Network diffusion under homophily and consolidation as a mechanism for social inequality

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Abstract

DiMaggio and Garip (2011) define *network externalities* (where the value of a practice is a function of network alters that have already adopted the practice) as a mechanism exacerbating social inequality under the condition of *homophily* (where advantaged individuals poised to be primary adopters are socially connected to other advantaged individuals). The authors use an agent-based model of diffusion on a real-life population for empirical illustration, and thus, do not consider *consolidation* (correlation between traits), a population parameter that shapes network structure and diffusion (Blau and Schwartz 1984, Centola 2015). Using an agent-based model, this paper shows that prior findings linking homophily to segregated social ties and to differential diffusion outcomes are contingent on high levels of consolidation. Homophily, under low consolidation, is not sufficient to exacerbate existing differences in adoption probabilities across groups, and can even end up alleviating inter-group inequality by facilitating diffusion.

Sociologists are interested in how social networks shape the distribution of resources (Lin 1993; Portes 1998), attitudes (Small, Lamont and Harding 2010), and behaviors (Boyd 1989, Marsden and Gorman 2001, Smith and Christakis 2010) in society. One line of inquiry focuses on relating network formation processes to social stratification outcomes. This work suggests that *homophily* – the tendency for actors to associate with similar others – leads to segregated social networks, and accordingly, to inter-group inequality in outcomes for which network peers offer a positive influence (DiMaggio and Garip 2011, Manzo 2013, Montgomery 1991).

Researchers have used formal analysis or agent-based models to theorize on network-induced unequal distributions in particular domains. Montgomery (1991), for example, has developed a mathematical model to connect job referral networks to wage inequality. Manzo (2013) has proposed a computational model to link network-based educational choice to educational disparities in France. In both examples, the authors argued that higher degrees of homophily in social ties (by ability in the former study, and by socio-economic status in the latter) lead to higher degrees of inequality (in wages in the former, and in educational attainment in the latter).

In a recent article, DiMaggio and Garip (2011) – DG hereafter – generalized this argument to any good or practice that displays *network externalities*, that is, becomes more valuable (or less risky) to a person as more network peers adopt that good or practice. Network externalities, the authors argued, exacerbate inter-group inequality under the condition of homophily, that is, if advantaged individuals who are the likely primary adopters of a good or practice are socially linked to other advantaged individuals in the population. The authors illustrated this process with an agent-based model of Internet adoption in the United States,

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sampling the agents from the 2002 General Social Survey (GSS) to produce realistic distributions of income, educational attainment, and race. Similar to earlier work, the authors found, higher degrees of homophily (by income, education, and race) generate higher degrees of inequality in adoption.

By using real-life data, DG's empirical illustration presumed a particular state of the world as given, and did not fully take into account the context for homophilous tie formation. The fact that income, education, and race are highly correlated in the U.S. setting, for example, likely produced highly clustered and segregated networks even under low levels of homophily.

In this paper, we argue that prior results linking homophily to network-based inequality depend on presumed correlations between different characteristics in a population. We are inspired by Blau and Schwartz's (1984) seminal work which suggested *consolidation* – the correlation between traits in a population – as a key population parameter shaping social interactions. Centola (2015) recently used an agent-based model to investigate how homophily and consolidation jointly alter network structure and diffusion outcomes.

We follow a similar strategy, but modify Centola's model in two ways. Like DG, we first introduce status differences among individuals which affect adoption probability, and second compare group-specific adoption rates and equilibrium levels under different conditions of homophily and consolidation. We find that whether (and how much) homophily exacerbates inter-group inequality is contingent on the level of consolidation in the population. In what follows, we first situate our approach in the existing literature, then describe the novelty of our model, and finally discuss the implications of our results.

SOCIAL NETWORKS AS A MECHANISM FOR INEQUALITY

Cumulative advantage from social networks?

Sociologists have long regarded 'cumulative advantage' as a general mechanism for inequality that accrues greater increments of benefits to individuals that possess an initial advantage (Merton 1968; DiPrete and Eirich 2006). Empirical evidence has consistently found success leading to further success across a range of reward systems, most notably, in scholarly publications (Allison, Long and Krauze 1982, Lazega and Jourda 2016) and recognition (Cole 1970, Reskin 1977), although the extent of support has varied by definition and method (van de Rijt et al. 2014, Salganik, Dodds and Watts 2006).

A large sociological literature has also shown that social networks provide access to various resources – such as information on jobs (Granovetter 1974) or migration opportunities (Massey and Espinosa 1997), normative pressures to assume healthy behaviors (Smith and Christakis 2008) or to improve school performance (Burke and Sass 2008, Sacerdote 2011) – that help individuals get ahead. Research has suggested that social networks can perpetuate inequality to the extent that such network-based resources are uneven in their distribution or benefits across groups (e.g., Garip 2008, Lin 2002, Smith 2005).

Scholars have only recently begun to connect these two lines of research, and consider social networks as a path toward cumulative advantage. In the area of labor markets, for example, scholars have argued that job referrals will increase wage inequality to the extent that workers of similar productivity are socially connected (Montgomery 1991, Arrow and Borzekowski 2004). In health research, studies have suggested that network effects in healthy behaviors will compound initial differences if high socio-economic status individuals associate

with one another (Pampel et al. 2010). In the field of education, researchers have attributed a wider gap in academic achievement to tracking, which puts students of similar academic standing together (Gamoran 2011).

There are two common elements to these arguments. First, social networks are presumed to provide a positive influence in adopting a practice (in finding a job, taking up a healthy habit, or aiming for academic success). Second, social networks are assumed to be homophilous, that is, stratified by traits that are related to adoption probability (productivity, financial resources, or academic ability).

There is vast evidence for each of these assumptions. Reviews of research on labor markets (Marsden and Gorman 2001), health (Smith and Christakis 2008), and education (Epple and Romano 2011) all suggest strong positive network effects in various outcomes. And studies of social network composition reveal a strong tendency towards homophily in many settings (Kandel 1978; McPherson et al. 2001; Rivera et al. 2010). But there is only limited empirical evidence for how network effects and homophily in social ties, in combination, compound initial advantages and widen existing disparities in the adoption of a practice.

Challenges in empirically linking social networks to inequality

It is difficult to establish a unified causal chain from network formation to network diffusion and inequality. The first obstacle is the lack of data. Longitudinal data sets that simultaneously track individuals' network ties and behavior are rare, and when available, typically restricted to an institutional setting (e.g., schools in the AddHealth data). Such incomplete data, although useful for some questions, do not offer reliable measures of homophily or adoption levels in individuals' social networks.

The second obstacle is the notorious difficulties in the identification of network effects (also referred to as *network diffusion*, *peer effects*, or *endogenous interactions*). Individuals might adopt a practice because prior adopters in their network offer information, help, or influence that makes that practice less risky or more beneficial. Or, individuals might adopt a practice simply because they are subject to similar unobserved contextual factors as the prior adopters. To discard the latter possibility, researchers search for instances where individuals in the same environment vary in their exposure to network effects (e.g., Liu et al. 2010). But, even then, it is hard to address the so-called 'reflection problem', that is, to establish that each individual is truly responding to the group-level behavior (rather than the group-level behavior simply reflecting the sum of individual choices) (Manski 1993).

The third, and perhaps the thorniest, obstacle is the potential confounding of network formation and network diffusion. Individuals might self-select into a network in anticipation of engaging in a practice (for example, a student looking to improve academic performance might join a study group, and start working harder) (Elwert and Winship 2014). To address this issue of endogenous selection, researchers typically seek natural experiments assigning individuals to particular networks (e.g., Sacerdote 2001), or test the sensitivity of results to varying degrees of confounding (e.g., VanderWeele 2011).

Needless to say, these issues become even more intractable in combination, making it very difficult to provide empirical evidence to existing claims in the literature that positive network effects in adoption and homophilous tie formation together increase inequality.

Formal and computational models of social networks and inequality

A number of researchers have used formal analysis and computational models to investigate the network dynamics underlying cumulative advantage. Montgomery (1991) has proposed a social-learning model of a labor market, where employers can hire through referrals, and if so, pay higher wages. A mathematical model illustrated that, if workers are matched to their contacts in productivity, then the wage differences between high- and low-productivity workers will increase over time. Interestingly, if workers are matched to their contacts on characteristics unrelated to productivity (e.g., gender), and if there are initial differences in employment based on those characteristics (e.g., lower employment among women), wage inequality along those characteristics will also expand over time.

More recent models have built on this set-up, and reached similar conclusions on the role of networks on labor market inequality (Arrow and Borzekowski 2004, Calvó-Armengol and Jackson 2004). But, these formal analyses relied on simple models to remain tractable. For example, Calvó-Armengol and Jackson's (2004) work specified job search as a finite state Markov process, where transition in an agent's employment state is dependent on the states of its network ties. The authors took network configuration as given, not emergent, although they did consider potential drop-outs from the network. Unlike Montgomery (1991), the authors also did not take into account homophily, that is, the tendency for high-ability workers to be connected to high-ability job candidates.

Researchers have turned to agent-based models for more flexible specifications of network formation and diffusion. Agent-based models use computer-generated agents that follow rules for interacting with other agents and with their environment. The models simulate

agents in interaction, and typically produce emergent macro-levels patterns that cannot be deduced from a simple aggregation of micro-level rules. Consequently, the models provide a critical tool for linking micro and macro level analysis, and for developing new theory (Bruch and Atwell 2015). Agent-based models do not solve the identification problems stated above, but they do allow researchers to create a complete (albeit synthetic) data set with no unobserved heterogeneity or endogenous selection, where the pure network effects can be isolated with counterfactual manipulations.

These advantages led Manzo (2013) to employ an agent-based model to investigate the sources of educational inequality in France. In his model, agents of different socio-economic groups make educational choices based on their ability, perceived pay-offs, and (in some cases) choices of other agents in their own group. The results showed that the empirical stratification in the French data can only be generated *in silico* if the model incorporates network influences from within one's own socio-economic group. In other words, network effects in educational choice, and homophily in social ties, together, provide a plausible explanation for the observed inequality in educational attainment in France.

DiMaggio and Garip (2011) followed a similar strategy, and used an agent-based model to understand the racial disparities in Internet adoption in the United States. The authors argued that initial differences in income and education between whites and African-Americans would translate into an enduring gap in adoption rates if one presumes (in line with the empirical evidence) that prior adopters in an ego's network encourage adoption, and that network alters are likely to resemble the ego in terms of income and education.

To fully grasp this idea, consider the first subscribers to home Internet service. These early adopters are likely to have sufficient financial and cultural resources (i.e., high income and education) to afford the new technology, and such individuals are disproportionately white in the U.S. context. Now consider the next round of subscribers. These individuals still need to have the requisite financial and cultural resources, but some also enjoy *network externalities*, that is, higher returns to the Internet as they can use the service to communicate with the earlier adopters. Now, if social ties were established at random, such externalities would be uniformly distributed in the population, and not change existing levels of inequality in adoption. But, as research shows, there is a high degree of homophily by education in personal networks in the United States, and even a higher degree of homophily by race (Marsden 1987, 1988). Introducing this pattern into the example, then, one can see that network externalities are bigger for the rich, better-educated and white individuals who are more likely to be connected to earlier adopters (who are also rich, better-educated and white). In this case, network externalities do not just perpetuate initial differences between the rich and the poor (or whites and African Americans), but externalities also make such differences larger than would be expected based on income or education differences alone.

