

A Network SIS Meta-Population Model with Transportation Flow ^{*}

Mengbin Ye ^{*}, Ji Liu ^{***}, Carlo Cenedese ^{**}, Zhiyong Sun ^{****},
Ming Cao ^{**}

^{*} *Optus-Curtin Centre of Excellence in Artificial Intelligence, Curtin
University, Perth, Australia*

^{**} *Faculty of Science and Engineering, ENTEG, University of
Groningen, Groningen 9747 AG, Netherlands*

^{***} *Department of Electrical and Computer Engineering, Stony Brook
University, New York, USA*

^{****} *Department of Electrical Engineering, Eindhoven University of
Technology, the Netherlands.*

*E-mail: mengbin.ye@curtin.edu.au, {c.cenedese, m.cao}@rug.nl,
ji.liu@stonybrook.edu, z.sun@tue.nl*

Abstract: This paper considers a deterministic Susceptible-Infected-Susceptible (SIS) meta-population model for the spread of a disease in a strongly connected network, where each node represents a large population. Individuals can travel between the nodes (populations). We derive a necessary and sufficient condition for the healthy equilibrium to be the unique equilibrium of the system, and then in fact it is asymptotically stable for all initial conditions (a sufficient condition for exponential stability is also given). If the condition is not satisfied, then there additionally exists a unique endemic equilibrium which is exponentially stable for all nonzero initial conditions. We then consider time-delay in the travel between nodes, and further investigate the role of the mobility rate that governs the flow of individuals between nodes in determining the convergence properties. We find that sometimes, increasing mobility helps the system converge to the healthy equilibrium.

Keywords: SIS model, transportation flow, meta-population networked models

1. INTRODUCTION

The mathematical modelling of disease outbreaks in a large interconnected population is a fundamental area of research in epidemiology and public health studies (Anderson and May, 1991; Nowzari et al., 2016), in part because experimental approaches are either too expensive or impossible in large human populations. Various models have been proposed to capture such epidemic outbreaks, with the Susceptible-Infected-Susceptible (SIS) and Susceptible-Infected-Removed (SIR) models being two fundamental ones (Pastor-Satorras and Vespignani, 2001; Kermack and McKendrick, 1927; Mieghem et al., 2009).

Both deterministic and probabilistic versions of networked SIS models exist (Fagnani and Zino, 2017; Mieghem et al., 2009; Fall et al., 2007; Lajmanovich and Yorke, 1976). Deterministic models are often easier to analyse, especially when the modelling context is considering a large population interacting over a network (Mei et al., 2017), and can be captured by either a discrete-time system (Ahn and Hassibi, 2013) or a continuous-time system (Mieghem

et al., 2009). This paper will consider a deterministic continuous-time networked SIS model from the following perspective: spreading of a disease across a network of interconnected populations, viz. a *meta-population* (each node represents one large and well-mixed population).

Among deterministic networked SIS models, the most popular version dates back to (Lajmanovich and Yorke, 1976). Various versions have since been studied (Mei et al., 2017; Mieghem et al., 2009). These models capture disease spreading from *interaction between the nodes*, i.e., via physical contact between individuals from different populations in the meta-population network.

However, one can appreciate that if individuals can travel between populations (nodes), such as if the populations are geographically separated, then disease spread occurs due to *infected individuals flowing between populations*. Several works, primarily focusing on SIR models, have used statistical analysis on real-world data, and computational frameworks to illustrate how meta-population epidemic models that explicitly consider individual flow between populations can accurately capture real-world epidemics such as the H1N1 (Swine Influenza) and SARS (Severe Acute Respiratory Syndrome) viruses (Khan et al., 2009; Brockmann and Helbing, 2013; Colizza et al., 2006).

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In terms of modelling individual flow between populations in the SIS framework, one model was proposed in (Arino and Van den Driessche, 2003). However, the model had high complexity, and the focus was on establishing the convergence of the flow dynamics; only some limited local stability results were obtained for the epidemic dynamics. A “patchy environment” model was proposed and studied in (Wang and Zhao, 2004; Jin and Wang, 2005). It is found that either the healthy equilibrium (the disease is eradicated from each node) is the unique equilibrium and it is asymptotically stable for all ¹ initial conditions, or, and in addition to the healthy equilibrium, there exists a unique endemic equilibrium (the disease exists in a nonzero proportion of the population of each node) which is convergent for all nonzero initial conditions.

In this paper, we derive, using an approach inspired by Brockmann and Helbing (2013), a deterministic meta-population SIS networked model with individual transport flow between the populations. Each population has a constant recovery and infection parameter to capture intra-population disease dynamics. The amount of flow of each population is captured by a possibly heterogeneous mobility rate. We analyse the system on strongly connected networks and provide a necessary and sufficient condition for the healthy equilibrium to be unique and asymptotically stable for all initial conditions. If the condition is not satisfied, then there additionally exists a unique endemic equilibrium that is exponentially stable for all nonzero initial conditions. The possible limiting behaviour of the proposed model is therefore similar to the “patchy environment” model. However, by using Metzler and M -matrix theory, our equilibria and convergence analysis is greatly simplified compared to (Wang and Zhao, 2004; Jin and Wang, 2005), and we establish exponential stability properties (only asymptotic convergence is obtained for the “patchy environment” model). We then provide one necessary and one sufficient condition for convergence to the healthy equilibrium. Last, we analyse the role of the mobility rate in affecting the convergence behaviour.

We conclude by introducing some mathematical preliminaries. Section 2 will propose the SIS model, with analysis presented in Section 3. Conclusions are given in Section 4.

