

GLOBAL STABILITY OF THE ENDEMIC EQUILIBRIUM OF MULTIGROUP SIR EPIDEMIC MODELS

HONGBIN GUO, MICHAEL Y. LI AND ZHISHENG SHUAI

ABSTRACT. For a class of multigroup SIR epidemic models with varying subpopulation sizes, we establish that the global dynamics are completely determined by the basic reproduction number R_0 . More specifically, we prove that, if $R_0 \leq 1$, then the disease-free equilibrium is globally asymptotically stable; if $R_0 > 1$, then there exists a unique endemic equilibrium and it is globally asymptotically stable in the interior of the feasible region. Our proof of global stability utilizes the method of global Lyapunov functions and results from graph theory.

1 Introduction Multigroup models have been proposed in the literature to describe the transmission dynamics of infectious diseases in heterogeneous host populations. Heterogeneity in host population can be the result of many factors. Individual hosts can be divided into groups according to different contact patterns such as those among children and adults for Measles and Mumps, or to distinct number of sexual partners for sexually transmitted diseases and HIV/AIDS. Groups can be geographical such as communities, cities, and countries, or epidemiological, to incorporate differential infectivity or co-infection of multiple strains of the disease agent. Multigroup models can also be used to investigate infectious diseases with multiple hosts such as West-Nile virus and vector borne diseases such as Malaria. For a recent survey of multigroup models, we refer the reader to [34].

A multigroup model is, in general, formulated by dividing the population of size $N(t)$ into n distinct groups. For $1 \leq k \leq n$, the k -th group is further partitioned into three compartments: the susceptibles, infectious, and recovered, whose numbers of individuals at time t are

AMS subject classification: 34D23, 92D30.

Keywords: Multigroup SIR model, basic reproduction number, endemic equilibrium, global stability.

Copyright ©Applied Mathematics Institute, University of Alberta.

denoted by $S_k(t), I_k(t)$ and $R_k(t)$, respectively. For $1 \leq i, j \leq n$, the disease transmission coefficient between compartments S_i and I_j is denoted by β_{ij} , so that the new infection occurred in the k -th group is given by

$$(1.1) \quad \sum_{j=1}^n \beta_{kj} S_k I_j.$$

The form of incidence in (1.1) is bilinear. Other incidence forms have been used in the literature, depending on the assumptions made about the mixing among different groups. The matrix $B = (\beta_{ij})_{n \times n}$ is the contact matrix, where $\beta_{ij} \geq 0$. Within the k -th group, it is assumed that natural death occurs in S_k, I_k and R_k compartments with rate constants d_k^S, d_k^I and d_k^R , respectively. Individuals in I_k suffer an additional death due to disease with rate constant ϵ_k . The influx of individuals into the k -th group is given by a constant Λ_k , of which a fraction p_k is assumed to be immuned, and remaining fraction $1 - p_k$ is susceptible. A simple immunization policy is considered where a fraction θ_k of the compartment S_k is vaccinated. We assume that individuals in I_k recover with a rate constant γ_k , and once recovered they remain permanently immuned for the disease. Based on these assumptions, the following system of differential equations can be derived:

$$(1.2) \quad \begin{aligned} S'_k &= (1 - p_k)\Lambda_k - (d_k^S + \theta_k)S_k - \sum_{j=1}^n \beta_{kj} S_k I_j, \\ I'_k &= \sum_{j=1}^n \beta_{kj} S_k I_j - (d_k^I + \epsilon_k + \gamma_k)I_k, \\ R'_k &= p_k\Lambda_k + \theta_k S_k + \gamma_k I_k - d_k^R R_k, \end{aligned}$$

where $k = 1, 2, \dots, n$. The parameters in the model are summarized in the following list:

- β_{ij} : transmission coefficient between compartments S_i and I_j ,
- d_k^S, d_k^I, d_k^R : natural death rates of S, I, R compartments in the k -th group, respectively,
- Λ_k : influx of individuals into the k -th group,
- p_k : fraction of new individuals into the k -th group who are immuned,
- θ_k : fraction of individuals in S_k who are vaccinated,
- γ_k : recovery rate of infectious individuals in the k -th group,
- ϵ_k : disease-caused death rate in the k -th group.

All parameter values are assumed to be nonnegative and $d_k^S, d_k^I, d_k^R, \Lambda_k > 0$ for all k .

For each k , adding the three equations in (1.2), gives

$$\begin{aligned} (S_k + I_k + R_k)' &= \Lambda_k - d_k^S S_k - (d_k^I + \epsilon_k) I_k - d_k^R R_k \\ &\leq \Lambda_k - d_k^*(S_k + I_k + R_k), \end{aligned}$$

where $d_k^* = \min\{d_k^S, d_k^I + \epsilon_k, d_k^R\}$. Hence $\limsup_{t \rightarrow \infty} (S_k + I_k + R_k) \leq \Lambda_k / d_k^*$. Similarly, it follows from the first equation in (1.2) that

$$\limsup_{t \rightarrow \infty} S_k \leq \frac{(1 - p_k)\Lambda_k}{d_k^S + \theta_k}.$$

Observe that the variable R_k does not appear in the first two equations of (1.2). This allows us to consider first the following reduced system for S_k and I_k

$$\begin{aligned} (1.3) \quad S_k' &= (1 - p_k)\Lambda_k - (d_k^S + \theta_k)S_k - \sum_{j=1}^n \beta_{kj} S_k I_j, \\ I_k' &= \sum_{j=1}^n \beta_{kj} S_k I_j - (d_k^I + \epsilon_k + \gamma_k)I_k, \end{aligned}$$

where $k = 1, 2, \dots, n$, in the feasible region

$$(1.4) \quad \Gamma = \left\{ (S_1, I_1, \dots, S_n, I_n) \in \mathbb{R}_+^{2n} \mid S_k \leq \frac{\Lambda_k(1 - p_k)}{d_k^S + \theta_k}, S_k + I_k \leq \frac{\Lambda_k}{d_k^*}, k = 1, 2, \dots, n \right\}.$$

Behaviors of R_k can then be determined from the last equation in (1.2). It can be verified that Γ in (1.4) is positively invariant with respect to (1.3). Let $\overset{\circ}{\Gamma}$ denote the interior of Γ . Our results in this paper will be stated for system (1.3) in Γ , and can be translated straightforwardly to system (1.2).

System (1.3) always has the disease-free equilibrium

$$P_0 = (S_1^0, 0, S_2^0, 0, \dots, S_n^0, 0),$$

where

$$(1.5) \quad S_k^0 = \frac{\Lambda_k(1-p_k)}{d_k^S + \theta_k}, \quad k = 1, 2, \dots, n,$$

is the equilibrium of the S_k population in the absence of disease ($I_1 = I_2 = \dots = I_n = 0$). An endemic equilibrium $P^* = (S_1^*, I_1^*, S_2^*, I_2^*, \dots, S_n^*, I_n^*)$ of (1.3) belongs to $\overset{\circ}{\Gamma}$, namely, $S_k^* > 0, I_k^* > 0, k = 1, 2, \dots, n$. Set

$$(1.6) \quad R_0 = \rho(M_0),$$

where

$$(1.7) \quad M_0 = M(S_1^0, S_2^0, \dots, S_n^0) = \left(\frac{\beta_{ij} S_i^0}{d_i^I + \epsilon_i + \gamma_i} \right)_{n \times n},$$

and ρ denotes the spectral radius. As we will show, R_0 is the key threshold parameter whose values completely characterize the global dynamics of (1.3). Furthermore, R_0 is the basic reproduction number for system (1.3) (see, e.g., [35]).

