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An Overview of Diffusion in Complex Networks

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An Overview of Diffusion in Complex Networks

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Abstract

We survey a series of theoretical contributions on diffusion in random networks. We start with a benchmark contagion process, referred in the epidemiology literature as the Susceptible-Infected-Susceptible model, which describes the spread of an infectious disease in a population. To make this model tractable, the interaction structure is considered as a heterogeneous sampling process characterized by the degree distribution. Within this framework, we distinguish between the case of *unbiased-degree* networks and *biased-degree* networks. We focus on the characterization of the *diffusion threshold*; that is, a condition on the primitives of the model that guarantees the spreading of the product to a significant fraction of the population, and its persistence. We also extend the analysis introducing a general diffusion model with features that are more appropriate for describing the diffusion of a new product, idea, behavior, etc.

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1 Introduction

In this chapter we discuss a number of different models of diffusion, where by *diffusion* (or contagion) we mean the process by which information (or any kind of signal) travels along a

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population of agents that are influenced by each other in some well defined way. The general objective is to understand how the network structure determines the reach of the process. This question is relevant for many different disciplines, ranging from sociology and economics to molecular biology and neurology.

In economics, technological diffusion has been a central topic of industrial organization and development which has lead to many well-known contributions (e.g., Rogers, 1995; Conley and Udry, 2001, among others). The issue of diffusion has also been extensively analyzed in the game theoretic literature where we can distinguish between models of learning (Bala and Goyal, 1998), opinion formation (Golub and Jackson, 2012a, 2012b, 2012c) and network games (Morris, 2000; Galeotti et al., 2010; Jackson and Yariv, 2007). Finally, a direct application of diffusion is the study of disease transmission in a population, an issue which has been addressed widely in the epidemiology literature (e.g., Bailey, 1975; Pastor-Satorrás and Vespignani, 2001a, 2001b). These last contributions build on the theoretical framework of random networks which provides a natural setup for the study of complex systems (Bollobás, 2001; Erdös and Rényi, 1959).

The purpose of this chapter is to present a series of models to extend those proposed in epidemiology. In doing so, we aim to understand diffusion not only of an infectious disease in a population, but also of an idea, a product, a cultural fad, or a technology. Our results focus on the characterization of the *diffusion threshold*, a condition on the primitives of the model which guarantees the spreading of the product (to a significant fraction of the population) and its persistence.

In Section 1 we study a benchmark contagion process referred in the literature as the Susceptible-Infected-Susceptible (SIS) model. The interaction structure is considered as the realization of a random sampling process characterized by the degree distribution, where the degree of an agent refers to the number of agents sampled by this agent. Within this framework, we distinguish between the case of *unbiased-degree* networks and *biased-degree* networks. In the first case, agents are homogeneous with respect to how much they are observed by others. Thus, heterogeneity in this framework is only related to the number of observations taken by agents before making a choice, but all agents are equally influential. In the second case, however, the number of agents observed by an agent roughly coincides with the number of agents observing such an agent. Thus, this framework can be considered as an approximation of an undirected network, where if agent i is influenced by agent j then j is influenced by i. The results we present shed light on the relevance of the degree distribution on the predictions of the model. In particular, we report how the diffusion threshold changes due to first order stochastic dominance shifts and mean-preserving spreads in the degree distribution.

In Section 2, we extend the previous analysis to account for general contagion processes which embody different models, including those based on best-response dynamics of coordination games, imitation dynamics, etc. We find that the diffusion threshold crucially depends on the contagion process. Thus, it becomes a relevant empirical question to determine which models are more appropriate for which applications. For instance, the well-known result that scale-free degree distributions exhibit a zero epidemic threshold for the SIS model is not robust to other contagion processes.[1] In particular, for those contagion processes in which the relative number of adopters (with respect to the size of the sample) is what determines the adoption rate (and not just absolute exposure), degree distributions with intermediate variance might be more appropriate for fostering diffusion.

In Section 3, we generalize the model even further to include the issue of homophily (i.e., the tendency of agents to associate with others similar to themselves). To do so, agents are distinguished by their types (e.g., race, gender, age, religion, profession). The interaction patterns are biased by types and different types of individuals might have different proclivities for adoption. In this context, we can analyze how such biases in interactions together with heterogeneity in susceptibility for adopting the new product (idea, disease, etc.) affect the reach of the process. For example, how does the diffusion of a new product that is more attractive to one age group depend on the interaction patterns across age groups? The main result is that homophily actually facilitates diffusion. That is, having a higher rate of homophily allows the diffusion to get started within the more vulnerable type and this can generate the critical mass necessary to diffuse the behavior or infection to the wider society.

2 The SIS model

Consider a new product, an infectious disease, or an idea spreading in a population. Our objective is to analyze whether diffusion occurs. That is, if we start with an infinitesimal small fraction of initial adopters, would the *product* be adopted by a significant fraction of the population and become endemic? In order to answer this question theoretically we make several crucial assumptions. On the one hand, the contagion process considered is the standard Susceptible-Infected-Susceptible model (SIS hereafter) introduced in the epidemiology literature

[1] The existence of a zero epidemic threshold for scale-free networks was first shown by Pastor-Satorrás and Vespignani (2001).

to study the diffusion of an infectious disease in a population.[2] On the other hand, we introduce a *directed* random sampling process to describe how agents are influenced by each other.