1.1 Notation

The n -column vector of all ones and zeros is given by $\mathbf{1}_n$ and $\mathbf{0}_n$, respectively. The $n \times n$ identity and $n \times m$ zero matrix are given by \mathbf{I}_n and $\mathbf{0}_{n \times m}$, respectively. For a vector $\mathbf{a} \in \mathbb{R}^n$ and matrix $\mathbf{A} \in \mathbb{R}^{n \times m}$, the i th entry of \mathbf{a} and i jth entry of \mathbf{A} are denoted by a_i and a_{ij} , respectively. For any two vectors $\mathbf{a}, \mathbf{b} \in \mathbb{R}^n$, we write $\mathbf{a} \geq \mathbf{b}$ if $a_i \geq b_i$ for all $i \in \{1, \dots, n\}$, $\mathbf{a} > \mathbf{b}$ if $\mathbf{a} \geq \mathbf{b}$ and $\mathbf{a} \neq \mathbf{b}$, and $\mathbf{a} \gg \mathbf{b}$ if $a_i > b_i$ for all $i \in \{1, \dots, n\}$. Similarly, for any two matrices $\mathbf{A}, \mathbf{B} \in \mathbb{R}^{m \times n}$, we write $\mathbf{A} \geq \mathbf{B}$ if $a_{ij} \geq b_{ij}$ for all $i \in \{1, \dots, m\}$ and $j \in \{1, \dots, n\}$. We write $\mathbf{A} > \mathbf{B}$ if $\mathbf{A} \geq \mathbf{B}$ and $\mathbf{A} \neq \mathbf{B}$, and $\mathbf{A} \gg \mathbf{B}$ if $a_{ij} > b_{ij}$ for all $i \in \{1, \dots, m\}$ and $j \in \{1, \dots, n\}$. A matrix \mathbf{A} satisfying $\mathbf{A} > \mathbf{0}_{n \times n}$ and $\mathbf{A} \gg \mathbf{0}_{n \times n}$ is said to be nonnegative and positive, respectively. A matrix $\mathbf{A} > \mathbf{0}_{n \times n}$ is said to be column-stochastic if $\sum_{j=1}^n a_{ji} =$

¹ In most epidemic models, only initial conditions which are meaningful and of interest in the epidemic context are considered.

1 for all $i = 1, \dots, n$. For a square matrix \mathbf{M} with spectrum $\sigma(\mathbf{M})$, define $\rho(\mathbf{M}) = \max\{|\lambda| : \lambda \in \sigma(\mathbf{M})\}$ and $s(\mathbf{M}) = \max\{\text{Re}(\lambda) : \lambda \in \sigma(\mathbf{M})\}$ as the spectral radius and the largest real part among the eigenvalues of \mathbf{M} , respectively. A matrix \mathbf{M} is said to be *Hurwitz* if $s(\mathbf{M}) < 0$. For a set \mathcal{M} with boundary, denote the boundary as $\partial\mathcal{M}$, and the interior $\text{Int}(\mathcal{M}) \triangleq \mathcal{M} \setminus \partial\mathcal{M}$. We define $\Xi_n = \{x \in \mathbb{R}_{\geq 0}^n : 0 \leq x_i \leq 1, i \in \{1, \dots, n\}\}$.

1.2 Metzler matrices and M -matrices

We introduce two important classes of matrices and associated results for the analysis. Let $\mathcal{Z} \subset \mathbb{R}^{n \times n}$ denote the set of all matrices whose offdiagonal entries are nonpositive. A Metzler matrix is a matrix whose offdiagonal entries are all nonnegative (Berman and Plemmons, 1979). Clearly, if $\mathbf{A} \in \mathcal{Z}$, then $-\mathbf{A}$ is Metzler. A matrix $\mathbf{A} \in \mathcal{Z}$ is called an M -matrix if it can be written as $\mathbf{A} = c\mathbf{I}_n - \mathbf{B}$, with $c > 0$, $\mathbf{B} > \mathbf{0}_{n \times n}$ and $c \geq \rho(\mathbf{B})$ (Berman and Plemmons, 1979).

Lemma 1. ((Varga, 2009, Section 2.1)). Suppose that \mathbf{M} is an irreducible Metzler matrix. Then, $s(\mathbf{M})$ is a simple eigenvalue of \mathbf{M} and there exists a unique (up to a scaling) vector $\mathbf{x} \gg \mathbf{0}_n$ such that $\mathbf{M}\mathbf{x} = s(\mathbf{M})\mathbf{x}$. Let $\mathbf{z} > \mathbf{0}_n$ be a given vector. If $\mathbf{M}\mathbf{z} < \lambda\mathbf{z}$ for some scalar λ , then $s(\mathbf{M}) < \lambda$. If $\mathbf{M}\mathbf{z} = \lambda\mathbf{z}$ for some scalar λ , then $s(\mathbf{M}) = \lambda$. If $\mathbf{M}\mathbf{z} > \lambda\mathbf{z}$ for some scalar λ , then $s(\mathbf{M}) > \lambda$.

Lemma 2. ((Qu, 2009, Theorem 4.27)). Let $\mathbf{R} \in \mathcal{Z}$ be given. Then, the following statements are equivalent

- (1) \mathbf{R} is an M -matrix
- (2) The eigenvalues of \mathbf{R} have nonnegative real parts.