One of the earliest work on multigroup models is the seminal paper by Lajmanovich and Yorke [24] on a class of SIS multigroup models for the transmission dynamics of Gonorrhoea. A complete analysis of the global dynamics is established. The global stability of the unique endemic equilibrium is proved using a global Lyapunov function. Subsequently, much research has been done on multigroup models, see, e.g., [1, 2, 7, 11–17, 25, 26, 28, 29, 31, 32, 33] and references therein. Due to the large scale and complexity of multigroup models, progresses in the mathematical analysis of their global dynamics have been slow. In particular, the question of uniqueness and global stability of the endemic equilibrium, when the basic reproduction number R_0 is greater than 1, has largely been open. Hethcote [15] proved global stability of the endemic equilibrium for multigroup SIR model without vital dynamics. Beretta and Capasso [2] derived sufficient conditions for global stability of the endemic equilibrium for multigroup SIR model with constant population in each group. Thieme [33] proved global stability of the endemic equilibrium of multigroup SEIRS models under certain restrictions. The most recent result on global stability is Lin and So [27] for a class of SIRS models with constant group sizes, in which they proved that the endemic equilibrium is globally asymptotically stable if the cross-group

contact rates are small or if the recovery rates in each group are small. The complete resolution of the global stability of endemic equilibrium when $R_0 > 1$ has been a well-known open problem in mathematical epidemiology. On the other hand, results in the opposite direction also exist in the literature. For n -group SIR models with proportionate incidence, uniqueness of endemic equilibria may not hold when $R_0 > 1$ (see [19, 34]). In light of these results, complete determination of the global dynamics of these models is essential for their application and further development. It is also crucial to determine how incidence forms or other epidemiological factors influence the uniqueness and global stability of endemic equilibria.

The aim of the present paper is to establish the global dynamics of the class of n -group SIR models with varying group sizes as defined in (1.2). In particular, we prove that, when $R_0 > 1$, the endemic equilibrium of the model is unique and globally asymptotically stable. For this class of multigroup models, our results completely resolve the open problem on the uniqueness and global stability of endemic equilibrium. Our proof relies on the use of a class of global Lyapunov functions. Lyapunov functions of this type has been used in the literature (e.g., see [8], [10], [18], [20]) and was recently rediscovered (e.g., see [22]) and successfully applied to several classes of epidemic models (see [11, 21]). It has the potential for a much wider applicability. The key to our analysis is a complete description of the complicated patterns exhibited in the derivative of the Lyapunov function, using graph theory.

In the next section, we quote some results from graph theory which will be used in the proof of our main results. In Section 3, our main results are stated. In Section 4, the global stability of the disease-free equilibrium when $R_0 \leq 1$ is proved. In Section 5, the global stability of the endemic equilibrium when $R_0 > 1$ is proved. In Section 6, we relate our definition of R_0 to earlier definitions in the literature. Extension of our results to multigroup models with other forms of incidence are discussed in Section 7.

2 Preliminaries Let $E = (e_{ij})_{n \times n}$, $F = (f_{ij})_{n \times n}$ be *nonnegative matrices*, namely, all of their entries are nonnegative. We write $E \geq F$ if $e_{kj} \geq f_{kj}$ for all k and j , and $E > F$ if $E \geq F$ and $E \neq F$. For $n > 1$, an $n \times n$ matrix E is *reducible* if, for some permutation matrix Q ,

$$QEQT = \begin{bmatrix} E_1 & 0 \\ E_2 & E_3 \end{bmatrix},$$

where E_1 and E_3 are square matrices. Otherwise, E is *irreducible*. The following properties of nonnegative matrices are standard (e.g., see [4]).

- P1. If E is nonnegative, then the spectral radius $\rho(E)$ of E is an eigenvalue, and E has a nonnegative eigenvector corresponding to $\rho(E)$.
- P2. If E is nonnegative and irreducible, then $\rho(E)$ is a simple eigenvalue, and E has a positive eigenvector x corresponding to $\rho(E)$.
- P3. If $0 \leq E \leq F$, then $\rho(E) \leq \rho(F)$. Moreover, if $0 \leq E < F$ and $E + F$ is irreducible, then $\rho(E) < \rho(F)$.
- P4. If E is nonnegative and irreducible, and F is diagonal and positive (namely, all of its entries are positive), then EF is irreducible.

Irreducibility of matrices can be easily tested using the associated directed graphs. A *directed graph* G_n is a set of n vertices and a set of directed arcs joining two vertices. A directed graph is *strongly connected* if any two distinct vertices are joined by an oriented path. The directed graph $G(E)$ associated with an $n \times n$ matrix E is a directed graph of n vertices, $1, 2, \dots, n$, such that there exists an arc (j, k) leading from j to k if and only if $e_{kj} \neq 0$. We have the following property.

- P5. Matrix E is irreducible if and only if $G(E)$ is strongly connected.

In Figure 1, examples of reducible and irreducible matrices and their associated directed graphs are shown.

An *oriented cycle* in a directed graph is a simple oriented path from a vertex to itself. A *directed tree* is a connected directed graph with no cycles. A directed tree is said to be *rooted* at a vertex, called root, if every path between a non-root vertex and the root is oriented towards the root. We refer the reader to [23, 29] for more details.

Consider the linear system

$$(2.1) \quad \bar{B}v = 0,$$

where

$$(2.2) \quad \bar{B} = \begin{bmatrix} \sum_{l \neq 1} \bar{\beta}_{1l} & -\bar{\beta}_{21} & \cdots & -\bar{\beta}_{n1} \\ -\bar{\beta}_{12} & \sum_{l \neq 2} \bar{\beta}_{2l} & \cdots & -\bar{\beta}_{n2} \\ \vdots & \vdots & \ddots & \vdots \\ -\bar{\beta}_{1n} & -\bar{\beta}_{2n} & \cdots & \sum_{l \neq n} \bar{\beta}_{nl} \end{bmatrix},$$

and $\bar{\beta}_{ij} \geq 0$.

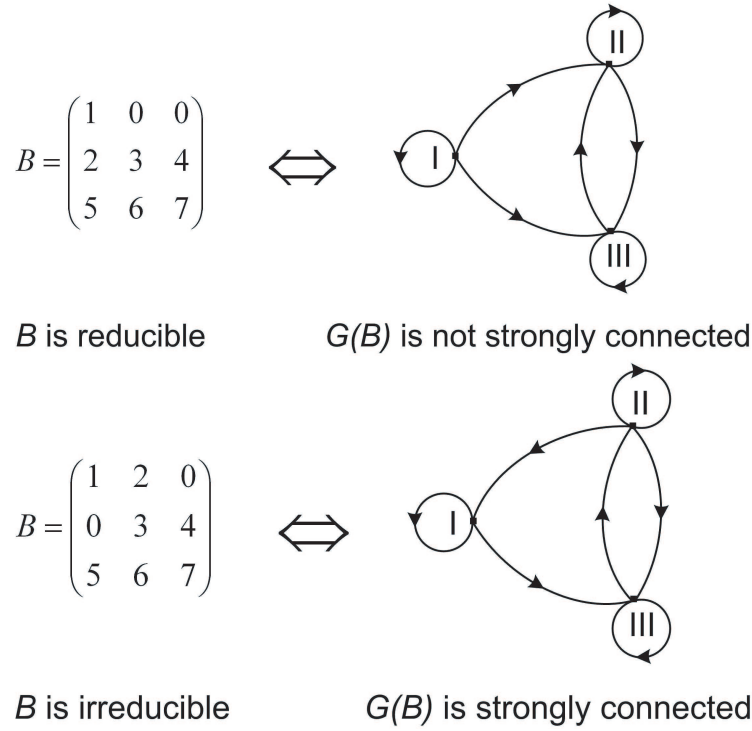


FIGURE 1: Examples of reducible and irreducible matrices and their associated directed graphs.

Lemma 2.1. *Assume that the matrix $(\bar{\beta}_{ij})_{n \times n}$ is irreducible and $n \geq 2$. Then the followings hold.*

(1) *The solution space of system (2.1) has dimension 1.*

(2) *A basis of the solution space is given by*

(2.3)
$$(v_1, v_2, \dots, v_n) = (C_{11}, C_{22}, \dots, C_{nn}),$$

where C_{kk} denotes the cofactor of the k -th diagonal entry of \bar{B} , $1 \leq k \leq n$.

(3) For all $1 \leq k \leq n$,

$$(2.4) \quad C_{kk} = \sum_{T \in \mathbb{T}_k} \prod_{(j,h) \in E(T)} \bar{\beta}_{jh},$$

where \mathbb{T}_k is the set of all directed trees of n vertices rooted at the k -th vertex, and $E(T)$ denotes the set of arcs in a directed tree T .

(4) For all $1 \leq k \leq n$,

$$C_{kk} > 0.$$

Proof. Since the sum of each column in \bar{B} equals zero, we have

$$(2.5) \quad C_{jk} = C_{lk}, \quad 1 \leq j, k, l \leq n,$$

where C_{jk} denotes the cofactor of the (j, k) entry of \bar{B} . Since \bar{B} is singular, we know that $(C_{11}, C_{12}, \dots, C_{1n})$ is a solution of system (2.1). Therefore, by (2.5), $(C_{11}, C_{22}, \dots, C_{nn})$ is also a solution of system (2.1).

