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Threshold dynamics of an SIR epidemic model with hybrid of multigroup and patch structures

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Abstract. In this paper, we formulate an SIR epidemic model with hybrid of multigroup and patch structures, which can be regarded as a model for the geographical spread of infectious diseases or a multi-group model with perturbation. We show that if a threshold value, which corresponds to the well-known basic reproduction number R_0, is less than or equal to unity, then the disease-free equilibrium of the model is globally asymptotically stable. We also show that if the threshold value is greater than unity, then the model is uniformly persistent and has an endemic equilibrium. Moreover, using a Lyapunov functional technique, we obtain a sufficient condition under which the endemic equilibrium is globally asymptotically stable. The sufficient condition is satisfied if the transmission coefficients in the same groups are large or the per capita recovery rates are small.

Keywords: SIR epidemic model, multigroup, patch, global asymptotic stability, Lyapunov functional.
MSC2010: Primary: 34D20, 34D23; Secondary: 92D30.

1 Introduction

From the beginning of the 20th century, for the sake of clarifying the pattern of disease spread, various mathematical models have been formulated as systems of differential or difference equations (see, for instance, Anderson [1] and Diekmann and Heesterbeek [6]). Studying the mathematical properties of such models contributes to obtain a suitable measure for the control of diseases and therefore, authors have studied various epidemic models and obtained many results on the analytical properties such as the existence, uniqueness of solutions and stability of each equilibrium of the models (see [1–3, 6–10, 12, 13, 16–21, 23, 24, 26, 27] and references therein).

The recent development of worldwide transportation is thought to be one of the causes of the global pandemic of diseases. Thus, some types of space-structured models are expected to play an important role in clarifying how such transportation affects the pattern of disease prevalence. In this paper, we focus on the dynamics of the following SIR epidemic model with hybrid of multi-group and patch structures, which can be regarded as a type of space-structured model:

$$\left\{\begin{array}{l} \dfrac{\mathrm{d}S_k}{\mathrm{d}t} = b_k - \left\{\mu_k + \displaystyle\sum_{j=1}^{n}(1-\delta_{jk})\,\alpha_{jk}\right\} S_k - S_k \sum_{j=1}^{n}\beta_{kj} I_j + \sum_{j=1}^{n}(1-\delta_{kj})\,\alpha_{kj} S_j, \\ \dfrac{\mathrm{d}I_k}{\mathrm{d}t} = S_k \displaystyle\sum_{j=1}^{n}\beta_{kj} I_j - \left\{\mu_k + \gamma_k + \sum_{j=1}^{n}(1-\delta_{jk})\,\alpha_{jk}\right\} I_k + \sum_{j=1}^{n}(1-\delta_{kj})\,\alpha_{kj} I_j, \\ \dfrac{\mathrm{d}R_k}{\mathrm{d}t} = \gamma_k I_k - \left\{\mu_k + \displaystyle\sum_{j=1}^{n}(1-\delta_{jk})\,\alpha_{jk}\right\} R_k + \sum_{j=1}^{n}(1-\delta_{kj})\,\alpha_{kj} R_j, \quad k = 1, 2, \cdots, n \end{array}\right. \tag{1.1}$$

with initial condition

$$\left\{\begin{array}{l} S_k(0) = \phi_1^k, \quad I_k(0) = \phi_2^k, \quad R_k(0) = \phi_3^k, \quad k = 1, 2, \cdots, n, \\ \left(\phi_1^1, \phi_2^1, \phi_3^1, \cdots, \phi_1^n, \phi_2^n, \phi_3^n\right) \in \mathbb{R}_+^{3n}, \end{array}\right.$$

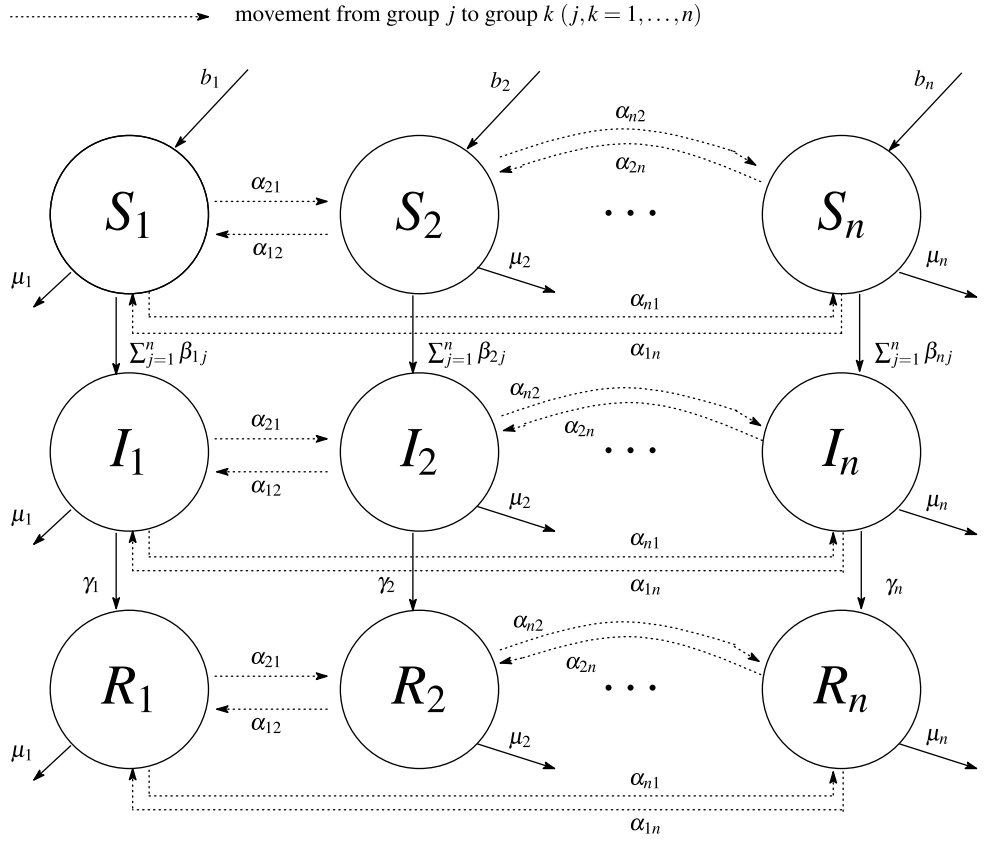


Figure 1: Diagram of the SIR epidemic model (1.1) with hybrid of multi-group and patch structures

where $\mathbb{R}_+^{3n} := \left\{(x_1, y_1, z_1, \cdots, x_n, y_n, z_n) \in \mathbb{R}^{3n} : x_k, y_k, z_k \geq 0,\ k = 1, 2, \cdots, n\right\}$.

In system (1.1), $S_k(t)$, $I_k(t)$ and $R_k(t)$ denote the densities of susceptible, infective and recovered individuals in group k at time t, respectively. $b_k > 0$ denotes the number of newborns per unit time in group k, $\mu_k > 0$ denotes the per capita mortality rate for individuals in group k (we do not consider the disease-induced mortality rates here), $\gamma_k \geq 0$ denotes the per capita recovery rate for infective individuals in group k, $\alpha_{kj} \geq 0$ denotes the per capita rate at which an individual in group j moves to group k, $\beta_{kj} \geq 0$ denotes the disease transmission coefficient between a susceptible individual in group k and an infective individual in group j, and δ_{kj} denotes the Kronecker delta such that $\delta_{kj} = 1$ if $k = j$ and $\delta_{kj} = 0$ otherwise. For a diagram of system (1.1), see Figure 1.

Note that Li and Shuai [17] investigated the case $\beta_{kj} = 0$, $j \neq k$, $k = 1, 2, \ldots, n$ with three restricted cases for more general patch structures than (1.1). In this model (1.1), the disease transmission can occur not only individuals in the same groups but also different groups, that is, it can occur that $\beta_{kj} > 0$ for some $k \neq j$. We call this kind of system the model with hybrid of multi-group (see, for instance, Guo *et al.* [9]) and patch (see, for instance, Arino [2], Wang and Zhao [26], Jin and Wang [12] and Li and Shuai [17]) structures. One of the previous studies on such a model was done by Bartlett [3, Section 8]. In the reference, the author considered the following two-group model:

$$\begin{cases} \dfrac{\mathrm{d}S_1}{\mathrm{d}t} = b_1 - S_1\left(\beta_1 I_1 + \beta_2 I_2\right) + m_S\left(S_2 - S_1\right), \\ \dfrac{\mathrm{d}I_1}{\mathrm{d}t} = S_1\left(\beta_1 I_1 + \beta_2 I_2\right) - (d+\rho)\,\mu I_1 + m_I\left(I_2 - I_1\right), \\ \dfrac{\mathrm{d}S_2}{\mathrm{d}t} = b_2 - S_2\left(\beta_1 I_1 + \beta_2 I_2\right) + m_S\left(S_1 - S_2\right), \\ \dfrac{\mathrm{d}I_2}{\mathrm{d}t} = S_2\left(\beta_1 I_1 + \beta_2 I_2\right) - (d+\rho)\,\mu I_2 + m_I\left(I_1 - I_2\right). \end{cases}$$

Here the symbols are slightly modified from the original ones. In Bartlett [3, Section 8], this system was explained as the model for the "interaction" of the actual diffusion or migration of individuals between groups and the chance of infection over the groups due to the visit of infective individuals to other groups and then returning. In Faddy [7], this type of model with hybrid of multi-group and patch structures was also studied. In the reference, such a system with hybrid structure was proposed as the model for considering both the mobility of infective individuals with respect to the space-region system and the contact infection among the neighborhood of each region. Recently, Muroya *et al.* [20] investigated a multi-group SIR epidemic model with general patch structure and Kuniya and Muroya [14] established

the complete global dynamics of a multi-group SIS epidemic model.

