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# GLOBAL BEHAVIOR OF A MULTI-GROUP SIR EPIDEMIC MODEL WITH AGE STRUCTURE AND AN APPLICATION TO THE CHLAMYDIA EPIDEMIC IN JAPAN\*

TOSHIKAZU KUNIYA†

**Abstract.** In this paper, we are concerned with the global behavior of a multi-group SIR epidemic model with age structure. A similar model was studied in [T. Kuniya, J. Wang, and H. Inaba, *Discrete Contin. Dyn. Syst. Ser. B*, 21 (2016), pp. 3515–3550] under some restrictive assumptions. In this paper, we weaken some of these assumptions for the purpose of application, and show that the global behavior of our model is completely determined by the basic reproduction number  $\mathcal{R}_0$ : if  $\mathcal{R}_0 < 1$ , then the disease-free equilibrium is globally attractive, whereas if  $\mathcal{R}_0 > 1$ , then the endemic equilibrium is globally attractive. The proofs are done by constructing suitable Lyapunov functions for total trajectories in compact attractors. In the application, we consider the chlamydia epidemic in Japan in 2015, and compare the estimation results of  $\mathcal{R}_0$  in four special cases of our model: a homogeneous model, an age-independent two-sex model, an age-dependent one-sex model, and an age-dependent two-sex model. In conclusion, we see that  $\mathcal{R}_0$  for the chlamydia epidemic in Japan in 2015 is in the range 1.0148–1.0535, and the introduction of the age structure has more influence on the value of  $\mathcal{R}_0$  than that of the two-group structure.

**Key words.** SIR epidemic model, global attractivity, basic reproduction number, Lyapunov function, compact attractor, chlamydia

**AMS subject classifications.** 35Q92, 37N25, 92D30

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**1. Introduction.** Mathematical epidemic models for the dynamics of infectious diseases in populations have been studied for decades since the pioneering work by Kermack and McKendrick [17]. One of the most important concepts in this field is the basic reproduction number  $\mathcal{R}_0$  that represents the expected number of secondary cases produced by a typical infected individual in a fully susceptible population (see [4]). From this definition, we can expect that an outbreak never occurs if  $\mathcal{R}_0 < 1$ , whereas it occurs if  $\mathcal{R}_0 > 1$ . Mathematically,  $\mathcal{R}_0$  is defined by the spectral radius of a linear operator called the next generation operator, and the global behavior of solutions in some basic epidemic models is completely determined by  $\mathcal{R}_0$ : if  $\mathcal{R}_0 \leq 1$ , then the solution converges to the trivial disease-free equilibrium, whereas if  $\mathcal{R}_0 > 1$ , then it converges to the positive endemic equilibrium (see, for instance, [14, section 5.5.2]). However, in some models with more complex structure, this threshold property of  $\mathcal{R}_0$  is not obvious, and some irregular cases, such as an unstable endemic equilibrium for  $\mathcal{R}_0 > 1$  (see, for instance, [9]) and a stable endemic equilibrium for  $\mathcal{R}_0 < 1$  (see, for instance, [10]), are known.

The SIR epidemic models are one of the most basic epidemic models in mathematical epidemiology, in which the total population is divided into three classes called susceptible, infective, and recovered (see [17]). For an SIR epidemic model with age structure, some conjectures on the threshold property of  $\mathcal{R}_0$  were proposed in [8], and

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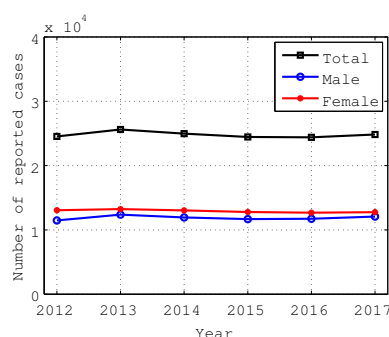


FIG. 1. Number of reported cases of chlamydia in Japan from 2012 to 2017 [16].

the answers to them were given in [13]: if  $\mathcal{R}_0 < 1$ , then the disease-free equilibrium is globally stable, whereas if  $\mathcal{R}_0 > 1$ , then the endemic equilibrium is locally asymptotically stable under some additional assumptions. However, the global stability of the endemic equilibrium for  $\mathcal{R}_0 > 1$  was not proved in [13]. In fact, endemic equilibria of age-structured SIR epidemic models are not always globally stable for  $\mathcal{R}_0 > 1$ ; they can be unstable, and periodic solutions can occur through the Hopf bifurcation under some assumptions (see [1, 3, 6, 26]). On the other hand, under some assumptions in which only the susceptible population has the age structure, endemic equilibria can be globally stable for  $\mathcal{R}_0 > 1$  (see [19, 20, 23]).

Epidemiologically, the estimation of  $\mathcal{R}_0$  is important as it indicates the intensity of each epidemic of diseases. For an endemic disease in which the number of infective individuals in the real data is almost unchanging, we can regard the infective population as being in the endemic equilibrium, and we can estimate  $\mathcal{R}_0$  for the disease by applying a mathematical model. For instance, in Figure 1, the number of reported cases of chlamydia in Japan was almost unchanged from 2012 to 2017, and thus we can regard the infective population as being in the endemic equilibrium.

In order to apply a mathematical model for the estimation of  $\mathcal{R}_0$  by using such data, we should clarify the stability of the endemic equilibrium of the model as the solution behavior of the model cannot be consistent with the real data if the endemic equilibrium is unstable for  $\mathcal{R}_0 > 1$ .

In this paper, we investigate the global behavior of a multi-group SIR epidemic model with age structure, and apply the model to estimate the basic reproduction number  $\mathcal{R}_0$  for the recent chlamydia epidemic in Japan as shown in Figure 1. A similar model was studied in [20], and the global stability of the endemic equilibrium for  $\mathcal{R}_0 > 1$  was proved under some additional assumptions (see (B1)–(B6) in the subsequent sections). However, these assumptions seem to be restrictive from the viewpoint of application. In this paper, we weaken them to new assumptions (see (A1)–(A6) in the subsequent sections) for the purpose of application and prove that  $\mathcal{R}_0$  completely determines the global behavior of the model: if  $\mathcal{R}_0 < 1$ , then the solution converges to the disease-free equilibrium, whereas if  $\mathcal{R}_0 > 1$ , then it converges to the unique endemic equilibrium. Thus, we can rule out the possibility of an unstable endemic equilibrium for  $\mathcal{R}_0 > 1$ , and we can apply our model to the estimation of  $\mathcal{R}_0$ . In the application, we consider four special cases of our model: a homogeneous model, an age-independent two-sex model, an age-dependent one-sex model, and an age-dependent two-sex model. By comparing these four cases, we obtain the estimation range of  $\mathcal{R}_0$  for the recent chlamydia epidemic in Japan and discuss the influence of

the model structure on the value of  $\mathcal{R}_0$ .

The remainder of this paper is organized as follows. In section 2, we formulate the multi-group SIR epidemic model with age structure. Under assumptions (A1)–(A5), it is reformulated into a model with age-dependent susceptibility. In section 3, we define the basic reproduction number  $\mathcal{R}_0$  for our model by the spectral radius of the next generation matrix. In section 4, we prove the existence and uniqueness of the endemic equilibrium for  $\mathcal{R}_0 > 1$ . In section 5, we prove the existence of a compact attractor that consists of total trajectories. In section 6, we prove the global attractivity of the disease-free equilibrium for  $\mathcal{R}_0 < 1$  by showing that the compact attractor is the singleton of the disease-free equilibrium. In section 7, we show the existence of a persistence attractor for  $\mathcal{R}_0 > 1$  in which a Lyapunov function is well defined, and we prove the global attractivity of the endemic equilibrium for  $\mathcal{R}_0 > 1$  by showing that the persistence attractor is the singleton of the endemic equilibrium. In section 8, we apply our model to the estimation of  $\mathcal{R}_0$  for the recent chlamydia epidemic in Japan. Finally, section 9 is devoted to a discussion.

**2. Model formulation.** In [20], the following multi-group SIR epidemic model with age structure was studied:

$$(2.1) \quad \begin{cases} \left( \frac{\partial}{\partial t} + \frac{\partial}{\partial a} \right) S_j(t, a) = -[\lambda_j(t, a) + \mu_j(a)] S_j(t, a), \\ \left( \frac{\partial}{\partial t} + \frac{\partial}{\partial a} \right) I_j(t, a) = \lambda_j(t, a) S_j(t, a) - [\mu_j(a) + \gamma_j(a)] I_j(t, a), \\ \left( \frac{\partial}{\partial t} + \frac{\partial}{\partial a} \right) R_j(t, a) = \gamma_j(a) I_j(t, a) - \mu_j(a) R_j(t, a), \\ S_j(t, 0) = b_j, \quad I_j(t, 0) = 0, \quad R_j(t, 0) = 0, \\ S_j(0, a) = S_{j,0}(a) \geq 0, \quad I_j(0, a) = I_{j,0}(a) \geq 0, \quad R_j(0, a) = R_{j,0}(a) \geq 0, \\ t > 0, \quad a \geq 0, \quad j = 1, 2, \dots, n, \end{cases}$$

where  $S_j(t, a)$ ,  $I_j(t, a)$ , and  $R_j(t, a)$  denote the susceptible, infective, and recovered populations of age  $a$  at time  $t$  in group  $j$ , respectively.  $\mu_j(a)$  and  $\gamma_j(a)$  denote the age-specific mortality and recovery rates in group  $j$ , respectively.  $\lambda_j(t, a) := \sum_{k=1}^n \int_0^{+\infty} \beta_{jk}(a, \sigma) I_k(t, \sigma) d\sigma$  denotes the force of infection to susceptible individuals of age  $a$  at time  $t$  in group  $j$ , where  $\beta_{jk}(a, \sigma)$  denotes the disease transmission coefficient between susceptible individuals of age  $a$  in group  $j$  and infective individuals of age  $\sigma$  in group  $k$ . In [20], it was assumed that all newborns are susceptible and the demographic steady state has been reached:

$$S_j(t, a) + I_j(t, a) + R_j(t, a) = P_j^*(a) := b_j e^{-\int_0^a \mu_j(\sigma) d\sigma}, \quad t \geq 0, \quad a \geq 0, \quad j = 1, 2, \dots, n.$$

Thus, the rate at which newborns are born in group  $j$  is given by  $b_j > 0$ .  $S_{j,0}(\cdot)$ ,  $I_{j,0}(\cdot)$ , and  $R_{j,0}(\cdot)$  are the initial age-distributions of each population. As in [20], we make the following assumptions:

- (A1) For each  $j \in \{1, 2, \dots, n\}$ ,  $\mu_j(\cdot) \in L_+^\infty(0, +\infty)$  and there exists a positive constant  $\underline{\mu} > 0$  such that  $\mu_j(a) > \underline{\mu}$  for all  $a \geq 0$ .
- (A2) For each  $j \in \{1, 2, \dots, n\}$ ,  $\gamma_j(\cdot) \in L_+^\infty(0, +\infty)$ .
- (A3) For each  $j, k \in \{1, 2, \dots, n\}$ ,  $\beta_{jk}(\cdot, \cdot) \in L_+^\infty((0, +\infty) \times (0, +\infty))$ .

In [20], the following additional assumptions were also made:

- (B1) For each  $j, k \in \{1, 2, \dots, n\}$ ,  $\beta_{jk}(\cdot, \sigma)$  is independent of age  $\sigma$  and state  $k$  of infective individuals, that is,  $\beta_{jk}(\cdot, \sigma) = \beta_j(\cdot) \in L_+^\infty(0, +\infty)$  for all  $\sigma \geq 0$ .

- (B2) For each  $j \in \{1, 2, \dots, n\}$ ,  $\mu_j(a)$  and  $\gamma_j(a)$  are positive constants, that is,  $\mu_j(a) = \mu_j > 0$  and  $\gamma_j(a) = \gamma_j > 0$  for all  $a \geq 0$ .

In this paper, we weaken (B1) and (B2) as follows:

- (A4) For each  $j, k \in \{1, 2, \dots, n\}$ ,  $\beta_{jk}(\cdot, \sigma)$  is independent of age  $\sigma$  of infective individuals, that is,  $\beta_{jk}(\cdot, \sigma) = \beta_{jk}(\cdot) \in L_+^\infty(0, +\infty)$  for all  $\sigma \geq 0$ .  
 (A5) For each  $j \in \{1, 2, \dots, n\}$ , there exists a positive constant  $r_j > 0$  such that  $\mu_j(a) + \gamma_j(a) = r_j$  for all  $a \geq 0$ .