For $1 \leq k \leq n$, in the k -th column of \bar{B} , the diagonal entry, $\sum_{l \neq k} \bar{\beta}_{kl}$, equals the negative of the sum of nondiagonal entries. By a result on directed graphs in [29, p. 47, Theorem 5.5], we obtain

$$C_{kk} = \sum_{T \in \mathbb{T}_k} \prod_{(j,h) \in E(T)} \bar{\beta}_{jh}.$$

Since $(\bar{\beta}_{ij})$ is irreducible, its associated directed graph is strongly connected, by P5. Thus, for each k , at least one term in $\sum_{T \in \mathbb{T}_k} \prod_{(j,h) \in E(T)} \bar{\beta}_{jh}$ is positive. Therefore, $C_{kk} > 0$ for $k = 1, 2, \dots, n$. Since C_{11} is a $(n-1)$ minor of \bar{B} , we know $\text{rank}(\bar{B}) = n-1$, and the solution space of (2.1) has dimension 1, completing the proof of Lemma 2.1. \square

As an illustration of C_{kk} , let $n = 3$ and \mathbb{T}_1 be the set of all directed trees rooted at the first vertex. Then, as shown in Figure 2, $\mathbb{T}_1 = \{T_1^1, T_1^2, T_1^3\}$, and $E(T_1^1) = \{(3, 2), (2, 1)\}$, $E(T_1^2) = \{(2, 1), (3, 1)\}$, $E(T_1^3) = \{(2, 3), (3, 1)\}$. Therefore,

$$(2.6) \quad C_{11} = \sum_{T_1^i \in \mathbb{T}_1} \prod_{(j,h) \in E(T_1^i)} \bar{\beta}_{jh} = \bar{\beta}_{32}\bar{\beta}_{21} + \bar{\beta}_{31}\bar{\beta}_{21} + \bar{\beta}_{23}\bar{\beta}_{31}.$$

A *unicyclic graph* is a directed graph that is obtained from a collection of directed rooted trees by joining their roots to form an oriented cycle.

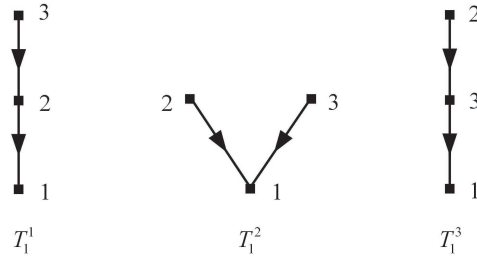


FIGURE 2: All directed trees with three vertices and rooted at 1.

For $1 \leq l \leq n$, let $D(n, l)$ denote the number of unicyclic graphs with n vertices whose cycle has length l . Then

$$(2.7) \quad D(n, l) = \binom{n}{l} n^{n-l-1} l!$$

and

$$(2.8) \quad n^n = \sum_{l=1}^n D(n, l)l.$$

For proofs of these relations, we refer the reader to ([3, Chapter 2]). A unicyclic graph with an oriented cycle of length l can produce l directed rooted trees by deleting different arcs in the oriented cycle, and the vertex from which the deleted arc starts becomes the root. Conversely, a unicyclic graph is obtained from a directed rooted tree by adding a directed arc from the root to any non-root vertex, see Figure 3.

3 Main results System (1.3) is said to be uniformly persistent [6, 36] in $\overset{\circ}{\Gamma}$ if there exists constant $c > 0$ such that

$$\liminf_{t \rightarrow \infty} S_k(t) > c \quad \text{and} \quad \liminf_{t \rightarrow \infty} I_k(t) > c, \quad k = 1, \dots, n,$$

provided $(S_1(0), I_1(0), \dots, S_n(0), I_n(0)) \in \overset{\circ}{\Gamma}$.

Let R_0 be defined in (1.6). We have the following results.

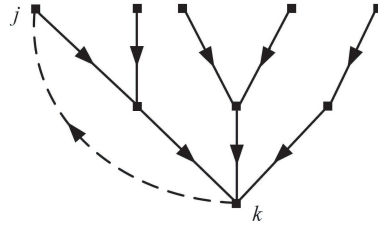


FIGURE 3: Forming a unicyclic graph from a directed tree rooted at vertex k by adding a directed arc from k to j .

Proposition 3.1. *Assume $B = (\beta_{ij})$ is irreducible. Then the following hold.*

- (1) *If $R_0 \leq 1$, then P_0 is the unique equilibrium of (1.3) and it is globally stable in Γ .*
- (2) *If $R_0 > 1$, then P_0 is unstable and system (1.3) is uniformly persistent in $\overset{\circ}{\Gamma}$.*

Results like Proposition 3.1 are known in the literature, at least for some special classes of model (1.3) (see [15, 27, 34]). We will provide a proof in the next section for completeness and to demonstrate our derivation of R_0 .

Uniform persistence of (1.3), together with uniform boundedness of solutions in $\overset{\circ}{\Gamma}$ (follows from the positive invariance of the bounded region Γ), implies the existence of an equilibrium of (1.3) in $\overset{\circ}{\Gamma}$ (see Theorem D.3 in [32] or Theorem 2.8.6 in [5]).

Corollary 3.2. *Assume $B = (\beta_{ij})$ is irreducible. If $R_0 > 1$, then (1.3) has at least one endemic equilibrium.*

Denote the endemic equilibrium by

$$P^* = (S_1^*, I_1^*, S_2^*, I_2^*, \dots, S_n^*, I_n^*),$$

$S_k^* > 0$ and $I_k^* > 0$ for $k = 1, 2, \dots, n$. We have the following main result on the uniqueness and global stability of P^* when $R_0 > 1$.

Theorem 3.3. *Assume that $B = (\beta_{ij})$ is irreducible. If $R_0 > 1$, then there exists a unique endemic equilibrium P^* , and P^* is globally asymptotically stable in $\overset{\circ}{\Gamma}$.*

Proposition 3.1 and Theorem 3.3 completely determine the global dynamics of (1.3) and those of (1.2). They establish the basic reproduction number R_0 as a sharp threshold parameter. Biologically, our results imply that, if $R_0 \leq 1$, then the disease always dies out from all groups; if $R_0 > 1$, then the disease always persists at the unique endemic equilibrium level in all groups, irrespective of the initial conditions.

The proof of Proposition 3.1 will be given in the next section, and that of Theorem 3.3 in Section 5.

4 Proof of Proposition 3.1 Let $S = (S_1, S_2, \dots, S_n)$ and $S^0 = (S_1^0, S_2^0, \dots, S_n^0)$. Then $M_0 = M(S^0)$. For $1 \leq k \leq n$, $0 \leq S_k \leq S_k^0$, we have $0 \leq M(S) \leq M(S_0) = M_0$. If $S \neq S^0$, then $M(S) < M_0$. On the other hand, since B is irreducible, we know $M(S)$ and M_0 are irreducible. Furthermore, $M(S) + M_0$ is also irreducible. Therefore, $\rho(M(S)) < \rho(M_0)$ provided $S \neq S^0$, by P3 of Section 2.

If $R_0 = \rho(M_0) \leq 1$ and $S \neq S^0$, then $\rho(M(S)) < 1$, and

$$M(S)I = I$$

has only the trivial solution $I = 0$. Thus P_0 is the only equilibrium of system (1.3) in Γ if $R_0 \leq 1$.