Driven to explain a real-life puzzle, DG struck a fine balance between using an agent-based model to push theory on the one hand, and calibrating that model to fit the empirical case, on the other. Crucially, the authors did not create synthetic agents, but used the sample from the network module of the 2002 GSS to replicate the observed marginal and joint distributions of income, education, race, and network size in the United States.

Their algorithm first generates a network of connections among agents with a given degree of homophily.[1] Each agent has a reservation price – a price at which it will subscribe to Internet service. The reservation price is an increasing function of income, education, and the share of network alters who have already adopted.[2] The price of Internet service is a declining function of overall adoption level to reflect economies of scale. This set-up implies that an agent can adopt because its reservation price has increased due to prior adopters in its network, or because the price of the service has dropped below its reservation price due to adoption in the population. At each time period, the algorithm computes each agent's adoption outcome by comparing its reservation price to the price of the Internet, updates reservation prices and the price of the service, and runs until adoption reaches an equilibrium level in the population.

The results showed that, as homophily increases in the network, the slope of the diffusion curve (which plots the cumulative proportion of adopters across time) becomes steeper. This is because individuals with an initial advantage (i.e., high income and education) become more likely to be connected to other advantaged individuals, who have lower reservation prices, compounding the network effects within this select group. But, this speed in adoption comes at a cost. As homophily rises in the network, the equilibrium adoption level in the population declines. While the practice diffuses quickly among the advantaged, it fails to spread to less advantaged groups.

Considering the context for homophily

Prior empirical, formal and computational analyses discussed above (and more comprehensively in DiMaggio and Garip's (2012) review) put forth a common argument: Social

networks exacerbate inequality if social ties facilitate the adoption of beneficial practices, and if those ties exhibit homophily, that is, similarity in individual traits related to adoption.

But, interestingly, in both Montgomery (1991) and DG, one observes significant disparities in adoption by a trait when social ties display homophily in that trait – even when the trait itself is *unrelated* to adoption advantage. Montgomery's model implies surplus wage inequality by gender (which cannot be attributed to ability differences alone) if social networks exhibit homophily by gender (which itself does not affect employment outcomes, but only the size of the initial employed pool). Similarly, DG find inequality in Internet adoption by race (above and beyond what would be expected based on income and education differences) when social ties are homophilous with respect to race (a characteristic unrelated to individuals' adoption propensity).

These patterns should not surprise us given that homophily in a trait changes the network structure, and thus network diffusion, even if that trait does not directly affect individuals' adoption probability. Then, any structural factor that relates to homophily should also have implications for inequality.

One structural factor that moderates the implications of homophily is *consolidation* – the correlation among different traits in a society. Indeed, in their influential work, Blau and Schwartz (1984) declared homophily and consolidation as key parameters shaping social interactions. Low levels of homophily and consolidation, the authors predicted, ensure cross-cutting social ties, and as a result, social cohesion in a community.[3]

Centola (2015) represented this intuition with an agent-based model, and reached unexpected conclusions. Low levels of homophily and consolidation lead to a random network

structure, and fail to support the diffusion of a common norm (a proxy for social cohesion).

Middle levels of homophily and consolidation, however, induce overlapping patterns of

connections (or 'wide bridges') that are optimal for *complex contagion* – the process by which

norms diffuse via reinforcement from multiple network alters (Centola and Macy 2007).

Centola also showed that homophily and consolidation interact in their effect on

diffusion. When consolidation is relatively high, for example, only low levels of homophily can

create the social structure necessary to support successful diffusion. Because various traits are

highly correlated, even slight increases in homophily lead to a highly-balkanized network, and

stop diffusion in its tracks. When consolidation is at middle levels, however, middle and high

levels homophily can also support effective diffusion. Because the traits are not as correlated in

this case, increases in homophily do not immediately translate into a segregated network.

Implications of homophily and consolidation for inequality

Centola's model is concerned only with network formation and diffusion, but his results

could be used to understand how homophily and consolidation, in concert, can contribute to

inter-group inequality. In this paper, we use Centola's model, but modify it to resemble the DG

set-up, where there is status differentiation in adoption probability. In effect, then, we replicate

DG's analysis with synthetic (rather than real-life) agents and generic (rather than calibrated)

parameters, which allows us to vary not just homophily, but also consolidation (a factor the

authors could not consider as they relied on the GSS sample with a fixed covariance structure).

We argue that the effect of homophily on inter-group inequality depends on the level of

consolidation in a society. Consider the extreme case of full consolidation, where traits in a

population are perfectly correlated. If we know a person's income, for example, we can

perfectly predict his or her education, residential neighborhood, and so on. There is, effectively, a single axis of differentiation. Now consider the other extreme of no consolidation, where individuals are randomly scattered in the multi-dimensional trait space. If we know a person's income, in this case, we still have no idea what their education or neighborhood is. There are multiple axes of differentiation.

We expect that the contribution of homophily to inter-group differences in diffusion will vary greatly across these two cases. In the full consolidation case, even low levels of homophily will be sufficient to concentrate advantage, and generate differential diffusion across groups. Let's presume (like DG) that there exists a status dimension, defined to be positively related to adoption probability, for instance, income. In a full consolidation setting, if individuals have a slight preference for similar alters (in terms of multiple characteristics, say income and education), then high income individuals will be more exclusively connected because they are also highly educated. Due to consolidation (even with dimensions that are not status related), an individual's advantage in the status dimension will also be reflected in network alters, further compounding the differences in adoption between high- and low-income groups.

In the lower consolidation case, by contrast, the power of homophily in connecting high-status individuals, and in concentrating advantage, will be diluted by the lack of relational concentration in the status characteristic. Even under high homophily, since high earners could have any level of education, the preference for similar alters will not generate well-defined and exclusively high-earning groups. The advantage in adoption that comes from the status attribute of income, in other words, will not be consolidated.

This logic leads us to qualify DG's findings. We argue that the high levels of inter-group inequality the authors observed, and connected to homophily, are in part due to the high level of consolidation in the sample from which the agents are drawn. Specifically, in the GSS sample, income, education and race are strongly correlated. Therefore, even a small degree of homophily (based on all three characteristics) is likely to generate a highly- balkanized network structure, and lead to inter-group differences in adoption. We argue that homophily bias alone will not be sufficient to generate inter-group inequality under lower levels of consolidation. Below, we describe our modeling strategy to theoretically investigate the implications of consolidation for the link between homophily and inter-group inequality.

METHODS

We use an agent-based model to create individuals with social identities and social ties. Similar to Centola's (2015) model, individuals are first assigned social identities, or sets of characteristics. An individual's identity defines his or her social distance to the other members of the population. Individuals then form connections based on social distance. As in DG, individuals form connections based on social distance across important dimensions. Once ties are established, individuals have the opportunity to influence behaviors of their network alters. This set-up closely resembles DG's model, but differs in using synthetic (rather than real) identities for individuals.

Generating the population

To formalize, we assign individuals to a set of positions that can take on *H* possible values (heterogeneity) within *D* social dimensions (complexity). There are *G* individuals with each social position, and hence, *N* (= *H* x *G*) individuals in the population. DG consider a fixed number

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of social dimensions (income, education, and race) with a fixed degree of heterogeneity. There are three equal-sized groups based on income (high, medium, and low), three groups based on educational degree (bachelor's, high school, middle school or less), and two groups based on race (white and black). In our model, we make the number of dimensions (*D*), the number of social positions in each dimension (*H*), and the number of individuals in each position *(G)* flexible to be able to vary the extent of social differentiation.

Establishing network ties

DG compute the social distance between all pairs of individuals (defined as the Euclidean distance based on standardized values of three observed social dimensions: income, education, and race), and then establish ties between individuals such that homophily bias occurs with a given probability. We follow a similar logic, but create a more complex architecture. In a nutshell, this architecture allows us not only to define the distance between individuals according to their social positions to control homophily, but also to define the distance between positions across those dimensions, in order to control consolidation in a similar way.

[FIGURE 1 HERE]

Figure 1 illustrates the set-up that is developed originally by Watts, Dodds and Newman (2002), and refined subsequently by Centola (2015). The figure shows a branching tree of *L* = 4 levels with a branching ratio of *B* = 2. This tree offers a visual representation of a population with a single social dimension (*D* = 1), and a hierarchical structure of *H* = 8 social positions (circles) that include a group of *G* = 6 individuals (black dots) each. Social distance between

individuals in the same group is defined as $x = 1$. Social distance between individuals in different

groups equals one plus the number of steps it takes to reach the fork in the tree where the

individuals share the closest common branch. (e.g., distance between individuals i and j in the

figure is $x_{ij} = 3$). To see how this construction defines a hierarchy, imagine that the social

dimension in the figure is occupation, where the left four positions (circles) represent

management, and the right four positions represent workers. The first branching point in the

tree, then, captures the social difference between management and workers – two classes of

positions that are maximally distant ($x = 4$). The second branching point within management

allows for finer-grained social distances, for instance, between executives and middle

management.

Occupation is a single dimension of social life, and one can think of many other

dimensions, such as education, income, or residential neighborhood. Similar to Centola (2015),

we introduce multiple dimensions in our model by replicating the tree-like structure in Figure 1

for each dimension. In order to generate different levels of consolidation, we then apply the

same scale used to measure social distance between individuals within a given dimension to

capture the distance between a single individual's social positions across different dimensions.

This, latter, distance equals the number of steps up the branching tree to find a common

ancestor if the two trees were to be super-imposed on one another. For example, when an

individual is located in the same position (e.g., the left-most circle) across two social dimensions

(e.g., income and education), the distance between positions is 1. When an individual is located

in positions that are at the opposite ends of the spectrum for the two dimensions (e.g., the left-

most circle for income, and the right-most circle for education), the distance between positions is 4.

Using the distance between positions within a single dimension, and the distance between positions across dimensions, we control degrees of consolidation (and later homophily) as follows. For each of the N individuals, we start with a dimension, d_1, and place individuals in a position randomly. To determine positions in the other dimensions, we rely on the consolidation parameter (β). That is, for each subsequent dimension, d, we draw a random social distance (y) among positions for each individual with probability

$$P(y) = c \cdot e^{-\beta y} \tag{1}$$

where β is the consolidation parameter and c is a normalizing constant. We assign social position at random among all positions in dimension d less than or equal to social distance y from the individual's position in d_1. For intuition, note that when consolidation is at its minimum ($\beta_{min} = -1$), the probability for the maximum social distance y is the highest. This can be interpreted as lack of consolidation as an individual is assigned a position at random, regardless of position in d_1. As consolidation increases, individual's positions become more correlated across dimensions ($\beta_{max} = 3$).

