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

Yuan Wang ∗ Sebin Gracy ∗ Hideaki Ishii ∗∗ and Karl Henrik Johansson ∗

∗ Division of Decision and Control Systems, School of Electrical Engineering and Computer Science, KTH Royal Institute of Technology, and Digital Futures, Stockholm, Sweden.
yuanwang@kth.se, gracy@kth.se, kallej@kth.se

∗∗ Department of Computer Science, Tokyo Institute of Technology, Yokohama, Japan. ishii@c.titech.ac.jp

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 $\beta$, scaled by the interactions it has with its neighboring agents; in a similar manner, an infected agent recovers based on the healing rate $\gamma$. 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 designed...
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., 2021), 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 $\mathbf{1} = [1, 1, \ldots, 1]^T$ and $\mathbf{0} = [0, 0, \ldots, 0]^T$ to denote the vectors of all-ones and all-zeros, respectively. Given a matrix $A$, $A < 0$ (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 $G = (V, E)$, where $V = \{1, 2, \ldots, n\}$ denotes the set of agents and $E$ denotes the set of interconnections between the agents. More precisely, $E = \{(i, j) \in V \times V \mid a_{ij} \neq 0\}$. That is, there is a directed edge from agent $j$ to agent $i$ if agent $i$ can infect agent $j$.

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

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

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):

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

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 $\beta$ to, at each time instant, $b_i(k)\beta$. Hence, the dynamics in (2) can be written as

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

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
\( x_i(k+1) = x_i(k) + \Delta T \beta (1 - 2x_i(k))(1 - x_i(k)) \times \sum_{j=1}^n a_{ij}x_j(k) - \Delta T \gamma x_i(k). \) \hspace{1cm} (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 \( x(k) = [x_1(k), x_2(k), \ldots, x_n(k)]^T \). Then, in vector form, (4) can be written as:

\[
(1 + \Delta T \beta (I - 2\text{diag}(x(k)))(I - \text{diag}(x(k)))A - \Delta T \gamma I)x(k).
\] \hspace{1cm} (5)

Observe that (5) can be further rewritten as:

\[
x(k+1) = \hat{M}(k)x(k),
\] \hspace{1cm} (6)

where

\[
\hat{M}(k) = M - B(k)A,
\] \hspace{1cm} (7)

\[
M = I + \Delta T \beta A - \Delta T \gamma I,
\] \hspace{1cm} (8)

\[
B(k) = \Delta T \beta \text{diag}(x(k))(3I - 2\text{diag}(x(k)) ).
\] \hspace{1cm} (9)

We need the following assumptions for our analysis.

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

Note that the adjacency matrix \( A \) is irreducible if and only if the underlying graph \( G \) is strongly connected.

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

**Assumption 3.** \( \Delta T \) 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 \( \forall i \in [n], \lim_{k \to \infty} x_i(k) = 0 \). Also it is said to reach an endemic equilibrium if the states converge to a positive constant, i.e., \( \forall i \in [n], \lim_{k \to \infty} x_i(k) = x_i^* \), 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 \( [0, 1/2]^n \). \hspace{1cm} (9)

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 \( x_{\lambda(A)} \) be the eigenvector for the eigenvalue \( \lambda(A) \). Then

\[
Mx_{\lambda(A)} = [I + \Delta T \beta A - \Delta T \gamma I]x_{\lambda(A)}
\] \hspace{1cm} (10)

\[
= [1 + \Delta T (\beta \lambda(A) - \gamma)]x_{\lambda(A)}
\]

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., \( \beta > \gamma \)). \hspace{1cm} \Box

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

\[
\bar{x} = 3R_0 - \sqrt{R_0^2 + 8R_0} \over 4R_0.
\]

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

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 \( \bar{x} \cdot 1 < 1/2 \) and thus \( \lim_{k \to \infty} x_i(k) < 1/2 \). 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 \( 100 \times 100 \). 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.

REFERENCES

Anderson, R.M. and May, R.M. (1992). Infectious Diseases of Humans: Dynamics and Control. Oxford University Press.

Bernoulli, D. (1760). Essai d’une nouvelle analyse de la mortalité causée par la petite vérole, et des avantages de l’incubation pour la prévenir. Histoire de l’Acad., Roy. Sci.(Paris) avec Mem., 1–45.

Fall, A., Iggidir, A., Sallet, G., and Tewa, J.J. (2007). Epidemic models and Lyapunov functions. Mathematical Modelling of Natural Phenomena, 2(1), 62–83.

