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Abstract

In this paper, I develop and estimate a dynamic model of strategic network formation with heterogeneous agents. The main theoretical result is the existence of a unique stationary equilibrium, which characterizes the probability of observing a specific network in the data. As a consequence, the structural parameters can be estimated using *only one observation* of the network at a single point in time. The estimation is challenging, since the exact evaluation of the likelihood function is computationally infeasible even for very small networks. To overcome this problem, I propose a Bayesian Markov Chain Monte Carlo algorithm that avoids the direct evaluation of the likelihood. This method drastically reduces the computational burden of estimating the posterior distribution and allows inference in high dimensional models.

I present an application to the study of segregation in school friendship networks, using data from Add Health. The latter contains the actual social network of each student in a representative sample of US schools. My results suggest that for White students, the value of a same-race friend decreases with the fraction of whites in the school. This relationship is of opposite sign for African American students.

The model is used to study how different desegregation policies may affect the structure of the network in equilibrium. I find an inverted U-shape relationship between the fraction of students belonging to a racial group and the expected equilibrium segregation levels. These results suggests that these policies should be carefully designed in order to be effective.

JEL Codes: D85, C15, C73
Keywords: Social Networks, Bayesian Estimation, Markov Chain Monte Carlo

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1 Introduction

In this paper, I develop and estimate a dynamic model of strategic network formation with heterogeneous agents. The main theoretical result is the existence of a unique stationary equilibrium, which characterizes the probability of observing a specific network in the data. As a consequence, the structural parameters can be estimated using *only one observation* of the network at a single point in time. The estimation is challenging, since the exact evaluation of the likelihood function is computationally infeasible even for very small networks. To overcome this problem, I propose a Bayesian Markov Chain Monte Carlo algorithm that avoids the direct evaluation of the likelihood. This method drastically reduces the computational burden of estimating the posterior distribution and allows inference in high dimensional models.

The methodological contributions of this work are motivated by a growing evidence documenting how the structure of social networks is related to individual performance. The number and socioeconomic composition of friends affect employment prospects, school performance, risky behavior, adoption of new technologies and health outcomes.[1] The literature has proposed two alternative approaches to study the determinants of network structure.[2] The strategic models interpret the network as the equilibrium outcome of a strategic game. Rational individuals invest in social ties and choose friends by considering the cost and benefits of each relationship. The network structure is thus the result of strategic interactions among agents. In models of random network formation each link occurs with a certain probability, and the network structure is the realization of a stochastic process. While random models provide a better fit of social network data, they lack any microfoundation. This feature severely limits their use for policy evaluation. At the same time, strategic models provide sharp predictions about networks observed in the real world, but they are unable to fit many structural properties of the data.

Several recent contributions[3] show that the development and estimation of an empirical model for strategic network formation faces two main challenges. First, strategic network formation models tend to have multiple equilibria, which makes the identification of structural parameters problematic; furthermore, estimation requires data containing multiple observations of the network. Second, strategic models have inherent computational complexity:

[1] For example, see the recent contributions of Topa (2001); Laschever (2009); Cooley (2010); Giorgi et al. (2010); Nakajima (2007); Bandiera and Rasul (2006); Conley and Udry (forthcoming).

[2] For a survey see Jackson (2008).

[3] See for example Currarini et al. (2009, 2010); Comola (2008); Mayer and Puller (2008); Christakis et al. (2010)

the number of possible network configurations increases exponentially with the number of players. This feature makes the computation of equilibria for large networks extremely hard. This curse of dimensionality imposes a severe limit to the estimation of these models, allowing inference only for small networks or specifications with few parameters.

The model developed in this work eliminates the first problem and drastically reduces the second. First, the existence of a unique stationary equilibrium allows estimation and identification of the structural parameters using only one observation of the network at a single point in time. Second, the proposed estimation algorithm eliminates the curse of dimensionality by avoiding the direct evaluation of the likelihood. The computational burden is reduced even further by exploiting the properties and characterization of the stationary equilibrium.

I present an application to the study of segregation in school friendship networks, using data from the *National Longitudinal Study of Adolescent Health* (Add Health). This unique dataset contains detailed information on the actual friendship network of each student in a representative sample of US schools. My final sample contains 14 schools with a total of 1139 students.[4] I find that race, gender and grade are important determinants of network formation in schools. There is evidence of homophily, i.e. students tend to interact and form social ties with similar people, other things being equal. My results suggest that for White students the value of a same-race friend decreases with the fraction of whites in the school. Viceversa, for African American students the value of an African American friend increase with the proportion of blacks in the school. Hispanic preferences seem to reflect the same pattern of whites.

This model is extremely useful in policy analysis, since it allows the researcher to simulate counterfactual policy experiments.[5] If policymakers are interested in promoting policies to affect the structure of the network, my model provides a useful guidance. As an example, I consider two schools from the sample, one with 98% whites and the other with 96% blacks. I simulate alternative swaps of students across schools and then measure the average segregation in the new stationary equilibrium of the model. I find that there is an *inverted U-shape* relationship between the fraction of students belonging to a racial group and the

[4] I use only the schools from the *saturated sample*. The sampling scheme of Add Health involved in-school interviews for all the students. A subsample of 20745 students was also interviewed at home, to collect detailed individual information. The saturated sample contains schools for which both interviews were administered to *each* student enrolled. Therefore this sample does not contain any missing information about individual controls. This is not the case for most schools in Add Health.

[5] Alternatively, it could be used as a guide for designing randomized experiments that modify students assignments.

expected equilibrium segregation levels.[6] For example, a change in the white student share from 90% to 80% implies an average increase of expected segregation by .20, as measured by the Freeman (1972) segregation index.[7]

The model incorporates ingredients from both strategic and random network formation literature (Jackson, 2008). The link formation is sequential: in each period only one agent is active and he updates only one link. At the beginning of the period, a random agent (John) is drawn from the population and he meets another agent (Liz) according to a random matching technology. At this point he has the opportunity to update his social tie to Liz. The implicit assumption is that meetings are very frequent and the agents have the opportunity to revise their strategies very often.

John cares about the socioeconomic composition of his friends: his utility from linking Liz depends on her socioeconomic attributes; additionally, he values the socioeconomic composition of her friends and how befriending her could affect his popularity among the other players. Finally, a link provides additional utility when it is reciprocated. When updating the link, John receives a random shock to his preferences, which is unobserved by the econometrician. This shock models unobservables: for example, John may be in a bad mood when he meets Liz, and this affects his linking strategy. The link is formed when the social relationship provides positive utility; otherwise the agent does not form (or severs, if already in place) the friendship.

A crucial assumption is that individuals do not take into account how their current linking strategy affects the shape of future networks: they follow a stochastic best-response dynamics *à la* Blume (1993).[8] This assumption reduces the computational complexity and provides a tractable dynamics.[9]

The model has two desirable features. First, there are two levels of heterogeneity. Each individual is endowed with a set of *exogenous* attributes. Furthermore, the dynamics of network formation generates *endogenous* heterogeneity: each individual has a different set of friends and a different composition of friends' attributes. In equilibrium two agents with exactly the same exogenous attributes may have different linking strategies, because of their

[6] Currarini et al. (2010) use a different model and find the same relationship.

[7] The index measures the difference between the expected and actual number of links among individuals of different groups. An index of 0 means that the actual network closely resembles one in which links are formed at random. Higher values indicate more segregation. The maximum of 1 corresponds to a network in which there are no inter-group links.

[8] It is possible to relax the assumption of myopic agents, but the computational burden becomes challenging. The simple characterization of equilibrium behavior, long run dynamics and the estimation strategy depend on the best-response dynamics and may not extend to an economy with forward-looking agents.

[9] Alternatively, it is possible to interpret this model as an equilibrium selection device, that selects one of the possible networks as the result of an evolutionary game.

different endogenous positions in the network and the socioeconomic composition of their friends. Most models of strategic network formation incorporate the first level of heterogeneity but they are unable to generate different equilibrium behavior, because the agents in these models care only about their direct links.[10]

Second, I can characterize the network formation game as a *potential game*.[11] All the players' incentives in any state of the network are completely summarized by an aggregate function, *the potential*, mapping networks and socioeconomic characteristics into potential levels. When an agent updates a link, the change in his utility is equal to the change in the potential. This simple characterization is very useful when studying a network with many agents, since the potential summarizes the incentives of all players with a single number: there is no need to keep track of the choices and utility levels of all n players. The existence of a potential allows me to characterize the stationary equilibrium in closed form. Assuming that preference shocks follow an extreme value distribution (i.i.d. over time and across agents), and that any pair of agents can meet with positive probability, I prove that the unique stationary equilibrium characterizes the probability of observing a specific network structure as an exponential function of the potential. This result provides the likelihood function for the estimation.

The estimation of the posterior distribution imposes a computational challenge: both the posterior and the likelihood are functions of normalizing constants which are intractable. [12]

To solve this problem, I propose a Markov Chain Monte Carlo algorithm that removes the need to evaluate the likelihood. This method belongs to the class of exchange algorithms, first developed by Murray et al. (2006) for a similar family of distributions. [13] I prove that the algorithm generates a Markov chain of parameters whose invariant distribution is the posterior. Therefore, samples from the algorithm can be used as (correlated) samples from the posterior. Using the properties of the stationary equilibrium and following a suggestion in Liang (2010), I modify the algorithm to reduce the computational burden even further.

[10] An exception is the model of De Marti and Zenou (2009), where the cost of linking an individual also depends on the composition of friends of friends. While the structure of the preference is similar to mine, they present a static model and the link formation requires mutual agreement of the players. The consequence is that their model has multiple equilibria.

[11] See Monderer and Shapley (1996) for a description of games with a potential. **?** investigates a model of network formation with a potential function. Their model only considers direct links utility, while mine includes indirect links, mutual links and popularity.

[12] To evaluate the likelihood function, one needs to compute the sum of exponential functions of the potential, where the sum is computed over all possible network configurations. To be concrete, a network with $n = 10$ agents has $2^{90} \approx 10^{27}$ possible network configurations. A state of the art supercomputer will take several years to evaluate the likelihood once.

[13] Similar algorithms have been proposed in the Exponential Random Graph literature by Caimo and Friel (2010), Koskinen (2008),Liang (2010).

This method allows estimation of high dimensional models in reasonable time. When data from multiple networks are available, the algorithm is easily extended.[14]

The remainder of the paper is organized as follows. Section 2 describes the model and the stationary equilibrium. Section 3 develops the estimation method and describes the Add Health data. Section 4 discusses the empirical results and the policy experiments. Section 5 concludes. Appendix A collects all the proofs for the theoretical model, while Appendix B provides the details about the MCMC algorithm and convergence.

2 A Model of Network Formation

2.1 Setup

Let $\mathcal{I} = \{1, 2, ..., n\}$ be the set of agents, each identified by a vector of A (exogenous) attributes $X_i = \{X_{i1}, ..., X_{iA}\}$, e.g. gender, wealth, age, location, etc. The attributes of the population are contained in the matrix $X = \{X_1, X_2, ..., X_n\}$ and $\mathcal{X}$ denotes the set of all possible matrices X. Time is discrete.

The social network is represented as a (random) $n \times n$ binary matrix $G \in \mathcal{G}$, where $\mathcal{G}$ is the set of all $n \times n$ binary matrices. The generic element of the matrix G is

$$G_{ij} = \begin{cases} 1 & \text{if individual } i \text{ nominates individual } j \text{ as friend} \\ 0 & \text{otherwise} \end{cases}$$

and I follow the convention in the literature, assuming $G_{ii} = 0$, for any i.

The network represented by G is *directed*: the existence of a link from i to j does not imply the existence of the link from j to i, i.e. $g_{ij} \neq g_{ji}$. This modeling choice reflects the structure of the Add Health data, where friendship nominations are not necessarily mutual. Some authors refer to this data as *perceived* networks.[15]

Let the *realization* of the network at time t be denoted as g^t and the *realization* of the link between i and j at time t be g^t_{ij}. The network including all the current links but g^t_{ij}, i.e. $g^t \backslash g^t_{ij}$, is denoted as g^t_{-ij}.

The preferences are defined over network realizations and population characteristics and I assume there is an utility function $U_i : \mathcal{G} \times \mathcal{X} \to \mathbb{R}$ for each i, mapping networks and individual characteristics into utility levels.

[14] In the estimation section I use a parallel version of this algorithm for the estimation with multiple school networks. The details are discussed in the computational appendix.

[15] See Wasserman and Faust (1994) for some references.

2.1.1 Network Formation Process

Individuals form links over time through a *stochastic best-response dynamics*, generating a Markov chain of networks. The main ingredients of this process are random matching and utility maximization. The implicit assumption is that individuals meet frequently and have the opportunity to revise their links very often.

Matching Technology. At the beginning of each period an agent i is randomly selected from the population, and he meets another individual j according to a matching technology. Formally, the *meeting process* is a stochastic sequence $m = \{m^t\}_{t=1}^{\infty}$ with support $\mathcal{I} \times \mathcal{I}$. The realizations of the meeting process are ordered pairs $m^t = \{i, j\}$, indicating which agent i should play and which link g_{ij} can be updated at period t.[16]

Player i meets agent j with probability

$$\Pr\left(m^t = ij | g^{t-1}, X\right) = \rho\left(g^{t-1}, X_i, X_j\right) \tag{1}$$

where $\sum_{i=1}^{n}\sum_{j=1}^{n}\rho\left(g^{t-1}, X_i, X_j\right) = 1$ for any $g \in \mathcal{G}$. The matching probability depends on the current network (e.g. the existence of a common friend between i and j) and the characteristics of the pair. This structure includes matching technologies with a bias for same-type individuals as in Currarini et al. (2009). The simplest example of (1) is an i.i.d. discrete uniform process with $\rho\left(g^{t-1}, X_i, X_j\right) = \frac{1}{n(n-1)}$. An example with bias for same-type agents is $\rho\left(g^{t-1}, X_i, X_j\right) \propto \exp\left[-d\left(X_i, X_j\right)\right]$, where $d\left(\cdot,\cdot\right)$ is a distance function.

Utility Maximization Conditional on the meeting $m^t = ij$, player i updates the link ij to maximize his current utility, taking the previous period network g^t_{-ij} as given. The agents have *complete information* since they can observe the entire network shape and the individual attributes of all agents.

Before updating his link to j, individual i receives an idiosyncratic shock $\varepsilon \sim F\left(\varepsilon\right)$ to his preferences, that the econometrician cannot observe. The latter shock is meant to model unobservable events that could influence the utility of a link, e.g. mood, gossips, fights, etc.

Player i links player j at time t, i.e. $g^t_{ij} = 1$, if it is a best response to the current network configuration

$$U_i\left(g^t_{ij} = 1, g^{t-1}_{-ij}, X\right) + \varepsilon\left(g^t_{ij} = 1\right) \geq U_i\left(g^t_{ij} = 0, g^{t-1}_{-ij}, X\right) + \varepsilon\left(g^t_{ij} = 0\right) \tag{2}$$

[16] Several models incorporate a matching technology in the network formation process. Jackson and Watts (2002) assume individuals meet randomly according to a discrete uniform distribution. Currarini et al. (2009) introduce a matching process that is biased towards individuals of the same type, similar to the one modeled here.

I assume that when the equality holds, the agent plays the status quo.[17] The stochastic process described above generates a sequence $[g^0, g^1, ..., g^t]$ of networks. In each period only one element of the random matrix G is updated, conditioning on previous period network. Therefore the sequence is a Markov chain, with transition probabilities determined by the meeting process and agents' linking choices. [18]

2.1.2 Preferences

The preferences are defined over networks and individual characteristics. The utility of player i from a network g and population attributes $X = (X_1, ..., X_n)$ is given by

$$U_i(g, X) = \underbrace{\sum_{j=1}^{n} g_{ij} u_{ij}}_{\text{direct friends}} + \underbrace{\sum_{j=1}^{n} g_{ij} g_{ji} m_{ij}}_{\text{mutual friends}} + \underbrace{\sum_{j=1}^{n} g_{ij} \sum_{\substack{k=1 \\ k \neq i,j}}^{n} g_{jk} v_{ik}}_{\text{friends of friends}} + \underbrace{\sum_{j=1}^{n} g_{ij} \sum_{\substack{k=1 \\ k \neq i,j}}^{n} g_{ki} w_{kj}}_{\text{popularity}} \quad (4)$$

where $u_{ij} \equiv u(X_i, X_j)$, $m_{ij} \equiv m(X_i, X_j)$, $v_{ij} \equiv v(X_i, X_j)$ and $w_{ij} \equiv w(X_i, X_j)$ are (bounded) real-valued functions of the attributes. The utility of the network is the sum of the net benefits received from each link, and links are considered perfect substitutes. The total benefit from an *additional link* has four components.