1.3 Graph Theory

Given a not necessarily symmetric matrix $\mathbf{A} > \mathbf{0}_{n \times n}$, we can associate with it a directed graph $\mathcal{G}[\mathbf{A}] = (\mathcal{V}, \mathcal{E}[\mathbf{A}], \mathbf{A})$, where $\mathcal{V} = \{v_1, \dots, v_n\}$ is the set of nodes. An edge $e_{ij} = (v_i, v_j)$ is in the set of ordered edges $\mathcal{E}[\mathbf{A}] \subseteq \mathcal{V} \times \mathcal{V}$ if and only if $a_{ji} > 0$. The edge e_{ij} is said to be incoming with respect to v_j and outgoing with respect to v_i . We define the incoming and outgoing neighbour sets of v_i as

$$\mathcal{N}_i^+ \triangleq \{v_j : e_{ji} = (v_j, v_i) \in \mathcal{E}[\mathbf{A}]\} \quad (1a)$$

$$\mathcal{N}_i^- \triangleq \{v_j : e_{ij} = (v_i, v_j) \in \mathcal{E}[\mathbf{A}]\} \quad (1b)$$

A directed path is a sequence of edges of the form $(v_{p_1}, v_{p_2}), (v_{p_2}, v_{p_3}), \dots$, where $v_{p_i} \in \mathcal{V}$ are distinct and $e_{p_i p_{i+1}} \in \mathcal{E}[\mathbf{A}]$. A graph $\mathcal{G}[\mathbf{A}]$ is *strongly connected* if and only if there is a path from every node to every other node, which is equivalent to \mathbf{A} being *irreducible* (Berman and Plemmons, 1979).

2. AN SIS MODEL WITH INDIVIDUAL FLOW

This section will propose a meta-population networked SIS model, with the model analysed in Section 3. We present the model, then provide explanations of the derivations, and compare it to others in the existing literature.

Consider n distinct large populations of individuals. Each population is well-mixed and represented by a node v_i in a network with $i \in \mathcal{I} \triangleq \{1, \dots, n\}$, and N_i the size of the population represented by node v_i . (We will sometimes refer to node v_i as population v_i for convenience). Each

individual is either *susceptible* (S) to, or *infected* (I) with, some disease. An individual may transition from being susceptible to being infected, and vice versa. The total numbers of susceptible and infected individuals in node v_i are given by S_i and I_i , respectively, which implies that $N_i = S_i + I_i$. Let $x_i = I_i/N_i$ denote the proportion of infected individuals in population v_i . Under the mild assumption that N_i is constant, reasonable for large populations, modelling and analysing $x_i(t)$ fully captures the disease dynamics over the meta-population network.

Formally, the dynamics of $x_i, i \in \mathcal{I}$, is given by

$$\dot{x}_i = -(\delta_i + \gamma_i)x_i + \alpha_i(1 - x_i)x_i + \sum_{j=1, j \neq i}^n \gamma_j w_{ij} x_j \frac{N_j}{N_i}. \quad (2)$$

The parameters $\delta_i > 0$ and $\alpha_i > 0$ capture the recovery and infection rate of the individuals in node v_i from the disease, while $\gamma_i \in (0, 1)$, for all $i \in \mathcal{I}$ is the constant *mobility rate* of node v_i . Roughly speaking, γ_i captures the proportion of individuals who are leaving v_i to travel to another node. The quantity $w_{ij} \in [0, 1]$ represents the proportion of all individuals leaving node v_j , that travel to node v_i . This implies that a natural constraint exists on the w_{ij} s: $\sum_{j=1}^n w_{ji} = 1$ and $w_{ii} = 0$, for all $i \in \mathcal{I}$.

By defining $\mathbf{x}(t) = [x_1(t), \dots, x_n(t)]^\top$ and $\mathbf{X}(t) = \text{diag}(x_1(t), \dots, x_n(t))$, the dynamics of the metapopulation network can be expressed as

$$\dot{\mathbf{x}}(t) = (-\mathbf{D} + \mathbf{\Gamma}) + \mathbf{A} - \mathbf{A}\mathbf{X}(t) + \mathbf{N}^{-1}\mathbf{W}\mathbf{\Gamma}\mathbf{N} \mathbf{x}(t), \quad (3)$$

where the $n \times n$ diagonal matrices \mathbf{D} , \mathbf{A} , \mathbf{N} , and $\mathbf{\Gamma}$ have i th diagonal entry δ_i , α_i , N_i , and γ_i , respectively. The column-stochastic matrix \mathbf{W} is associated with the graph $\mathcal{G}[\mathbf{W}]$, which represents the transportation network that allows individuals to travel between the nodes. For simplicity, we will sometimes analyse the dynamics Eq. (3) expressed as:

$$\dot{\mathbf{x}}(t) = (-\mathbf{U} - \mathbf{A}\mathbf{X}(t) + \mathbf{M}) \mathbf{x}(t), \quad (4)$$

where $\mathbf{U} = \mathbf{D} + \mathbf{\Gamma} - \mathbf{A}$ is a diagonal matrix. The nonnegative matrix $\mathbf{M} \triangleq \mathbf{N}^{-1}\mathbf{W}\mathbf{\Gamma}\mathbf{N}$ has entries $m_{ii} = 0$ and $m_{ij} = \gamma_j w_{ij} N_j / N_i$ for $i \neq j$. Because $m_{ij} > 0 \Leftrightarrow w_{ij} > 0$, $\mathcal{G}[\mathbf{W}]$ and $\mathcal{G}[\mathbf{M}]$ have the same node and edge set but different weights.

2.1 Derivation of Networked SIS Model with Flow

To begin, we recall the deterministic SIS model for a well-mixed population v_i (Anderson and May, 1991):

$$\dot{I}_i = -\delta_i I_i + \alpha_i \frac{S_i}{N_i} I_i + \pi_i. \quad (5)$$

The recovery and infection rates are $\delta_i > 0$ and $\alpha_i > 0$, respectively, and N_i is assumed to be constant. The term π_i represents the increase in the number of infected individuals in v_i due to effects from neighbouring nodes v_j . When $\pi_i \equiv 0$, i.e., the population is isolated, Eq. (5) reduces to the classical single population SIS model. A specific form of π_i for infection by flow of individuals between nodes is now described, which will yield Eq. (2).