Formally, assume a continuum of agents $N = [0, 1]$. Agents can be in two possible states: *active* (infected) or *passive* (susceptible). A passive agent can become active, and conversely, an active agent can become passive. The SIS model assumes the simplest possible process of contagion characterized by the following parameters. A passive agent becomes active with a probability $\nu > 0$ when interacting with an active agent. Conversely, with a probability $\delta > 0$ an active agent can become passive again.[3] The crucial parameter of the model is the (effective) *spreading rate* denoted by $\lambda = \frac{\nu}{\delta}$, which measures how contagious the behavior is. In this setting, the system must always remain in continuous flux since the particular identity of active and passive agents is permanently changing. The objective in this context is to predict the convergence to some population profile where the frequency of active agents remains stable over time. To make the approach tractable, the dynamics is described in continuous time. Thus, the previously defined probabilities ν and δ are instead interpreted as rates. In addition, the stochastic process is approximated by its deterministic counterpart. [4]

Let us consider that individuals observe each other before changing their states. Assume that each agent is characterized by her degree. In particular, an agent has degree d if she samples from the population (and is potentially influenced by) d other agents per unit of time. Observation is typically directed; that is, if an agent observes agent i, this does not imply that j observes i, although an approximation of an undirected network will be considered as well. Let $P(d)$ be the degree distribution; that is, the fraction of the population with degree d. Equivalently, $P(d)$ can be viewed as the probability that a randomly selected node has degree d.

There are several focal degree distributions. For instance, if the population is homogeneous then $P(\overline{d}) = 1$ for some degree $\overline{d} \geq 1$. Moreover, empirical studies have led to the conclusion that many complex networks are characterized by a scale-free degree distribution (i.e., a fat-

[2] The so-called SIS model has extensively been studied in the literature (see e.g., Pastór-Satorrás and Vespignani, 2001; Jackson and Rogers, 2007, etc.).

[3] Note that in the context of a disease, it is implicitly assumed that there is no full immunization and therefore a recovered person can catch the disease again. An obvious instance is the standard flu.

[4] Benaim and Weibull (2003) show that the continuous (deterministic) approximation is appropriate when dealing with large populations. In particular, they find that if the deterministic population flow remains forever in some subset of the state space, then the stochastic process will remain in the same subset space for a very long time with a probability arbitrarily close to one, provided the population is large enough.

tailed property). Price (1965) was the first to find such distributions in a network setting (in particular, in citation networks among scientific articles). The scale-free distribution, or power-law distribution, can be expressed as

$$P(d) = bd^{-\gamma}$$

where $2 < \gamma \leq 3$ and b is a positive normalizing constant. The main feature of this distribution is that the relative probabilities of two different degrees (d, $\widehat{d}$) only depend on their ratio ($\frac{d}{\widehat{d}}$) and not on their absolute values. In these distributions, the average degree cannot be conceived as a good estimate of the typical node degree found in the network. In particular, the population has a significant fraction of *hubs*, i.e., nodes with very high degree compared to the average.

Within the context of directed random networks, we consider two paradigmatic cases depending on how agents choose who to observe: *unbiased-degree* (case 1) and *biased-degree* (case 2). In case 1, agents select other agents completely at random and, thus, the probability of choosing an agent with degree d is precisely $P(d)$. In case 2, agents are biased by the degree of others, so that an agent with degree d is sampled d times more often than an agent with degree 1. Therefore, the probability of selecting an agent with degree d is proportional to $dP(d)$. More precisely, let $Q(d)$ be the probability of selecting an agent with degree d. Then

$$Q(d) = P(d) \text{ in case 1}$$

whereas

$$Q(d) = \frac{dP(d)}{\langle d \rangle_P} \text{ in case 2}$$

where $\langle d \rangle_P = \sum_{d \geq 1} dP(d)$ is the average degree.

Note that Case 2 can be considered as an approximation of an undirected network, as the number of agents observed by an agent is the same as the (expected) number of agents the agent is observed by. Note that, for some applications (e.g., the diffusion of a disease) it is a more accurate description of the reality as personal interaction is required for contagion. We analyze next the two cases separately.

2.1 The SIS model and unbiased-degree random networks

In this section we focus on the unbiased-degree network case which represents the simplest framework to study random interactions characterized by a degree distribution.

Let us first introduce some notation. Let $\rho_d(t)$ denote the frequency of active agents among those with degree d at time t and $\rho(t)$ be the total frequency of active agents in the population at time t. Thus,

$$\rho(t) = \sum_d P(d)\rho_d(t).$$

The adoption dynamics describes the evolution of $\rho_d(t)$ as a function of the parameters of the SIS model. For each $d \geq 1$ we have the following differential equation:

$$\rho_d'(t) = -\rho_d(t)\delta + (1 - \rho_d(t))\nu d\rho(t),$$

where the first term on the sum $(-\rho_d(t)\delta)$ tracks the transitions from active to passive, whereas the second term tracks the transitions from passive to active $((1-\rho_d(t))\nu d\rho(t))$. To understand this term, note that the expected number of active agents in the sample of an agent with degree d is $d\rho(t)$. Thus, the probability that a passive agent becomes active in the small interval of time from t to $t + dt$ is given by $[1 - (1 - \upsilon dt)^{d\rho(t)}]$ and $\lim_{dt\to 0} \frac{[1-(1-\upsilon dt)^{d\rho(t)}]}{dt} = \nu d\rho(t)$.

The stationary states of this dynamics can be computed by imposing that $\rho_d'(t) = 0$ for all d. Therefore, for each d,

$$\rho_d = \frac{\lambda d\rho}{1 + \lambda d\rho},$$

where $\lambda = \frac{\nu}{\delta}$ is the (effective) *spreading rate*. The following fixed-point equation characterizes the fraction of adopters in the stationary state:

$$\rho = H_{\lambda,P}(\rho), \tag{1}$$

where

$$H_{\lambda,P}(\rho) = \sum_d P(d)\frac{\lambda d\rho}{1 + \lambda d\rho}.$$

Notice that $\rho = 0$ is always a solution of equation (1), which implies that the state where all agents are passive is stationary. Thus, in order to spread the "active state" in the population, there must be an initial seed of active agents. To be more precise, let us introduce the following two definitions:

We say that there is *diffusion* in the population if by seeding it randomly with an infinitesimally small initial fraction of active agents, the behavior spreads to a positive fraction of the population and becomes persistent.

We say that λ^* is the *diffusion threshold* if there is diffusion if and only if $\lambda > \lambda^*$.

