



On a Discrete-Time Network SIS Model with Opinion Dynamics*

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Abstract: This extended abstract proposes a discrete-time network susceptible-infected-susceptible (SIS) model coupled with opinion dynamics, where the opinion dynamics models each individual's perceived severity of illness or perceived susceptibility. The effects of the opinion dynamics on the network SIS model are studied by analyzing the limiting behaviors of the system and providing illustrative simulations.

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1. INTRODUCTION

Study of epidemiological models has a long history dating back to (Kermack and McKendrick, 1927) and has received increasing attention due to outbreaks of contagious diseases such as SARS, Ebola, MERS, and the current coronavirus (COVID-19). Probably the most important epidemiological models are SIS and SIR (susceptible-infected-recovered) models. Earlier models mainly focus on a well-mixed population, in which each individual has an equal probability of interaction with any other individual. A notable exception is the work of Lajmanovich and Yorke (1976) which studies a continuous-time network SIS model for gonorrhea, where the interactions among the individuals are described by a possibly sparse graph. Recently, network models have attracted considerable attention (Fall et al., 2007; Mieghem et al., 2009; Khanafer et al., 2016; Paré et al., 2017; Liu et al., 2019). For recent development in this area, see surveys by Mei et al. (2017); Nowzari et al. (2016).

It is clear that individuals' opinions (i.e., perceived severity of the illness or perceived susceptibility) affect the spread of infectious diseases. For example, an individual's perceived susceptibility influences his/her behavior including how frequently to interact with others, how much medical treatment to take, and whether to travel or not, as shown in the current COVID-19 pandemic. However, there are very few existing mathematical models combining epidemic spreading and opinion dynamics. The work of Ni et al. (2011) only studies a well-mixed population and thus cannot be applied to network models. A related line of research is the recent literature on combining network epidemic models with human awareness (Funk et al., 2009; Paarporn et al., 2017; Liu et al., 2017; Paré et al., 2020b) and human behavior (Rizzo et al., 2014; Funk et al., 2010). Although these models capture a new state of an

individual, for example, in the transition from completely unaware to alerted of the disease, they do not take opinion dynamics into account, which are particularly important in modern epidemiology in the presence of rapid development of communication technology and fast-growing online social media.

In our recent paper Xuan et al. (2020), we proposed a continuous-time network SIS model coupled with opinion dynamics, where the opinion dynamics models each individual's perceived severity of illness or perceived susceptibility. Considering the facts that there exist both continuous- and discrete-time network SIS models (Nowzari et al., 2016) and that discrete-time opinion dynamics models are more popular and natural than continuous-time ones, this extended abstract aims to propose a discrete-time counterpart of the model in Xuan et al. (2020) and study the model by characterizing its limiting behavior, equilibria, and their stability.

2. THE MODEL

Consider a social network of $n > 1$ agents representing n individuals, labeled 1 through n . Each agent i can only learn, and be influenced by, the opinions of certain other agents called its neighbors. Neighbor relationships among the n agents are described by a directed graph \mathbb{G} , called the neighbor graph, in that agent j is a neighbor of agent i whenever (j, i) is an arc in \mathbb{G} . Thus, the directions of arcs indicate the directions of information flow and infection. Each agent i has an opinion z_i which represents agent i 's opinion about the severity of the epidemic virus spreading over the network. Each agent i 's opinion, z_i , is a real-valued quantity which evolves as a function of the opinions of its neighbors and its probability of being infected, with the precise dynamics being defined shortly.

We consider a discrete-time network SIS model recently proposed by Paré et al. (2020a) as follows:

$$x_i(k+1) = x_i(k) + h \left(-\delta_i x_i(k) + (1-x_i(k)) \sum_{j \in \mathcal{N}_i} \beta_{ij} x_j(k) \right),$$

* All the proofs of the assertions in this extended abstract are omitted due to space limitation and will be provided in an expanded version.

where $x_i(k) \in [0, 1]$ denotes the probability of agent i being infected at discrete-time index k , δ_i is the curing rate of agent i , \mathcal{N}_i is the set of the neighbors of agent i , β_{ij} is the infection rate from agent j to agent i , and $h > 0$ is the sampling parameter. The item $-\delta_i x_i(k)$ represents how each agent i cures itself, and $(1 - x_i(k)) \sum_{j \in \mathcal{N}_i} \beta_{ij} x_j(k)$ represents how each agent i can be infected by its neighbors.

