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Global stability of a multi-group SIS epidemic model with varying total population size

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Abstract

In this paper, to analyze the effect of the cross patch infection between different groups to the spread of gonorrhea in a community, we establish the complete global dynamics of a multi-group SIS epidemic model with varying total population size by a threshold parameter. In the proof, we use special Lyapunov functional techniques, not only one proposed by the paper [J. Prüss, L. Pujo-Menjouet, G.F. Webb and R. Zacher, Analysis of a model for the dynamics of prions, *Dis. Con. Dyn. Sys. Series B*, **6** (2006), 225–235], but also the other one for a varying total population size with some ideas specified to our model and no longer need a grouping technique derived from the graph theory which is commonly used for the global stability analysis of multi-group epidemic models.

Key words: multi-group SIS epidemic model; varying total population size; global stability; Lyapunov function
2000 MSC: 34K20, 34K25, 92D30

1. Introduction

Multi-group epidemic models have been studied in the literature of mathematical epidemiology to clarify the transmission dynamics of various infectious diseases such as measles, mumps, gonorrhea, West-Nile virus, HIV/AIDS and so on. In such multi-group epidemic models, a heterogeneous host population is divided into several homogeneous groups according to modes of transmission, contact patterns, or geographic distributions, so that within-group and inter-group interactions can be modeled separately.

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In 1976, Lajmanovich and Yorke [13] proposed a multi-group SIS model with constant total populations in each group for the spread of gonorrhea in a community, in which the global stability of the model is studied.

Then, there are many studies on SIS epidemic models (see for example, Huang and Takeuchi [10] and Vargas-De-León [33] and references therein) and multi-group epidemic models (see for example, Wang and Xiao [35], Arino [1] Liu and Zhou [18], Liu and Takeuchi [19] and Nakata [25]).

Moreover, we are also interested in the ideas of Lyapunov functional techniques proposed in Prüss *et al.* [27] for an SEIS epidemic model with no delay, Muroya *et al.* [22, Lemma 5.1] for a discrete version of the model and Nakata *et al.* [26] and Enatsu *et al.* [5] in which a simple idea is proposed to extend the Lyapunov functional techniques in McCluskey [20] for SIR epidemic models to SIRS epidemic models with delays.

On the other hand, in 2006, Guo *et al.* [8] have first succeeded in a complete global analysis of a multi-group SIR model by making use of the theory of non-negative matrices and the graph theory to Lyapunov functional techniques. Hereafter, there are many researchers follow this graph-theoretic approach on the global stability of various multi-group SIR models (see for example, [4], [9], [11], [16], [17], [29], [30], [36], [37] and references therein).

Recently, under the assumption that the total population is constant, Kuniya and Muroya [12] and Muroya *et al.* [24] established the complete global dynamics of multi-group SIS epidemic models in a patchy environment without and with the time delay, respectively. Moreover, Wang *et al.* extended the result of Kuniya and Muroya [12] to delayed multi-group SIS models with general nonlinear incidence rates. Muroya [21] investigated an equivalent conditions between a Lotka-Volterra system with patch structure and a multi-group SI epidemic model with patch structure.

To analyze the effect of the cross patch infection between different groups to the spread of gonorrhea in a community, by a multi-group SIS epidemic model with varying total population size, we can not use the relation that the total population size of each group is assentially constant in the Lyapunov functions, as in Kuniya and Muroya [12] and Muroya *et al.* [24].

Therefore, to analyze the multi-group SIS epidemic model with varying total population size, we need to use another technique of the Lyapunov functional with varying total population size, for example, Enatsu *et al.* [5, Proof of Theorem 1.1] for a SIRS epidemic model and Muroya *et al.* [23, Lemma 4.5] for a multi-group SIRS epidemic model.

Motivated by these, in this paper, by a threshold parameter, we establish the complete global dynamics of the following multi-group SIS epidemic model with no delay, cross patch infection and varying total population size in each

group:

$$\begin{cases} \dfrac{dS_k}{dt} = b_k - \mu_k^S S_k - S_k\left(\sum\limits_{j=1}^{n} \beta_{kj} I_j\right) + \delta_k I_k, \\ \dfrac{dI_k}{dt} = S_k\left(\sum\limits_{j=1}^{n} \beta_{kj} I_j\right) - (\mu_k^I + \delta_k) I_k, \quad k = 1, 2, \cdots, n. \end{cases} \tag{1.1}$$

$S_k(t)$ and $I_k(t)$ denote the numbers of susceptible and infected individuals in group k at time t, respectively. b_k is the recruitment rate of the population in group k. μ_k^S and μ_k^I are the natural death rates of susceptible and infected individuals, respectively, in group k. δ_k is the rate at which an infectious individual returns to the susceptible class in group k. β_{kj} is the rate of disease transmission between a susceptible individual in group k and an infectious individual in group j. We assume that each parameters $b_k,\ \mu_{k1},\ \mu_{k2}$ are positive constants and $\beta_{kj},\ \delta_k$ are nonnegative constants. We set the initial condition of system (1.1) as

$$\begin{cases} S_k(0) = \phi_1^k \geq 0,\ I_k(0) = \phi_2^k \geq 0,\ k = 1, 2, \ldots, n \\ (\phi_1^1, \phi_2^1, \phi_1^2, \phi_2^2, \ldots, \phi_1^n, \phi_2^n) \in \mathbb{R}_+^{2n}, \end{cases} \tag{1.2}$$

where $\mathbb{R}_+^{2n} = \{(x_1, y_1, x_2, y_2, \ldots, x_n, y_n) : x_k,\ y_k \geq 0,\ k = 1, 2, \ldots, n\}$.

For the biological justification, we assume that

$$\mu_k^S \leq \mu_k^I, \qquad k = 1, 2, \ldots, n. \tag{1.3}$$

Moreover, we assume that

$$\text{the } n \times n \text{ matrix } \mathbf{B} = \Big(\beta_{kj}\Big)_{n\times n} \text{ is irreducible,} \tag{1.4}$$

whose biological meaning is that every pair of groups is joined by an infectious path so that the presence of an infectious individual in the first group can cause infection in the second group.

Let

$$\tilde{R}_0 := \rho(\tilde{\mathbf{M}}(\mathbf{S}^0)), \tag{1.5}$$

where

$$\mathbf{S}^0 := \left(S_1^0, S_2^0, \ldots, S_n^0\right)^T = \left(\frac{b_1}{\mu_1^S}, \frac{b_2}{\mu_2^S}, \ldots, \frac{b_n}{\mu_n^S}\right)^T \in \mathbb{R}_+^n$$

and $\rho(\tilde{\mathbf{M}}(\mathbf{S}^0))$ denotes the spectral radius of matrix $\tilde{\mathbf{M}}(\mathbf{S}^0)$ defined by

$$\tilde{\mathbf{M}}(\mathbf{S}^0) := \left(\frac{\beta_{kj} S_k^0}{\mu_k^I + \delta_k}\right)_{n\times n}.$$

The following theorem is the main result in this paper.

Theorem 1.1 *For system (1.1), we have*

(i) If $\tilde{R}_0 \leq 1$, then the disease-free equilibrium $\mathbf{E}^0 = (S_1^0, 0, S_2^0, 0, \ldots, S_n^0, 0)$ is globally asymptotically stable in $\mathbf{\Gamma}$.