Under (i) of the following assumption, system (1.1) can be regarded as the generalization of usual patch models such that $\beta_{kj} = 0$ for $k \neq j$ and $\beta_{kj} > 0$ for $k = j$ and therefore, the analysis would have much mathematical interest:

Assumption 1.1. *Either one of the following conditions holds.*

(i) *The n-square matrix* $\mathbf{A} := (\alpha_{kj})_{1\leq k,j\leq n}$ *is irreducible.*

(ii) *The n-square matrix* $\mathbf{B} := (\beta_{kj})_{1\leq k,j\leq n}$ *is irreducible.*

(i) of Assumption 1.1 implies that there exists a path such that an individual in each group can move to any other group. (ii) of Assumption 1.1 implies that there exists an infection path such that an infective individual in each group can contact to a susceptible individual in any other group. Note that now we are also assuming that the rates $\alpha_{kj},\ k, j = 1, 2, \ldots, n$ are independent of the class (that is, S, I or R) of each individual. Similar assumption is found in, for instance, Arino [2] and Hyman and LaForce [11]. Note also that we have

$$\sum_{k=1}^{n}\sum_{j=1}^{n}(1-\delta_{jk})\,\alpha_{jk}S_k = \sum_{k=1}^{n}\sum_{j=1}^{n}(1-\delta_{kj})\,\alpha_{kj}S_j \tag{1.2}$$

(similar equalities hold also for I_j and R_j, $j = 1, 2, \ldots, n$) and hence, in each class, the total emigration is always in balance with the total immigration and the only input to the system is the recruitment of newborns.

Biologically, we can regard system (1.1) as a model for the geographical spread of disease (see Section 7.1). In this case, as explained in Bartlett [3] and Faddy [7], $\beta_{kj},\ k \neq j$ can imply the effect of contact infection among the neighborhood of each region, which is not due to the actual diffusion or migration. On the other hand, we can also regard (1.1) as a multi-group model with perturbation with respect to coefficient α_{kj}. In this case, as in the model of a sexually transmitted disease in Section 7.2, $\alpha_{kj},\ k \neq j$ imply the transfer rate from a state to other states (e.g., sexual transformation).

Due to the complex form, to our knowledge, there are very few studies on the models with hybrid of multi-group and patch structures (see for example, Muroya *et al.* [20] for a general SIR model with patch structure). In this paper, we study the global dynamics of system (1.1) and obtain a threshold condition which can determine the global asymptotic stability of each equilibrium.

From the viewpoint of application, we expect that the threshold condition can play an important role in controlling the geographical spread of diseases.

Note that the first and second equations of system (1.1) are independent from $R_k,\ k = 1, 2, \ldots, n$. This allows us hereafter to consider only the following reduced system:

$$\begin{cases} \dfrac{\mathrm{d}S_k}{\mathrm{d}t} = b_k - \left\{\mu_k + \displaystyle\sum_{j=1}^{n}(1-\delta_{jk})\,\alpha_{jk}\right\}S_k - S_k\sum_{j=1}^{n}\beta_{kj}I_j + \sum_{j=1}^{n}(1-\delta_{kj})\,\alpha_{kj}S_j, \\ \dfrac{\mathrm{d}I_k}{\mathrm{d}t} = S_k\displaystyle\sum_{j=1}^{n}\beta_{kj}I_j - \left\{\mu_k + \gamma_k + \sum_{j=1}^{n}(1-\delta_{jk})\alpha_{jk}\right\}I_k + \sum_{j=1}^{n}(1-\delta_{kj})\,\alpha_{kj}I_j, \quad k = 1, 2, \cdots, n \end{cases} \tag{1.3}$$

with initial condition

$$\begin{cases} S_k(0) = \phi_1^k, \quad I_k(0) = \phi_2^k, \quad k = 1, 2, \cdots, n, \\ \left(\phi_1^1, \phi_2^1, \phi_1^2, \phi_2^2, \cdots, \phi_1^n, \phi_2^n\right) \in \mathbb{R}_+^{2n}. \end{cases}$$

We define the feasible region for system (1.3) by

$$\Gamma := \left\{(S_1, I_1, \cdots, S_n, I_n) \in \mathbb{R}_+^{2n} :\ S_k \leq S_k^0,\ \sum_{k=1}^{n}(S_k + I_k) \leq \frac{\bar{b}}{\underline{\mu}},\quad k = 1, 2, \cdots, n\right\}, \tag{1.4}$$

where $\bar{b} := \sum_{k=1}^{n} b_k$ and $\underline{\mu} := \min_{1\leq k\leq n}\mu_k$.

As in the previous studies of multi-group epidemic models (see, for instance, [9, 10, 18, 19, 21, 23, 27]), we can expect that a threshold value for the global dynamics of system (1.3) is obtained as the spectral radius of a nonnegative irreducible matrix, which corresponds to the well-known *next generation matrix* (see, for instance, van den Driessche and Watmough [24]). Let $\mathbf{H}$ and $\mathbf{b}$ be a matrix and a vector defined by

$$\mathbf{H} := \begin{bmatrix} \mu_1 + \tilde{\alpha}_{11} & -\alpha_{12} & \cdots & -\alpha_{1n} \\ -\alpha_{21} & \mu_2 + \tilde{\alpha}_{22} & \cdots & -\alpha_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ -\alpha_{n1} & -\alpha_{n2} & \cdots & \mu_n + \tilde{\alpha}_{nn} \end{bmatrix} \quad \text{and} \quad \mathbf{b} := \begin{bmatrix} b_1 \\ b_2 \\ \vdots \\ b_n \end{bmatrix}, \tag{1.5}$$

respectively, where

$$\tilde{\alpha}_{kk} := \sum_{j=1}^{n}(1-\delta_{jk})\alpha_{jk}. \tag{1.6}$$

We define a positive n-column vector $\mathbf{S}^0 := (S_1^0, S_2^0, \cdots, S_n^0)^T$ by

$$\mathbf{S}^0 = \mathbf{H}^{-1}\mathbf{b}, \tag{1.7}$$

where T denotes the transpose operation for a vector or a matrix. Note that it follows from (1.6) that $\mathbf{H}$ is an M-matrix and hence, the positive inverse $\mathbf{H}^{-1}$ exists (see, for instance, Berman and Plemmons [4] or Varga [25]). Let $\tilde{\mathbf{V}}$ be an n-dimensional diagonal matrix defined by

$$\begin{aligned}\tilde{\mathbf{V}} &:= \mathrm{diag}_{1\le k\le n}\,(\mu_k+\gamma_k+\tilde{\alpha}_{kk}) \\ &= \begin{bmatrix} \mu_1+\gamma_1+\tilde{\alpha}_{11} & 0 & \cdots & 0 \\ 0 & \mu_2+\gamma_2+\tilde{\alpha}_{22} & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \mu_n+\gamma_n+\tilde{\alpha}_{nn} \end{bmatrix}\end{aligned} \tag{1.8}$$

and $\tilde{\mathbf{F}}$ be a matrix-valued operator on $\mathbb{R}_+^n$ defined by

$$\tilde{\mathbf{F}}(\mathbf{S}) := \begin{bmatrix} S_1\beta_{11} & S_1\beta_{12}+\alpha_{12} & \cdots & S_1\beta_{1n}+\alpha_{1n} \\ S_2\beta_{21}+\alpha_{21} & S_2\beta_{22} & \cdots & S_2\beta_{2n}+\alpha_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ S_n\beta_{n1}+\alpha_{n1} & S_n\beta_{n2}+\alpha_{n2} & \cdots & S_n\beta_{nn} \end{bmatrix},$$

where $\mathbf{S} := (S_1, S_2, \cdots, S_n)^T$. Under these settings, we define a matrix

$$\begin{cases} \tilde{\mathbf{M}}(\mathbf{S}) := \tilde{\mathbf{V}}^{-1}\tilde{\mathbf{F}}(\mathbf{S}) = (\tilde{M}_{kj})_{n\times n}, \\ \tilde{M}_{kj} := \dfrac{S_k\beta_{kj}+(1-\delta_{kj})\alpha_{kj}}{\mu_k+\gamma_k+\tilde{\alpha}_{kk}}, \quad k,j=1,2,\cdots,n \end{cases}$$