Lajmanovich, A. and Yorke, J.A. (1976). A deterministic model for gonorrhea in a nonhomogeneous population. Mathematical Biosciences, 36(3-4), 221–236.

Liu, F., Cui, S., Li, X., and Buss, M. (2020). On the stability of the endemic equilibrium of a discrete-time networked epidemic model. IFAC-PapersOnLine, 53(2), 2576–2581.

Meyer, C. (2000). Matrix Analysis and Applied Linear Algebra. SIAM.

Morris, D.H., Rossine, F.W., Plotkin, J.B., and Levin, S.A. (2021). Optimal, near-optimal, and robust epidemic control. Communications Physics, 4(1), 1–8.

Nowzari, C., Preciado, V.M., and Pappas, G.J. (2016). Analysis and control of epidemics: A survey of spreading processes on complex networks. IEEE Control Systems Magazine, 36(1), 26–46.

Paré, P.E., Gracy, S., Sandberg, H., and Johansson, K.H. (2020a). Data-driven distributed mitigation strategies and analysis of mutating epidemic processes. In Proc. 59th IEEE Conference on Decision and Control (CDC), 6138–6143.

Paré, P.E., Liu, J., Beck, C.L., Kirwan, B.E., and Başar, T. (2020b). Analysis, estimation, and validation of discrete-time epidemic processes. IEEE Transactions on Control Systems Technology, 28(1), 79–93.

Rantzer, A. (2011). Distributed control of positive systems. In Proc. 50th IEEE Conference on Decision and Control and European Control Conference, 6608–6611.

Torres, J.A., Roy, S., and Wan, Y. (2016). Sparse resource allocation for linear network spread dynamics. IEEE Transactions on Automatic Control, 62(4), 1714–1728.

Varga, R. (2000). Matrix iterative analysis. Springer.

Vidyasagar, M. (2002). Nonlinear Systems Analysis. SIAM.

Wang, Y., Ishii, H., Bonnet, F., and Défago, X. (2021). Resilient consensus against epidemic malicious attacks. In Proc. European Control Conference, to appear. Also, arXiv preprint arXiv:2012.13757.

Watkins, N.J., Nowzari, C., Preciado, V.M., and Pappas, G.J. (2016). Optimal resource allocation for competitive spreading processes on bilayer networks. IEEE Trans. Control of Network Systems, 5(1), 298–307.

APPENDIX

We first introduce the following two lemmas for positive and non-negative matrices.

Lemma 2. (Rantzer, 2011, Lemma 2) Suppose that $M$ is an irreducible non-negative matrix such that $\rho(M) < 1$. Then, there exists a positive diagonal matrix $P$ such that $M^TPM - P < 0$.

Lemma 3. (Paré et al., 2020b, Lemma 3) Suppose that $M$ is an irreducible non-negative matrix such that $\rho(M) = 1$. Then, there exists a positive diagonal matrix $P$ such that $M^TPM - P \leq 0$.

Proof of Theorem 1: Due to Assumption 1, and since $a_{ij} \geq 0$, we know that $A$ is an irreducible non-negative matrix. Therefore, from (8), it also follows that $M$ is irreducible non-negative. We separately consider the cases $\rho(M) < 1$ and $\rho(M) = 1$.

Case 1 $\rho(M) < 1$: From Lemma 2, we know that there exists a positive diagonal matrix $P_1$ such that $M^TP_1M - P_1 < 0$. Consider the Lyapunov candidate given by $V_1(x) = x^TP_1x$ and it is immediate that $V_1(x) > 0$ for every $x \neq 0$. Let $\Delta V_1(x(k)) = V_1(x(k+1)) - V_1(x(k))$.

For $x(k) \neq 0, k \in \mathbb{Z}_+$, we have

$$\Delta V_1(x(k)) = x^T(k) \left[ M^TP_1M - P_1 \right] x(k) - x^T(k) P_1x(k+1) - x^T(k) P_1x(k)$$

$$= x^T(k) \left[ (M - B(k)A)P_1(M - B(k)A) - P_1 \right] x(k)$$

$$= x^T(k) \left[ (M - B(k)A)P_1 - M^TP_1M - P_1 - M^TP_1B(k)A \right] x(k) - M^TP_1B(k)A + A^T B^T(k) P_1 B(k)A \right] x(k).$$

(11)

Since $M^TP_1M - P_1$ is negative definite we have

$$\Delta V_1(x(k)) < x^T(k) \left[ -M^TP_1B(k)A - A^T B^T(k) P_1 M + A^T B^T(k) P_1 B(k)A \right] x(k).$$

(12)

