not significantly different from 1 (\( t = -1.401, \) with \( 11.994 \) d.f., \( p = .161 \)). Consistent with our earlier findings, the effect of density is negative (\( t = -20.642, \) with \( 11.994 \) d.f., \( p < .001 \)): as the density of W increases, the estimate of \( \rho \) at a given level of population \( \rho \) becomes increasingly negatively biased. In model 2 we add the interaction between the population \( \rho \) (RHOPOP) and density. Although the coefficient is in the expected direction, it is not statistically significant. This does not support the findings in our earlier work (Mizruchi and Neuman, 2008), in which we found that the negative bias at \( \rho \) is high of density increased at increasing levels of population \( \rho \).  

12 We further examined this interaction effect by running regression models on each network type (random, star, caveman, and small-world) separately. The main effect of population \( \rho \) was significantly less than 1 in the random, star, and small-world models; it was greater than 1, but not significantly, in the caveman model. As expected, the main effect of density was negative and significant for each network type. The RHOPOP \( \times \) DENSITY interaction was significantly negative for random and small-world networks, negative but not significant for caveman networks, and marginally positive for star networks. Even in the models where the interaction term
was significant, it explained a very small percentage of the overall model variance. The lack of consistency in the significance of the interaction term across network types as well as lack of the interaction’s explanatory power overall was surprising to us given our previous work. It is important to note, however, that these simulations, unlike our previous work, were not run across the full range of possible target densities. We therefore advise caution before making any general claims about whether the underestimation of $\rho$ is related to the true network effect of the model. Results of these regression models are available from the authors upon request.

### Table 2: Linear regression models of the estimated network effect, $\rho$(RHOEST).

<table>
<thead>
<tr>
<th>Variable</th>
<th>(1) All network types, main effects</th>
<th>(2) All network types, interaction</th>
</tr>
</thead>
<tbody>
<tr>
<td>Constant</td>
<td>0.0896 (0.0177)*</td>
<td>0.1611 (0.0139)*</td>
</tr>
<tr>
<td>RHOPop†</td>
<td>0.9525 (0.0339)</td>
<td>0.9525 (0.0339)</td>
</tr>
<tr>
<td>Density</td>
<td>−0.8834 (0.0428)**</td>
<td>−0.8834 (0.0428)**</td>
</tr>
<tr>
<td>RHOPop × Density</td>
<td>−0.2139 (0.0208)</td>
<td></td>
</tr>
<tr>
<td>STAR</td>
<td>−0.0292 (0.0197)</td>
<td>−0.0292 (0.0197)</td>
</tr>
<tr>
<td>CAVEMAN</td>
<td>−0.1659 (0.0197)**</td>
<td>−0.1659 (0.0197)**</td>
</tr>
<tr>
<td>SMALL WORLD</td>
<td>−0.0201 (0.0197)</td>
<td>−0.0201 (0.0197)</td>
</tr>
<tr>
<td>Observations</td>
<td>12,000</td>
<td>12,000</td>
</tr>
<tr>
<td>R-Squared</td>
<td>.097</td>
<td>.097</td>
</tr>
</tbody>
</table>

Probabilities are two-tailed; unstandardized coefficients are presented, with standard errors in parentheses; the dependent variable is RHOEST (the estimated value for $\rho$).

† Significance tests for RHOPop are performed with respect to 1 rather than 0.

5. Bias in low-density networks

In this section we examine the degree of underestimation bias at low densities by analyzing networks exclusively in the low-density range for three different network configurations: random, star, and line.

1. Random: In the previous section, we created random networks by allowing every pair of nodes in $W_{\text{random}}$ to be connected with the same probability, which was equal to the target density, $d$. Based on this, the expected value of the density of $W_{\text{random}} = d$. One change in these subsequent simulations is that here we created only enough random ties so that the density of $W_{\text{random}} = d$ exactly. We made this change because our focus on low densities required more precision in our design.

2. Star: We constructed star networks as before, except with different target densities. The minimal star network, in which one node is connected to all other nodes and no other connections exist, provides us with our lowest target density, $2/N$. For target densities greater than this, we added ties at random such that the density of the total network $W_{\text{star}}$—the minimal star plus these “random” ties—equals the target density.

3. Line: The minimal line configuration has every node connected to exactly two other nodes except for two “end” nodes, each of which is connected to only one other node. As with the minimal star configuration, the minimal line configuration yields $N − 1$ ties and a density of $2/N$. To achieve target densities greater than this, we added ties at random such that the density of the total network $W_{\text{line}}$—the minimal line plus these “random” ties—equals the target density.