These assumptions are similar to [19, Assumptions 1 and 3]. Note that (A5) can approximately hold if the recovery rates are age-independent and sufficiently larger than the mortality rates. Under (A4) and (A5), the equations of  $S_j$  and  $I_j$ ,  $j = 1, 2, \dots, n$ , in (2.1) can be rewritten as follows:

$$(2.2) \quad \begin{cases} \left( \frac{\partial}{\partial t} + \frac{\partial}{\partial a} \right) S_j(t, a) = - \left[ \sum_{k=1}^n \beta_{jk}(a) \int_0^{+\infty} I_k(t, \sigma) d\sigma + \mu_j(a) \right] S_j(t, a), \\ \left( \frac{\partial}{\partial t} + \frac{\partial}{\partial a} \right) I_j(t, a) = \sum_{k=1}^n \beta_{jk}(a) \int_0^{+\infty} I_k(t, \sigma) d\sigma S_j(t, a) - r_j I_j(t, a), \\ t > 0, \quad a > 0, \quad j = 1, 2, \dots, n. \end{cases}$$

Note that we can omit the equations of  $R_j$ ,  $j = 1, 2, \dots, n$ , since they do not appear in (2.2). Let  $J_j(\cdot) := \int_0^{+\infty} I_j(\cdot, a) da$  and  $J_{j,0} := \int_0^{+\infty} I_{j,0}(a) da$ ,  $j = 1, 2, \dots, n$ . Then, by integrating the second equation in (2.2), we obtain the following multi-group model with age-dependent susceptibility:

$$(2.3) \quad \begin{cases} \left( \frac{\partial}{\partial t} + \frac{\partial}{\partial a} \right) S_j(t, a) = - \left[ \sum_{k=1}^n \beta_{jk}(a) J_k(t) + \mu_j(a) \right] S_j(t, a), \\ \frac{d}{dt} J_j(t) = \sum_{k=1}^n \int_0^{+\infty} \beta_{jk}(a) S_j(t, a) da J_k(t) - r_j J_j(t), \\ S_j(t, 0) = b_j, \quad S_j(0, a) = S_{j,0}(a) \geq 0, \quad J_j(0) = J_{j,0} \geq 0, \\ t > 0, \quad a \geq 0, \quad j = 1, 2, \dots, n. \end{cases}$$

In sections 3–7, we focus on the reformulated system (2.3).

**3. The basic reproduction number.** In [20], in addition to (B1) and (B2), the following assumptions were also made:

- (B3) For each  $j \in \{1, 2, \dots, n\}$ , the domain of  $\beta_j(\cdot)$  is extended to  $\mathbb{R}$  by assuming that  $\beta_j(a) = 0$  for all  $a \in (-\infty, 0)$ .  
 (B4) For each  $j \in \{1, 2, \dots, n\}$ , it holds that  $\lim_{h \rightarrow 0} \int_0^{+\infty} |\beta_j(a+h) - \beta_j(a)| da = 0$ .  
 (B5) For each  $j \in \{1, 2, \dots, n\}$ , there exists a positive constant  $\epsilon_0 > 0$  such that  $\beta_j(a) \geq \epsilon_0$  for all  $a \geq 0$ .

In this paper, we make the following assumption, which is weaker than (B3)–(B5):

- (A6) Matrix  $(\int_0^{+\infty} \beta_{jk}(a) P_j^*(a) da)_{1 \leq j, k \leq n}$  is irreducible.

In fact, if (B5) holds, then matrix  $(\int_0^{+\infty} \beta_{jk}(a) P_j^*(a) da)_{1 \leq j, k \leq n}$  is irreducible since  $P_j^*(\cdot) \in L_+^1(0, +\infty)$  for all  $j \in \{1, 2, \dots, n\}$  under (A1). Thus, (A6) holds.

Let  $X := L^1(0, +\infty; \mathbb{R}^n)$ , and let  $X_+$  be the positive cone of  $X$ . Let us define the

following state space for system (2.3):

$$\Omega := \left\{ (\varphi, \psi)^T : \varphi = (\varphi_1, \varphi_2, \dots, \varphi_n)^T \in X_+, \psi = (\psi_1, \psi_2, \dots, \psi_n)^T \in \mathbb{R}_+^n, \right. \\ \left. 0 \leq \varphi_j(a) \leq P_j^*(a), \quad 0 \leq \psi_j \leq \int_0^{+\infty} P_j^*(\sigma) d\sigma \text{ for all } a \geq 0 \text{ and } j = 1, 2, \dots, n \right\}.$$

It is obvious that system (2.3) has the unique disease-free equilibrium  $\mathbf{E}_0 : (\mathbf{S}, \mathbf{J})^T = (\mathbf{P}^*, \mathbf{0})^T \in \Omega$ , where  $\mathbf{S} := (S_1, S_2, \dots, S_n)^T$ ,  $\mathbf{J} := (J_1, J_2, \dots, J_n)^T$ , and  $\mathbf{P}^* := (P_1^*, P_2^*, \dots, P_n^*)^T$ . The second equation in (2.3) can be linearized around the disease-free equilibrium  $\mathbf{E}_0$  as follows:  $J_j'(t) = \sum_{k=1}^n \int_0^{+\infty} \beta_{jk}(a) P_j^*(a) da J_k(t) - r_j J_j(t)$ ,  $t > 0$ ,  $j = 1, 2, \dots, n$ . According to the theory of basic reproduction number (see, for instance, [4, 27] and [14, section 9.3.1]), the basic reproduction number  $\mathcal{R}_0$  for system (2.3) is defined by the spectral radius of the next generation matrix  $\mathbf{K} := \mathbf{FV}^{-1}$ :  $\mathcal{R}_0 := r(\mathbf{K})$ , where

$$\mathbf{F} := \begin{pmatrix} \int_0^{+\infty} \beta_{11}(a) P_1^*(a) da & \cdots & \int_0^{+\infty} \beta_{1n}(a) P_1^*(a) da \\ \vdots & \ddots & \vdots \\ \int_0^{+\infty} \beta_{n1}(a) P_n^*(a) da & \cdots & \int_0^{+\infty} \beta_{nn}(a) P_n^*(a) da \end{pmatrix}, \quad \mathbf{V} := \text{diag}(r_j)_{1 \leq j \leq n}, \\ \mathbf{K} = \mathbf{FV}^{-1} = \begin{pmatrix} \frac{\int_0^{+\infty} \beta_{11}(a) P_1^*(a) da}{r_1} & \cdots & \frac{\int_0^{+\infty} \beta_{1n}(a) P_1^*(a) da}{r_n} \\ \vdots & \ddots & \vdots \\ \frac{\int_0^{+\infty} \beta_{n1}(a) P_n^*(a) da}{r_1} & \cdots & \frac{\int_0^{+\infty} \beta_{nn}(a) P_n^*(a) da}{r_n} \end{pmatrix}.$$

Since matrix  $\mathbf{K}$  is nonnegative and irreducible under assumption (A6), it follows from the Perron–Frobenius theorem (see, for instance, [2]) that  $\mathcal{R}_0 = r(\mathbf{K})$  is a simple eigenvalue of  $\mathbf{K}$  corresponding to a strictly positive eigenvector.

**4. Existence and uniqueness of the endemic equilibrium.** The endemic equilibrium of system (2.3) can be written as  $\mathbf{E}^* := (\mathbf{S}, \mathbf{J})^T = (\mathbf{S}^*, \mathbf{J}^*)^T \in \Omega$ , where  $\mathbf{S}^* := (S_1^*, S_2^*, \dots, S_n^*)^T$  and  $\mathbf{J}^* := (J_1^*, J_2^*, \dots, J_n^*)^T$ , and  $S_j^*$  and  $J_j^*$ ,  $j = 1, 2, \dots, n$ , satisfy the following equations:

$$(4.1) \quad \begin{cases} \frac{d}{da} S_j^*(a) = - \left[ \sum_{k=1}^n \beta_{jk}(a) J_k^* + \mu_j(a) \right] S_j^*(a), & a > 0, \quad S_j^*(0) = b_j, \\ 0 = \sum_{k=1}^n \int_0^{+\infty} \beta_{jk}(a) S_j^*(a) da J_k^* - r_j J_j^*, & j = 1, 2, \dots, n. \end{cases}$$

Solving the first two equations in (4.1), we have, for  $a \geq 0$  and  $j = 1, 2, \dots, n$ ,

$$(4.2) \quad S_j^*(a) = b_j e^{-\int_0^a \{\sum_{k=1}^n \beta_{jk}(\sigma) J_k^* + \mu_j(\sigma)\} d\sigma} = P_j^*(a) e^{-\sum_{k=1}^n \int_0^a \beta_{jk}(\sigma) d\sigma J_k^*}.$$

Substituting (4.2) into the last equation in (4.1) and rearranging it, we have

$$(4.3) \quad J_j^* = \sum_{k=1}^n \frac{\int_0^{+\infty} \beta_{jk}(a) P_j^*(a) e^{-\sum_{\ell=1}^n \int_0^a \beta_{j\ell}(\sigma) d\sigma J_\ell^*} da}{r_j} J_k^*, \quad j = 1, 2, \dots, n.$$

Let us define the following matrix-valued function on  $\mathbb{R}^n$  to  $\mathbb{R}^{n \times n}$ :

$$\mathbf{M}(\psi) := \begin{pmatrix} \frac{\int_0^{+\infty} \beta_{11}(a) P_1^*(a) e^{-\sum_{\ell=1}^n \int_0^a \beta_{1\ell}(\sigma) d\sigma \psi_\ell} da}{r_1} & \cdots & \frac{\int_0^{+\infty} \beta_{1n}(a) P_1^*(a) e^{-\sum_{\ell=1}^n \int_0^a \beta_{1\ell}(\sigma) d\sigma \psi_\ell} da}{r_1} \\ \vdots & \ddots & \vdots \\ \frac{\int_0^{+\infty} \beta_{n1}(a) P_n^*(a) e^{-\sum_{\ell=1}^n \int_0^a \beta_{n\ell}(\sigma) d\sigma \psi_\ell} da}{r_n} & \cdots & \frac{\int_0^{+\infty} \beta_{nn}(a) P_n^*(a) e^{-\sum_{\ell=1}^n \int_0^a \beta_{n\ell}(\sigma) d\sigma \psi_\ell} da}{r_n} \end{pmatrix},$$

$$\psi := (\psi_1, \psi_2, \dots, \psi_n)^T \in \mathbb{R}^n.$$

Then, (4.3) can be rewritten as the following vector-matrix form:

$$(4.4) \quad \mathbf{J}^* = \mathbf{M}(\mathbf{J}^*) \mathbf{J}^*.$$

On the existence of the endemic equilibrium  $\mathbf{E}^*$  of system (2.3), we prove the following proposition.

**PROPOSITION 4.1.** *Suppose that (A1)–(A6) and  $\mathcal{R}_0 > 1$  hold. Then system (2.3) has at least one endemic equilibrium  $\mathbf{E}^*$  in  $\Omega$ .*

*Proof.* From (4.4), we now show that the nonlinear operator  $\Psi(\psi) := \mathbf{M}(\psi)\psi$ ,  $\psi \in \mathbb{R}_+^n$ , has at least one positive fixed point  $\psi^* \in \mathbb{R}_+^n \setminus \{\mathbf{0}\}$ . For each  $j \in \{1, 2, \dots, n\}$  and  $\psi \in \mathbb{R}_+^n$ , by integration by parts, we have

$$\begin{aligned} (\Psi(\psi))_j &= \sum_{k=1}^n \frac{\int_0^{+\infty} \beta_{jk}(a) P_j^*(a) e^{-\sum_{\ell=1}^n \int_0^a \beta_{j\ell}(\sigma) d\sigma \psi_\ell} da}{r_j} \psi_k \\ &= \frac{\int_0^{+\infty} P_j^*(a) \sum_{k=1}^n \beta_{jk}(a) \psi_k e^{-\sum_{\ell=1}^n \int_0^a \beta_{j\ell}(\sigma) d\sigma \psi_\ell} da}{r_j} \\ (4.5) \quad &= \frac{\left[ -P_j^*(a) e^{-\sum_{\ell=1}^n \int_0^a \beta_{j\ell}(\sigma) d\sigma \psi_\ell} \right]_0^{+\infty} - \int_0^{+\infty} \mu_j(a) P_j^*(a) e^{-\sum_{\ell=1}^n \int_0^a \beta_{j\ell}(\sigma) d\sigma \psi_\ell} da}{r_j} \\ &= \frac{b_j}{r_j} - \frac{1}{r_j} \int_0^{+\infty} \mu_j(a) P_j^*(a) e^{-\sum_{\ell=1}^n \int_0^a \beta_{j\ell}(\sigma) d\sigma \psi_\ell} da, \end{aligned}$$

where  $(\cdot)_j$  denotes the  $j$ th entry of a vector. Hence, operator  $\Psi(\psi)$  is monotone increasing with respect to  $\psi \in \mathbb{R}_+^n$  and uniformly bounded above by  $\max_{1 \leq j \leq n} (b_j/r_j)$ :  $\|\Psi(\psi)\| := \max_{1 \leq j \leq n} |(\Psi(\psi))_j| \leq \max_{1 \leq j \leq n} (b_j/r_j)$ .