(ii) If $\tilde{R}_0 > 1$, then system (1.1) is uniformly persistent in $\mathbf{\Gamma}^0$ and there exists an endemic equilibrium $\mathbf{E}^* = (S_1^*, I_1^*, S_2^*, I_2^*, \ldots, S_n^*, I_n^*)$ which is globally asymptotically stable in $\mathbf{\Gamma}^0$,

where $\mathbf{\Gamma}^0$ is the interior of the feasible region $\mathbf{\Gamma}$ defined by

$$\mathbf{\Gamma} = \Big\{ (S_1, I_1, S_2, I_2, \ldots, S_n, I_n) \in \mathbb{R}_+^{2n} \\ \mid S_k \leq S_k^0,\ S_k + I_k \leq \frac{b_k}{\mu_k^S},\ k = 1, 2, \ldots, n \Big\}.$$

The organization of this paper is as follows. In Section 2, we prove the eventual boundedness of solutions for system (1.1). In Section 3, following the proof techniques in Guo *et al.* [8], we prove the global asymptotic stability of the disease-free equilibrium for $\tilde{R}_0 \leq 1$. We further prove the uniform persistence of system (1.1) and the existence of an endemic equilibrium $\mathbf{E}^*$ of system (1.1) for $\tilde{R}_0 > 1$ (see Proposition 3.1 and Corollary 3.1). In Section 4, for $\tilde{R}_0 > 1$, using Lyapunov function techniques to the system (1.1) (see Lemmas 4.1-4.4), we prove the global asymptotic stability of an endemic equilibrium of system (1.1). Finally, in Section 5 to show the validity of our theoretical results, we offer two numerical examples, one is a sexually transmitted disease and the other is a geographical spread of disease.

2. Positivity and Eventual boundedness of solutions of (1.1)

In this section we prove the positivity and eventual boundedness of solutions of system (1.1). Let $N_k(t) = S_k(t) + I_k(t)$ be the total population of group $k,\ k = 1, 2, \ldots, n$ at time t. Then we have the following lemma on the positivity and eventual boundedness of solutions $S_k,\ I_k,\ k = 1, 2, \ldots, n$ of system (1.1).

Lemma 2.1 *(i) Solutions of system (1.1) with initial condition (1.2) satisfy*

$$S_k(t) > 0,\ I_k(t) \geq 0,\ k = 1, 2, \ldots, n \quad \text{for all } t > 0.$$

(ii) Under the condition (1.3) it holds that

$$\begin{cases} \lim_{t\to+\infty} N_k(t) \leq S_k^0, \\ \text{in particular,} \\ \limsup_{t\to+\infty} S_k(t) \leq S_k^0,\ \limsup_{t\to+\infty} I_k(t) \leq S_k^0,\ k = 1, 2, \ldots, n. \end{cases}$$

Proof. First we prove (i). By (1.1), we have that $\frac{d}{dt} S_k(+0) \geq b_k > 0$ and $S_k(0) \geq 0$ for any $k = 1, 2, \ldots, n$, which imply that there exist positive constants $t_{k0},\ k = 1, 2, \ldots, n$ such that $S_k(t) > 0$ for any $0 < t < t_{k0},\ k = 1, 2, \ldots, n$.

Now, we prove that $S_k(t) > 0$ for any $0 < t < +\infty$ and $k = 1, 2, \ldots, n$. On the contrary, suppose that there exist $t_1 > 0$ and $k_1 \in \{1, 2, \ldots, n\}$ such that $S_k(t) > 0,\ k = 1, 2, \ldots, n$ for all $t \in [0, t_1)$ and $S_{k_1}(t_1) = 0$. Then, from the first equation of system (1.1), it follows that $\frac{d}{dt} S_{k_1}(t_1) \geq b_{k_1} > 0$ which is a contradiction to the fact that $S_{k_1}(t) > 0 = S_{k_1}(t_1)$ for $t \in [0, t_1)$. Hence, we obtain that $S_k(t) > 0$ for any $0 < t < +\infty$ and $k = 1, 2, \ldots, n$.

Next, we prove that $I_k(t) \geq 0$ for any $0 < t < +\infty$ and $k = 1, 2, \ldots, n$. On the contrary, suppose that there exist $t_2 > 0$ and $k_2 \in \{1, 2, \ldots, n\}$ such that $I_{k_2}(t_2) < 0$. Set $t_{k_2} = \inf\{0 < t < t_2 : I_{k_2}(t) < 0\}$. Then, $0 \leq t_{k_2} < t_2$ and $I_{k_2}(t_{k_2}) = 0$. Then, it follows from the second equation of system (1.1) that $\frac{d}{dt} I_{k_2}(+t_{k_2}) \geq 0$. Hence, we have $I_{k_2}(t) \geq 0$ for all $t \geq 0$, because if there exists a small $\varepsilon_1 > 0$ such that $I_{k_2}(t_2 + \varepsilon_1) < 0$, then it must follow that $I'_{k_2}(t_2) < 0$. Thus, from the second equation of system (1.1), it follows that there exists a sufficiently small $\varepsilon_2 > 0$ such that $I'_{k_2}(t) \geq -\left(\mu_k^I + \gamma_k\right) I_{k_2}(t)$ for $t \in [t_2 - \varepsilon_2, t_2]$, which implies $I_{k_2}(t_2) \geq I(t_2 - \varepsilon_2) e^{-(\mu_k^I + \gamma_k)\varepsilon_2} > 0$ and this is a contradiction.

Next we prove (ii). From (1.1) and (1.3) we have

$$\begin{aligned} \frac{\mathrm{d}}{\mathrm{d}t} N_k(t) &= \frac{\mathrm{d}}{\mathrm{d}t} \{S_k(t) + I_k(t)\} \\ &= b_k - \mu_k^S S_k(t) - \mu_k^I I_k(t) \\ &\leq b_k - \mu_k^S N_k(t), \quad k = 1, 2, \ldots, n. \end{aligned} \tag{2.1}$$

Hence we have $\lim_{t \to +\infty} N_k(t) \leq S_k^0,\ k = 1, 2, \ldots, n$ and the remainder of (ii) immediately follows from this inequality. □

3. Global stability of the disease-free equilibrium $\mathbf{E^0}$ for $\tilde{R}_0 \leq 1$

We can obtain the following Proposition, whose proof is similar to that in Guo *et al.* [8, Proposition 3.1]

Proposition 3.1 *(i) If $\tilde{R}_0 \leq 1$, then the disease-free equilibrium $\mathbf{E}^0$ is the unique equilibrium of system (1.1) and it is globally asymptotically stable in $\mathbf{\Gamma}$.*

(ii) If $\tilde{R}_0 > 1$, then $\mathbf{E}^0$ is unstable and system (1.1) is uniformly persistent in $\mathbf{\Gamma}^0$.

For the proof, see Appendix A.

Proof of (i) of Theorem 1.1. It immediately follows from (i) of Proposition 3.1. □

The uniform persistence of system (1.1), together with the uniform boundedness of solutions in $\mathbf{\Gamma}^0$ (which follows from Lemma 2.1), implies the existence of an endemic equilibrium $\mathbf{E}^*$ of system (1.1) in $\mathbf{\Gamma}^0$ (see [28, Theorem D.3] or Bhatia *et al.*[2, Theorem 2.8.6]).

Corollary 3.1 *If $\tilde{R}_0 > 1$, then system* (1.1) *has at least one endemic equilibrium* $\mathbf{E}^* = (S_1^*, I_1^*, S_2^*, I_2^*, \ldots, S_n^*, I_n^*)$ *in* $\mathbf{\Gamma}^0$.