We now modify the above model to incorporate each agent's opinion of how severe the virus is, using the same idea in Xuan et al. (2020). Without loss of generality, we assume that each z_i takes values between 0 and 1. The case $z_i = 0$ means that agent i believes the virus does not have any threat, and the case $z_i = 1$ means that agent i believes the virus poses a maximal threat. It is reasonable to expect that the larger z_i is, the less agent i may interact with its neighbors and the more likely it will take treatment when being infected. Thus, we propose the following modified discrete-time network SIS dynamics:

$$\begin{aligned} x_i(k+1) = & x_i(k) + h \left(-(\delta_{\min} + (\delta_i - \delta_{\min}) z_i(k)) x_i(k) \right. \\ & \left. + (1 - x_i(k)) \sum_{j \in \mathcal{N}_i} (\beta_{ij} - (\beta_{ij} - \beta_{\min}) z_i(k)) x_j(k) \right), \end{aligned}$$

where δ_{\min} and β_{\min} denote the minimum curing rate and infection rate, respectively. In the case when $z_i = 0$, which implies that agent i does not consider the virus a threat, it will take no action to protect itself and thus is maximally exposed to the infection. In the case when $z_i = 1$, which implies that agent i believes the virus is extremely serious, it will interact with others as little as possible and seek out all the medical treatment options possible.

Next we model how each agent i 's opinion z_i evolves, which is as follows:

$$z_i(k+1) = \theta_i x_i(k) + (1 - \theta_i) \left(w_{ii} z_i(k) + \sum_{j \in \mathcal{N}_i} w_{ij} z_j(k) \right), \quad (1)$$

where $\theta_i \in (0, 1)$ is a constant, and w_{ii} and w_{ij} are positive weights such that $w_{ii} + \sum_{j \in \mathcal{N}_i} w_{ij} = 1$.

Remark 1. In Xuan et al. (2020), a continuous-time opinion dynamics model was proposed as

$$\dot{z}_i(t) = (x_i(t) - z_i(t)) + \sum_{j \in \mathcal{N}_i} (z_j(t) - z_i(t)),$$

which has the following two properties. First, if $x_i(k) = z_i(k)$, then the model simplifies to a continuous-time consensus model, the canonical Abelson model, which will lead all agents' opinions to a consensus. Second, if agent i 's opinion has reached a consensus with its neighbors, i.e., $\sum_{j \in \mathcal{N}_i} (z_j(k) - z_i(k)) = 0$, it will finally converge to x_i . Such a model is consistent with the health belief model (Glanz et al., 2008; Rosenstock, 1974). Now consider the same two cases for the discrete-time counterpart (1). First, if $x_i(k) = z_i(k)$, then (1) simplifies to a discrete-time consensus model, the classical DeGroot model, which will also lead all agents' opinions to a consensus. Second, if agent i 's opinion has reached a consensus with its neighbors, i.e., $z_i(k) = z_j(k)$ for all $j \in \mathcal{N}_i$, it will also finally converge to x_i . Therefore, (1) shares the same

behavior as the model in Xuan et al. (2020), and thus is a valid discrete-time counterpart. \square

Following Xuan et al. (2020) and Paré et al. (2020a), we impose the following natural restrictions on the parameters of the model throughout the extended abstract. For convenience, we use $[n]$ to denote the index set $\{1, 2, \dots, n\}$.

Assumption 1. For all $i \in [n]$, there hold $x_i(0), z_i(0) \in [0, 1]$, $\delta_i \geq \delta_{\min} > 0$, and $\beta_{ij} \geq \beta_{\min} > 0$ for all $j \in \mathcal{N}_i$. The neighbor graph \mathbb{G} is strongly connected. The sampling period h is positive and for every agent i , there hold $h\delta_i \leq 1$ and $h \sum_{j=1}^n \beta_{ij} \leq 1$.

The following lemma shows that the system is well-posed.

Lemma 1. If $x_i(0), z_i(0) \in [0, 1]$ for all $i \in [n]$, then $x_i(k), z_i(k) \in [0, 1]$ for all $i \in [n]$ and $k \in \{0, 1, 2, \dots\}$.

It is easy to see that $x = z = \mathbf{0}_n$ is an equilibrium of the system, where $\mathbf{0}_n$ denotes the n -dimensional vector whose entries all equal to 0. Since $x = \mathbf{0}_n$ corresponds to the case when no individual is infected and implies that $z = \mathbf{0}_n$ is the only equilibrium of (1), we call this trivial equilibrium the healthy state.

In the sequel, we define $D_{\min} = \delta_{\min} I_n$ for simplicity, where I_n denotes the $n \times n$ identity matrix, and use $\rho(M)$ to denote the spectral radius of a real square matrix M .

We first characterize the local stability of the healthy state.

Proposition 1. If $\rho(I_n - hD_{\min} - hB) < 1$, the healthy state is locally exponentially stable. If $\rho(I_n - hD_{\min} - hB) > 1$, the healthy state is unstable.

The following theorem states that in the case when $\rho(I_n - hD_{\min} - hB) \leq 1$, the healthy state is globally stable.

Theorem 1. If $\rho(I_n - hD_{\min} - hB) \leq 1$, then the healthy state is asymptotically stable for all initial conditions.