We include the star networks in our analysis because that is the configuration at which we detected the negative bias at very low densities. The random networks serve as a control group. The purpose of including networks based on the line structure in addition to the star and random networks is to control for a potential confound between the star and random networks. Star and random networks differ in their level of centralization; networks with a star configuration are highly centralized whereas networks whose ties appear more or less at random are not. For the low densities of this test, star and random networks also differ in that star networks are connected whereas random networks are generally not connected. The line configuration allows us to disentangle these two properties. Like star networks, line networks are connected; yet like random networks, line networks are decentralized. Distinguishing between these two network features could be useful in determining just what is causing the observed phenomenon.

In the previous analysis, we used matrices of $N = 400$. The estimation procedure takes an extremely long time to run on models of that size, so we scaled back the matrices in these simulations to $N = 50$. Past results have shown that networks of size 50 are large enough to produce systematic underestimation in $\rho$ and that, if anything, underestimation of $\rho$ becomes more pronounced with increasing $N$ (Mizruchi and Neuman, 2008). Simulations with $N = 50$ therefore represent a conservative test of whether the network
autocorrelation model underestimates \( \rho \) at low densities for networks of a given structure.

We began our simulations by using the base configurations of a pure star network and a pure line network:
density = 2/N = 2/50 = .04. We created random networks with this exact same number of ties, \( N = 1.13 \). From these base configurations, we increased the density of \( W \) by adding new ties at random, from 1 to 11 ties. The number of total ties in each \( W \) matrix thus ranged from 49 to 60, corresponding to densities from .04 to .05.

As in the previous section, we repeated each simulation at three target densities: \( \rho = 0, 0.2, \) and 0.5. The number of total ties in each \( W \) matrix was row-normalized. We computed “observed” values of \( Y \) as \((I - \rho W)^{-1}(X \beta + \varepsilon)\) and used this \( Y \) along with \( W \) and \( \rho \) to estimate the model parameters \( \rho \) and \( \beta \).

Table 3 presents scatterplots of the estimated \( \rho \) for each replication as a function of the actual density of \( W \). Panels 1–3 of Table 3 each consist of replications for a specific network type at one of the three population values of \( \rho \). Table 3 (panels a–i) presents the 95% confidence intervals around the sample mean of \( \rho \) for a given target density. Each panel consists of replications for a specific network type at one of the three population values of \( \rho \).

In both Fig. 3 and Table 3, results for random and line networks are shown in the first two rows, respectively. At first glance, there appears to be little evidence of bias in the estimates of \( \rho \) for either type of network. Both networks generate estimates that appear “flat” and centered near the population \( \rho \). The mean estimates for \( \rho \) are greater than the population \( \rho \) more often than they were in the simulations from our previous section. Closer inspection, however,
Table 4
Linear regression models of the estimated network effect, ρ(RHOEST), at low levels of density.

<table>
<thead>
<tr>
<th>Variable</th>
<th>(1) Random main effects</th>
<th>(2) Random interaction</th>
<th>(3) Line main effects</th>
<th>(4) Line interaction</th>
<th>(5) Star main effects</th>
<th>(6) Star interaction</th>
</tr>
</thead>
<tbody>
<tr>
<td>Constant</td>
<td>-0.0433 (0.0261)**</td>
<td>0.2230 (0.0016)**</td>
<td>0.0277 (0.0262)**</td>
<td>0.2159 (0.0017)**</td>
<td>-1.0328 (0.0681)**</td>
<td>0.1202 (0.0043)**</td>
</tr>
<tr>
<td>RHOPOP‡</td>
<td>0.9909 (0.0080)</td>
<td>0.9909 (0.0080)</td>
<td>0.9802 (0.0080)†</td>
<td>0.9802 (0.0081)†</td>
<td>0.7629 (0.0209)**</td>
<td>0.7629 (0.0208)**</td>
</tr>
<tr>
<td>DENSITY</td>
<td>0.7880 (0.5836)</td>
<td>0.7880 (0.5836)</td>
<td>-0.9096 (0.5872)</td>
<td>-0.9096 (0.5873)</td>
<td>21.9140 (1.5247)**</td>
<td>21.9140 (1.5174)**</td>
</tr>
<tr>
<td>RHOPOP × DENSITY</td>
<td>0.5220 (2.8405)</td>
<td>-1.4281 (2.8581)</td>
<td>44.0004 (7.3846)</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Observations 3600, R-squared .810, .818, .805, .805, .300, .306

Probabilities are two-tailed; unstandardized coefficients are presented, with standard errors in parentheses; the dependent variable is RHOEST (the estimated value for ρ).