The travel of individuals between nodes occurs over a network, captured by $\mathcal{G}[\mathbf{W}]$. An edge $e_{ji} \in \mathcal{E}[\mathbf{W}]$ indicates that individuals travel from node v_j to node v_i , and we define the incoming and outgoing neighbour set \mathcal{N}_i^+ and \mathcal{N}_i^- , of v_i as in Eq. (1), see Fig. 1. Let F_i^+ and F_i^-

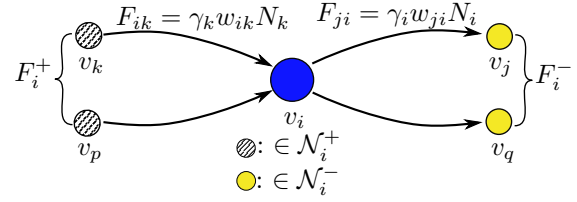


Fig. 1. Flow in and out of a node v_i . Individuals from node $v_k \in \mathcal{N}_i^+$ (striped nodes) flow into v_i , with a flux F_{ik} , while individuals leave v_i and travel to node $v_j \in \mathcal{N}_i^-$ (yellow nodes) with flux F_{ji} . For v_i , the total entering and leaving fluxes are $F_i^+ = \sum_{k \in \mathcal{N}_i^+} F_{ik}$ and $F_i^- = \sum_{j \in \mathcal{N}_i^-} F_{ji}$, respectively.

represent the *constant* flux of individuals (i.e. individuals per unit time) entering and leaving node v_i , respectively. By denoting the flux from node v_j to v_i as F_{ij} , one obtains $\sum_{j \in \mathcal{N}_i^+} F_{ij} = F_i^+$ and $\sum_{j \in \mathcal{N}_i^-} F_{ji} = F_i^-$. The assumption that N_i is constant leads to $F_i^+ = F_i^- \triangleq F_i$. Moreover, we argue that it is reasonable to assume that $F_i < N_i$, because $F_i = N_i$ implies that the entire population of v_i is on the move at any given time. We define the mobility rate of node v_i as $\gamma_i = \frac{F_i}{N_i}$, i.e. the portion of individuals in node v_i who are travelling, and it is constant since F_i and N_i are constant. Last, for $\mathcal{G}[\mathbf{W}]$ we define the weight of the edge e_{ij} as $w_{ji} \triangleq F_{ji}/F_i^-$: the proportion of individuals leaving v_i that travel to v_j . We have $F_{ji} = \gamma_i w_{ji} N_i$, and $\sum_{j \in \mathcal{N}_i^-} w_{ji} = 1$, which implies that \mathbf{W} is column stochastic with zero diagonal entries.

We now show how Eq. (2) is obtained. By assuming that infected and susceptible individuals are equally likely to travel, we propose that Eq. (5) takes the form of

$$\dot{I}_i = -\delta_i I_i + \alpha_i \frac{S_i}{N_i} I_i + \sum_{j=1, j \neq i}^n (F_{ij} \frac{I_j}{N_j} - F_{ji} \frac{I_i}{N_i}). \quad (6)$$

Thus, the last term in Eq. (6) identifies the difference in the flux of infected individuals flowing into $F_{ij} \frac{I_j}{N_j}$ and out $F_{ji} \frac{I_i}{N_i}$ of node v_i . With $x_i = I_i/N_i$, and recalling that (i) $F_{ij} = \gamma_j w_{ij} N_j$, and (ii) $S_i = N_i - I_i$, we obtain

$$\dot{x}_i = -\delta_i x_i + \alpha_i (1 - x_i)x_i + \sum_{j=1, j \neq i}^n (\gamma_j w_{ij} \frac{N_j}{N_i} x_j - \gamma_i w_{ji} x_i).$$

Eq. (2) is recovered by recalling that $\sum_{j=1, j \neq i}^n w_{ji} = 1$.

Notice that the population size N_i appears in the dynamics Eq. (2) explicitly. This is a direct consequence of the method used to model individuals *flowing* or travelling between nodes. Intuitively, for a fixed γ_i , the number of individuals leaving node v_i will increase linearly with N_i .

2.2 Existing Deterministic SIS Models

We briefly compare the dynamics in Eq. (2) with those in the literature. The most well known networked SIS model (Lajmanovich and Yorke, 1976) assumes that Eq. (5) is given with $\pi_i = \sum_{j \neq i} \beta_{ij} \frac{S_j}{N_j} I_j$, where $\beta_{ij} \geq 0$ is an infection rate from v_j to v_i . This extends Eq. (5) by assuming that individuals in node v_j and v_i *come into contact* if $\beta_{ij} > 0$, since $\beta_{ij} \frac{S_j}{N_j} I_j$ is simply the second term in Eq. (5)

but with I_j and β_{ij} replacing I_i and α_i , respectively². Such a model may be appropriate for capturing a meta-population where individuals from different populations come into regular physical contact, e.g. suburbs in a city, but not for geographically-separated populations. Our approach to modelling the flow of individuals is heavily inspired Brockmann and Helbing (2013), who study an SIR network model by which individuals travel between cities and spread diseases.

Some works in the mathematical biology community have considered flow-based “patchy” SIS models (Wang and Zhao, 2004; Jin and Wang, 2005; Arino and Van den Driessche, 2003, 2006) After a transient in which each population size N_i converges to a constant, the model of (Jin and Wang, 2005; Wang and Zhao, 2004), is given by

$$\dot{x}_i = -(\mu_i + \delta_i)x_i + \alpha_i(1 - x_i)x_i + \sum_{j=1}^n a_{ij}x_j, \quad (7)$$

where δ_i, α_i are as in Eq. (2), $\mu_i > 0$ is a natural death rate, and $a_{ii} \leq 0$ and $a_{ij} \geq 0$ for $j \neq i$. However, there are no constraints on the a_{ij} or a_{ii} , unlike the constraints of $\gamma_i \in (0, 1)$ and $\sum_{j=1}^n w_{ji} = 1$ in Eq. (2). These differences arise from differences in the derivation of the model, leading to significantly different conclusions regarding the role of the flow rate γ_i in the spread of the disease, as we will report in Section 3.2.