It is obvious that  $\Psi(\mathbf{0}) = \mathbf{0}$  and  $\mathbf{M}(\mathbf{0})$  is the strong Fréchet derivative of  $\Psi(\cdot)$  at the origin. Since  $\mathbf{M}(\mathbf{0}) = \mathbf{V}^{-1}\mathbf{F}$ , we have  $r(\mathbf{M}(\mathbf{0})) = r(\mathbf{V}^{-1}\mathbf{F}) = r(\mathbf{F}\mathbf{V}^{-1}) = r(\mathbf{K}) = \mathcal{R}_0 > 1$ . Thus, it follows from the Perron–Frobenius theorem (see [2]) that  $r(\mathbf{M}(\mathbf{0})) > 1$  is a simple eigenvalue of  $\mathbf{M}(\mathbf{0})$  corresponding to a strictly positive eigenvector, and there exists no nonnegative eigenvector of  $\mathbf{M}(\mathbf{0})$  corresponding to eigenvalue 1. Hence, we can apply the technique of Krasnoselskii as in [18, Theorem 4.11] (see also [13, Proposition 4.6]) to conclude that operator  $\Psi(\cdot)$  has at least one positive fixed point  $\psi^* \in \mathbb{R}_+^n \setminus \{\mathbf{0}\}$ .

For  $\mathbf{J}^* = \psi^*$ , we have from (4.5) that for each  $j \in \{1, 2, \dots, n\}$ ,

$$\begin{aligned} J_j^* &= \sum_{k=1}^n \frac{\int_0^{+\infty} \beta_{jk}(a) P_j^*(a) e^{-\int_0^a \sum_{\ell=1}^n \beta_{j\ell}(\sigma) d\sigma J_\ell^*} da}{r_j} J_k^* \leq \frac{b_j}{r_j} = b_j \int_0^{+\infty} e^{-r_j a} da \\ &\leq b_j \int_0^{+\infty} e^{-\int_0^a \mu_j(\sigma) d\sigma} da = \int_0^{+\infty} P_j^*(a) da. \end{aligned}$$

Furthermore, it is obvious from (4.2) that  $S_j^*(a) \leq P_j^*(a)$  for all  $a \geq 0$  and  $j \in \{1, 2, \dots, n\}$ . This implies that  $\mathbf{E}^* := (\mathbf{S}^*, \mathbf{J}^*)^T$  belongs to  $\Omega$ . This completes the proof.  $\square$

Note that  $J_j^* > 0$  for all  $j \in \{1, 2, \dots, n\}$  in the endemic equilibrium  $\mathbf{E}^*$  by virtue of (A6) and (4.3). On the uniqueness of the endemic equilibrium  $\mathbf{E}^*$  of system (2.3), we prove the following proposition.

**PROPOSITION 4.2.** *Suppose that (A1)–(A6) and  $\mathcal{R}_0 > 1$  hold. Then system (2.3) has at most one endemic equilibrium  $\mathbf{E}^*$  in  $\Omega$ .*

*Proof.* It suffices to show that operator  $\Psi(\cdot)$  has at most one positive fixed point. Let  $\psi^* := (\psi_1^*, \psi_2^*, \dots, \psi_n^*)^T \in \mathbb{R}_+^n$  and  $\tilde{\psi} := (\psi_1, \tilde{\psi}_2, \dots, \tilde{\psi}_n)^T \in \mathbb{R}_+^n$  be two positive fixed points of operator  $\Psi(\cdot)$ . Let  $\eta^* := \sup\{\eta \geq 0 : \psi_j^* \geq \eta \tilde{\psi}_j \text{ for all } j \in \{1, 2, \dots, n\}\}$ , and suppose that  $\eta^* < 1$ . Note that  $\eta^* > 0$  since  $\psi_j^* > 0$  and  $\tilde{\psi}_j > 0$  for all  $j \in \{1, 2, \dots, n\}$ . From the monotonicity of operator  $\Psi(\cdot)$ , we have, for  $j = 1, 2, \dots, n$ ,

$$\begin{aligned} \psi_j^* &= (\Psi(\psi^*))_j \geq (\Psi(\eta^* \tilde{\psi}))_j = \sum_{k=1}^n \frac{\int_0^{+\infty} \beta_{jk}(a) P_j^*(a) e^{-\sum_{\ell=1}^n \int_0^a \beta_{j\ell}(\sigma) d\sigma} \eta^* \tilde{\psi}_\ell da}{r_j} \eta^* \tilde{\psi}_k \\ &> \eta^* \sum_{k=1}^n \frac{\int_0^{+\infty} \beta_{jk}(a) P_j^*(a) e^{-\sum_{\ell=1}^n \int_0^a \beta_{j\ell}(\sigma) d\sigma} \tilde{\psi}_\ell da}{r_j} \tilde{\psi}_k = \eta^* (\Psi(\tilde{\psi}))_j = \eta^* \tilde{\psi}_j, \end{aligned}$$

which contradicts the definition of  $\eta^*$ . Hence,  $\eta^* \geq 1$  and we have  $\psi_j^* \geq \eta^* \tilde{\psi}_j \geq \tilde{\psi}_j$  for all  $j \in \{1, 2, \dots, n\}$ . By exchanging the roles of  $\psi^*$  and  $\tilde{\psi}$ , we can show in a similar way that  $\tilde{\psi}_j \geq \psi_j^*$  for all  $j \in \{1, 2, \dots, n\}$ . Hence, we obtain  $\psi^* = \tilde{\psi}$ . This completes the proof.  $\square$

**5. Existence of a compact attractor.** Let  $Y := X \times \mathbb{R}^n$  and  $\|(\varphi, \psi)^T\|_Y := \sum_{j=1}^n \int_0^{+\infty} |\varphi_j(a)| da + \sum_{j=1}^n |\psi_j|$ ,  $(\varphi, \psi)^T \in Y$ . Let  $Y_+ := X_+ \times \mathbb{R}_+^n$  be the positive cone of  $Y$ . As in [20, section 8], we can define a  $C_0$ -semigroup  $\{U(t)\}_{t \geq 0} : Y_+ \rightarrow Y_+$  for the solution of system (2.3) by  $U(t)(\mathbf{S}_0(\cdot), \mathbf{J}_0) := (\mathbf{S}(t, \cdot), \mathbf{J}(t))^T$ ,  $t \geq 0$ , where  $\mathbf{S}_0 := (S_{1,0}, S_{2,0}, \dots, S_{n,0})^T \in X_+$  and  $\mathbf{J}_0 := (J_{1,0}, J_{2,0}, \dots, J_{n,0})^T \in \mathbb{R}_+^n$ . We first prove the following lemma on the boundedness of semigroup  $U(\cdot)$ .

**LEMMA 5.1.** *Suppose that (A1)–(A6) hold. Then  $U(\cdot)$  is point dissipative and eventually bounded on bounded subsets of  $Y_+$ .*

*Proof.* Let  $\bar{b} := \max_{1 \leq j \leq n} \{b_j\} \in (0, +\infty)$ . It is easy to see from (2.3) that

$$\begin{aligned} \frac{d}{dt} \left( \int_0^{+\infty} S_j(t, a) da + J_j(t) \right) &= b_j - \int_0^{+\infty} \mu_j(a) S_j(t, a) da - r_j J_j(t) \\ &\leq \bar{b} - \underline{\mu} \left( \int_0^{+\infty} S_j(t, a) da + J_j(t) \right), \quad t > 0, \quad j = 1, 2, \dots, n. \end{aligned}$$

By adding these inequalities for all  $j \in \{1, 2, \dots, n\}$ , we have

$$\frac{d}{dt} \|U(t)(\mathbf{S}_0(\cdot), \mathbf{J}_0)\|_Y \leq n\bar{b} - \underline{\mu} \|U(t)(\mathbf{S}_0(\cdot), \mathbf{J}_0)\|_Y, \quad t > 0.$$



Then, as in [22, Proposition 1], we have

$$(5.1) \quad \begin{aligned} \|U(t)(\mathbf{S}_0(\cdot), \mathbf{J}_0)\|_Y &\leq \max \left\{ \frac{n\bar{b}}{\underline{\mu}}, \left\| (\mathbf{S}_0(\cdot), \mathbf{J}_0)^T \right\|_Y \right\} \text{ for all } t \geq 0, \\ \limsup_{t \rightarrow +\infty} \|U(t)(\mathbf{S}_0(\cdot), \mathbf{J}_0)\|_Y &\leq \frac{n\bar{b}}{\underline{\mu}}. \end{aligned}$$

The second inequality in (5.1) implies that  $U(\cdot)$  is point dissipative. For any bounded subset of  $Y_+$  such that  $\|(\mathbf{S}_0(\cdot), \mathbf{J}_0)^T\|_Y < M$  for some  $M > 0$ , the first inequality in (5.1) implies that  $U(\cdot)$  is eventually bounded. This completes the proof.  $\square$

We next prove the following lemma on the asymptotic smoothness of  $U(\cdot)$ .

**LEMMA 5.2.** *Suppose that (A1)–(A6) hold. Then  $U(\cdot)$  is asymptotically smooth.*

*Proof.* By [25, Theorem 2.46] (see also [22, Theorem 5.1]), it suffices to show that there exist two maps  $V, W : \mathbb{R}_+ \times Y_+ \rightarrow Y_+$  such that  $U(t)(\mathbf{S}_0(\cdot), \mathbf{J}_0) = V(t)(\mathbf{S}_0(\cdot), \mathbf{J}_0) + W(t)(\mathbf{S}_0(\cdot), \mathbf{J}_0)$  for all  $t \geq 0$ , and such that the following two conditions hold for any bounded closed set  $C \subset Y_+$  that is forward invariant under  $U(\cdot)$ :

(C1)  $\lim_{t \rightarrow +\infty} \text{diam } V(t)(C) = 0$ .

(C2) There exists a  $t_C \geq 0$  such that  $W(t)(C)$  has compact closure for all  $t \geq t_C$ .

Here, the diameter of set  $A \subset Y_+$  is defined by  $\text{diam } A := \sup \{\|x - y\|_Y : x, y \in A\}$ . For  $V(\cdot)$  and  $W(\cdot)$  defined as in [20, section 8], we can prove (C1) and (C2) in a way similar to that in [20, the proofs of Lemmas 8.1 and 8.2]. Therefore, we omit the details. This completes the proof.  $\square$

From Lemmas 5.1 and 5.2, we can apply [25, Theorem 2.33] to obtain the following proposition on the existence of a compact attractor.

**PROPOSITION 5.3.** *Suppose that (A1)–(A6) hold. Then there exists a compact attractor  $\mathcal{A} \subset Y_+$  of bounded sets.*

*Proof.* The assertion directly follows from Lemmas 5.1 and 5.2 and [25, Theorem 2.33]. This completes the proof.  $\square$

Let  $\mathcal{U} : \mathbb{R} \rightarrow Y_+$  be a total trajectory such that  $U(t)(\mathcal{U}(s)) = \mathcal{U}(t+s)$  holds for all  $t \geq 0$  and  $s \in \mathbb{R}$ . From a well-known fact, we see that compact attractor  $\mathcal{A}$  consists of total trajectories; that is, for any  $(\mathbf{S}_0(\cdot), \mathbf{J}_0)^T \in \mathcal{A}$ , there exists a total trajectory  $\mathcal{U}(\cdot)$  such that  $\mathcal{U}(0) = (\mathbf{S}_0(\cdot), \mathbf{J}_0)^T$  and  $\mathcal{U}(t) \in \mathcal{A}$  for all  $t \in \mathbb{R}$ . For a total trajectory, we can write  $\mathcal{U}(t) := (\mathbf{S}(t, \cdot), \mathbf{J}(t))^T$ ,  $t \in \mathbb{R}$ , where

$$(5.2) \quad \begin{aligned} S_j(t, a) &= S_j(t - a, 0) e^{-\int_0^a [\sum_{k=1}^n \beta_{jk}(\sigma) J_k(t-a+\sigma) + \mu_j(\sigma)] d\sigma} \\ &= b_j e^{-\int_0^a [\sum_{k=1}^n \beta_{jk}(\sigma) J_k(t-a+\sigma) + \mu_j(\sigma)] d\sigma}, \quad t \in \mathbb{R}, \quad a \geq 0, \quad j = 1, 2, \dots, n. \end{aligned}$$

In sections 6 and 7, we investigate the global behavior of system (2.3) by focusing on total trajectory  $\mathcal{U}(\cdot)$ .

**6. Global attractivity of the disease-free equilibrium for  $\mathcal{R}_0 < 1$ .** We now prove the global attractivity of the disease-free equilibrium  $\mathbf{E}_0 := (\mathbf{S}, \mathbf{J})^T = (\mathbf{P}^*, \mathbf{0})^T \in \Omega$  for  $\mathcal{R}_0 < 1$  by constructing a Lyapunov function, which is similar to the one in [11, section 4]. Since matrix  $\mathbf{M}(\mathbf{0}) = \mathbf{V}^{-1}\mathbf{F}$  is nonnegative and irreducible, it follows from the Perron–Frobenius theorem (see [2]) that it has a strictly positive left eigenvector  $\mathbf{w} := (w_1, w_2, \dots, w_n)$ ,  $w_j > 0$ ,  $j = 1, 2, \dots, n$ , corresponding to eigenvalue  $r(\mathbf{M}(\mathbf{0})) = r(\mathbf{V}^{-1}\mathbf{F}) = r(\mathbf{F}\mathbf{V}^{-1}) = \mathcal{R}_0$ . That is,  $\mathbf{w}\mathbf{M}(\mathbf{0}) = \mathcal{R}_0\mathbf{w}$ . Let

us define the following Lyapunov function for total trajectory  $\mathcal{U}(\cdot)$  in  $\mathcal{A}$ :  $L_1(t) := \sum_{j=1}^n (w_j/r_j) J_j(t)$ ,  $t \in \mathbb{R}$ . Note that  $L_1(t)$  is bounded on  $\mathbb{R}$  since total trajectory  $\mathcal{U}(t) = (\mathbf{S}(t, \cdot), \mathbf{J}(t))^T$  belongs to compact set  $\mathcal{A}$  for all  $t \in \mathbb{R}$ . We prove the following theorem.