First, when the agent links another individual, she receives an additional *direct* net benefit u_{ij}. The direct utility includes both costs and benefits and it may possibly be negative: in case of homophily, the net utility u_{ij} is positive if i and j belong to the same group, while it is negative when they are of different types. This is illustrated in Panel A of Figure 1 with a simple network of 8 agents. Each agent can belong to either the blue group or the yellow group. The link that agent 4 forms to individual 5 provides different direct utility in the two networks, since the identity of 5 is different: blue for the left network and yellow for the right one. In many models this component is parameterized as $u_{ij} = b_{ij} - c_{ij}$, where b_{ij} indicates the (gross) benefit and c_{ij} the cost of forming the additional link g_{ij}. I use the notation u_{ij}, since it does not require assumptions on the cost function.

[17] This assumption does not affect the main result and it is relevant only when the distribution of the preference shocks is degenerate.

[18] I do not go over the tedious but straightforard derivation of the actual transition matrix for the chain. The set of all possible states is $\mathcal{G}$, the probability of transition from a network $g^t = g$ to next period network $g^{t+1} = (g'_{ij}, g_{-ij})$ is

$$\rho(g, X_i, X_j) I_{\{U_i(g'_{ij}, g_{-ij}, X) + \varepsilon(g'_{ij}) \geq U_i(g_{ij}, g_{-ij}, X) + \varepsilon(g_{ij})\}} \quad (3)$$

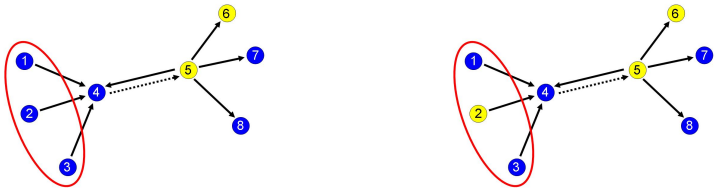
where $I_{\{...\}}$ is an indicator function. The transition probability is zero if the networks differ in more than one element.

Figure 1: Components of the utility function

A. Direct friends

B. Mutual friends

C. Friends of friends



D. Popularity

The network contains $n = 8$ agents, belonging to two groups: blue and yellow. All the panels show a situation in which 4 is forming a new link to individual 5 (the dashed arrow from 4 to 5). Agent 4 receives different direct utility when he links a blue (Panel A, left) or a yellow (Panel A, right) individual. Agent 4's utility for an additional link is different if the link is unilateral (Panel B, left) or reciprocated (Panel B, right). Furthermore, agent 4's utility from friends of friends varies with their socioeconomic composition: 3 blue individuals (Panel C, left) provide different utility with respect to 2 blue and 1 yellow (Panel C, right). Finally, agent 4 values how his new link affects his popularity, since he creates a new indirect friendship for those who already have a link to him (agents 1,2 and 3). The utility of link to agent 5 (which is yellow) when agents 1,2 and 3 are all blue (Panel D, left) is different when agent 2 is yellow and 1 and 2 are blue (Panel D, right).

Agents receive additional utility m_{ij} if the link is mutual. A friendship is valued differently if the other agent reciprocates. The idea is that an agent may perceive another

individual as a friend, but that person may not perceive the relationship in the same way. Panel B of Figure 1 isolates this component: a link from agent 4 to agent 5 has a different value if agent 5 reciprocates (right network).

The players value the composition of friends of friends. When i is deciding whether to link j, she observes j's friends and their socioeconomic characteristics. Each of j's friend provides additional utility $v(X_i, X_k)$ to i. In this model, an agent who has the opportunity to form an additional link, values a white student with three Hispanic friends as a different "good" than a white student with two white friends and one African American friend.[19] In other words, individuals value both *exogenous* heterogeneity and *endogenous* heterogeneity: the former is determined by the socioeconomic characteristics of the agents, while the latter arises endogenously with the process of network formation. I assume that only friends of friends are valuable and they are considered as perfect substitutes: individuals do not receive utility two-links-away friends. In Panel C of Figure 1, in the eyes of agent 4, agent 5 in the left network is a different "good" than agent 5 in the right network, since the composition of his friends is different.

The fourth component corresponds to a *popularity effect*. Consider Panel D in Figure 1. When agent 4 forms a link to agent 5, he automatically creates an indirect link for agents 1, 2 and 3. Thus agent 4 generates an externality. Let's assume there is homophily in indirect links: in the left network the externality is negative for all three agents (1, 2 and 3); in the right network it is negative for 1 and 3, but positive for 2. Therefore in the left network the popularity of 4 goes down, while in the right network the change in popularity is less pronounced. [20]

2.2 Equilibrium Analysis

I impose an additional assumption on the functional forms of the utility functions. The assumption is not too strong, but it provides an important identification restriction. I assume that the utility m_{ij} obtained from mutual links is symmetric and that the utility of an indirect link v_{ij} has the same functional form as the utility from the popularity effect w_{ij}.

[19] A similar assumption is used in De Marti and Zenou (2009) where the agents' cost of linking depend on the racial composition of friends of friends. Their model is an extension of the connection model of Jackson and Wolinsky (1996), and the links are formed with mutual consent. The corresponding network is undirected.

[20] There is an alternative interpretation of this last component. In some sense it introduces some reduced form *forward-looking* behavior in the model, since the popularity is referred to how more/less likely are the other agents to maintain or create a link to individual i in future meetings.

ASSUMPTION 1 ***(Preferences)*** *The utility function satisfies the following restrictions*

$$\begin{aligned} m(X_i, X_j) &= m(X_j, X_i) \text{ for all } i, j \in \mathcal{I} \\ w(X_k, X_j) &= v(X_k, X_j) \text{ for all } k, j \in \mathcal{I} \end{aligned}$$

therefore the utility function is

$$U_i(g, X) = \sum_{j=1}^{n} g_{ij} u_{ij} + \sum_{j=1}^{n} g_{ij} g_{ji} m_{ij} + \sum_{j=1}^{n} g_{ij} \sum_{\substack{k=1 \\ k \neq i,j}}^{n} g_{jk} v_{ik} + \sum_{j=1}^{n} g_{ij} \sum_{\substack{k=1 \\ k \neq i,j}}^{n} g_{ki} v_{kj} \tag{5}$$

The symmetry in m_{ij} does not imply that a mutual link between i and j gives both the same utility. Indeed if i and j have a mutual link, they receive the same common utility component (m_{ij}) but they may perceive that particular friendship in a different way, as long as the utility from direct or indirect links are different for i and j. In other words, two individuals with the same exogenous characteristics $X_i = X_j$ (say two males, whites, enrolled in eleventh grade) that form a mutual link receive the same u_{ij} and m_{ij}, but they may have different utilities from that additional link because of the composition of their friends of friends and their popularity. Therefore, I argue that this restriction is not too strong.

The second restriction is more technical. When i forms a link to j, i creates an externality for all k's that have linked her: any such k has now an additional indirect friend, i.e. j, that agent k will value an amount $v(X_k, X_j)$. An individual i values his popularity effect as much as k values the indirect link to j, i.e. i internalizes the externality he creates.

Assumption 1 is the main ingredient that guarantees a closed form solution for the stationary equilibrium of the model. Without this assumption, the model would still have a unique stationary equilibrium, however it would be impossible to characterize the likelihood function in closed form.[21] The first part of the assumption is a normalization of the utility function. The second part of the assumption is an identification restriction, that guarantees the model's coherency in the sense of Tamer (2003). In simple words, this part of the assumption guarantees that the system of conditional linking probabilities implied by the model generates a proper joint distribution of the network matrix.[22]

The assumption delivers a very simple characterization of the stationary equilibrium. The following proposition highlights one of the crucial results of this paper

[21] Estimation of such a model could be performed using Approximate Bayesian Computations (see Marjoram et al. (2003) for example), but the computational burden is even more challenging.

[22] For example in bivariate discrete response models, the system of conditional probabilities generates a joint distribution that does not sum to one. The restriction in Assumption 1 gets rid of this problem. Similar restrictions are also encountered in spatial econometrics models. See Besag (1974) for an example.

PROPOSITION 1 ***(Potential Function)*** *Under the restrictions of Assumption 1, the deterministic incentives of any player in any state of the network are summarized by a* ***potential function****,* $Q : \mathcal{G} \times \mathcal{X} \to \mathbb{R}$

$$Q(g, X) = \sum_{i=1}^{n} \sum_{j=1}^{n} g_{ij} u_{ij} + \sum_{i=1}^{n} \sum_{j>i}^{n} g_{ij} g_{ji} m_{ij} + \sum_{i=1}^{n} \sum_{\substack{j=1 \\ j \neq i}}^{n} \sum_{\substack{k=1 \\ k \neq i,j}}^{n} g_{ij} g_{jk} v_{ik} \tag{6}$$

and the network formation game is a Potential Game.

Proof. In Appendix A ■

The intuition for the result is simple. Under the restrictions of Assumption 1, for any player i and any link g_{ij} we have

$$Q(g_{ij}, g_{-ij}, X) - Q(1 - g_{ij}, g_{-ij}, X) = U_i(g_{ij}, g_{-ij}, X) - U_i(1 - g_{ij}, g_{-ij}, X)$$

Consider two networks, $g = (g_{ij}, g_{-ij})$ and $g' = (1 - g_{ij}, g_{-ij})$, that differ only with respect to one link, g_{ij}, chosen by individual i: the difference in utility that agent i receives from the two networks, $U_i(g, X) - U_i(g', X)$, is exactly equal to the difference of the *potential* function evaluated at the two networks, $Q(g, X) - Q(g', X)$. Therefore the potential is an aggregate function that summarizes the state of the network and the deterministic incentives of the players in each state.

There is an advantage in characterizing the network formation as a potential game. In order to compute the equilibria of the model, there is no need to keep track of each player's behavior: the potential function contains all the relevant information. This property is extremely useful for the analysis of networks with many players: the usual check for existence of profitable deviations from the Nash equilibrium can be performed using the potential instead of checking each player's possible deviation in sequence.

The potential $Q(g, X)$ is not equivalent to the welfare function $W(g, X)$,

$$\begin{aligned} W(g, X) &= \sum_{i=1}^{n} U_i(g, X) \\ &= Q(g, X) + \sum_{i=1}^{n} \sum_{j>i}^{n} g_{ij} g_{ji} m_{ij} + \sum_{i=1}^{n} \sum_{j=1}^{n} \sum_{\substack{k=1 \\ k \neq i,j}}^{n} g_{ij} g_{ki} v_{kj} \end{aligned}$$

To analyze the long run behavior of the model, I impose more structure on the matching technology.[23]

[23] Christakis et al. (2010) assume that individuals can meet only once and their link remains in place forever. This assumption is convenient when estimating a large network, but it does not allow the characterization of the stationary equilibrium.

ASSUMPTION 2 ***(Meeting Process)*** *Any meeting is possible, i.e. for any* $ij \in \mathcal{I} \times \mathcal{I}$

$$\rho(g^{t-1}, X_i, X_j) > 0 \tag{7}$$

The meeting process is such that any individual can be chosen and any pair of agents can meet. This assumption is needed to guarantee that any Nash network can be reached with positive probability. For example, a discrete uniform distribution satisfies this assumption.[24]

It is useful to consider a *special case* of the model, in which there are no preference shocks: the characterization of equilibria and long run behavior for such model provides more intuition about the dynamic of the full structural model.

Let $\mathcal{N}(g)$ be the set of networks that differ from g by only one element of the matrix, i.e.

$$\mathcal{N}(g) \equiv \{g' : g' = (g'_{ij}, g_{-ij}), \text{ for all } g'_{ij} \neq g_{ij}, \text{ for all } i, j \in \mathcal{I}\} \tag{8}$$

A Nash network is defined as a network in which any player has no profitable deviations from his current linking strategy, when randomly selected from the population. The following results characterize the set of the pure-strategy Nash equilibria and the long run behavior of the model with no shocks.

PROPOSITION 2 ***(Model without Shocks: Equilibria and Long Run)*** *Consider the model without idiosyncratic preference shocks. Under Assumption 1 and 2:*

1. *There exist at least one pure-strategy Nash equilibrium network*
2. *The set* $\mathcal{NE}(\mathcal{G}, X, U)$ *of all pure-strategy Nash equilibria of the network formation game is completely characterized by the local maxima of the potential function.*

$$\mathcal{NE}(\mathcal{G}, X, U) = \left\{ g^* : g^* = \arg \max_{g \in \mathcal{N}(g^*)} Q(g, X) \right\} \tag{9}$$

3. *Any pure-strategy Nash equilibrium is an* ***absorbing*** *state.*
4. *As* $t \to \infty$*, the network converges to one of the Nash networks with probability 1*

[24] A symmetric distribution such that $\rho_{ij}(X_i, X_j) > 0$ for any ij satisfies the assumption. An example is

$$\rho(X_i, X_j) \propto \frac{1}{n} \exp[-d(X_i, X_j)]$$

where $d(\cdot, \cdot)$ is a distance function.

Proof. In Appendix A ■

Suppose that the current network is a Nash network. As a consequence, if an agent deviates from the current linking strategy, he receives less utility. Since the change in utility for any agent is equivalent to the change in potential, any deviation from the Nash network must decrease the potential. It follows that the Nash network must be a local maximizer of the potential function over the set of networks that differ from the current network for at most one link.

Furthermore, the model will converge to one of the Nash Equilibria in the long run, independent of the initial network. Suppose an agent is drawn from the meeting process. Such agent will play a best response to the current network configuration, therefore his utility cannot decrease. This holds for any player and any period, thus the potential is nondecreasing over time. Since there is a finite number of possible networks, in the long run the sequence of networks will reach a local maximum of the potential, i.e. a Nash equilibrium.

With the intuition from the simpler model in mind, we can now analyze the full structural model with preference shocks. In the full model there is a high probability of hitting a Nash network. However, the shocks allow the network to escape from such networks: this makes the model ergodic and eliminates absorbing states.

I make a parametric assumption on the shocks that provides the characterization of the stationary distribution and the transition probabilities.[25]

ASSUMPTION 3 ***(Idiosyncratic Shocks)*** *The shock follows a Type I extreme value distribution, i.i.d. among links and across time*

The probability of a link between i and j, given a meeting $m^t = ij$ and previous period network configuration g^{t-1}

$$\begin{aligned}
\Pr\left(g_{ij}^t = 1 \middle| g_{-ij}^{t-1}, X\right) &= \Pr\left[\varepsilon_{ij}^t(0) - \varepsilon_{ij}^t(1) \leq U_i\left(1, g_{-ij}^{t-1}, X\right) - U_i\left(0, g_{-ij}^{t-1}, X\right)\right] \\
&= \frac{\exp\left[u_{ij} + g_{ji}^{t-1} m_{ij} + \sum_{k \neq i,j} g_{jk}^{t-1} v_{ik} + \sum_{k \neq i,j} g_{ki}^{t-1} v_{kj}\right]}{1 + \exp\left[u_{ij} + g_{ji}^{t-1} m_{ij} + \sum_{k \neq i,j} g_{jk}^{t-1} v_{ik} + \sum_{k \neq i,j} g_{ki}^{t-1} v_{kj}\right]} \qquad (10)
\end{aligned}$$

[25] An alternative assumption is that shocks follow a Gaussian distribution. The extreme value assumption implies a nice characterization of the stationary distribution and a simpler simulation and estimation strategy, which I need to overcome the computational complexity as explained in the empirical section.

Under assumptions 1-3, the network evolves as a Markov chain with transition probability given by the conditional choice probabilities (10) and the probability law of the meeting process m^t.

It can be shown that the sequence $[g^0, g^1, ..., g^t]$ is:

1. *irreducible*, i.e. every state of the network can be reached with positive probability in a finite number of steps

2. *aperiodic*, i.e. the chain does not get trapped in cycles, because the probability of moving from a state to another is always positive under the extreme value assumption

Intuitively, assuming $P(m^t = ij) > 0$ for any ij, implies that there is always a positive probability to reach a new network in which the link g_{ij} can be updated. The logistic assumption implies that there is always a positive probability of switching to another state of the network, thus eliminating absorbing states.