Let $(\omega_1, \omega_2, \dots, \omega_n)$ be a left eigenvector of M_0 corresponding to $\rho(M_0)$, i.e.,

$$(\omega_1, \omega_2, \dots, \omega_n) \rho(M_0) = (\omega_1, \omega_2, \dots, \omega_n) M_0.$$

Since M_0 is irreducible, we know $\omega_k > 0$ for $k = 1, 2, \dots, n$, by P2 of Section 2. Set

$$L = \sum_{k=1}^n \frac{\omega_k}{d_k^I + \epsilon_k + \gamma_k} I_k.$$

Differentiation gives

$$\begin{aligned} L' &= \sum_{k=1}^n \frac{\omega_k}{d_k^I + \epsilon_k + \gamma_k} I_k' = (\omega_1, \omega_2, \dots, \omega_n) [M(S)I - I] \\ &\leq (\omega_1, \omega_2, \dots, \omega_n) [M_0I - I] \end{aligned}$$

$$= [\rho(M_0) - 1](\omega_1, \omega_2, \dots, \omega_n)I \leq 0, \quad \text{if } R_0 \leq 1.$$

If $R_0 = \rho(M_0) < 1$, then $L' = 0 \Leftrightarrow I = 0$. If $R_0 = 1$, then $L' = 0$ implies

$$(4.1) \quad (\omega_1, \omega_2, \dots, \omega_n)M(S)I = (\omega_1, \omega_2, \dots, \omega_n)I.$$

If $S \neq S^0$, then

$$(\omega_1, \omega_2, \dots, \omega_n)M(S) < (\omega_1, \omega_2, \dots, \omega_n)M_0 = (\omega_1, \omega_2, \dots, \omega_n).$$

Thus (4.1) has only the trivial solution $I = 0$. Therefore, $L' = 0 \Leftrightarrow I = 0$ or $S = S^0$ provided $R_0 \leq 1$. It can be verified that the only compact invariant subset of the set where $L' = 0$ is the singleton $\{P_0\}$. By LaSalle's Invariance Principle [25], P_0 is globally asymptotically stable in Γ if $R_0 \leq 1$.

If $R_0 = \rho(M_0) > 1$ and $I \neq 0$, we know that

$$\begin{aligned} & (\omega_1, \omega_2, \dots, \omega_n)M_0 - (\omega_1, \omega_2, \dots, \omega_n) \\ &= [\rho(M_0) - 1](\omega_1, \omega_2, \dots, \omega_n) > 0, \end{aligned}$$

and thus $L' = (\omega_1, \omega_2, \dots, \omega_n)[M(S)I - I] > 0$ in a neighborhood of P_0 in $\overset{\circ}{\Gamma}$, by continuity. This implies P_0 is unstable. Using a uniform persistence result from [9] and a similar argument as in the proof of Proposition 3.3 of [26], we can show that, when $R_0 > 1$, the instability of P_0 implies the uniform persistence of (1.3). This completes the proof of Proposition 3.1.

5 Proof of Theorem 3.3 In this section, we prove that the endemic equilibrium P^* is globally asymptotically stable when $R_0 > 1$. In particular, this implies that the endemic equilibrium is unique in the region $\overset{\circ}{\Gamma}$ when it exists.

Let $(S_1^*, I_1^*, S_2^*, I_2^*, \dots, S_n^*, I_n^*) \in \overset{\circ}{\Gamma}$ be an endemic equilibrium. Set

$$(5.1) \quad \bar{\beta}_{ij} = \beta_{ij}S_i^*I_j^*, \quad 1 \leq i, j \leq n, \quad n \geq 2,$$

and

$$(5.2) \quad \bar{B} = \begin{bmatrix} \sum_{l \neq 1} \bar{\beta}_{1l} & -\bar{\beta}_{21} & \cdots & -\bar{\beta}_{n1} \\ -\bar{\beta}_{12} & \sum_{l \neq 2} \bar{\beta}_{2l} & \cdots & -\bar{\beta}_{n2} \\ \vdots & \vdots & \ddots & \vdots \\ -\bar{\beta}_{1n} & -\bar{\beta}_{2n} & \cdots & \sum_{l \neq n} \bar{\beta}_{nl} \end{bmatrix}.$$

Then, by Lemma 2.1, a basis for the solution space of the linear system

$$(5.3) \quad \overline{B}v = 0$$

can be written as

$$(5.4) \quad (v_1, \dots, v_n) = (C_{11}, \dots, C_{nn}),$$

where C_{kk} denotes the cofactor of the k -th diagonal entry of \overline{B} , $1 \leq k \leq n$. By the irreducibility of B , we know that (β_{ij}) is irreducible and $v_k = C_{kk} > 0$, $k = 1, \dots, n$, by Lemma 2.1.

For $n = 1$, i.e., the case of single group SIR model, Theorem 3.3 is well known (e.g., see [14]). We only consider the case $n \geq 2$. Let v_1, \dots, v_n be chosen as in (5.4). Set

$$(5.5) \quad V = \sum_{k=1}^n v_k (S_k - S_k^* \ln S_k + I_k - I_k^* \ln I_k).$$

Differentiating V and using the equilibrium equations

$$(5.6) \quad (1 - p_k)\Lambda_k = (d_k^S + \theta_k)S_k^* + \sum_{j=1}^n \beta_{kj}S_k^*I_j^*,$$

and

$$(5.7) \quad (d_k^I + \epsilon_k + \gamma_k)I_k^* = \sum_{j=1}^n \beta_{kj}S_k^*I_j^*,$$

we obtain

$$\begin{aligned} V' &= \sum_{k=1}^n v_k \left(S_k' - \frac{S_k^*}{S_k} S_k' + I_k' - \frac{I_k^*}{I_k} I_k' \right) \\ &= \sum_{k=1}^n v_k \left[(1 - p_k)\Lambda_k - (d_k^S + \theta_k)S_k - \sum_{j=1}^n \beta_{kj}S_k I_j \right. \\ &\quad \left. - (1 - p_k)\Lambda_k \frac{S_k^*}{S_k} + (d_k^S + \theta_k)S_k^* + \sum_{j=1}^n \beta_{kj}S_k^* I_j \right. \\ &\quad \left. + \sum_{j=1}^n \beta_{kj}S_k I_j - (d_k^I + \epsilon_k + \gamma_k)I_k \right. \\ &\quad \left. - \sum_{j=1}^n \beta_{kj}S_k I_j \frac{I_k^*}{I_k} + (d_k^I + \epsilon_k + \gamma_k)I_k^* \right] \end{aligned}$$

$$\begin{aligned}
&= \sum_{k=1}^n v_k \left[-S_k^*(d_k^S + \theta_k) \left(\frac{S_k^*}{S_k} + \frac{S_k}{S_k^*} - 2 \right) \right. \\
&\quad + \left(\sum_{j=1}^n \beta_{kj} S_k^* I_j - (d_k^I + \epsilon_k + \gamma_k) I_k \right) \\
&\quad \left. + \left(2 \sum_{j=1}^n \beta_{kj} S_k^* I_j^* - \sum_{j=1}^n \beta_{kj} I_j^* \frac{(S_k^*)^2}{S_k} - \sum_{j=1}^n \beta_{kj} S_k I_j \frac{I_k^*}{I_k} \right) \right].
\end{aligned}$$

Since

$$\frac{S_k^*}{S_k} + \frac{S_k}{S_k^*} - 2 \geq 0,$$

we have

$$(5.8) \quad -S_k^*(d_k^S + \theta_k) \left(\frac{S_k^*}{S_k} + \frac{S_k}{S_k^*} - 2 \right) \leq 0,$$

and the equal sign holds if and only if $S_k = S_k^*$. Next, we claim

$$(5.9) \quad \sum_{k=1}^n v_k \left(\sum_{j=1}^n \beta_{kj} S_k^* I_j - (d_k^I + \epsilon_k + \gamma_k) I_k \right) = 0,$$

for all $(I_1, I_2, \dots, I_n) \in \mathbb{R}_+^n$. To see this, we note that

$$(5.10) \quad \sum_{k=1}^n v_k \sum_{j=1}^n \beta_{kj} S_k^* I_j = \sum_{j=1}^n v_j \sum_{k=1}^n \beta_{jk} S_j^* I_k = \sum_{k=1}^n \left(\sum_{j=1}^n \beta_{jk} S_j^* v_j \right) I_k.$$

It suffices to show

$$\sum_{j=1}^n \beta_{jk} S_j^* v_j = v_k (d_k^I + \epsilon_k + \gamma_k), \quad k = 1, 2, \dots, n.$$