**THEOREM 6.1.** *Suppose that (A1)–(A6) and  $\mathcal{R}_0 < 1$  hold. Then  $\mathcal{A} = \{\mathbf{E}_0\}$ ; that is, the disease-free equilibrium  $\mathbf{E}_0$  is globally attractive in any bounded sets of  $Y_+$ .*

*Proof.* For any total trajectory  $\mathcal{U}(t) = (\mathbf{S}(t, \cdot), \mathbf{J}(t))^T$ ,  $t \in \mathbb{R}$  in  $\mathcal{A}$ , the derivative of Lyapunov function  $L_1(\cdot)$  is calculated as follows:

$$\begin{aligned}
 \frac{d}{dt} L_1(t) &= \sum_{j=1}^n \frac{w_j}{r_j} \frac{d}{dt} J_j(t) = \sum_{j=1}^n \frac{w_j}{r_j} \left[ \sum_{k=1}^n \int_0^{+\infty} \beta_{jk}(a) S_j(t, a) da J_k(t) - r_j J_j(t) \right] \\
 &= \sum_{j=1}^n w_j \left[ \sum_{k=1}^n \frac{\int_0^{+\infty} \beta_{jk}(a) b_j e^{-\int_0^a [\sum_{\ell=1}^n \beta_{j\ell}(\sigma) J_\ell(t-a+\sigma) + \mu_j(\sigma)] d\sigma} da}{r_j} J_k(t) - J_j(t) \right] \\
 &\leq \sum_{j=1}^n w_j \left[ \sum_{k=1}^n \frac{\int_0^{+\infty} \beta_{jk}(a) P_j^*(a) da}{r_j} J_k(t) - J_j(t) \right] \\
 &= \mathbf{w} [\mathbf{M}(\mathbf{0}) \mathbf{J}(t) - \mathbf{J}(t)] = (\mathcal{R}_0 - 1) \mathbf{w} \mathbf{J}(t) \leq 0.
 \end{aligned}
 \tag{6.1}$$

Thus,  $L_1(t)$  is nonincreasing on  $\mathbb{R}$ . Since  $L_1(\cdot)$  is bounded, the alpha limit set of  $\mathcal{U}(\cdot)$  is included in the largest invariant subset  $\mathcal{M}$  of set  $\{(\mathbf{S}, \mathbf{J})^T \in \mathcal{A} \subset Y_+ : L_1' = 0\}$ . We claim that  $\mathcal{M} = \{\mathbf{E}_0\}$ . In fact, it follows from (6.1) that  $\mathbf{J} = \mathbf{0}$  in  $\mathcal{M}$ . We then have from (5.2) that  $\mathbf{S} = \mathbf{P}^*$  and thus,  $\mathcal{M} = \{(\mathbf{P}^*, \mathbf{0})^T\} = \{\mathbf{E}_0\}$ . Since  $L_1(\cdot)$  attains its minimum 0 at  $\mathbf{E}_0$  and it is nonincreasing,  $\mathcal{U}(t) = \mathbf{E}_0$  holds for all  $t \in \mathbb{R}$ , which implies  $\mathcal{A} = \{\mathbf{E}_0\}$ . This completes the proof.  $\square$

**7. Global attractivity of the endemic equilibrium for  $\mathcal{R}_0 > 1$ .** In [20], to define a suitable Lyapunov function for  $\mathcal{R}_0 > 1$ , the following assumption was also made in addition to (B1)–(B5):

(B6) For each  $j \in \{1, 2, \dots, n\}$ ,  $S_{j,0}(\cdot) \in L_+^1(0, +\infty)$ , it holds that  $J_{j,0} > 0$  and  $\int_0^{+\infty} |\ln S_{j,0}(a)| e^{-\int_0^a \mu_j(\sigma) d\sigma} da < +\infty$ .

In this paper, we do not have to assume the last inequality in (B6) since we consider total trajectory  $\mathcal{U}(\cdot) \in \mathcal{A}$ . We define the persistence attractor  $\mathcal{A}_0 \subset \mathcal{A}$  by a set such that for any total trajectory  $\mathcal{U}(\cdot) \in \mathcal{A}_0$ , there exists an  $\epsilon > 0$  such that  $J_j(t) > \epsilon$  holds for all  $t \in \mathbb{R}$  and  $j \in \{1, 2, \dots, n\}$ . Let  $\varrho : Y_+ \rightarrow \mathbb{R}_+$  be a function defined by  $\varrho((\varphi, \psi)^T) := \max_{1 \leq j \leq n} \{\psi_j\}$ ,  $(\varphi, \psi)^T \in Y_+$ . Let  $\Gamma$  be a set defined by

$$\Gamma := \left\{ (\varphi, \psi)^T \in Y_+ : \psi_j > 0 \text{ for some } j \in \{1, 2, \dots, n\} \right\}.$$

We first prove the uniform weak  $\varrho$ -persistence of system (2.3) for  $\mathcal{R}_0 > 1$ .

**LEMMA 7.1.** *Suppose that (A1)–(A6) and  $\mathcal{R}_0 > 1$  hold. Then system (2.3) is uniformly weakly  $\varrho$ -persistent for nontrivial initial conditions. That is, there exists an  $\epsilon_1 > 0$  such that  $\limsup_{t \rightarrow +\infty} \varrho(\mathcal{U}(t)(\mathbf{S}_0(\cdot), \mathbf{J}_0)) > \epsilon_1$ , provided  $(\mathbf{S}_0(\cdot), \mathbf{J}_0)^T \in \Gamma$ .*

*Proof.* Since  $(\mathbf{S}_0(\cdot), \mathbf{J}_0)^T \in \Gamma$ , there exists a  $j^* \in \{1, 2, \dots, n\}$  such that  $J_{j^*,0} > 0$ . Then, we see from the second equation in (2.3) that  $J_{j^*}(t) > 0$  for all  $t > 0$ . Since  $S_j(t, a) = b_j e^{-\int_0^a [\sum_{k=1}^n \beta_{jk}(\sigma) J_k(t-a+\sigma) + \mu_j(\sigma)] d\sigma} > 0$  for all  $t > a \geq 0$  and  $j \in \{1, 2, \dots, n\}$ , it follows from the second equation in (2.3) and assumption (A6) that there exists a  $t^* > 0$  such that  $J_j(t) > 0$  for all  $t > t^*$  and  $j \in \{1, 2, \dots, n\}$ .

For  $\epsilon \geq 0$  and  $T \geq 0$ , let us define the following  $n \times n$ -matrix:

$$\mathbf{F}(\epsilon, T) := \begin{pmatrix} \int_0^T \beta_{11}(a)P_1^*(a)e^{-\epsilon \int_0^a \sum_{\ell=1}^n \beta_{1\ell}(\sigma)d\sigma} da & \cdots & \int_0^T \beta_{1n}(a)P_1^*(a)e^{-\epsilon \int_0^a \sum_{\ell=1}^n \beta_{1\ell}(\sigma)d\sigma} da \\ \vdots & \ddots & \vdots \\ \int_0^T \beta_{n1}(a)P_n^*(a)e^{-\epsilon \int_0^a \sum_{\ell=1}^n \beta_{n\ell}(\sigma)d\sigma} da & \cdots & \int_0^T \beta_{nn}(a)P_n^*(a)e^{-\epsilon \int_0^a \sum_{\ell=1}^n \beta_{n\ell}(\sigma)d\sigma} da \end{pmatrix}.$$

Since  $\lim_{T \rightarrow +\infty} \mathbf{F}(0, T) = \mathbf{F}$  and  $\mathcal{R}_0 = r(\mathbf{F}\mathbf{V}^{-1}) > 1$ , there exist sufficiently small  $\epsilon_1 > 0$  and large  $T_1 > 0$  such that  $r(\mathbf{F}(\epsilon_1, T_1)\mathbf{V}^{-1}) > 1$ . For such an  $\epsilon_1$ , suppose on the contrary that  $\limsup_{t \rightarrow +\infty} \varrho(U(t)(\mathbf{S}_0(\cdot), \mathbf{J}_0)) \leq \epsilon_1$ . Then there exists a sufficiently large  $T_0 > t^* > 0$  such that  $J_j(t) \leq \epsilon_1$  for all  $t \geq T_0$  and  $j \in \{1, 2, \dots, n\}$ . Without loss of generality, by taking  $U(T_0)(\mathbf{S}_0(\cdot), \mathbf{J}_0)$  as a new initial condition, we can assume that  $0 < J_j(t) \leq \epsilon_1$  holds for all  $t \geq 0$  and  $j \in \{1, 2, \dots, n\}$ . We then have from (2.3) that, for all  $t \geq T_1$ ,

$$\begin{aligned} \frac{d}{dt} J_j(t) &\geq \sum_{k=1}^n \int_0^t \beta_{jk}(a) b_j e^{-\int_0^a [\epsilon_1 \sum_{\ell=1}^n \beta_{j\ell}(\sigma) + \mu_j(\sigma)] d\sigma} da J_k(t) - r_j J_j(t) \\ &\geq \sum_{k=1}^n \int_0^{T_1} \beta_{jk}(a) P_j^*(a) e^{-\epsilon_1 \int_0^a \sum_{\ell=1}^n \beta_{j\ell}(\sigma) d\sigma} da J_k(t) - r_j J_j(t), \quad j = 1, 2, \dots, n. \end{aligned}$$

These inequalities can be rewritten as  $\mathbf{J}'(t) \geq [\mathbf{F}(\epsilon_1, T_1) - \mathbf{V}]\mathbf{J}(t)$ ,  $t \geq T_1$ . Note that  $r(\mathbf{F}(\epsilon_1, T_1)\mathbf{V}^{-1}) > 1$  implies that the spectral bound of matrix  $\mathbf{F}(\epsilon_1, T_1) - \mathbf{V}$  is positive (see, for instance, [14, Proposition 9.5]). Hence, we have  $J_j(t) \rightarrow +\infty$  ( $t \rightarrow +\infty$ ) for all  $j \in \{1, 2, \dots, n\}$ , which contradicts  $J_j(t) \leq \epsilon_1$  for all  $t \geq 0$ . Hence, we obtain  $\limsup_{t \rightarrow +\infty} \varrho(U(t)(\mathbf{S}_0(\cdot), \mathbf{J}_0)) > \epsilon_1$ . This completes the proof.  $\square$

Using Lemma 7.1 and an approach as in [7, proof of Theorem 1], we next prove the uniform strong  $\varrho$ -persistence of system (2.3) for  $\mathcal{R}_0 > 1$ .