Plugging (8) into (12), and due to Assumption 3, we have

$$\Delta V_1(x(k)) < x^T(k) \left[ -P_1 B(k)A - \Delta T \beta A^T P_1 B(k)A \right. \right.$$
It can be immediately seen that satisfying $0 < \varepsilon < \frac{3R_0R_1}{4\Delta T}$ and, hence, we arrive at

$$\Delta V_1(x(k)) = \mathbf{x}^T(k)A^T[-\Delta T \beta P_1(k) + \Delta T \beta B^T(k)P_1 + B^T(k)P_1(k)Ax(k)].$$

Note the inequality in (13) holds since $P_1$ and $B(k)$ are both positive diagonal matrices and $A$ is a non-negative matrix. The term $\Delta T \gamma - 1$ is negative, due to Assumption 3. Since $B(k)$ and $P_1(k)$ are diagonal and $P_1(k)B(k) = B(k)P_1(k)$, from (14), we have

$$\Delta V_1(x(k)) < \mathbf{x}^T(k)A^T(-2\Delta T \beta I + B(k))P_1(k)B(k)Ax(k).$$

Next we consider the matrix $\tilde{B}(k) = -2\Delta T \beta I + B(k)$:

$$\tilde{B}(k) = -2\Delta T \beta I + B(k) = -2\Delta T \beta I + \Delta T \beta \text{diag}(x(k))(3I - 2\text{diag}(x(k))) = \Delta T \beta [\text{diag}(x(k))(3I - 2\text{diag}(x(k))) - 2I].$$

Clearly, $B(k)$ is a diagonal matrix and its ith element is $[B(k)]_{ii} = \Delta T \beta (2x_i^2(k) + 3x_i(k) - 2)$. Since $0 < x_i(k) \leq 1$, we know that $[B(k)]_{ii} \leq (-7/8)\Delta T \beta < 0$, which indicates that $B(k)$ is negative definite. Moreover, since $A^T$, $P_1$ and $B(k)$ are all non-negative matrices, we conclude that $\Delta V_1(x(k)) < 0$ from (15). Therefore, from (Vidyasagar, 2002), the system converges asymptotically to the DFE for this case.

**Case 2** $\rho(M) = 1$: Due to Lemma 3, the condition $\rho(M) = 1$ guarantees the existence of a positive diagonal matrix $P_2$ such that $M^T P_2 M - P_2 \leq 0$. Consider the Lyapunov candidate given by $V_2(x(k)) = \mathbf{x}^T(k)P_2\mathbf{x}(k)$. The rest of the proof is quite similar to the case of $\rho(M) < 1$, and, hence, we arrive at $\Delta V_2(x(k)) < 0$. Therefore, from (Vidyasagar, 2002) it follows that the system converges asymptotically to the DFE for this case as well.

**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 equilibrium of the model. Subsequently, we establish, for all non-zero initial conditions, asymptotic convergence to the said equilibrium.

**Step 1: Existence/Uniqueness of the equilibrium**

By (5), an equilibrium $\mathbf{x}^* = [x_1^*, x_2^*, \ldots, x_n^*]^T$ satisfies

$$\mathbf{x}^* = \left[I + \Delta T \beta I(1 - 2\text{diag}(\mathbf{x}^*))(I - \text{diag}(\mathbf{x}^*))A - \Delta T \gamma I\right] \mathbf{x}^*.$$

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

$$[I + \text{diag}(3R_0A\mathbf{x}^*) - \text{diag}(2R_0A\mathbf{x}^*)\text{diag}(\mathbf{x}^*)] \mathbf{x}^* = R_0 A \mathbf{x}^*.$$

Define $H(\mathbf{x}^*) = I + \text{diag}(3R_0A\mathbf{x}^*) - \text{diag}(2R_0A\mathbf{x}^*)\text{diag}(\mathbf{x}^*)$. 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

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

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

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

Hence, it follows that

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

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

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

It is clear that $\mathbf{r} = \frac{3R_0 - \sqrt{R_0^2 + 8R_0}}{4\Delta T}$ satisfies