Similar to Watts et al. (2002) and Centola (2015), we set homophily based on the *shortest* social distance (i.e., one plus the number of steps up the tree to reach a common root) between a pair of individuals across *all social dimensions*. This captures the intuitive notion that closeness in one dimension (e.g., education) is sufficient to connote affiliation, for example,

when geographically and ethnically distinct researchers collaborate on the same project given

the same social position in the occupational dimension. A useful property of this metric is that it

violates the triangle inequality, which states that if individuals i and j share a group in one

dimension such that $x_{ij} = 1$, and similarly, if individuals j and k share a group in another

dimension such that $x_{jk} = 1$, it is perfectly feasible to have person i and person k be socially

distant such that $x_{ik} > x_{jk} + x_{ij}$.[4] These features reflect how social psychologists have come to

model perceived similarity in social relationships (Shepard 1987, Tenenbaum and Griffiths

2002). Yet closeness in just one dimension (shortest social distance) is but a special case of

social distance. Sensitivity analyses consider alternative metrics for social distance, such as the

mean social distance between a number of social dimensions.

After defining social distance between all individuals in the population, we introduce the

homophily parameter (α) and start building social ties among individuals. Individuals start with

no ties. We select an individual i randomly from among all individuals with available ties (that is,

remaining individuals whose existing ties < degree size, Z). For each individual, we draw a

random social distance x with probability

$$P(x) = c \cdot e^{-\alpha x} \qquad\qquad (2)$$

where α is the homophily parameter and c is a normalizing constant. We then choose a random

individual j to establish a social tie from among all individuals at distance x or less from the

individual i. Note that homophily parameter defines the maximum social distance an individual

is able to tolerate when making a tie, and thus effectively sets an individual's "search radius" in

selecting network alters. High values of the homophily parameter imply a small search radius, and a strong preference for similar others. For intuition, consider that under the maximum level of homophily (α_{max} = 3), individuals are most likely to make social contacts with other individuals at a social distance of 1 (with constant c set accordingly). Decreasing the homophily parameter increases the search radius.

We continue the tie formation process until individuals in the population, on average, have the same pre-set degree size, Z. An important simplification (similar to DG and Centola) is to assume ties to be symmetrical. That is, if individual i establishes a tie with individual j, individual j is also considered to have established a tie to individual i.

Modeling diffusion and inequality

We use Centola's (2015) architecture outlined above to generate a population of particular characteristics, to establish network ties among individuals, and to model the diffusion of a beneficial practice. Similar to DG, however, our goal is to observe group-specific diffusion rates, and consider their implications for social inequality. This goal requires a modification in Centola's set-up, which assigns all individuals the same *adoption threshold*, defined as the number of adopters in ego's network necessary to induce the ego to adopt a practice. Centola's model considers practices that diffuse through *complex contagion*, that is, those with an adoption threshold of 2 or higher. DG's analysis also focuses on complex contagion, but allows the adoption threshold to vary in the population. Indeed, a particular feature of their model is to make the adoption threshold an inverse function of an individual's economic and cultural resources. In this model, each individual has a *reservation price* – a price at which he or she is willing to adopt the practice. This price is an increasing function of one's income, education,

and the number of network alters who have already adopted. Then, all else equal, high income and high education individuals have the highest reservation prices (and hence the lower implied thresholds for adoption).

We introduce this important feature into Centola's set-up as follows. First, we let an arbitrarily chosen social dimension, d, indicate status for all individuals (similar to income or education in the DG model). We designate a given proportion (P) of the population as high status, an identical proportion as low status, and the remainder as medium status. Similar to Gondal (2014), we vary the proportion of high status individuals in order to test the sensitivity of our results to the size of the elite.

Second, we make the adoption threshold an inverse function of status. Specifically, we assign high status individuals an adoption threshold of 2, medium-status individuals a threshold of 3, and low-status individuals a threshold of 4. Note that an adoption threshold of 2 and higher bring about a *complex contagion* process (to use Centola and Macy's (2007) terminology). Our results at the population level closely follow those of Centola (see Figure 2).[5]

To initiate the diffusion process, like Centola (2015), we randomly seed one high-status individual and their network (that is, individual's first-order ties) as the first adopters. We also randomly seed one low-status individual and one medium-status individual (and their corresponding networks) such that network externalities are independent of status, and there is no inequality in adoption initially. Following the initial seeding, at each time period, all individuals who have not adopted the practice simultaneously make decisions on whether or not to adopt, and the algorithm outputs the cumulative and group-specific percentages of

adopters by status. The process ends after *T* = 50 time periods, which, as the results indicate,

provides ample time to reach equilibrium diffusion levels.

Parameters and robustness checks

In this study, we focus on the effects of homophily (α) and consolidation (β) on network

diffusion and inequality; therefore, we keep the remaining parameters fixed. Below, we list all

the parameters used in generating our results. Centola (2015) has investigated the robustness

of the results to variations of all parameters, but one. Therefore, here, we report the sensitivity

of our findings to *P* (the proportion of high-status individuals in the population), which is the

only parameter not included in Centola's analysis, and refer the reader to the original paper for

all other checks. We have run our models with *P* ranging from 1/16 to 4/16 and found nearly

identical results (available upon request) for *P* equal to 2/16 and 3/16. The implications of

lower and of higher values of P are discussed in sensitivity analyses.

Population parameters

- *D* = complexity (number of dimensions) = 10

- *H* = heterogeneity (number of social positions) in a dimension = 16

- *G* = group size (number of people in each position) = 50

- *N* = population size = *H x G* = 800

- *P* = proportion of high status individuals = 2/16

Network parameters

- α = level of homophily, ranging from -1 to 3

- β = level of consolidation, ranging from -1 to 3

- *Z* = average degree (number of ties for each person) = 5

Adoption parameters

- *T* = time intervals = 50

We code our algorithm in R (version 3.3.1). To account for the randomness in initial seeding, and in the social positions of individuals by status, we run the simulations 100 times for each set of parameters, repeating the entire process of population construction, network formation, and diffusion. These repeat runs give us means and standard deviations across all realizations of specific sets of social conditions. In what follows, we report not just the average diffusion outcomes (as both Centola (2015) and DG do), but also the distribution of diffusion outcomes across repetitions. As a methodological point, we note that conclusions based on average observations might be misleading for particular parameter combinations, and at particular time-points.

RESULTS

Overall diffusion under homophily and consolidation

Before considering group-specific diffusion rates, we investigate overall diffusion patterns, and confirm that our results are similar to Centola's (2015) findings. This is important because our model has implemented adoption thresholds that vary inversely with individuals' status, which might disrupt the diffusion dynamics in the original model based on fixed adoption thresholds. While we keep the average adoption threshold equal to that in Centola, it is still not obvious that diffusion patterns will remain similar with a given proportion (*P* = 2/16) of high- and low-status individuals (who require less and more social reinforcement to adopt, respectively). In Figure 2, we plot overall equilibrium cumulative adoption rates (z-axis) under status-based

thresholds while varying consolidation (y-axis) and homophily (x-axis), keeping all other

parameters at values listed in the preceding section.

[FIGURE 2 HERE]

Figure 2A and Figure 2B present identical data on the relationship between diffusion,

consolidation, and homophily (in a 3-dimensional and 2-dimensional representation,

respectively). In both figures, homophily and consolidation are varied from -1 to 3. Introducing

status-based thresholds as in DG does not change the relationship between homophily,

consolidation, and diffusion at the population level. Similar to Centola (2015), we observe that

(i) homophily and consolidation interact in their effect on diffusion, and (ii) diffusion is most

successful when neither homophily nor consolidation are very low and at least one is at a

moderate level.

We now turn to the implications of our model for DG's conclusions on how homophily

affects diffusion and inter-group inequality. While DG treat consolidation as fixed, our model

allows us to vary it. For the sake of simplicity, in the remainder of this paper, instead of showing

the full range of values for homophily and consolidation (as in Figure 2), we display results for

(i) four levels of homophily, including very low (α = -1), low (α = 0), medium (α = 1), and high

homophily (α = 2), and (ii) two levels of consolidation, low (β = 0.5) and high (β = 2). This

exposition allows us to observe adoption rates under varying degrees of homophily and

consolidation, and also over time, similar to DG.

We present not just average diffusion patterns, but also the 95 percent confidence bands around the average across multiple realizations. To clarify, the variance in simulations is not generated by different parameter values, but by randomly occurring differences in the social positions or networks of initial seeds under a given set of parameter values. It is important to consider the full distribution of simulations to ensure that our results are stable (and not driven by volatile realizations of the model), and that the differences we point to across multiple scenarios are statistically significant.

Panel B in Figure 3 shows the cumulative adoption (y-axis) over time (x-axis) by homophily in a high-consolidation world. Note that Figure 3 can be understood as a cross-section of Figure 2, but with the added dimension of time, and confidence bands (gray regions) around the average diffusion curve across 100 realizations per a given set of parameters.

We observe several patterns. First, low homophily (α = 0) leads to the highest diffusion level in equilibrium, where the practice consistently reaches full saturation in the population. Medium (α = 1) and high (α = 2) levels of homophily lead to much lower – and statistically indistinguishable – adoption levels in equilibrium. Second, low homophily (α = 0) leads to a slower rate of diffusion initially, compared to medium and high homophily, but then later surpasses the equally fast medium and high levels of homophily. In line with DG's observations, then, while homophily boosts adoption speed initially (as the practice can spread quickly among the advantaged individuals socially connected to one another), it hurts the equilibrium adoption level (as the practice fails to reach the less advantaged individuals).

[FIGURE 3 HERE]

Yet, another pattern in the figure seems to defy DG's expectations. The very low homophily case (α = -1) leads not only to the slowest diffusion rate, but also to low overall adoption levels in equilibrium. Centola (2015) explains this finding with reference to complex contagion. When a practice requires reinforcement from multiple social ties to be adopted, networks need to have 'wide bridges', that is, overlapping social ties, to effectively spread that practice. Such wide bridges are only possible with some degree of homophily and consolidation. Under very little homophily, even high levels of consolidation are not sufficient to produce the social structure needed to sustain diffusion. (Note that, in Figure 2B, when homophily is less than -0.5, diffusion is nearly flat at zero, regardless of the level of consolidation.) Why then, one can ask, did DG not observe this pattern in their analysis?

The answer, we believe, is simple. Because DG base individual's positions in social dimensions on GSS data, and also take a fixed number of individuals (N=2,257) to establish a large number of social ties (an average of 28 ties per person, as given by the actual degree sizes reported by each individual), the resulting networks ended up with some degree of (incidental) homophily even when DG set homophily bias to zero in simulations. After all, even no homophily can still bring about homophilous tie formation (especially if there are few network alters to choose from). (By comparison, in our model, there are 800 individuals to establish an average of 5 ties per person.) Then, DG's no homophily case is likely to resemble our low homophily condition, and there is no contradiction in the findings.

This significant overlap between DG and our results, however, disappears under low consolidation, as shown in panel A in Figure 3. In this case, medium (α = 1) and high (α = 2)

levels of homophily, although not statistically distinguishable from one another, lead to much

higher adoption rates and equilibrium levels compared to low (α = 0) and very low homophily

(α = -1) conditions. Under low consolidation, then, homophily actually helps both the speed and

level of diffusion, directly opposing DG's conclusions based on a high-consolidation setting.

The explanation for this pattern, again, comes from the conditions for complex

contagion. Under low consolidation, only higher degrees of homophily can create overlapping

social ties that are key to successful diffusion. When consolidation and homophily are both low,

diffusion fails to take off as quickly, and never catches up.