In fact, by (5.2), (5.3) and (5.7), we have

$$\begin{bmatrix} \beta_{11} S_1^* I_1^* & \beta_{21} S_2^* I_1^* & \cdots & \beta_{n1} S_n^* I_1^* \\ \beta_{12} S_1^* I_2^* & \beta_{22} S_2^* I_2^* & \cdots & \beta_{n2} S_n^* I_2^* \\ \vdots & \vdots & \ddots & \vdots \\ \beta_{1n} S_1^* I_n^* & \beta_{2n} S_2^* I_n^* & \cdots & \beta_{nn} S_n^* I_n^* \end{bmatrix} \begin{bmatrix} v_1 \\ v_2 \\ \vdots \\ v_n \end{bmatrix}$$

$$= \begin{bmatrix} \sum_{j=1}^n \beta_{1j} S_1^* I_j^* v_1 \\ \sum_{j=1}^n \beta_{2j} S_2^* I_j^* v_2 \\ \vdots \\ \sum_{j=1}^n \beta_{nj} S_n^* I_j^* v_n \end{bmatrix} = \begin{bmatrix} (d_1^I + \epsilon_1 + \gamma_1) I_1^* v_1 \\ (d_2^I + \epsilon_2 + \gamma_2) I_2^* v_2 \\ \vdots \\ (d_n^I + \epsilon_n + \gamma_n) I_n^* v_n \end{bmatrix},$$

and thus

$$\begin{bmatrix} \beta_{11} S_1^* & \beta_{21} S_2^* & \cdots & \beta_{n1} S_n^* \\ \beta_{12} S_1^* & \beta_{22} S_2^* & \cdots & \beta_{n2} S_n^* \\ \vdots & \vdots & \ddots & \vdots \\ \beta_{1n} S_1^* & \beta_{2n} S_2^* & \cdots & \beta_{nn} S_n^* \end{bmatrix} \begin{bmatrix} v_1 \\ v_2 \\ \vdots \\ v_n \end{bmatrix} = \begin{bmatrix} (d_1^I + \epsilon_1 + \gamma_1) v_1 \\ (d_2^I + \epsilon_2 + \gamma_2) v_2 \\ \vdots \\ (d_n^I + \epsilon_n + \gamma_n) v_n \end{bmatrix}.$$

Using inequality (5.8), identity (5.9), and notation $\bar{\beta}_{kj}$ as given in (5.1), we have

$$\begin{aligned} (5.11) \quad V' &\leq \sum_{k=1}^n v_k \left(2 \sum_{j=1}^n \bar{\beta}_{kj} - \sum_{j=1}^n \bar{\beta}_{kj} \frac{S_k^*}{S_k} - \sum_{j=1}^n \bar{\beta}_{kj} \frac{I_j S_k I_k^*}{I_k S_k^* I_j^*} \right) \\ &= \sum_{k,j=1}^n v_k \bar{\beta}_{kj} \left(2 - \frac{S_k^*}{S_k} - \frac{I_j S_k I_k^*}{I_k S_k^* I_j^*} \right). \end{aligned}$$

Denote

$$\begin{aligned} (5.12) \quad H_n &= H_n(S_1, I_1, S_2, I_2, \dots, S_n, I_n) \\ &= \sum_{k,j=1}^n v_k \bar{\beta}_{kj} \left(2 - \frac{S_k^*}{S_k} - \frac{I_j S_k I_k^*}{I_k S_k^* I_j^*} \right). \end{aligned}$$

In the following we show $H_n \leq 0$ for all $(S_1, I_1, S_2, I_2, \dots, S_n, I_n) \in \mathring{\Gamma}$. Since the proof for the general case is rather complicated, we first give detailed proofs for $n = 2$ and $n = 3$. Then major steps of the proof for arbitrary $n \geq 2$ is given.

Case $n = 2$: We have

$$H_2 = H_2(S_1, I_1, S_2, I_2) = \sum_{k,j=1}^2 v_k \bar{\beta}_{kj} \left(2 - \frac{S_k^*}{S_k} - \frac{I_j S_k I_k^*}{I_k S_k^* I_j^*} \right).$$

From (2.3) we obtain $v_1 = \bar{\beta}_{21}$ and $v_2 = \bar{\beta}_{12}$. Expanding H_2 gives

$$(5.13) \quad H_2 = \bar{\beta}_{21}\bar{\beta}_{11} \left(2 - \frac{S_1^*}{S_1} - \frac{I_1 S_1 I_1^*}{I_1 S_1^* I_1^*} \right) + \bar{\beta}_{21}\bar{\beta}_{12} \left(2 - \frac{S_1^*}{S_1} - \frac{I_2 S_1 I_1^*}{I_1 S_1^* I_2^*} \right) \\ + \bar{\beta}_{12}\bar{\beta}_{21} \left(2 - \frac{S_2^*}{S_2} - \frac{I_1 S_2 I_2^*}{I_2 S_2^* I_1^*} \right) + \bar{\beta}_{12}\bar{\beta}_{22} \left(2 - \frac{S_2^*}{S_2} - \frac{I_2 S_2 I_2^*}{I_2 S_2^* I_2^*} \right).$$

Write the subindices of $\bar{\beta}_{ij}$'s in (5.13) in the form

$$(5.14) \quad \left\{ \begin{array}{cc} 2 & 1 \\ 1 & 1 \end{array} \right\}, \quad \left\{ \begin{array}{cc} 2 & 1 \\ 1 & 2 \end{array} \right\}, \quad \left\{ \begin{array}{cc} 1 & 2 \\ 2 & 1 \end{array} \right\} \quad \text{and} \quad \left\{ \begin{array}{cc} 1 & 2 \\ 2 & 2 \end{array} \right\},$$

respectively. Each expression in (5.14) defines a transformation from row 1 to row 2. Observe that each transformation in (5.14) possesses one cycle of length 1 or 2. Moreover, both terms in (5.13) corresponding to the transformations with a 2-cycle (i.e., a cycle with length 2) have the same coefficients. Therefore, the sum H_2 can be naturally grouped according to the length of cycles appearing in the subindices of $\bar{\beta}_{ij}$'s.

$$H_2 = \bar{\beta}_{21}\bar{\beta}_{11} \left(2 - \frac{S_1^*}{S_1} - \frac{S_1}{S_1^*} \right) + \bar{\beta}_{12}\bar{\beta}_{22} \left(2 - \frac{S_2^*}{S_2} - \frac{S_2}{S_2^*} \right) \\ + \bar{\beta}_{21}\bar{\beta}_{12} \left(4 - \frac{S_1^*}{S_1} - \frac{I_2 S_1 I_1^*}{I_1 S_1^* I_2^*} - \frac{S_2^*}{S_2} - \frac{I_1 S_2 I_2^*}{I_2 S_2^* I_1^*} \right).$$

Note that

$$\bar{\beta}_{21}\bar{\beta}_{11} \left(2 - \frac{S_1^*}{S_1} - \frac{S_1}{S_1^*} \right) \leq 0, \\ \bar{\beta}_{12}\bar{\beta}_{22} \left(2 - \frac{S_2^*}{S_2} - \frac{S_2}{S_2^*} \right) \leq 0,$$

and

$$(5.15) \quad \bar{\beta}_{21}\bar{\beta}_{12} \left(4 - \frac{S_1^*}{S_1} - \frac{I_2 S_1 I_1^*}{I_1 S_1^* I_2^*} - \frac{S_2^*}{S_2} - \frac{I_1 S_2 I_2^*}{I_2 S_2^* I_1^*} \right) \leq 0,$$

we obtain $H_2(S_1, I_1, S_2, I_2) \leq 0$ for all $(S_1, I_1, S_2, I_2) \in \overset{\circ}{\Gamma}$. From (5.8), we know $V' = 0$ if and only if $S_k = S_k^*$, $k = 1, 2$, and $H_2 = 0$. Moreover, irreducibility of matrix B , or equivalently, the strong connectedness of the directed graph $G(B)$, implies $\bar{\beta}_{21}\bar{\beta}_{12} > 0$. Consequently, we obtain from (5.15)

$$V' = 0 \iff S_k = S_k^*, \quad I_k = aI_k^*, \quad k = 1, 2,$$

where a is an arbitrary positive number.