and a threshold value

$$\tilde{R}_0 := \rho(\tilde{\mathbf{M}}(\mathbf{S}^0)), \tag{1.9}$$

where ρ denotes the spectral radius of a matrix. The definition of this value $\tilde{R}_0$ is slightly different from that of the well-known *basic reproduction number* R_0 (see Diekmann and Heesterbeek [6] or van den Driessche and Watmough [24]). But on analysis of multi-group SIR epidemic models, a lot of researchers used this $\tilde{R}_0$ in place of R_0 (see for example, Guo *et al.* [9]). In this paper, we shall use $\tilde{R}_0$ in our analysis mainly for a technical reason such that we can construct a suitable Lyapunov function L making use of the form of matrix $\tilde{\mathbf{M}}(\mathbf{S})$ (see Section 3), because we shall show that $\tilde{R}_0$ has an equivalent threshold condition to that of R_0, Hence, we can use both of them as the threshold value for system (1.3) (see Section 5). The main purpose of this paper is to establish the following theorem which states that $\tilde{R}_0$ (and thus, R_0) plays the role of the threshold value for the global asymptotic stability of equilibria of system (1.3):

Theorem 1.1. *Let* Γ *and* $\tilde{R}_0$ *be defined by* (1.4) *and* (1.9)*, respectively.*

(1) *If* $\tilde{R}_0 \le 1$*, then the disease-free equilibrium* $\mathbf{E}^0 = (S_1^0, 0, S_2^0, 0, \cdots, S_n^0, 0)$ *of system* (1.3) *is globally asymptotically stable in region* Γ*.*

(2) *If* $\tilde{R}_0 > 1$*, then system* (1.3) *is uniformly persistent in the interior* Γ^0 *of* Γ *and has at least one endemic equilibrium* $\mathbf{E}^* = (S_1^*, I_1^*, S_2^*, I_2^*, \cdots, S_n^*, I_n^*)$ *in* Γ^0*. Moreover, if*

$$\min_{1\le k\le n}\{\beta_{kk}(S_k^*+I_k^*)-\gamma_k\} \ge 0, \tag{1.10}$$

then the endemic equilibrium $\mathbf{E}^*$ *is globally asymptotically stable in* Γ^0*.*

Remark 1.1. *Condition* (1.10) *holds if* β_{kk} *is large or* γ_k *is small* (*for details, see Corollary 6.1*)*. Moreover, this condition* (1.10) *is a sufficient condition of* (4.16) *which is satisfied for a sufficiently small patch parameters of* α_{jk}*. In this meaning, the condition* (1.10) *can be seen as a perturbation result from a well known result of Guo et al. for a multi-group SIR epidemic model.*

For the proof of Theorem 1.1, we shall use a Lyapunov functional method (see also Korobeinikov [13]). One of the core ideas of the construction of such a Lyapunov function is using a Laplacian matrix $\tilde{\mathbf{B}}$ and linear system $\tilde{\mathbf{B}}\mathbf{v} = 0$ as in Guo *et al.* [9]. The other one of the core ideas is using function $g(x) = x - 1 - \ln x$ to evaluate the derivative of the Lyapunov function in an appropriate way. Then, we succeed in omitting the argument about the cycles, which was needed in the graph theoretic approach in Guo *et al.* [9]. The result would remind us the importance of using function $g(x) = x - 1 - \ln x$ in the Lyapunov functional methods to analysis for epidemic models.

The organization of this paper is as follows: In Section 2, we show the positivity and boundedness of solutions of system (1.3). In Section 3, we prove (1) of Theorem 1.1. In Section 4, we prove (2) of Theorem 1.1. In Section 5, we derive the basic reproduction number R_0 for system (1.3) and show that it has a similar threshold property as $\tilde{R}_0$ in the sense that $R_0 \leq 1$ if and only if $\tilde{R}_0 \leq 1$. In Section 7, we perform some numerical simulations to show the validity of Theorem 1.1.

2 Positivity and boundedness of solutions

In this section, we prove the following proposition.

Proposition 2.1. *For system* (1.3)*, it holds that*

$$S_k(t) > 0, \quad I_k(t) \geq 0, \quad \forall k = 1, 2, \cdots, n, \quad t \in (0, +\infty)$$

and

$$\limsup_{t\to+\infty} \sum_{k=1}^{n} \{S_k(t) + I_k(t)\} \leq \frac{\bar{b}}{\underline{\mu}}, \quad \limsup_{t\to+\infty} S_k(t) \leq S_k^0, \quad k = 1, 2, \cdots, n, \tag{2.1}$$

where $\bar{b} > 0$ *and* $\underline{\mu} > 0$ *are positive constants defined in* (1.4).

Proof. It follows from the first equation of (1.3) that $\lim_{S_k\to+0} \frac{\mathrm{d}}{\mathrm{d}t} S_k \geq b_k > 0$. Hence, initial condition $S_k(0) = \phi_1^k \geq 0$ implies that there exists a positive constant t_{k0} such that $S_k(t) > 0$ for all $0 < t < t_{k0}$. Let $t_0 := \min_{1\leq k\leq n} t_{k0}$.

First, we claim that $S_k(t) > 0$ for all $k = 1, 2, \cdots, n$ and $0 < t < +\infty$. In fact, if it is not true, then there exist a positive constant $t_1 > t_0$ and a positive integer $k_1 \in \{1, 2, \cdots, n\}$ such that $S_{k_1}(t_1) = 0$ and $S_{k_1}(t) > 0$ for all $0 < t < t_1$. However, the first equation of (1.3) yields $\frac{\mathrm{d}}{\mathrm{d}t} S_{k_1}(t_1) \geq b_{k_1} > 0$, which contradicts to the fact that $S_{k_1}(t) > 0 = S_{k_1}(t_1)$ for all $0 < t < t_1$.

Next, we claim that $I_k(t) \geq 0$ for all $k = 1, 2, \cdots, n$ and $0 < t < +\infty$. In fact, if it is not true, then there exist positive constant $t_2 > 0$ and positive integer $k_2 \in \{1, 2, \cdots, n\}$ such that $I_{k_2}(t_2) < 0$. Let $s_2 := \inf\{0 < t < t_2 : I_{k_2}(t) < 0\}$, which must satisfy $0 \leq s_2 < t_2$ and $I_{k_2}(s_2) = 0$. However, the second equation of (1.3) yields $\frac{\mathrm{d}}{\mathrm{d}t} I_{k_2}(s_2) \geq 0$, which contradicts to the fact that $I_{k_2}(t) < 0 = I_{k_2}(s_2)$ for all $s_2 < t < t_2$.

Finally, we prove (2.1). It follows from (1.2) and (1.6) that

$$\begin{aligned}
\frac{\mathrm{d}}{\mathrm{d}t}\left\{\sum_{k=1}^{n}(S_k + I_k)\right\} &= \sum_{k=1}^{n}\left\{b_k - (\mu_k + \tilde{\alpha}_{kk})S_k - (\mu_k + \gamma_k + \tilde{\alpha}_{kk})I_k + \sum_{j=1}^{n}(1-\delta_{kj})(\alpha_{kj}S_j + \alpha_{kj}I_j)\right\} \\
&= \sum_{k=1}^{n}\{b_k - \mu_k S_k - (\mu_k + \gamma_k)I_k\} \leq \sum_{k=1}^{n} b_k - \left(\min_{1\leq k\leq n}\mu_k\right)\sum_{k=1}^{n}(S_k + I_k),
\end{aligned}$$

from which we obtain the first inequality of (2.1). It follows from the first equation of (1.3) that

$$\frac{\mathrm{d}S_k}{\mathrm{d}t} \leq b_k - (\mu_k + \tilde{\alpha}_{kk})S_k + \sum_{j=1}^{n}(1-\delta_{kj})\alpha_{kj}S_j, \quad k = 1, 2, \cdots, n.$$

Then, it follows from (1.7) and the theory of linear differential equations that

$$\frac{\mathrm{d}\mathbf{S}}{\mathrm{d}t} \leq \left(\mathbf{S}(0) - \mathbf{S}^0\right)\exp(-\mathbf{H}t) + \mathbf{S}^0.$$

Since $\mathbf{H}$ defined by (1.5) is an M-matrix, all of its eigenvalues have negative real parts. Therefore, we have

$$\limsup_{t\to+\infty} \exp(-\mathbf{H}t) = \mathbf{0}$$

and hence, $\limsup_{t\to+\infty} S_k(t) \leq S_k^0$, $k = 1, 2, \cdots, n$. □

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

In this section, we give the proof of (1) of Theorem 1.1.