Comparing panels A and B reveals another insight that is not obvious from Figure 2 (and,

thus, Centola's original analysis). The low-consolidation condition (panel A) creates more

variance in diffusion than its high-consolidation counterpart (panel B), especially for low

homophily (α = 0). Because Figure 2 only displays the average outcome, it is hard to know

whether, say, a diffusion level of 0.5 indicates that diffusion consistently reaches half the

population, or that diffusion is at full saturation (100%) half the time, and fails completely in the

other half. In Figure 3, we see that the former interpretation (of stable results) is only

reasonable for high-consolidation worlds, where the confidence bands around the outcome are

very tight. But, the latter interpretation (of highly volatile realizations) is more accurate for low-

consolidation worlds, where the confidence bands cover a broad range of outcomes. For

example, for low consolidation and low homophily (α = 0), diffusion reaches 75% at equilibrium

as many times as it lingers at 25%. The average diffusion curve settles at 50%, and hides this

large variation. This observation is important for empirical work. Given the greater inherent

volatility of diffusion outcomes, researchers working in low-consolidation settings might be

more likely to reach faulty conclusions based on their observations (compared to those operating in high-consolidation settings).

Group-specific diffusion under homophily and consolidation

We now turn to diffusion outcomes for different status groups, and inequality in those outcomes across groups. Figure 4 shows the log odds ratios of adoption rates between high-status and low-status adopters (1/8th of the population each) under varying levels of homophily, contrasting low consolidation (panel A) and high consolidation (panel B) worlds. [6] Lower log odds ratios indicate lower inequality.

[FIGURE 4 HERE]

First, it is important to note that the 95% confidence bands (gray region) around the inequality curves are much wider under low homophily when consolidation is low than when consolidation is high. This is consistent with the earlier observation that low consolidation condition can generate a lot more variance in diffusion outcomes (figure 3, panel A) compared to its high consolidation counterpart.

Second, we observe that, when homophily is at moderate to high levels, log odds ratios are larger when consolidation is high. For example, log odds ratios are greater than 1.5 for high ($\alpha = 2$) and medium ($\alpha = 1$) homophily cases when consolidation is high, but they approach null when consolidation is low. This observation is perhaps not surprising. When individuals strongly prefer to associate with similar others, less correlation between different dimensions of social

life generates less social reinforcement for exclusive groups based on status dimension. Thus, one finds less difference between high- and low-status individuals' outcomes when different dimensions of social life are not strongly correlated (i.e., under low consolidation).

Third, and conversely, when homophily is low ($\alpha = 0$), log odds ratios are smaller at equilibrium when consolidation is high ($\beta = 2$) rather than low ($\beta = 0.5$). And the reason is simple. Under low homophily, a practice reaches full saturation (and hence, zero inequality) only under high consolidation (see $\alpha = 0$ condition in Figure 3, panel B). The practice remains moderately diffused (around 50%) under low consolidation (see the same condition in panel A), and presents some inequality by status.

Fourth, when individuals establish ties randomly ($\alpha = -1$), there is no statistically significant difference between high- and low-consolidation worlds in terms of equilibrium inequality. The practice remains minimally diffused in both cases: only slightly above 10% under low consolidation (Figure 3, panel A), and around 25% but with a larger variance under high consolidation (panel B). In both cases, the differences are likely driven by the status imbalance in initial seeding, that is, by the fact that there are more initial adopters that are high rather than low status.

Another way of thinking about these results is that, save for the $\alpha = -1$ case, the relative implications of homophily levels on inequality in diffusion become *flipped* in equilibrium for high and low consolidation worlds. The conditions that generate the most to least inequality are $\alpha = 0, 1, 2$ versus $\alpha = 2, 1, 0$ for low and high consolidation worlds, respectively. The reasons why homophily exacerbates inequality in the high consolidation world is intuitive and consistent with DG. The counterintuitive finding or "flip" in low consolidation worlds can be

explained by the following intuition. In low consolidation worlds, homophily helps reduce

inequality at equilibrium by supporting diffusion. Over time, homophily creates the bridge

width that is necessary for successful diffusion. And inequality is always the lowest when

diffusion reaches the whole network. Thus, in low consolidation worlds, high homophily

decreases inequality by supporting overall diffusion. Although there is an initial exacerbating

effect of homophily on inequality (when diffusion is still taking off, homophily implies that

diffusion takes place more quickly among higher status individuals), the benefit to diffusion of

high homophily for high status adopters is eventually tempered by its later support for overall

diffusion (this starts to occur at $T = 15$). By contrast in the low consolidation world where

homophily is also low, diffusion remains incomplete, so inequality stays at the same moderate

initial level.

SENSITIVITY ANALYSES

Centola (2015) has investigated the robustness of the results to variations of all parameters, but

one (P). Therefore, here, we report the sensitivity of our findings to P (the proportion of high-

status individuals in the population), which is the only parameter not included in Centola's

analysis, and refer the reader to the original paper for all other checks. Results are nearly

identical for P = 2/16, P = 3/16. So when high and low status individuals make up roughly a

quarter to a third of the population (combined), high homophily can decrease inequality in low

consolidation worlds by supporting overall diffusion. Figure 5 represents overall adoption

diffusion success, varying status distribution.

[FIGURE 5 HERE]

To understand why the results do not hold for lower (1/4) and higher (4/16 or greater) values of P, recall that homophily creates a balkanized network structure that is necessary for complex contagions. Recall also that contagion in our set-up is at first more likely among higher status individuals who have lower adoption thresholds, but it eventually spills over to the rest of the population. When P is too low, there are too few high-status individuals to support the level of adoption that then spreads to the entire network. As a result, overall diffusion remains low, and the level of inequality remains high, regardless of the level of homophily. When P is too high, the opposite happens: Diffusion is very successful, owing to the presence of more high-status individuals with lower adoption thresholds. This results in minimal inequality regardless of the level of homophily or consolidation.

In addition to considering different distributions of status, we have also checked the sensitivity of our results to the metric for social distance, which is fixed in Watts et al. (2002) and Centola (2015) as the *shortest* social distance across *all social dimensions*. The shortest distance metric has a number of desirable properties and is consistent with how social psychologists have come to model perceived similarity in social relationships (Shepard 1987; Tenenbaum and Griffiths 2002). While a change in position in *any* social position can change shortest distance, and *different* social dimensions determine social distance for different pairs of individuals, some might consider this metric relatively "univariate" due to the fact that closeness in just one dimension can render distance in other dimensions irrelevant. We recognize that although this precise property makes it attractive to some scholars, it is but one way to conceptualize social distance. Therefore, we consider alternative metrics here.

In particular, we set homophily based on the mean distance within the closest X

dimensions between a pair of individuals, incrementally increasing X from 1 (as in the main

results). Our findings are robust for X = 1, 2, and 3 dimensions, indicating that even when

individuals are using a more "multivariate" metric of social distance, there are some, low, levels

of consolidation in which higher homophily improves diffusion and diminishes inequality.

Evidence of this pattern is presented in Figure 6, which replicates Figure 4 but uses a mean of 3

dimensions rather than shortest distance to inform homophily. Here, the point remains that

under some levels of low consolidation, moderate homophily (α = 2 and α = 1) can yield lower

inequality than low homophily (α = -0.5).

[FIGURE 6 HERE]

When homophily is based on the average distance between increasingly many social

dimensions, diffusion starts to be increasingly unsuccessful at low consolidation, and is not

redeemed by high homophily. This is because this metric necessarily results in greater or equal

(but never smaller) distances such that the implications of any level of homophily are

intensified. As Figure 7 demonstrates, diffusion begins to become depressed at low

consolidation and high homophily when homophily is based on the average of four social

dimensions. (See figure A2 in the Appendix for a two-dimensional representation of diffusion

outcomes.) Put differently, as the number of salient dimensions increases, our population

becomes too differentiated. In a highly-differentiated population, one needs lower levels of

consolidation to make up for the network segregation brought on by homophily (in order to

observe successful diffusion). When we include four or more social dimensions in our social distance measure, we start to see that there is no level of consolidation that is low enough to counter the effect of homophily, and therefore, no parameter combination under which diffusion is successful.

This pattern indicates that the Centola architecture may not be ideal for considering a world in which more than a few social dimensions are relevant. While the work that is immediately relevant to ours tends to model distance in terms of the shortest distance or the mean of just a few (such as 3 in the case of DG), there are other ways to conceptualize social distance (e.g., Boutyline 2017), and it is important to recognize the limited scope of our model.

[FIGURE 7 HERE]

Finally, it is worth noting that our findings hold even when we consider *effective homophily* – that is, observed homophily (which can be higher than *affective homophily* that is set by our model parameter, α). We define effective homophily here as the ratio of average social distance between dyads in the population that do not share a tie and average social distance between dyads that do share a tie. The intuition here is that larger effective homophily means smaller social distance among dyads that share a tie compared to dyads that do not share a tie. Basically, consistent with existing ABMs (Centola 2011, DiMaggio and Garip 2011) and recent empirical work (Smith et al. 2016, Wimmer and Lewis 2010), our model represents homophily as the probability of association based on social distance between individuals. But, consolidation can also induce homophily independent of our homophily parameter, α.

Therefore, it is important to see if our results remain similar when we consider *effective homophily* in the population. Below, we show that our core finding, that inequality can *decrease* with homophily under low consolidation, is robust to using a measure of *effective* rather than *affective* homophily.

[FIGURE 8 HERE]

Figure 8 replicates Figure 4 but with labels for *effective* instead of *affective* homophily, and shows similar patterns. (The four homophily levels displayed in the high and consolidation panels are not identical across the two figures, which is expected given that consolidation feeds into *effective* homophily, and makes it higher than the *affective* homophily set by the model). Similar to Figure 4, in Figure 8, we see that high levels of *effective* homophily can diminish, not exacerbate, inequality under low consolidation (panel 8A). (Figure A1 in the Appendix displays a two-dimensional representation of diffusion outcomes.)

DISCUSSION

DG's work unequivocally argues that homophily exacerbates inequality in adoption if a practice is subject to network externalities, and if the practice is initially more likely to be adopted by high-status individuals. Our findings confirm some of their findings, while qualifying or extending others.

Confirming DG, we find that homophily exacerbates adoption inequality if consolidation is moderate to high. When social dimensions are strongly correlated, increasing homophily

makes networks more segregated by status, and locks the practice into network regions where high-status actors cluster.

Qualifying DG, we show that homophily reduces adoption inequality if consolidation is low. When social dimensions are largely independent, increasing homophily is not sufficient to segregate social networks, but it is helpful to create overlapping social ties, or 'wide bridges', across which behaviors can spread. Regardless of level of consolidation, homophily creates an advantage for high status initial adopters because it makes it more likely for other high-status adopters to be closely connected to the initial adopters. When consolidation is low, this advantage disappears if homophily is high enough to generate the overlapping social ties for diffusion to reach lower status individuals who require more social reinforcement for adoption. In this case, eventual successful diffusion by low status individuals overcomes inequality.

Extending DG, we observe that some homophily is needed for effective diffusion. Under very low homophily (a case DG could not test effectively due to the constraints of their data), a network does not have the sufficient structure to coordinate behavior, regardless of the level of consolidation in the population.