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

We prove uniqueness by a contradiction argument. Suppose that there is another equilibrium $\mathbf{x}^* = [x_1^*, x_2^*, \ldots, x_n^*]$. Let $\zeta = \max_{i \in [n]} x_i^*$. We would like to show that $\zeta \leq 1$. By way of contradiction, assume that $\zeta > 1$. This implies that $\mathbf{x}^* \leq \zeta \mathbf{r} \cdot 1$ and there exists an $i_0$ such that $\mathbf{r}_{i_0} = \zeta_{i_0} \mathbf{r}$. We note that $\mathbf{r}_{i_0} \leq 1$ so that $1 < \zeta \leq 1/\mathbf{r}$. Define a map $f(ix) : \mathbb{R}_+ \rightarrow \mathbb{R}_+$ such that $f(ix) = [H^{-1}(ix) R_0 A \mathbf{x}^*]_i$. Then, for the aforementioned node $i_0$, based on (17) and since $f(\mathbf{r}_{i_0}) = f(\zeta_{i_0})$, we have

$$\mathbf{r}_{i_0} = \frac{[R_0 A \mathbf{x}^*]_{i_0}}{1 + 3[R_0 A \mathbf{x}^*]_{i_0} \varepsilon - 2[R_0 A \mathbf{x}^*]_{i_0} \varepsilon^2}.$$

Let

$$g(\zeta) = [1 + 3R_0 \mathbf{r} - 2R_0(\mathbf{r})^2] - [1 + 3R_0 \mathbf{r} - 2R_0(\mathbf{r}^2)] = 3R_0 \mathbf{r}(\zeta - 1) - 2R_0(\mathbf{r})(\zeta - 1)(\zeta + 1) = R_0 \mathbf{r}(\zeta - 1) (3 - 2\mathbf{r} - 2\mathbf{r^2}).$$

Since $\mathbf{r} \leq 1$ and $\zeta > 1$, we have

$$g(\zeta) > R_0 \mathbf{r}(\zeta - 1)(1 - 2\mathbf{r}) > 0.$$
\[ \Delta y_i(k) = \Delta T \beta (1 - 2\theta - 2y_i(k)) (1 - \theta - y_i(k)) \times \sum_{j=1}^{a_i} a_{ij}(y_j(k) + \theta) - \Delta T \gamma (1 - \theta - y_i(k)) \]
\[ = - \Delta T \gamma y_i(k) + \Delta T \beta (1 - 2\theta) \sum_{j=1}^{a_i} a_{ij}(y_j(k) + \theta) \]
\[ + \Delta T \beta (2y_i^2(k) + (4\theta - 3)y_i(k)) \sum_{j=1}^{a_i} a_{ij}x_j(k) \]
\[ + \Delta T \beta (1 - 2\theta) (1 - \theta - \gamma) \]
From (20), \[ \Delta T \beta (1 - 2\theta)(1 - \theta - \gamma) = 0, \]
and hence \[ \Delta y_i(k) = \Delta T \beta (1 - 2\theta) \sum_{j=1}^{a_i} a_{ij}(y_j(k) + \theta) \]
\[ + \Delta T \beta (2y_i^2(k) + (4\theta - 3)y_i(k)) \sum_{j=1}^{a_i} a_{ij}x_j(k). \] (21)

Since \( \theta > 0, \frac{1}{\theta} \) exists. From (21), we have the following:
\[ y_i(k+1) = \left[ (1 - \Delta T \gamma) + \Delta T \beta (1 - 2\theta)(1 - \theta) \right] y_i(k) \]
\[ + 2\Delta T \beta [1 - 2\theta] + \Delta T \beta [1 - 2\theta] \Delta T \beta (2y_i^2(k) + (4\theta - 3)y_i(k)) \sum_{j=1}^{a_i} a_{ij}y_j(k). \] (22)

Rewriting (20) in terms of \( \beta \), and plugging it into (22) yields:
\[ y_i(k+1) = \left[ (1 - \Delta T \gamma) + \Delta T \beta (1 - 2\theta)(1 - \theta) \right] y_i(k) \]
\[ + \Delta T \beta [1 - 2\theta] + \Delta T \beta (2y_i^2(k) + (4\theta - 3)y_i(k)) \sum_{j=1}^{a_i} a_{ij}x_j(k). \]

Thus we have \( D_1 = 1 \). Since \( \Delta T \) is sufficiently small and for every \( i \in [a], \Delta T \beta \sum_{j \neq i} a_{ij} \) is sufficiently small as well. From (26), we have \( |D|_{ji} > 0 \). Then \( D \) is a non-negative irreducible matrix and moreover, \( 1 > 0 \). 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 \( v^T > 0^T \) such that \( v^T D = v^T \).