Theorem 1 (López-Pintado, 2012) *Let P be the degree distribution of a (unbiased-degree) random network. The diffusion threshold for the SIS model is:*

$$\lambda^* = \frac{1}{\langle d \rangle_P}$$

The outline of the proof is the following. In this context, diffusion occurs whenever equation (1) has a positive solution. It is straightforward to show that $H_{\lambda,P}(\rho)$ is an increasing and concave function of ρ. Moreover, $H_{\lambda,P}(0) = 0$ and $H_{\lambda,P}(1) < 1$. Therefore, as depicted in Figure 1, there exists a positive solution of equation (1) if and only if $\frac{dH_{\lambda,P}(\rho)}{d\rho}\rfloor_{\rho=0} = \lambda \sum_d P(d)d > 1$.

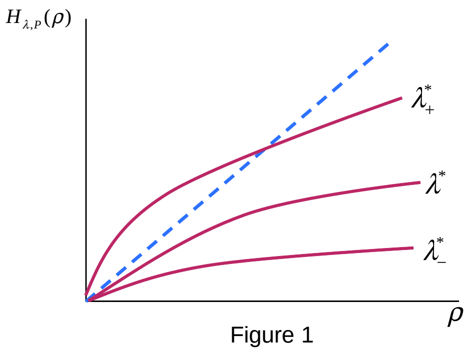

Fig. 1 Representation of $H_{\lambda,P}$ when (i) λ equals the diffusion threshold λ^* (ii) λ is above the diffusion threshold $\lambda = \lambda^*_+$ and (ii) λ is below the diffusion threshold $\lambda = \lambda^*_-$

The diffusion threshold is inversely proportional to the average degree. That is, the higher the average degree the easier it is to foster diffusion. Nevertheless, Theorem 1 does not provide information about the reach of the process whenever there is diffusion. We analyze this issue next.

We say that the adoption dynamics has reached an *endemic state* with a fraction of adopters ρ^* if this fraction remains constant in the upcoming periods. Equation (1) provides a characterization of the endemic states as a function of the degree distribution. Notice that equation (1) has one solution ($\rho = 0$) when $\lambda \leq \lambda^*$ and two solutions ($\rho = 0$ and a positive one) when $\lambda > \lambda^*$, as depicted in Figure 1. Nevertheless, $\rho = 0$ is not a stable solution whenever $\lambda > \lambda^*$. Thus, we define as $\rho^*(P)$ to the (stable) endemic state of the diffusion process.

Two definitions are required before presenting the next result. Consider the degree distributions P and $\widetilde{P}$. We say that $\widetilde{P}$ *first order stochastic dominates* P if

$$\sum_{d=0}^{x} \widetilde{P}(d) \leq \sum_{d=0}^{x} P(d) \text{ for all } x.$$

The intuitive idea is that $\widetilde{P}$ is obtained by shifting mass from P to place it on higher values.

We can also say that $\widetilde{P}$ is a *mean-preserving spread* of P if $\widetilde{P}$ and P have the same mean and

$$\sum_{z=0}^{x}\sum_{d=0}^{z}\widetilde{P}(d) \leq \sum_{z=0}^{x}\sum_{d=0}^{z}P(d) \text{ for all } x.$$

This condition implies that $\widetilde{P}$ has a (weakly) higher variance than P, but it also implies a more structured relationship between the two. In fact the reverse is not true, having a higher variance and the same mean is not sufficient for one distribution to be a mean-preserving spread of another.

Proposition 1 *Let P be the degree distribution of a (unbiased-degree) random network and consider the SIS model. The following holds:*

(1) If $\widetilde{P}$ first order stochastic dominates P then $\rho^*(\widetilde{P}) \geq \rho^*(P)$.

(2) If $\widetilde{P}$ is a mean-preserving spread of P then $\rho^*(\widetilde{P}) \leq \rho^*(P)$.

Before showing this result, let us describe the following two well-known *properties*.

- Property 1: If $\widetilde{P}$ first order stochastic dominates P then, for all non-decreasing functions f,

$$\sum_{d} f(d)\widetilde{P}(d) \geq \sum_{d} f(d)P(d).$$

  and

- Property 2: If $\widetilde{P}$ is a mean-preserving spread of P then, for all concave functions f,

$$\sum_{d} f(d)P(d) \geq \sum_{d} f(d)\widetilde{P}(d).$$

Notice that the endemic state is characterized by equation (1) and since ρ_d is nondecreasing and concave (as a function of d), applying properties (1) and (2) we obtain the desired result.

As illustrated in Figure 2, the diffusion threshold decreases and the endemic state increases with a first order stochastic dominance shift of the degree distribution (see the graph on the left). This is a consequence of the fact that in the SIS contagion process the higher the degree of an agent, the easier it is to become an adopter. We also illustrate how, even though the diffusion threshold does not vary if we shift the degree distribution with a mean-preserving spread, the endemic state decreases with such a shift (see the graph on the right). The intuition for this is that an increase in the degree of an agent increases her adoption rate, but it has a decreasing marginal effect.

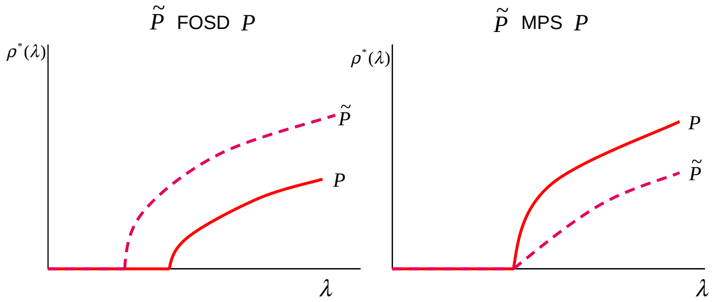

Figure 2

Fig. 2 The graphs represent qualitatively the endemic state (ρ^*) as function of the spreading rate (λ) for the degree distribution P and $\widetilde{P}$, where $\widetilde{P}$ first order stochastic dominates (FOSD) P in the graph on the left and $\widetilde{P}$ is a mean-preserving spread of P (MPS) in the graph on the right

In the next section we analyze a biased-degree random network instead and find critical differences with the degree-unbiased case.