Proof of (1) **of Theorem 1.1.** First we show that there do not exist any endemic equilibria $\mathbf{E}^*$ in Γ. Since solutions belong to Γ, we have $0 < S_k \leq S_k^0$ for $1 \leq k \leq n$ and hence $\mathbf{0} \leq \tilde{\mathbf{M}}(\mathbf{S}) \leq \tilde{\mathbf{M}}(\mathbf{S}^0)$. Assumption 1.1 guarantees the irreducibility of matrices $\tilde{\mathbf{M}}(\mathbf{S})$, $\tilde{\mathbf{M}}(\mathbf{S}^0)$ and $\tilde{\mathbf{M}}(\mathbf{S}) + \tilde{\mathbf{M}}(\mathbf{S}^0)$. Therefore, it follows from the Perron-Frobenius theorem on nonnegative irreducible matrices (see, for instance, Berman and Plemmons [4, Corollary 2.1.5]) that

$$\rho(\tilde{\mathbf{M}}(\mathbf{S})) < \rho(\tilde{\mathbf{M}}(\mathbf{S}^0)) = \tilde{R}_0 \leq 1$$

for $\mathbf{S} \neq \mathbf{S}^0$. Hence,

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

has only the trivial solution $\mathbf{I} = \mathbf{0}$. This implies that the disease-free equilibrium $\mathbf{E}^0$ is the only equilibrium of system (1.3) in Γ.

Let $(\omega_1, \omega_2, \cdots, \omega_n)$ be a left eigenvector of matrix $\tilde{\mathbf{M}}(\mathbf{S}^0)$ corresponding to the eigenvalue $\rho(\tilde{\mathbf{M}}(\mathbf{S}^0))$, that is,

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

The irreducibility of matrix $\tilde{\mathbf{M}}(\mathbf{S}^0)$ yields the strict positive vector $(\omega_1, \omega_2, \cdots, \omega_n)$ with $\omega_k > 0$ for $k = 1, 2, \cdots, n$ (see Berman and Plemmons [4, Theorem 2.1.4]). Let L be a Lyapunov function on $\mathbb{R}^n_+$ defined by

$$L := (\omega_1, \omega_2, \cdots, \omega_n) \begin{bmatrix} \mu_1 + \gamma_1 + \tilde{\alpha}_{11} & 0 & \cdots & 0 \\ 0 & \mu_2 + \gamma_2 + \tilde{\alpha}_{22} & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \mu_n + \gamma_n + \tilde{\alpha}_{nn} \end{bmatrix}^{-1} \begin{bmatrix} I_1 \\ I_2 \\ \vdots \\ I_n \end{bmatrix}.$$

The derivative along the trajectories of system (1.3) is

$$\begin{aligned} L' &= (\omega_1, \omega_2, \cdots, \omega_n)\left[\tilde{\mathbf{M}}(\mathbf{S})\,\mathbf{I} - \mathbf{I}\right] \leq (\omega_1, \omega_2, \cdots, \omega_n)\left[\tilde{\mathbf{M}}(\mathbf{S}^0)\,\mathbf{I} - \mathbf{I}\right] \\ &= \left\{\rho\left(\tilde{\mathbf{M}}(\mathbf{S}^0)\right) - 1\right\}(\omega_1, \omega_2, \cdots, \omega_n)\,\mathbf{I} \\ &= (\tilde{R}_0 - 1)\,(\omega_1, \omega_2, \cdots, \omega_n)\,\mathbf{I} \leq 0. \end{aligned} \tag{3.1}$$

Thus, for $\tilde{R}_0 < 1$, we have that $L' = 0$ if and only if $\mathbf{I} = \mathbf{0}$. For $\tilde{R}_0 = 1$, we see from the first equality of (3.1) that $L' = 0$ implies

$$(\omega_1, \omega_2, \cdots, \omega_n)\,\tilde{\mathbf{M}}(\mathbf{S})\,\mathbf{I} = (\omega_1, \omega_2, \cdots, \omega_n)\,\mathbf{I}. \tag{3.2}$$

In this situation, if $\mathbf{S} \neq \mathbf{S}^0$, then we have

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

and hence, (3.2) has only the trivial solution $\mathbf{I} = \mathbf{0}$. Consequently, for $\tilde{R}_0 \leq 1$, we have that $L' = 0$ if and only if $\mathbf{I} = \mathbf{0}$ or $\mathbf{S} = \mathbf{S}^0$. This implies that the only compact invariant subset of the set where $L' = 0$ is the singleton $\{\mathbf{E}^0\}$. Therefore, it follows from the LaSalle invariance principle (see LaSalle [15]) that the disease-free equilibrium $\mathbf{E}^0$ is globally asymptotically stable in Γ. □

4 Global stability of the endemic equilibrium $\mathbf{E}^*$ for $\tilde{\mathbf{R}}_\mathbf{0} > \mathbf{1}$

We first prove the following proposition.

Proposition 4.1. *Let Γ and $\tilde{R}_0$ be defined by* (1.4) *and* (1.9)*, respectively. If $\tilde{R}_0 > 1$, then the disease-free equilibrium $\mathbf{E}^0 = (S_1^0, 0, \cdots, S_n^0, 0) \in \Gamma$ is unstable.*

Proof. Let ω_k, $k = 1, 2, \ldots, n$ and L be as in the proof of (1) of Theorem 1.1. Since

$$\begin{aligned} (\omega_1, \omega_2, \cdots, \omega_n)\,\tilde{\mathbf{M}}(\mathbf{S}^0) - (\omega_1, \omega_2, \cdots, \omega_n) &= \left\{\rho\left(\tilde{\mathbf{M}}(\mathbf{S}^0)\right) - 1\right\}(\omega_1, \omega_2, \cdots, \omega_n) \\ &= \left(\tilde{R}_0 - 1\right)(\omega_1, \omega_2, \cdots, \omega_n) > \mathbf{0}, \end{aligned}$$

it follows from the continuity of $\tilde{\mathbf{M}}(\mathbf{S})$ with respect to $\mathbf{S}$ that

$$L' = (\omega_1, \omega_2, \cdots, \omega_n)\left[\tilde{\mathbf{M}}(\mathbf{S})\,\mathbf{I} - \mathbf{I}\right] > 0$$

in a neighborhood of $\mathbf{E}^0$ in Γ^0. This implies that $\mathbf{E}^0$ is unstable. □

From Freedman *et al.* [8], using an argument as in the proof of Proposition 3.3 of Li *et al.* [16], we can prove that the instability of $\mathbf{E}^0$ implies the uniform persistence of system (1.3).

From Smith and Waltman [22, Theorem D.3], we see that the uniform persistence of system (1.3) together with the uniform boundedness of solutions in Γ^0 implies the existence of an endemic equilibrium in Γ^0. Consequently, from Propositions 2.1 and 4.1, we obtain the following proposition.

Proposition 4.2. *Let Γ and $\tilde{R}_0$ be defined by* (1.4) *and* (1.9)*, respectively. If $\tilde{R}_0 > 1$, then system (1.3) is uniformly persistent and has at least one endemic equilibrium $\mathbf{E}^* = (S_1^*, I_1^*, S_2^*, I_2^*, \cdots, S_n^*, I_n^*)$ in the interior Γ^0 of Γ.*

In the remainder of this section, we assume that $\tilde{R}_0 > 1$. It follows from (1.3) that each component of the endemic equilibrium $\mathbf{E}^* = (S_1^*, I_1^*, S_2^*, I_2^*, \cdots, S_n^*, I_n^*) \in \Gamma^0$ satisfies the following equations:

$$b_k = (\mu_k + \tilde{\alpha}_{kk})\,S_k^* + \sum_{j=1}^{n}\left\{\beta_{kj}S_k^*I_j^* - (1-\delta_{kj})\,\alpha_{kj}S_j^*\right\}, \tag{4.1}$$

$$(\mu_k + \gamma_k + \tilde{\alpha}_{kk})\,I_k^* = \sum_{j=1}^{n}\left\{\beta_{kj}S_k^*I_j^* + (1-\delta_{kj})\,\alpha_{kj}I_j^*\right\},\ k = 1, 2, \cdots, n. \tag{4.2}$$

Let

$$\tilde{\beta}_{kj} := \{\beta_{kj}S_k^* + (1-\delta_{kj})\alpha_{kj}\}\,I_j^*, \quad 1 \le k, j \le n,$$

$$\tilde{\mathbf{B}} := \begin{bmatrix} \sum_{j\neq 1}\tilde{\beta}_{1j} & -\tilde{\beta}_{21} & \cdots & -\tilde{\beta}_{n1} \\ -\tilde{\beta}_{12} & \sum_{j\neq 2}\tilde{\beta}_{2j} & \cdots & -\tilde{\beta}_{n2} \\ \vdots & \vdots & \ddots & \vdots \\ -\tilde{\beta}_{1n} & -\tilde{\beta}_{2n} & \cdots & \sum_{j\neq n}\tilde{\beta}_{nj} \end{bmatrix}$$

and

$$(v_1, v_2, \cdots, v_n) := (C_1, C_2, \cdots, C_n),$$

where C_k denotes the cofactor of the k-th diagonal entry of $\tilde{\mathbf{B}}$. Using arguments as in Guo *et al.* [9], we have

