

Suppressing the endemic equilibrium in SIS epidemics: A state dependent approach

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Abstract: This paper considers the susceptible-infected-susceptible (SIS) epidemic model with an underlying network structure and focuses on the effect of social distancing to regulate the epidemic level. We demonstrate that if each subpopulation is informed of its infection rate and reduces interactions accordingly, the fraction of the subpopulation infected stays below half for all time instants. To this end, we first modify the basic SIS model by introducing a state dependent parameter representing the frequency of interactions between subpopulations. Thereafter, we show that for this modified SIS model, the spectral radius of a suitably-defined matrix being not greater than one causes all the agents, regardless of their initial sickness levels, to converge to the healthy state; assuming non-trivial disease spread, the spectral radius being greater than one leads to the existence of a unique endemic equilibrium, which is also asymptotically stable. Finally, by leveraging the aforementioned results, we show that the fraction of (sub)populations infected never exceeds half.

Keywords: Epidemic processes, Infection reduction, Characterization of endemic equilibrium, Suppressing endemic equilibrium

1. INTRODUCTION

Spreading processes such as information, diseases, and so on play an outsized role in modern societies. Notably, the ongoing COVID-19 crisis has caused disruption to our daily lives on a scale not seen in decades. Hence, spreading processes have attracted the attention of researchers for centuries, starting from Bernoulli's seminal paper (Bernoulli, 1760), with the key objective being to understand and eradicate (or, at the very least, mitigate) the spread. The literature abounds with relevant models, viz. susceptible-infected-recovered (SIR), susceptible-exposed-infected-recovered (SEIR), etc. The focus of the present paper is on the susceptible-infected-susceptible (SIS) model.

In the SIS model, an agent, which could represent either a subpopulation or an individual, is either in the susceptible or infected state. A healthy agent can get infected depending on the infection rate β , scaled by the interactions it has with its neighboring agents; in a similar manner, an infected agent recovers based on the healing rate γ . It is assumed that the total number of agents is constant (Lajmanovich and Yorke, 1976) and sufficiently many. The latter implies that stochastic effects can be

discounted (Anderson and May, 1992). We say that the system is in the healthy state if all the agents are healthy, or equivalently, in the disease-free equilibrium (DFE). If the epidemic remains persistent, we say that the system is in the endemic state.

Stability analysis of SIS models has been a major focus in mathematical epidemiology; see, for instance, (Fall et al., 2007) and (Paré et al., 2020b) for continuous-time and discrete-time cases, respectively. Similarly, control of SIS models has also received significant attention; see, for instance (Torres et al., 2016; Watkins et al., 2016). We refer the interested readers to (Nowzari et al., 2016) for an overview of these topics. By leveraging the information regarding infection levels of agents, a state feedback strategy for eradicating epidemics has been proposed (Paré et al., 2020a). The strategy involves boosting the healing rates of all agents, presupposing the availability of medical resources such as vaccinations, drug administration and so on. In the absence of pharmaceutical intervention strategies, policymakers might have less stringent objectives.

In this paper, we approach the problem of epidemic peak control from the viewpoint of *social distancing*. Under the situation where the healthcare system is overwhelmed by the wide spread of infections, decreasing the frequency of interactions could be one of the very few effective options for mitigation; under serious conditions, its enforcement may require declarations of the state of emergency. In fact, for SIR epidemics such strategies have been de-

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signed previously. The work (Morris et al., 2021), using the SIR model demonstrates that if social distancing is enforced effectively at a proper level and an appropriate timing, the peak of infected population can be reduced. In (Wang et al., 2021b), this model is augmented by a multi-agent system performing consensus algorithms, where the infected agents may not behave as desired and resilience against such behaviors is sought. To the best of our knowledge, for SIS models, strategies for suppression of epidemics *by upper bounding the proportion of infected individuals in a subpopulation with a specific value* are not available. We aim to address the same in the present paper.

Contributions: The main contribution of this paper is to devise a control scheme for guaranteeing that the fraction of individuals in a subpopulation who are infected does not exceed half for all time instants. Our approach is as follows: First, we modify the discrete-time SIS model in (Paré et al., 2020b) by introducing a state dependent parameter. Then, we show that for this modified SIS model, the following properties hold:

- (i) The spectral radius of a suitably-defined matrix being not greater than one guarantees convergence to the DFE; see Theorem 1.
- (ii) If the spectral radius of the aforementioned matrix is greater than one, then there exists an endemic equilibrium, which has a specific characterization, and is asymptotically stable; see Theorem 2.
- (iii) Finally, leveraging the results in Theorems 1 and 2, we show that the fraction of infected individuals in a subpopulation never exceeds half; see Theorem 3.

Outline: The rest of the paper unfolds as follows. The problem being investigated is formally introduced in Section 2. The main results are provided in Section 3, while simulations illustrating our theoretical findings are given in Section 4. Finally, a summary of the paper and some concluding remarks are provided in Section 5.