3. ANALYSIS

We now analyse the system in Eq. (3) and fully characterise the equilibria and convergence properties. The proof of the main convergence theorem is given in the Appendix A, while other proofs are omitted due to spatial constraints and will be included in an extended version of this paper. To begin, we impose the following assumptions on the parameters.

Assumption 1. For all $i \in \mathcal{I}$, there holds $\delta_i > 0, \alpha_i > 0$, and $\gamma_i \in (0, 1)$. The matrix $\mathbf{W} > \mathbf{0}_{n \times n}$ is irreducible, with entries satisfying $w_{ii} = 0$ and $\sum_{j=1}^n w_{ji} = 1$ for all $i \in \mathcal{I}$.

It is worth emphasising that an irreducible \mathbf{W} implies that the graphs $\mathcal{G}[\mathbf{W}]$ and $\mathcal{G}[\mathbf{M}]$ are strongly connected.

3.1 Equilibria and Convergence Properties

Since each x_i denotes the proportion of infected individuals in population (node) v_i , it is natural to assume that the initial value $\mathbf{x}(0) \in \Xi_n$. We will now prove that Ξ_n is positively invariant for the system in Eq. (3), which ensures that $x_i(t)$ for all $t \geq 0$ retains its important physical meaning in the epidemic context. From here on, we focus on the analysis of the system Eq. (3) only in Ξ_n .

Lemma 3. Suppose that Assumption 1 holds. If $\mathbf{x}(0) \in \Xi_n$, then the system Eq. (3) satisfies $\mathbf{x}(t) \in \Xi_n$ for all $t \geq 0$. Moreover, if $\mathbf{x}(t) \in \partial\Xi_n \setminus \mathbf{0}_n$, then there exists a finite κ such that $\mathbf{x}(t + \kappa) \in \text{Int}(\Xi_n)$.

Clearly, $\mathbf{x} = \mathbf{0}_n$ is an equilibrium of the system Eq. (3), in which no population has any infected individuals. We call this trivial equilibrium the *healthy equilibrium*. In contrast,

² Often, the literature defines $\beta_{ii} = \alpha_i$ as a self-infection parameter, and combines the second and third summands of Eq. (5).

nonzero equilibria of the system (if they exist) reflect a diseased steady state, and are called *endemic or nontrivial equilibria*. An immediate consequence of Lemma 3 is the following characterisation of endemic equilibria.

Proposition 1. Suppose that Assumption 1 holds. If \mathbf{x}^* is an endemic equilibrium of Eq. (3), then $\mathbf{x}^* \in \text{Int}(\Xi_n)$.

We now present a result that shows the system Eq. (4) (equivalent to Eq. (3)) always converges, and the value $s(-\mathbf{U} + \mathbf{M})$ uniquely determines the equilibria and associated convergence properties.

Theorem 1. Suppose that Assumption 1 holds, and consider the system Eq. (4). Then the following hold:

- (1) If $s(-\mathbf{U} + \mathbf{M}) \leq 0$, then $\mathbf{0}_n$ is the unique equilibrium, and it is asymptotically stable for all $\mathbf{x}(0) \in \Xi_n$. If $s(-\mathbf{U} + \mathbf{M}) < 0$, then it is exponentially stable.
- (2) If $s(-\mathbf{U} + \mathbf{M}) > 0$, then in addition to $\mathbf{x} = \mathbf{0}_n$, there exists a unique endemic equilibrium $\bar{\mathbf{x}}$ which is exponentially stable for all $\mathbf{x}(0) \in \Xi_n \setminus \mathbf{0}_n$. Moreover, $\mathbf{x} = \mathbf{0}_n$ is unstable.

3.2 Effective Reproduction Number and the Impact of Changing Mobility Rates

In this subsection, we give a physically relevant interpretation to the result of Theorem 1. We then explore the role of the mobility rates γ_i in the epidemic process.

Because diagonal matrices commute, it follows that $-\mathbf{U} + \mathbf{M}$ is similar to $-\mathbf{U} + \mathbf{W}\mathbf{\Gamma}$ using the similarity transformation $\mathbf{N}(-\mathbf{U} + \mathbf{M})\mathbf{N}^{-1}$. This implies the results in Theorem 1 continue to hold if we replace $s(-\mathbf{U} + \mathbf{M})$ with $s(-\mathbf{U} + \mathbf{W}\mathbf{\Gamma})$. The convergence behaviour of the system Eq. (3) is therefore independent of the size N_i of the population v_i , for all $i \in \mathcal{I}$. However, transient behaviour may depend on $N_i, i \in \mathcal{I}$.