Extensive simulations show that in the case when $\rho(I_n - hD_{\min} - hB) > 1$, the system will asymptotically converge to a unique nonzero state, called the endemic equilibrium, as long as $x(0) \neq \mathbf{0}_n$, which will be provided in the next section. However, complete analysis of the uniqueness and stability of the endemic equilibrium has so far eluded us, which is a direction of our future work.

3. SIMULATIONS

This section provides several illustrative simulations. To visualize the system more clearly, an unique demonstrating scheme was employed. In each figure, the initial condition for the system is shown on the left side while the final state on the right. The trajectories of the virus and opinion are then depicted by the color of the corresponding node. Virus is depicted by the color red ($r = [1 \ 0 \ 0]$) and opinion is depicted by the color blue ($b = [0 \ 0 \ 1]$). When $x_i(k) = 0$ and $z_i(k) = 0$, the corresponding color goes to white. For all $i \in [n]$, the diameter of the node representing agent i is given by

$$d_{x_i(k)} = d_0 + r_0 x_i(k), \\ d_{z_i(k)} = d_0 + r_0 z_i(k),$$

with d_0 being the default diameter and r_0 being the scaling factor depending on the sickness and opinion of agent i .

Firstly, we illustrate Theorem 1 by considering the system with 20 nodes and $\rho(I_n - hD_{\min} - hB) = 0.8851$. Consistent with the result of Theorem 1, the virus is eradicated and the opinion goes to zero, as depicted in Figure 1.

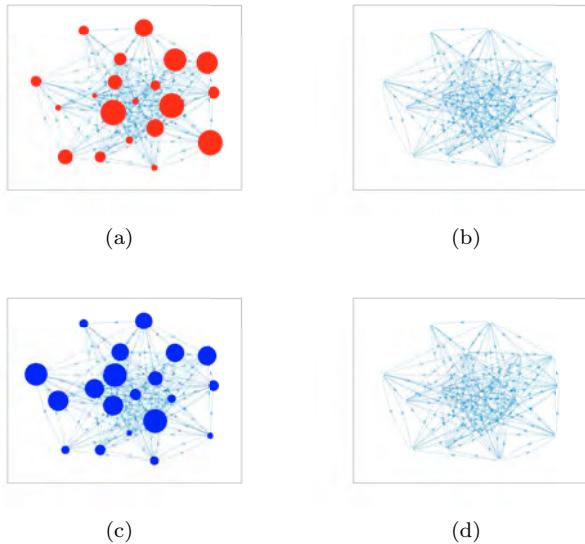


Fig. 1. This system meets the assumption of Theorem 1, with $\rho(I_n - hD_{\min} - hB) = 0.8851$. Figures on the left column denote system at time zero and figures on the right column denote system at time step 100 where (a), (b) denote epidemic dynamics, (c), (d) denote opinion dynamics. The virus is eradicated and the opinion goes to zero at time step 100.

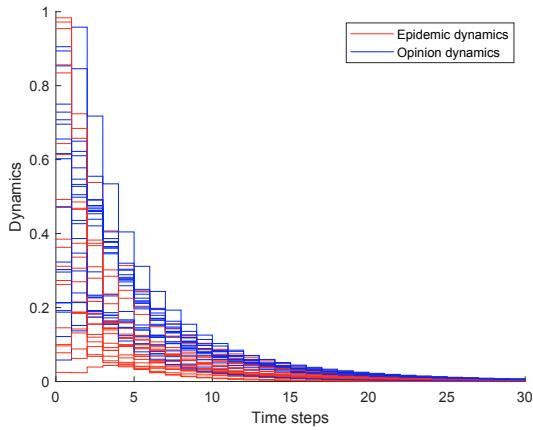


Fig. 2. Trajectories of the simulation in Fig. 1. Epidemic dynamics and opinion dynamics are depicted by red and blue, respectively.

An illustration of the case when $\rho(I_n - hD_{\min} - hB) > 1$ the system converges to a non-zero equilibrium, which based on numerous different initial conditions, appears to be unique and with a large basin of attraction is shown in