Notation: Let \mathbb{R}_+ and \mathbb{Z}_+ denote the sets of non-negative real numbers and integers, respectively. For any two vectors $\mathbf{a}, \mathbf{b} \in \mathbb{R}^n$, we write $\mathbf{a} > \mathbf{b}$ if $a_i > b_i$ for every $i \in [n]$. Let an eigenvalue of matrix A be denoted by $\lambda(A)$. Let $\rho(A)$ denote the largest absolute value of an eigenvalue of matrix A , which is also called the spectral radius of A . A diagonal matrix is denoted as $\text{diag}(\cdot)$. We use $\mathbf{1} = [1, 1, \dots, 1]^T$ and $\mathbf{0} = [0, 0, \dots, 0]^T$ to denote the vectors of all-ones and all-zeros, respectively. Given a matrix A , $A \prec 0$ (resp. $A \preceq 0$) indicates that A is negative definite (resp. negative semidefinite).

2. PROBLEM FORMULATION

2.1 Basic SIS model

Consider a network of n agents, with each agent representing a subpopulation, and suppose that a virus is spreading over this network. Coming into contact with an infectious agent possibly results in an otherwise healthy agent getting infected with the virus. Such a spreading process can be represented by a directed graph $\mathcal{G} = (\mathcal{V}, \mathcal{E})$, where $\mathcal{V} = \{1, 2, \dots, n\}$ denotes the set of agents and \mathcal{E} denotes the set of interconnections between the agents. More precisely, $\mathcal{E} = \{(i, j) \in \mathcal{V} \times \mathcal{V} \mid a_{ij} \neq 0\}$. That is, there is a directed edge from agent j to agent i if a

subpopulation j can infect subpopulation i . The strength of interconnection from agent j to i is captured by the weight $a_{ij} > 0$. Let $\beta > 0$ and $\gamma > 0$ denote the infection and healing rates of each agent, respectively.

Now, the continuous-time dynamics of each agent $i \in [n]$ can be represented as follows (Fall et al., 2007):

$$\dot{x}_i(t) = \beta(1 - x_i(t)) \sum_{j=1}^n a_{ij} x_j(t) - \gamma x_i(t), \quad (1)$$

where $x_i(t)$ is the infection level of agent i and time $t \in \mathbb{R}_+$. Observe that, since the state $x_i(t)$ here denotes the fraction of the subpopulation infected at time t , the state values must remain in the interval $[0, 1]$ and we restrict our analysis within this range for all agents.

The discrete-time version of (1) can be obtained by applying Euler's method to (1) as in (Paré et al., 2020b):

$$x_i(k+1) = x_i(k) + \Delta T [\beta(1 - x_i(k)) \sum_{j=1}^n a_{ij} x_j(k) - \gamma x_i(k)], \quad (2)$$

where $\Delta T > 0$ is the sampling period.

It is common to denote the basic reproduction number by $R_0 = \beta/\gamma > 0$. It represents the reproduction ability, indicating how many agents an infected agent can infect on average per time step.

2.2 Problem statement

Assuming that there is a non-trivial disease spread, our goal is to devise a control scheme through social distancing such that the infection levels $x_i(k)$ of all subpopulations are bounded from above by $1/2$ for all time instants k .

2.3 Modified SIS model with local policy makers

In order to achieve our goal, we modify the system in (2) by introducing an *infection reduction parameter*, denoted by $b_i(k) \in [0, 1]$. This can be interpreted as a parameter provided by a local policymaker who, based on available sickness data, estimates the realtime infection level for agent i and makes preventive decisions. Such decisions, in this context, correspond to reducing the interactions with other agents in the network. Consequently, for each agent i , the effective infection rate is reduced from β to, at each time instant, $b_i(k)\beta$. Hence, the dynamics in (2) can be written as

$$x_i(k+1) = x_i(k) + \Delta T [b_i(k)\beta(1 - x_i(k)) \sum_{j=1}^n a_{ij} x_j(k) - \gamma x_i(k)]. \quad (3)$$

Note that $b_i(k) = 0$ indicates that agent i removes all connections with its neighbors, while $b_i(k) = 1$ indicates all connections with neighbors are maintained as in the nominal case.

3. MAIN RESULTS

In this section, we present a control strategy for guaranteeing that, for $i \in [n]$, $x_i(k) \in [0, 1/2)$ for all time instants k . Towards this end, we set the infection reduction parameter for each agent i as $b_i(k) = 1 - 2x_i(k)$. This indicates that each agent i is asked by its local policymaker to reduce its contacts by $2x_i(k)$ at each time instant. Substituting this parameter into (3), the dynamics for agent i can be written as

$$x_i(k+1) = x_i(k) + \Delta T \beta (1 - 2x_i(k))(1 - x_i(k)) \times \sum_{j=1}^n a_{ij} x_j(k) - \Delta T \gamma x_i(k). \quad (4)$$

Since the values that $b_i(k)$ takes depend on the infection rate at time instant k , we say that it is a state dependent parameter.