Next, define the irreducible matrix $\tilde{\mathbf{W}} = \mathbf{A} + \mathbf{W}\mathbf{\Gamma} > \mathbf{0}_{n \times n}$, and the positive diagonal matrix $\tilde{\mathbf{D}} = \mathbf{D} + \mathbf{\Gamma}$, so that $-\mathbf{U} + \mathbf{W}\mathbf{\Gamma} = -\tilde{\mathbf{D}} + \tilde{\mathbf{W}}$. We define the effective reproduction number of Eq. (3) as

$$\mathcal{R}_0 \triangleq \rho(-\tilde{\mathbf{D}}^{-1}\tilde{\mathbf{W}}). \quad (8)$$

It can be shown that $s(-\tilde{\mathbf{D}} + \tilde{\mathbf{W}}) < 0 \Leftrightarrow \mathcal{R}_0 < 1$, $s(-\tilde{\mathbf{D}} + \tilde{\mathbf{W}}) = 0 \Leftrightarrow \mathcal{R}_0 = 1$, and $s(-\tilde{\mathbf{D}} + \tilde{\mathbf{W}}) > 0 \Leftrightarrow \mathcal{R}_0 > 1$ (Liu et al., 2019, Proposition 1). Thus, the \mathcal{R}_0 defined in Eq. (8) captures the salient epidemic behaviour in a way consistent with the general definition of the effective reproduction number for many epidemic models: the disease is eradicated if $\mathcal{R}_0 \leq 1$ and will persist as t goes to infinity if $\mathcal{R}_0 > 1$, see e.g. (Fall et al., 2007; Jin and Wang, 2005; Nowzari et al., 2016).

We now give two conditions, one necessary and one sufficient, to ensure that $s(-\mathbf{U} + \mathbf{M}) \leq 0$, i.e., $\mathcal{R}_0 \leq 1$.

Proposition 2. Suppose that Assumption 1 holds. Then:

- (1) $s(-\mathbf{U} + \mathbf{M}) \leq 0$ only if $\exists i \in \mathcal{I}$ such that $\delta_i + \gamma_i > \alpha_i$.
- (2) $s(-\mathbf{U} + \mathbf{M}) \leq 0$ if $\delta_i > \alpha_i$ for all $i \in \mathcal{I}$.

The first statement establishes that a network converges to the healthy equilibrium only if at least one population has a combined recovery rate and mobility rate (corresponding to the rate of decrease in infected individuals in that

population) greater than its infection rate. The second statement establishes that the network will converge to the healthy equilibrium if every population has a recovery rate greater than its infection rate. This is a sufficient condition, although it may not be realistic.

We now provide a result which identifies explicitly the effect of the mobility rate γ_i in contributing to or impeding the convergence towards the healthy equilibrium.

Theorem 2. Suppose that Assumption 1 holds, and consider the system Eq. (4). Define $\phi \triangleq s(-\mathbf{U} + \mathbf{M})$, and let \mathbf{r}^\top and \mathbf{y} be the left and right positive³ eigenvectors of $-\mathbf{U} + \mathbf{M}$ associated with the simple eigenvalue ϕ , respectively, normalised to satisfy $\mathbf{r}^\top \mathbf{y} = 1$. Then,

$$\frac{\partial \phi}{\partial \gamma_i} = -\frac{r_i y_i}{\gamma_i} (\alpha_i - \delta_i - \phi), \quad \forall i. \quad (9)$$

Moreover, the following hold:

- (1) Suppose $\phi \leq 0$. Then, $\frac{\partial \phi}{\partial \gamma_i} < 0$ **if** $\alpha_i \geq \delta_i$.
- (2) Suppose $\phi > 0$. Then, $\frac{\partial \phi}{\partial \gamma_i} < 0$ **only if** $\alpha_i > \delta_i$.

It is notable that $\frac{\partial \phi}{\partial \gamma_i}$ is dependent on node-level parameters $\delta_i, \alpha_i, \gamma_i$ and network-level parameters ϕ, r_i, y_i . Moreover, the sign of $\frac{\partial \phi}{\partial \gamma_i}$ only depends on α_i, δ_i , and ϕ .

Statements (1) and (2) in Theorem 2 also give illuminating insights. Statement (1) says that if Eq. (3) converges to the healthy equilibrium, then increasing γ_i at any node v_i satisfying $\alpha_i \geq \delta_i$ will introduce no risk in the sense of changing the convergence properties of Eq. (3). In fact, the system Eq. (3) will be more robust to the possibility of an outbreak since ϕ will decrease. Statement (2) elucidates that if Eq. (3) converges to the endemic equilibrium, then the only nodes v_i for which an increase in γ_i might possibly lead to a decreasing ϕ are those satisfying $\alpha_i > \delta_i$. Interestingly, nodes satisfying $\alpha_i > \delta_i$ when disconnected from the network will generically converge to an endemic equilibrium; $\lim_{t \rightarrow \infty} x_i(t) = 1 - \delta_i / \alpha_i$ if $b_{ij} = 0$ for all j and $x_i(0) \neq 0$. Similarly, one can also use Eq. (9) to determine those nodes v_j for which decreasing γ_j will decrease ϕ .

Remark 1. The conclusions of Proposition 2 and Theorem 2 are different to those of the ‘‘patchy’’ model of (Wang and Zhao, 2004; Jin and Wang, 2005). We first note that the analysis of flow impact in (Wang and Zhao, 2004; Jin and Wang, 2005) is limited only to the $n = 2$ node case, whereas we consider arbitrary n nodes. In the ‘‘patchy’’ model, the disease may die out in two disconnected nodes but persist when there is a flow between the two nodes, which directly contrasts Proposition 2, Statement (2).

4. CONCLUSION

This paper proposed an SIS networked model with flows of individuals between the nodes. We showed that a specific eigenvalue of a matrix of the system parameters uniquely determines the equilibria and limiting behaviour of the system. We then investigated the role of certain parameters associated with each node (population) in changing the limiting behaviour, including the mobility rates. For future work, we aim to extend our results for time-delay in system to better reflect real-world travels between populations.

³ See Lemma 1 for the positivity property.