We also make a few finer points. First, low consolidation worlds, all else equal, create more variance in diffusion and inequality outcomes compared to high consolidation cases. Second, the diffusion and inequality trajectories shift over time. For example, while diffusion is quite fast in a high homophily condition, its equilibrium level is low compared to a low homophily condition. Or, while inequality increases steeply at first in a high homophily setting, it can end up at a lower equilibrium compared to that in a low homophily case. Put differently,

one can settle on the wrong conclusions if one observes only average values, or collects data mid-process (that is, prior to equilibrium).

CONCLUSION

A major insight in sociology suggests that social networks can provide access to useful resources or positive influences that help individuals succeed (Portes 1998). Another key insight indicates that early advantages can lead to benefits that pre-dispose individuals to obtain more advantages over time (Merton 1986, DiPrete and Eirich 2006). These two ideas go well together in that social networks can be a mechanism for generating cumulative advantage.

Recent formal and computational analyses have made this connection explicit by studying homophily. Studies have linked, for example, network effects in job search to wage inequality (Montgomery 1991, Calvó-Armengol and Jackson 2004) or the peer effects in educational choice to disparities in educational attainment between groups (Manzo 2013). DiMaggio and Garip (2011) have offered arguably the most general theoretical statement, and identified three necessary conditions for network effects to exacerbate inequality in the adoption of a beneficial practice. First, the authors have argued, adoption should be more likely among the more advantaged individuals (for example, high earners or highly educated). Second, adoption should be more likely if one's peers have adopted. That is, network effects should be positive. And, third, and most importantly, networks should exhibit homophily (tendency for ties among similar individuals) with respect to traits related to adoption.

In this paper, we extend DiMaggio and Garip's (2011) analysis, and discover a fourth, and crucial, condition neglected in prior work. For social networks to exacerbate inequality, we argue, characteristics in a population need to consolidated (that is, highly correlated). Without

consolidation, homophily in any given characteristic is not be sufficient to segregate social networks, and isolate adoption to particular segments of the population.

Earlier work has not considered consolidation as a factor in network formation either because it has relied on formal analysis where networks were considered given (e.g., Calvó-Armengol and Jackson 2004) or because it has used computational models calibrated to a particular real-life setting (e.g., DiMaggio and Garip 2011, Manzo 2013).

We draw inspiration from Blau and Schwartz's work (1984, p.12), which declared consolidation to be of "prime significance for intergroup relations." Recently, Centola (2015) confirmed this insight with an agent-based model, and demonstrated that homophily and consolidation together shape network structure and diffusion outcomes.

In this paper, we start with Centola's generic model, and use it to first replicate, and then to extend, DiMaggio and Garip's findings. We generate a sample of synthetic agents, and introduce status differences between them. We then give high-status individuals a small advantage in adoption. We vary levels of homophily and consolidation, and observe whether initial advantages by status are compounded via network effects.

We report several findings. First, similar to DiMaggio and Garip, we find that homophily exacerbates adoption inequality, but only if consolidation is relatively high. Second, different from DiMaggio and Garip, we show that homophily actually alleviates adoption inequality if consolidation is low.

These patterns all owe to an important insight gained from Centola's (2015) analysis: Low to moderate levels of homophily and consolidation generate social networks with

overlapping ties, or 'wide bridges', that can support the diffusion of a practice through

reinforcement from multiple network alters (or, what Centola and Macy (2007) call 'complex

contagion'). Higher levels of homophily or consolidation, however, lead to segregated or

balkanized social ties, and can stop diffusion in its tracks.

In a high consolidation world, increasing homophily brings about the latter, detrimental,

structure for diffusion, and also makes the status-based divide in adoption deeper. But, in a low

consolidation world, rising homophily leads to the former, favorable, structure for contagion,

and alleviates status-based differences in adoption.

Our analysis allows us to make a number of methodological points. First, prior work

using agent-based models routinely presents the average diffusion curve (computed over

multiple simulation runs), but not the confidence bands around the average. We call future

research to be more attentive to, and report, the variation across multiple realizations. In our

case, the interpretation of our results would be quite different had we just relied on just the

average patterns. Second, while we recognize that agent-based models can be a useful tool

when calibrated to real-life cases (as in DiMaggio and Garip's work), we also argue that such

applications might not always lead to fully generalizable conclusions. Researchers should pay

more attention to how much of their results are driven by the model parameters, and how

much is due to the particular setting the parameters or data are set to capture.

We believe our work opens to doors to studying many other factors that we did not

consider in our analysis. For example, recent work considers the interactions between different

kinds of homophily (e.g., that based on individual choice and that induced by population

compositions in institutional settings) in producing particular network structure and diffusion

patterns (Kossinets and Watts 2006). Recent work also shows how adoption of a practice can

pave the way to establishing new dimensions for status differentiation, and deepen inequality

(Gondal 2014). Future work, therefore, can incorporate patterns of induced homophily or path-

dependent diffusion trajectories for multiple practices into our set-up.

Recent work also considers how population processes (such as in- and out-migration)

can affect population composition, network structures, as well as diffusion outcomes (Garip

and Zhao, forthcoming), suggesting another possible direction of extension. Finally, qualitative

work finds that individuals' perceptions of social norms (and their respective adherence to

them) may depend not just on their position in the network, but on the particular patterns of

social interactions, and in particular, to degrees of exposure to network peers (Shepherd 2017).

Therefore, future attention could also be given to incorporating social interaction and exposure

into modeling frameworks with differential impacts on contagion.

[APPENDIX FIGURES]

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ENDNOTES

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[1] The authors used Skvoretz's (1990) definition of homophily (or 'tau bias') which is the probability that an ego will select a similar alter above and beyond the probability of such a pairing under random choice.

[2] DG defined *network externalities* broadly as applicable to any practice whose value to an individual is an increasing function of the prior adopters in that individual's network. The authors operationalized this mechanism with a 'network term' included in the reservation price. This term implied that an individual's willingness to adopt a practice (i.e., the price he or she is accepting to pay for it) increases linearly with the *share* of adopters in his or her network. In a subsequent review article, DiMaggio and Garip (2012) offered a more specific definition for *network externalities*, and differentiated it from other mechanisms for network effects such as *social facilitation* or *normative influence*. (See Rossman, Chiu and Mol (2008) for a similar analytic framework.) According to the updated definition, the authors argued, network externalities need to be operationalized as a function of the *number* (not share) of adopters in an individual's network. In this paper, we use the updated definition, and operationalize network externalities with an adoption threshold that depends on the *number* of adopters. This choice carries an implicit assumption that an individual only cares about the adopters in his or

her network and is indifferent to the non-adopters (Granovetter 1978, Centola and Macy 2007). See the methods section for details.

[3] Another structural factor shaping homophily is the institutional setting. McPherson et al. (2001) distinguish homophily based on individual *choice* from homophily *induced* by institutions such as schools (Fischer 1977), voluntary associations (McPherson and Smith-Lovin 1987), or work environments (Reskin et al. 1999). Such institutions might include particular group compositions, and thus, exhibit induced homophily in ties even when individuals are selecting alters randomly. Induced homophily is a crucial concept, but it is hard to incorporate into a formal or computational modeling framework in abstract form (that is, without first defining relevant institutions and deciding on their recruitment criteria). Thus, we do not focus on it in this paper.

[4] We ran a robustness check with an alternative distance measure that takes the mean social distance across the three dimensions along which two actors are most similar. The results continued to support our main conclusions.

[5] We conducted a robustness check where we subjected all status groups to a complex contagion process. This exercise involved setting the adoption thresholds to 2, 3, and 4 for high, medium, and low status groups, respectively, and increasing the average degree size in the population from 5 to 10 (in order to allow for successful diffusion). Our results remained qualitatively similar.

[6] The log odds ratios between high-status and medium-status adopters are not reported because they are qualitatively similar to the log odds ratios between high-status and low-status adopters. The only difference is that they are, unsurprisingly, slightly smaller.

TABLES AND FIGURES

Figure 1 Architecture of a social dimension. Each group contains G individuals that share a common social position (circle). The distance x between individuals (black dots) in the same group is 1. The distance between individuals in different groups equals one plus the steps it takes to reach a common root in the tree. The structure has $L = 4$ levels, and a branching ratio of $B = 2$.
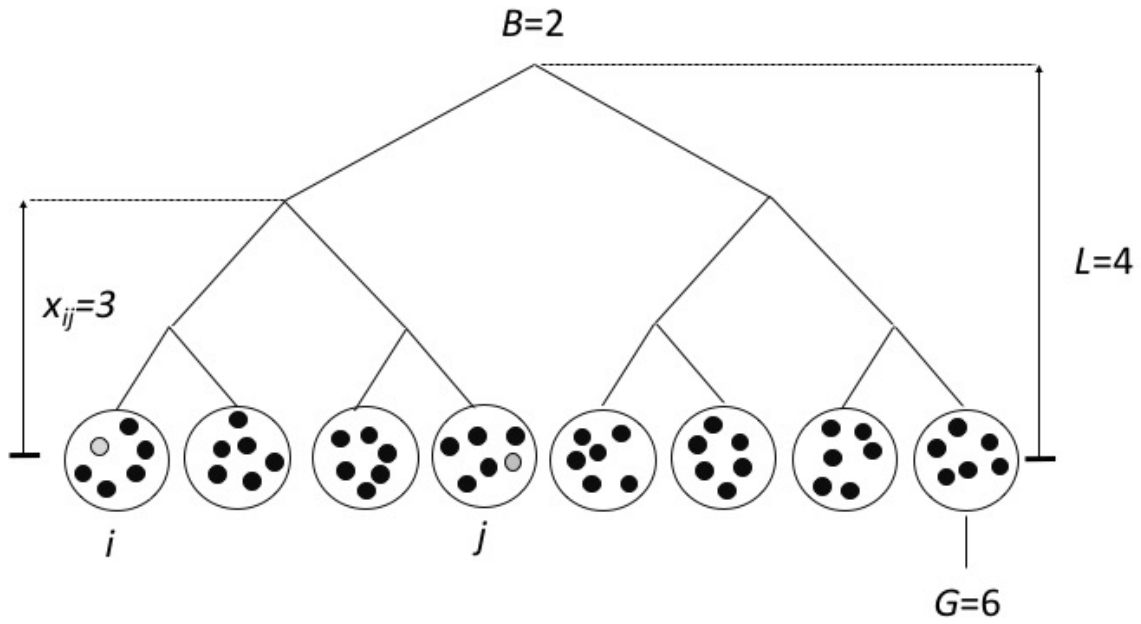
Figure 2 Overall diffusion with status-based adoption thresholds. Equilibrium cumulative adoption rate (z-axis) by homophily (x-axis) and consolidation (y-axis) over 100 realizations. All other parameters are fixed at: $D = 10$, $H = 16$, $G = 50$, $P = 2/16$, $Z = 10$.