Let $\mathbf{x}(k) = [x_1(k), x_2(k), \dots, x_n(k)]^T$. Then, in vector form, (4) can be written as:

$$\mathbf{x}(k+1) = [I + \Delta T \beta (I - 2\text{diag}(\mathbf{x}(k)))(I - \text{diag}(\mathbf{x}(k)))A - \Delta T \gamma I] \mathbf{x}(k). \quad (5)$$

Observe that (5) can be further rewritten as:

$$\mathbf{x}(k+1) = \hat{M}(k) \mathbf{x}(k), \quad (6)$$

where

$$\hat{M}(k) = M - B(k)A, \quad (7)$$

$$M = I + \Delta T \beta A - \Delta T \gamma I, \quad (8)$$

$$B(k) = \Delta T \beta \text{diag}(\mathbf{x}(k))(3I - 2\text{diag}(\mathbf{x}(k))). \quad (9)$$

We need the following assumptions for our analysis.

Assumption 1. (Paré et al., 2020b) The underlying graph \mathcal{G} is strongly connected.

Note that the adjacency matrix A is irreducible if and only if the underlying graph \mathcal{G} is strongly connected.

Assumption 2. For every $i \in [n]$, the initial state satisfies $x_i(0) \in (0, 1/2)$.

Assumption 3. ΔT is sufficiently small.

Assumption 2 ensures that when the control action based on infection reduction starts, less than half of the subpopulation in any agent is infected. Assumption 3 is a technical assumption on the sampling period.

We need the following definitions in the sequel.

Definition 1. The system (5) is said to reach the *disease free equilibrium (DFE)* if $\forall i \in [n], \lim_{k \rightarrow \infty} x_i(k) = 0$. Also it is said to reach an *endemic equilibrium* if the states converge to a positive constant, i.e., $\forall i \in [n], \lim_{k \rightarrow \infty} x_i(k) = x_i^*$, where $0 < x_i^* < 1$.

We now present our main results, whose proofs are given in the Appendix.

Theorem 1. Consider system (5) under Assumptions 1–3. If $\rho(M) \leq 1$, then the DFE is asymptotically stable with the domain of attraction $[0, 1/2)^n$.

Theorem 1 establishes that as long as $\rho(M) \leq 1$, our control scheme achieves convergence to the healthy state, irrespective of whether the agents are initially healthy or sick. Moreover, simulations indicate that the smaller the spectral radius of M is, the faster the convergence to the healthy state is; see Fig. 1.

It is natural to ask what the behavior of system (5) is when $\rho(M) > 1$. We analyse the same next. As a first step, we introduce the following assumption.

Assumption 4. The weights of the graph satisfy $0 \leq a_{ij} < 1$, and $\sum_{j=1}^n a_{ij} = 1, a_{ii} > 1/2, \forall i \in [n]$.

The following lemma establishes the relationship between $\rho(M)$ and R_0 .

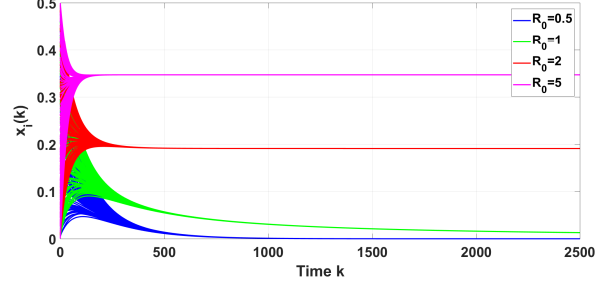


Fig. 1. Time responses for $x_i(k)$ with different R_0

Lemma 1. Suppose that Assumptions 1 and 4 hold. Then $\rho(M) > 1$ if and only if $R_0 > 1$.

Proof: Based on Assumptions 1, 4 and the Perron-Frobenius theorem (Meyer, 2000), it follows that $\rho(A) = 1$. Let $\mathbf{x}_{\lambda(A)}$ be the eigenvector for the eigenvalue $\lambda(A)$. Then

$$M \mathbf{x}_{\lambda(A)} = [I + \Delta T \beta A - \Delta T \gamma I] \mathbf{x}_{\lambda(A)} = [1 + \Delta T (\beta \lambda(A) - \gamma)] \mathbf{x}_{\lambda(A)}.$$

Then, $\lambda(M) = 1 + \Delta T (\beta \lambda(A) - \gamma)$ and thus $\rho(M) = 1 + \Delta T (\beta \rho(A) - \gamma) = 1 + \Delta T (\beta - \gamma)$. We have $\rho(M) > 1$ if and only if $R_0 > 1$ (i.e., $\beta > \gamma$). \square

Theorem 2. Consider system (5) under Assumptions 1–4. If $\rho(M) > 1$, then there exists a unique endemic equilibrium $\bar{x} \cdot \mathbf{1} > \mathbf{0}$, where

$$\bar{x} = \frac{3R_0 - \sqrt{R_0^2 + 8R_0}}{4R_0}. \quad (10)$$

Moreover, the endemic equilibrium $\bar{x} \cdot \mathbf{1}$ is asymptotically stable with the domain of attraction $[0, 1/2)^n \setminus \{\mathbf{0}\}$.

Theorem 2 states that the reproduction number being greater than one gives rise to an endemic behavior. That is, the epidemic becomes a “fact of life” for the community.

We have so far shown that with $b_i(k) = 1 - 2x_i(k)$, the endemic equilibrium $\bar{x} < 1/2$ and thus $\lim_{k \rightarrow \infty} x_i(k) < 1/2$. In the following theorem, we would like to show for all $k \in \mathbb{Z}_+$, $x_i(k)$ is upper bounded by $1/2$.