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

and hence, from (4.2), we have

$$\sum_{j=1}^{n} v_j\{\beta_{jk}S_j^* + (1-\delta_{jk})\alpha_{jk}\} = v_k(\mu_k + \gamma_k + \tilde{\alpha}_{kk}), \quad k = 1, 2, \cdots, n. \tag{4.3}$$

Using $(v_1, v_2, \cdots, v_n)$, we define a Lyapunov functional on $\mathbb{R}_+^{2n}$ by

$$U := \sum_{k=1}^{n} v_k\left\{S_k^* g\left(\frac{S_k}{S_k^*}\right) + I_k^* g\left(\frac{I_k}{I_k^*}\right)\right\}, \tag{4.4}$$

where $g(x) := x - 1 - \ln x$ is a function defined on $(0, +\infty)$. Note that $g(x) \ge 0$ for all $x > 0$ and the global minimum $g(x) = 0$ is attained if and only if $x = 1$. The derivative of U along the trajectories of system (1.3) is

$$U' = \sum_{k=1}^{n} v_k\left\{\left(1 - \frac{1}{x_k}\right)\frac{\mathrm{d}S_k}{\mathrm{d}t} + \left(1 - \frac{1}{y_k}\right)\frac{\mathrm{d}I_k}{\mathrm{d}t}\right\}, \tag{4.5}$$

where

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

It follows from the first equation of (1.3) and (4.1) that

$$\begin{aligned}\frac{\mathrm{d}S_k}{\mathrm{d}t} &= b_k - (\mu_k + \tilde{\alpha}_{kk}) S_k - \sum_{j=1}^{n} \{\beta_{kj} S_k I_j - (1-\delta_{kj}) \alpha_{kj} S_j\} \\ &= -(\mu_k + \tilde{\alpha}_{kk}) (S_k - S_k^*) - \sum_{j=1}^{n} \left\{\beta_{kj} \left(S_k I_j - S_k^* I_j^*\right) - (1-\delta_{kj}) \alpha_{kj} \left(S_j - S_j^*\right)\right\} \\ &= -(\mu_k + \tilde{\alpha}_{kk}) S_k^* (x_k - 1) - \sum_{j=1}^{n} \left\{\beta_{kj} S_k^* I_j^* (x_k y_j - 1) - (1-\delta_{kj}) \alpha_{kj} S_j^* (x_j - 1)\right\}. \end{aligned} \tag{4.6}$$

Furthermore it follows from the second equation of (1.3) and (4.2) that

$$\begin{aligned}\frac{\mathrm{d}I_k}{\mathrm{d}t} &= \sum_{j=1}^{n} \{\beta_{kj} S_k I_j + (1-\delta_{kj}) \alpha_{kj} I_j\} - (\mu_k + \gamma_k + \tilde{\alpha}_{kk}) I_k \\ &= \sum_{j=1}^{n} \left\{\beta_{kj} S_k^* I_j^* x_k y_j + (1-\delta_{kj}) \alpha_{kj} I_j^* y_j\right\} - (\mu_k + \gamma_k + \tilde{\alpha}_{kk}) I_k^* y_k \\ &= \sum_{j=1}^{n} \left\{\beta_{kj} S_k^* I_j^* (x_k y_j - y_k) + (1-\delta_{kj}) \alpha_{kj} I_j^* (y_j - y_k)\right\}. \end{aligned} \tag{4.7}$$

Substituting (4.6) and (4.7) into (4.5), we have

$$\begin{aligned} U' = &\sum_{k=1}^{n} v_k \left[\left(1 - \frac{1}{x_k}\right) \left\{-(\mu_k + \tilde{\alpha}_{kk}) S_k^* (x_k - 1) - \sum_{j=1}^{n} \left\{\beta_{kj} S_k^* I_j^* (x_k y_j - 1) - (1-\delta_{kj}) \alpha_{kj} S_j^* (x_j - 1)\right\}\right\}\right. \\ &\left. + \left(1 - \frac{1}{y_k}\right) \left\{\sum_{j=1}^{n} \left\{\beta_{kj} S_k^* I_j^* (x_k y_j - y_k) + (1-\delta_{kj}) \alpha_{kj} I_j^* (y_j - y_k)\right\}\right\}\right] \\ = &-\sum_{k=1}^{n} v_k \left[(\mu_k + \tilde{\alpha}_{kk}) S_k^* \left(1 - \frac{1}{x_k}\right) (x_k - 1) - \sum_{j=1}^{n} (1-\delta_{kj}) \alpha_{kj} S_j^* \left(1 - \frac{1}{x_k}\right) (x_j - 1)\right] \\ &+ \sum_{k=1}^{n} v_k \left[\sum_{j=1}^{n} \beta_{kj} S_k^* I_j^* \left\{\left(1 - \frac{1}{x_k}\right) (1 - x_k y_j) + \left(1 - \frac{1}{y_k}\right) (x_k y_j - y_k)\right\} + \sum_{j=1}^{n} (1-\delta_{kj}) \alpha_{kj} I_j^* \left(1 - \frac{1}{y_k}\right) (y_j - y_k)\right]. \end{aligned} \tag{4.8}$$

Now we prove the following lemma.

Lemma 4.1. *For $k, j = 1, 2, \cdots, n$, the following relations hold:*

$$\left(1 - \frac{1}{x_k}\right) (x_j - 1) = g(x_j) - g\left(\frac{x_j}{x_k}\right) + g\left(\frac{1}{x_k}\right), \tag{4.9}$$

$$\left(1 - \frac{1}{x_k}\right) (x_k - 1) = g(x_k) + g\left(\frac{1}{x_k}\right), \tag{4.10}$$

and

$$\left(1 - \frac{1}{x_k}\right) (1 - x_k y_j) + \left(1 - \frac{1}{y_k}\right) (x_k y_j - y_k) = -g\left(\frac{1}{x_k}\right) - g\left(\frac{x_k y_j}{y_k}\right) + \{g(y_j) - g(y_k)\}, \tag{4.11}$$

$$\left(1 - \frac{1}{y_k}\right) (y_j - y_k) = -g\left(\frac{y_j}{y_k}\right) + \{g(y_j) - g(y_k)\}. \tag{4.12}$$

Proof. For $k, j = 1, 2, \cdots, n$, we have

$$\left(1 - \frac{1}{x_k}\right) (x_j - 1) = x_j - \frac{x_j}{x_k} + \frac{1}{x_j} - 1 = g(x_j) - g\left(\frac{x_j}{x_k}\right) + g\left(\frac{1}{x_k}\right)$$

and hence, (4.9) holds. In particular, since $g(\frac{x_j}{x_k}) = g(1) = 0$ when $j = k$, (4.10) holds. Moreover, we have

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

and

$$\left(1-\frac{1}{y_k}\right)(y_j-y_k)=y_j-\frac{y_j}{y_k}-y_k+1=-g\left(\frac{y_j}{y_k}\right)+\{g(y_j)-g(y_k)\}.$$

Thus, (4.11) and (4.12) hold. □

Using Lemma 4.1, we give the proof of (2) of Theorem 1.1.

Proof of (2) **of Theorem 1.1.** Substituting (4.9)-(4.12) into (4.8), we have

$$\begin{aligned}
U'=&-\sum_{k=1}^{n}v_k(\mu_k+\tilde{\alpha}_{kk})S_k^*\left\{g(x_k)+g\left(\frac{1}{x_k}\right)\right\}+\sum_{k=1}^{n}v_k\sum_{j=1}^{n}(1-\delta_{kj})\alpha_{kj}S_j^*\left\{g(x_j)-g\left(\frac{x_j}{x_k}\right)+g\left(\frac{1}{x_k}\right)\right\}\\
&-\sum_{k=1}^{n}v_k\sum_{j=1}^{n}\left[\beta_{kj}S_k^*I_j^*\left\{g\left(\frac{1}{x_k}\right)+g\left(\frac{x_ky_j}{y_k}\right)\right\}+(1-\delta_{kj})\alpha_{kj}I_j^*g\left(\frac{y_j}{y_k}\right)\right]\\
&+\sum_{k=1}^{n}v_k\sum_{j=1}^{n}(\beta_{kj}S_k^*+(1-\delta_{kj})\alpha_{kj})I_j^*\{g(y_j)-g(y_k)\}. \qquad (4.13)
\end{aligned}$$