2.2 The SIS model and biased-degree random networks

The methodology applied in the previous section is useful for understanding the predictions on diffusion in a directed network, that is, a network where if i interacts with j this does not imply that j interacts with i. This, of course, is a strong assumption as many socioeconomic interactions among agents are bilateral in nature and thus links in the network are undirected. We therefore can extend the specification of the model proposed above in order to approximate an undirected interaction structure. A tractable attempt to do so is to assume that sampling is not performed uniformly at random but that, instead, it is biased by degree. That is, the probability that an agent samples an agent with degree d is proportional not only to $P(d)$ but also to d. This captures the idea that agents with higher degree are sampled more often.[5] Formally, as already highlighted in Section 1, in this case, the probability that an agent samples another agent with degree d is:

$$Q(d) = \frac{dP(d)}{\langle d \rangle_P},$$

where the average degree $\langle d \rangle_P$ is used for normalization purposes.

Some additional notation is required before presenting the dynamics. Let $\theta(t)$ be the probability that an agent samples an active agent at time t. Thus,

$$\theta(t) = \sum_d Q(d)\rho_d(t). \tag{2}$$

[5] Pastor-Satorrás and Vespignani (2001) used this specification.

This is due to the fact that the probability that at the end of a link an agent has degree d is $Q(d)$ (which in this case is different from $P(d)$). Following analogous steps to those already presented in Section 2.1 we find that the adoption dynamics is now described as follows:

$$\rho_d'(t) = -\rho_d(t)\delta + (1 - \rho_d(t))\nu d\theta(t),$$

where the first term of the sum $(-\rho_d(t)\delta)$ stands for the transition from active to passive. The second term stands for the transition from passive to active $((1 - \rho_d(t))\nu d\theta(t))$, where the expected number of adopters in a sample of size d is $d\theta(t)$. The stationary states of this dynamics can be computed by imposing that $\rho_d'(t) = 0$ for all d which leads to:

$$\rho_d = \frac{\lambda d\theta}{1 + \lambda d\theta} \text{ for all } d. \tag{3}$$

Substituting (3) in (2) we find that the fixed-point equation which characterizes the value of θ in the stationary state is

$$\theta = \widetilde{H}_{\lambda,P}(\theta), \tag{4}$$

where

$$\widetilde{H}_{\lambda,P}(\theta) = \frac{1}{\langle d\rangle_P} \sum_d P(d) \frac{\lambda d^2\theta}{1 + \lambda d\theta}.$$

The next result characterizes the diffusion threshold. To do so let us denote by $\langle d^2\rangle_P$ to the second order moment of the degree distribution P. That is,

$$\left\langle d^2 \right\rangle_P = \sum_d d^2 P(d).$$

Theorem 2 (Pastor-Satorrás and Vespignani, 2001) *Let P be the degree distribution of a (biased-degree) random network. The diffusion threshold for the SIS model is:*

$$\lambda^* = \frac{\langle d\rangle_P}{\langle d^2\rangle_P}.$$

The outline of the proof is the following. There is diffusion if there exists a positive solution of equation (4). In addition, it is straightforward to show that $\widetilde{H}_{\lambda,P}(\theta)$ is an increasing and concave function of θ, $\widetilde{H}_{\lambda,P}(0) = 0$ and $\widetilde{H}_{\lambda,P}(1) < 1$. Therefore, there is diffusion if and only if $\frac{d\widetilde{H}_{\lambda,P}(\theta)}{d\rho}\rfloor_{\theta=0} = \lambda \frac{\left\langle d^2\right\rangle_P}{\langle d\rangle_P} > 1$.

Note that, unlike for the unbiased case, now the variance of the degree distribution also determines the diffusion threshold as $\lambda^* = \frac{\langle d\rangle_P}{\langle d^2\rangle_P} = \frac{\langle d\rangle_P}{\langle d\rangle_P^2 + var(p)}$, where $var(P)$ denotes the variance of distribution P.

As a consequence of Theorem 2, we provide the following comparative statics results on the degree distribution.

Corollary 1 *Let P be the degree distribution of a (biased-degree) random network and consider the SIS model. The following holds:*

(1) If $\widetilde{P}$ first order stochastic dominates P then $\lambda^*(\widetilde{P}) \leq \lambda^*(P)$.

(2)If $\widetilde{P}$ is a mean-preserving spread of P then $\lambda^*(\widetilde{P}) \leq \lambda^*(P)$.

This proof of this corollary is straightforward given the expression for the diffusion threshold provided by Theorem 2. If we compare these results with those obtained for the unbiased-degree case (Proposition 1), we find that for both cases the diffusion threshold decreases with the density of the network. Nevertheless, the effect of a mean-preserving spread is different as in the biased-degree case diffusion is triggered more easily the higher the variance of the degree distribution. The intuition behind this finding relies on the relevant role that hubs (i.e., high-degree nodes) play for diffusion in the biased-degree case, which is not as important in the unbiased-degree case. In the biased-degree case, agents with high degree not only observe many others, but are also observed by many others. Therefore, they easily become infected and also infect others afterwards. For the unbiased-degree case, however, agents with high degree are observed equally as much as any other agent in the population and, thus, they do not necessary promote diffusion once they become infected.

The study of the endemic state and how it depends on the degree distribution is not straightforward (see Jackson and Rogers, 2007). The main reason for this is that the values of ρ (the fraction of adopters in the population) and θ (the probability of sampling an adopter) do not necessarily move in the same direction when there is a shift in P. The next result shows that θ increases with a mean-preserving spread of the degree distribution. Nevertheless, this does not imply that ρ also increases. A piece of notation is needed. Given P, let $\theta^*(P)$ denote the value of θ in the (stable) endemic state of the dynamics. Then the following result holds:

Proposition 2 (Jackson and Rogers, 2007) *Let P be the degree distribution of a (biased-degree) random network and consider the SIS model. If $\widetilde{P}$ is a mean-preserving spread of P, then $\theta^*(P) \leq \theta^*(\widetilde{P})$.*

The proof of this result is a direct consequence of equation (4), property (2) described in Section 2.1, and the fact that $\frac{\lambda d^2 \theta}{1+\lambda d \theta}$ is a convex function of d.[6]

[6] Jackson and Rogers (2007) were the first to analyze the diffusion proprieties of networks ordered through the stochastic dominance of their degree distributions.