† p < .10.
* p < .05.
*** p < .001.
‡ Significance tests for RHOPOP are performed with respect to 1 rather than 0.

Fig. 3. Scatterplot of the estimated network effect (ρ) against the actual density of W. Each point represents one replication of a trial at a combination of network type (Random, Star, or Line), target ρ (0, 0.2, or 0.5) and network density.

reveals that even at these low levels of density there are signs of a tendency for ρ to be underestimated. Although the mean estimates for ρ are sometimes greater than the target value for a particular network, they are still more likely to be lower than the target ρ value. For the random networks, only four of 36 sample means across all values of population ρ are greater than the population ρ,


\( \chi^2 = 21.78, \text{ with } 1 \text{ d.f.}, p < .001 \). This imbalance is larger with the line networks, in which only one\(^{14}\) of the sample means is greater than the population \( \rho \) (\( \chi^2 = 32.11, \text{ with } 1 \text{ d.f.}, p < .001 \)). Yet those are the only indicators of underestimation bias with these models. The 95\% confidence intervals for the estimated \( \rho \)'s do not fall below the target value of \( \rho \) more often than suggested by chance for either network type. In both sets of models, the upper bound of the confidence interval falls below the target value just one time (2.8\%), which is not statistically significant (\( \chi^2 = 0.37, \text{ with } 1 \text{ d.f.}, p = .54 \)). Consistent with our previous findings, the lower bound of the confidence interval never once lies above the population \( \rho \) for either type of network.

The results for the simulations using star networks (the third row of Fig. 3 and Table 3) exhibit much clearer signs of underestimation. Only two of the 36 sample means in panels g–i of Table 3 are greater than the population \( \rho \) (\( \chi^2 = 28.44, \text{ with } 1 \text{ d.f.}, p < .001 \)). More strikingly, the 95\% confidence interval for estimates of \( \rho \) fall below the population \( \rho \) 2 times (16.7\%) for \( \rho = 0.5 \text{ times (41.7\%)} \) for \( \rho = 0.2 \), and all 12 times for \( \rho = 0.5 \). Not only is the total of 19 times (52.8\%) far above what we would expect by chance (\( \chi^2 = 173.01, \text{ with } 1 \text{ d.f.}, p < .001 \)), but the pattern suggests that for star networks at low densities, underestimation is more prevalent at higher values of population \( \rho \).

In addition to underestimation being more common for the star networks as compared with the other types of networks, there is another important difference in the bias exhibited across network types. For the star networks, the bias occurs systematically. Specifically, in networks with a star structure the estimates of \( \rho \) become less biased as density increases for the low densities in our tests. We verified this with a series of regressions. For each of the three network types, we regressed the estimated value for \( \rho \) (RHOEST) on the population \( \rho \) (RHOPOP), the density of \( \text{DENSITY} \), and the interaction of population \( \rho \) and network density (RHOPOP \( \times \) DENSITY). As in the previous analysis, we centered RHOPOP and DENSITY on their means before computing the interaction and include the mean-centered variables in our regression.

For each of the three network types, we ran two regression models: one with just the main effects of population \( \rho \) (RHOPOP) and network density (DENSITY) and a second with the interaction term added (RHOPOP \( \times \) DENSITY). The results appear in models 1–6 of Table 4. The coefficient for the population \( \rho \) (RHOPOP) is not significantly different from 1 for the random networks (model 1) but is for the line networks (model 3) (\( t = 2.4750 \text{ with } 3597 \text{ d.f.}, p = .015 \)). In neither model do the estimates for \( \rho \) vary with the network density. The addition of RHOPOP \( \times \) DENSITY in models 2 and 4 shows no significant interaction between population \( \rho \) and network density for random networks and line networks. The star networks reveal a different story, however. In the main effects analysis (model 5) the coefficient for population \( \rho \) is significantly lower than the expected value of 1 (\( t = 11.3445 \text{ with } 3597 \text{ d.f.}, p < .001 \)), but more importantly, the coefficient for network density is positive and significant (\( t = 14.370 \text{ with } 3597 \text{ d.f.}, p < .001 \)). This latter result indicates that, controlling for population \( \rho \), the estimates of sample \( \rho \) become less negatively biased with increasing network density for star networks at the low densities of these simulations. And in model 6, the coefficient for the interaction term is positive and significant (\( t = 5.958 \text{ with } 3596 \text{ d.f.}, p < .001 \)), which indicates that the underestimation of \( \rho \) diminishes at higher values of density.