Theorem 3. Consider the system dynamics in (4) under Assumptions 1–4. Then, for $i \in [n]$, we have $x_i(k) < 1/2$ at all times $k \in \mathbb{Z}_+$.

In words, Theorem 3 guarantees that the proposed control strategy ensures that the fraction of infected individuals in a subpopulation never exceeds half. Hence, the burden on the healthcare facilities remains more manageable.

4. NUMERICAL EXAMPLE

We provide numerical examples to illustrate our results. Networks with 100 agents were generated by randomly placing agents having the communication radius of $r = 50$ in the area of 100×100 . For agents i and j that can communicate, select the weight $0 < a_{ij} < 1$. The initial state $x_i(0)$ is randomly chosen from $(0, 1/2)$, and $\Delta T = 0.01$. We confirmed that As a result, the conditions in Assumptions 1, 2 and 4 are fulfilled.

In this simulation, we would like to check our control strategy with different R_0 . We test four sets of parameters: i) $\beta = 0.5, \gamma = 1$, and hence $R_0 = 0.5$; ii) $\beta = 1, \gamma = 1$,

and hence $R_0 = 1$; iii) $\beta = 2, \gamma = 1$ and hence $R_0 = 2$; and iv) $\beta = 5, \gamma = 1$, and hence $R_0 = 5$. Applying the policy of $b_i(k) = 1 - 2x_i(k)$, the time responses for $x_i(k)$ are shown in Fig. 1. In line with the results in Theorem 1 for the cases where $R_0 = 0.5$ and $R_0 = 1$, the states $x_i(k)$ converge to 0 with $R_0 = 0.5$ achieving exponential convergence, while for $R_0 = 1$ the states decay to 0 asymptotically. The case when $R_0 = 2$ is consistent with Theorem 2, and we see that the endemic equilibrium is approximately 0.19, which indeed obeys (10). Moreover, as expected, the states go to this endemic equilibrium. A similar result also holds for the case $R_0 = 5$. Furthermore, all states are upper bounded by 0.5, consistent with the findings of Theorem 3.

5. CONCLUSION

In this paper, we have considered a discrete-time SIS epidemic process over a strongly connected network. By leveraging the information regarding sickness levels to reduce contacts between subpopulations, we have devised a control strategy which ensures that the fraction of infected individuals in a subpopulation never exceeds half.

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APPENDIX

Proof of Theorem 1: The proof of Theorem 1 follows a similar sketch as that of (Theorem 1 (Paré et al., 2020b)). Due to space restrictions, we omit the proofs here. The detailed proof may be found in (Wang et al., 2021a). \square

Proof of Theorem 2: The proof is inspired by Fall et al. (2007) and Liu et al. (2020). It consists of two steps: we first establish the existence and uniqueness of the endemic equilibrium. Subsequently, we establish, for all non-zero initial conditions, asymptotic convergence to the said equilibrium.

Step 1: Existence/Uniqueness of the endemic equilibrium
By (5), an equilibrium $\mathbf{x}^* = [x_1^*, x_2^*, \dots, x_n^*]^T$ satisfies

$$\mathbf{x}^* = [I + \Delta T \beta (I - 2\text{diag}(\mathbf{x}^*)) (I - \text{diag}(\mathbf{x}^*)) A - \Delta T \gamma I] \mathbf{x}^*.$$

Hence, it follows that

$$(I - R_0 A) \mathbf{x}^* = 2R_0 \text{diag}(\mathbf{x}^*) \text{diag}(\mathbf{x}^*) A \mathbf{x}^* - 3R_0 \text{diag}(\mathbf{x}^*) A \mathbf{x}^*.$$

Furthermore, we have

$[I + \text{diag}(3R_0 A \mathbf{x}^*) - \text{diag}(2R_0 A \mathbf{x}^*) \text{diag}(\mathbf{x}^*)] \mathbf{x}^* = R_0 A \mathbf{x}^*$,
Define $H(\mathbf{x}^*) = I + \text{diag}(3R_0 A \mathbf{x}^*) - \text{diag}(2R_0 A \mathbf{x}^*) \text{diag}(\mathbf{x}^*)$. It can be immediately seen that $H(\mathbf{x}^*)$ is a positive diagonal matrix with $[H(\mathbf{x}^*)]_{ii} \geq 1$, and as a consequence $H^{-1}(\mathbf{x}^*)$ exists. Thus we have

$$\mathbf{x}^* = H^{-1}(\mathbf{x}^*) R_0 A \mathbf{x}^* \quad (11)$$

By assumption, $\rho(M) > 1$. Hence, due to Lemma 1, it follows that $R_0 > 1$, and, hence we can choose a small ε satisfying $0 < \varepsilon < \frac{3R_0 - \sqrt{R_0^2 + 8R_0}}{4R_0}$. It then holds $0 < 1 + 3R_0\varepsilon - 2R_0\varepsilon^2 < R_0$ and thus $\varepsilon < \frac{R_0\varepsilon}{1 + 3R_0\varepsilon - 2R_0\varepsilon^2}$. Furthermore due to Assumption 4, it follows that $R_0 A \mathbf{1} = R_0 \mathbf{1}$. Then, for $i \in [n]$, we have

$$\varepsilon < \frac{[R_0 A \mathbf{1}]_i \varepsilon}{1 + 3[R_0 A \mathbf{1}]_i \varepsilon - 2[R_0 A \mathbf{1}]_i \varepsilon^2}.$$