Appendix A. PROOF OF THEOREM 1

For simplicity, we shall analyse the system as expressed in Eq. (4), first focusing on the existence and uniqueness of equilibria. Observe that any equilibrium \mathbf{x}^* must satisfy

$$(-\mathbf{U} + \mathbf{M} - \mathbf{A}\mathbf{X}^*)\mathbf{x}^* = \mathbf{0}_n. \quad (\text{A.1})$$

Define $\mathbf{Q} = \mathbf{U} - \mathbf{M}$. If $s(-\mathbf{Q}) \leq 0$, then \mathbf{Q} is *nonnegative stable*, i.e. real part of every eigenvalue of \mathbf{Q} is nonnegative. According to Lemma 2, this is equivalent to saying that \mathbf{Q} is an irreducible M -matrix. Suppose to the contrary, we have $s(-\mathbf{Q}) \leq 0$ and $\mathbf{x}^* \neq \mathbf{0}_n$ is an equilibrium of Eq. (3). Then, $\mathbf{A}\mathbf{X}^*$ is nonnegative diagonal with at least one positive entry. According to (Qu, 2009, Theorem 4.31), $\mathbf{Q} + \mathbf{A}\mathbf{X}^*$ is a nonsingular M -matrix, which implies that there does not exist a nonzero \mathbf{x}^* satisfying Eq. (A.1), and thus creating a contradiction. We have proved that $s(-\mathbf{U} + \mathbf{M}) \leq 0$ is sufficient for $\mathbf{0}_n$ to be the unique equilibrium of Eq. (3). To prove necessity, we need only to prove that there exists at least one endemic equilibrium if $s(-\mathbf{U} + \mathbf{M}) > 0$, which we shall now address.

Using the approach of (Lajmanovich and Yorke, 1976, Lemma 4.1), it can be shown that Eq. (3) has at least one endemic equilibrium if $s(-\mathbf{U} + \mathbf{M}) > 0$, with Proposition 1 indicating that it is in $\text{Int}(\Xi_n)$. Detailed steps are omitted here due to space limitations. We prove that the endemic equilibrium is unique by contradiction. Suppose to the contrary that $\mathbf{1}_n \gg \mathbf{k} \gg \mathbf{0}_n$ and $\mathbf{1}_n \gg \mathbf{h} \gg \mathbf{0}_n$ are two distinct endemic equilibria of Eq. (3). Since $\mathbf{k} \neq \mathbf{h}$, we assume without loss of generality, that $h_1 > k_1$ and $h_1/k_1 \geq h_i/k_i$ for all $i \in \mathcal{I}$. As below Eq. (4), let $m_{ij} = \gamma_j w_{ij} N_j / N_i$. Then, one obtains from Eq. (2) that $-(\delta_1 + \gamma_1)h_1 + \alpha_1(1 - h_1)h_1 + \sum_{j>1}^n m_{1j}h_j = -(\delta_1 + \gamma_1)k_1 + \alpha_1(1 - k_1)k_1 + \sum_{j>1}^n m_{1j}k_j = 0$. This yields

$$\begin{aligned} & -(\delta_1 + \gamma_1)k_1 + \alpha_1(1 - h_1)k_1 + \sum_{j>1}^n m_{1j} \frac{h_j k_1}{h_1} \\ & = -(\delta_1 + \gamma_1)k_1 + \alpha_1(1 - k_1)k_1 + \sum_{j>1}^n m_{1j}k_j. \end{aligned} \quad (\text{A.2})$$

The assumption that $h_1 > k_1$ and $h_1/k_1 \geq h_i/k_i$ for all i implies that $(1 - h_1)k_1 < (1 - k_1)k_1$ and $h_i k_1 / h_1 \leq k_i$ for all i . This in turn implies that

$$\alpha_1(1 - h_1)k_1 + \sum_{j>1}^n m_{1j} \frac{h_j k_1}{h_1} < \alpha_1(1 - k_1)k_1 + \sum_{j>1}^n m_{1j}k_j,$$

which contradicts Eq. (A.2); there exists a unique endemic equilibrium $\bar{\mathbf{x}} \in \text{Int}(\Xi_n)$ if $s(-\mathbf{U} + \mathbf{M}) > 0$.

Convergence when $s(-\mathbf{U} + \mathbf{M}) \leq 0$: Since $\mathbf{Q} = \mathbf{U} - \mathbf{M}$ is an irreducible M -matrix, there exists a positive diagonal \mathbf{P} such that $\mathbf{T} \triangleq \mathbf{P}\mathbf{Q} + \mathbf{Q}^\top \mathbf{P}$ is positive definite or positive semidefinite according as $s(\mathbf{Q}) > 0$ or $s(\mathbf{Q}) = 0$ (see (Berman and Plemmons, 1979, Theorem 2.3) and (Qu, 2009, Theorem 4.31), respectively).

Consider the candidate Lyapunov function $V(\mathbf{x}(t)) = \frac{1}{2} \mathbf{x}(t)^\top \mathbf{P} \mathbf{x}(t)$, being positive definite and decrescent in Ξ_n . Differentiating V with respect to t along the trajectory of Eq. (3) yields

$$\dot{V}(\mathbf{x}(t)) = -\mathbf{x}(t)^\top \left(\frac{1}{2} \mathbf{T} + \mathbf{P} \mathbf{A} \mathbf{X}(t) \right) \mathbf{x}(t). \quad (\text{A.3})$$

Because \mathbf{P} and \mathbf{A} are positive diagonal matrices, and $\mathbf{X} = \text{diag}(x_1, \dots, x_n)$, there holds $\mathbf{x}^\top \mathbf{P} \mathbf{A} \mathbf{X} \mathbf{x} \geq 0$ on the compact set Ξ_n , with equality if and only if $\mathbf{x} = \mathbf{0}_n$. This implies that $V(\mathbf{x}(t))$ is negative definite in Ξ_n . The Lyapunov Theorem (Sastry, 1999, Theorem 5.16) yields that $\mathbf{x} = \mathbf{0}_n$ is asymptotically stable for all $\mathbf{x}(0) \in \Xi_n$.