**LEMMA 7.2.** *Suppose that (A1)–(A6) and  $\mathcal{R}_0 > 1$  hold. Then system (2.3) is uniformly strongly  $\varrho$ -persistent for nontrivial initial conditions; that is, there exists an  $\epsilon_2 > 0$  such that  $\liminf_{t \rightarrow +\infty} \varrho(U(t)(\mathbf{S}_0(\cdot), \mathbf{J}_0)) > \epsilon_2$ , provided  $(\mathbf{S}_0(\cdot), \mathbf{J}_0)^T \in \Gamma$ .*

*Proof.* Suppose on the contrary that the assertion does not hold. Then, there exist sequences  $\{u_k\}_{k=1}^{+\infty}$  and  $\{e_k\}_{k=1}^{+\infty}$  such that

$$(7.1) \quad \liminf_{t \rightarrow +\infty} \varrho(U(t)u_k) < e_k < \epsilon_1, \quad u_k \in \Gamma, \quad e_k > 0, \quad k = 1, 2, \dots, \quad \lim_{k \rightarrow +\infty} e_k = 0,$$

where  $\epsilon_1 > 0$  is a positive constant defined as in Lemma 7.1. By Lemma 7.1 and (7.1), we see that there exist sequences  $\{\theta_k\}_{k=1}^{+\infty}$  and  $\{\tau_k\}_{k=1}^{+\infty}$  such that, for all  $k = 1, 2, \dots$ ,

$$(7.2) \quad \varrho(U(\theta_k)u_k) = \epsilon_1, \quad \varrho(U(\tau_k)u_k) < e_k < \epsilon_1 \text{ and } \varrho(U(t)u_k) < \epsilon_1 \text{ for all } t \in (\theta_k, \tau_k].$$

Let  $\tilde{u}_k := U(\theta_k)u_k \in Y_+$  for all  $k \in \mathbb{N}$ . Since it follows from the first inequality in (5.1) that  $\sup_{t \geq 0} \|U(t)u_k\|_Y \leq \max\{nb/\mu, \|u_k\|_Y\} < +\infty$ , we have from (C1)–(C2) in the proof of Lemma 5.2 and [28, Proposition 3.13] that  $\{U(t)u_k : t \geq 0\}$  has compact closure in  $Y$ . Hence, we can assume that  $\{\tilde{u}_k\}_{k=1}^{+\infty}$  is a convergent sequence in  $Y$  (otherwise, we can choose a convergent subsequence). Let  $u^* := \lim_{k \rightarrow +\infty} \tilde{u}_k \in Y$ . Since  $\varrho(u^*) = \epsilon_1 > 0$ , it follows that  $u^* \in \Gamma$ . By Lemma 7.1, we see that there exist positive constants  $\tau > 0$  and  $m > 0$  such that  $\varrho(U(\tau)u^*) > \epsilon_1$  and  $\varrho(U(t)u^*) > m$  for all  $t \in [0, \tau]$ . By the continuity and the semigroup property of  $U(\cdot)$ , we see that there exists a sufficiently large  $k^* \in \mathbb{N}$  such that

$$(7.3) \quad \varrho(U(\theta_{k^*} + \tau)u_{k^*}) > \epsilon_1 \quad \text{and} \quad \varrho(U(\theta_{k^*} + t)u_{k^*}) > m > e_{k^*} \quad \text{for all } t \in [0, \tau].$$

For such a  $k^* \in \mathbb{N}$ , we have from (7.2) that for  $t'_{k^*} = \tau_{k^*} - \theta_{k^*}$ ,

$$(7.4) \quad \varrho(U(\theta_{k^*} + t'_{k^*})u_{k^*}) < e_{k^*} < \epsilon_1 \quad \text{and} \quad \varrho(U(\theta_{k^*} + t)u_{k^*}) < \epsilon_1 \quad \text{for all } t \in (0, t'_{k^*}].$$

If  $\tau > t'_{k^*}$ , then the second inequality in (7.3) contradicts the first inequality in (7.4).

If  $\tau \leq t'_{k^*}$ , then the first inequality in (7.3) contradicts the second inequality in (7.4).

This completes the proof.  $\square$

Using Lemma 7.2, we prove the following proposition.

**PROPOSITION 7.3.** *Suppose that (A1)–(A6) and  $\mathcal{R}_0 > 1$  hold. Then there exists an  $\epsilon_3 > 0$  such that  $\liminf_{t \rightarrow +\infty} J_j(t) \geq \epsilon_3$  for all  $j \in \{1, 2, \dots, n\}$ , provided  $(\mathbf{S}_0(\cdot), \mathbf{J}_0)^T \in \Gamma$ .*

*Proof.* Let  $\tilde{\varrho} : Y_+ \rightarrow \mathbb{R}_+$  be a function defined by  $\tilde{\varrho}((\varphi, \psi)^T) := \min_{1 \leq j \leq n} \{\psi_j\}$ ,  $(\varphi, \psi)^T \in Y_+$ . Let  $\mathcal{U}(\cdot) \in \mathcal{A}$  be a total trajectory with precompact range such that  $\mathcal{U}(t) > 0$  for all  $t \in \mathbb{R}$ . By (5.1), we have that  $\sum_{k=1}^n J_k(t) \leq n\bar{b}/\underline{\mu}$  for all  $t \in \mathbb{R}$ . We then have from (5.2) that, for all  $t \in \mathbb{R}$  and  $j \in \{1, 2, \dots, n\}$ ,

$$S_j(t, a) = b_j e^{-\int_0^a [\sum_{k=1}^n \beta_{jk}(\sigma) J_k(t-a+\sigma) + \mu_j(\sigma)] d\sigma} \geq P_j^*(a) e^{-(\bar{\beta} n \bar{b}/\underline{\mu})a},$$

where  $\bar{\beta} := \max_{1 \leq j, k \leq n} \{\text{ess. sup}_{a \geq 0} \beta_{jk}(a)\} \in (0, +\infty)$ . Then, from the second equation in (2.3), we have, for all  $t \in \mathbb{R}$  and  $j \in \{1, 2, \dots, n\}$ ,

$$\frac{d}{dt} J_j(t) \geq \sum_{k=1}^n \int_0^{+\infty} \beta_{jk}(a) P_j^*(a) e^{-(\bar{\beta} n \bar{b}/\underline{\mu})a} da J_k(t) - r_j J_j(t).$$

By (A6), matrix  $(\int_0^{+\infty} \beta_{jk}(a) P_j^*(a) e^{-(\bar{\beta} n \bar{b}/\underline{\mu})a} da)_{1 \leq j, k \leq n} - \text{diag}(r_j)_{1 \leq j \leq n}$  is quasi-positive and irreducible. Then, we see from [25, Proposition A.28] that  $J_j(0) > 0$  for all  $j \in \{1, 2, \dots, n\}$ , and thus,  $\tilde{\varrho}(\mathcal{U}(0)) > 0$ . Then, by Lemmas 5.1, 5.2, and 7.2, we can apply [25, Corollary 4.22] to see that there exists an  $\epsilon_3 > 0$  such that  $\liminf_{t \rightarrow +\infty} \tilde{\varrho}(U(t)(\mathbf{S}_0(\cdot), \mathbf{J}_0)) \geq \epsilon_3$ , provided  $(\mathbf{S}_0(\cdot), \mathbf{J}_0)^T \in \Gamma$ . This implies that  $\liminf_{t \rightarrow +\infty} J_j(t) > \epsilon_3$  for all  $j \in \{1, 2, \dots, n\}$ . This completes the proof.  $\square$

Proposition 7.3 implies that if  $\mathcal{R}_0 > 1$ , then there exists a persistence attractor  $\mathcal{A}_0 \subset \mathcal{A}$  that attracts any bounded sets of  $\Gamma \subset Y_+$ . Note that for any total trajectory  $\mathcal{U}(\cdot)$  in  $\mathcal{A}_0$ , it holds that  $J_j(t) > \epsilon_3 > 0$  for all  $t \in \mathbb{R}$  and  $j \in \{1, 2, \dots, n\}$ .

To define a suitable Lyapunov function, we use a well-known Volterra-type function  $g(x) := x - 1 - \ln x$ ,  $x > 0$  (see, for instance, [21]). Note that  $g(x) \geq 0$  for all  $x > 0$ , and  $g(x) = 0$  if and only if  $x = 1$ . We now prove the following lemma.

**LEMMA 7.4.** *Suppose that (A1)–(A6) and  $\mathcal{R}_0 > 1$  hold. Then, for any total trajectory  $\mathcal{U}(t) = (\mathbf{S}(t, \cdot), \mathbf{J}(t))^T$ ,  $t \in \mathbb{R}$  in  $\mathcal{A}_0$ , the following inequalities hold:*

$$(7.5) \quad 0 \leq \int_0^{+\infty} S_j^*(a) g\left(\frac{S_j(t, a)}{S_j^*(a)}\right) da < +\infty, \quad 0 \leq g\left(\frac{J_j(t)}{J_j^*}\right) < +\infty,$$

$$t \in \mathbb{R}, \quad j = 1, 2, \dots, n.$$

*Proof.* The nonnegativity is obvious since  $g(x) \geq 0$  for all  $x > 0$ . We have from (4.2) and (5.2) that, for all  $t \in \mathbb{R}$  and  $j \in \{1, 2, \dots, n\}$ ,

$$(7.6) \quad \int_0^{+\infty} S_j^*(a) g\left(\frac{S_j(t, a)}{S_j^*(a)}\right) da = \int_0^{+\infty} \left[ S_j(t, a) - S_j^*(a) - S_j^*(a) \ln \frac{S_j(t, a)}{S_j^*(a)} \right] da$$

$$\leq \|S_j(t, \cdot)\|_{L^1} + \|S_j^*(\cdot)\|_{L^1} + \int_0^{+\infty} S_j^*(a) \int_0^a \sum_{k=1}^n \beta_{jk}(\sigma) [J_k(t-a+\sigma) - J_k^*] d\sigma da.$$

Note that the second inequality in (5.1) implies that  $\|\mathcal{U}(t)\|_Y \leq n\bar{b}/\underline{\mu}$  for all  $t \in \mathbb{R}$ , provided  $\mathcal{U}(\cdot) \in \mathcal{A}$ . That is,  $\max\{\|S_j(t, \cdot)\|_{L^1}, \sum_{k=1}^n J_k(t)\} \leq \|\mathcal{U}(t)\|_Y \leq n\bar{b}/\underline{\mu}$  for all  $t \in \mathbb{R}$  and  $j = \{1, 2, \dots, n\}$ . Furthermore, we see from (4.2) that  $\|S_j^*(\cdot)\|_{L^1} \leq n\bar{b}/\underline{\mu}$  for all  $j \in \{1, 2, \dots, n\}$ . Hence, it follows from (7.6) that

$$\begin{aligned} \int_0^{+\infty} S_j^*(a)g\left(\frac{S_j(t, a)}{S_j^*(a)}\right) da &\leq 2\frac{n\bar{b}}{\underline{\mu}} + \bar{\beta}\frac{n\bar{b}}{\underline{\mu}} \int_0^{+\infty} aS_j^*(a) da \\ &\leq \frac{n\bar{b}}{\underline{\mu}} \left(2 + \bar{\beta}\bar{b} \int_0^{+\infty} ae^{-\underline{\mu}a} da\right) = \frac{n\bar{b}}{\underline{\mu}} \left(2 + \frac{\bar{\beta}\bar{b}}{\underline{\mu}^2}\right) < +\infty, \quad t \in \mathbb{R}, \quad j = 1, 2, \dots, n, \end{aligned}$$

where  $\bar{\beta} = \max_{1 \leq j, k \leq n} \{\text{ess. sup}_{a \geq 0} \beta_{jk}(a)\} \in (0, +\infty)$ . Hence, the first estimation in (7.5) holds.

By (5.1) and Proposition 7.3, we have

$$(7.7) \quad 0 < \frac{\epsilon_3}{J_j^*} \leq \frac{J_j(t)}{J_j^*} \leq \frac{n\bar{b}}{J_j^* \underline{\mu}} < +\infty, \quad t \in \mathbb{R}, \quad j = 1, 2, \dots, n.$$

Note that  $J_j^* > 0$  for all  $j \in \{1, 2, \dots, n\}$  by virtue of (A6) and (4.3). From (7.7), the second estimation in (7.5) holds. This completes the proof.  $\square$

By virtue of Lemma 7.4, we can define the following Lyapunov function for total trajectory  $\mathcal{U}(\cdot)$  in  $\mathcal{A}_0$  as in [20, section 8]:

$$L_2(t) := \sum_{j=1}^n \kappa_j \left\{ \int_0^{+\infty} S_j^*(a)g\left(\frac{S_j(t, a)}{S_j^*(a)}\right) da + J_j^*g\left(\frac{J_j(t)}{J_j^*}\right) \right\}, \quad t \in \mathbb{R},$$

where  $\kappa_j$ ,  $j = 1, 2, \dots, n$ , are positive constants that satisfy

$$\sum_{k=1}^n \tilde{\beta}_{jk} \kappa_j = \sum_{k=1}^n \tilde{\beta}_{kj} \kappa_k, \quad \tilde{\beta}_{jk} := \int_0^{+\infty} \beta_{jk}(a) S_j^*(a) da, \quad J_k^*, \quad j, k = 1, 2, \dots, n.$$

In fact, the existence of such  $\kappa_j$ ,  $j = 1, 2, \dots, n$ , follows from [11, Lemma 2.1]. Then, the derivative of Lyapunov function  $L_2(\cdot)$  is calculated as follows (we omit the details since they are almost the same as in [20, Proof of Proposition 8.2]):

$$(7.8) \quad \begin{aligned} \frac{d}{dt} L_2(t) &= - \sum_{j=1}^n \kappa_j \left[ \int_0^{+\infty} \mu_j(a) S_j^*(a)g\left(\frac{S_j(t, a)}{S_j^*(a)}\right) da \right. \\ &\quad \left. + \sum_{k=1}^n \int_0^{+\infty} \beta_{jk}(a) S_j^*(a) J_k^*g\left(\frac{J_j^* J_k(t) S_j(t, a)}{J_j(t) J_k^* S_j^*(a)}\right) da \right] \leq 0, \quad t \in \mathbb{R}. \end{aligned}$$

Then, by using the method from the proof of Theorem 6.1, we can establish the following theorem on the global attractivity of the endemic equilibrium for  $\mathcal{R}_0 > 1$ .