The last term of the right-hand side of (4.13) is rewritten as

$$\begin{aligned}
&\sum_{k=1}^{n}v_k\sum_{j=1}^{n}(\beta_{kj}S_k^*+(1-\delta_{kj})\alpha_{kj})I_j^*\{g(y_j)-g(y_k)\}\\
=&\sum_{k=1}^{n}v_k\sum_{j=1}^{n}(\beta_{kj}S_k^*+(1-\delta_{kj})\alpha_{kj})I_j^*g(y_j)-\sum_{k=1}^{n}v_k\left\{\sum_{j=1}^{n}(\beta_{kj}S_k^*+(1-\delta_{kj})\alpha_{kj})I_j^*\right\}g(y_k)\\
=&\sum_{j=1}^{n}v_j\sum_{k=1}^{n}\left(\beta_{jk}S_j^*+(1-\delta_{jk})\alpha_{jk}\right)I_k^*g(y_k)-\sum_{k=1}^{n}v_k(\mu_k+\gamma_k+\tilde{\alpha}_{kk})I_k^*g(y_k)\\
=&\sum_{k=1}^{n}\left\{\sum_{j=1}^{n}v_j\left(\beta_{jk}S_j^*+(1-\delta_{jk})\alpha_{jk}\right)-v_k(\mu_k+\gamma_k+\tilde{\alpha}_{kk})\right\}I_k^*g(y_k). \qquad (4.14)
\end{aligned}$$

Substituting (4.14) into (4.13), we have

$$\begin{aligned}
U'=&-\sum_{k=1}^{n}v_k(\mu_k+\tilde{\alpha}_{kk})S_k^*\left\{g(x_k)+g\left(\frac{1}{x_k}\right)\right\}+\sum_{k=1}^{n}v_k\sum_{j=1}^{n}(1-\delta_{kj})\alpha_{kj}S_j^*\left\{g(x_j)-g\left(\frac{x_j}{x_k}\right)+g\left(\frac{1}{x_k}\right)\right\}\\
&-\sum_{k=1}^{n}v_k\sum_{j=1}^{n}\left[\beta_{kj}S_k^*I_j^*\left\{g\left(\frac{1}{x_k}\right)+g\left(\frac{x_ky_j}{y_k}\right)\right\}+(1-\delta_{kj})\alpha_{kj}I_j^*g\left(\frac{y_j}{y_k}\right)\right]\\
&+\sum_{k=1}^{n}\left\{\sum_{j=1}^{n}v_j\left(\beta_{jk}S_j^*+(1-\delta_{jk})\alpha_{jk}\right)-v_k(\mu_k+\gamma_k+\tilde{\alpha}_{kk})\right\}I_k^*g(y_k)\\
=&-\sum_{k=1}^{n}\left\{v_k(\beta_{kk}I_k^*+(\mu_k+\tilde{\alpha}_{kk}))-\sum_{j=1}^{n}v_j(1-\delta_{jk})\alpha_{jk}\right\}S_k^*g(x_k)\\
&-\sum_{k=1}^{n}v_k\left\{\left(\sum_{j=1}^{n}\beta_{kj}I_j^*+(\mu_k+\tilde{\alpha}_{kk})\right)S_k^*-\sum_{j=1}^{n}(1-\delta_{kj})\alpha_{kj}S_j^*\right\}g\left(\frac{1}{x_k}\right)\\
&-\sum_{k=1}^{n}v_k\sum_{j=1}^{n}(1-\delta_{kj})\alpha_{kj}S_j^*g\left(\frac{x_j}{x_k}\right)-\sum_{k=1}^{n}v_k\sum_{j=1}^{n}\left\{\beta_{kj}S_k^*I_j^*g\left(\frac{x_ky_j}{y_k}\right)+(1-\delta_{kj})\alpha_{kj}I_j^*g\left(\frac{y_j}{y_k}\right)\right\}\\
&+\sum_{k=1}^{n}\left\{\sum_{j=1}^{n}v_j\left(\beta_{jk}S_j^*+(1-\delta_{jk})\alpha_{jk}\right)-v_k(\mu_k+\gamma_k+\tilde{\alpha}_{kk})\right\}I_k^*g(y_k).
\end{aligned}$$

Hence, from (4.1) and (4.3), we have

$$U' = -\sum_{k=1}^{n}\left\{v_k\left(\beta_{kk}I_k^* + (\mu_k+\tilde{\alpha}_{kk})\right) - \sum_{j=1}^{n} v_j\left(1-\delta_{jk}\right)\alpha_{jk}\right\}S_k^* g\left(x_k\right)$$
$$-\sum_{k=1}^{n} v_k b_k g\left(\frac{1}{x_k}\right) - \sum_{k=1}^{n} v_k \sum_{j=1}^{n}\left(1-\delta_{kj}\right)\alpha_{kj}S_j^* g\left(\frac{x_j}{x_k}\right) - \sum_{k=1}^{n} v_k \sum_{j=1}^{n}\left\{\beta_{kj}S_k^* I_j^* g\left(\frac{x_k y_j}{y_k}\right) + \left(1-\delta_{kj}\right)\alpha_{kj}I_j^* g\left(\frac{y_j}{y_k}\right)\right\}. \tag{4.15}$$

We note that assumption (1.10) implies

$$\sum_{j=1}^{n} v_j\beta_{jk}S_j^* \geq v_k(\gamma_k - \beta_{kk}I_k^*), \quad \forall k = 1, 2, \cdots, n,$$

which is equivalent to

$$v_k(\beta_{kk}I_k^* + (\mu_k+\tilde{\alpha}_{kk})) - \sum_{j=1}^{n} v_j(1-\delta_{jk})\alpha_{jk} \geq 0, \quad \forall k = 1, 2, \cdots, n. \tag{4.16}$$

From (4.15) and (4.16), it follows that $U' \leq 0$. Furthermore, we see that the equality $U' = 0$ holds if and only if

$$x_k = 1 \ \text{ and } \ y_k = y_j \quad \forall k, j = 1, 2, \cdots, n. \tag{4.17}$$

(4.17) implies that there exists a positive constant $c > 0$ such that

$$\frac{I_k}{I_k^*} = c \quad \forall k = 1, 2, \cdots, n.$$

Thus, substituting

$$S_k = S_k^* \ \text{ and } \ I_k = cI_k^* \quad \forall k = 1, 2, \cdots, n$$

into the first equation of system (1.3), we have

$$0 = b_k - (\mu_k+\tilde{\alpha}_{kk}) + c\sum_{j=1}^{n}\beta_{kj}S_k^*I_j^* - (1-\delta_{kj})\alpha_{kj}S_j^*, \quad \forall k = 1, 2, \cdots, n. \tag{4.18}$$

Since the right-hand side of (4.18) is strictly monotone decreasing with respect to c, equality (4.18) holds if and only if $c = 1$. This implies that the only compact invariant subset where $U' = 0$ is the singleton $\{\mathbf{E}^*\}$.

From a similar argument as in Section 3, we can conclude that $\mathbf{E}^*$ is globally asymptotically stable in Γ^0. □

5 Relation between $\tilde{\mathbf{R}}_0$ and the basic reproduction number $\mathbf{R_0}$

In this section, we calculate the basic reproduction number R_0 for system (1.3) and investigate the relation between it and $\tilde{R}_0$. First we derive the next generation matrix (see van den Driessche and Watmough [24]) for system (1.3), whose spectral radius is the desired R_0. Let $\mathbf{V}$ be an n-square matrix defined by

$$\mathbf{V} = \begin{bmatrix} \mu_1+\gamma_1+\tilde{\alpha}_{11} & -\alpha_{12} & \cdots & -\alpha_{1n} \\ -\alpha_{21} & \mu_2+\gamma_2+\tilde{\alpha}_{22} & \cdots & -\alpha_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ -\alpha_{n1} & -\alpha_{n2} & \cdots & \mu_n+\gamma_n+\tilde{\alpha}_{nn} \end{bmatrix}. \tag{5.1}$$

Note that the diagonal entries of matrix $\mathbf{V}$ imply the rate of transfer of individuals out of each group, and the nondiagonal entries imply the rate of transfer of individuals into each group by means different from the new infection. Let $\mathbf{F}$ be a matrix-valued operator on $\mathbb{R}_+^n$ defined by

$$\mathbf{F}(\mathbf{S}) = \begin{bmatrix} S_1\beta_{11} & S_1\beta_{12} & \cdots & S_1\beta_{1n} \\ S_2\beta_{21} & S_2\beta_{22} & \cdots & S_2\beta_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ S_n\beta_{n1} & S_n\beta_{n2} & \cdots & S_n\beta_{nn} \end{bmatrix}.$$

Note that the (k, j) entry of matrix $\mathbf{F}(\mathbf{S})$ implies the rate at which an infective individual in group j produces a new infective individual in group k when the density of susceptible individuals is given by $\mathbf{S}$. Since $\mathbf{V}$ is an M-matrix, the

positive inverse $\mathbf{V}^{-1}$ exists and hence, $\mathbf{M}(\mathbf{S}) := \mathbf{F}(\mathbf{S})\,\mathbf{V}^{-1}$ exists. Following the definition in [24], we obtain the next generation matrix as $\mathbf{M}\left(\mathbf{S}^0\right)$ and hence, the basic reproduction number R_0 is obtained by the spectral radius

$$R_0 = \rho\left(\mathbf{M}\left(\mathbf{S}^0\right)\right). \tag{5.2}$$

Note that

$$\mathbf{F}(\mathbf{S}^*) - \mathbf{V} = \tilde{\mathbf{F}}(\mathbf{S}^*) - \tilde{\mathbf{V}} = \mathbf{0}, \tag{5.3}$$

where $\mathbf{S}^* = (S_1^*, S_2^*, \cdots, S_n^*)^T$.