THEOREM 1 ***(Uniqueness and Characterization of Stationary Equilibrium)*** *Consider the network formation game with idiosyncratic shocks, under Assumptions 1-3.*

1. *There exists a unique stationary distribution $\pi(g, X)$ such that*

$$\lim_{t\to\infty} P\left(G^t = g \middle| G^0 = g^0, X\right) = \pi(g, X) \tag{11}$$

2. *Assume that the meeting probability of i and j does not depend on the existence of a link between them, i.e.*

$$\rho\left(g^{t-1}, X_i, X_j\right) = \rho\left(g^{t-1}_{-ij}, X_i, X_j\right) \tag{12}$$

Then the stationary distribution $\pi(g, X)$ is

$$\pi(g, X) = \frac{\exp\left[Q(g, X)\right]}{\sum_{\omega\in\mathcal{G}} \exp\left[Q(\omega, X)\right]} \tag{13}$$

where $Q(g, X)$ is the potential function (6).

Proof. In Appendix A ■

The first part of the proposition follows directly from the irreducibility and aperiodicity of the Markov process generated by the network formation game. The uniqueness of the stationary distribution is useful in estimation, since there is no concern about multiple equilibria. Furthermore, the stationary equilibrium characterizes the likelihood of observing a specific network configuration in the data. As a consequence, I can estimate the structural

parameters by observing only *one network at a specific point in time.*

The second part of the proposition provides a closed form solution for the stationary distribution. The intuition is straightforward: in the long run, the system of interacting agents will visit more often those states/networks that have high potential. Networks with high potential correspond to Nash equilibria described in Proposition 2. Therefore an high proportion of the possible networks generated by the network formation game, will correspond to the Nash networks.

The stationary distribution $\pi(g, X)$ includes a normalizing constant

$$c(\mathcal{G}, X) \equiv \sum_{\omega \in \mathcal{G}} \exp\left[Q(\omega, X)\right] \tag{14}$$

to guarantee that it is a proper probability distribution. However, the normalizing constant complicates the estimation, since it cannot be evaluated exactly or approximated with precision. This is explained in the estimation section.

3 Estimation Strategy

3.1 Computational Problem

To estimate the model I assume that the utility functions depend on a vector of parameters $\theta = (\theta_u, \theta_m, \theta_v)$:

$$\begin{aligned} u_{ij} &= u(X_i, X_j, \theta_u) \\ m_{ij} &= m(X_i, X_j, \theta_m) \\ v_{ij} &= v(X_i, X_j, \theta_v) \end{aligned}$$

The goal is to recover the parameters' posterior distribution, given the data and the prior. Let $p(\theta)$ be the prior distribution. Given the likelihood function $\pi(g, X, \theta)$ of the observed data (g, X), the posterior distribution of θ can be written as

$$p(\theta|g, X) = \frac{\pi(g, X, \theta)\, p(\theta)}{\int_\Theta \pi(g, X, \theta)\, p(\theta)\, d\theta} \tag{15}$$

The estimation of the posterior imposes two computational challenges. First, the posterior depends on the normalizing integral $\int_\Theta \pi(g, X, \theta)\, p(\theta)\, d\theta$. This problem is common to any Bayesian analysis, and it is usually solved using a Metropolis-Hastings algorithm that avoids direct computation of the integral. This algorithm generates a Markov chain of parameters whose unique invariant distribution is the posterior (15). The empirical distribution of the

chain is used as estimate of the posterior.

At each iteration t, with current parameter $\theta_t = \theta$, a new parameter vector θ' is proposed from a distribution $q_\theta(\cdot|\theta)$. At iteration $t+1$ the new parameter θ_{t+1} is updated according to

$$\theta_{t+1} = \begin{cases} \theta' & \text{with prob. } \alpha(\theta, \theta') \\ \theta & \text{with prob. } 1 - \alpha(\theta, \theta') \end{cases} \tag{16}$$

where $\alpha(\theta, \theta')$ is computed as

$$\alpha(\theta, \theta') = \min\left\{1, \frac{p(\theta'|g, X)\, q_\theta(\theta|\theta')}{p(\theta|g, X)\, q_\theta(\theta'|\theta)}\right\} \tag{17}$$

The appealing feature of this scheme is that in order to compute $\alpha(\theta, \theta')$ we don't need to evaluate the integral, since the ratio of the posteriors is $p(\theta'|g, X)/p(\theta|g, X) = \frac{\pi(g,X,\theta')p(\theta')}{\pi(g,X,\theta)p(\theta)}$.

However, the naive version of the Metropolis-Hastings algorithm cannot be used for this model. The likelihood function $\pi(g|X, \theta)$ is known up to a normalizing constant that is computationally infeasible. Rewrite the acceptance probability in (17) to make the likelihood contribution explicit

$$\begin{aligned} \alpha(\theta, \theta') &= \min\left\{1, \frac{\frac{\exp[Q(g,X,\theta')]}{c(\mathcal{G},X,\theta)} p(\theta')\, q_\theta(\theta|\theta')}{\frac{\exp[Q(g,X,\theta)]}{c(\mathcal{G},X,\theta')} p(\theta)\, q_\theta(\theta'|\theta)}\right\} \\ &= \min\left\{1, \frac{\exp[Q(g, X, \theta')]}{\exp[Q(g, X, \theta)]} \frac{c(\mathcal{G}, X, \theta)}{c(\mathcal{G}, X, \theta')} \frac{p(\theta')}{p(\theta)} \frac{q_\theta(\theta|\theta')}{q_\theta(\theta'|\theta)}\right\} \end{aligned}$$

The Metropolis-Hastings acceptance $\alpha(\theta, \theta')$ depends on the ratio $c(\mathcal{G}, X, \theta)/c(\mathcal{G}, X, \theta')$, whose exact evaluation is computationally infeasible even for very small networks. To be concrete, let me consider a small network with $n = 10$ agents. From (14) we know that $c(\mathcal{G}, X, \theta) = \sum_{\omega \in \mathcal{G}} \exp[Q(\omega, X, \theta)]$. In order to compute the constant at the current parameter θ we need to evaluate the exponential of the potential function for all $2^{90} \backsimeq 10^{27}$ possible networks with 10 agents and compute their sum. This task would take several years even for a state-of-the art supercomputer. In general with a network containing n players, we have to sum over $2^{n(n-1)}$ possible network configurations.[26]

[26] A supercomputer that can compute 10^{12} potential functions in 1 second would take almost 40 million years to compute the constant once for a network with $n = 10$. The schools used in the empirical section have between 20 and 181 enrolled students. This translates into a minimum of 2^{380} and a maximum of 2^{32580} possible network configurations.

3.2 Estimation Algorithm

To solve the estimation problem, I propose a variation of the *exchange algorithm*, first developed by Murray et al. (2006). This algorithm uses a double Metropolis-Hastings step to avoid the computation of the normalizing constant $c(\mathcal{G}, X, \theta)$ in the likelihood. This improvement comes with a cost: the algorithm may produce MCMC chains that have very poor mixing (Caimo and Friel, 2010) and high autocorrelation. I partially correct for this problem by choosing the proposal distribution in an adaptive way.

While several authors have proposed similar algorithms in the related literature on Exponential Random Graphs Models (ERGM),[27] the models estimated with this methodology have very few parameters and use data from very small networks. To the best of my knowledge I am the first to estimate an high dimensional model using data from multiple networks.

In this section I describe the algorithm for a single network, while in the appendix I provide the extension for multiple independent networks.[28]

The idea of the algorithm is to sample from an augmented distribution using an auxiliary variable. At each iteration, the algorithm proposes a new parameter vector θ', drawn from a suitable proposal distribution $q_\theta(\theta'|\theta)$; in the second step, it samples a network g' from the likelihood $\pi(g', X, \theta')$; finally, the proposed parameter is accepted with a probability $\alpha_{ex}(\theta, \theta')$, such that the Markov chain of parameters generated by these update rules, has the posterior (15) as unique invariant distribution.

I first describe the algorithm used to sample a network from the stationary distribution of the model; then I provide the full algorithm for estimation of the posterior.

3.2.1 Network Simulations

In order to use the exchange algorithm, I need to draw random samples from the stationary distribution of the network formation model. Direct simulation is not possible because the normalizing constant $c(\mathcal{G}, X, \theta)$ is computationally infeasible, as described above. Therefore I rely on Markov Chain Monte Carlo simulation methods.

The algorithm used in this paper is similar to the Metropolis-Hastings algorithm proposed

[27] Caimo and Friel (2010) use the exchange algorithm to estimate ERGM. They improve the mixing of the sampler using the snooker algorithm. Koskinen (2008) proposes the Linked Importance Sampler Auxiliary variable (LISA) algorithm, which uses importance sampling to provide an estimate of the acceptance probability. Another variation of the algorithm is used in Liang (2010).

[28] When the data consist of several independent school networks, I use a parallel version of the algorithm that stores each network in a different processor. Each processor runs the simulations independently and the final results are summarized in the master processor, that updates the parameters for next iteration. Details in Appendix.

in Snijders (2002). [29] For a fixed parameter value θ, the algorithm simulates a Markov chain of networks whose unique invariant distribution is (13). As the number of iterations R becomes large, the simulated networks are (approximate) samples from the stationary distribution of the model evaluated at parameter θ.

ALGORITHM 1 *Fix a parameter value θ. At iteration t, with current network $g_t = g$*

1. *Propose a network g' from a proposal distribution*

$$g' \sim q_g(g'|g) \tag{18}$$

2. *Update the network according to*

$$g_{t+1} = \begin{cases} g' & \text{with prob. } \alpha_{mh}(g, g') \\ g & \text{with prob. } 1 - \alpha_{mh}(g, g') \end{cases} \tag{19}$$

where

$$\alpha_{mh}(g, g') = \min\left\{1, \frac{\exp\left[Q(g', X, \theta)\right]}{\exp\left[Q(g, X, \theta)\right]} \frac{q_g(g|g')}{q_g(g'|g)}\right\} \tag{20}$$

At each iteration a random network g' is proposed, and the update is accepted with probability $\alpha_{mh}(g, g')$. The main advantage of this simulation strategy is that the acceptance ratio (20) does not contain the normalizing constant $c(\mathcal{G}, X, \theta)$ of the stationary distribution. Each quantity in the acceptance ratio can be computed exactly.

The Metropolis-Hastings structure of the algorithm guarantees that the network sampled are drawn from the stationary equilibrium of the model.

PROPOSITION 3 *The updates in ALGORITHM 1 produce a Markov Chain of networks that has the stationary equilibrium of the model at parameter θ as unique stationary distribution.*

Proof. In Appendix B ■

In the practical implementation of this algorithm, I use several moves and proposals. First, a move that updates only one link per iteration, proposing to swap the link value. At each iteration a random pair of agents (i, j) is selected from a discrete uniform distribution,

[29] I also experimented with the Simulated Tempering algorithm proposed in Mele (2010). The latter is extremely useful when the stationary distribution of the network formation model has more than one mode. Furthermore, it improves the mixing of the chain. However it does so by increasing the time needed to collect a sample. Since in this context there was virtually no difference between the Simulated Tempering results and the simpler Metropolis-Hastings updates in a set of experiments with artificial data, I use the latter in the rest of the paper.

and it is proposed to swap the value of the link g_{ij} to $1 - g_{ij}$. Second, to improve the convergence I allow the sampler to propose bigger moves: instead of proposing to swap only one link, it proposes to swap the entire network matrix.[30] With a small probability p_{inv}, the sampler proposes a new network $g' = \mathbf{1} - g$, which is accepted with probability $\alpha_{mh}(g, g')$.

The algorithm has a very useful property that can be exploited in the posterior simulation to reduce the computational burden. I state the property in the following Lemma. Adapting the suggestion in Liang (2010), define $\mathcal{P}_{\theta'}^{(R)}(g'|g)$ as the transition probability of a Markov chain that generates g' with R Metropolis-Hastings updates of the algorithm, starting at the observed network g and using the proposed parameter θ'.

$$\mathcal{P}_{\theta'}^{(R)}(g'|g) = \mathcal{P}_{\theta'}(g^1|g)\mathcal{P}_{\theta'}(g^2|g^1) \cdots \mathcal{P}_{\theta'}(g'|g^{R-1}) \tag{21}$$

where $\mathcal{P}_{\theta'}(g^j|g^i) = q_g(g^j|g^i)\alpha_{mh}(g^i, g^j)$ is the transition probability of the network simulation algorithm above. Since the Metropolis-Hastings algorithm satisfies the detailed balance condition (see the proof), we can prove the following

LEMMA 1 *Simulate a network g' from the stationary distribution $\pi(\cdot, X, \theta')$ using a Metropolis-Hastings algorithm starting at the network g observed in the data. Then*

$$\frac{\mathcal{P}_{\theta'}^{(R)}(g|g')}{\mathcal{P}_{\theta'}^{(R)}(g'|g)} = \frac{\exp\left[Q(g, X, \theta')\right]}{\exp\left[Q(g', X, \theta')\right]} \tag{22}$$

Proof. In appendix B ■

One should notice that as long as the algorithm is started from the network g observed in the data (which is assumed to be a draw from the stationary equilibrium of the model), the equality in (22) is satisfied for any R.

3.2.2 Posterior Simulation

I propose a modified version of the exchange algorithm developed by Murray et al. (2006) to sample from distributions with intractable constants. In the original algorithm one needs to draw *exact* samples from the stationary equilibrium of the model. However, this would require an enormous amount of steps using the network simulation algorithm.
My strategy is to exploit the result in Lemma 1 to decrease the number of simulations needed to collect an approximate sample from the stationary equilibrium. The samples from the posterior distribution are generated using the following steps

[30] This move is suggested in Geyer (1992) and Snijders (2002). Snijders (2002) argues that this is particularly useful in case of a bimodal distribution.

ALGORITHM 2 ***(FAST EXCHANGE ALGORITHM)***
Fix the number of simulations R. At each iteration t, with current parameter $\theta_t = \theta$ and network data g

1. *Propose a new parameter θ' from a distribution $q_\theta(\cdot|\theta)$*

$$\theta' \sim q_\theta(\cdot|\theta) \tag{23}$$

2. *Start* ***ALGORITHM 1*** *at the observed network g, iterating for R steps using parameter θ' and collect the last simulated network g'*

$$g' \sim \mathcal{P}_{\theta'}^{(R)}(g'|g) \tag{24}$$

3. *Update the parameter according to*

$$\theta_{t+1} = \begin{cases} \theta' & \text{with prob. } \alpha_{ex}(\theta, \theta') \\ \theta & \text{with prob. } 1 - \alpha_{ex}(\theta, \theta') \end{cases}$$

where

$$\alpha_{ex}(\theta, \theta') = \min\left\{1, \frac{\exp\left[Q(g', X, \theta)\right]}{\exp\left[Q(g, X, \theta)\right]} \frac{p(\theta')}{p(\theta)} \frac{q_\theta(\theta|\theta')}{q_\theta(\theta'|\theta)} \frac{\exp\left[Q(g, X, \theta')\right]}{\exp\left[Q(g', X, \theta')\right]}\right\} \tag{25}$$

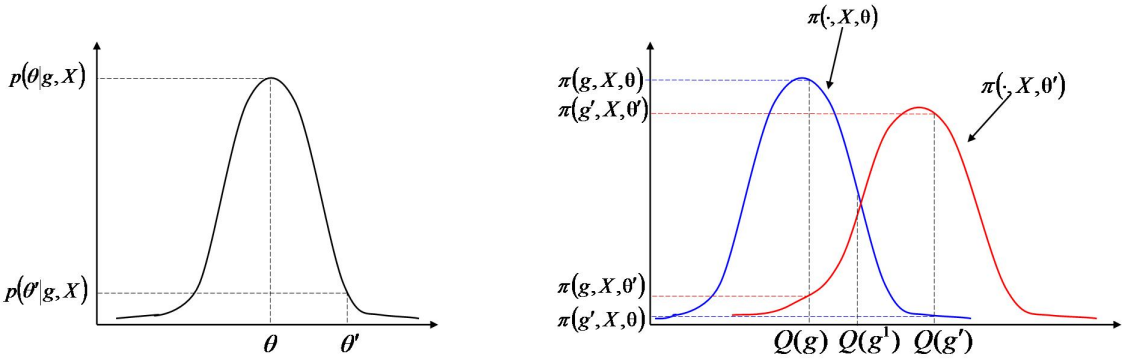
The appeal of this algorithm is that all the quantities in the acceptance ratio (34) can be evaluated: there are no integrals or normalizing constants to compute. I provide the algorithm details, and the relative proofs of convergence to the posterior and some evidence on mixing in Appendix B. The algorithm used to estimate the model using multiple school networks on parallel processors is an extension of ALGORITHM 2, therefore it is presented in Appendix B. Here I explain intuitively why the sampler works, with the help of Figure 2.