**THEOREM 7.5.** *Suppose that (A1)–(A6) and  $\mathcal{R}_0 > 1$  hold. Then  $\mathcal{A}_0 = \{\mathbf{E}^*\}$ ; that is, the endemic equilibrium  $\mathbf{E}^*$  is globally attractive in any bounded sets of  $\Gamma \subset Y_+$ .*

*Proof.* By (7.8), we see that  $L_2(t)$  is nonincreasing on  $\mathbb{R}$ . Since  $L_2(\cdot)$  is bounded, the alpha limit set of total trajectory  $\mathcal{U}(\cdot) \in \mathcal{A}_0$  is included in the largest invariant subset  $\tilde{\mathcal{M}}$  of set  $\{(\mathbf{S}, \mathbf{J})^T \in \mathcal{A}_0 \subset Y_+ : L_2' = 0\}$ . We claim that  $\tilde{\mathcal{M}} = \{\mathbf{E}^*\}$ . In fact, by (7.8),  $L_2' = 0$  implies that

$$(7.9) \quad S_j(t, \cdot) = S_j^*(\cdot), \quad J_j(t) = cJ_j^*, \quad t \in \mathbb{R},$$

where  $c > 0$  is a positive constant. Substituting them into the first equation in (2.3), we have

$$\frac{d}{da} S_j^*(a) = - \left[ c \sum_{k=1}^n \beta_{jk}(a) J_k^* + \mu_j(a) \right] S_j^*(a), \quad a > 0, \quad j = 1, 2, \dots, n,$$

and hence,  $S_j^*(a) = b_j e^{-\int_0^a \{c \sum_{k=1}^n \beta_{jk}(\sigma) J_k^* + \mu_j(\sigma)\} d\sigma}$ ,  $a \geq 0$ ,  $j = 1, 2, \dots, n$ . By the uniqueness of the endemic equilibrium  $\mathbf{E}^*$  (see Proposition 4.2), we have  $c = 1$ . Hence, (7.9) implies that  $\mathcal{M} = \{\mathbf{E}^*\}$ . Since  $L_2(\cdot)$  attains its minimum  $L_2 = 0$  at  $\mathbf{E}^*$  and it is nonincreasing,  $\mathcal{U}(t) = \mathbf{E}^*$  holds for all  $t \in \mathbb{R}$ . This implies that  $\mathcal{A}_0 = \{\mathbf{E}^*\}$ . This completes the proof.  $\square$

From (2.2), we see that if  $(\mathbf{S}, \mathbf{J})^T$  attains the endemic equilibrium  $\mathbf{E}^*$ , then the infective populations  $I_j$ ,  $j = 1, 2, \dots, n$ , should satisfy the following equations:

$$\left( \frac{\partial}{\partial t} + \frac{\partial}{\partial a} \right) I_j(t, a) = \sum_{k=1}^n \beta_{jk}(a) J_k^* S_j^*(a) - r_j I_j(t, a), \quad I_j(t, 0) = 0, \\ t > 0, \quad a > 0, \quad j = 1, 2, \dots, n.$$

Hence, we see that  $I_j(t, \cdot)$ ,  $j = 1, 2, \dots, n$ , converge to positive distributions  $I_j^*(\cdot)$ ,  $j = 1, 2, \dots, n$ , as  $t \rightarrow +\infty$ , where  $I_j^*(a) = \int_0^a e^{-r_j(a-\sigma)} \sum_{k=1}^n \beta_{jk}(\sigma) J_k^* S_j^*(\sigma) d\sigma$ ,  $a \geq 0$ ,  $j = 1, 2, \dots, n$ . Similarly, we see that if  $(\mathbf{S}, \mathbf{J})^T$  attains the disease-free equilibrium  $\mathbf{E}^0$ , then  $I_j(t, \cdot)$ ,  $j = 1, 2, \dots, n$ , converge to zero as  $t \rightarrow +\infty$ . Consequently, from Theorems 6.1 and 7.5, we obtain the following main theorem in this paper.

**THEOREM 7.6.** *Suppose that (A1)–(A6) hold. If  $\mathcal{R}_0 > 1$ , then infective populations  $I_j(t, \cdot)$ ,  $j = 1, 2, \dots, n$ , of system (2.2) converge to positive distributions  $I_j^*(\cdot)$ ,  $j = 1, 2, \dots, n$ , as  $t \rightarrow +\infty$ , provided  $I_{j,0}(a) > 0$  for some  $j \in \{1, 2, \dots, n\}$  on some nonempty interval. If  $\mathcal{R}_0 < 1$ , then infective populations  $I_j(t, \cdot)$ ,  $j = 1, 2, \dots, n$ , of system (2.2) converge to zero as  $t \rightarrow +\infty$ , provided  $I_{j,0}(a) \geq 0$  for all  $a \geq 0$ .*

**8. Application.** By Theorem 7.6, we see that the global behavior of model (2.2) is completely determined by the basic reproduction number  $\mathcal{R}_0$  under assumptions (A1)–(A6). Hence, we can apply our model to estimate  $\mathcal{R}_0$  for the recent chlamydia epidemic in Japan (see Figure 1). As stated in section 1, we can regard the infective population of the recent chlamydia epidemic in Japan as being in the endemic equilibrium. Hence, in what follows, we choose the data in 2015 (see Table 1) as the reference data since the complete demographic data in Japan in 2015 is available in [15].

In what follows, we consider four special cases of our model: a homogeneous model, an age-independent two-sex model, an age-dependent one-sex model, and an age-dependent two-sex model.

**8.1. A homogeneous model.** We first consider the case of constant parameters for  $n = 1$ , that is,  $b_1 = b > 0$ ,  $\mu_1(a) = \mu > 0$ ,  $\gamma_1(a) = \gamma > 0$ , and  $\beta_{11}(a) = \beta > 0$  for all  $a \geq 0$ . In this case, it is obvious that assumptions (A1)–(A6) hold, and model (2.2) is equivalent to the following classical SI(R) epidemic model with demography:

$$(8.1) \quad \begin{cases} \frac{dS(t)}{dt} = b - \beta S(t)I(t) - \mu S(t), \\ \frac{dI(t)}{dt} = \beta S(t)I(t) - (\mu + \gamma)I(t), \\ S(0) = S_0 \geq 0, \quad I(0) = I_0 \geq 0, \quad t > 0. \end{cases}$$

TABLE 1

*Age-distributions of reported cases of chlamydia in Japan in 2015 [16].*

| Age-group | Total | Male  | Female |
|-----------|-------|-------|--------|
| 0–4       | 3     | 2     | 1      |
| 5–9       | 1     | 0     | 1      |
| 10–14     | 28    | 3     | 25     |
| 15–19     | 2438  | 562   | 1876   |
| 20–24     | 6377  | 2135  | 4242   |
| 25–29     | 5306  | 2397  | 2909   |
| 30–34     | 3766  | 2054  | 1712   |
| 35–39     | 2562  | 1558  | 1004   |
| 40–44     | 1721  | 1184  | 537    |
| 45–49     | 1075  | 799   | 276    |
| 50–54     | 573   | 447   | 126    |
| 55–59     | 305   | 266   | 39     |
| 60–       | 295   | 263   | 32     |
| Total     | 24450 | 11670 | 12780  |

Following the classical result (see, for instance, [14, section 5.5.2]), the basic reproduction number is given by  $\mathcal{R}_0 = \beta(b/\mu)/(\mu + \gamma)$ , and if  $\mathcal{R}_0 > 1$  and  $I_0 > 0$ , then  $\lim_{t \rightarrow +\infty} I(t) = I^* > 0$ , where

$$(8.2) \quad I^* = \frac{b}{\mu + \gamma} \left(1 - \frac{1}{\mathcal{R}_0}\right).$$

Note that we can also obtain this result by applying Theorem 7.6 to this case.

As stated above, we use data from 2015. From Table 1, we can set  $I^* = 24450$ . Let the time unit be 1 year. Using data in [15], we can derive the average life span of all individuals as  $L = 74.3849$ , and hence,  $\mu = 1/L = 0.0134$ . From data in [24], we fix the total population as  $N = 127095000$ . Hence, we can determine  $b$  as  $b = N\mu = 1703073$ . Following [12], we assume that the average infectious period is  $1/\gamma = 1$  (year), and hence,  $\gamma = 1$ . Using these parameters and (8.2), we obtain the following estimation of  $\mathcal{R}_0$ :  $\mathcal{R}_0 = (1 - (\mu + \gamma)I^*/b)^{-1} \approx 1.0148$ . This value is not so different from the value  $\mathcal{R}_0 = 1.02$  obtained in a previous study [12], which was based on the prevalence measured for the population in Britain from 1999 to 2001 [5].

**8.2. An age-independent two-sex model.** We next consider the case of constant parameters for  $n = 2$ , in which groups 1 and 2 imply male and female populations, respectively. That is,  $b_j > 0$ ,  $\mu_j(a) = \mu_j > 0$ ,  $\gamma_j(a) = \gamma_j > 0$ , and  $\beta_{jk}(a) = \beta_{jk} \geq 0$  for all  $a \geq 0$  and  $j, k \in \{1, 2\}$ . For simplicity, we assume that  $\beta_{11} = \beta_{22} = 0$ ,  $\beta_{12} > 0$ , and  $\beta_{21} > 0$ . That is, there is only the heterosexual disease transmission. In this case, we see that assumptions (A1)–(A6) hold, and model (2.2) is equivalent to the following two-sex SI(R) epidemic model:

$$(8.3) \quad \begin{cases} \frac{dS_1(t)}{dt} = b_1 - [\beta_{12}I_2(t) + \mu_1]S_1(t), & \frac{dI_1(t)}{dt} = \beta_{12}S_1(t)I_2(t) - (\mu_1 + \gamma_1)I_1(t), \\ \frac{dS_2(t)}{dt} = b_2 - [\beta_{21}I_1(t) + \mu_2]S_2(t), & \frac{dI_2(t)}{dt} = \beta_{21}S_2(t)I_1(t) - (\mu_2 + \gamma_2)I_2(t), \\ S_j(0) = S_{j,0} \geq 0, \quad I_j(0) = I_{j,0} \geq 0, \quad t > 0, \quad j = 1, 2. \end{cases}$$

From the definition in section 3, we obtain the basic reproduction number as

$$(8.4) \quad \mathcal{R}_0 = \sqrt{\frac{\beta_{12}}{\mu_2 + \gamma_2} \frac{b_1}{\mu_1} \frac{\beta_{21}}{\mu_1 + \gamma_1} \frac{b_2}{\mu_2}}.$$

Following the result in [11], we see that if  $\mathcal{R}_0 > 1$  and  $I_{j,0} > 0$ ,  $j = 1, 2$ , then  $\lim_{t \rightarrow +\infty} I_j(t) = I_j^* > 0$ ,  $j = 1, 2$ , where

$$(8.5) \quad I_1^* = \frac{\lambda_1^*}{\mu_1 + \gamma_1} \frac{b_1}{\lambda_1^* + \mu_1}, \quad I_2^* = \frac{\lambda_2^*}{\mu_2 + \gamma_2} \frac{b_2}{\lambda_2^* + \mu_2},$$

and  $\lambda_1^* = \beta_{12}I_2^*$  and  $\lambda_2^* = \beta_{21}I_1^*$  denote the forces of infection to male and female susceptible individuals at the endemic equilibrium, respectively. Note that this result can also be obtained by applying Theorem 7.6 to this case.

From Table 1, we set  $I_1^* = 11670$  and  $I_2^* = 12780$ . Using data in [15], we can derive the average life spans of male and female individuals as  $L_1 = 71.3404$  and  $L_2 = 78.0806$ , respectively. We then have  $\mu_1 = 1/L_1 = 0.0140$  and  $\mu_2 = 1/L_2 = 0.0128$ . From data in [24], we fix the male and female populations as  $N_1 = 61842000$  and  $N_2 = 65253000$ , respectively. We then have  $b_1 = N_1\mu_1 = 865788$  and  $b_2 = N_2\mu_2 = 835240$ . As in section 8.1, we assume that  $\gamma_1 = \gamma_2 = 1$ . By using these parameters and (8.5), we obtain  $\lambda_1^* = I_1^*(\mu_1 + \gamma_1)\mu_1/[b_1 - I_1^*(\mu_1 + \gamma_1)] \approx 1.94 \times 10^{-4}$  and  $\lambda_2^* = I_2^*(\mu_2 + \gamma_2)\mu_2/[b_2 - I_2^*(\mu_2 + \gamma_2)] \approx 2.0148 \times 10^{-4}$ , and hence,  $\beta_{12} = \lambda_1^*/I_2^* \approx 1.5180 \times 10^{-8}$  and  $\beta_{21} = \lambda_2^*/I_1^* \approx 1.7265 \times 10^{-8}$ . Substituting these parameters into (8.4), we obtain the estimation of  $\mathcal{R}_0$  as  $\mathcal{R}_0 \approx 1.0148$ . This is similar to the one obtained in section 8.1.