3 Beyond the SIS model: general adoption rules

The SIS model corresponds with a specific contagion process, which is directly imported from epidemiology. In social contexts, however, the diffusion of information, or a behavior, often exhibits features that do not match well those of the epidemic models. For instance, in the SIS formulation of diffusion, the transmission of infection to a healthy agent depends on her total exposure to the disease, i.e., the absolute number of infected neighbors. In the spread of many social phenomena, there is a factor of coordination (or persuasion) involved and therefore relative considerations are important (i.e., the number of infected versus non-infected). Moreover, unlike in the SIS model, the adoption rate does not necessarily need to increase linearly with the number of adopters. For instance, if agents adopt only if a significant fraction of others have adopted (a threshold rule). Finally, in the SIS model, the transition from active to passive occurs at a constant rate and therefore does not depend on the behavior of others, something which seems artificial for diffusion in many socioeconomic contexts. For all the reasons listed above, we now present a general family of contagion models which extend the SIS model in several directions.

We assume that in each period agents are in one of two states: active or passive (as before). The agents' actions are influenced by the actions of others, but in a stochastic manner. A passive agent adopts the behavior at a rate described by an adoption rule $f_d(a)$ where d is her degree and a is the number of sampled agents who have adopted the behavior. Conversely, an active agent becomes passive at a rate given by $g_d(a)$ where, again, d is her degree and a is the number of sampled agents who have adopted the behavior. The adoption rules $f_d(a)$ and $g_d(a)$ are the primitives of the diffusion process and must satisfy the following assumptions:

- $f_d(0) = 0$ for each d. In words, a passive agent cannot become active unless she samples at least one active agent.
- $f_d(a)$ is a non-decreasing function of a. In words, the adoption rate is non-decreasing in the number of adopters in the sample.
- $f_d(1) > 0$ for some d such that $P(d) > 0$. This is a technical condition and it implies that there exists a certain degree such that the rate of adoption for agents with such a degree, when only one agent in the sample is active, is positive.[7]

[7] For example, a rule where agents adopt only if at least two sampled agents have adopted does not satisfy this assumption.

- $g_d(0) = \delta > 0$ for all d. That is, the transition rate from active to passive, when all agents in the sample are passive, is positive and constant for all degrees.

- $g_d(a)$ is a non-increasing function of a. That is, the transition rate from active to passive is non-increasing in the number of active agents in the sample.

This general approach encompasses a number of different models. Three simple examples are the following.

First, the SIS model presented in the previous section corresponds with the adoption rules $f_d(a) = \nu a$ and $g_d(a) = \delta$.

Second, consider the following *Imitation model*. Every period, a non-smoker considers the possibility of smoking at a rate $\nu > 0$. This agent engages in smoking if he or she happens to sample a smoker among those agents that influence him or her. Conversely, at a rate δ a smoker considers the possibility of quitting smoking. This agent decides to quit if him or her happens to sample among those agents that influence him or her a non-smoker. This diffusion process corresponds with the following specification of the adoption rules: $f_d(a) = \nu \frac{a}{d}$ and $g_d(a) = \delta \frac{d-a}{d}$.

Third, consider the following *Majority threshold model*.[8] We consider again the example of choosing whether to smoke or not. Every period, a non-smoker considers the possibility of smoking at a rate $\nu > 0$. This agent engages in smoking behavior if he or she observes that more than half of the agents that influence him or her are smokers. Conversely, a smoker considers the possibility of quitting smoking at a rate δ. This agent decides to quit if him or her observes that at least half of the agents that influence him or her are non-smoker. This diffusion process corresponds with the following specification of the adoption rules: $f_d(a) = \nu$ if $\frac{a}{d} > 0.5$ and $f_d(a) = 0$ otherwise. Also, $g_d(a) = \delta$ if $\frac{a}{d} \leq 0.5$ and $g_d(a) = 0$ otherwise.

Notice that both in the Imitation model and the Majority threshold model relative considerations (i.e., $\frac{a}{d}$ instead of a) are important. Moreover, in the Majority threshold model the adoption rules do not depend linearly on a. Finally, the transition from active to passive, in both models, is not constant and crucially depends on the behavior observed by the agent when making such a decision.

The diffusion threshold can also be calculated for these general models as presented in the next result.

[8]These threshold models have been extensively analyzed in the literature (see Granovetter, 1978; Watts, 2002; López-Pintado, 2006 and Jackson and Yariv, 2007).

Theorem 3 (Jackson and López-Pintado, 2013) *Let P be the degree distribution of a random network. The diffusion threshold for the general model is:*

$$\sum_d Q(d)d\frac{f_d(1)}{\delta} > 1$$

where $Q(d) = P(d)$ in an unbiased-degree random network, whereas $Q(d) = \frac{dP(d)}{\langle d \rangle_P}$ in a biased-degree random network.

Notice that Theorem 3 shows that the diffusion threshold depends on the degree distribution and on the values of the adoption rules $f_d(1)$ and $g_d(0)$. The reason why $f_d(a)$ and $g_d(a)$ for $a > 1$ does not appear in the condition is that in the initial periods of the dynamics there is only a small fraction of adopters in the population and, thus, the probability that an agent observes more than one adopter in her sample is negligible. Nevertheless, as briefly explained below, further properties of the adoption rule (e.g., the concavity of the rule) crucially affect other properties of the diffusion process, as for example, the type of transition occurring at the diffusion threshold (i.e., whether it is a second order phase transition or not).