Note that elements of an endemic equilibrium $\mathbf{E}^*$ satisfy

$$\{\tilde{\mathbf{F}}(\mathbf{S}^*) - \tilde{\mathbf{V}}\}\mathbf{I}^* = \mathbf{0},$$

where

$$\tilde{\mathbf{F}}(\mathbf{S}) = \left(\beta_{kj} S_k\right)_{n\times n}, \quad \tilde{\mathbf{V}} = \operatorname{diag}\left(\mu_1^I + \delta_1,\ \mu_2^I + \delta_2,\ \ldots,\ \mu_n^I + \delta_n\right)$$

and

$$\mathbf{S} = (S_1, S_2, \ldots, S_n)^T, \quad \mathbf{S}^* = (S_1^*, S_2^*, \ldots, S_n^*)^T, \quad \mathbf{I}^* = (I_1^*, I_2^*, \ldots, I_n^*)^T.$$

Now, we consider the relation between the reproduction number R_0 (see for instance, van den Driessche and Watmough [31]) for system (1.1) and $\tilde{R}_0$. The basic reproduction number R_0 is calculated as the spectral radius

$$R_0 := \rho(\mathbf{M}(\mathbf{S}^0)), \tag{3.1}$$

of the next generation matrix $\mathbf{M}(\mathbf{S}^0)$, where

$$\mathbf{M}(\mathbf{S}) = \left(\frac{\beta_{kj} S_k}{\mu_j^I + \delta_j}\right)_{n\times n}.$$

We have the following lemma.

Lemma 3.1

$$\begin{cases} R_0 < 1 & \textit{if and only if} \quad \tilde{R}_0 < 1, \\ R_0 = 1 & \textit{if and only if} \quad \tilde{R}_0 = 1, \\ R_0 > 1 & \textit{if and only if} \quad \tilde{R}_0 > 1. \end{cases}$$

For the proof, see Appendix B. From Lemma 3.1, for convenience, we use $\tilde{R}_0$ defined by (1.5) as a threshold parameter (see Guo *et al.* [8]) in place of the reproduction number R_0 given by (3.1).

4. Global stability of an endemic equilibrium $\mathbf{E}^*$ for $\tilde{R}_0 > 1$

In this section, we prove that if $\tilde{R}_0 > 1$, then an endemic equilibrium $\mathbf{E}^*$ of system (1.1) is globally asymptotically stable in $\mathbf{\Gamma}^0$. For $\tilde{R}_0 > 1$, from Corollary 3.1, it follows that there exists an endemic equilibrium $\mathbf{E}^* \in \mathbf{\Gamma}^0$ whose elements satisfy

$$\begin{cases} b_k = \mu_k^S S_k^* + \displaystyle\sum_{j=1}^{n} \beta_{kj} S_k^* I_j^* - \delta_k I_k^*, \\ \left(\mu_k^I + \delta_k\right) I_k^* = \displaystyle\sum_{j=1}^{n} \beta_{kj} S_k^* I_j^*, \quad k = 1, 2, \ldots, n. \end{cases} \tag{4.1}$$

Now, to eliminate the terms $\delta_k I_k,\ k = 1, 2, \ldots, n$ essentially from the Lyapunov functionals on (1.1), we first apply the techniques of Prüss *et al.* [27] for an SEIS epidemic model with no delay. Let

$$\begin{cases} \tilde{\beta}_{kk} = \beta_{kk}\left(1 - \dfrac{\delta_k}{\beta_{kk}S_k^*}\right), \\ \tilde{\beta}_{kj} = \beta_{kj} \ \text{ for } \ k \neq j, \quad k, j = 1, 2, \ldots, n. \end{cases}$$

Then we have

$$\begin{aligned} &-\beta_{kk}\left(S_k I_k - S_k^* I_k^*\right) + \delta_k\left(I_k - I_k^*\right) \\ &\quad = -\beta_{kk}\left(1 - \frac{\delta_k}{\beta_{kk}S_k^*}\right)\left(S_k I_k - S_k^* I_k^*\right) + \delta_k\left(1 - \frac{S_k}{S_k^*}\right) I_k \\ &\quad = -\tilde{\beta}_{kk}\left(S_k I_k - S_k^* I_k^*\right) + \delta_k\left(1 - \frac{S_k}{S_k^*}\right) I_k, \quad k = 1, 2, \ldots, n \end{aligned} \tag{4.2}$$

and

$$\begin{cases} \beta_{kk} S_k I_k - \delta_k I_k = \tilde{\beta}_{kk} S_k I_k - \delta_k\left(1 - \dfrac{S_k}{S_k^*}\right) I_k, \\ \beta_{kk} S_k^* I_k^* - \delta_k I_k^* = \tilde{\beta}_{kk} S_k^* I_k^*, \quad k = 1, 2, \ldots, n. \end{cases} \tag{4.3}$$

and

$$\sum_{j=1}^{n} \tilde{\beta}_{kj} S_k^* I_j^* - \mu_k^I I_k^* = \sum_{j=1}^{n} \beta_{kj} S_k^* I_j^* - \left(\mu_k^I + \delta_k\right) I_k^* = 0. \tag{4.4}$$

Using (4.1)-(4.3) we can rewrite system (1.1) as

$$\begin{cases} \dfrac{\mathrm{d}S_k}{\mathrm{d}t} = -\mu_k^S(S_k - S_k^*) - \displaystyle\sum_{j=1}^{n} \tilde{\beta}_{kj}(S_k I_j - S_k^* I_j^*) + \delta_k\left(1 - \frac{S_k}{S_k^*}\right) I_k, \\ \dfrac{\mathrm{d}I_k}{\mathrm{d}t} = \displaystyle\sum_{j=1}^{n} \tilde{\beta}_{kj} S_k I_j - \mu_k^I I_k - \delta_k\left(1 - \frac{S_k}{S_k^*}\right) I_k, \quad k = 1, 2, \ldots, n. \end{cases} \tag{4.5}$$

Let

$$U_1 := \sum_{k=1}^{n} v_k \left\{ S_k^* g\left(\frac{S_k}{S_k^*}\right) + I_k^* g\left(\frac{I_k}{I_k^*}\right) \right\}, \tag{4.6}$$

where $v_1, v_2, \cdots, v_n$ are positive constants defined below. Let

$$x_k = \frac{S_k}{S_k^*}, \quad y_k = \frac{I_k}{I_k^*}, \quad k = 1, 2, \ldots, n.$$

and

$$g(x) = x - 1 - \ln x,$$

where $x \in \mathbb{R}_+ \setminus \{0\}$. Note that $g(x) \geq g(1) = 0$ for any $x \in \mathbb{R}_+ \setminus \{0\}$. We have the following lemma.