From (5.3) we have

$$\mathbf{F}(\mathbf{S}^*)\,\mathbf{V}^{-1} = \tilde{\mathbf{V}}^{-1}\tilde{\mathbf{F}}(\mathbf{S}^*) = \mathbf{E},$$

where $\mathbf{E}$ denotes the identity matrix. Hence

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

and it follows from (1.9), (5.2), Proposition 2.1 and the theory of nonnegative irreducible matrices (see, for instance, Varga [25, Chapter 2]) that

$$R_0 < 1 \quad \text{if and only if} \quad \tilde{R}_0 < 1,$$

that is,

$$\operatorname{sign}(R_0 - 1) = \operatorname{sign}(\tilde{R}_0 - 1).$$

Hence, we conclude that R_0 plays the role of a threshold for system (1.3) similar to $\tilde{R}_0$ and Theorem 1.1 can be rewritten as follows.

Theorem 5.1. *Let Γ and R_0 be defined by (1.4) and (5.2), respectively.*

(1) *If $R_0 \le 1$, then the disease-free equilibrium $\mathbf{E}^0 = (S_1^0, 0, S_2^0, 0, \cdots, S_n^0, 0)$ of system (1.3) is globally asymptotically stable in region Γ.*

(2) *If $R_0 > 1$, then system (1.3) is uniformly persistent in the interior Γ^0 and has at least one endemic equilibrium $\mathbf{E}^* = (S_1^*, I_1^*, S_2^*, I_2^*, \cdots, S_n^*, I_n^*)$ in Γ^0. Moreover, if (1.10) holds, then the endemic equilibrium $\mathbf{E}^*$ is globally asymptotically stable in Γ^0.*

6 Corollary

In this section, we provide a sufficient condition under which condition (1.10) holds. The condition is expressed only by given coefficients in (1.3) and therefore, it plays an important role in checking whether the condition (1.10) holds.

If $\tilde{R}_0 > 1$ (or, equivalently, $R_0 > 1$), then it follows from the first statement of (2) of Theorem 1.1 (or Theorem 5.1) that system (1.3) has an endemic equilibrium $\mathbf{E}^*$ in Γ^0. Adding the first and second equations of system (1.3), we have

$$\frac{\mathrm{d}}{\mathrm{d}t}(S_k + I_k) = b_k - \left\{\mu_k + \sum_{j=1}^{n}(1-\delta_{jk})\,\alpha_{jk}\right\}(S_k + I_k) + \sum_{j=1}^{n}(1-\delta_{kj})\,\alpha_{kj}\,(S_j + I_j) - \gamma_k I_k, \quad k = 1, 2, \cdots, n.$$

Thus, each component of the endemic equilibrium $\mathbf{E}^* = (S_1^*, I_1^*, \cdots, S_n^*, I_n^*)$ must satisfy the following relation:

$$\begin{aligned} 0 &= b_k - \left\{\mu_k + \sum_{j=1}^{n}(1-\delta_{jk})\,\alpha_{jk}\right\}(S_k^* + I_k^*) + \sum_{j=1}^{n}(1-\delta_{kj})\,\alpha_{kj}\left(S_j^* + I_j^*\right) - \gamma_k I_k^* \\ &\ge b_k - \left\{\mu_k + \gamma_k + \sum_{j=1}^{n}(1-\delta_{jk})\,\alpha_{jk}\right\}(S_k^* + I_k^*) + \sum_{j=1}^{n}(1-\delta_{kj})\,\alpha_{kj}\left(S_j^* + I_j^*\right) \end{aligned}$$

for $k = 1, 2, \cdots, n$. Thus, we have $\mathbf{0} \ge \mathbf{b} - \mathbf{V}\,(S_1^* + I_1^*, \cdots, S_n^* + I_n^*)^T$. Hence, it holds that

$$(S_1^* + I_1^*, \cdots, S_n^* + I_n^*)^T \ge \mathbf{V}^{-1}\mathbf{b},$$

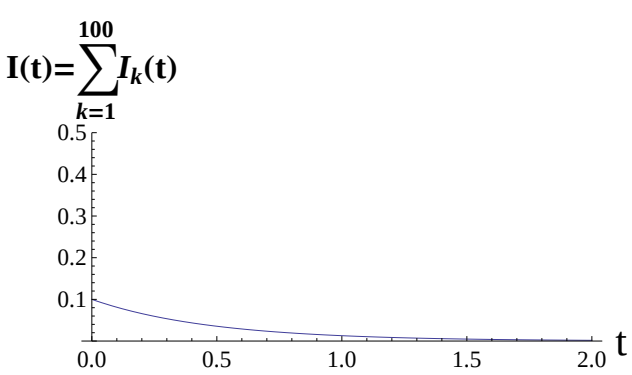
where $\mathbf{b}$ and $\mathbf{V}$ are given by (1.5) and (5.1), respectively. Thus, we obtain the following sufficient condition:

$$\min_{1\le k\le n}\left\{\beta_{kk}\left(\mathbf{V}^{-1}\mathbf{b}\right)_k - \gamma_k\right\} \ge 0, \quad (\cdot)_k \text{ denotes the } k\text{-th entry of a vector}, \tag{6.1}$$

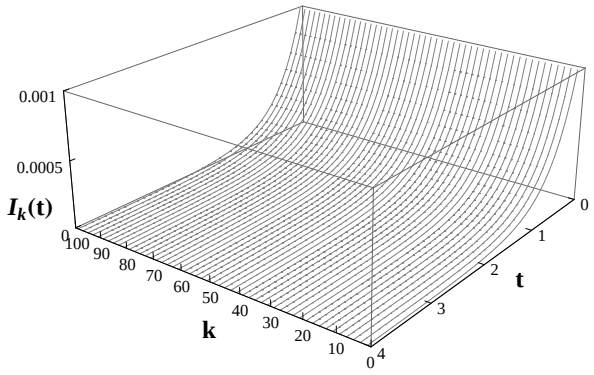
under which the condition (1.10) holds.

Corollary 6.1. *Let Γ, $\tilde{R}_0$ and R_0 be defined by (1.4), (1.9) and (5.2), respectively. If $\tilde{R}_0 > 1$ (or, equivalently, $R_0 > 1$) and (6.1) holds, then system (1.3) has a globally stable endemic equilibrium $\mathbf{E}^*$ in the interior Γ^0 of Γ.*

Since the left-hand side of (6.1) is explicitly expressed by the given coefficients in (1.3), we can easily check whether it holds by performing numerical calculations.



(a) Fraction of the total density of infective individuals $I = \sum_{k=1}^{100} I_k$ versus time t



(b) Fractions of the total densities of infective individuals I_k $(k = 1, 2, \cdots, 100)$ versus time t

Figure 1: Behavior of the solution of infective individuals of system (1.1) for (7.1) and $p = 1$. In this case, $\tilde{R}_0 = 0.44046\cdots \leq 1$.

7 Numerical examples

In this section, we perform numerical simulations to verify the validity of Theorem 1.1. First, based on the interpretation in Bartlett [3] and Faddy [7], we regard system (1.1) as a model for a geographically spreading disease. Next, we regard system (1.1) as a multi-group model with perturbation with respect to α_{kj} and simulate the spread of a sexually transmitted disease.

7.1 A geographically spreading disease

To model the geographical spread of a disease, we fix $n = 100$ as the number of regions. We further fix the following coefficients.

$$\begin{cases} b_k = \left\{3 + 2\sin\left(\dfrac{2\pi}{100}k\right)\right\} \times 10^{-2},\ \mu_k = 3 + 2\sin\left(\dfrac{2\pi}{100}k\right), \\ \gamma_k = \left\{1 + 0.5\sin\left(\dfrac{2\pi}{100}k\right)\right\} \times 10^{-2}, \\ \alpha_{kj} = \left\{1 + 0.5\sin\left(\dfrac{2\pi}{100}(k-j)\right)\right\} \times 10^{2},\ k \neq j, \quad \alpha_{kj} = 0,\ k = j, \\ \beta_{kj} = p \times \left(\alpha_{kj} \times 10^{-1} + 1\right), \quad k, j = 1, 2, \cdots, 100. \end{cases} \tag{7.1}$$

We observe the behavior of solution of (1.1) with varying p. Note that the asymmetric case $\alpha_{kj} \neq \alpha_{jk}$ for $j \neq k$ is considered in (7.1). Under (7.1), we have

$$N(t) := \sum_{k=1}^{100} \{S_k(t) + I_k(t) + R_k(t)\} \ \to\ N^* = 1 \ \text{ as } \ t \to +\infty$$

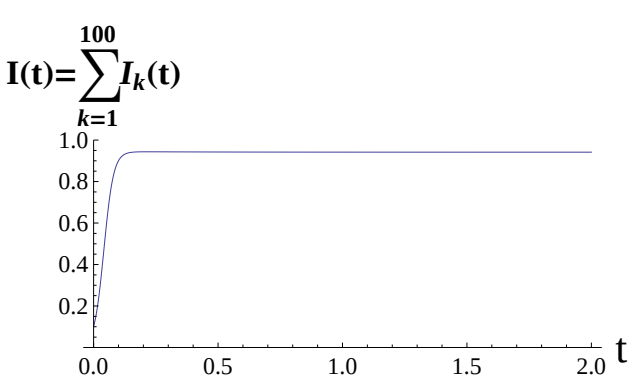
for any $N(0) > 0$. Thus, setting $(S_k(0), I_k(0), R_k(0)) = (0.009, 0.001, 0)$ for all $k \in \{1, 2, \cdots, 100\}$, we let the total population $N(t)$ attains its equilibrium $N^* = 1$ at $t = 0$.