The results obtained for the Imitation model are striking. The diffusion threshold is $\lambda^* = 1$, both for the unbiased-degree and biased-degree random network. The reason is that, in this case, all agents have the same probability of becoming an adopter, independently of their degree. To see this, consider two agents i and j where i has degree d and j has degree $2d$. It is straightforward to show that the probability that agent i observes a active agents in the sample coincides with the probability that agent j observes $2a$. Moreover, the Imitation model assumes that both agents, i and j, would have the same probability of adopting as $\frac{a}{d} = \frac{2a}{2d}$).

For the Majority threshold model, we obtain that the diffusion threshold is $\lambda^* = 1/p(1)$ for the unbiased random network, and $\lambda^* = \langle d \rangle_P / p(1)$ for the biased random network. Notice that, in this case, only agents with degree 1 that happen to sample an adopter will adopt in the initial periods of the dynamics, which is why the diffusion threshold decreases with respect to $p(1)$. The diffusion threshold is higher for the biased-degree case than for the unbiased-degree case. The reason is that, in the former case, the agents with degree 1 are observed (in expectation) only by 1 agent and thus are less efficient in spreading the behavior than in the later case where an agent with degree 1 is observed by the same number of agents as any other agent in the population (i.e., roughly by $\langle d \rangle_P$ other agents in each unit of time). [9]

[9] The study of how collective outcomes depend on the details of the contagion process has also been highlighted by Young (2009), Galeotti and Goyal (2009), López-Pintado and Watts (2008), etc.

To conclude, let us concentrate on *absolute adoption rules*, that is, on rules satisfying that it is the total exposure to the activity what determines the adoption rate. Formally, $f_d(a) = f(a)$ and $g_d(a) = g(a)$ for all d and $0 \leq a \leq d$. We can distinguish three focal absolute adoption rules, which are the following:

(a) $f(a) = \upsilon a$ and $g(a) = \delta$ (i.e., the SIS model), where the marginal impact on adoption of having one more adopter in an agents's sample is constant.

(b) $f(a) = \upsilon\sqrt{a}$ and $g(a) = \delta$, where the marginal impact on adoption of having one more adopter in an agent's sample is decreasing.

(c) $f(a) = \upsilon a^2$ and $g(a) = \delta$, where the marginal impact on adoption of having one more adopter in an agents's sample is increasing.

Corollary 2 *Let P be the degree distribution of a random network. The diffusion threshold for the absolute adoption rules (a), (b) and (c) is*

$$\lambda^* = \frac{1}{\langle d \rangle_P}$$

for an unbiased-degree random network, whereas it is

$$\lambda^* = \frac{\langle d \rangle_P}{\langle d^2 \rangle_P}$$

for a biased-degree random network.

This corollary is a direct application of Theorem 3. Notice that the diffusion threshold coincides for all the absolute adoption rules considered. Nevertheless, as described in López-Pintado (2008), for cases (a) and (b) the endemic state $\rho^*(\lambda)$ exhibits a second order phase transition at the diffusion threshold $\lambda = \lambda^*$. In other words, the endemic state $\rho^*(\lambda)$ is a continuous function of the spreading rate and, therefore, as λ converges to λ^*, $\rho^*(\lambda)$ converges to $\rho(\lambda^*)$. For case (c), however, we obtain a discontinuity in the endemic fraction of adopters at $\lambda = \lambda^*$ (first order phase transition or hysteresis) as illustrated in Figure 3. This is due to the existence of multiple stationary states of the adoption dynamics, depending on the size of the initial seed of adopters.

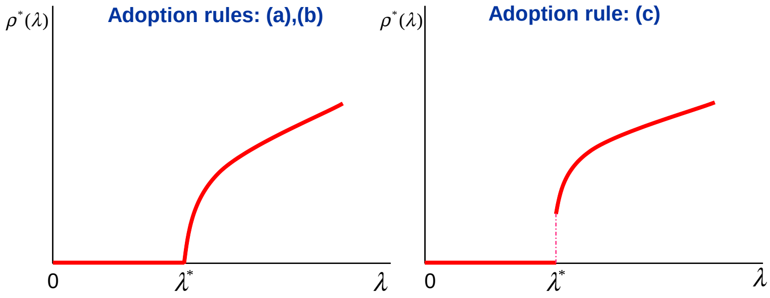

Figure 3

Fig. 3: The graphs represent qualitatively the endemic state (ρ^*) as function of the spreading rate (λ). The graph on the left corresponds to concave adoption rules such as (a) and (b), where there is a second order phase transition at λ^*. The graph on the right corresponds to adoption rule (c), where there is a first order phase transition at λ^*

4 Homophily

In this section we want to understand the effect that homophily has on diffusion, something which despite its importance has received little attention in the diffusion literature.[10] Homophily is the tendency of agents to associate with others similar to themselves. For example, young children in day care have higher rates of interaction with other young children than with older children. Adults of a certain profession, religion and education are more likely to interact with other adults with similar characteristics. In addition we allow for heterogeneity in preferences regarding the new product or behavior (or different susceptibilities for catching a disease). For instance, children can be more vulnerable to some diseases than adults, a new movie can be more attractive to women than men, etc. In particular, we examine whether or not diffusion occurs in a heterogeneous and homophilous society.

To be consistent with the rest of the paper, we start analyzing homophily in the SIS model, and extend later the analysis to more general models of diffusion in random networks.