For ease of exposition, let me assume that the prior is flat, so that $p(\theta)/p(\theta') \simeq 1$. Suppose we start the sampler from a parameter θ that has high posterior probability, given the data g. That is, there is good agreement between the data and the parameter, so it is likely that the data are generated from a model with parameter θ. This is displayed on the left graph of Figure 2. Now, suppose we propose a parameter θ' that belongs to a low probability region of the posterior. This means that there is a low probability that the observed network g is generated by parameter θ'. As a consequence we would have that the ratio

$$\frac{p(\theta'|g, X)}{p(\theta|g, X)} \simeq \frac{\pi(g, X, \theta')}{\pi(g, X, \theta)}$$

is small, as indicated in the right graph of Figure 2. Let's start the network simulations using parameter θ'. The sequence of simulated networks will start approaching the new

Figure 2: The Exchange Algorithm



A. Posterior Distribution B. Two Stationary Equilibria

The graph on the left is the posterior distribution, given the data. The graph on the right represents two stationary equilibria of the model, one at parameter θ (blue) and one at parameter θ' (red). The iteration t starts with parameter θ. It is proposed to update the parameter using proposal θ'. The algorithm start sampling networks from the stationary distribution at parameter θ' (red) and quickly moves from g to g'. The probability of accepting the proposed parameter θ' is proportional to the ratio $\frac{\pi(g',X,\theta)}{\pi(g',X,\theta')}\frac{\pi(g,X,\theta')}{\pi(g,X,\theta)}$, which is small as indicated in the graph. In summary, a move from the high density region of the posterior (θ) to a low density region (θ') is likely to be rejected. For the same reasoning a move from θ' to θ is very likely to be accepted. Therefore the algorithm produces samples from the correct posterior distribution.

stationary distribution $\pi(\cdot, X, \theta')$, moving away from the stationary distribution $\pi(\cdot, X, \theta)$. This is indicated in Figure 2 with a simulation of 2 steps: starting from g we obtain two networks, g^1 and g'. The network g' is closer to a high probability region of $\pi(\cdot, X, \theta')$ than to a high probability region of $\pi(\cdot, X, \theta)$, providing that the algorithm was run for a sufficiently high number of steps R. It follows that also the ratio

$$\frac{\pi(g', X, \theta)}{\pi(g', X, \theta')}$$

is small. Notice that

$$\begin{aligned}\frac{\pi(g', X, \theta)}{\pi(g', X, \theta')}\frac{\pi(g, X, \theta')}{\pi(g, X, \theta)} &= \frac{\exp\left[Q(g', X, \theta)\right]}{\exp\left[Q(g, X, \theta)\right]}\frac{\exp\left[Q(g, X, \theta')\right]}{\exp\left[Q(g', X, \theta')\right]}\frac{c(\mathcal{G}, X, \theta')}{c(\mathcal{G}, X, \theta)}\frac{c(\mathcal{G}, X, \theta)}{c(\mathcal{G}, X, \theta')} \\ &= \frac{\exp\left[Q(g', X, \theta)\right]}{\exp\left[Q(g, X, \theta)\right]}\frac{\exp\left[Q(g, X, \theta')\right]}{\exp\left[Q(g', X, \theta')\right]}\end{aligned}$$

This ratio is contained in (34). As a consequence the acceptance ratio of the exchange algorithm is low and the proposed parameter θ' is very likely to be rejected. Let's repeat the

reasoning while starting the sampler at θ' and proposing an update θ: this proposal is very likely to be accepted for the same intuitive argument just explained.

In summary, the sampler is very likely to accept proposals that move towards high density regions of the posterior while it is very likely to reject proposals that move towards low density regions of the posterior. Therefore it produces samples of parameters that closely resemble the posterior distribution.

An important tuning parameter of the algorithm is R, the number of network simulations to be performed in the second step. Clearly, as $R \to \infty$ the algorithm converges to the original exchange algorithm of Murray et al. (2006), producing exact samples from the posterior distribution. While I do not propose an *optimal* way to choose R, in Appendix B I provide some evidence with simulated data showing that there is not much difference in the estimates or convergence using different length of simulations. The value of R has a stronger effect on the standard deviation than on the mean of the posterior, as it is expected.

3.3 Likelihood Function and Exponential Random Graphs

Scholars in statistics and sociology have recently devoted a lot of attention to the Exponential Random Graph models (ERGM).[31] The latter are statistical models of random network formation, with complex dependence structures among links. These models have been successfully used to fit real world social networks, providing a useful benchmark for alternative models.

A remarkable feature of my model is that it contains the ERGMs model as a special case. The ERGM's likelihood has the exponential family form (Lehman, 1983). Assume that the utility functions u, m and v depend *linearly* on a vector of parameters. Define $\theta_u = (\theta_{u1}, \theta_{u2}, ..., \theta_{uP})'$, $\theta_m = (\theta_{m1}, \theta_{m2}, ..., \theta_{mL})'$ and $\theta_v = (\theta_{v1}, \theta_{v2}, ..., \theta_{vS})'$. Define the function $H : \mathbb{R}^A \times \mathbb{R}^A \to \mathbb{R}$.

[31] Frank and Strauss (1986) developed the theory of Markov Random Graphs. These are random network formation models in which there is markovian dependence among links: the probability that a links occur depends on the existence of other links. See Snijders (2002) for a review of these models and the relative estimation techniques.

ASSUMPTION 4 ***(Linearity of Utility)*** *The utility functions are linear in parameters*

$$\begin{aligned} u_{ij} &= u\left(X_i, X_j, \theta_u\right) = \sum_{p=1}^{P} \theta_{up} H_{up}\left(X_i, X_j\right) = \theta_u' \mathbf{H}_u\left(X_i, X_j\right) \\ m_{ij} &= m\left(X_i, X_j, \theta_m\right) = \sum_{l=1}^{L} \theta_{ml} H_{ml}\left(X_i, X_j\right) = \theta_m' \mathbf{H}_m\left(X_i, X_j\right) \\ v_{ij} &= v\left(X_i, X_j, \theta_v\right) = \sum_{s=1}^{S} \theta_{vs} H_{vs}\left(X_i, X_j\right) = \theta_v' \mathbf{H}_v\left(X_i, X_j\right) \end{aligned}$$

This assumption leaves room for many interesting specifications. In particular the functions H do not rule out interactions among different characteristics, for example interactions of race and gender of both individuals. We can consider different specifications and include different sets of variables for the direct, mutual and indirect links.

PROPOSITION 4 ***(Exponential Family Likelihood)*** *Under assumptions 1-3, the stationary distribution $\pi\left(g, X\right)$ belongs to the* ***exponential family****, i.e. it can be written in the form*

$$\pi\left(g, X\right) = \frac{\exp\left[\theta' \mathbf{t}\left(g, X\right)\right]}{\sum_{\omega \in \mathcal{G}} \exp\left[\theta' \mathbf{t}\left(\omega, X\right)\right]} \tag{26}$$

where $\theta = \left(\theta_u, \theta_m, \theta_v\right)'$ is a (column) vector of parameters and $\mathbf{t}\left(g, X\right)$ is a (column) vector of canonical statistics

Proof. In Appendix A ■

The vector $\mathbf{t}\left(g, X\right) = \left(t_1\left(g, X\right), ..., t_K\left(g, X\right)\right)$ is a vector of statistics for the network formation model. This vector can contain the number of links, the number of whites-to-whites links, the number of male-to-female links and so on. Interactions of different variables are possible, e.g. the number of black-males-to-white-females links, or interactions of individual controls with school-level controls. Furthermore, the statistics are sufficient for the network.

This likelihood is very similar to the one of exponential random graph models. My model can be thought of as a microfoundation of the exponential random graph models. In this sense, we can interpret the ERGM as the stationary equilibrium of a strategic game of network formation with myopic agents following a stochastic best response dynamics, when utility are linear functions of the parameters.

The identification of parameters for the linear utility case follows from the theory of exponential family distributions (Lehman, 1983). Identification is guaranteed as long as the

sufficient statistics $t(g, X)$ are not linearly dependent. The nonlinear case is more complex and there are no general conditions that guarantee identification.[32] For this reason, I estimate the model in the linear case.

The Bayesian framework can help to achieve identification of the parameters in the nonlinear case, by using the prior distributions. This is common in the DSGE models estimation literature, where parameters are often ill-identified and prior distributions can be used to produce more precise estimates. This possibility is not explored here and it is left to future research.

The linear case also allows for specifications of the utility function involving network-level controls, when estimation is performed using multiple networks. This can be achieved by specifying parameters

$$\theta_p = \theta_{p0} + \sum_{c=1}^{C} \theta_{pc} Z_c \tag{27}$$

where Z_c is a network-level variable. This specification allow network fixed effects and interactions of network controls with individual controls. The estimation methodology presented above can be applied to this specification without any change. However, the estimation of a model with random coefficients would require some additional computational cost.

3.4 Practical Implementation

As noted above, it is possible to modify the precision of the estimates when there is some previous information that can be incorporated in the prior. I choose somewhat vague priors for the parameters, in order to get most of the information from the data. One could think of the estimates as conservative. I assume independent normal priors

$$p(\theta) = \mathcal{N}(\mathbf{0}, 3\mathbf{I}_P) \tag{28}$$

where P is the number of parameters.

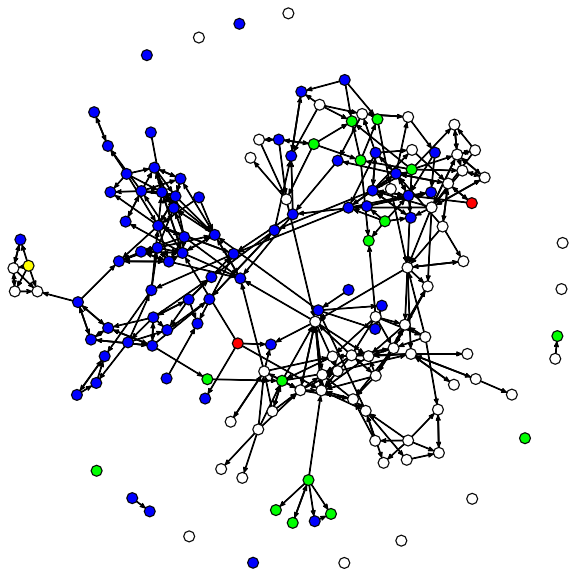
The proposal distribution for the posterior simulation is

$$q_\theta(\cdot|\theta) = \mathcal{N}(\mathbf{0}, \delta\mathbf{\Sigma}) \tag{29}$$

where δ is a scaling factor and $\mathbf{\Sigma}$ is a covariance matrix. I use an adaptive procedure to determine a suitable $\mathbf{\Sigma}$. I start the iterations with $\mathbf{\Sigma} = \lambda\mathbf{I}_P$, where λ is a vector of standard deviations. I choose λ so that the sampler accepts at least $20\% - 25\%$ of the proposed

[32] Geyer (1992) provides some guidance in this matter. He shows conditions that guarantee the convergence of the Monte Carlo Maximum Likelihood estimate to the exact MLE. However, to the best of my knowledge there are no sufficient conditions that guarantee identification in this setting.

Figure 3: A School Network



white=Whites; blue = African Americans; yellow = Asians; green = Hispanics; red = Others

Note: The graphs represent the friendship network of a school extracted from AddHealth. Each dot represents a student, each arrow is a friend nomination. The colors represent racial groups.

parameters, as standard in the literature (Gelman et al., 2003; Robert and Casella, 2005). I run the chain and monitor convergence using standard methods. Once the chains have reached approximate convergence, I estimate the covariance matrix of the chains and use it as an approximate $\mathbf{\Sigma}$. The scaling factor is $\delta = 2.38/\sqrt{(P)}$ as suggested in Gelman et al. (1996).

The network sampler uses a proposal $q_g\left(g|g'\right)$ which selects a link to be updated at each period according to a discrete uniform distribution. The probability of network inversion is $p_{inv} = 0.01$.

The posterior distributions shown in the graphs are obtained with a simulation of 50000 Metropolis-Hastings updates of the parameters. These simulations start from values found after long experimentation with different starting values and burn-in periods, monitoring

convergence using standard methods. For each parameter update, I simulate the network for 3000 iterations to collect a sample from the stationary distribution.

3.5 The Add Health Data

The *National Longitudinal Study of Adolescent Health* (Add Health) is a dataset containing information on a nationally representative sample of US schools. The survey started in 1994, when the 90118 participants were entering grades 7-12, and the project collected data in four successive waves.[33] Each student responded to an *in-school* questionnaire, and a subsample of 20745 was given an *in-home* interview to collect more detailed information about behaviors, characteristics and health status. In this paper I use only data from the *saturated sample* of Wave I, containing information on 16 schools. Each student in this sample completed both the in-school and in-home questionnaires. I exclude the two largest schools, 58 and 77: they have respectively 811 and 1664 students, while the third largest school has 159 students. To keep the sample as homogeneous as possible I prefer to not use these schools. My final sample includes 1139 students in 14 schools.

The *in-school* questionnaire collects the social network of each participant. Each student was given a school roster and was asked to identify up to five male and five female friends.[34] I use the friendship nominations as proxy for the social network in a school. The resulting network is *directed*: Paul may nominate Jim but this does not necessarily implies that Jim nominates Paul.[35] The model developed in this paper takes this feature of the data into account.

A sub-sample of 20745 students was also given an *in-home* questionnaire, that collected most of the sensible data. I use data on racial group, grade and gender of individuals. A student with a missing value in any of these variables is dropped from the sample. Each students that declares to be of Hispanic origin is considered Hispanic. The remaining non-Hispanic students are assigned to the racial group they declared. Therefore the racial categories are: White, Black, Asian, Hispanic and Other race. Other race contains Native Americans.

Descriptive statistics are in Table 1. The smallest school has 20 enrolled students while the largest used in estimation has 159 students. There is a certain amount of variation in the number of links: some schools are more "social" and form many links per capita, while

[33] More details about the sampling design and the representativeness are contained in Moody (2002) and the Add Health website http://www.cpc.unc.edu/projects/addhealth/projects/addhealth

[34] One can think that this limit could bias the friendship data, but only 3% of the students nominated 10 friends (Moody (2002).

[35] Some authors do not take into account this feature of the data and they recode the friendships as mutual: if a student nominates another one, the opposite nomination is also assumed. Echenique and Fryer (200?)

Table 1: **Descriptive Statistics for the schools in the Saturated Sample**

School	1	2	3	7	8	28	58	77	81	88	106	115	126	175	194	369
Students	44	60	117	159	110	150	811	1664	98	90	81	20	53	52	43	52
Links	12	120	125	344	239	355	3290	3604	163	308	162	44	123	171	42	48
Females	0.5	0.517	0.419	0.44	0.5	0.587	0.473	0.483	0.531	0.522	0.531	0.55	0.491	0.538	0.512	0.654
A. Racial Composition																
Whites	0.5	0.95	0.983	0.981	0.973	0.42	0.978	0.055	0.98	0.989	0	1	0.472	0.769	0.977	0.942
Blacks	0.136	0	0	0.006	0.018	0.453	0.002	0.233	0	0	0.963	0	0.151	0.019	0	0
Asians	0	0	0	0	0.009	0.007	0.005	0.299	0.01	0	0	0	0.038	0.038	0	0
Hispanics	0.364	0.05	0.017	0.006	0	0.107	0.011	0.392	0.01	0	0.025	0	0.302	0.154	0.023	0.058
Others	0	0	0	0	0	0.013	0.004	0.02	0	0.011	0	0	0.038	0.019	0	0
Racial Fragm	0.599	0.095	0.034	0.037	0.053	0.606	0.044	0.699	0.04	0.022	0.072	0	0.661	0.382	0.045	0.109
B. Grade Composition																
7th Grade	0.159	0.2	0.128	0.145	0.227	0.173	0.002	0.001	0.112	0.144	0.506	0.4	0.491	0.462	0.488	0.538
8th Grade	0.159	0.217	0.154	0.157	0.2	0.173	0.004	0.003	0.153	0.178	0.481	0.6	0.472	0.538	0.488	0.462
9th Grade	0.114	0.2	0.12	0.214	0.136	0.2	0.289	0.004	0.153	0.122	0.012	0	0.038	0	0	0
10th Grade	0.273	0.133	0.205	0.157	0.182	0.167	0.277	0.346	0.214	0.167	0	0	0	0	0	0
11th Grade	0.136	0.167	0.179	0.164	0.118	0.14	0.223	0.345	0.265	0.211	0	0	0	0	0.023	0
12th Grade	0.159	0.083	0.214	0.164	0.136	0.147	0.205	0.301	0.102	0.178	0	0	0	0	0	0
C. Segregation																
Segr Whites	0	0	0	0	0	0.720	0.005	0.266	0	0	-	-	0.573	0.115	0	0
Segr Blacks	0	-	-	0	0	0.764	0	0.790	-	-	0	-	0.179	0	-	-
Segr Asian	-	-	-	-	0	0	0	0.744	0	-	-	-	0	0	-	-
Segr Hisp	0	0	0	0	-	0.429	0	0.691	-	-	0	-	0.227	0.025	0	0
Segr Other	-	-	-	-	-	0	0	0.026	-	0	-	-	0	0	-	-
Seg Gender	0.250	0.100	0.140	0.341	0.069	0.255	0.221	0.287	0.264	0.176	0.258	0.168	0.129	0.122	0.262	0.156

other schools have very few friendship nominations. The ratio of boys to girls is balanced in almost all schools, excluding school 369: here female students are large majority.