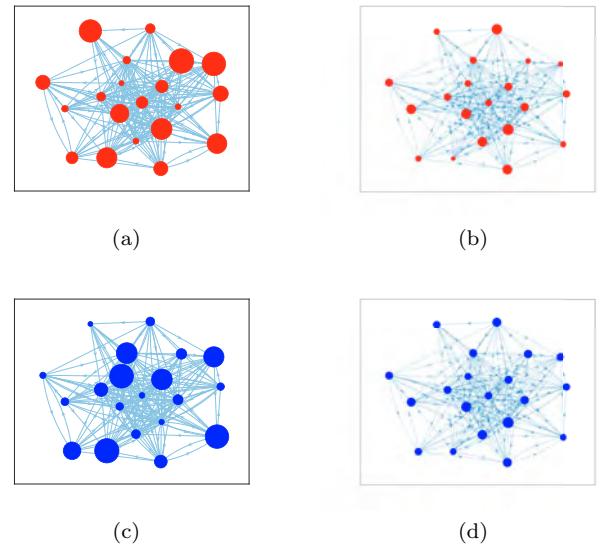


Fig. 3. This system meets the assumption that an unique non-zero endemic equilibrium is asymptotically stable if the initial values are not all equal to zero, with $\rho(I_n - hD_{\min} - hB) = 1.0602$. Figures on the left column denote system at time zero and figures on the right column denote system at time step 200 where (a), (b) denote epidemic dynamics, (c), (d) denote opinion dynamics. The virus and opinion reach endemic state at time step 200.

Figure 3, where we set the total node number to 20 and $\rho(I_n - hD_{\min} - hB) = 1.0602$.

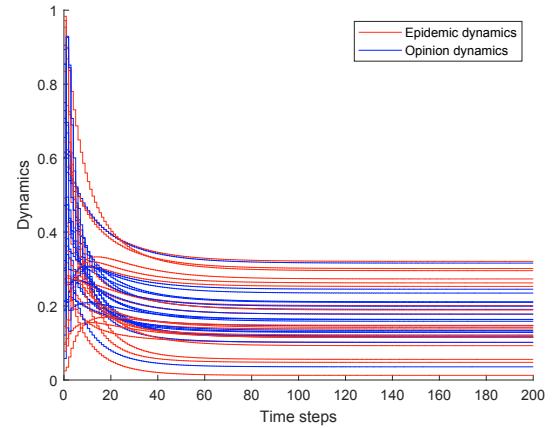


Fig. 4. Trajectories of the simulation in Fig. 3. Epidemic dynamics and opinion dynamics are depicted by red and blue, respectively.

A question of interest is to ascertain whether conditions exist for the system to have multiple attractive equilibria, or have limit cycles. In the following simulation we start the system with parameters as in Figure 3, with two different initial conditions; in both cases, the system converges to the same nonzero equilibrium as depicted in Figure 5. Moreover, the system appears to have a unique equilibrium which, via simulation, appears to be initial condition independent.

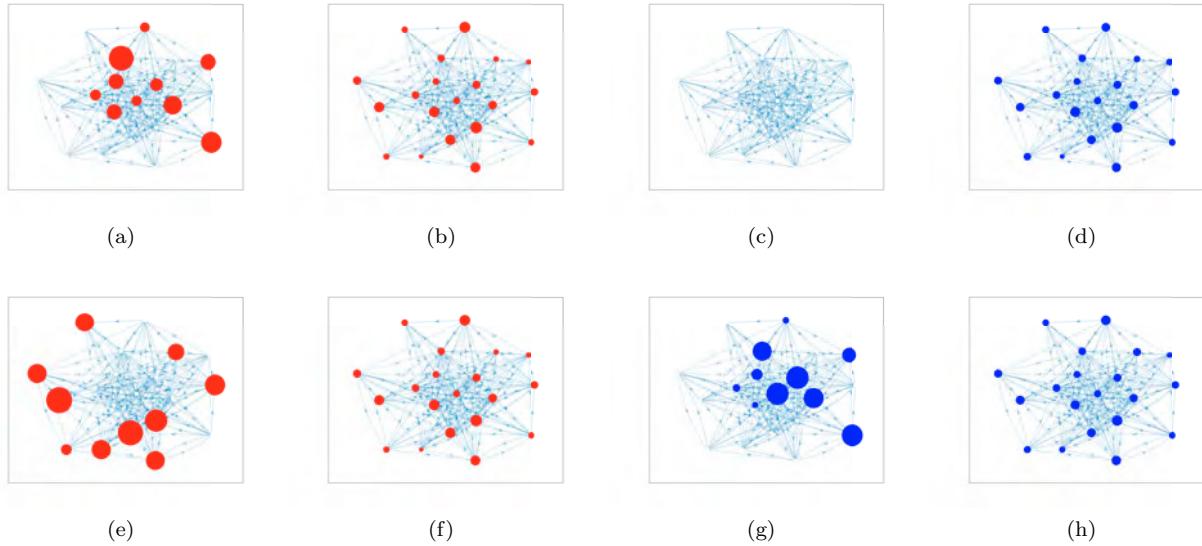


Fig. 5. This system meets the assumption that an unique non-zero endemic equilibrium is asymptotically stable if the initial values of epidemics $x_i(0)$ are not all equal to zero. The the epidemic state and opinion state converge to the same parallel equilibrium for all two initial conditions. Figures on row one and row two demonstrate the system with different initial conditions. (a), (c), (e), (g) denote the system at time step zero, and (b), (d), (f), (h) denote the system at time step 200.

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