4.1 Homophily in the SIS model

For ease of exposition, we assume that the population is only made of two groups (the young and the elder). Agents in each group have different proclivities for getting infected of a certain

[10] There are some exceptions such as Currarini et al. (2009), Golub and Jackson (2012), among others.

disease. In particular, imagine that the elder are more vulnerable to this disease than the young. More precisely, if λ_1 is the spreading rate of the young and λ_2 of the elder then $\lambda_1 < \lambda_2$. Let π be the probability that an individual interacts with an individual of the same age range. We also allow for heterogeneity with respect to the degree distribution. In particular, let $P_i(d)$ be the degree distribution of individuals of type i. In this example it is reasonable to assume bilateral interaction and, thus, let us focus on the biased-degree network case. Hence, conditional on sampling an agent of type i, this agent will have degree d with probability $Q_i(d) = \frac{dP_i(d)}{\langle d \rangle_i}$. The result on diffusion is the following:

Proposition 3 (Jackson and López-Pintado, 2013) *Let* $\pi_0 = \frac{1-\widetilde{d}_1\lambda_1\widetilde{d}_2\lambda_2}{\frac{\widetilde{d}_1\lambda_1+\widetilde{d}_2\lambda_2}{2}-\widetilde{d}_1\lambda_1\widetilde{d}_2\lambda_2}$, *where* $\widetilde{d}_i = \frac{\langle d^2 \rangle_i}{\langle d \rangle_i}$. *Diffusion occurs for the SIS model with homophily if and only if one of the following conditions hold:*

1) $\lambda_1\lambda_2 > \frac{1}{\widetilde{d}_1\widetilde{d}_2}$ *or*

2) $\lambda_1\lambda_2 \leq \frac{1}{\widetilde{d}_1\widetilde{d}_2}$ *and* $\pi > \pi_0$

Recall that the condition for diffusion in the standard (homogenous) SIS model is $\lambda > \frac{1}{\widetilde{d}}$, which is a particular case of the previous result. Note also that if we considered, instead, an unbiased-degree random network, we obtain the same result as in Proposition 3, but with $\widetilde{d}_i = \frac{1}{\langle d \rangle_i}$.

The most interesting scenario turns out to be one where one of the types would foster diffusion if isolated, whereas the other would not (i.e., $\lambda_1 < \frac{1}{\widetilde{d}_1}$ and $\lambda_2 > \frac{1}{\widetilde{d}_2}$). In that scenario, we show that homophily either plays no role (if $\lambda_1\lambda_2 > \frac{1}{\widetilde{d}_1\widetilde{d}_2}$) or it actually facilitates diffusion (if $\lambda_1\lambda_2 < \frac{1}{\widetilde{d}_1\widetilde{d}_2}$). Note that in the latter case diffusion occurs only if the two types are sufficiently biased in interactions towards their own types (i.e., π is sufficiently large).

4.2 Homophily beyond the SIS model

We now generalize the previous analysis beyond the SIS model with two types. Let us assume that all relevant characteristics are captured by a finite set of m types where $m \geq 1$ (e.g., agents in type i are male, aged 30-40, atheist and university professors). Formally, the continuum of agents $N = [0, 1]$ is partitioned by types where n_i denotes the fraction of agents of type i. Thus, $\sum_{i=1}^{m} n_i = 1$. Again, we assume that agents have a degree which measures the number of individuals sampled per unit of time. The distribution of degrees can be different across types (i.e., the elderly might have lower mean and variance in degrees than teenagers) and thus $P_i(d)$ indicates the degree distribution of individuals of type i.

The random meeting process now incorporates biases across types. In particular, the rate at which an agent of type i meets agents of other types is described by the following matrix:

$$\Pi = \begin{pmatrix} \pi_{11} & \dots & \pi_{1m} \\ \vdots & \dots & \vdots \\ \pi_{m1} & \dots & \pi_{mm} \end{pmatrix},$$

where π_{ij} is the probability that an agent of type i meets an agent of type j in any given meeting. Thus, $\sum_{j=1}^{m} \pi_{ij} = 1$. To guarantee that a behavior that starts spreading in one group reaches any other group we must assume that Π is a primitive matrix, that is, $\Pi^t > 0$ for some t.[11]

In any given period, an agent of type i with degree d expects to meet $d\pi_{ij}$ agent of type j, and conditional on meeting an agents of type j, the probability that this agent has degree d is

$$Q_j(d) = P_j(d),$$

in the unbiased-degree network case, and

$$Q_j(d) = \frac{dP_j(d)}{\langle d \rangle_{P_j}},$$

in the biased-degree network case, where $\langle d \rangle_{P_j}$ is the average degree of P_j.[12]

Let $\rho_{i,d}(t)$ denote the frequency of active agents at time t among those of type i with degree d. Thus,

$$\rho_i(t) = \sum_d P_i(d)\rho_{i,d}(t)$$

is the frequency of active agents at time t among those of type i, and

$$\rho(t) = \sum_d n_i \rho_i(t)$$

is the overall fraction of active agents in the population at time t.

Finally, the contagion model is defined with the general adoption rules $f_{i,d}(a)$ and $g_{i,d}(a)$ presented in Section 2 but note that these rules can differ across types. This allows us to define $\theta_i(t)$ as the probability that an agent of type i samples an active agent. Note that

$$\theta_i(t) = \sum_j \pi_{ij} \sum_d Q_j(d)\rho_{j,d}(t). \tag{5}$$

[11] Notice that $\Pi^t = \Pi * \Pi * ... * \Pi$, t times.

[12] In the biased-degree case, certain constraints on the parameters of the model would be required in order to approximate it to an undirected network. For example, the number of interactions from type i to type j should coincide with the number of interactions from type j to type i in a unit of time. That is, $n(i) \langle d \rangle_i \pi_{ij} = n(j) \langle d \rangle_j \pi_{ji}$.

Let us now define the rates at which a passive agent becomes active and vice versa. To do so, let $rate_{i,d}^{0\to1}(t)$ be the rate at which a passive agent of type i and with degree d becomes active, whereas $rate_{i,d}^{1\to0}(t)$ stands for the reverse transition. We assume that the number of infected agents in a sample follows a binomial distribution with parameters d (number of draws) and $\theta_i(t)$ (probability of each draw being active). That is,

$$\begin{aligned} rate_{i,d}^{0\to1}(t) &= \sum_{a=0}^{d} f_{i,d}(a)\binom{d}{a}\theta_i(t)^a(1-\theta_i(t))^{(d-a)}, \\ rate_{i,d}^{1\to0}(t) &= \sum_{a=0}^{d} g_{i,d}(a)\binom{d}{a}\theta_i(t)^a(1-\theta_i(t))^{(d-a)}. \end{aligned}$$

The diffusion dynamics is described as follows:

$$\rho'_{i,d}(t) = -\rho_{i,d}(t)rate_{i,d}^{1\to0}(t) + (1-\rho_{i,d}(t))rate_{i,d}^{0\to1}(t) \tag{6}$$

where the right-hand side represents the increase in the level of active agents, whereas the left-hand side represents the decrease in such a level due to the transition of some active agents to passive.