Hence, it follows that

$$\varepsilon \cdot \mathbf{1} < H^{-1}(\varepsilon \cdot \mathbf{1}) R_0 A (\varepsilon \cdot \mathbf{1}).$$

Similarly, by taking μ satisfying $\frac{3R_0 - \sqrt{R_0^2 + 8R_0}}{4R_0} < \mu < 1$, we have

$$\mu \cdot \mathbf{1} > H^{-1}(\mu \cdot \mathbf{1}) R_0 A (\mu \cdot \mathbf{1}).$$

It is clear that $\bar{x} = \frac{3R_0 - \sqrt{R_0^2 + 8R_0}}{4R_0}$ satisfies

$$\bar{x} \cdot \mathbf{1} = H^{-1}(\bar{x} \cdot \mathbf{1}) R_0 A (\bar{x} \cdot \mathbf{1}).$$

We prove uniqueness by a contradiction argument. Suppose that there is another endemic equilibrium $\bar{\mathbf{x}}^* = [\bar{x}_1^*, \bar{x}_2^*, \dots, \bar{x}_n^*]$. Let $\zeta = \max_{i \in [n]} \frac{\bar{x}_i^*}{\bar{x}}$. We would like to show that $\zeta \leq 1$. By way of contradiction, assume that $\zeta > 1$. This implies that $\bar{\mathbf{x}}^* \leq \zeta \bar{\mathbf{x}} \cdot \mathbf{1}$ and there exists an i_0 such that $\bar{x}_{i_0}^* = \zeta \bar{x}$. We note that $\bar{x}_{i_0}^* \leq 1$ so that $1 < \zeta \leq 1/\bar{x}$. Define a map $f(x_i) : \mathbb{R}_+ \rightarrow \mathbb{R}_+$ such that $f(x_i) = [H^{-1}(\mathbf{x}^*)R_0A\mathbf{x}^*]_i$. Then, for the aforementioned node i_0 , based on (11) and since $f(\bar{x}_{i_0}^*) = f(\zeta \bar{x})$, we have

$$\begin{aligned} \bar{x}_{i_0}^* &= \frac{[R_0A\bar{\mathbf{x}}^*]_{i_0}}{1 + 3[R_0A\bar{\mathbf{x}}^*]_{i_0} - 2[R_0A\text{diag}(\bar{\mathbf{x}}^*)\bar{\mathbf{x}}^*]_{i_0}} \\ &= \frac{[R_0A\zeta \bar{\mathbf{x}} \cdot \mathbf{1}]_{i_0}}{1 + 3[R_0A\zeta \bar{\mathbf{x}} \cdot \mathbf{1}]_{i_0} - 2[R_0A\text{diag}(\zeta \bar{\mathbf{x}} \cdot \mathbf{1})\zeta \bar{\mathbf{x}} \cdot \mathbf{1}]_{i_0}} \\ &= \frac{\zeta [R_0A\bar{\mathbf{x}} \cdot \mathbf{1}]_{i_0}}{1 + 3\zeta [R_0A\bar{\mathbf{x}} \cdot \mathbf{1}]_{i_0} - 2\zeta^2 [R_0A\text{diag}(\bar{\mathbf{x}} \cdot \mathbf{1})\bar{\mathbf{x}} \cdot \mathbf{1}]_{i_0}} \\ &= \frac{R_0\zeta \bar{x}}{1 + 3R_0\zeta \bar{x} - 2R_0\zeta^2 \bar{x}^2}. \end{aligned} \quad (12)$$

Let

$$\begin{aligned} g(\zeta) &= [1 + 3R_0\zeta \bar{x} - 2R_0(\zeta \bar{x})^2] - [1 + 3R_0\bar{x} - 2R_0\bar{x}^2] \\ &= 3R_0\bar{x}(\zeta - 1) - 2R_0\bar{x}^2(\zeta - 1)(\zeta + 1) \\ &= R_0\bar{x}(\zeta - 1)(3 - 2\zeta \bar{x} - 2\bar{x}). \end{aligned}$$

Since $\zeta \bar{x} \leq 1$ and $\zeta > 1$, we have

$$g(\zeta) \geq R_0\bar{x}(\zeta - 1)(1 - 2\bar{x}) > 0.$$

Thus, from (12), we have

$$\bar{x}_{i_0}^* < \frac{\zeta R_0\bar{x}}{1 + 3R_0(\bar{x}) - 2R_0(\bar{x})^2} = \zeta \bar{x} = \bar{x}_{i_0}^*. \quad (13)$$

Hence, we obtain a contradiction of the assumption that $\zeta > 1$, thus implying $\zeta \leq 1$. Therefore, if there exists another equilibrium $\bar{\mathbf{x}}^*$, it must satisfy $\bar{\mathbf{x}}^* \leq \bar{\mathbf{x}} \cdot \mathbf{1}$. By exchanging the roles of $\bar{\mathbf{x}}^*$ and $\bar{\mathbf{x}} \cdot \mathbf{1}$, by a similar analysis as before, we obtain $\bar{\mathbf{x}}^* \geq \bar{\mathbf{x}} \cdot \mathbf{1}$. This implies $\bar{\mathbf{x}}^* = \bar{\mathbf{x}} \cdot \mathbf{1}$, thus concluding the proof of uniqueness.