**8.3. An age-dependent one-sex model.** We next consider the case of the age-dependent transmission coefficient for  $n = 1$ , that is,  $b_1 = b > 0$ ,  $\mu_1(a) = \mu > 0$ ,  $\gamma_1(a) = \gamma > 0$ , and  $\beta_{11}(a) = \beta(a) \geq 0$  for all  $a \geq 0$ ,  $\beta(\cdot) \in L_+^\infty(0, +\infty)$ , and  $\int_0^{+\infty} \beta(a)be^{-\mu a}da > 0$ . In this case, we see that assumptions (A1)–(A6) hold, and model (2.2) is equivalent to the following age-dependent one-sex SI(R) epidemic model:

$$(8.6) \quad \begin{cases} \left( \frac{\partial}{\partial t} + \frac{\partial}{\partial a} \right) S(t, a) = - \left[ \beta(a) \int_0^{+\infty} I(t, \sigma) d\sigma + \mu \right] S(t, a), \\ \left( \frac{\partial}{\partial t} + \frac{\partial}{\partial a} \right) I(t, a) = \beta(a) \int_0^{+\infty} I(t, \sigma) d\sigma S(t, a) - (\mu + \gamma) I(t, a), \\ S(t, 0) = b, \quad I(t, 0) = 0, \\ S(0, a) = S_0(a) \geq 0, \quad I(0, a) = I_0(a) \geq 0, \quad t > 0, \quad a \geq 0. \end{cases}$$

From the definition in section 3, we obtain the basic reproduction number as

$$(8.7) \quad \mathcal{R}_0 = \frac{\int_0^{+\infty} \beta(a)be^{-\mu a}da}{\mu + \gamma}.$$

By Theorem 7.6, we see that if  $\mathcal{R}_0 > 1$  and  $I_0(\cdot) > 0$  on some nonempty interval, then infective population  $I(t, \cdot)$  of system (8.6) converges to positive distribution  $I^*(\cdot)$  as  $t \rightarrow +\infty$ , where

$$(8.8) \quad \begin{aligned} I^*(a) &= \int_0^a \lambda^*(\sigma) S^*(\sigma) e^{-(\mu+\gamma)(a-\sigma)} d\sigma, \quad S^*(a) = be^{-\mu a} e^{-\int_0^a \lambda^*(\sigma) d\sigma}, \\ \lambda^*(a) &= \beta(a) \int_0^{+\infty} I^*(\sigma) d\sigma, \quad a \geq 0. \end{aligned}$$

As in section 8.1, we fix  $b = 1703073$ ,  $\mu = 0.0134$ , and  $\gamma = 1$ . To estimate  $\mathcal{R}_0$  given by (8.7), we have to determine transmission coefficient  $\beta(\cdot)$ . To this end, we fix  $I^*(\cdot)$  as a spline function that interpolates the data of age-distribution of the total infective population in Table 1 (see Figure 2).



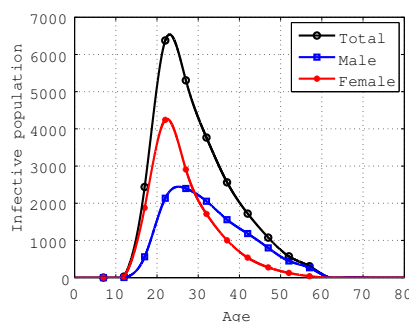


FIG. 2. Spline functions that interpolate age-distributions in Table 1.

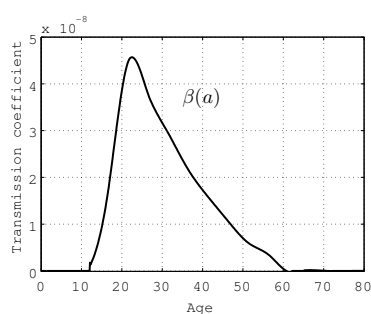


FIG. 3. Transmission coefficient  $\beta(\cdot)$  calculated by (8.9).

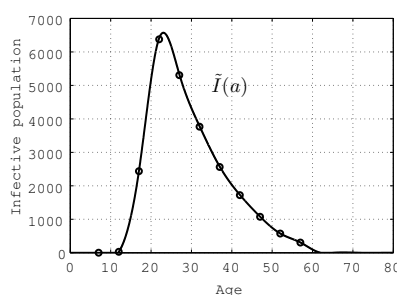


FIG. 4. Infective population  $\tilde{I}(\cdot)$  reconstructed by (8.10) (dots indicate the data of the total infective population in Table 1).

Let  $u^*(a) := S^*(a)/(be^{-\mu a})$  and  $v^*(a) := I^*(a)/(be^{-\mu a})$ ,  $a \geq 0$ . We then have, at the endemic equilibrium,

$$\frac{du^*(a)}{da} = -\lambda^*(a)u^*(a), \quad u^*(0) = 1, \quad \frac{dv^*(a)}{da} = \lambda^*(a)u^*(a) - \gamma v^*(a), \quad v^*(0) = 0, \quad a \geq 0.$$

Hence, we have  $u^*(a) = e^{-\int_0^a \lambda^*(\sigma) d\sigma}$  and  $v^*(a) = \int_0^a \lambda^*(\sigma) u^*(\sigma) d\sigma - \gamma \int_0^a v^*(\sigma) d\sigma$  for all  $a \geq 0$ , and thus,  $v^*(a) + \gamma \int_0^a v^*(\sigma) d\sigma = \int_0^a \lambda^*(\sigma) e^{-\int_0^\sigma \lambda^*(\rho) d\rho} d\sigma = 1 - e^{-\int_0^a \lambda^*(\sigma) d\sigma}$  for all  $a \geq 0$ . Solving this equation with respect to  $\lambda^*(\cdot)$ , we obtain  $\lambda^*(a) = \{[v^*(a)]' + \gamma v^*(a)\} / \{1 - [v^*(a) + \gamma \int_0^a v^*(\sigma) d\sigma]\}$  for all  $a \geq 0$ , and thus,

$$(8.9) \quad \beta(a) = \frac{1}{\int_0^{+\infty} I^*(\sigma) d\sigma} \frac{[v^*(a)]' + \gamma v^*(a)}{1 - [v^*(a) + \gamma \int_0^a v^*(\sigma) d\sigma]}, \quad a \geq 0.$$

Note that we can numerically calculate the right-hand side of (8.9) by using the parameters chosen above (see Figure 3). To confirm the validity of this  $\beta(\cdot)$ , we reconstruct the infective population  $\tilde{I}(\cdot)$  from (8.8) as follows:

$$(8.10) \quad \tilde{I}(a) = be^{-\mu a} \int_0^{+\infty} I^*(a) da \int_0^a \beta(\sigma) e^{-\int_0^{\sigma} \lambda^*(a) da \int_0^{\sigma} \beta(\rho) d\rho} e^{-\gamma(a-\sigma)} d\sigma, \quad a \geq 0.$$

In Figure 4, we see that the reconstructed infective population  $\tilde{I}(\cdot)$  is almost the same as the infective population  $I^*(\cdot)$  obtained as a spline function in Figure 2. Hence, we see that this choice of  $\beta(\cdot)$  is reasonable. Using the parameters chosen in this way, we obtain the estimation of  $\mathcal{R}_0$  from (8.7) as  $\mathcal{R}_0 \approx 1.0531$ . This value is slightly different from those obtained in sections 8.1 and 8.2.

**8.4. An age-dependent two-sex model.** We finally consider the case of age-dependent transmission coefficients for  $n = 2$ . As in section 8.2, we assume that there is only the heterosexual disease transmission, that is,  $b_j > 0$ ,  $\mu_j(a) = \mu_j > 0$ ,  $\gamma_j(a) = \gamma_j > 0$ , and  $\beta_{jj}(a) = 0$  for all  $a \geq 0$  and  $j = 1, 2$ , and  $\beta_{12}(\cdot), \beta_{21}(\cdot) \in L_+^\infty(0, +\infty)$ ,  $\int_0^{+\infty} \beta_{12}(a)b_1e^{-\mu_1a}da > 0$ , and  $\int_0^{+\infty} \beta_{21}(a)b_2e^{-\mu_2a}da > 0$ . In this case, we see that assumptions (A1)–(A6) hold, and model (2.2) is equivalent to the following age-dependent two-sex SI(R) epidemic model:

$$(8.11) \quad \begin{cases} \left(\frac{\partial}{\partial t} + \frac{\partial}{\partial a}\right) S_1(t, a) = - \left[ \beta_{12}(a) \int_0^{+\infty} I_2(t, \sigma) d\sigma + \mu_1 \right] S_1(t, a), \\ \left(\frac{\partial}{\partial t} + \frac{\partial}{\partial a}\right) I_1(t, a) = \beta_{12}(a) \int_0^{+\infty} I_2(t, \sigma) d\sigma S_1(t, a) - (\mu_1 + \gamma_1) I_1(t, a), \\ \left(\frac{\partial}{\partial t} + \frac{\partial}{\partial a}\right) S_2(t, a) = - \left[ \beta_{21}(a) \int_0^{+\infty} I_1(t, \sigma) d\sigma + \mu_2 \right] S_2(t, a), \\ \left(\frac{\partial}{\partial t} + \frac{\partial}{\partial a}\right) I_2(t, a) = \beta_{21}(a) \int_0^{+\infty} I_1(t, \sigma) d\sigma S_2(t, a) - (\mu_2 + \gamma_2) I_2(t, a), \\ S_j(t, 0) = b_j, \quad I_j(t, 0) = 0, \quad S_j(t, 0) = b_j, \quad I_j(t, 0) = 0, \\ S_j(0, a) = S_{j,0}(a), \quad I_j(0, a) = I_{j,0}(a), \quad t > 0, \quad a \geq 0, \quad j = 1, 2. \end{cases}$$

From the definition in section 3, we obtain the basic reproduction number as

$$(8.12) \quad \mathcal{R}_0 = \sqrt{\frac{\int_0^{+\infty} \beta_{12}(a)b_1e^{-\mu_1a}da}{\mu_2 + \gamma_2} \frac{\int_0^{+\infty} \beta_{21}(a)b_2e^{-\mu_2a}da}{\mu_1 + \gamma_1}}.$$

By Theorem 7.6, we see that if  $\mathcal{R}_0 > 1$  and  $I_{j,0}(\cdot) > 0$ ,  $j = 1, 2$ , on some nonempty interval, then infective populations  $I_j(t, \cdot)$ ,  $j = 1, 2$ , converge to positive distributions  $I_j^*(\cdot)$ ,  $j = 1, 2$ , as  $t \rightarrow +\infty$ , where

$$(8.13) \quad \begin{aligned} I_j^*(a) &= \int_0^a \lambda_j^*(\sigma) S_j^*(\sigma) e^{-(\mu_j + \gamma_j)(a - \sigma)} d\sigma, \quad S_j^*(a) = b_j e^{-\mu_j a} e^{-\int_0^a \lambda_j^*(\sigma) d\sigma}, \quad j = 1, 2, \\ \lambda_1^*(a) &= \beta_{12}(a) \int_0^{+\infty} I_2^*(\sigma) d\sigma, \quad \lambda_2^*(a) = \beta_{21}(a) \int_0^{+\infty} I_1^*(\sigma) d\sigma, \quad a \geq 0. \end{aligned}$$

As in section 8.2, we fix  $b_1 = 865788$ ,  $b_2 = 835240$ ,  $\mu_1 = 0.0140$ ,  $\mu_2 = 0.0128$ , and  $\gamma_1 = \gamma_2 = 1$ . To estimate  $\mathcal{R}_0$ , we have to determine  $\beta_{12}(\cdot)$  and  $\beta_{21}(\cdot)$ . As in section 8.3, we fix  $I_1^*(\cdot)$  and  $I_2^*(\cdot)$  as spline functions that interpolate the data of age-distributions of male and female infective populations in Table 1, respectively (see Figure 2). Let  $u_j^*(a) := S_j^*(a)/(b_j e^{-\mu_j a})$  and  $v_j^*(a) := I_j^*(a)/(b_j e^{-\mu_j a})$ ,  $a \geq 0$ ,  $j = 1, 2$ . We then have, for  $a \geq 0$  and  $j \in \{1, 2\}$ ,

$$\frac{du_j^*(a)}{da} = -\lambda_j^*(a)u_j^*(a), \quad u_j^*(0) = 1, \quad \frac{dv_j^*(a)}{da} = \lambda_j^*(a)u_j^*(a) - \gamma_j v_j^*(a), \quad v_j^*(0) = 0.$$

In a fashion similar to that in section 8.3, we obtain, for all  $a \geq 0$  and  $j = 1, 2$ ,  $\lambda_j^*(a) = \{[v_j^*(a)]' + \gamma_j v_j^*(a)\} / \{1 - [v_j^*(a) + \gamma_j \int_0^a v_j^*(\sigma) d\sigma]\}$ , and thus,

$$(8.14) \quad \begin{aligned} \beta_{12}(a) &= \frac{1}{\int_0^{+\infty} I_2^*(\sigma) d\sigma} \frac{[v_1^*(a)]' + \gamma_1 v_1^*(a)}{1 - [v_1^*(a) + \gamma_1 \int_0^a v_1^*(\sigma) d\sigma]}, \\ \beta_{21}(a) &= \frac{1}{\int_0^{+\infty} I_1^*(\sigma) d\sigma} \frac{[v_2^*(a)]' + \gamma_2 v_2^*(a)}{1 - [v_2^*(a) + \gamma_2 \int_0^a v_2^*(\sigma) d\sigma]}, \quad a \geq 0. \end{aligned}$$

Note that we can numerically calculate the right-hand sides of both equations in (8.14) by using the parameters chosen above (see Figure 5). To confirm the validity of these

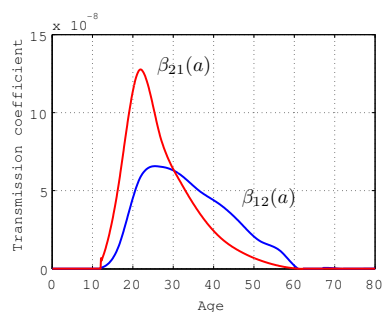


FIG. 5. Transmission coefficients  $\beta_{12}(\cdot)$  and  $\beta_{21}(\cdot)$  calculated by (8.14).