Case $n = 3$: We have

$$(5.16) \quad \begin{aligned} H_3 &= H_3(S_1, I_1, S_2, I_2, S_3, I_3) \\ &= \sum_{k,j=1}^3 v_k \bar{\beta}_{kj} \left(2 - \frac{S_k^*}{S_k} - \frac{I_j S_k I_k^*}{I_k S_k^* I_j^*} \right). \end{aligned}$$

From (2.3) we obtain

$$(5.17) \quad \begin{aligned} v_1 &= \bar{\beta}_{32} \bar{\beta}_{21} + \bar{\beta}_{31} \bar{\beta}_{21} + \bar{\beta}_{23} \bar{\beta}_{31}, \\ v_2 &= \bar{\beta}_{31} \bar{\beta}_{12} + \bar{\beta}_{13} \bar{\beta}_{32} + \bar{\beta}_{12} \bar{\beta}_{32}, \\ v_3 &= \bar{\beta}_{12} \bar{\beta}_{23} + \bar{\beta}_{21} \bar{\beta}_{13} + \bar{\beta}_{13} \bar{\beta}_{23}. \end{aligned}$$

Substituting expressions of v_k in (5.17) into H_3 , we observe that H_3 is the sum of $3^3 = 27$ terms of forms

$$(5.18) \quad \bar{\beta}_{rl} \bar{\beta}_{lk} \bar{\beta}_{kj} \left(2 - \frac{S_k^*}{S_k} - \frac{I_j S_k I_k^*}{I_k S_k^* I_j^*} \right),$$

or

$$(5.19) \quad \bar{\beta}_{rk} \bar{\beta}_{lk} \bar{\beta}_{kj} \left(2 - \frac{S_k^*}{S_k} - \frac{I_j S_k I_k^*}{I_k S_k^* I_j^*} \right),$$

where $\{r, l, k\}$ is a permutation of $\{1, 2, 3\}$, and $1 \leq j \leq 3$. Write the subindices of $\bar{\beta}_{ij}$'s in (5.18) and (5.19) in the form of transformations

$$(5.20) \quad \left\{ \begin{matrix} r & l & k \\ l & k & j \end{matrix} \right\} \quad \text{and} \quad \left\{ \begin{matrix} r & l & k \\ k & k & j \end{matrix} \right\},$$

respectively. When $j = k, l$ or r , both transformations in (5.20) possesses cycles of length 1, 2 or 3. The terms in H_3 will be grouped together according to the length of cycles appearing in (5.20).

When $j = k$, both transformations in (5.20) have a 1 cycle $\{ \begin{smallmatrix} * & * & k \\ * & * & k \end{smallmatrix} \}$, and accordingly, the terms in (5.18) and (5.19) satisfy

$$\bar{\beta}_{rl} \bar{\beta}_{lk} \bar{\beta}_{kk} \left(2 - \frac{S_k^*}{S_k} - \frac{I_k S_k I_k^*}{I_k S_k^* I_k^*} \right) = \bar{\beta}_{rl} \bar{\beta}_{lk} \bar{\beta}_{kk} \left(2 - \frac{S_k^*}{S_k} - \frac{S_k}{S_k^*} \right) \leq 0,$$

and

$$\bar{\beta}_{rk}\bar{\beta}_{lk}\bar{\beta}_{kk}\left(2 - \frac{S_k^*}{S_k} - \frac{I_k S_k I_k^*}{I_k S_k^* I_k^*}\right) = \bar{\beta}_{rk}\bar{\beta}_{lk}\bar{\beta}_{kk}\left(2 - \frac{S_k^*}{S_k} - \frac{S_k}{S_k^*}\right) \leq 0.$$

When $j = r$, the first transformation in (5.20) produces two distinct 3-cycle patterns $\left\{\begin{smallmatrix} r & l & k \\ l & k & r \end{smallmatrix}\right\}$ and $\left\{\begin{smallmatrix} r & k & l \\ k & l & r \end{smallmatrix}\right\}$. There are 6 terms in H_3 of a 3-cycle form, three of them correspond to each cycle pattern, and thus have the same coefficients $\bar{\beta}_{rl}\bar{\beta}_{lk}\bar{\beta}_{kr}$ or $\bar{\beta}_{rk}\bar{\beta}_{kl}\bar{\beta}_{lr}$. These six terms can be divided into two groups and each has a sum of form

$$\begin{aligned} (5.21) \quad & \bar{\beta}_{rl}\bar{\beta}_{lk}\bar{\beta}_{kr}\left(2 - \frac{S_k^*}{S_k} - \frac{I_r S_k I_k^*}{I_k S_k^* I_r^*}\right) + \bar{\beta}_{lk}\bar{\beta}_{kr}\bar{\beta}_{rl}\left(2 - \frac{S_r^*}{S_r} - \frac{I_l S_r I_r^*}{I_r S_r^* I_l^*}\right) \\ & + \bar{\beta}_{kr}\bar{\beta}_{rl}\bar{\beta}_{lk}\left(2 - \frac{S_l^*}{S_l} - \frac{I_k S_l I_l^*}{I_l S_l^* I_k^*}\right) \\ & = \bar{\beta}_{rl}\bar{\beta}_{lk}\bar{\beta}_{kr}\left(6 - \frac{S_k^*}{S_k} - \frac{I_r S_k I_k^*}{I_k S_k^* I_r^*} - \frac{S_r^*}{S_r} \right. \\ & \quad \left. - \frac{I_l S_r I_r^*}{I_r S_r^* I_l^*} - \frac{S_l^*}{S_l} - \frac{I_k S_l I_l^*}{I_l S_l^* I_k^*}\right) \leq 0. \end{aligned}$$

When $j = r$, the second transformation in (5.20) has a 2-cycle $\left\{\begin{smallmatrix} r & * & k \\ k & * & r \end{smallmatrix}\right\}$. Also, when $j = l$, both transformations in (5.20) have a 2 cycle $\left\{\begin{smallmatrix} * & l & k \\ * & k & l \end{smallmatrix}\right\}$. There are altogether 12 terms in H_3 corresponding to 2-cycle patterns. Each 2-cycle pattern corresponds to 2 terms in H_3 with the same coefficients (products of $\bar{\beta}$'s). These 12 terms can be grouped into 6 pairs and each has a sum of form

$$\begin{aligned} (5.22) \quad & \bar{\beta}_{rk}\bar{\beta}_{lk}\bar{\beta}_{kr}\left(2 - \frac{S_k^*}{S_k} - \frac{I_r S_k I_k^*}{I_k S_k^* I_r^*}\right) \\ & + \bar{\beta}_{kr}\bar{\beta}_{lk}\bar{\beta}_{rk}\left(2 - \frac{S_r^*}{S_r} - \frac{I_k S_r I_r^*}{I_r S_r^* I_k^*}\right) \\ & = \bar{\beta}_{rk}\bar{\beta}_{lk}\bar{\beta}_{kr}\left(4 - \frac{S_k^*}{S_k} - \frac{I_r S_k I_k^*}{I_k S_k^* I_r^*} - \frac{S_r^*}{S_r} - \frac{I_k S_r I_r^*}{I_r S_r^* I_k^*}\right) \leq 0, \end{aligned}$$

or

$$(5.23) \quad \bar{\beta}_{rl}\bar{\beta}_{lk}\bar{\beta}_{kl}\left(2 - \frac{S_k^*}{S_k} - \frac{I_l S_k I_k^*}{I_k S_k^* I_l^*}\right) + \bar{\beta}_{rl}\bar{\beta}_{kl}\bar{\beta}_{lk}\left(2 - \frac{S_l^*}{S_l} - \frac{I_k S_l I_l^*}{I_l S_l^* I_k^*}\right)$$

$$= \bar{\beta}_{rl}\bar{\beta}_{lk}\bar{\beta}_{kl} \left(4 - \frac{S_k^*}{S_k} - \frac{I_l S_k I_k^*}{I_k S_k^* I_l^*} - \frac{S_l^*}{S_l} - \frac{I_k S_l I_l^*}{I_l S_l^* I_k^*} \right) \leq 0.$$