Step 2: Stability of the endemic equilibrium

First, note that any equilibrium \bar{x} of (4) satisfies:

$$\bar{x} = \bar{x} + \Delta T(\beta(1 - 2\bar{x})(1 - \bar{x}) \cdot \sum_{j=1}^n a_{ij}\bar{x} - \gamma \bar{x}).$$

Since, by Assumption 4, $\sum_{j=1}^n a_{ij} = 1$, and since $\bar{x} > 0$,

$$\beta(1 - 2\bar{x})(1 - \bar{x}) - \gamma = 0. \quad (14)$$

Let, for all $i \in [n]$, $y_i(k) = x_i(k) - \bar{x}$ and $\Delta y_i(k) = y_i(k+1) - y_i(k)$. Substituting $x_i(k) = y_i(k) + \bar{x}$ into (4) yields

$$\begin{aligned} \Delta y_i(k) &= \Delta T\beta(1 - 2\bar{x} - 2y_i(k))(1 - \bar{x} - y_i(k)) \\ &\quad \times \sum_{j=1}^n a_{ij}(y_j(k) + \bar{x}) - \Delta T\gamma \bar{x} - \Delta T\gamma y_i(k) \\ &= -\Delta T\gamma y_i(k) + \Delta T\beta(1 - 2\bar{x})(1 - \bar{x}) \sum_{j=1}^n a_{ij}y_j(k) \\ &\quad + \Delta T\beta(2y_i^2(k) + (4\bar{x} - 3)y_i(k)) \sum_{j=1}^n a_{ij}x_j(k) \\ &\quad + \Delta T(\beta(1 - 2\bar{x})(1 - \bar{x}) - \gamma) \bar{x}. \end{aligned}$$

From (14), $\Delta T(\beta(1 - 2\bar{x})(1 - \bar{x}) - \gamma) \bar{x} = 0$, and hence

$$\begin{aligned} \Delta y_i(k) &= \Delta T\beta(1 - 2\bar{x})(1 - \bar{x}) \sum_{j=1}^n a_{ij}y_j(k) - \Delta T\gamma y_i(k) \\ &\quad + \Delta T\beta(2y_i^2(k) + (4\bar{x} - 3)y_i(k)) \sum_{j=1}^n a_{ij}x_j(k). \end{aligned} \quad (15)$$

Since $\bar{x} > 0$, $\frac{1}{\bar{x}}$ exists. From (15), we have the following:

$$\begin{aligned} y_i(k+1) &= [(1 - \Delta T\gamma) + \Delta T\beta(4\bar{x} - 3)\bar{x}] y_i(k) \\ &\quad + 2\Delta T\beta\bar{x}y_i^2(k) + \Delta T\beta[(1 - 2\bar{x})(1 - \bar{x}) \\ &\quad + (4\bar{x} - 3)y_i(k) + 2y_i^2(k)] \sum_{j=1}^n a_{ij}y_j(k). \end{aligned} \quad (16)$$

Rewriting (14) in terms of β , and plugging it into (16) yields:

$$\begin{aligned} y_i(k+1) &= \left[(1 - \Delta T\gamma) + \Delta T\frac{\gamma(4\bar{x} - 3)\bar{x}}{(1 - 2\bar{x})(1 - \bar{x})} \right] \\ &\quad \times y_i(k) + \Delta T\frac{2\gamma\bar{x}}{(1 - 2\bar{x})(1 - \bar{x})} \times y_i^2(k) \\ &\quad + \Delta T\beta[(1 - 2\bar{x})(1 - \bar{x}) + (4\bar{x} - 3)y_i(k) + 2y_i^2(k)] \\ &\quad \times \sum_{j=1}^n a_{ij}y_j(k) \\ &= \left[1 - \Delta T\gamma \cdot \frac{1 - 2\bar{x}^2}{(1 - 2\bar{x})(1 - \bar{x})} \right] \times y_i(k) \\ &\quad + \Delta T\gamma \cdot \frac{2\bar{x}}{(1 - 2\bar{x})(1 - \bar{x})} \times y_i^2(k) \\ &\quad + \Delta T\beta[1 - 2(y_i(k) + \bar{x})][1 - (y_i(k) + \bar{x})] \\ &\quad \times \sum_{j=1}^n a_{ij}y_j(k). \\ &= \left[1 - \Delta T\gamma \cdot \frac{1 - 2\bar{x} \cdot (\bar{x} + y_i(k))}{(1 - 2\bar{x})(1 - \bar{x})} \right] \times y_i(k) \\ &\quad + \Delta T\beta[1 - 2(y_i(k) + \bar{x})][1 - (y_i(k) + \bar{x})] \\ &\quad \times \sum_{j=1}^n a_{ij}y_j(k). \quad (17) \\ &= \left[1 - \Delta T\gamma \cdot \frac{1 - 2\bar{x}x_i(k)}{(1 - 2\bar{x})(1 - \bar{x})} \right] \times y_i(k) \\ &\quad + \Delta T\beta(1 - 2x_i(k))(1 - x_i(k)) \sum_{j=1}^n a_{ij}y_j(k). \quad (18) \end{aligned}$$