This systematic decrease in the underestimation of \( \rho \) as density increases is a new phenomenon to us. We saw no evidence of this in our previous study, and it did not appear in either the random or line networks in this analysis. As we have noted, almost all other simulations we have run have shown bias to increase with increasing levels of density. Furthermore, the underestimation bias is typically not evident at densities below .20. Yet for the star structure, the lowest estimates of \( \rho \) occur at or near the lowest network density target, and there is a clear pattern for the estimates of \( \rho \) to increase as density increases (at least at density levels up to .05). This effect holds at each of the three values for population \( \rho \) and becomes even more pronounced at higher target values of \( \rho \).

### 6. Conclusion

In our earlier work (Mizruchi and Neuman, 2008), we showed that the estimates of the autocorrelation parameter \( \rho \) in the network autocorrelation model exhibited a systematic negative bias, especially at high levels of network density. Because these findings were based on simulations drawn from random networks, however, this raised the question of whether a similar bias would hold in network structures that resembled those encountered in real-life situations. Extending our analyses to three well-known network structures—star, caveman, and small-world—we have shown that the negative bias in \( \rho \) continues to hold in non-random networks. This is especially interesting given that networks which exhibit these characteristics are by definition of relatively low density. In fact, we were able to show that the negative bias exists even when our range of density (from .05 to .5) was only half that which we had examined in our earlier study, in which we included networks with densities as high as .95.

Beyond replicating our earlier findings on networks of defined structures, our simulations also yielded an unexpected and intriguing result. For one network—the star—we found an especially large negative bias at the lowest density level that we examined. A detailed investigation of the relation between the population \( \rho \) and its sampling distribution at very low levels of density further confirmed this finding. The negative bias was greatest at the lowest value and became less pronounced as the density increased.

We are thus left with three conclusions from this analysis. First, it is increasingly difficult to deny that the parameter estimate \( \rho \) in the network autocorrelation model contains a systematic negative bias. This bias has now been shown to occur not only in randomly generated networks but in well-established network structures as well. Second, the underestimation bias is not confined strictly to networks of high density. At least in one structure, the star, we have shown that the bias can exist at very low levels of density as well. Third, although we have learned more about the specific points at which the negative bias exists, we still do not know why it occurs. Identifying the sources of this bias is the next order of business.

### Appendix A. Derivation of the probability of ties between non-central nodes for the star network

The base star network model consists of every node being tied to the same node with no other existing ties. As explained in the text, in networks with \( N \) nodes, the density of this base star configuration is \( 2/N \). To achieve target densities greater than \( 2/N \), we added ties at random between non-central nodes. Achieving a target density, \( d \), greater than \( 2/N \) required us to calculate the probability, \( q \), that any two non-central nodes should be tied given \( d \) and \( N \). This probability equals the number of ties between non-central nodes divided by the total number of ties between non-central nodes that are possible.

For density \( d \), the total number of ties in the network is \( d(N(N − 1))/2 \). The base star configuration accounts for \( N − 1 \) of these ties, leaving \( d(N(N − 1))/2 − (N − 1) = ((dN − 2)/2)(N − 1) \) ties between non-central nodes.

The number of possible ties between non-central nodes in the star model equals the total number of possible ties among \( N \) nodes.

\(^{14}\) Panel d (target \( \rho = 0 \)) in Table 1 shows means of 0.000 for density targets of .0424. At greater precision, this mean is actually \( −0.000327 \).
minus the number of ties in the base star configuration, or \((N(N - 1)/2) - (N - 1)\).

With these calculations, we can derive the probability, \(q\), that any two non-central nodes are connected as a function of the number of nodes in the network, \(N\), and the target density, \(d\).

\[
q(N,d) = \frac{\text{# of ties between non-central nodes}}{\text{# of possible ties between non-central nodes}}
\]

\[
= \frac{(dN - 2)(N - 1)/2 - (N - 1)}{dN - 2}
\]

\[
= \frac{N - 2}{N}
\]

**Appendix B. Derivation of network density for the caveman network**

In the caveman network model, we let \(N\) equal the total number of nodes in the network and \(m\) equal the number of nodes in each completely connected group. The number of completely connected groups is therefore equal to \(N/m\). Density is defined as the number of total ties in the network divided by the number of possible ties in the network. The number of total ties can be split into two parts: intragroup ties and intergroup ties.

Using the definition of density as the number of total ties in the network divided by the number of possible ties in the network, we can substitute and solve as follows:

\[
\text{Density (N,m)} = \frac{\text{(# of intragroup ties) + (# of intergroup ties)}}{\text{(# of possible ties)}}
\]

\[
= \frac{N(m - 1)/2 + N/m}{m(m - 1)/2 + N/m}
\]

\[
= \frac{N(m - 1) + 2}{m(N - 1)}
\]

**References**