In summary, each term in H_3 corresponds to a transformation in (5.20) which possesses a unique cycle of length 1, 2 or 3. The number of transformations in (5.20) with an l -cycle is given by $D(n, l) \times l$, $l = 1, 2, 3$. In particular, by (2.7), the number of 1-cycles in (5.20) is $D(3, 1) \times 1 = 9$, the number of 2-cycles is $D(3, 2) \times 2 = 12$, and the number of 3-cycles is $D(3, 3) \times 3 = 6$. Therefore, by (2.8),

$$3^3 = 27 = D(3, 1) \times 1 + D(3, 2) \times 2 + D(3, 3) \times 3.$$

This shows that all terms in H_3 are accounted for in our grouping according to cycle patterns and lengths in (5.20). Therefore, we have shown $H_3(S_1, I_1, S_2, I_2, S_3, I_3) \leq 0$ for all $(S_1, I_1, S_2, I_2, S_3, I_3) \in \overset{\circ}{\Gamma}$. From (5.8) we know $V' = 0$ if and only if $S_k = S_k^*$, $k = 1, 2, 3$, and $H_3 = 0$. We claim that if $S_k = S_k^*$, $k = 1, 2, 3$, then

$$(5.24) \quad H_3 = 0 \iff I_k = aI_k^*, \quad k = 1, 2, 3,$$

where a is an arbitrary positive number. It suffices to show that $H_3 = 0$ implies

$$(5.25) \quad \frac{I_k}{I_k^*} = \frac{I_r}{I_r^*}, \quad 1 \leq k, r \leq 3.$$

If $\beta_{kr} = 0$, for some $k \neq r$, then, by the irreducibility of $B = (\beta_{ij})$, or equivalently, the strong connectedness of the $G(B)$, we necessarily have $\bar{\beta}_{kl}\bar{\beta}_{lr} \neq 0$ for $l \neq k, r$. Therefore, either a 3-cycle $\left\{ \begin{smallmatrix} k & l & r \\ l & r & k \end{smallmatrix} \right\}$ exists or both 2-cycles $\left\{ \begin{smallmatrix} k & l & * \\ l & k & * \end{smallmatrix} \right\}$ and $\left\{ \begin{smallmatrix} l & r & * \\ r & l & * \end{smallmatrix} \right\}$ exist. In either case, (5.25) follows from $H_3 = 0$, and from relations (5.21), (5.22) and (5.23). If all $\beta_{ij} \neq 0$, $i \neq j$, then $\bar{\beta}_{kl}\bar{\beta}_{lr} \neq 0$ for $l \neq k, r$, and the same argument shows that (5.25) holds. We thus obtain

$$V' = 0 \iff S_k = S_k^*, \quad I_k = aI_k^*, \quad k = 1, 2, 3,$$

where a is an arbitrary positive number.

Case $n \geq 2$: We have

$$(5.26) \quad \begin{aligned} H_n &= H_n(S_1, I_1, S_2, I_2, \dots, S_n, I_n) \\ &= \sum_{k,j=1}^n v_k \bar{\beta}_{kj} \left(2 - \frac{S_k^*}{S_k} - \frac{I_j S_k I_k^*}{I_k S_k^* I_j^*} \right). \end{aligned}$$

Here $v_k = C_{kk}$ as given in (2.4) is a sum of n^{n-2} terms, each of which is a product of $n-1$ $\bar{\beta}_{ij}$'s whose subindices can be represented by all arcs in a directed tree T rooted at the k -th vertex, by Lemma 2.1(3). Therefore, $v_k \bar{\beta}_{kj}$ is the sum of n^{n-2} terms. Each term in $v_k \bar{\beta}_{kj}$ is a product of n $\bar{\beta}_{ij}$'s whose subindices define transformations as in (5.14) and (5.20), and are represented by directed arcs in a unicyclic graph Q . From our discussion at the end of Section 2, we know Q is formed by adding an oriented arc (k, j) to the directed tree T . Each unicyclic graph Q has a unique cycle CQ of length $1 \leq l \leq n$. Furthermore, there are l terms in H_n , whose coefficients correspond to all l rotations of the same l -cycle and thus are the same, are naturally grouped together. We can show, as in the cases of $n = 2, 3$, the sum of these l terms is nonpositive. More specifically, we can group all terms in H_n according to the length of cycles, and further group the terms of the same cycle length according to their cycle patterns and using (2.4), as shown in the following.

$$\begin{aligned}
 (5.27) \quad H_n &= \sum_{k,j=1}^n v_k \bar{\beta}_{kj} \left(2 - \frac{S_k^*}{S_k} - \frac{I_j S_k I_k^*}{I_k S_k^* I_j^*} \right) \\
 &= \sum_{l=1}^n \left[\sum_{Q \in \mathcal{D}(n,l)} \sum_{(r,m) \in E(CQ)} \left(\prod_{(j,h) \in E(Q)} \bar{\beta}_{jh} \right) \right. \\
 &\quad \left. \times \left(2 - \frac{S_r^*}{S_r} - \frac{S_r I_m I_r^*}{S_r^* I_r I_m^*} \right) \right] \\
 &= \sum_{l=1}^n \left[\sum_{Q \in \mathcal{D}(n,l)} \left(\prod_{(j,h) \in E(Q)} \bar{\beta}_{jh} \right) \right. \\
 &\quad \left. \times \sum_{(r,m) \in E(CQ)} \left(2 - \frac{S_r^*}{S_r} - \frac{S_r I_m I_r^*}{S_r^* I_r I_m^*} \right) \right],
 \end{aligned}$$

where $\mathcal{D}(n, l)$ presents the set of all unicyclic graphs of n vertices with an oriented cycle of length l , CQ is the oriented cycle with length l in a unicyclic graph $Q \in \mathcal{D}(n, l)$, and $E(CQ)$ and $E(Q)$ represent the sets of arcs in CQ and Q , respectively. Since the cardinality of $E(Q)$ is n , the coefficient of each term in (5.27), $\prod_{(j,h) \in E(Q)} \bar{\beta}_{jh}$, is a product of n $\bar{\beta}_{ij}$'s. The cardinality of the set $\mathcal{D}(n, l)$ is

$$(5.28) \quad D(n, l) = \binom{n}{l} n^{n-l-1} l!,$$

and the cardinality of $E(CQ)$ is the length l of the cycle CQ . By the identity (2.8)

$$(5.29) \quad n^n = \sum_{l=1}^n D(n, l)l,$$

we see that all terms in H_n are accounted for in our grouping (5.27). For the oriented cycle CQ in any $Q \in \mathcal{D}(n, l)$, we have

$$(5.30) \quad \sum_{(r,m) \in E(CQ)} \left(2 - \frac{S_r^*}{S_r} - \frac{S_r I_m I_r^*}{S_r^* I_r I_m^*} \right) \leq 0.$$

By (5.27) and (5.30), we know $H_n(S_1, I_1, S_2, I_2, \dots, S_n, I_n) \leq 0$ for all $(S_1, I_1, S_2, I_2, \dots, S_n, I_n) \in \overset{\circ}{\Gamma}$. Therefore, we have

$$V' \leq 0.$$

We claim that if $S_k = S_k^*$, $1 \leq k \leq n$, then

$$(5.31) \quad H_n = 0 \iff I_k = aI_k^*, \quad k = 1, 2, \dots, n,$$

where a is an arbitrary positive number. It suffices to show that $I_k/I_k^* = I_r/I_r^*$ when $\bar{\beta}_{kr} \neq 0$. By the irreducibility of (β_{ij}) , there exists $1 \leq m_1, m_2, \dots, m_s \leq n$, $0 \leq s \leq n - 2$ such that k, r, m_1, \dots, m_s are distinct, and the product $\bar{\beta}_{kr} \bar{\beta}_{r m_1} \bar{\beta}_{m_1 m_2} \cdots \bar{\beta}_{m_s k} \neq 0$. Furthermore, there exists a unicyclic graph $Q \in \mathcal{D}(n, l)$ such that $E(CQ) = \{(k, r), (r, m_1), \dots, (m_s, k)\}$ and $\prod_{(j,h) \in E(Q)} \bar{\beta}_{jh} \neq 0$. Therefore, from

(5.27) and (5.30), we know $I_k/I_k^* = I_r/I_r^*$ if $H_n = 0$.

From (5.8) and (5.31) we know that $V' = 0 \iff S_k = S_k^*$, $I_k = aI_k^*$, $k = 1, 2, \dots, n$. Substituting $S_k = S_k^*$ and $I_k = aI_k^*$ into the first equation of system (1.3), we obtain

$$(5.32) \quad 0 = (1 - p_k)\Lambda_k - (d_k^S + \theta_k)S_k^* - a \sum_{j=1}^n \beta_{kj} S_k^* I_j^*.$$

Since the right-hand-side of (5.32) is strictly decreasing in a , by (5.6), we know (5.32) holds if and only if $a = 1$, namely, at P^* . Therefore, the only compact invariant subset of the set where $V' = 0$ is the singleton $\{P^*\}$. By LaSalle's Invariance Principle, P^* is global asymptotically stable in $\overset{\circ}{\Gamma}$ if $R_0 > 1$. This completes the proof of Theorem 3.3.