Panel A summarizes the racial composition. Most school are extremely racially homogeneous. School 1, 28, 126 and 175 are more diverse as reflected in the Racial Fragmentation index. This is an index that measure the degree of heterogeneity of a population. It is interpreted as the probability that two randomly chosen students in the school belong to different racial groups.[36] An index of 0 indicates that there is only one racial group and the population is perfectly homogeneous. Higher values of the index represents increasing levels of racial heterogeneity. Panel B summarizes the Grade composition. Most school offer all the grades from 7th to 12th, with homogeneous population across grades. Several schools offer only lower grades.

Panel C analyzes the racial and gender segregation of each school friendship network. The level of segregation is measured with the Freeman (1972) segregation index. If there is no segregation, the number of links among individuals of different groups does not depend on the group identity. The index measures the difference between the expected and actual number of links among individuals of different groups. An index of 0 means that the actual network closely resembles one in which links are formed at random. Higher values indicate more segregation. The index varies between 0 and 1, where the maximum corresponds to a network in which there are no cross-group links.

Since most schools are racially homogeneous, the measured segregation is zero. Schools with a racially diverse student population show high level of segregation for each racial group. On the other hand gender segregation is quite low and homogeneous across schools.

4 Empirical Results

4.1 Parameter Estimates

4.1.1 One school network

An important feature of the model is that it allows estimation using only one network observation. In this section, I estimate the model using data from school 28 of Add Health. The school has 150 enrolled students and 58.7% girls, with a total of 355 friend nominations. The

[36] If there are K racial groups and the share of each race is s_k, the index is

$$FRAG = 1 - \sum_{k=1}^{K} (s_k)^2 \tag{30}$$

clustering coefficient is 0.2906 and the racial fragmentation is 0.606. The racial composition is as follows: 42% whites, 45.3% blacks, 0.667% asians, 10.6% hispanics. Figure 3 shows the network of friendship nomination: each dot corresponds to a student, the color represents his racial group and an arrow is a friend nomination.

The results for three alternative specifications of the model are presented in Table 2.

Table 2: Three Specifications, School 28

	Model 1		Model 2		Model 3	
	mean	s.d.	mean	s.d.	mean	s.d.
Direct utility (u_{ij})						
constant	-4.6448	0.4555	-4.1779	0.5330	-4.5947	0.6502
same gender					0.2199	0.4942
same grade					0.7720	0.5558
white-white	1.3013	0.4812	0.4012	0.7681	0.4624	0.8419
black-black	1.4942	0.4463	0.7709	0.7670	0.7132	0.7985
hispanic-hispanic	0.7628	1.1791	0.8504	1.4012	1.5408	1.1437
Mutual utility (m_{ij})						
constant	3.5171	0.5036	2.8197	1.0779	0.9503	1.3547
same gender					1.5864	1.0896
same grade					0.0060	1.0120
white-white			0.4614	1.2300	0.3804	1.1925
black-black			0.7945	1.2114	0.7624	1.1534
hispanic-hispanic			-0.2865	1.9812	0.3745	1.7842
Indirect utility (v_{ij})						
constant	-0.0745	0.0596	-0.2629	0.1353	-0.3628	0.1849
same gender					-0.0152	0.1835
same grade					0.3559	0.1665
white-white			0.3249	0.1879	0.3354	0.2027
black-black			0.2426	0.1825	0.2761	0.1767
hispanic-hispanic			-0.0404	0.7695	-0.3136	0.9793

Posterior mean and standard deviation for three alternative specifications of the model. The estimates are obtained with a sample of 50000 simulations for the parameters, and 3000 network simulations for each parameter proposal.

I report the posterior mean and standard deviation. Each estimate measures the marginal effect of the variable: for example, the parameter associated with the direct utility of *white-white* measures the marginal utility of a white individual forming a link to another white, other things being equal.

The first column contains posterior mean and standard deviation of a specification in

which the direct utility is a function of total number of links (constant), total number of links in which both are Whites, Blacks or Hispanic. This specification tests for the presence of differential homophily: each racial group may have different homophily levels. A positive coefficient for the variable white-white would indicate that white students have a bias towards same race friends. The remaining controls are for the number of reciprocated links (mutual constant) and for the number of indirect friends (friends of friends).
These results points to strong racial homophily effects for each racial group. Each additional link is costly as indicated by the negative coefficient of the constant. However, an additional link is more valuable if the pair belongs to the same racial group: all the homophily coefficients are positive. A mutual link increases utility as expected, while linking to an individual with many friends decreases it. The latter effect can be due to congestion: an individual with many links has less time to devote to each of his friends.[37]

Model 2 includes controls for the racial composition of mutual friends and friends of friends. This model confirms the existence of homophily in direct links, but also in mutual and indirect links. The only exception is for links that involve hispanics: mutual and indirect links decrease utility.

Model 3 includes controls for homophily in gender and grade. In this dataset more than 50% of all friendships are within the same grade. At the same time, it is known that gender differences are an important explanatory variable of interaction, especially among adolescents. The estimates show that there are homophily effects for both grade and gender.

4.1.2 Multiple networks

The algorithm and the estimation methodology are easily extended to the case with multiple independent networks. In this section, I report results from an estimation performed using data from all the 14 schools in my sample. In the first column of Table 3 I report the results for school 28 as a useful comparison. Not surprisingly the standard deviation of the marginal posteriors are smaller by several magnitudes when compared to the estimation with only one network. In Column 2 there is evidence of racial homophily in the direct links. Other things being equal the student prefer form links to student of the same gender, grade and race. The racial homophily is not present for blacks.

Data from multiple schools allow the inclusion of school level variables, that may help in identifying the homophily effects. In the third column I show results where the homophily

[37] At the same time one should notice that the homophily effect for Hispanics is estimated with higher variability: this is because there are very few Hispanics in the dataset, and they form few links. A partial solution is to run more simulations. Alternatively one could estimate a model with multiple schools and exploit the variability among schools as a source of identification.

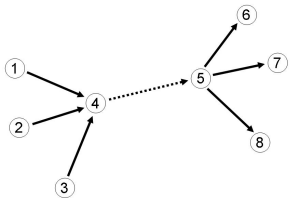
Table 3: Estimation results, full sample

	School 28		Full Sample		Full Sample	
	mean	s.d.	mean	s.d.	mean	s.d.
Direct utility (u_{ij})						
constant	-4.5947	0.6502	-5.0269	0.1701	-4.9742	0.1842
same gender	0.2199	0.4942	0.1475	0.1069	0.1644	0.1065
same grade	0.7720	0.5558	1.9400	0.1364	1.9745	0.1165
white-white	0.4624	0.8419	0.3268	0.1561	0.5575	0.2017
black-black	0.7132	0.7985	0.0039	0.2485	-0.2858	0.2101
hispanic-hispanic	1.5408	1.1437	0.5230	0.4267	0.6662	0.3216
white-white * whites					-0.4289	0.1316
black-black * blacks					2.0846	0.3656
hisp-hisp * hisp					-1.0826	0.8320
Mutual utility (m_{ij})						
constant	0.9503	1.3547	2.9716	0.3910	2.8194	0.3756
same gender	1.5864	1.0896	1.1868	0.2479	1.1686	0.2430
same grade	0.0060	1.0120	-1.6454	0.2791	-1.7988	0.2230
white-white	0.3804	1.1925	0.2342	0.3230	0.5027	0.3257
black-black	0.7624	1.1534	0.4118	0.4275	0.6010	0.3428
hispanic-hispanic	0.3745	1.7842	-0.4523	0.8312	-0.3575	0.2487
Indirect utility (v_{ij})						
constant	-0.3628	0.1849	0.0263	0.0388	0.0141	0.0424
same gender	-0.0152	0.1835	-0.1223	0.0481	-0.1335	0.0470
same grade	0.3559	0.1665	0.0839	0.0281	0.0890	0.0273
white-white	0.3354	0.2027	0.0290	0.0314	0.0433	0.0339
black-black	0.2761	0.1767	-0.0206	0.0459	0.0010	0.0434
hispanic-hispanic	-0.3136	0.9793	0.1104	0.1712	0.1424	0.1565

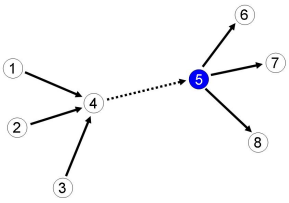
effects are interacted with the proportions of each racial group in the school. White students receive lower utility from same race friends as the white student body increases. Viceversa, African American students value friends of the same racial group more when the proportion of blacks in the school increases. Hispanic preferences seem to reflect the same pattern of whites.

It is important to highlight that the estimated marginal utilities for direct links are obtained controlling for the structure of the network. The homophily effects are therefore net of the network structure. Homophily effects are present in the mutual and indirect links. The interpretation of these estimates is not as simple as with the direct utility. Therefore I present several examples in Figure 4. In Panel A a network with 8 students is shown. The students are assumed to be all whites, male and enrolled in the same grade. Agent 4 has

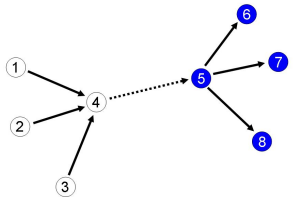
Figure 4: Change in the probability of forming a link



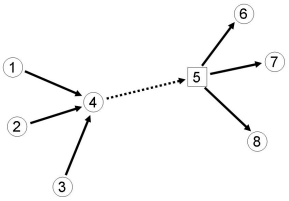
A. Baseline



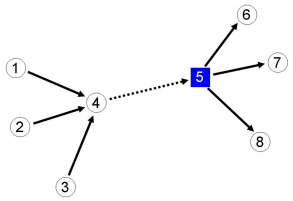
B. Agent 5 is black
Direct effect: −11.4%
Total effect: −21.5%



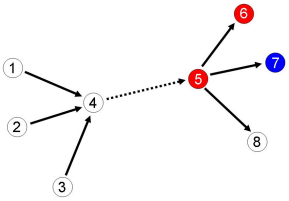
C. Agents 5, 6, 7 and 8 are black
Direct effect: −11.4%
Total Effect: −30.7%



D. Agent 5 is female
Direct effect: −14.3%
Total effect: 24.5%



E. Agent 5 is black female
Direct effect: −24.2%
Total Effect: −2.1%



F. Agent 5 has diverse friends
Direct effect: −11.4%
Total effect: −27.7%

The network contains $n = 8$ agents. In each panel agent 4 is deciding whether to create a link to agent 5. Panel A is the baseline situation, where all the students are white. For simplicity assume they are all males enrolled in the same grade. The remaining panels show the change in the probability that the link is formed, when the structure of the network is altered. The direct effect is the change in probability (with respect to Panel A) arising only because of the change in the direct utility. The total effect is the change in the probability of linking when considering all the components of the utility function. In Panel B, agent 5 is black: if we consider only the effect on the direct utility the probability of a link among 4 and 5 goes down by 11%. When we consider the full utility of agent 4, the probability of the link decrease by almost twice as much. Similar results hold for the remaining panels.

to choose whether to form a new link to agent 5. To make exposition simple, let's assume that the utility is evaluated at the posterior mean. The probability that Agent 4 forms the

link is 0.067, according to the estimate in column 3 of Table 3. Considering only the direct utility, this probability would be a little lower, 0.062. In Panel B agent 5 is now African American. If we were to consider only the direct effect of this change the probability of the link would drop by 11.4%. When we consider the effect of the network structure (effect on the popularity and friends of friends), this change implies a decline in the probability of that link of 21.5%. The remaining graphs are variations of this simple example and all the percentage changes are measured with respect to the baseline network in Panel A. The most intriguing result is in Panels D and E. In Panel D, agent 5 is female. When considering only the direct effect, this would imply a decrease in utility and therefore in the probability of linking. However, the indirect and popularity effects counterbalance the decrease in direct utility, implying an increase in the linking probability. A similar mechanism is in place in Panel E.

4.2 Policy Experiments

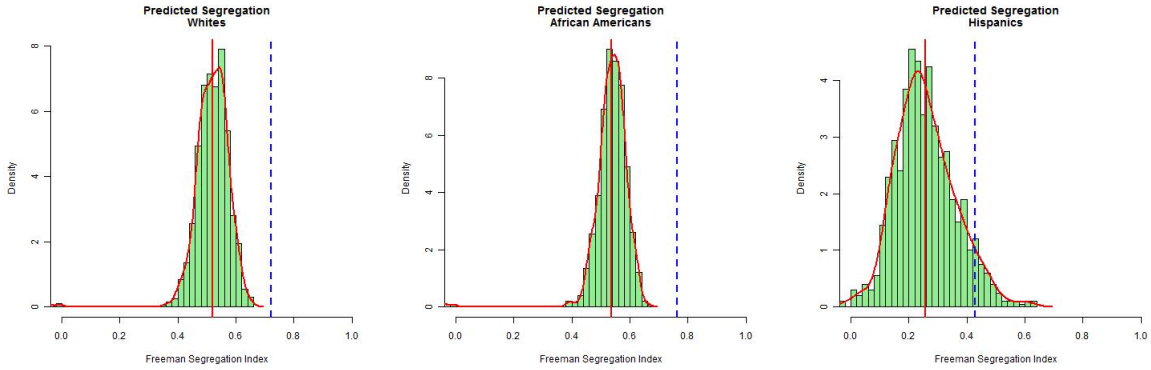
The estimated model can be used to predict how alternative policies affect the structure of the network. Policy makers may be interested in pursuing policies that may promote racial integration, or they may consider policies that create separate schools for boys and girls. My model can provide some guidance in this matter.

For example one could be interested in evaluating the effectiveness of busing programs in promoting interracial integration. School 28 has an extremely segregated friendship network: if the school administration starts a busing program that modifies the composition of the school, does segregation increase or decrease?

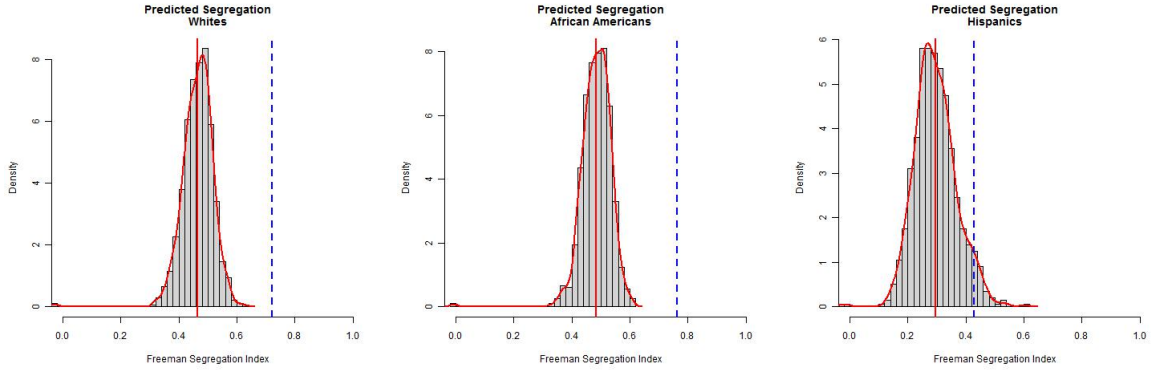
Using the posterior distribution estimated in column 3 of Table 2, I simulate two policies. The first policy increases the African American enrollment by transferring 8 African-American students from a random school to school 28. The second is a reassignment of 16 Hispanic students from the same random school to school 28. In both cases, I compute the segregation levels in the stationary equilibrium before and after the implementation of the policy. I use the Freeman's Segregation Index (see Freeman (1972)) to measure segregation for the three relevant groups: Whites, African-Americans and Hispanics.