Note that (18) holds since $x_i(k) = y_i(k) + \bar{x}$. Let $\mathbf{y}(k) = [y_1(k), y_2(k), \dots, y_n(k)]^T$ and we write (18) in matrix form so as to obtain $\mathbf{y}(k+1) = \Phi(k)\mathbf{y}(k)$,

$$\begin{aligned} \text{where } \Phi(k) &= I - \Delta T\gamma \text{diag} \left(\frac{1}{(1 - 2\bar{x})(1 - \bar{x})} \right) \\ &\quad + \Delta T\gamma \text{diag} \left(\frac{2\bar{x}}{(1 - 2\bar{x})(1 - \bar{x})} \right) \text{diag}(\mathbf{x}(k)) \\ &\quad + \Delta T\beta(I - 2\text{diag}(\mathbf{x}(k)))(I - \text{diag}(\mathbf{x}(k)))A. \end{aligned} \quad (19)$$

Construct a matrix D such that

$$D = I - \Delta T\gamma \text{diag} \left(\frac{1}{(1 - 2\bar{x})(1 - \bar{x})} \right) + \Delta T\beta A.$$

We can check that $[D]_{ij} = \Delta T\beta a_{ij}, \forall i \neq j$ and

$$\begin{aligned} [D]_{ii} &= 1 - \Delta T\gamma \frac{1}{(1 - 2\bar{x})(1 - \bar{x})} + \Delta T\beta a_{ii} \\ &= 1 - \Delta T\beta + \Delta T\beta a_{ii} \\ &= 1 - \Delta T\beta \sum_{j \neq i} a_{ij}. \end{aligned} \quad (20)$$

Thus we have $D\mathbf{1} = \mathbf{1}$. Since ΔT is sufficiently small and for every $i \in [n]$, $\Delta T\beta \sum_{j \neq i} a_{ij}$ is sufficiently small as well.

From (20), we have $[D]_{ii} > 0$. Then D is a non-negative irreducible matrix and moreover, $\mathbf{1} > \mathbf{0}$. Hence, we have $\rho(D) = 1$. In addition, based on the Perron-Frobenius Theorem for irreducible nonnegative matrices (Theorem 2.7 (Varga, 2000)), we can also find a left vector $\mathbf{v}^T > \mathbf{0}^T$ such that $\mathbf{v}^T D = \mathbf{v}^T$.

Construct an auxiliary system as follows

$$\mathbf{z}(k+1) = \Phi(k)\mathbf{z}(k), \quad (21)$$

where $\mathbf{z}(0) = |\mathbf{y}(0)|$. Since $\Phi(k)$ is a non-negative matrix, we have $\mathbf{z}(k) \geq \mathbf{0}$ and $-\mathbf{z}(k) \leq \mathbf{y}(k) \leq \mathbf{z}(k), \forall k \in \mathbb{Z}_+$. Therefore, $\mathbf{y}(k)$ is asymptotically stable if the origin is asymptotically stable for $\mathbf{z}(k)$. Consider Lyapunov candidate $V(k) = \mathbf{v}^T \mathbf{z}(k)$, and it can be readily seen that

$V(k) \geq 0$ since $\mathbf{v}^T > \mathbf{0}^T$, $\mathbf{z}(k) \geq \mathbf{0}$. We note that $V(k) = 0$ only if $\mathbf{z}(k) = \mathbf{0}$. Therefore, we have

$$\begin{aligned} V(k+1) - V(k) &= \mathbf{v}^T (\mathbf{z}(k+1) - \mathbf{z}(k)) \\ &= \mathbf{v}^T (\Phi(k) - I)\mathbf{z}(k) \\ &= \mathbf{v}^T (\Phi(k) - D)\mathbf{z}(k). \end{aligned} \quad (22)$$

$$\begin{aligned} \Phi(k) - D &= \Delta T \gamma \text{diag} \left(\frac{2\bar{x}}{(1-2\bar{x})(1-\bar{x})} \right) \text{diag}(\mathbf{x}(k)) \\ &\quad + \Delta T \beta \text{diag}(\mathbf{x}(k))(2\text{diag}(\mathbf{x}(k)) - 3I)A. \end{aligned} \quad (23)$$