Lemma 4.1 *The derivative of U_1, which is defined by* (4.6)*, along the trajectories of system* (1.1) *is calculated as*

$$\begin{aligned}\frac{\mathrm{d}U_1(t)}{\mathrm{d}t} &= -\sum_{k=1}^{n} v_k\left(\mu_k^S S_k^* + \delta_k I_k^* y_k\right)\left(1-\frac{1}{x_k}\right)(x_k-1)\\ &\quad -\sum_{k=1}^{n} v_k \sum_{j=1}^{n} \tilde{\beta}_{kj} S_k^* I_j^* \left\{ g\left(\frac{1}{x_k}\right) + g\left(\frac{x_k y_j}{y_k}\right)\right\}\\ &\quad +\sum_{k=1}^{n}\left(\sum_{j=1}^{n} v_j \tilde{\beta}_{jk} S_j^* - v_k \mu_k^I\right) I_k^* g(y_k)\\ &\quad +\sum_{k=1}^{n} v_k \delta_k I_k^* (y_k-1)(x_k-1). \end{aligned} \tag{4.7}$$

Proof. Differentiation gives

$$\frac{\mathrm{d}U_1(t)}{\mathrm{d}t} = \sum_{k=1}^{n} v_k \left\{ \left(1-\frac{S_k^*}{S_k}\right)\frac{\mathrm{d}S_k}{\mathrm{d}t} + \left(1-\frac{I_k^*}{I_k}\right)\frac{\mathrm{d}I_k}{\mathrm{d}t}\right\}. \tag{4.8}$$

Now, from (4.1) and (4.5), we have

$$\frac{\mathrm{d}S_k}{\mathrm{d}t} = -\mu_k^S S_k^*(x_k-1) - \sum_{j=1}^{n} \tilde{\beta}_{kj} S_k^* I_j^* \left(x_k y_j - 1\right) + \delta_k I_k^*(1-x_k) y_k \tag{4.9}$$

and

$$\frac{\mathrm{d}I_k}{\mathrm{d}t} = \sum_{j=1}^{n} \tilde{\beta}_{kj} S_k^* I_j^* \left(x_k y_j - y_k\right) - \delta_k I_k^* \left(1-x_k\right) y_k. \tag{4.10}$$

Substituting (4.9) and (4.10) into (4.8), we have

$$\begin{aligned}\frac{\mathrm{d}U_1(t)}{\mathrm{d}t} &= \sum_{k=1}^{n} v_k \Bigg[\left(1-\frac{1}{x_k}\right)\Bigg\{ -\mu_k^S S_k^*(x_k-1)\\ &\qquad -\sum_{j=1}^{n} \tilde{\beta}_{kj} S_k^* I_j^* (x_k y_j - 1) + \delta_k I_k^*(1-x_k) y_k \Bigg\}\\ &\qquad +\left(1-\frac{1}{y_k}\right)\left\{ \sum_{j=1}^{n} \tilde{\beta}_{kj} S_k^* I_j^* (x_k y_j - y_k) - \delta_k I_k^*(1-x_k) y_k \right\}\Bigg]\\ &= -\sum_{k=1}^{n} v_k (\mu_k^S S_k^* + \delta_k I_k^* y_k)\left(1-\frac{1}{x_k}\right)(x_k-1)\\ &\quad +\sum_{k=1}^{n} v_k \sum_{j=1}^{n} \tilde{\beta}_{kj} S_k^* I_j^* \left\{ \left(1-\frac{1}{x_k}\right)(1-x_k y_j) + \left(1-\frac{1}{y_k}\right)(x_k y_j - y_k)\right\}\\ &\quad +\sum_{k=1}^{n} v_k \delta_k I_k^*(y_k-1)(x_k-1). \end{aligned} \tag{4.11}$$

Note that we have

$$\begin{aligned}
&\left(1-\frac{1}{x_k}\right)(1-x_ky_j)+\left(1-\frac{1}{y_k}\right)(x_ky_j-y_k)\\
=\;&\left(1-\frac{1}{x_k}-x_ky_j+y_j\right)+\left(x_ky_j-\frac{x_ky_j}{y_k}-y_k+1\right)\\
=\;&2-\frac{1}{x_k}+y_j-\frac{x_ky_j}{y_k}-y_k\\
=\;&-g\left(\frac{1}{x_k}\right)-g\left(\frac{x_ky_j}{y_k}\right)+\{g(y_j)-g(y_k)\}.
\end{aligned}$$

Thus, the second term of the last equation in (4.11) is calculated as

$$\begin{aligned}
&\sum_{k=1}^{n}v_k\sum_{j=1}^{n}\tilde{\beta}_{kj}S_k^*I_j^*\left\{\left(1-\frac{1}{x_k}\right)(1-x_ky_j)+\left(1-\frac{1}{y_k}\right)(x_ky_j-y_k)\right\}\\
=\;&-\sum_{k=1}^{n}v_k\sum_{j=1}^{n}\tilde{\beta}_{kj}S_k^*I_j^*\left\{g\left(\frac{1}{x_k}\right)+g\left(\frac{x_ky_j}{y_k}\right)\right\}\\
&+\sum_{k=1}^{n}v_k\sum_{j=1}^{n}\tilde{\beta}_{kj}S_k^*I_j^*\{g(y_j)-g(y_k)\}. \qquad (4.12)
\end{aligned}$$

From (4.4) we have

$$\begin{aligned}
&\sum_{k=1}^{n}v_k\sum_{j=1}^{n}\tilde{\beta}_{kj}S_k^*I_j^*\{g(y_j)-g(y_k)\}\\
=&\sum_{k=1}^{n}v_k\sum_{j=1}^{n}\tilde{\beta}_{kj}S_k^*I_j^*g(y_j)-\sum_{k=1}^{n}v_k\sum_{j=1}^{n}\tilde{\beta}_{kj}S_k^*I_j^*g(y_k)\\
=&\sum_{j=1}^{n}v_j\sum_{k=1}^{n}\tilde{\beta}_{jk}S_j^*I_k^*g(y_k)-\sum_{k=1}^{n}v_k\mu_k^II_k^*g(y_k)\\
=&\sum_{k=1}^{n}\left\{\sum_{j=1}^{n}v_j\tilde{\beta}_{jk}S_j^*-v_k\mu_k^I\right\}I_k^*g(y_k). \qquad (4.13)
\end{aligned}$$

Hence, from (4.11)-(4.13), we have the expression (4.7). □

Now we are in a position to consider the following condition.

$$\sum_{k=1}^{n}\left\{\sum_{j=1}^{n}v_j\tilde{\beta}_{jk}S_j^*-v_k\mu_k^I\right\}I_k^*g(y_k)=0.$$

We prove the following lemma which comes from a well-known technique used by Guo *et al.* [8].

Lemma 4.2 *The following system*

$$\sum_{j=1}^{n} v_j \tilde{\beta}_{jk} S_j^* = v_k \mu_k^I, \quad k = 1, 2, \ldots, n, \tag{4.14}$$

has a positive solution $(v_1, v_2, \ldots, v_n)$ *defined by*

$$(v_1, v_2, \cdots, v_n) = (C_1, C_2, \ldots, C_n), \tag{4.15}$$

where C_k $(k = 1, 2, \ldots, n)$ *denotes the cofactor of the* k*-th diagonal entry of matrix*

$$\tilde{\mathbf{B}} = \begin{bmatrix} \sum\limits_{j\neq 1} \tilde{\sigma}_{1j} & -\tilde{\sigma}_{21} & \cdots & -\tilde{\sigma}_{n1} \\ -\tilde{\sigma}_{12} & \sum\limits_{j\neq 2} \tilde{\sigma}_{2j} & \cdots & -\tilde{\sigma}_{n2} \\ \cdots & & & \\ -\tilde{\sigma}_{1n} & -\tilde{\sigma}_{2n} & \cdots & \sum\limits_{j\neq n} \tilde{\sigma}_{nj} \end{bmatrix},$$

where

$$\tilde{\sigma}_{kj} = \tilde{\beta}_{kj} S_k^* I_j^*, \quad k, j = 1, 2, \ldots, n.$$