First we set $p = 0.1$. In this case, we have $\tilde{R}_0 = 0.999797\cdots \leq 1$ and hence, from (1) of Theorem 1.1, the disease-free equilibrium $\mathbf{E}^0$ of system (1.1) is globally asymptotically stable in region Γ. In fact, we obtain Figure 1 which exhibits this result.

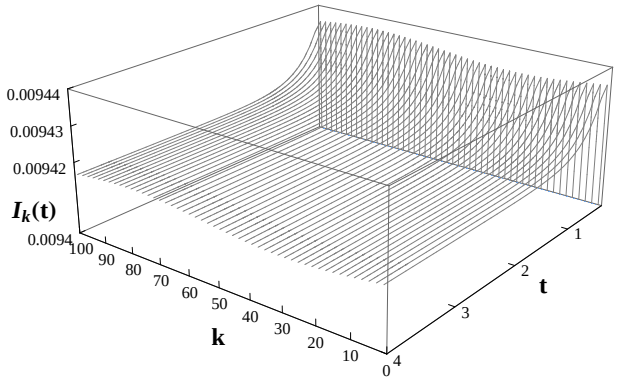
Next we set $p = 5$. In this case, we have $\tilde{R}_0 = 1.0052\cdots > 1$ and

$$\min_{1 \leq k \leq 100} \left\{\beta_{kk}\left(\mathbf{V}^{-1}\mathbf{b}\right)_k - \gamma_k\right\} = 0.0348339\cdots > 0.$$

Hence, from Corollary 6.1, system (1.1) has a unique endemic equilibrium $\mathbf{E}^*$ in Γ^0 which is globally asymptotically stable. In fact, we obtain Figure 2 which exhibits this result.



(a) Fraction of the total density of infective individuals $I = \sum_{k=1}^{100} I_k$ versus time t



(b) Fractions of the total densities of infective individuals I_k $(k = 1, 2, \cdots, 100)$ versus time t

Figure 2: Behavior of the solution of infective individuals of system (1.1) for (7.1) and $p = 5$. In this case, $\tilde{R}_0 = 1.0052\cdots > 1$.

7.2 A sexually transmitted disease

Next, to model a sexually transmitted disease, we let $n = 2$ and $k = 1$ and $k = 2$ be subscripts representing female and male, respectively. Fix

$$\begin{cases} b_1 = b_2 = 1.5, \quad \mu_1 = \mu_2 = 3, \\ \gamma_1 = \gamma_2 = 0.01, \\ \alpha_{11} = \alpha_{22} = 0, \quad \alpha_{12} = \alpha_{21} = 0.1, \\ \beta_{11} = p, \quad \beta_{22} = 0.5 \times p, \quad \beta_{12} = \beta_{21} = 1 \end{cases} \tag{7.2}$$

and observe the behavior of solution of system (1.1) with varying p. Under (7.2), we have

$$N(t) := \sum_{k=1}^{2} \{S_k(t) + I_k(t) + R_k(t)\} \ \rightarrow \ N^* = 1 \ \text{ as } \ t \rightarrow +\infty$$

for any $N(0) > 0$. Thus, let us set the initial condition as $(S_k(0), I_k(0), R_k(0)) = (0.49, 0.01, 0)$ for $k = 1, 2$.

First we set $p = 5$. In this case, we have $\tilde{R}_0 = 0.881475\cdots \leq 1$ and hence, from (1) of Theorem 1.1, the disease-free equilibrium $\mathbf{E}^0$ of system (1.1) is globally asymptotically stable in region Γ. In fact, we obtain Figure 3 (a) which exhibits this result.

Next we set $p = 6$. In this case, we have $\tilde{R}_0 = 1.03231\cdots > 1$ and

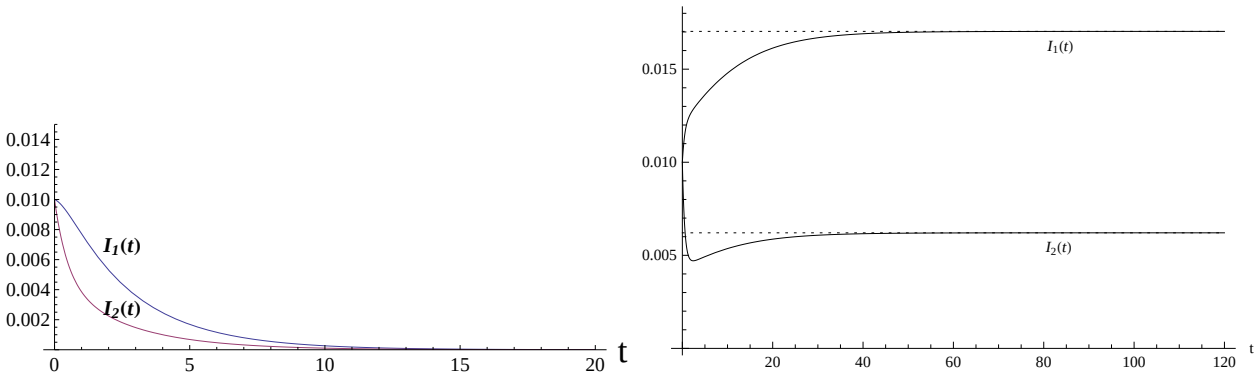
$$\min_{1 \leq k \leq 100} \left\{ \beta_{kk} \left(\mathbf{V}^{-1} \mathbf{b} \right)_k - \gamma_k \right\} = 1.48502\cdots > 0.$$

Hence, from Corollary 6.1, system (1.1) has a unique endemic equilibrium $\mathbf{E}^*$ in Γ^0 which is globally asymptotically stable. In fact, we obtain Figure 3 (b) which exhibits this result.

8 Discussion

In this paper, we have formulated an SIR epidemic model (1.1) with hybrid of multi-group and patch structures. We have defined a threshold value $\tilde{R}_0$ by the spectral radius of a nonnegative irreducible matrix $\tilde{\mathbf{M}}(\mathbf{S}^0)$ (see (1.9)), and we have shown that if $\tilde{R}_0 \leq 1$, then the disease-free equilibrium $\mathbf{E}^0$ of the system is globally asymptotically stable, while if $\tilde{R}_0 > 1$, then the system is uniformly persistent and there exists an endemic equilibrium $\mathbf{E}^*$. Moreover, under the condition (1.10), we have shown that if $\tilde{R}_0 > 1$, then the endemic equilibrium $\mathbf{E}^*$ is globally asymptotically stable. Moreover, we obtained a sufficient condition for (1.10), which is expressed only by given coefficients and therefore, we can easily testify whether it holds or not by numerical calculation (see Section 7). We have also shown that $\tilde{R}_0 \leq 1$ if and only if $R_0 \leq 1$. This implies that we can use both $\tilde{R}_0$ and R_0 to predict the eventual size of epidemic.

Compared to Li and Shuai [17], we see that from (6.1), the condition (1.10) holds if the transmission coefficients β_{kk}, $k = 1, 2, \ldots, n$ in the same groups are sufficiently large and/or the per capita recovery rates γ_k, $k = 1, 2, \ldots, n$ are sufficiently small. This situation seems to be realistic for a disease with high infectiousness and long (or, lifelong) infection period. Thus, the geographical spread of HIV/AIDS infection might be thought to be the one of important examples for applications of our stability results.



(a) Fractions of infective individuals I_1 and I_2 versus time t for $p = 5$. In this case, $\tilde{R}_0 = 0.881475\cdots < 1$.

(b) Fractions of infective individuals I_1 and I_2 versus time t for $p = 6$. In this case, $\tilde{R}_0 = 1.03231\cdots > 1$ ($I_1^* = 0.0170\cdots$, $I_2^* = 0.0062\cdots$)

Figure 3: Behavior of the solution of infective individuals of system (1.1) for (7.2)

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