The results are reported in Figure 5. Panel A shows the segregation level without policy (blue) and the distribution after the implementation of the policy (red) when we reassign 8 African-Americans to school 28. For all the racial groups the expected segregation goes down. The probability of an increase in racial segregation is null for Whites and African Americans and it is minimal for Hispanics (0.06). Panel B shows that the second policy has

Figure 5: Policy Experiments



Panel A. Busing program transporting 8 African American students to School 28.



Panel B. Busing program transporting 16 Hispanic students to School 28.

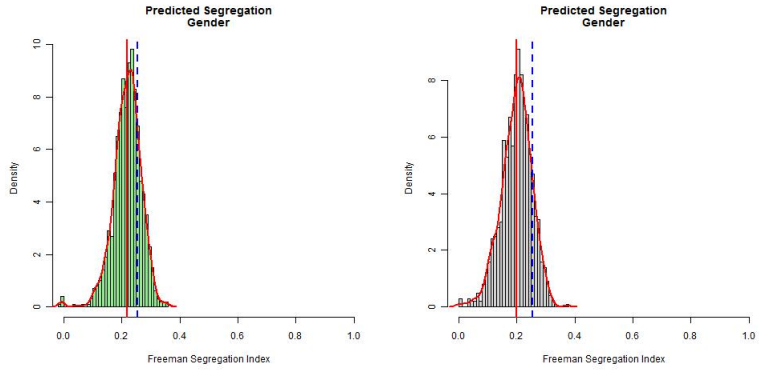
The graphs show the distribution and average of Freeman's Segregation Index for the 3 racial groups after the policy is implemented (red solid) and the segregation before the policy (blue dashed). The graphs also show the histogram of the simulated segregation and a kernel smoothed density. The graphs in Panel A row shows a reassignment of 8 African-American students to school 28. The graphs in Panel B refer to a policy that reassigns 16 Hispanic students to school 28.

similar results. Furthermore in Figure 6, I analyze the effects of the policies on gender segregation. The policy is successful in decreasing both racial and gender expected segregation. The probability of an increase in gender segregation is 0.213 and 0.131 for the two policies respectively.

The previous examples would lead to the conclusion that policies that modify the racial composition within schools reduce segregation in the social network of friendship. However, this is not always the case.

I simulate several swaps of students among school 88 and 106. These are two schools with an homogeneous student population: 98.9% whites and 96.3% African American re-

Figure 6: Policy Experiments



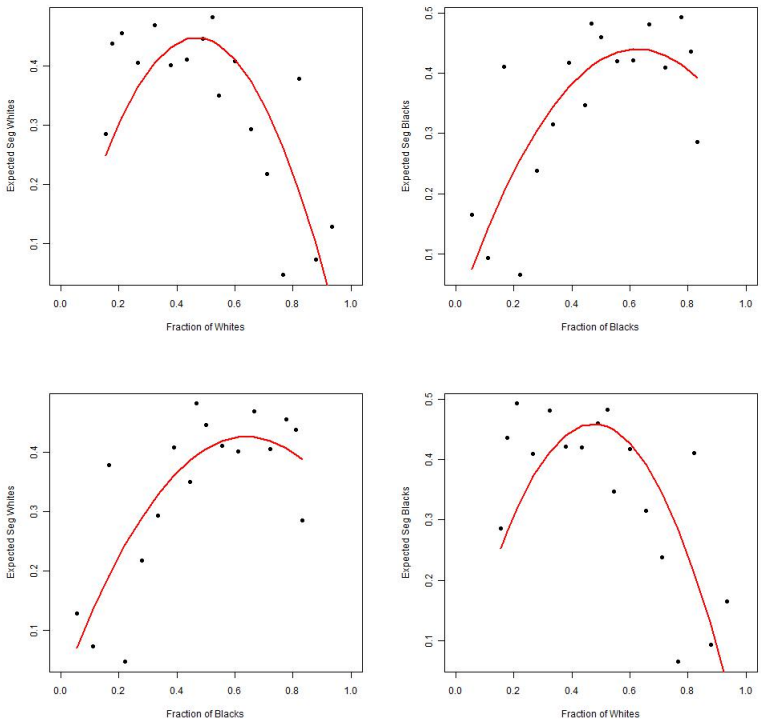
Panel A. Policy 1 Panel B. Policy 2

The graphs show the distribution and average of Freeman's Segregation Index for the gender segregation after the policy is implemented (red solid) and the segregation before the policy (blue dashed). The graphs also show the histogram of the simulated segregation and a kernel smoothed density. The graphs in Panel A row shows a reassignment of 8 African-American students to school 28. The graphs in Panel B refer to a policy that reassigns 16 Hispanic students to school 28.

spectively. The simulated policies take several (white) students from school 88 and enroll them in school 106, while the same number of (black) students in school 106 are enrolled in school 88. This allows me to modify the ratio of Whites and African Americans in the two schools and predict the level of segregation in the two schools.

The results of these simulations are in Figure 7. There is evidence of an inverted U-shaped relationship between fraction of a racial group and the expected segregation levels. The graph suggests that the implementation of a policy that modifies the fraction of whites from .9 to .8 will increase segregation on average by .2. The main lesson from this graph is that equalizing the racial shares between the two schools is a really bad idea if integration is one of the policymaker's goals. An alternative concern for the busing programs is that a recent decision of the Supreme Court declared unconstitutional the use of race to determine the assignment of children to schools. Therefore, school district administrators that want to promote racial integration have to find alternative ways to assign students to schools. For example, one may be tempted to create one gender schools. Table 4 presents the results from such a policy using school 28. I create two schools, one only with the male students and one only with female students. The results are clear: the expected racial segregation decreases in both schools. This could provide an alternative to the busing programs based on race.

Figure 7: Policy Experiments, School 88



The graphs shows the results of policy experiments in which students are swapped between school 88 and school 106. The expected segregation in the stationary equilibrium after the policy is plotted against the fraction of each racial group. Each dot represents a different simulated policy. The red solid line is the fitted value of a regression where the expected segregation is a function of fraction of the racial group and fraction of the racial group squared.

Table 4: Same gender schools, school 28

	Current	Female	Male
White	0.7202	0.2768	0.3507
African Americans	0.7636	0.2791	0.3752
Hispanic	0.4288	0.0970	0.2221

5 Conclusions

This paper has developed a dynamic model of strategic network formation with heterogeneous agents that allows estimation of the structural parameters using only one observation of the network at a single point in time. The characterization of the unique stationary equi-

librium of the model provides the likelihood of observing a specific network structure in the data. I propose a Bayesian Markov Chain Monte Carlo method that reduces the computational complexity of the estimation and allows inference in high dimensional models.

The model can be used to infer the effect of alternative policies on the network structure. As an example I provide an application to the study of desegregation policies in US schools. The model provides prediction on the expected levels of segregation implied by busing programs: there is an inverted U-shape relationship between the share of a racial group in the school and the expected segregation level. These results suggest that these policies should be carefully designed in order to avoid unexpected outcomes. The model presented here can be used as a guidance in the design of such programs.

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A Proofs

Proof of Proposition 1

The potential is a function Q from the space of actions to the real line such that $Q\left(g_{ij}, g_{-ij}, X\right) - Q\left(g'_{ij}, g_{-ij}, X\right) = U_i\left(g_{ij}, g_{-ij}, X\right) - U_i\left(g'_{ij}, g_{-ij}, X\right)$, for any ij.[38] A back-of-the-envelope computation shows that, for any ij

$$\begin{aligned} Q\left(g_{ij}=1, g_{-ij}, X\right) - Q\left(g_{ij}=0, g_{-ij}, X\right) &= u_{ij} + g_{ji}m_{ij} + \sum_{\substack{k=1 \\ k\neq i,j}}^{n} g_{jk}v_{ik} + \sum_{\substack{k=1 \\ k\neq i,j}}^{n} g_{ki}v_{kj} \\ &= U_i\left(g_{ij}=1, g_{-ij}, X\right) - U_i\left(g_{ij}=0, g_{-ij}, X\right) \end{aligned}$$

therefore Q is the potential of the network formation game.

Incidentally, the welfare function is computed as

$$\begin{aligned} W\left(g, X\right) &= \sum_{i=1}^{n} U_i\left(g, X\right) \\ &= \sum_{i=1}^{n}\sum_{j=1}^{n} g_{ij}u_{ij} + \sum_{i=1}^{n}\sum_{j=1}^{n} g_{ij}g_{ji}m_{ij} + \sum_{i=1}^{n}\sum_{j=1}^{n}\sum_{\substack{k=1 \\ k\neq i,j}}^{n} g_{ij}g_{jk}v_{ik} + \sum_{i=1}^{n}\sum_{j=1}^{n}\sum_{\substack{k=1 \\ k\neq i,j}}^{n} g_{ij}g_{ki}v_{kj} \\ &= \sum_{i=1}^{n}\sum_{j=1}^{n} g_{ij}u_{ij} + 2\sum_{i=1}^{n}\sum_{j>i}^{n} g_{ij}g_{ji}m_{ij} + \sum_{i=1}^{n}\sum_{j=1}^{n}\sum_{\substack{k=1 \\ k\neq i,j}}^{n} g_{ij}g_{jk}v_{ik} + \sum_{i=1}^{n}\sum_{j=1}^{n}\sum_{\substack{k=1 \\ k\neq i,j}}^{n} g_{ij}g_{ki}v_{kj} \\ &= Q\left(g, X\right) + \sum_{i=1}^{n}\sum_{j>i}^{n} g_{ij}g_{ji}m_{ij} + \sum_{i=1}^{n}\sum_{j=1}^{n}\sum_{\substack{k=1 \\ k\neq i,j}}^{n} g_{ij}g_{ki}v_{kj} \end{aligned}$$

Proof of Proposition 2

1) This follows directly from the fact that the network formation game is a potential game

[38] For more details and definitions see Monderer and Shapley (1996).

with finite strategy space. (see Monderer and Shapley (1996) for details)
2) The set of Nash equilibria is defined as the set of g^* such that, for every i and for every $g_{ij} \neq g^*_{ij}$

$$U_i\left(g^*_{ij}, g^*_{-ij}, X\right) \geq U_i\left(g_{ij}, g^*_{-ij}, X\right)$$

Therefore, since Q is a potential function, for every $g_{ij} \neq g^*_{ij}$

$$Q\left(g^*_{ij}, g^*_{-ij}, X\right) \geq Q\left(g_{ij}, g^*_{-ij}, X\right)$$

Therefore g^* is a maximizer of Q. The converse is easily checked using the opposite reasoning.
3) Suppose $g^t = g^*$. Since this is a Nash equilibrium, no player will be willing to change her linking decision when her turn to play comes. Therefore, once the chain reaches a Nash equilibrium, it will not escape from that state.
4) The probability that the potential will increase from t to $t+1$ is

$$Pr\left[Q\left(g^{t+1}, X\right) \geq Q\left(g^t, X\right)\right] =$$

$$= \sum_i \sum_j Pr\left(m^{t+1} = ij\right) \underbrace{Pr\left[U_i\left(g^{t+1}_{ij}, g^t_{-ij}, X\right) \geq U_i\left(g^t_{ij}, g^t_{-ij}, X\right) \middle| m^{t+1} = ij\right]}_{=1 \text{ because agents play Best Response, conditioning on } m^{t+1}}$$

$$= \sum_i \sum_j \rho_{ij} = 1$$

By part 3) of the proposition, a Nash network is an absorbing state of the chain. Therefore any probability distribution that puts probability 1 on a Nash network is a stationary distribution. For any initial network, the chain will converge to one of the stationary distributions. It follows that in the long run the model will be in a Nash network, i.e. for any $g^0 \in \mathcal{G}$

$$\lim_{t \to \infty} Pr\left[g^t \in NE \middle| g^0\right] = 1$$

Proof of Theorem 1
1. The sequence of networks $[g^0, g^1, ...]$ generated by the network formation game is a markov chain. Inspection of the transition probability proves that the chain is irreducible and aperiodic, therefore it is ergodic. The result then follows form the ergodic theorem.
2. A sufficient condition for stationarity is the *detailed balance*. In our case this means to prove

$$P_{gg'}\pi_g = P_{g'g}\pi_{g'} \tag{31}$$

where

$$\begin{aligned} P_{gg'} &= \Pr\left(g^{t+1} = g' \middle| g^t = g\right) \\ \pi_g &= \pi\left(g^t = g\right) \end{aligned}$$

Notice that the transition from g to g' is possible if these networks differ by only one element g_{ij}. Otherwise the transition probability is zero and the detailed balance condition is satisfied. Let's consider the nonzero probability transitions, with $g = (1, g_{-ij})$ and $g' = (0, g_{-ij})$. Define $\Delta Q \equiv Q(1, g_{-ij}, X) - Q(0, g_{-ij}, X)$.

$$\begin{aligned} P_{gg'}\pi_g &= \Pr\left(m^t = ij\right) Pr\left(g_{ij} = 0 \middle| g_{-ij}\right) \frac{\exp\left[Q\left(1, g_{-ij}, X\right)\right]}{\sum_{\omega \in \mathcal{G}} \exp\left[Q\left(\omega, X\right)\right]} \\ &= \rho\left(g_{-ij}, X_i, X_j\right) \times \frac{1}{1 + \exp\left[\Delta Q\right]} \times \frac{\exp\left[Q\left(1, g_{-ij}, X\right) + Q\left(0, g_{-ij}, X\right) - Q\left(0, g_{-ij}, X\right)\right]}{\sum_{\omega \in \mathcal{G}} \exp\left[Q\left(\omega, X\right)\right]} \\ &= \rho\left(g_{-ij}, X_i, X_j\right) \times \frac{1}{1 + \exp\left[\Delta Q\right]} \times \frac{\exp\left[Q\left(1, g_{-ij}, X\right) - Q\left(0, g_{-ij}, X\right)\right] \exp\left[Q\left(0, g_{-ij}, X\right)\right]}{\sum_{\omega \in \mathcal{G}} \exp\left[Q\left(\omega, X\right)\right]} \\ &= \rho\left(g_{-ij}, X_i, X_j\right) \frac{\exp\left[\Delta Q\right]}{1 + \exp\left[\Delta Q\right]} \frac{\exp\left[Q\left(0, g_{-ij}, X\right)\right]}{\sum_{\omega \in \mathcal{G}} \exp\left[Q\left(\omega, X\right)\right]} \\ &= \Pr\left(m^t = ij\right) \Pr\left(g_{ij} = 1 \middle| g_{-ij}\right) \frac{\exp\left[Q\left(0, g_{-ij}, X\right)\right]}{\sum_{\omega \in \mathcal{G}} \exp\left[Q\left(\omega, X\right)\right]} \\ &= P_{g'g}\pi_{g'} \end{aligned}$$

So the distribution (13) satisfies the detailed balance condition. Therefore it is a stationary distribution for the network formation model. From part 1) of the proposition, we know that the process is ergodic and it has a unique stationary distribution. Therefore $\pi(g, X)$ is also the unique stationary distribution.