Proof. Consider a basis for the solution space of the linear system

$$\tilde{\mathbf{B}}\mathbf{v} = 0 \tag{4.16}$$

which can be written as (4.15) (see, for example, Berman and Plemmons [3]). From the irreducibility of matrix $\mathbf{B} = (\beta_{kj})_{n\times n}$, we see that matrix $(\tilde{\sigma}_{kj})_{n\times n}$ is also irreducible and $v_k = C_k > 0,\ k = 1, 2, \ldots, n$. Then, from (4.16), we have

$$\begin{bmatrix} \tilde{\sigma}_{11} & \tilde{\sigma}_{21} & \cdots & \tilde{\sigma}_{n1} \\ \tilde{\sigma}_{12} & \tilde{\sigma}_{22} & \cdots & \tilde{\sigma}_{n2} \\ \cdots & & & \\ \tilde{\sigma}_{1n} & \tilde{\sigma}_{2n} & \cdots & \tilde{\sigma}_{nn} \end{bmatrix} \begin{bmatrix} v_1 \\ v_2 \\ \vdots \\ v_n \end{bmatrix} = \begin{bmatrix} \left(\sum\limits_{j=1}^{n} \tilde{\sigma}_{1j}\right) v_1 \\ \left(\sum\limits_{j=1}^{n} \tilde{\sigma}_{2j}\right) v_2 \\ \vdots \\ \left(\sum\limits_{j=1}^{n} \tilde{\sigma}_{nj}\right) v_n \end{bmatrix}.$$

Hence we have

$$\sum_{j=1}^{n} v_j \tilde{\sigma}_{jk} = v_k \sum_{j=1}^{n} \tilde{\sigma}_{kj}, \quad k = 1, 2, \ldots, n,$$

which is equivalent to

$$\sum_{j=1}^{n} v_j \tilde{\beta}_{jk} S_j^* I_k^* = v_k \sum_{j=1}^{n} \tilde{\beta}_{kj} S_k^* I_j^* = v_k \mu_k^I I_k^*, \quad k = 1, 2, \ldots, n. \tag{4.17}$$

From (4.17) and the positivity of $I_k^*,\ k = 1, 2, \ldots, n$, we can conclude that $(v_1, v_2, \ldots, v_n)$ defined by (4.15) is a positive solution of (4.14). □

Now, for the case $\delta_k > 0$, we offer the following Lemmas 4.3-4.4. Similar Lyapunov functional techniques are used in Nakata *et al.* [26] and Enatsu *et al.* [5] with McCluskey [20].

Lemma 4.3 *Under the condition* (1.3) *we have*

$$\begin{aligned}\frac{\mathrm{d}}{\mathrm{d}t}\left(\frac{(N_k - N_k^*)^2}{2}\right) = &-\mu_k^S (N_k^*)^2 (n_k - 1)^2 - \varepsilon_k S_k^* I_k^* (x_k - 1)(y_k - 1) \\ &-\varepsilon_k (I_k^*)^2 (y_k - 1)^2, \quad k = 1, 2, \ldots, n,\end{aligned} \tag{4.18}$$

where

$$\begin{cases} N_k^* = S_k^* + I_k^*, \quad \varepsilon_k = \mu_k^I - \mu_k^S \geq 0, \\ \textit{and} \quad n_k = \dfrac{N_k}{N_k^*}, \quad k = 1, 2, \ldots, n. \end{cases}$$

In particular, if $\mu_k^S = \mu_k^I = \mu_k$, *then we have* $\varepsilon_k = 0$ *and*

$$\begin{aligned}\frac{\mathrm{d}}{\mathrm{d}t}\left(\frac{(N_k - N_k^*)^2}{2}\right) = &-\mu_k (S_k^*)^2 (x_k - 1)^2 - 2\mu_k S_k^* I_k^* (x_k - 1)(y_k - 1) \\ &-\mu_k (I_k^*)^2 (y_k - 1)^2, \quad k = 1, 2, \ldots, n.\end{aligned} \tag{4.19}$$

Proof. From the second equation of (2.1), we have

$$\frac{\mathrm{d}N_k}{\mathrm{d}t} = -\mu_k^S (N_k - N_k^*) - \varepsilon_k (I_k - I_k^*),$$

and hence,

$$\begin{aligned}&\frac{\mathrm{d}}{\mathrm{d}t}\left(\frac{(N_k - N_k^*)^2}{2}\right) \\ &= (N_k - N_k^*)\{-\mu_k^S (N_k - N_k^*) - \varepsilon_k (I_k - I_k^*)\} \\ &= -\mu_k^S (N_k - N_k^*)^2 - \varepsilon_k \{(S_k - S_k^*) + (I_k - I_k^*)\}(I_k - I_k^*) \\ &= -\mu_k^S (N_k^*)^2 (n_k - 1)^2 - \varepsilon_k S_k^* I_k^* (x_k - 1)(y_k - 1) - \varepsilon_k (I_k^*)^2 (y_k - 1)^2.\end{aligned}$$

Hence, we obtain (4.18). In particular, if $\mu_k^S = \mu_k^I = \mu_k$, then $\varepsilon_k = 0$ and

$$\begin{aligned}&\frac{\mathrm{d}}{\mathrm{d}t}\left(\frac{(N_k - N_k^*)^2}{2}\right) \\ &= (N_k - N_k^*)\{-\mu_k (N_k - N_k^*)\} \\ &= -\mu_k \{(S_k - S_k^*) + (I_k - I_k^*)\}^2 \\ &= -\mu_k \{(S_k - S_k^*)^2 + 2(S_k - S_k^*)(I_k - I_k^*) + (I_k - I_k^*)^2\} \\ &= -\mu_k (S_k^*)^2 (x_k - 1)^2 - 2\mu_k S_k^* I_k^* (x_k - 1)(y_k - 1) - \mu_k (I_k^*)^2 (y_k - 1)^2,\end{aligned}$$

and hence, we obtain (4.19). □

Now we consider

$$U = U_1 + U_2, \tag{4.20}$$

where

$$U_2 = \sum_{k=1}^{n} v_k w_k \frac{(N_k - N_k^*)^2}{2}$$

and

$$w_k = \begin{cases} \dfrac{\delta_k}{2\mu_k S_k^*} & \text{if } \mu_k^S = \mu_k^I = \mu_k, \\ \dfrac{\delta_k}{(\mu_k^I - \mu_k^S) S_k^*} & \text{if } \mu_k^S < \mu_k^I, \end{cases}$$

for $k = 1, 2, \ldots, n$. From Lemmas 4.1-4.3, one can easily obtain the following lemma.

Lemma 4.4 *Suppose that $\tilde{R}_0 > 1$. Let $\mathbf{v} = (v_1, v_2, \ldots, v_n)$ be chosen as in (4.14) in Lemma 4.2. Then we have*

$$\begin{aligned} \frac{\mathrm{d}U(t)}{\mathrm{d}t} = & -\sum_{k=1}^{n} v_k (\mu_k^S S_k^* + \delta_k I_k^* y_k) \left(1 - \frac{1}{x_k}\right)(x_k - 1) \\ & -\sum_{k=1}^{n} v_k \sum_{j=1}^{n} \beta_{kj} S_k^* I_j^* \left\{ g\left(\frac{1}{x_k}\right) + g\left(\frac{x_k y_j}{y_k}\right) \right\} \\ & -\sum_{k=1}^{n} v_k W_k, \end{aligned} \tag{4.21}$$

where

$$W_k = \begin{cases} \dfrac{\delta_k S_k^*}{2}(x_k - 1)^2 + \dfrac{\delta_k (I_k^*)^2}{2 S_k^*}(y_k - 1)^2 & \text{if } \mu_k^S = \mu_k^I = \mu_k, \\ \dfrac{\mu_k^S \delta_k (N_k^*)^2}{(\mu_k^I - \mu_k^S) S_k^*}(n_k - 1)^2 + \dfrac{\delta_k (I_k^*)^2}{S_k^*}(y_k - 1)^2 & \text{if } \mu_k^S < \mu_k^I \end{cases}$$

for $k = 1, 2, \ldots, n$.