A. 3D Contour Plot
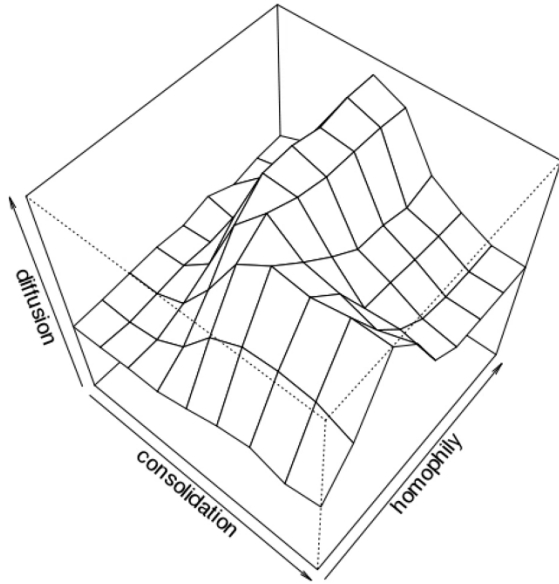
B. Image Plot
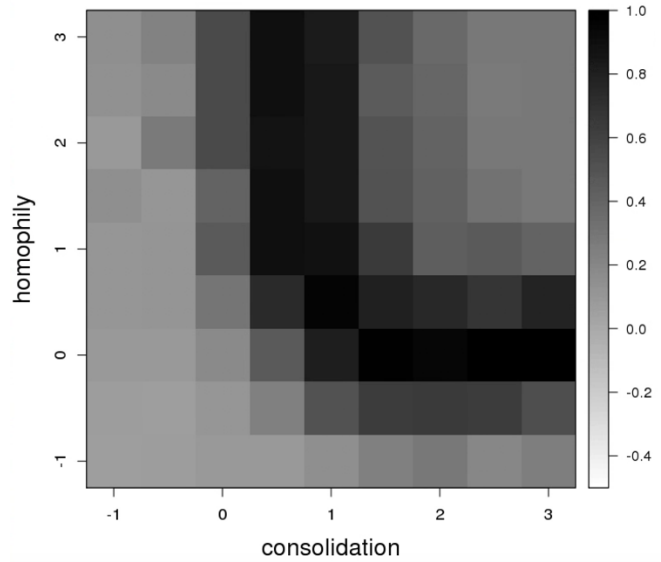
Figure 3 Overall diffusion by homophily at low and high consolidation. Cumulative adoption rate (y-axis) over time (x-axis) by homophily, with 95% confidence bands (gray region), at low consolidation (panel A) and high consolidation (panel B). All other parameters are fixed at: D = 10, H = 16, G = 50, P = 2/16, Z = 10. Means and variances are calculated from 100 realizations per set of parameters.
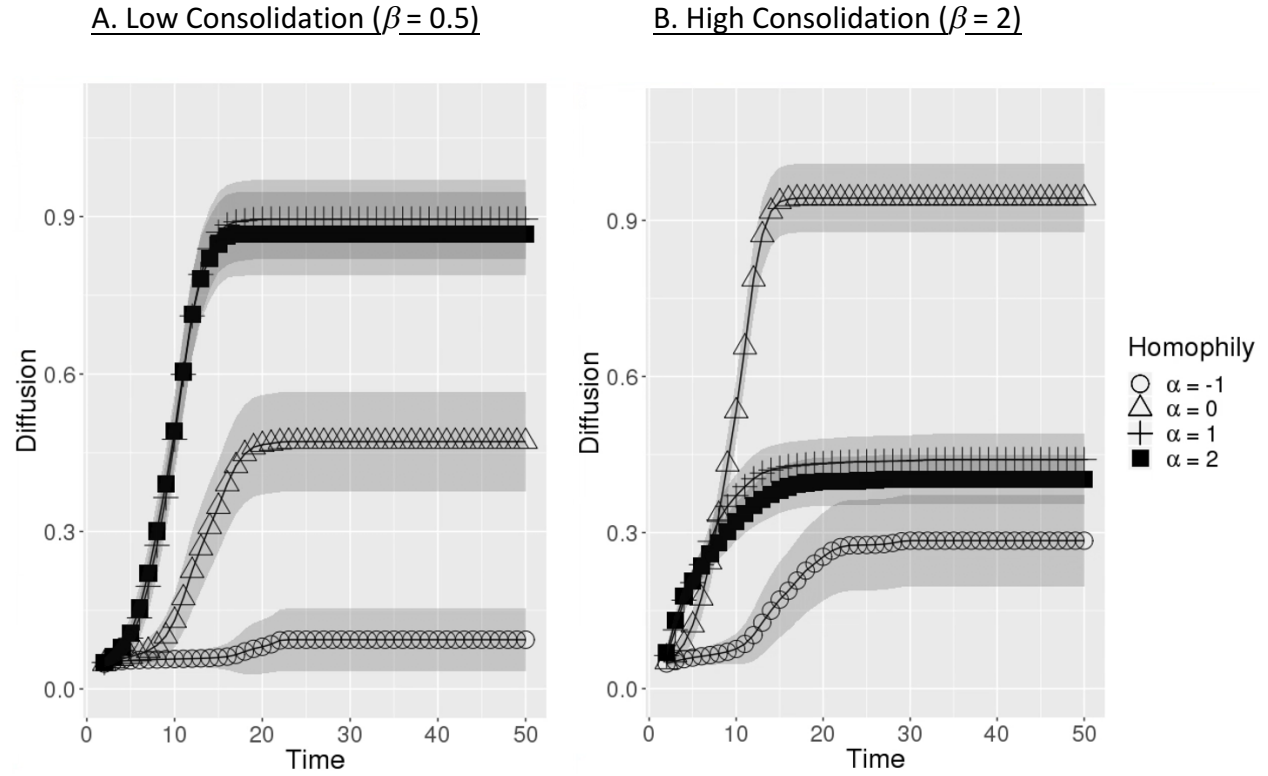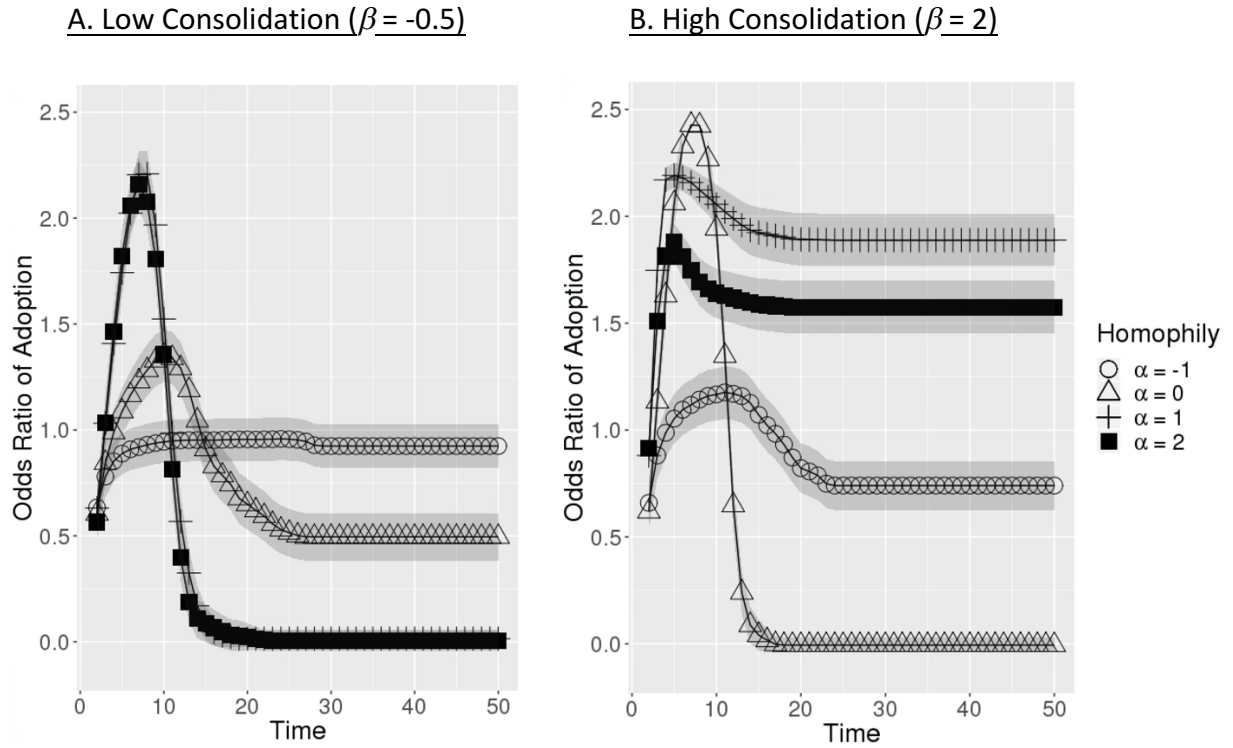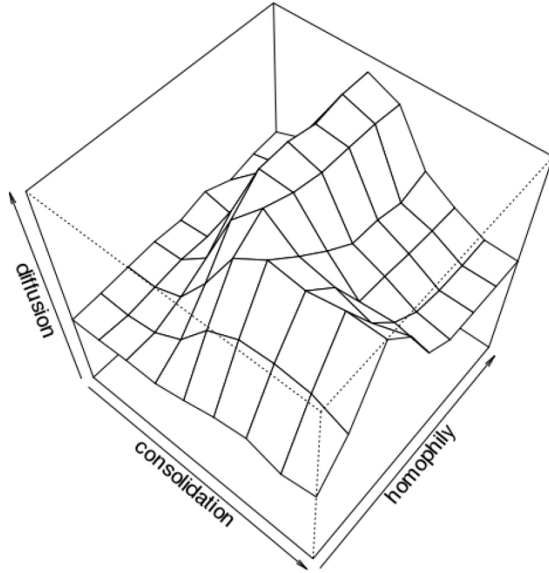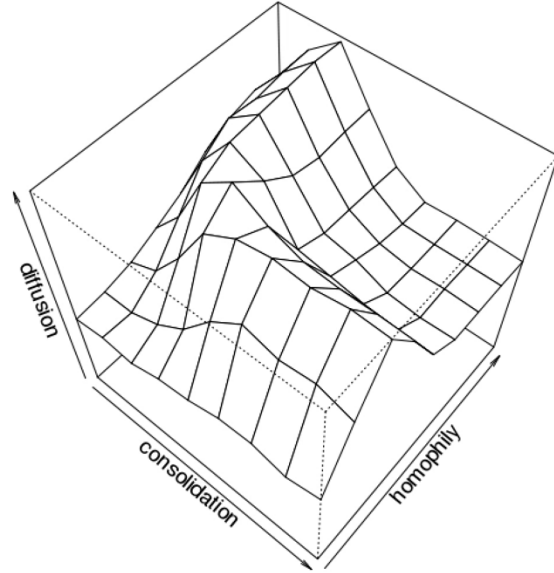
Figure 4 Inequality in diffusion by homophily under low and high consolidation. Log odds ratios of adoption probabilities between high-status and low-status individuals (y-axis) over time (x-axis) by homophily, with 95% confidence bands (gray region), under low (panel A) and high (panel B) consolidation. All other parameters are fixed at: $D = 10$, $H = 16$, $G = 50$, $P = 2/16$, $Z = 10$. Means and variances are calculated from 100 realizations per set of parameters.
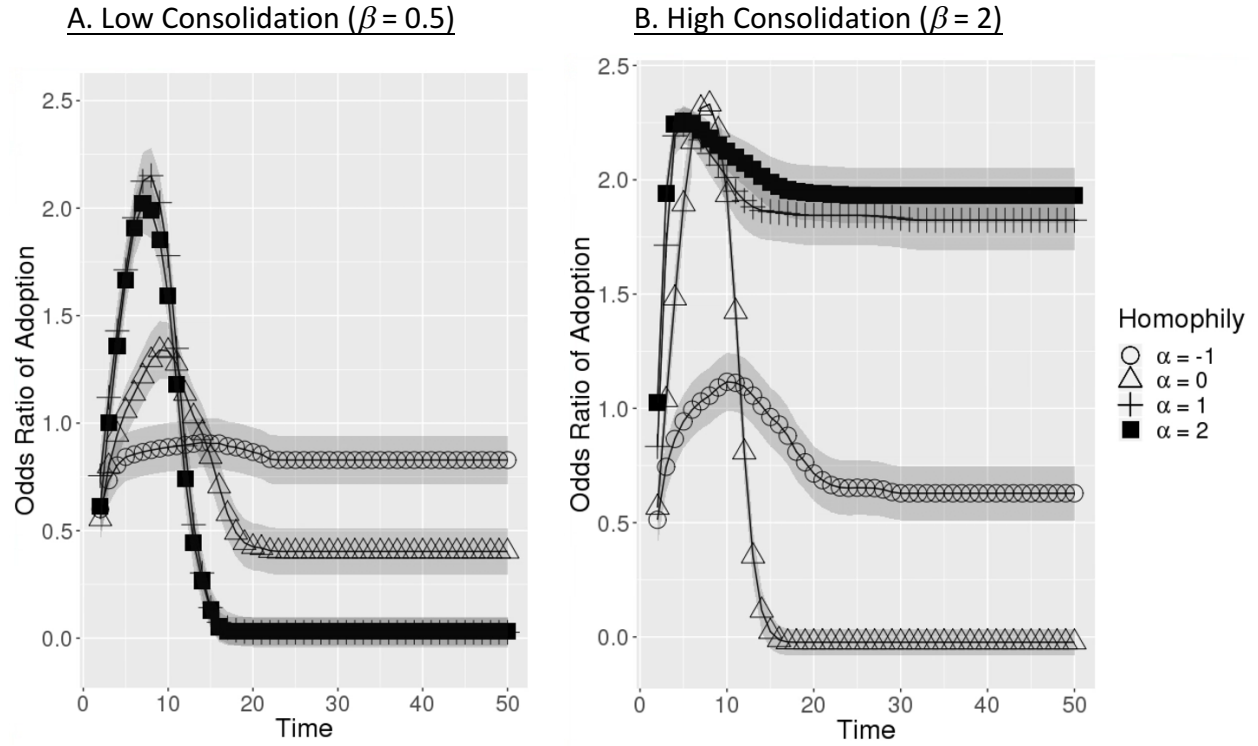
Figure 5 Overall diffusion with status-based adoption thresholds, varying status distribution (P). Equilibrium cumulative adoption rate (z-axis) by homophily (x-axis) and consolidation (y-axis) over 100 realizations. All other parameters are fixed at: *D* = 10, *H* = 16, *G* = 50, *Z* = 10.