Proof of Proposition 4

The proof consists of showing that $Q(g, X)$ can be written in the form $\theta' \mathbf{t}(g, X)$. Consider

the first part of the potential

$$\begin{aligned}
\sum_i \sum_j g_{ij} u_{ij} &= \sum_i \sum_j g_{ij} \sum_{p=1}^{P} \theta_{up} H_{up}(X_i, X_j) \\
&= \sum_{p=1}^{P} \theta_{up} \sum_i \sum_j g_{ij} H_{up}(X_i, X_j) \\
\text{define } t_{up}(g, X) &\equiv \sum_i \sum_j g_{ij} H_{up}(X_i, X_j), \text{ therefore} \\
&= \sum_{p=1}^{P} \theta_{up} t_{up}(g, X) \\
&= \theta_u' \mathbf{t}_u(g, X)
\end{aligned}$$

where $\theta_u = (\theta_{u1}, \theta_{u2}, ..., \theta_{uP})'$ and $\mathbf{t}_u(g, X) = (t_{u1}(g, X), t_{u2}(g, X), ..., t_{uP}(g, X))'$. Analogously define $\theta_m = (\theta_{m1}, \theta_{m2}, ..., \theta_{mL})'$ and $\mathbf{t}_m(g, X) = (t_{m1}(g, X), t_{m2}(g, X), ..., t_{mL}(g, X))'$ and $\theta_v = (\theta_{v1}, \theta_{v2}, ..., \theta_{vS})'$ and $\mathbf{t}_v(g, X) = (t_{v1}(g, X), t_{v2}(g, X), ..., t_{vS}(g, X))'$. It follows that

$$\begin{aligned}
\sum_i \sum_{j>i} g_{ij} g_{ji} m_{ij} &= \sum_i \sum_{j>i} g_{ij} g_{ji} \sum_{l=1}^{L} \theta_{ml} H_{ml}(X_i, X_j) \\
&= \sum_{l=1}^{L} \theta_{ml} \sum_i \sum_{j>i} g_{ij} g_{ji} H_{ml}(X_i, X_j) \\
&= \sum_{l=1}^{L} \theta_{ml} t_{ml}(g, X) \\
&= \theta_m' \mathbf{t}_m(g, X)
\end{aligned}$$

and

$$\begin{aligned}
\sum_i \sum_j g_{ij} \sum_{k \neq i,j} g_{jk} v_{ij} &= \sum_i \sum_j g_{ij} \sum_{k \neq i,j} g_{jk} \sum_{s=1}^{S} \theta_{vs} H_{vs}(X_i, X_k) \\
&= \sum_{s=1}^{S} \theta_{vs} \sum_i \sum_j g_{ij} \sum_{k \neq i,j} g_{jk} H_{vs}(X_i, X_k) \\
&= \sum_{s=1}^{S} \theta_{vs} t_{vs}(g, X) \\
&= \theta_v' \mathbf{t}_v(g, X)
\end{aligned}$$

Therefore $Q(g,X)$ can be written in the form $\theta'\mathbf{t}(g,X)$, where $\theta=(\theta_u,\theta_m,\theta_v)'$ and $\mathbf{t}(g,X)=[\mathbf{t}_u(g,X),\mathbf{t}_m(g,X),\mathbf{t}_v(g,X)]'$

$$\begin{aligned} Q(g,X) &= \theta_u'\mathbf{t}_u(g,X)+\theta_m'\mathbf{t}_m(g,X)+\theta_v'\mathbf{t}_v(g,X) \\ &= \theta'\mathbf{t}(g,X) \end{aligned}$$

and the stationary distribution is then

$$\pi(g,X)=\frac{\exp\left[\theta'\mathbf{t}(g,X)\right]}{\sum_{\omega\in\mathcal{G}}\exp\left[\theta'\mathbf{t}(\omega,X)\right]}$$

B Computational Details

B.1 Exchange algorithm

In this section I provide the technical details for the algorithm proposed in the empirical part of the paper. The first set of results show that the exchange algorithm generate (approximate) samples from the posterior distribution (15).

The original exchange algorithm developed in Murray et al. (2006) is slightly different from the one used here. The main modification is in Step 2: the original algorithm requires to generate an *exact* sample from the stationary equilibrium of the model.

ALGORITHM 3 ***(Exchange Algorithm)***
Start at current parameter $\theta_t=\theta$ and network data g.

1. *Propose a new parameter vector θ'*

$$\theta'\sim q_\theta(\cdot|\theta) \tag{32}$$

2. *Draw an exact sample network g' from the likelihood*

$$g'\sim\pi(\cdot|X,\theta') \tag{33}$$

3. *Compute the acceptance ratio*

$$\begin{aligned} \alpha_{ex}(\theta,\theta') &= \min\left\{1,\frac{\exp\left[Q(g',X,\theta)\right]}{\exp\left[Q(g,X,\theta)\right]}\frac{p(\theta')}{p(\theta)}\frac{q_\theta(\theta|\theta')}{q_\theta(\theta'|\theta)}\frac{\exp\left[Q(g,X,\theta')\right]}{\exp\left[Q(g',X,\theta')\right]}\frac{c(\theta)c(\theta')}{c(\theta)c(\theta')}\right\} \\ &= \min\left\{1,\frac{\exp\left[Q(g',X,\theta)\right]}{\exp\left[Q(g,X,\theta)\right]}\frac{p(\theta')}{p(\theta)}\frac{q_\theta(\theta|\theta')}{q_\theta(\theta'|\theta)}\frac{\exp\left[Q(g,X,\theta')\right]}{\exp\left[Q(g',X,\theta')\right]}\right\} \end{aligned} \tag{34}$$

4. Update the parameter according to

$$\theta_{t+1} = \begin{cases} \theta' & \textit{with prob. } \alpha_{ex}(\theta, \theta') \\ \theta & \textit{with prob. } 1 - \alpha_{ex}(\theta, \theta') \end{cases} \tag{35}$$

The exchange algorithm works because it satisfies detailed balance condition for the posterior distribution, i.e. for any couple of parameters $(\theta_i, \theta_j) \in \Theta$ we have

$$\Pr[\theta_j|\theta_i, g, X]\, p(\theta_i|g, X) = \Pr[\theta_i|\theta_j, g, X]\, p(\theta_j|g, X) \tag{36}$$

The detailed balance condition is sufficient condition for the Markov chain generated by the algorithm to have stationary distribution the posterior (15) (for details see Robert and Casella (2005) or Gelman et al. (2003)).

LEMMA 2 *The exchange algorithm produces a Markov chain with invariant distribution (15).*

Proof. Define $\mathcal{Z} \equiv \int_\Theta \pi(g|X, \theta)\, \rho(\theta)\, d\theta$. In the algorithm the probability $\Pr[\theta_j|\theta_i, g, X]$ of transition to θ_j, given the current parameter θ_i and the observed data (g, X), can be computed as

$$\Pr[\theta_j|\theta_i, g, X] = q_\theta(\theta_j|\theta_i) \frac{\exp[Q(g', X, \theta_j)]}{c(\mathcal{G}, X, \theta_j)} \alpha_{ex}(\theta_i, \theta_j) \tag{37}$$

This is the probability of proposing θ_j, $q_\theta(\theta_j|\theta_i)$, times the probability of generating the new network g' from the model's stationary distribution, $\frac{\exp[Q(g', X, \theta_j)]}{c(\mathcal{G}, X, \theta_j)}$ and accepting the proposed parameter $\alpha_{ex}(\theta_i, \theta_j)$. Therefore the left-hand side of (36) can be written as

$$\begin{aligned}
\Pr[\theta_j|\theta_i, g, X]\, p(\theta_i|g, X) = \;& q_\theta(\theta_j|\theta_i) \frac{\exp[Q(g', X, \theta_j)]}{c(\mathcal{G}, X, \theta_j)} \alpha_{ex}(\theta_i, \theta_j)\, p(\theta_i|g, X) \\
= \;& q_\theta(\theta_j|\theta_i) \frac{\exp[Q(g', X, \theta_j)]}{c(\mathcal{G}, X, \theta_j)} \alpha_{ex}(\theta_i, \theta_j) \frac{\frac{\exp[Q(g, X, \theta_i)]}{c(\mathcal{G}, X, \theta_i)} p(\theta_i)}{\mathcal{Z}} \\
= \;& q_\theta(\theta_j|\theta_i) \frac{\exp[Q(g', X, \theta_j)]}{c(\mathcal{G}, X, \theta_j)} \\
\times \;& \min\left\{1, \frac{\exp[Q(g', X, \theta_i)]}{\exp[Q(g, X, \theta_i)]} \frac{p(\theta_j)}{p(\theta_i)} \frac{q_\theta(\theta_i|\theta_j)}{q_\theta(\theta_j|\theta_i)} \frac{\exp[Q(g, X, \theta_j)]}{\exp[Q(g', X, \theta_j)]}\right\} \\
\times \;& \frac{\frac{\exp[Q(g, X, \theta_i)]}{c(\mathcal{G}, X, \theta_i)} p(\theta_i)}{\mathcal{Z}}
\end{aligned}$$

$$= \min\left\{q_\theta(\theta_j|\theta_i) \frac{\exp[Q(g', X, \theta_j)]}{c(\mathcal{G}, X, \theta_j)} \frac{\exp[Q(g, X, \theta_i)]}{c(\mathcal{G}, X, \theta_i)} \frac{p(\theta_i)}{\mathcal{Z}}, q_\theta(\theta_i|\theta_j) \frac{\exp[Q(g', X, \theta_i)]}{c(\mathcal{G}, X, \theta_i)} \frac{\exp[Q(g, X, \theta_j)]}{c(\mathcal{G}, X, \theta_j)} \frac{p(\theta_j)}{\mathcal{Z}}\right\}$$

$$
\begin{aligned}
&= q_\theta\left(\theta_i|\theta_j\right)\frac{\exp\left[Q(g',X,\theta_i)\right]}{c(\mathcal{G},X,\theta_i)}\frac{\exp\left[Q(g,X,\theta_j)\right]}{c(\mathcal{G},X,\theta_j)}\frac{p\left(\theta_j\right)}{\mathcal{Z}}\times \\
&\times \min\left\{1,\frac{\exp\left[Q(g',X,\theta_j)\right]}{\exp\left[Q(g,X,\theta_j)\right]}\frac{p\left(\theta_i\right)}{p\left(\theta_j\right)}\frac{q_\theta\left(\theta_j|\theta_i\right)}{q_\theta\left(\theta_i|\theta_j\right)}\frac{\exp\left[Q(g,X,\theta_i)\right]}{\exp\left[Q(g',X,\theta_i)\right]}\right\} \\
&= q_\theta\left(\theta_i|\theta_j\right)\frac{\exp\left[Q(g',X,\theta_i)\right]}{c(\mathcal{G},X,\theta_i)}\alpha(\theta_j,\theta_i)\frac{\exp\left[Q(g,X,\theta_j)\right]}{c(\mathcal{G},X,\theta_j)}\frac{p\left(\theta_j\right)}{\mathcal{Z}} \\
&= q_\theta\left(\theta_i|\theta_j\right)\frac{\exp\left[Q(g',X,\theta_i)\right]}{c(\mathcal{G},X,\theta_i)}\alpha(\theta_j,\theta_i)p\left(\theta_j|g,X\right) \\
&= \Pr\left[\theta_i|\theta_j,g,X\right]p\left(\theta_j|g,X\right)
\end{aligned}
$$

The latter step proves the detailed balance for a generic network g'. Since the condition is satisfied for any network, the detailed balance follows. ■

Unfortunately the exchange algorithm's computational burden is phenomenal. To generate an exact sample from the stationary equilibrium it may be necessary to run the algorithm for an enormous amount of iterations.

The algorithm presented in this paper removes the requirement of exact sampling by exploiting a property of the stationary equilibrium characterization, described in Lemma 1. Following a suggestion in Liang (2010), it is possible to show that for this model it is sufficient to run a simulation of moderate size, starting at the observed network. Lemma 1 shows that if we sample from the stationary distribution of the model using a Metropolis-Hastings algorithm satisfying detailed balance for $\pi\left(g,X,\theta'\right)$, we only need a finite number of network updates.

Proof of Lemma 1

Let $\mathcal{P}_{\theta'}^{(R)}(g'|g)$ be defined as in (21). This is the transition probability of the chain that generates g' with R Metropolis-Hastings updates, starting at the observed network g and using the proposed parameter θ'. Notice that the Metropolis-Hastings algorithm satisfies the detailed balance for $\pi\left(g,X,\theta'\right)$, therefore we have

$$
\begin{aligned}
\mathcal{P}_{\theta'}^{(R)}(g|g')\pi\left(g',X,\theta'\right) &= \mathcal{P}_{\theta'}(g_{R-1}|g')\mathcal{P}_{\theta'}(g_{R-2}|g_{R-1})\cdots\mathcal{P}_{\theta'}(g|g_1)\pi\left(g',X,\theta'\right) \\
&= \mathcal{P}_{\theta'}(g_1|g)\mathcal{P}_{\theta'}(g_2|g_1)\cdots\mathcal{P}_{\theta'}(g'|g_{R-1})\pi\left(g,X,\theta'\right) \\
&= \mathcal{P}_{\theta'}^{(R)}(g'|g)\pi\left(g,X,\theta'\right)
\end{aligned}
$$

It follows that

$$\begin{aligned}\frac{\mathcal{P}_{\theta'}^{(R)}(g|g')}{\mathcal{P}_{\theta'}^{(R)}(g'|g)} &= \frac{\pi\left(g,X,\theta'\right)}{\pi\left(g',X,\theta'\right)} \\ &= \frac{\exp\left[Q(g,X,\theta')\right]}{\exp\left[Q(g',X,\theta')\right]}\frac{c\left(\mathcal{G},X,\theta'\right)}{c\left(\mathcal{G},X,\theta'\right)} \\ &= \frac{\exp\left[Q(g,X,\theta')\right]}{\exp\left[Q(g',X,\theta')\right]}\end{aligned}$$

This concludes the proof.

It remains to prove that the algorithm used to simulate the network produces samples from the stationary equilibrium of the model. This is the result of Proposition 3.

Proof of Proposition 3

The network simulation model satisfies the detailed balance condition for the stationary distribution 13. Indeed for any given θ

$$\begin{aligned}\Pr\left(g'|g,X,\theta\right)\pi\left(g,X,\theta\right) &= q_g\left(g'|g\right)\min\left\{1,\frac{\exp\left[Q\left(g',X,\theta\right)\right]}{\exp\left[Q\left(g,X,\theta\right)\right]}\frac{q_g\left(g|g'\right)}{q_g\left(g'|g\right)}\right\}\frac{\exp\left[Q\left(g,X,\theta\right)\right]}{c\left(\mathcal{G},X,\theta\right)} \\ &= \min\left\{q_g\left(g'|g\right)\frac{\exp\left[Q\left(g,X,\theta\right)\right]}{c\left(\mathcal{G},X,\theta\right)},\frac{\exp\left[Q\left(g',X,\theta\right)\right]}{c\left(\mathcal{G},X,\theta\right)}q_g\left(g|g'\right)\right\} \\ &= q_g\left(g|g'\right)\min\left\{\frac{q_g\left(g'|g\right)}{q_g\left(g|g'\right)}\frac{\exp\left[Q\left(g,X,\theta\right)\right]}{c\left(\mathcal{G},X,\theta\right)},\frac{\exp\left[Q\left(g',X,\theta\right)\right]}{c\left(\mathcal{G},X,\theta\right)}\right\} \\ &= q_g\left(g|g'\right)\min\left\{\frac{q_g\left(g'|g\right)}{q_g\left(g|g'\right)}\frac{\exp\left[Q\left(g,X,\theta\right)\right]}{\exp\left[Q\left(g',X,\theta\right)\right]},1\right\}\frac{\exp\left[Q\left(g',X,\theta\right)\right]}{c\left(\mathcal{G},X,\theta\right)} \\ &= \Pr\left(g|g',X,\theta\right)\pi\left(g',X,\theta\right)\end{aligned}$$

This concludes the proof.

Using Lemma 1 and 2, together with Proposition 3, it is easy to see that the algorithm proposed in the estimation section is an approximate version of the exchange algorithm. For $R \to \infty$ the two algorithms coincide. The main advantage of my approach is the decreased computational burden.

B.2 Convergence Experiments

In this section, I provide an overview of the convergence properties of the algorithm using examples with artificial data. Assume a toy model with three parameters, with an utility

function of the following form

$$U_i(g, X) = \sum_{j=1}^{n} g_{ij}\theta_1 + \sum_{j=1}^{n} g_{ij}g_{ji}\theta_2 + \sum_{j=1}^{n} g_{ij} \sum_{k\neq i,j;k=1}^{n} g_{jk}\theta_3 + \sum_{j=1}^{n} g_{ij} \sum_{k\neq i,j;k=1}^{n} g_{ki}\theta_3 \tag{38}$$

The artificial data are generated using the vector of parameters

$$\theta = (-2.0, 0.5, 0.01) \tag{39}$$

To obtain the network dataset for the estimation, the network simulation algorithm is started at a random network and then ran for 1 million iterations. The initial random network is generated by assuming each link is independent and the probability of a link is $p = .2$. The last iteration of this long simulation is used as dataset in all the estimation exercises below. I report results for a network with $n = 50$ agents, but I ran the same simulations using a network with $n = 30$ and $n = 100$, with similar results.