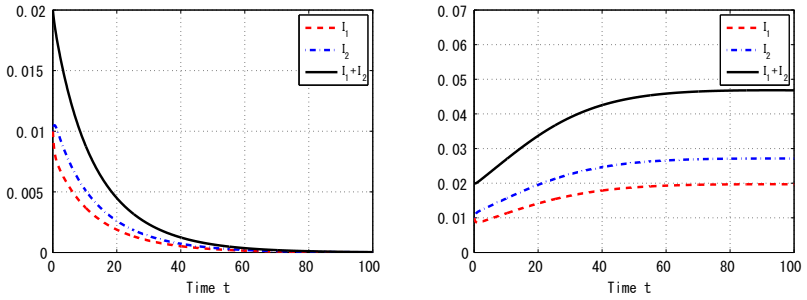
Proof. It follows from Proposition 3.1 that system (1.1) is uniformly persistent in $\mathbf{\Gamma}^0$. Thus, from Corollary 3.1, we see that there exists at least one endemic equilibrium $\mathbf{E}^* = (S_1^*, I_1^*, S_2^*, I_2^*, \ldots, S_n^*, I_n^*)$. Let $\mathbf{v} = (v_1, v_2, \ldots, v_n)$ be chosen as in (4.14) in Lemma 4.2. Then, we have (4.21) for (4.20) and hence, $\frac{dU(t)}{dt} \leq 0$. We see that $\frac{dU(t)}{dt} = 0$ if and only if

$$x_k = 1, \ y_k = 1, \ (\text{and } n_k = 1), \ \text{for any } t > 0, \ k = 1, 2, \ldots, n,$$

that is,

$$S_k(t) = S_k^*, \ I_k(t) = I_k^*, \ (\text{and } N_k(t) = N_k^*), \ \text{for any } t > 0, \ k = 1, 2, \ldots, n.$$

Thus, we see that the only compact invariant subset where $\frac{dU(t)}{dt} = 0$ is the singleton $\{\mathbf{E}^*\}$. From Proposition 3.1 and a similar argument as in Section 3, we can conclude that $\mathbf{E}^*$ is globally asymptotically stable in $\mathbf{\Gamma}^0$. □



(a) $\tilde{R}_0 \simeq 0.9746 < 1$ (b) $\tilde{R}_0 \simeq 1.0259 > 1$

Figure 1: Infected populations of female ($I_1(t)$) and male ($I_2(t)$) and total infected population ($I_1(t) + I_2(t)$) versus time t

5. Numerical examples

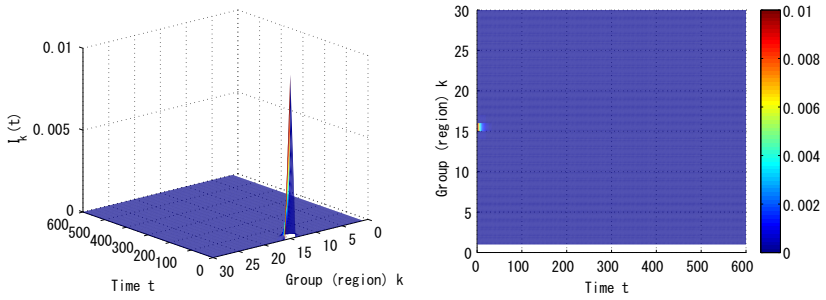
In this section, we perform numerical simulation to show the validity of our theoretical results.

5.1. A sexually transmitted disease

We first consider the two-group case ($n = 2$), which is thought to be suitable for sexually transmitted diseases since we can regard groups 1 and 2 as the female and male groups, respectively.

To model the long-term spread of disease, set the unit of time as a year. Since the average life expectancy is given by the inverse of the mortality rate, here we fix $\mu_1^S = 1/85$, $\mu_2^S = 1/80$, $\mu_1^I = 1/75$ and $\mu_2^I = 1/70$ to consider the situation that female individuals tend to live longer than male individuals and there is the risk of the disease-induced death. $b_k,\ k = 1, 2$ are set in terms of normalization, that is, $b_k = \mu_k^S,\ k = 1, 2$ and thus, the each subpopulation is equal to 1 in the disease-free steady state. Therefore, in the feasible region Γ, we can regard each solution as the ratio to each total subpopulation. We fix $\delta_k = 12,\ k = 1, 2$, which implies that the average infectious period $(1/\delta_k,\ k = 1, 2)$ is equal to a month. Under these settings, we observe the change of global stability of each equilibrium when the disease transmission rate $\beta_{kj},\ k, j = 1, 2$ is changed.

First we set $\beta_{kj} = 1.9\,(k + j)\,,\ k, j = 1, 2$. In this case, $\tilde{R}_0 \approx 0.9746 < 1$ and therefore, we expect from Theorem 1.1 (i) that the disease-free equilibrium $\mathbf{E}^0$ is globally asymptotically stable. In fact, in Fig. 1 (a), each infected population converges to zero. Next we set $\beta_{kj} = 2\,(k + j)\,,\ k, j = 1, 2$. In this case, $\tilde{R}_0 \approx 1.0259 > 1$ and therefore, we expect from Theorem 1.1 (ii) that the endemic equilibrium $\mathbf{E}^*$ is globally asymptotically stable. In fact, in Fig. 1 (b), each infected population converges to some positive steady state.



(a) (b)

Figure 2: Time evolution of the infected population $I_k(t)$, $k = 1, 2, \cdots, 30$ with $\tilde{R}_0 \approx 0.9921 < 1$. The discrete groups are connected smoothly by the MATLAB command "surf".

5.2. A geographical spread of disease

We next consider the 30-group case ($n = 30$) as the model of geographical spread of disease. For simplicity, referring to the previous example, we fix the following coefficients:

$$b_k = \frac{1}{80}, \quad \mu_k^S = \frac{1}{80}, \quad \mu_k^I = \frac{1}{70}, \quad \delta_k = 12, \quad k = 1, 2, \cdots, 30.$$

In what follows, we shall observe the stability change with different β_{kj}, $k, j = 1, 2, \cdots, 30$. To simulate the spatially spreading phenomenon, we employ the following diffusive-like form for matrix $\mathbf{B} = (\beta_{kj})_{1 \le k,j \le 30}$:

$$\mathbf{B} = (\beta_{kj})_{1 \le k,j \le 30} = \begin{pmatrix} \beta & \alpha & 0 & \cdots & 0 \\ \alpha & \beta & \alpha & \cdots & 0 \\ 0 & \ddots & \ddots & \ddots & \vdots \\ \vdots & & \alpha & \beta & \alpha \\ 0 & \cdots & 0 & \alpha & \beta \end{pmatrix},$$

where α and β are positive constants. It is easy to see that this matrix $\mathbf{B}$ is irreducible. In what follows, we fix $\alpha = 0.01$ and change β. The initial condition is fixed as follows.

$$S_k(0) = 1, \quad I_k(0) = 0, \quad k \neq 15, \quad S_{15}(0) = 0.99, \quad I_{15}(0) = 0.01.$$

First, we set $\beta = 11.9$. In this case, $\tilde{R}_0 \approx 0.9921 < 1$. Hence, from Theorem 1.1 (i), we can expect that the disease-free equilibrium $\mathbf{E}^0$ is globally asymptotically stable. In fact, in Fig. 2, we can observe that each infected population converges to zero.