A. P = 1/16
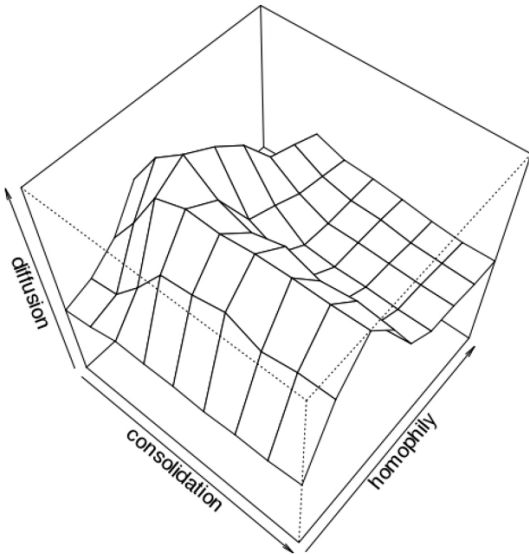
B. P = 2/16
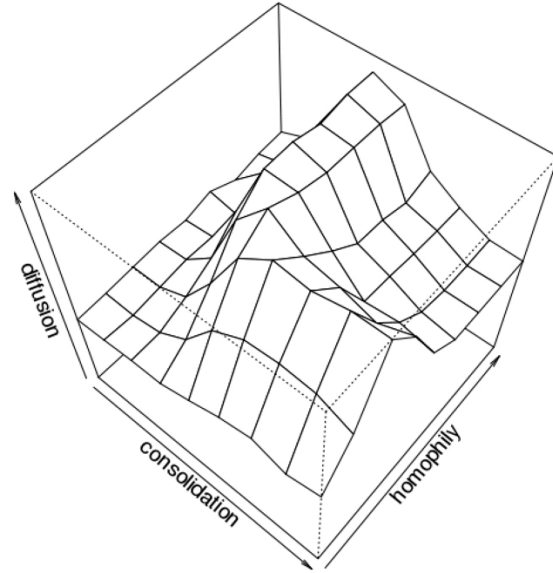
C. P = 3/16
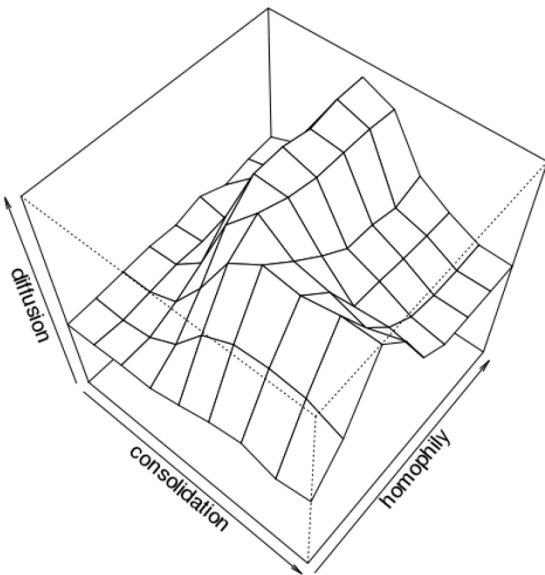
D. P = 4/16
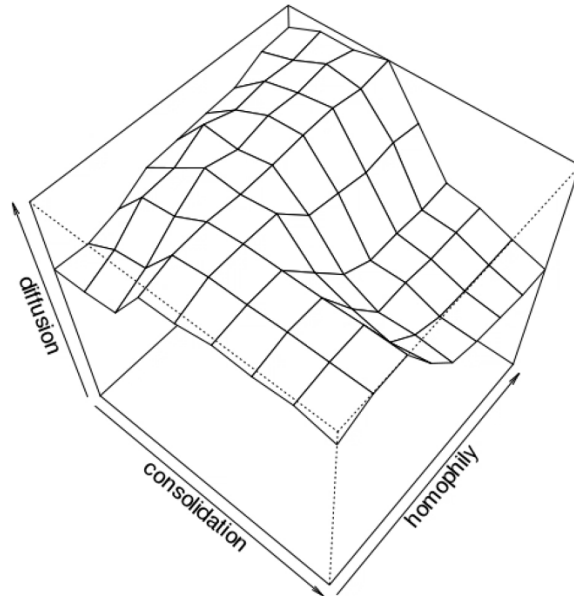
**Figure 6 Inequality in diffusion by homophily under low and high consolidation with distance based on mean of 3 social dimensions**. Log odds ratios of adoption probabilities between high-status and low-status individuals (y-axis) over time (x-axis) by homophily, with 95% confidence bands (gray region), under low (panel A) and high (panel B) consolidation. All other parameters are fixed at: $D = 10$, $H = 16$, $G = 50$, $P = 2/16$, $Z = 10$. Means and variances are calculated from 100 realizations per set of parameters.
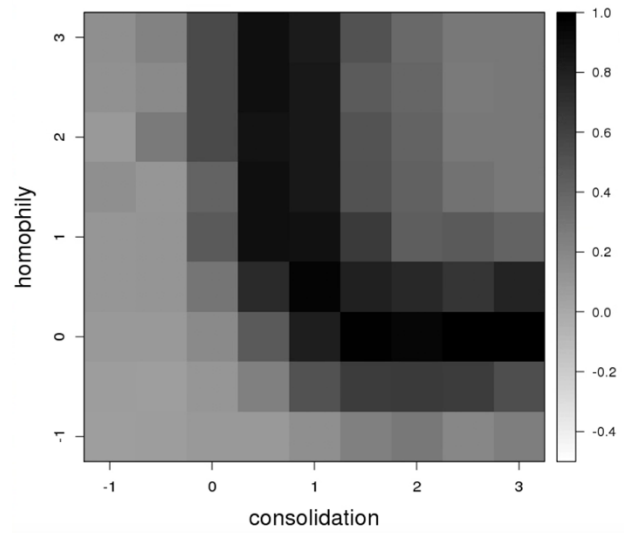

A. Low Consolidation ($\beta = -0.5$)

B. High Consolidation ($\beta = 2$)

Figure 7 Overall diffusion with status-based adoption thresholds, varying distance metric.
Equilibrium cumulative adoption rate (z-axis) by homophily (x-axis) and consolidation (y-axis) over 100 realizations. All other parameters are fixed at: $D = 10$, $H = 16$, $G = 50$, $P = 2/16$, $Z = 10$.
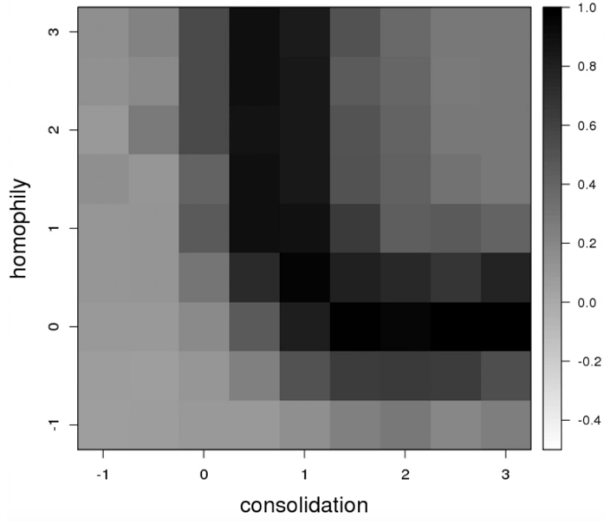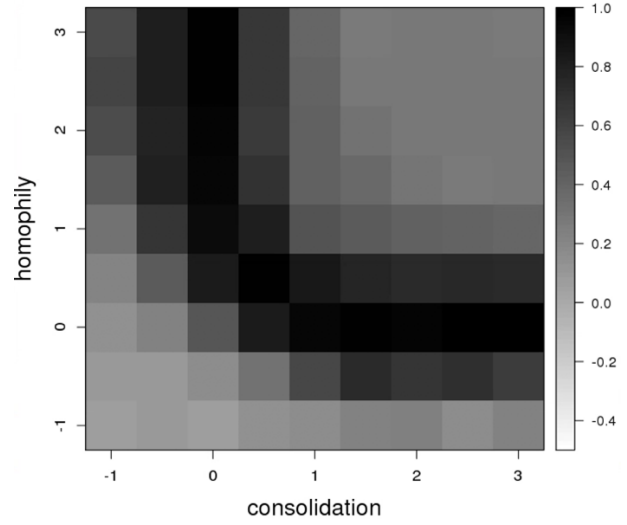
A. Minimum