We note that $[\Phi(k) - D]_{ij} = \Delta T \beta_i (2x_i(k) - 3)a_{ij} < 0$, $i \neq j$. Observe that

$$\begin{aligned} [\Phi(k) - D]_{ii} &= \Delta T x_i(k) \left[\frac{2\gamma\bar{x}}{(1-2\bar{x})(1-\bar{x})} \right. \\ &\quad \left. + \beta(2x_i(k) - 3)a_{ii} \right] \\ &= \Delta T x_i(k) [2\beta\bar{x} + \beta(2x_i(k) - 3)a_{ii}] \\ &< \Delta T \beta x_i(k) [1 - 2a_{ii}] < 0 \end{aligned} \quad (24)$$

$$(25)$$

We note that (24) is based on (14). Moreover, based on $\bar{x}_i < 1/2$, $\forall i$, $x_i(k) < 1/2$, $a_{ii} > 1/2$ and Assumption 4, we obtain (25). Thus, $\Phi(k) - D$ is a matrix in which every element is negative. Then we have $V(k+1) - V(k) \leq 0$ from (22), and the equality holds if and only if $\mathbf{z}(k) = \mathbf{0}$. Thus, from (Vidyasagar, 2002), it follows that the auxiliary system (21) converges asymptotically to the origin. Thus, the system (4) converges asymptotically to the endemic equilibrium. \square

Proof of Theorem 3: We first consider the case where $R_0 \leq 1$. Based on Assumptions 1–4 and the results in Lemma 1 and Theorem 1, for an initial state $0 < x_i(0) < 1/2$, the state $x_i(k)$ asymptotically converges to 0. Define $x_{\max}(k) = \max_{i \in [n]} \{x_i(k)\}$. Then, based on (4), we have

$$\begin{aligned} x_i(k+1) &= x_i(k) + \Delta T (\beta(1 - 2x_i(k))(1 - x_i(k)) \\ &\quad \times \sum_{j=1}^n a_{ij} x_j(k) - \gamma x_i(k)) \\ &\leq x_i(k) + \Delta T [\beta(1 - 2x_i(k))(1 - x_i(k))x_{\max}(k) - \gamma x_i(k)] \\ &\quad (26) \\ &< x_i(k) + \Delta T [\gamma(1 - x_i(k))x_{\max}(k) - \gamma x_i(k)] \\ &\quad (27) \\ &\leq (1 - \Delta T \gamma)x_{\max}(k) + \Delta T \gamma(1 - x_i(k))x_{\max}(k) \\ &\quad (28) \\ &< x_{\max}(k). \end{aligned} \quad (29)$$

The inequality (26) is due to $x_j(k) \leq x_{\max}(k)$ and Assumption 4, whereas inequality (27) follows due to the fact that the assumption $R_0 \leq 1$ implies $\beta \leq \gamma$ and, due to $1 - 2x_i(k) < 1$. Inequality (28) follows due to $x_i(k) \leq x_{\max}(k)$ while inequality (29) is immediate. Thus, for every $i \in [n]$ and $x_i(k) \neq 0$, we have $x_i(k+1) < x_{\max}(k) < x_{\max}(0) < 1/2$.

Next, we consider the case where $\rho(M) > 1$. Suppose that $\rho(M) > 1$, then, since system (4) satisfies Assumptions 1–4, from Theorem 2, we know that there exists endemic equilibrium $\bar{\mathbf{x}}$ such that for every $i \in [n]$, $0 < \bar{x}_i < 1/2$.

We note that $R_0 > 1$ if $\rho(M) > 1$. In the following analysis, we would like to consider the following two cases:

Case 1: The local states that satisfies

$$\frac{1}{2} \left(1 - \frac{1}{R_0} \right) < x_i(k) < \frac{1}{2}.$$

Based on (3), we have the following inequalities:

$$\begin{aligned} x_i(k+1) &\leq x_i(k) + \Delta T \gamma ((1 - 2x_i(k))(1 - x_i(k)) \\ &\quad \times x_{\max}(k)R_0 - x_i(k)) \end{aligned} \quad (30)$$

$$< x_i(k) + \Delta T \gamma ((1 - x_i(k))x_{\max}(k) - x_i(k)) \quad (31)$$

$$< x_{\max}(k). \quad (32)$$

We note that (31) hold since $\frac{1}{2} \left(1 - \frac{1}{R_0} \right) < x_i(k) < 1/2$, then we have $(1 - 2x_i(k))R_0 < 1$. Inequality (32) follows from the same line of reasoning as inequality (26).

Case 2: The local states that satisfies

$$0 < x_i(k) < \frac{1}{2} \left(1 - \frac{1}{R_0} \right).$$

Since the initial states satisfies $0 < x_i(0) < 1/2$, we have that $x_i(k) < 1/2$, $\forall i \in [n]$. The monotonicity is unclear in this case. If $x_i(k)$ does not exceed the interval, it is clear that we have $0 < x_i(k) < 1/2$, $\forall k \in \mathbb{Z}_+$. Otherwise, from (4), we have

$$x_i(k+1) \leq x_i(k) + \Delta T \beta \sum_{j=1}^n a_{ij}.$$

Based on Assumption 3, ΔT is sufficiently small such that the increment $\Delta T \beta \sum_{j=1}^n a_{ij}$ is sufficiently small as well. Then there must exists some time $k' > k$ such that $x_i(k')$ satisfies Case 1.

Thus, for all agents with initial local states that satisfies Assumption 2, we always have $x_i(k) < 1/2$ for all $k \in \mathbb{Z}_+$. \square