We now prove the exponential stability for $s(-\mathbf{U} + \mathbf{M}) < 0$. Let $\lambda_{\min}(\cdot)$ and $\lambda_{\max}(\cdot)$ denote the smallest and largest eigenvalue of a symmetric matrix. When $s(-\mathbf{U} + \mathbf{M}) < 0$, one has $\lambda_{\min}(\mathbf{P})\|\mathbf{x}\|^2 \leq V(\mathbf{x}) \leq \lambda_{\max}(\mathbf{P})\|\mathbf{x}\|^2$ and $\dot{V}(\mathbf{x}) \leq -\frac{1}{2}\lambda_{\min}(\mathbf{T})\|\mathbf{x}\|^2$ for all $\mathbf{x} \in \Xi_n$. It follows from (Sastry, 1999, Theorem 5.17) that $\mathbf{x} = \mathbf{0}_n$ is exponentially stable with domain of attraction Ξ_n , with a rate of convergence of at least $\lambda_{\min}(\mathbf{T})/(2\lambda_{\max}(\mathbf{P}))$.

Convergence when $s(-\mathbf{U} + \mathbf{M}) > 0$: Let $\bar{\mathbf{x}} \in \text{Int}(\Xi_n)$ be the unique endemic equilibrium of Eq. (3). Define the coordinate transform $\mathbf{y}(t) = \mathbf{x}(t) - \bar{\mathbf{x}}$, and let $\mathbf{Y} = \text{diag}(y_1, \dots, y_n)$ and $\bar{\mathbf{Q}} = \mathbf{U} - \mathbf{M} + \mathbf{A}\bar{\mathbf{X}}$. Observe that

$$\begin{aligned} \dot{\mathbf{y}}(t) &= -(\mathbf{U} - \mathbf{M})(\mathbf{x}(t) + \bar{\mathbf{x}}) - \mathbf{A}(\mathbf{Y}(t) + \bar{\mathbf{X}})(\mathbf{y}(t) + \bar{\mathbf{x}}) \\ &= -(\bar{\mathbf{Q}} + \mathbf{A}\bar{\mathbf{X}})\mathbf{y}(t) - \mathbf{A}\mathbf{Y}(t)\mathbf{y}(t), \end{aligned} \quad (\text{A.4})$$

with the last equality holding because Eq. (A.1) yields $-\bar{\mathbf{Q}}\bar{\mathbf{x}} = \mathbf{0}_n$. Since $-\bar{\mathbf{Q}}$ is a Metzler matrix, and because we have $-\bar{\mathbf{Q}}\bar{\mathbf{x}} = \mathbf{0}_n$ with $\bar{\mathbf{x}} \gg \mathbf{0}_n$, Lemma 1 yields $s(\bar{\mathbf{Q}}) = 0$. Lemma 2 establishes that $\bar{\mathbf{Q}} \in \mathcal{Z}$ is a singular M -matrix, and $\bar{\mathbf{Q}}$ is irreducible because \mathbf{M} is irreducible. According to (Qu, 2009, Theorem 4.31), $\mathbf{L} \triangleq \bar{\mathbf{Q}} + \mathbf{A}\bar{\mathbf{X}}$ is a non-singular M -matrix. According to (Berman and Plemmons, 1979, Theorem 2.3), there exists a positive diagonal matrix \mathbf{P} such that $\mathbf{T} \triangleq \mathbf{P}\mathbf{L} + \mathbf{L}^\top \mathbf{P}$ is positive definite.

Define $\mathcal{S} = \Xi_n - \bar{\mathbf{x}}$ as the set of points of Ξ_n translated from the origin by $\bar{\mathbf{x}}$. Clearly, \mathcal{S} is a positive invariant set of the transformed system Eq. (A.4), and a simple adjustment to Lemma 3 will prove that for all $\mathbf{y}(0) \in \partial\mathcal{S} \setminus -\bar{\mathbf{x}}$, there exists a $\kappa > 0$ such that $\mathbf{y}(\kappa) \in \text{Int}(\mathcal{S})$. Consider the candidate Lyapunov function $V(\mathbf{y}(t)) = \frac{1}{2}\mathbf{y}(t)^\top \mathbf{P}\mathbf{y}(t)$, which is positive definite and decrescent in \mathcal{S} . Differentiating V with respect to t along the trajectories of Eq. (A.4), leads to $\dot{V}(\mathbf{y}(t)) = -\mathbf{y}(t)^\top (\frac{1}{2}\mathbf{T} + \mathbf{P}\mathbf{A}\mathbf{Y}(t))\mathbf{y}(t)$. Using the same arguments as below Eq. (A.3), one can show that $\mathbf{0}_n$ is exponentially stable for the system Eq. (A.4) for all $\mathbf{y}(0) \in \mathcal{S} \setminus -\bar{\mathbf{x}}$, which in turn implies that $\lim_{t \rightarrow \infty} \mathbf{x}(t) = \bar{\mathbf{x}}$ exponentially fast for all $\mathbf{x}(0) \in \Xi_n \setminus \mathbf{0}_n$.

It remains to prove that $\mathbf{0}_n$ is unstable if $s(-\mathbf{U} + \mathbf{M}) > 0$. The Jacobian of the system in Eq. (3) at $\mathbf{x} = \mathbf{0}_n$ is given by $\mathbf{J} = -\mathbf{U} + \mathbf{M}$. Since $s(-\mathbf{U} + \mathbf{M}) > 0$, \mathbf{J} is unstable and by the Linearization Theorem (Sastry, 1999, Theorem 5.42), $\mathbf{0}_n$ is an unstable equilibrium of Eq. (3). ■

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