Next, we set $\beta = 12.1$. In this case, $\tilde{R}_0 \approx 1.0088 > 1$. Hence, from Theorem 1.1 (ii), we can expect that the endemic equilibrium $\mathbf{E}^*$ is globally asymptotically stable. In fact, in Fig. 3, we can observe that each infected population

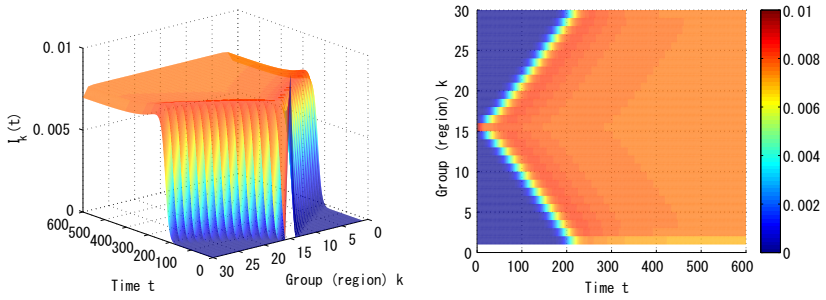


Figure 3: Time evolution of the infected population $I_k(t)$, $k = 1, 2, \cdots, 30$ with $\tilde{R}_0 \approx 1.0088 > 1$. The discrete groups are connected smoothly by the MATLAB command "surf".

converges to some positive value. In particular, by virtue of the form of matrix $\mathbf{B}$, we can observe the wave-like spreading pattern connecting the disease-free equilibrium $\mathbf{E}^0$ and the endemic equilibrium $\mathbf{E}^*$.

5.3. An age-dependent disease

Finally we consider the 100-group case ($n = 100$) as the model of an age-dependent disease. In this case, k denotes the age of each individual which maximum is assumed to be 100.

Similar to the previous examples, we set the unit of time as a year. First we consider the following age-dependent continuous mortality:

$$\mu(a) = \begin{cases} 0.1000\,(a-5)^2/25 + 0.0063, & 0 \le a < 5; \\ 0.0058\,(a-5)/45 + 0.0063, & 5 \le a < 50; \\ 0.1622\,(a-50)^2/1156 + 0.0121, & 50 \le a \le 100, \end{cases}$$

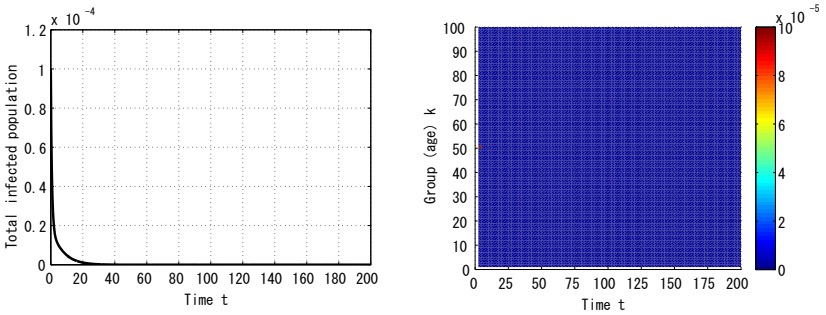
which was used in [11] to approximate the mortality for the population of Zimbabwe reported by Garnett and Anderson [7]. Let

$$\tilde{\mu}_k^S = \mu(k), \quad \mu_k^I = 1.1 \times \mu(k), \quad k = 1, 2, \cdots, 100.$$

In order to consider the aging process, we assume that the rate at which a susceptible individual grows up to the next age (that is, 1 per year) is incorporated into μ_k^S:

$$\mu_k^S = \tilde{\mu}_k^S + 1, \ k = 1, 2, \cdots, 99, \quad \mu_{100}^S = \tilde{\mu}_{100}^S.$$

We assume that the aging process of infective individuals can be ignored under the assumption that the recovery rate is relatively larger than the aging rate. Thus, we fix $\delta_k = 365/14, \ k = 1, 2, \cdots, 100$ assuming that the average infectious period is two weeks. As in [11], we fix the rate of birth at the first age as $b_1 = 1/46.6495$. Since b_k $(k \ge 2)$ can be regarded as the inflow into the new age group k, we fix them as $b_k = b_{k-1}/\mu_{k-1}^S$, $k = 2, 3, \cdots, 100$ by virtue of which



(a) Total infected population $\sum_{k=1}^{100} I_k(t)$ (b) Distribution of $I_k(t)$ for each k and t versus time t

Figure 4: Time evolution of the infected population $I_k(t)$, $k = 1, 2, \cdots, 100$ with $\tilde{R}_0 \approx 0.9942 < 1$.

we can consider the population at the demographic steady state. Under these settings, we observe the stability change of each equilibrium when the value of β_{kj}, $k, j = 1, 2, \cdots, 100$ is changed. The initial condition is fixed as follows.

$$S_k(0) = 0.01, \quad I_k(0) = 0, \quad k \neq 50, \quad S_{50}(0) = 0.0099, \quad I_{50}(0) = 0.0001.$$

First we set $\beta_{kj} = 25$, $k, j = 1, 2, \cdots, 100$. In this case, $\tilde{R}_0 \approx 0.9942 < 1$ and hence, from Theorem 1.1 (i), we can expect that the disease-free equilibrium $\mathbf{E}^0$ is globally asymptotically stable. In fact, in Fig. 4, the infected population converges to zero.

Next we set $\beta_{kj} = 26$, $k, j = 1, 2, \cdots, 100$. In this case, $\tilde{R}_0 \approx 1.0340 > 1$ and hence, from Theorem 1.1 (ii), we can expect that the endemic equilibrium $\mathbf{E}^*$ is globally asymptotically stable. In fact, in Fig. 5, the infected population converges to some positive value. In particular, although the group is discrete, we can observe the continuous PDE-like solution behavior across the difference of ages in Fig. 5 (b).

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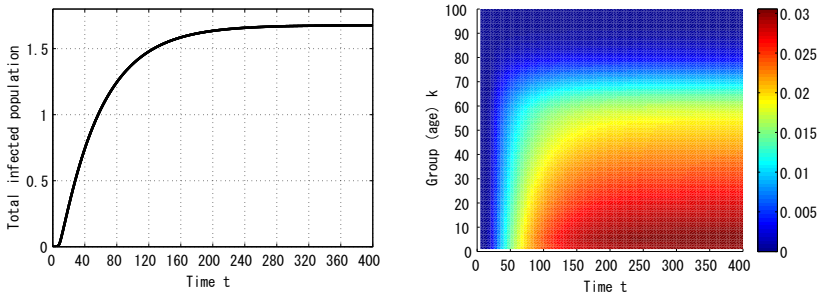

(a) Total infected population $\sum_{k=1}^{100} I_k(t)$ (b) Distribution of $I_k(t)$ for each k and t versus time t

Figure 5: Time evolution of the infected population $I_k(t)$, $k = 1, 2, \cdots, 100$ with $\tilde{R}_0 \approx 1.0340 > 1$.