As in a stationary state $\rho'_{i,d}(t) = 0$ then

$$\rho_{i,d} = \frac{rate_{i,d}^{0\to1}}{rate_{i,d}^{0\to1} + rate_{i,d}^{1\to0}}. \tag{7}$$

We substitute equation (7) in equation (5) and find that the values for θ_i in the steady states are

$$\theta_i = H_i(\theta_1, \theta_2 ... \theta_n),$$

where

$$H_i(\theta_1, \theta_2 ... \theta_n) = \sum_j \pi_{ij} \sum_d Q_j(d) \frac{rate_{i,d}^{0\to1}}{rate_{i,d}^{0\to1} + rate_{i,d}^{1\to0}}.$$

This system of equations characterizes the steady states for θ_i, but from here we can compute the steady states for the fraction of adopters of each type ρ_i and ultimately the overall fraction of adopters ρ.

The objective is to find conditions for diffusion. Note that $\boldsymbol{\theta} = \mathbf{0}$ (i.e., $(\theta_1, \theta_2 ... \theta_n) = (0, 0, ..., 0)$) is a steady state of the diffusion dynamics. We must explore the stability of such state. If $\boldsymbol{\theta} = \mathbf{0}$ is not stable, following fixed-point arguments applied to monotone correspondences on lattices, it can be shown that there exists another strictly positive steady state of the dynamics (see Jackson and López-Pintado, 2013 for details on this argument). From (5) and

(6) we find

$$\theta_i'(t) = \sum_j \pi_{ij} \sum_d Q_j(d) \left[-\rho_{j,d}(t) rate_{j,d}^{1\to 0}(t) + (1-\rho_{j,d}(t)) rate_{j,d}^{0\to 1}(t) \right].$$

Note that near $\boldsymbol{\theta} = \mathbf{0}$ (and assuming that there is an upper bound on the degree of agents) we have that:

$$rate_{j,d}^{1\to 0}(t) = \delta \text{ and } (1-\rho_{j,d}(t)) rate_{j,d}^{0\to 1}(t) = df_{jd}(1)\theta_j(t)$$

and thus we can rewrite

$$\theta_i'(t) = \sum_j \pi_{ij} \sum_d Q_j(d) df_{jd}(1)\theta_j(t) - \theta_i(t)\delta,$$

which can be expressed in matricial form as

$$\boldsymbol{\theta}'(\mathbf{t}) = [A\boldsymbol{\theta} - \boldsymbol{\theta}]\,\delta$$

where

$$A = \begin{pmatrix} \pi_{11}x_1 & \dots & \pi_{1m}x_m \\ \vdots & \dots & \vdots \\ \pi_{m1}x_1 & \dots & \pi_{mm}x_m \end{pmatrix},$$

and

$$x_i = \sum_d Q_i(d) d \frac{f_{i,d}(1)}{\delta}.$$

The term x_i can be interpreted as the relative growth of adoption due to type i and adjusted by the relative rates at which agents of type i will be met by other agents.

With this information we can now state the following result.

Theorem 4 (Jackson and López-Pintado, 2013.) *Diffusion occurs if the largest eigenvalue of A is larger than* 1*.*

Note that if we only have *one type* in the population then we can drop subindex i and the condition for diffusion is

$$x = \sum_d Q(d) d \frac{f_d(1)}{\delta} > 1$$

which coincides with the condition provided in Theorem 3.

Assume now that there are *two types* with symmetry in how introspective groups are in their meetings. Therefore, $\pi_{11} = \pi_{22} = \pi$. The result in this case is the following:

Proposition 4 (Jackson and López-Pintado, 2013) *Let* $\pi_0 = \frac{1-x_1x_2}{x_1+x_2-x_1x_2}$. *Diffusion occurs if and only if one of the following conditions hold:*

1) $x_1x_2 > 1$ *or*

2) $x_1x_2 < 1$ *and* $\pi > \pi_0$.

Note that if diffusion occurs within each type when isolated, it would also occur when there is interaction among the two (in such a case $x_1 > 1$ and $x_2 > 1$ and thus part (1) of the proposition holds). If diffusion does not occur among either type when isolated, then it would not occur if there is interaction between them (note that $\pi > \pi_0$ cannot occur if both x_1 and x_2 are below 1). Finally, if diffusion occurs among only one of the types when isolated, then it would occur among the entire population if homophily is high enough. The intuition behind this result is that having a higher rate of homophily allows the diffusion to get started within the more vulnerable type, and this can generate the critical mass necessary to diffuse the behavior to the wider society.

5 Conclusions

In this chapter we have surveyed a series of stylized models of diffusion in networks. In order to make the analysis tractable, the interaction or influence structure is described by an explicit sampling process where two extreme cases have been considered: the unbiased-degree and the biased-degree case. In the former case out-degree (information level) and expected in-degree (visibility level) of agents are uncorrelated, whereas in the latter case these two measures coincide. López-Pintado (2012) and Jackson and López-Pintado (2013) extend this idea to comprise a wide array of sampling options depending on the level of correlation assumed between agent's in and out degree. The main focus of most of the work surveyed in this chapter, however, is to discuss the hypothesis that more dense and heterogeneous networks always favor diffusion, something which is true for standard epidemiology models but that does not generalize to other models of diffusion based on coordination and imitation behavioral rules.

We have also tried to understand the effect that homophily has on diffusion, concentrating on the concept of the diffusion threshold. That is, the spreading to a significant fraction of the population of a new behavior when starting with a small initial seed. Nevertheless, there are other issues which are not addressed here, but that are relevant. For example, one could evaluate the size of the adoption endemic state as a function of the homophily level.

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