To check if the exchange algorithm converges to the right region of the parameter space, the parameter simulations are started from 5 different starting values

$$\begin{aligned}
\theta^1 &= (-2.0, 0.5, 0.01) \\
\theta^2 &= (-10.0, 5.0, 1.0) \\
\theta^3 &= (10.0, -5.0, -1.0) \\
\theta^4 &= (-3.0, -0.05, 0.3) \\
\theta^5 &= (-20.0, 15.0, -0.3)
\end{aligned}$$

The first is the parameter vector that generates the data, while the others are overdispersed initial values. In Figure 8 I display the convergence of the simulations to the high density region of the posterior. In this example the number of network simulations per parameter proposal is $R = 3000$.[39] The solid horizontal black line represents the parameter that generated the data. Each color represents a simulation started at one of the initial values above. After 2000 iterations all the chains have converged to the region of the posterior that contains the data generating parameters. In Figure 9 I show the autocorrelation functions for the same example. In this example the autocorrelation disappears after 200 lags. This is mainly due to the small amount of parameters in this toy model. High dimensional models show more persistent autocorrelation of the chains. In Figure 10 I show the same convergence properties of Figure 8 by plotting two parameters in each graph. I show 3 snapshots of the simulations: at 500, 1000 and 2000 iterations. The dashed lines intersect

[39] Similar results hold for different R values.

at the parameter values that generated the data. After 500 iterations (Panel A) almost all chains have converged to the high density region. The purple chain converges after 2000 iterations: this is because this chain corresponds to the 5th starting value, which is the quite far from the parameter that generated the network. In summary, convergence in this toy model is quite fast. In general this is the case also for higher dimensional models. One possible strategy is to use a small R for the initial simulations: when the chain reaches approximate convergence we can increase the number of network simulations and estimate the posterior with higher precision.

B.3 Parallel estimation with multiple networks

When data from multiple independent networks are available the estimation routines are easily adapted. Assume the researcher has data from C networks: let g_c and X_c denote the network matrix and the individual controls for network c, $c = 1, ..., C$. The aggregate data are denoted as $g = \{g_1, ..., g_c\}$ and $X = \{X_1, ..., X_c\}$.

Assuming each network is drawn from the stationary equilibrium of the model, each network has distribution

$$\pi(g_c, X_c, \theta) = \frac{\exp[Q(g_c, X_c, \theta)]}{\sum_{\omega \in \mathcal{G}_c} \exp[Q(\omega_c, X_c, \theta)]} \tag{40}$$

Since each network is independent, the likelihood of the data (g, X) can be written as

$$\begin{aligned}
\pi(g, X, \theta) &= \prod_{c=1}^{C} \pi(g_c, X_c, \theta) \\
&= \prod_{c=1}^{C} \left\{ \frac{\exp[Q(g_c, X_c, \theta)]}{c(\mathcal{G}_c, X_c, \theta)} \right\} \\
&= \frac{\exp\left[\sum_{c=1}^{C} Q(g_c, X_c, \theta)\right]}{\prod_{c=1}^{C} c(\mathcal{G}_c, X_c, \theta)} \\
&= \frac{\exp\left[\sum_{c=1}^{C} Q(g_c, X_c, \theta)\right]}{\mathcal{C}(\mathcal{G}, X, \theta)}
\end{aligned}$$

where $\mathcal{G} = \bigcup_{c=1}^{C} \mathcal{G}_c$. The likelihood for multiple independent networks is of the same form as the likelihood for one network observation. The structure of this likelihood makes parallelization extremely easy: each network can be simulated independently using the network

Table 5: Convergence Experiments

Starting value 1						
	true		R=1000	R=2000	R=3000	R=5000
θ_1	-2.000	mean	-2.0165	-2.0643	-2.077	-2.0838
		s.d.	0.2629	0.2018	0.1845	0.1635
		mc s.e.	0.0125	0.0069	0.0063	0.0051
θ_2	0.500	mean	0.5387	0.6083	0.6207	0.6158
		s.d.	0.5519	0.4435	0.4144	0.4076
		mc s.e.	0.0338	0.0294	0.0189	0.0279
θ_3	0.010	mean	0.0043	0.0121	0.0147	0.0175
		s.d.	0.0262	0.0201	0.0187	0.0165
		mc s.e.	0.0002	0.0001	0.0001	0.0001
Starting value 2						
	true		R=1000	R=2000	R=3000	R=5000
θ_1	-2.000	mean	-2.0131	-2.0651	-2.0688	-2.0673
		s.d.	0.2643	0.2013	0.1814	0.1655
		mc s.e.	0.0137	0.0067	0.0057	0.0046
θ_2	0.500	mean	0.5542	0.6181	0.6149	0.6571
		s.d.	0.5506	0.4425	0.4228	0.4046
		mc s.e.	0.0363	0.0279	0.029	0.022
θ_3	0.010	mean	0.0041	0.0119	0.0143	0.0157
		s.d.	0.0267	0.0201	0.0185	0.0167
		mc s.e.	0.0002	0.0001	0.0001	0.0001
Starting value 3						
	true		R=1000	R=2000	R=3000	R=5000
θ_1	-2.000	mean	-2.0287	-2.0583	-2.0656	-2.0686
		s.d.	0.2548	0.2072	0.1883	0.164
		mc s.e.	0.0099	0.0081	0.0085	0.0043
θ_2	0.500	mean	0.5723	0.6028	0.6275	0.6593
		s.d.	0.5418	0.4473	0.4084	0.3844
		mc s.e.	0.034	0.0224	0.0283	0.0207
θ_3	0.010	mean	0.0058	0.0113	0.0128	0.016
		s.d.	0.0255	0.0211	0.0203	0.0167
		mc s.e.	0.0002	0.0001	0.0001	0.0001
Starting value 4						
	true		R=1000	R=2000	R=3000	R=5000
θ_1	-2.000	mean	-2.016	-2.0727	-2.0884	-2.0724
		s.d.	0.2574	0.2033	0.1842	0.1625
		mc s.e.	0.01	0.0064	0.007	0.0051
θ_2	0.500	mean	0.5612	0.5993	0.6354	0.6576
		s.d.	0.5436	0.4442	0.4163	0.4044
		mc s.e.	0.0346	0.027	0.0252	0.0256
θ_3	0.010	mean	0.0047	0.0128	0.0158	0.0162
		s.d.	0.0254	0.0205	0.0181	0.0165
		mc s.e.	0.0002	0.0001	0.0001	0.0001
Starting value 5						
	true		R=1000	R=2000	R=3000	R=5000
θ_1	-2.000	mean	-2.0309	-2.056	-2.0823	-2.0794
		s.d.	0.2522	0.2059	0.1803	0.1648
		mc s.e.	0.0113	0.007	0.0056	0.0051
θ_2	0.500	mean	0.5668	0.6246	0.654	0.6539
		s.d.	0.5464	0.4389	0.416	0.3966
		mc s.e.	0.0399	0.0244	0.0249	0.0213
θ_3	0.010	mean	0.0061	0.0104	0.0153	0.0168
		s.d.	0.0253	0.0209	0.0183	0.0169
		mc s.e.	0.0002	0.0001	0.0001	0.0001

simulation algorithm; at the end of the simulation we collect the last network and compute the potential; then we compute the sum of potentials and use it to compute the probability

of update.
Therefore, the algorithm is modified as follows

ALGORITHM 4 ***(Parallel FAST EXCHANGE ALGORITHM)***
Fix the number of simulations R. Store each network data (g_c, X_c) in a different processor/core. At each iteration t, with current parameter $\theta_t = \theta$ and network data g

1. *Propose a new parameter θ' from a distribution $q_\theta(\cdot|\theta)$*

$$\theta' \sim q_\theta(\cdot|\theta) \tag{41}$$

2. *For each processor c, start* ***ALGORITHM 1*** *at the observed network g_c, iterating for R steps using parameter θ' and collect the last simulated network g'_c*

$$g'_c \sim \mathcal{P}^{(R)}_{\theta'}(g'_c|g_c) \tag{42}$$

3. *Update the parameter according to*

$$\theta_{t+1} = \begin{cases} \theta' & \text{with prob. } \alpha_{pex}(\theta, \theta') \\ \theta & \text{with prob. } 1 - \alpha_{pex}(\theta, \theta') \end{cases}$$

where

$$\alpha_{pex}(\theta, \theta') = \min\left\{1, \frac{\exp\left[\sum_{c=1}^{C} Q(g'_c, X_c, \theta)\right]}{\exp\left[\sum_{c=1}^{C} Q(g_c, X_c, \theta)\right]} \frac{p(\theta')}{p(\theta)} \frac{q_\theta(\theta|\theta')}{q_\theta(\theta'|\theta)} \frac{\exp\left[\sum_{c=1}^{C} Q(g_c, X_c, \theta')\right]}{\exp\left[\sum_{c=1}^{C} Q(g'_c, X_c, \theta')\right]}\right\} \tag{43}$$

The speed of the algorithm depends on the largest network in the data. Since each parameter update requires the result of each processor simulation there is some idle time, since small networks are simulated much faster.

B.4 Freeman Segregation Index

The Freeman Segregation Index measures the degree of segregation in a population with two groups (Freeman, 1972). Assume there are two groups, A and B. Let n_{AB} be the total number of links that individuals of group A form to individuals of group B. Let n_{BA}, n_{BB} and n_{AA} be analogously defined. The original index developed by Freeman (1972) is defined as

$$FSI = \frac{\mathbb{E}[n_{AB}] + \mathbb{E}[n_{BA}] - (n_{AB} + n_{BA})}{\mathbb{E}[n_{AB}] + \mathbb{E}[n_{BA}]} \tag{44}$$

When the link formation does not depend on the identity of individuals, then the links should be randomly distributed with respect to identity. Therefore, the index measures the

difference between the expected and actual number of links among individuals of different groups, as a fraction of the expected links. An index of 0 means that the actual network closely resembles one in which links are formed at random. Higher values indicate more segregation. In this paper segregation is measured using the index[40]

$$SEG = \max\{0, FSI\} \tag{45}$$

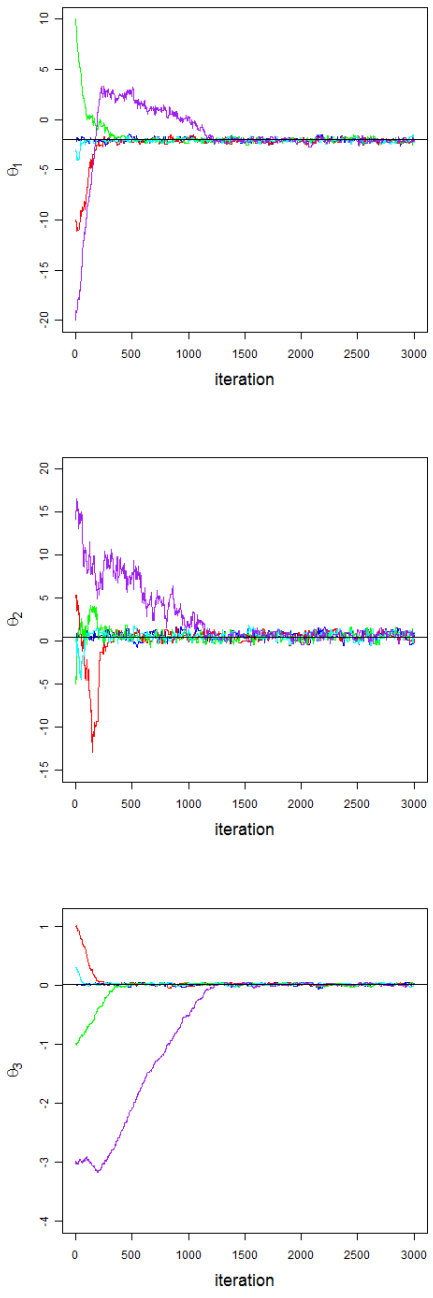
The index varies between 0 and 1, where the maximum corresponds to a network in which there are no cross-group links.

To complete the derivation of the index, the expected number of cross-group links is computed as

$$\begin{aligned} \mathbb{E}[n_{AB}] &= \frac{(n_{AA}+n_{AB})(n_{AB}+n_{BB})}{n_{AA}+n_{AB}+n_{BA}+n_{BB}} \\ \mathbb{E}[n_{BA}] &= \frac{(n_{BA}+n_{BB})(n_{AA}+n_{BA})}{n_{AA}+n_{AB}+n_{BA}+n_{BB}} \end{aligned}$$

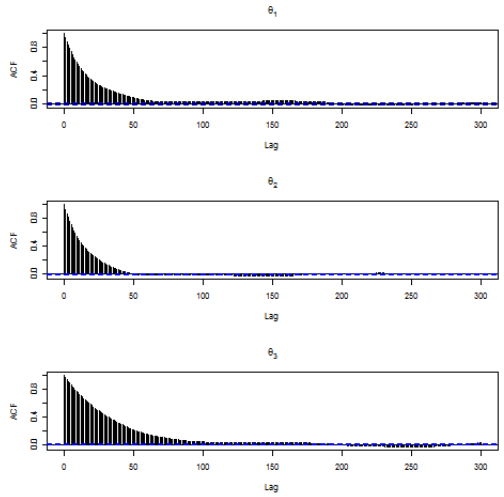
[40]The index (44) varies between -1 and 1. However, the interpretation of the index when it assumes negative values is not clear. Therefore Freeman (1972) suggests to use only when it is nonnegative, to measure the presence of segregation

Figure 8: Convergence to the high density posterior region



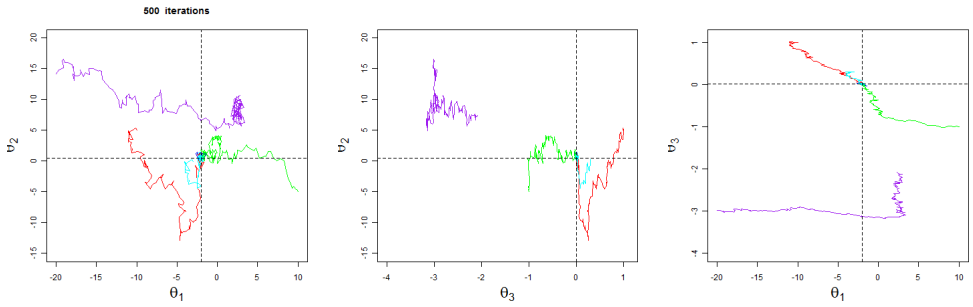
Each graph shows convergence to the high density region of the posterior distribution. The curves with different colors represent chains started at overdispersed initial values. The solid black line represent the parameter that generated the data. Convergence is very fast and we can use the initial 2000 iterations as burn-in. In this example the network has $n = 50$ agents and the number of network simulations per proposal is $R = 3000$.

Figure 9: Convergence to the high density posterior region

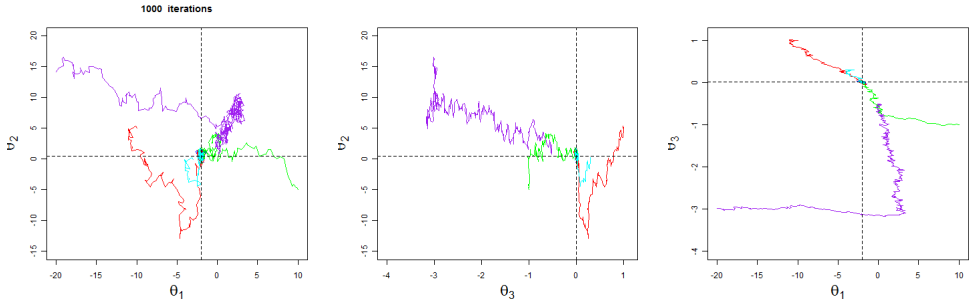


Each graph is the autocorrelation function of the chains generated by the exchange algorithm.

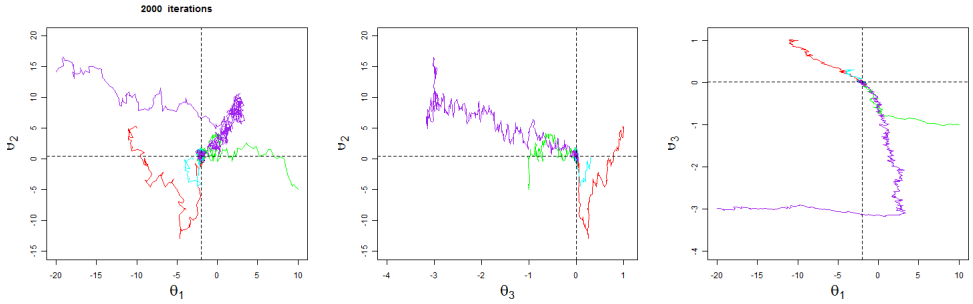
Figure 10: Convergence to the high density posterior region



Panel A. 500 iterations



Panel B. 1000 iterations



Panel C. 2000 iterations

Three snapshots of the simulations at 500, 1000 and 2000 iterations of the fast exchange algorithm. The true parameter value is indicated by the intersection of the dashed lines. After 500 iterations only few chains have converged close to the true parameters. After 1000 the remaining chains have almost reached the high density region of the posterior. At 2000 iterations the algorithm has reached approximate convergence for all the chains.