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A. Proof of Proposition 3.1

First we prove (i). Let

$$\tilde{\mathbf{M}}(\mathbf{S}) := \left(\frac{\beta_{kj} S_k}{\mu_k^I + \delta_k} \right)_{n \times n}.$$

Since solution $(S_1, I_1, S_2, I_2, \ldots, S_n, I_n)$ is in $\mathbf{\Gamma}$, it holds that $0 \le S_k \le S_k^0$ for $k = 1, 2, \ldots, n$ and $\mathbf{0} \le \tilde{\mathbf{M}}(\mathbf{S}) \le \tilde{\mathbf{M}}(\mathbf{S}^0)$. Since it follows from (1.4) that matrix $\mathbf{B}$ is irreducible, we see that matrices $\tilde{\mathbf{M}}(\mathbf{S})$ and $\tilde{\mathbf{M}}(\mathbf{S}^0)$ are also irreducible. Thus, we have $\rho(\tilde{\mathbf{M}}(\mathbf{S})) < \rho(\tilde{\mathbf{M}}(\mathbf{S}^0)) = \tilde{R}_0 \le 1$, provided $\mathbf{S} \ne \mathbf{S}^0$ (see, for example, [32, Lemma 2.3]). Therefore, we see that

$$\tilde{\mathbf{M}}(\mathbf{S})\mathbf{I} = \mathbf{I}$$

has only the trivial solution $\mathbf{I} = \mathbf{0}$. Thus, $\mathbf{E}^0$ is the only equilibrium of system (1.1) in $\mathbf{\Gamma}$.

Let $(\omega_1, \ldots, \omega_n)$ be a left eigenvector of $\tilde{\mathbf{M}}(\mathbf{S}^0)$ corresponding to $\rho(\tilde{\mathbf{M}}(\mathbf{S}^0))$, i.e.,

$$(\omega_1, \omega_2, \ldots, \omega_n)\rho(\tilde{\mathbf{M}}(\mathbf{S}^0)) = (\omega_1, \omega_2, \ldots, \omega_n)\tilde{\mathbf{M}}(\mathbf{S}^0).$$

Since matrix $\tilde{\mathbf{M}}(\mathbf{S}^0)$ is irreducible, we have $\omega_k > 0$ for $k = 1, 2, \ldots, n$. Let

$$\begin{aligned} L &:= (\omega_1, \omega_2, \ldots, \omega_n) \\ &\times \begin{bmatrix} \mu_1^I + \delta_1 & 0 & \cdots & 0 \\ 0 & \mu_2^I + \delta_2 & \cdots & 0 \\ \cdots & & & \\ 0 & 0 & \cdots & \mu_n^I + \delta_n \end{bmatrix}^{-1} \begin{bmatrix} I_1 \\ I_2 \\ \vdots \\ I_n \end{bmatrix}. \end{aligned}$$

Differentiation gives

$$\begin{aligned} L' &= (\omega_1, \omega_2, \ldots, \omega_n) \left[\tilde{\mathbf{M}}(\mathbf{S})\mathbf{I} - \mathbf{I} \right] \le (\omega_1, \omega_2, \ldots, \omega_n) \left[\tilde{\mathbf{M}}(\mathbf{S}^0)\mathbf{I} - \mathbf{I} \right] \\ &= \left\{ \rho(\tilde{\mathbf{M}}(\mathbf{S}^0)) - 1 \right\} (\omega_1, \omega_2, \ldots, \omega_n)\, \mathbf{I} \le 0. \end{aligned}$$

If $\tilde{R}_0 = \rho(\tilde{\mathbf{M}}(\mathbf{S}^0)) < 1$, then $L' = 0 \iff \mathbf{I} = \mathbf{0}$. If $\tilde{R}_0 = 1$, then $L' = 0$ implies

$$(\omega_1, \omega_2, \ldots, \omega_n)\, \tilde{\mathbf{M}}(\mathbf{S})\mathbf{I} = (\omega_1, \omega_2, \ldots, \omega_n)\, \mathbf{I}. \tag{A.1}$$

If $\mathbf{S} \ne \mathbf{S}^0$, then

$$(\omega_1, \omega_2, \ldots, \omega_n)\tilde{\mathbf{M}}(\mathbf{S}) < (\omega_1, \omega_2, \ldots, \omega_n)\tilde{\mathbf{M}}(\mathbf{S}^0) = (\omega_1, \omega_2, \ldots, \omega_n).$$

Thus, (A.1) has only the trivial solution $\mathbf{I} = \mathbf{0}$. Therefore, $L' = 0 \iff \mathbf{I} = \mathbf{0}$ or $\mathbf{S} = \mathbf{S}^0$, provided $\tilde{R}_0 \le 1$. It can be verified that the only compact invariant subset of the set where $L' = 0$ is the singleton $\{\mathbf{E}^0\}$. Thus, from LaSalle's Invariance Principle (see [14]), it follows that $\mathbf{E}^0$ is globally asymptotically stable in $\mathbf{\Gamma}$ if $\tilde{R}_0 \le 1$.

Next we prove (ii). If $\tilde{R}_0 = \rho(\tilde{\mathbf{M}}(\mathbf{S}^0)) > 1$ and $\mathbf{I} \neq \mathbf{0}$, then we have

$$(\omega_1, \omega_2, \ldots, \omega_n)\tilde{\mathbf{M}}(\mathbf{S}^0) - (\omega_1, \omega_2, \ldots, \omega_n) = \{\rho(\tilde{\mathbf{M}}(\mathbf{S}^0)) - 1\}(\omega_1, \omega_2, \ldots, \omega_n) > 0$$

and thus, it follows from the continuity that $L' = (\omega_1, \omega_2, \ldots, \omega_n)[\tilde{\mathbf{M}}(\mathbf{S})\mathbf{I} - \mathbf{I}] > 0$ in a neighborhood of $\mathbf{E}^0$ in $\mathbf{\Gamma}^0$. This implies the instability of $\mathbf{E}^0$. Using a uniform persistence result obtained by Freedman *et al.* [6] and an argument as in the proof of Proposition 3.3 of Li *et al.* [15], we see that the instability of $\mathbf{E}^0$ implies the uniform persistence of system (1.1), which completes the proof. □

B. Proof of Lemma 3.1

Since

$$S_k^* \left(\sum_{j=1}^{n} \beta_{kj} I_j^* \right) - \left(\mu_k^I + \delta_k \right) I_k^* = 0, \quad k = 1, 2, \ldots, n,$$

we have

$$\begin{aligned} &\left(\frac{\beta_{kj} S_k^*}{\mu_j^I + \delta_j} \right)_{n \times n} \left((\mu_1^I + \delta_1) I_1^*, (\mu_2^I + \delta_2) I_2^*, \ldots, (\mu_n^I + \delta_n) I_n^* \right)^T \\ &\qquad = ((\mu_1^I + \delta_1) I_1^*, (\mu_2^I + \delta_2) I_2^*, \ldots, (\mu_n^I + \delta_n) I_n^*)^T \end{aligned} \tag{B.1}$$

and

$$\left(\frac{\beta_{kj} S_k^*}{\mu_k^I + \delta_k} \right)_{n \times n} \left(I_1^*, I_2^*, \ldots, I_n^* \right)^T = \left(I_1^*, I_2^*, \ldots, I_n^* \right)^T. \tag{B.2}$$

From (B.1) and (B.2) we obtain

$$\rho\left(\left(\frac{\beta_{kj} S_k^*}{\mu_j^I + \delta_j} \right)_{n \times n} \right) = \rho\left(\left(\frac{\beta_{kj} S_k^*}{\mu_k^I + \delta_k} \right)_{n \times n} \right) = 1,$$

that is,

$$\rho(\mathbf{M}(\mathbf{S}^*)) = \rho(\tilde{\mathbf{M}}(\mathbf{S}^*)) = 1.$$

Thus, from (1.5), (3.1), Lemma 2.1 and the arguments in the proof of (i) of Proposition 3.1 on the theory of nonnegative irreducible matrices (see for example, Varga [32, Chapter 2]), we complete the proof. □