B. Mean of 2

C. Mean of 3
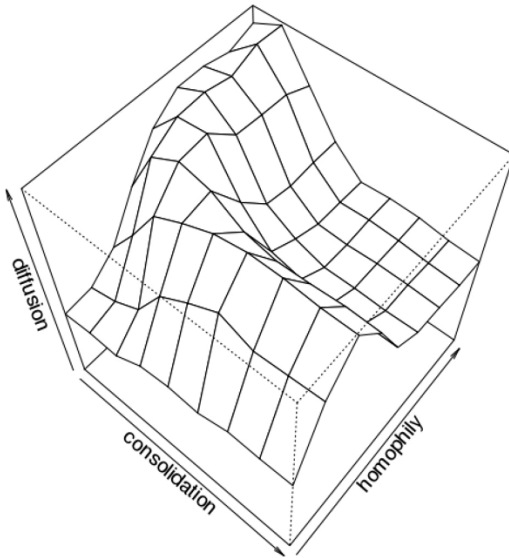
D. Mean of 4
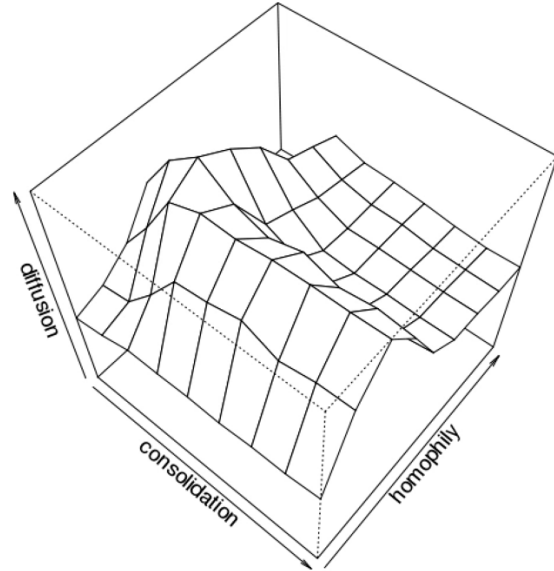
Figure 8 Inequality in diffusion by "effective" homophily under low and high consolidation.
Log odds ratios of adoption probabilities between high-status and low-status individuals (y-axis) over time (x-axis) by homophily, with 95% confidence bands (gray region), under low (panel A) and high (panel B) consolidation. All other parameters are fixed at: $D = 10$, $H = 16$, $G = 50$, $P = 2/16$, $Z = 10$. Means and variances are calculated from 100 realizations per set of parameters.

A. Low Consolidation ($\beta = 0.5$)

B. High Consolidation ($\beta = 2$)
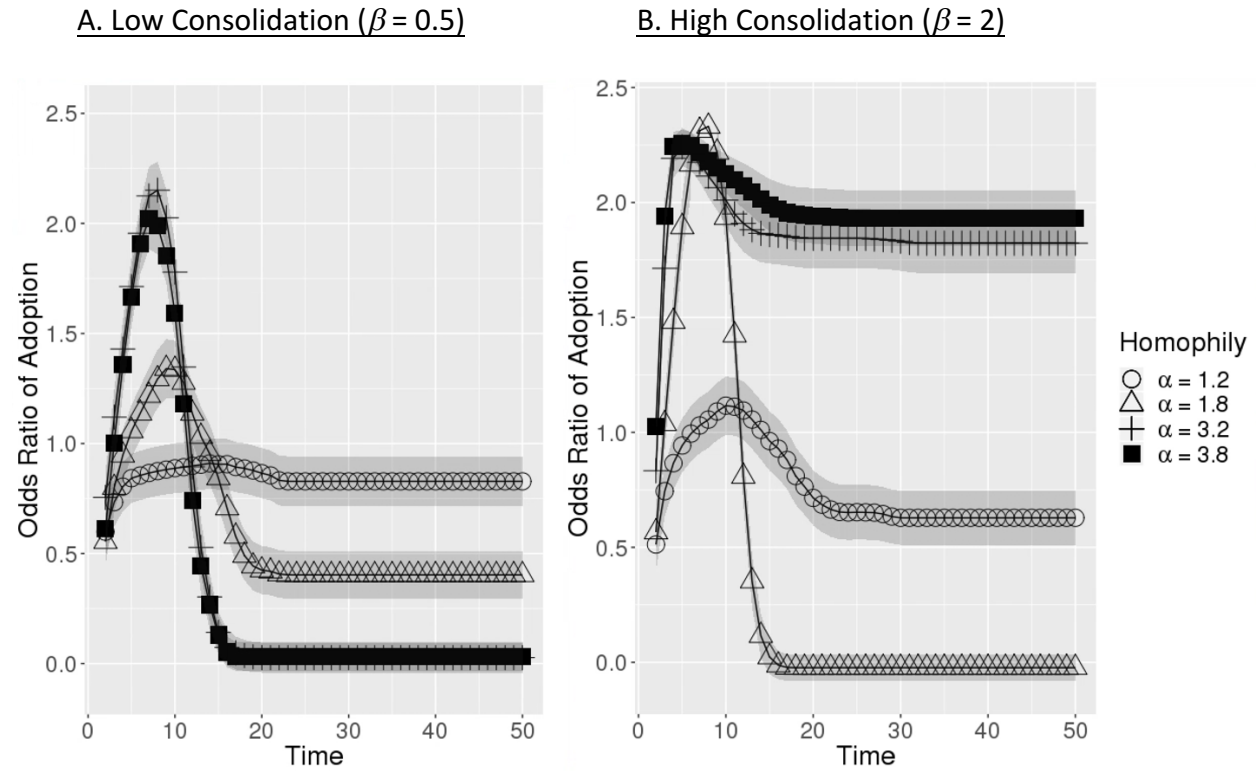
Homophily
$\bigcirc$ $\alpha = 1.2$
$\triangle$ $\alpha = 1.8$
$+$ $\alpha = 3.2$
$\blacksquare$ $\alpha = 3.8$

Figure A1 Overall diffusion with status-based adoption thresholds, varying status distribution (P). Equilibrium cumulative adoption rate (z-axis) by homophily (x-axis) and consolidation (y-axis) over 100 realizations. All other parameters are fixed at: $D = 10$, $H = 16$, $G = 50$, $Z = 10$.

A. P = 1/16
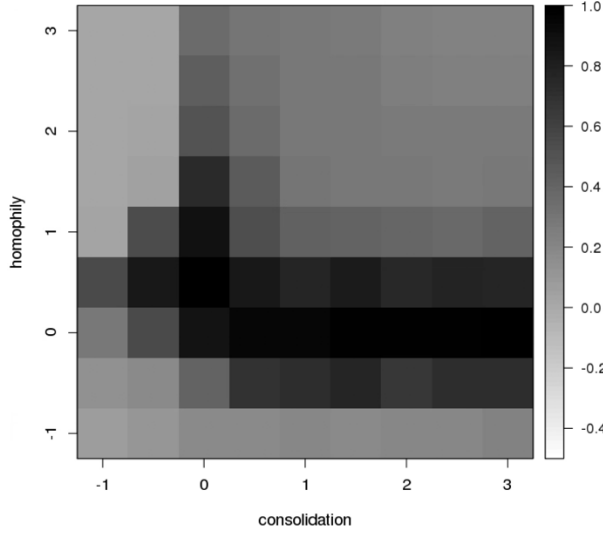
B. P = 2/16

C. P = 3/16
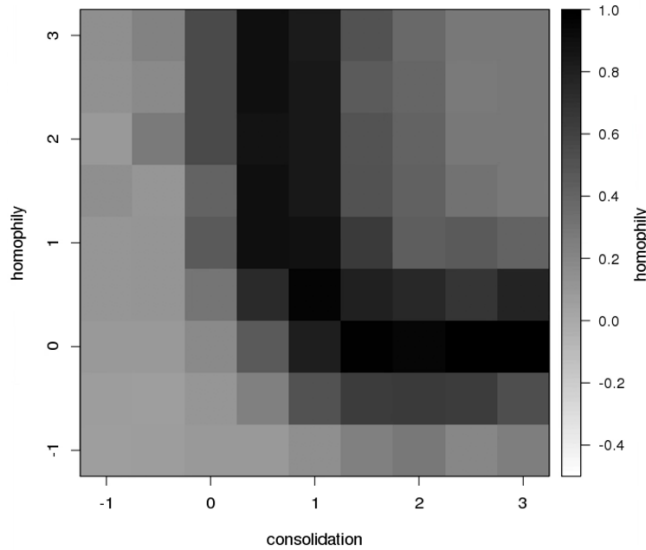
D. P = 4/16
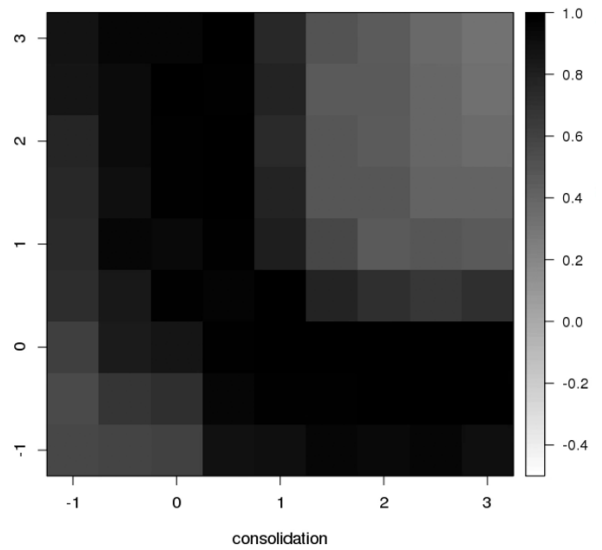
Figure A2 Overall diffusion with status-based adoption thresholds, varying distance metric.
Equilibrium cumulative adoption rate (z-axis) by homophily (x-axis) and consolidation (y-axis) over 100 realizations. All other parameters are fixed at: $D = 10$,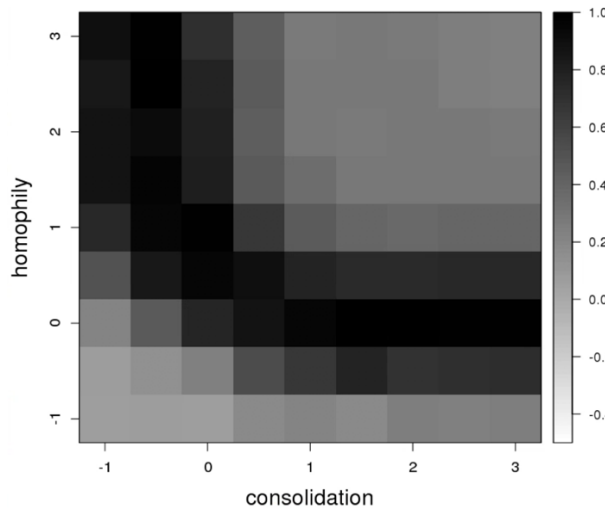 $H = 16$, $G = 50$, $P = 2/16$, $Z = 10$.