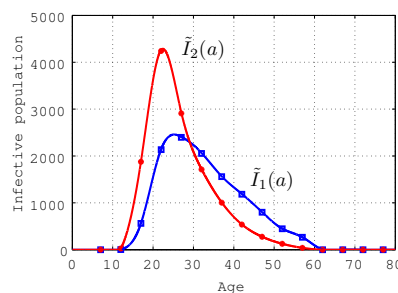


FIG. 6. Infective populations  $\tilde{I}_1(\cdot)$  and  $\tilde{I}_2(\cdot)$  reconstructed by (8.15) (dots indicate the data of male and female infective populations in Table 1).

choices of  $\beta_{12}(\cdot)$  and  $\beta_{21}(\cdot)$ , we reconstruct the infective populations  $\tilde{I}_1(\cdot)$  and  $\tilde{I}_2(\cdot)$  from (8.13) as follows, for  $a \geq 0$ :

$$(8.15) \quad \begin{aligned} \tilde{I}_1(a) &= b_1 e^{-\mu_1 a} \int_0^{+\infty} I_2^*(a) da \int_0^a \beta_{12}(\sigma) e^{-\int_0^{+\infty} I_2^*(a) da \int_0^\sigma \beta_{12}(\rho) d\rho} e^{-\gamma_1(a-\sigma)} d\sigma, \\ \tilde{I}_2(a) &= b_2 e^{-\mu_2 a} \int_0^{+\infty} I_1^*(a) da \int_0^a \beta_{21}(\sigma) e^{-\int_0^{+\infty} I_1^*(a) da \int_0^\sigma \beta_{21}(\rho) d\rho} e^{-\gamma_2(a-\sigma)} d\sigma. \end{aligned}$$

In Figure 6, we see that the reconstructed infective populations  $\tilde{I}_1(\cdot)$  and  $\tilde{I}_2(\cdot)$  are almost the same as the infective populations  $I_1^*(\cdot)$  and  $I_2^*(\cdot)$  obtained as spline functions in Figure 2, respectively. Hence, we see that these choices of  $\beta_{12}(\cdot)$  and  $\beta_{21}(\cdot)$  are reasonable. Using the parameters determined in this way, we obtain the estimation of  $\mathcal{R}_0$  from (8.12) as  $\mathcal{R}_0 \approx 1.0535$ . This value is close to the one obtained in section 8.3 and slightly different from those obtained in sections 8.1 and 8.2.

**9. Discussion.** In this paper, we have studied the multi-group SIR epidemic model (2.1) with age structure. Under assumptions (A1)–(A6), we have reformulated the model into the multi-group model (2.3) with age-dependent susceptibility. We have defined the basic reproduction number  $\mathcal{R}_0$  of system (2.3) as the spectral radius of the next generation matrix  $\mathbf{K}$ , and have shown that if  $\mathcal{R}_0 > 1$ , then system (2.3) has the unique endemic equilibrium  $\mathbf{E}^*$  (Propositions 4.1 and 4.2). We have further shown the existence of compact attractor  $\mathcal{A}$  (Proposition 5.3) that consists of total trajectories  $\mathcal{U}(\cdot)$ . Then, defining Lyapunov function  $L_1(\cdot)$  for total trajectory  $\mathcal{U}(\cdot)$  in  $\mathcal{A}$ , we have proved that if  $\mathcal{R}_0 < 1$ , then the disease-free equilibrium  $\mathbf{E}_0$  is globally attractive (Theorem 6.1). For  $\mathcal{R}_0 > 1$ , we have shown Proposition 7.3, which implies the existence of the persistence attractor  $\mathcal{A}_0 \subset \mathcal{A}$ . Then, by defining the Lyapunov function  $L_2(\cdot)$  for total trajectory  $\mathcal{U}(\cdot)$  in  $\mathcal{A}_0$ , we have proved that if  $\mathcal{R}_0 > 1$ , then the endemic equilibrium  $\mathbf{E}^*$  is globally attractive (Theorem 7.5). Through this analysis, we have succeeded in weakening additional assumptions (B1)–(B6) in the previous study [20].

In section 8, we have applied our main theorem (Theorem 7.6) to the estimation of the basic reproduction number  $\mathcal{R}_0$  for the chlamydia epidemic in Japan in 2015. We have obtained the estimation values of  $\mathcal{R}_0$  for four special cases of our model:  $\mathcal{R}_0 \approx 1.0148$  for the homogeneous model (8.1),  $\mathcal{R}_0 \approx 1.0148$  for the age-independent two-sex model (8.3),  $\mathcal{R}_0 \approx 1.0531$  for the age-dependent one-sex model (8.6), and  $\mathcal{R}_0 \approx 1.0535$  for the age-dependent two-sex model (8.11) (see Table 2).

TABLE 2

The basic reproduction number  $\mathcal{R}_0$  estimated for four special cases of model (2.2) in section 8.

|                 | One-sex | Two-sex |
|-----------------|---------|---------|
| Age-independent | 1.0148  | 1.0148  |
| Age-dependent   | 1.0531  | 1.0535  |

All of these estimation values are not so different from the value  $\mathcal{R}_0 = 1.02$  obtained in [12]. However, we see from Table 2 that the introduction of the age structure has more influence on the value of  $\mathcal{R}_0$  than that of the two-group structure. In particular, in our case,  $\mathcal{R}_0$  values for the models with age structure are greater than those for the models without age structure. This indicates that although ODE models without age structure are usually easier to use than PDE models with age structure, it could lead to the underestimation of  $\mathcal{R}_0$ .

Finally, we mention some future tasks. In our model (2.2) under (A4) and (A5), we assume that the disease transmission coefficient is independent of the age of infective individuals, and that the sum of the mortality and recovery rates is constant. Of course, a model without these assumptions is more realistic. However, the stability of the endemic equilibrium for  $\mathcal{R}_0 > 1$  does not always hold in such a model (see, for instance, [1, 6, 26]). To reveal whether the endemic equilibrium of an age-structured SIR epidemic model can be globally stable for  $\mathcal{R}_0 > 1$  under some epidemiologically reasonable assumptions is an important future task from both the mathematical and epidemiological viewpoints. In section 8, we considered models with at most two groups. Our main theorem (Theorem 7.6) can be applied to more general models with finitely many groups. To consider such a model, we need a more detailed dataset subdivided according to the heterogeneity (for instance, sexual activity) of each individual. To apply our main theorem to such more general models is also an important future task. In the estimation of  $\mathcal{R}_0$  values, we have implicitly assumed that all infective individuals are reported and have neglected the possibility that some of them are not reported. For this reason, our  $\mathcal{R}_0$  values would be underestimated. Improving the accuracy of the estimation by determining the fraction that are unreported is also an important future task.

## REFERENCES

- [1] V. ANDREASEN, *Instability in an SIR-model with age-dependent susceptibility*, in Mathematical Population Dynamics, Wuerz Publishing, Winnipeg, 1995, pp. 3–14.
- [2] A. BERMAN AND R. J. PLEMMONS, *Nonnegative Matrices in the Mathematical Sciences*, Academic Press, New York, 1979.
- [3] Y. CHA, M. IANNELLI, AND F. A. MILNER, *Stability change of an epidemic model*, Dynam. Systems Appl., 9 (2000), pp. 361–376.
- [4] O. DIEKMANN, J. A. P. HEESTERBEEK, AND J. A. J. METZ, *On the definition and the computation of the basic reproduction ratio  $R_0$  in models for infectious diseases in heterogeneous populations*, J. Math. Biol., 28 (1990), pp. 365–382.
- [5] K. A. FENTON, C. KOROVESIS, A. M. JOHNSON, A. MCCADDEN, S. MCMANUS, K. WELLINGS, C. H. MERCER, C. CARDER, A. J. COPAS, K. NANCHAHAL, W. MACDOWALL, G. RIDGWAY, J. FIELD, AND B. ERENS, *Sexual behaviour in Britain: Reported sexually transmitted infections and prevalent genital Chlamydia trachomatis infection*, Lancet, 358 (2001), pp. 1851–1854.
- [6] A. FRANCESCHETTI, A. PUGLIESE, AND D. BREDI, *Multiple endemic states in age-structured SIR epidemic models*, Math. Biosci. Eng., 9 (2012), pp. 577–599.
- [7] H. I. FREEDMAN AND P. MOSON, *Persistence definitions and their connections*, Proc. Amer. Math. Soc., 109 (1990), pp. 1025–1033.
- [8] D. GREENHALGH, *Threshold and stability results for an epidemic model with an age-structured meeting rate*, IMA J. Math. Med. Biol., 5 (1988), pp. 81–100.

- [9] D. GREENHALGH, *Hopf bifurcation in epidemic models with a latent period and nonpermanent immunity*, Math. Comput. Modelling, 25 (1997), pp. 85–107.
- [10] A. B. GUMEL, *Causes of backward bifurcations in some epidemiological models*, J. Math. Anal. Appl., 395 (2012), pp. 355–365.
- [11] H. GUO, M. Y. LI, AND Z. SHUAI, *Global stability of the endemic equilibrium of multigroup SIR epidemic models*, Can. Appl. Math. Q., 14 (2006), pp. 259–284.
- [12] J. C. M. HEIJNE, S. A. HERZOG, C. L. ALTHAUS, N. LOW, AND M. KRETZSCHMAR, *Case and partnership reproduction numbers for a curable sexually transmitted infection*, J. Theoret. Biol., 331 (2013), pp. 38–47.
- [13] H. INABA, *Threshold and stability results for an age-structured epidemic model*, J. Math. Biol., 28 (1990), pp. 414–434.
- [14] H. INABA, *Age-Structured Population Dynamics in Demography and Epidemiology*, Springer, Singapore, 2017.
- [15] JAPANESE MINISTRY OF HEALTH, LABOUR, AND WELFARE, *The 22nd Life Tables*, <https://www.mhlw.go.jp/english/database/db-hw/lifetb22nd/index.html> (accessed 2018/07/24).
- [16] JAPANESE MINISTRY OF HEALTH, LABOUR, AND WELFARE, *Reported Cases of Sexually Transmitted Diseases* (in Japanese), <http://www.mhlw.go.jp/topics/2005/04/tp0411-1.html> (accessed 2018/06/27).
- [17] W. O. KERMACK AND A. G. MCKENDRICK, *Contributions to the mathematical theory of epidemics—I*, Proc. R. Soc. London, 115 (1927), pp. 700–721.
- [18] M. A. KRASNOSELSKII, *Positive Solutions of Operator Equations*, Groningen, Noordhoff, 1964.
- [19] T. KUNIYA, *Global stability analysis with a discretization approach for an age-structured multi-group SIR epidemic model*, Nonlinear Anal. Real World Appl., 12 (2011), pp. 2640–2655.
- [20] T. KUNIYA, J. WANG, AND H. INABA, *A multi-group SIR epidemic model with age structure*, Discrete Contin. Dyn. Syst. Ser. B, 21 (2016), pp. 3515–3550.
- [21] C. C. MCCLUSKEY, *Complete global stability for an SIR epidemic model with delay—distributed or discrete*, Nonlinear Anal. Real World Appl., 11 (2010), pp. 55–59.
- [22] C. C. MCCLUSKEY, *Global stability for an SEI epidemiological model with continuous age-structure in the exposed and infectious classes*, Math. Biosci. Eng., 9 (2012), pp. 819–841.
- [23] A. V. MELNIK AND A. KOROBEINIKOV, *Lyapunov functions and global stability for SIR and SEIR models with age-dependent susceptibility*, Math. Biosci. Eng., 10 (2013), pp. 369–378.
- [24] *Population Estimates by Age (5-Year Age Group) and Sex—Total Population, Japanese Population*, Portal Site of Official Statistics of Japan, <https://www.stat.go.jp/english/data/jinsui/tsuki/index.html> (accessed 2018/07/24).
- [25] H. L. SMITH AND H. R. THIEME, *Dynamical Systems and Population Persistence*, American Mathematical Society, Providence, RI, 2011.
- [26] H. R. THIEME, *Stability change of the endemic equilibrium in age-structured models for the spread of  $S \rightarrow I \rightarrow R$  type infectious diseases*, in Differential Equations Models in Biology, Epidemiology and Ecology, Springer, Berlin, 1991, pp. 139–158.
- [27] P. VAN DEN DRIESSCHE AND J. WATMOUGH, *Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission*, Math. Biosci., 180 (2002), pp. 29–48.
- [28] G. F. WEBB, *Theory of Nonlinear Age-Dependent Population Dynamics*, Marcel Dekker, New York, 1985.