Construct an auxiliary system as follows
\[
\zeta(k+1) = \Phi(\zeta(k)),
\]
where \( \zeta(0) = \gamma(0) \), since \( \Phi(\cdot) \) is a non-negative matrix, we have \( \zeta(k) \geq 0 \) and \( -z(k) \leq \gamma(k) \leq z(k) \), \( \forall k \in \mathbb{Z}_+ \). Therefore, \( \gamma(k) \) is asymptotically stable if the origin is asymptotically stable for \( z(k) \). Consider Lyapunov candidate \( V(k) = v^T z(k) \), and it can be readily seen that \( V(k) \geq 0 \) since \( v^T > 0^T, z(k) \geq 0 \). We note that \( V(k) = 0 \) only if \( z(k) = 0 \). Therefore, we have
\[
V(k+1) - V(k) = v^T (z(k+1) - z(k)) = v^T (\Phi(k) - I) z(k)
= v^T (\Phi(k) - D) z(k).
\]

Thus, \( \Phi(k) = D - \Delta T \gamma \text{diag} \left( \frac{2\theta}{(1 - 2\theta)(1 - \theta)} \right) \text{diag}(x(k)) \]
\[ + \Delta T \beta \text{diag}(x(k))(2 \text{diag}(x(k)) - 3I)A. \] (29)

We note that \( |\Phi(k) - D|_{ji} = |\Delta T \beta (2x_i(k) - 3a_{ij}| < 0, i \neq j \). Observe that
\[
\Phi(k) - D|_{ii} = \Delta T x_i(k) \left[ \frac{2\theta}{(1 - 2\theta)(1 - \theta)} \right] \text{diag}(x(k))
+ \beta (2x_i(k) - 3a_{ii}) \]
\[ = \Delta T x_i(k) \left[ \frac{2\theta}{(1 - 2\theta)(1 - \theta)} \right] \text{diag}(x(k))
+ \beta (2x_i(k) - 3a_{ii}). \] (30)

We note that (30) is based on (20). Moreover, based on \( \theta_t < 1/2, \forall i, x_i(k) < 1/2, a_{ii} > 1/2 \) and Assumption 4, we obtain (31). Thus, \( \Phi(k) - D \) is a matrix in which every element is negative. Then we have \( V(k+1) - V(k) \leq 0 \) from (28), and the equality holds if and only if \( z(k) = 0 \). Thus, from (Vidyasagar, 2002), it follows that the auxiliary system (27) converges asymptotically to the origin. Thus, the system (4) converges asymptotically to the endeminc equilibrium. □

**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 \( x_{\text{max}}(k) = \max_{i \in [a]} x_i(k) \). Then, based on (4), we have
\[
x_i(k+1) = x_i(k) + \Delta T \beta (1 - 2x_i(k))(1 - x_i(k)) \sum_{j=1}^{a_i} a_{ij}x_j(k) - \gamma x_i(k) \leq x_i(k) + \Delta T \beta (1 - 2x_i(k))(1 - x_i(k))x_{\text{max}}(k) - \gamma x_i(k)
\]
\[ < x_i(k) + \Delta T \beta (1 - x_i(k))x_{\text{max}}(k) \gamma x_i(k). \] (32)

We can check that \( |D|_{ji} = |\Delta T \beta a_{ij}, \forall i \neq j \) and
\[
|D|_{ij} = 1 - \Delta T \beta \sum_{j \neq i} a_{ij}.
\]

The inequality (32) is due to \( x_i(k) \leq x_{\text{max}}(k) \) and Assumption 4, whereas inequality (33) 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 (34) follows due to...
\(x_i(k) \leq x_{\text{max}}(k)\) while inequality (35) is immediate. Thus, for every \(i \in [n]\) and \(x_i(k) \neq 0\), we have \(x_i(k + 1) < x_{\text{max}}(k) < x_{\text{max}}(0) < 1/2\).

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 \(\overline{x}\) such that for every \(i \in [n]\), \(0 < \overline{x}_i < 1/2\).

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:
\[
\begin{align*}
x_i(k + 1) &\leq x_i(k) + \Delta T \gamma ((1 - 2x_i(k))(1 - x_i(k)) \times x_{\text{max}}(k)R_0 - x_i(k)) \leq x_i(k) + \Delta T \gamma ((1 - x_i(k))x_{\text{max}}(k) - x_i(k)) \leq x_{\text{max}}(k). \quad (36) \\
&< x_i(k) + \Delta T \gamma ((1 - x_i(k))x_{\text{max}}(k) - x_i(k)) \leq x_{\text{max}}(k). \quad (37) \\
&< x_{\text{max}}(k). \quad (38)
\end{align*}
\]

We note that (37) 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 (38) follows from the same line of reasoning as inequality (32).

**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, \(\Delta T\) 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 \(k \in \mathbb{Z}^+\).