6 Basic reproduction number R_0 We have derived our threshold parameter

$$(6.1) \quad R_0 = \rho \left(\begin{bmatrix} \frac{\beta_{11}S_1^0}{d_1^l + \epsilon_1 + \gamma_1} & \cdots & \frac{\beta_{1n}S_1^0}{d_1^l + \epsilon_1 + \gamma_1} \\ \vdots & \ddots & \vdots \\ \frac{\beta_{n1}S_n^0}{d_n^l + \epsilon_n + \gamma_n} & \cdots & \frac{\beta_{nn}S_n^0}{d_n^l + \epsilon_n + \gamma_n} \end{bmatrix} \right)$$

from the stability analysis of the disease-free equilibrium P_0 using the method of Lyapunov functions. We have shown that R_0 plays the role expected of the basic reproduction number, namely, if $R_0 \leq 1$ the disease always dies out, and if $R_0 > 1$, the disease persists. In [35], a method of deriving the basic reproduction number for epidemic models in heterogeneous populations is proposed. Apply the method of [35] to our model (1.3), we can derive the basic reproduction number as

$$(6.2) \quad R_0 = \rho \left(\begin{bmatrix} \frac{\beta_{11}S_1^0}{d_1^l + \epsilon_1 + \gamma_1} & \cdots & \frac{\beta_{1n}S_1^0}{d_n^l + \epsilon_n + \gamma_n} \\ \vdots & \ddots & \vdots \\ \frac{\beta_{n1}S_n^0}{d_1^l + \epsilon_1 + \gamma_1} & \cdots & \frac{\beta_{nn}S_n^0}{d_n^l + \epsilon_n + \gamma_n} \end{bmatrix} \right),$$

where the matrix $\left(\frac{\beta_{kj}S_k^0}{d_j^l + \epsilon_j + \gamma_j} \right)$ is called the next generation matrix in [7] (see Example 4.2 in [35]). Biological interpretation of R_0 in (6.2) as the basic reproduction number is given in [7, 35]. It is straightforward to verify that two expressions of R_0 in (6.1) and (6.2) are equivalent.

7 Other incidence forms Our analysis in Sections 4 and 5 completely determines the global dynamics of multigroup SIR model (1.2). The same analysis applies to models with certain proportionate incidence forms.

Consider an n -group SIR model

$$(7.1) \quad \begin{aligned} S_k' &= dN_k(1 - p_k) - (d + \theta_k)S_k - \sum_{j=1}^n \lambda_{kj} \frac{S_k}{N_k} I_j, \\ I_k' &= \sum_{j=1}^n \lambda_{kj} \frac{S_k}{N_k} I_j - (d + \gamma_k)I_k, \\ R_k' &= dN_k p_k + \theta_k S_k + \gamma_k I_k - dR_k, \end{aligned}$$

for $k = 1, 2, \dots, n$. In this model, the incidence is of proportionate form. It can be verified that the total population in each group $N_k = S_k + I_k + R_k$ is a constant. Consequently, system (7.1) reduces to system (1.2) if we choose $\Lambda_k = dN_k$ and $\beta_{ij} = \lambda_{ij}/N_i$. Therefore, the global dynamics of (7.1) is completely determined by Proposition 3.1 and Theorem 3.3.

Another class of n -group SIR models that can be reduced to the form of (1.2) is the following.

$$\begin{aligned}
 (7.2) \quad S'_k &= bNq_k(1 - p_k) - (d + \theta_k)S_k - \sum_{j=1}^n \beta_{kj} \frac{S_k}{N} I_j, \\
 I'_k &= \sum_{j=1}^n \beta_{kj} \frac{S_k}{N} I_j - (d + \gamma_k)I_k, \\
 R'_k &= bNp_kq_k + \theta_k S_k + \gamma_k I_k - dR_k,
 \end{aligned}$$

for $k = 1, 2, \dots, n$, where $N = \sum_{k=1}^n (S_k + I_k + R_k)$ denotes the total population size, b and d respectively represent the birth and death rate constants, q_k is the ratio of new birth to enter the k -th group, and $\sum_{k=1}^n q_k = 1$. The differences between (7.2) and (1.2) are in the influx of susceptibles and the incidence forms.

The total population size $N(t)$ can be determined by the differential equation

$$(7.3) \quad N' = (b - d)N,$$

which is derived by adding the equations in (7.2). Let $s_k = S_k/N$, $i_k = I_k/N$ and $r_k = R_k/N$ denote the fractions of the classes S_k, I_k and R_k in the total population, respectively. It can be verified that s_k, i_k and r_k satisfy the following system of differential equations

$$\begin{aligned}
 (7.4) \quad s'_k &= bq_k(1 - p_k) - (b + \theta_k)s_k - \sum_{j=1}^n \beta_{kj} s_k i_j, \\
 i'_k &= \sum_{j=1}^n \beta_{kj} s_k i_j - (b + \gamma_k)i_k, \\
 r'_k &= bp_kq_k + \theta_k s_k + \gamma_k i_k - br_k.
 \end{aligned}$$

System (7.4) is a special case of system (1.2). From (1.6), we obtain the

basic reproduction number for system (7.4)

$$(7.5) \quad R_0 = \rho \left(\begin{bmatrix} \frac{bq_1\beta_{11}(1-p_1)}{(b+\gamma_1)(b+\theta_1)} & \cdots & \frac{bq_1\beta_{1n}(1-p_1)}{(b+\gamma_1)(b+\theta_1)} \\ \vdots & \ddots & \vdots \\ \frac{bq_n\beta_{n1}(1-p_n)}{(b+\gamma_n)(b+\theta_n)} & \cdots & \frac{bq_n\beta_{nn}(1-p_n)}{(b+\gamma_n)(b+\theta_n)} \end{bmatrix} \right).$$

The feasible region for (7.4) is given as follows:

$$(7.6) \quad \Delta = \{ (s_1, i_1, r_1, s_2, i_2, r_2, \dots, s_n, i_n, r_n) \in \mathbb{R}_+^{3n} \mid s_k + i_k + r_k = q_k, k = 1, 2, \dots, n \}.$$

System (7.4) always has the disease-free equilibrium

$$P_0 = (s_1^0, 0, r_1^0, s_2^0, 0, r_2^0, \dots, s_n^0, 0, r_n^0),$$

where

$$s_k^0 = \frac{bq_k(1-p_k)}{b+\theta_k}, \quad r_k^0 = \frac{q_k(bp_k+\theta_k)}{b+\theta_k}, \quad k = 1, 2, \dots, n.$$

An endemic equilibrium $P^* = (s_1^*, i_1^*, r_1^*, s_2^*, i_2^*, r_2^*, \dots, s_n^*, i_n^*, r_n^*)$ of (7.4) belongs to $\overset{\circ}{\Delta}$, namely, $s_k^* > 0, i_k^* > 0, r_k^* > 0$ for $k = 1, 2, \dots, n$. Applying Proposition 3.1 and Theorem 3.3 to system (7.4), we obtain the following result.

Theorem 7.1. *Assume $B = (\beta_{ij})$ is irreducible. Then the following results hold for system (7.4).*

- (1) *If $R_0 \leq 1$, then the disease-free equilibrium P_0 is globally asymptotically stable in Δ .*
- (2) *If $R_0 > 1$, then P_0 is unstable. There exists a unique endemic equilibrium P^* , and P^* is globally asymptotically stable in $\overset{\circ}{\Delta}$.*

Biologically, Theorem 7.1 implies that, if the basic reproduction number $R_0 \leq 1$, then the diseases dies out in the sense that infectious fractions go to zero from all the groups, and if $R_0 > 1$, then any initial infections will lead to endemic disease in the sense that the infectious fractions tend to a positive constant in all the groups.

Acknowledgments This research is supported in part by grants from the Natural Science and Engineering Research Council of Canada (NSERC) and Canada Foundation for Innovation (CFI). Both HG and ZS acknowledge the support of the Josephine Mitchell Graduate Scholarships from the Department of Mathematical and Statistical Sciences at the University of Alberta. The authors also acknowledge the financial support from NCE-MITACS Project “Transmission Dynamics and Spatial Spread of Infectious Diseases: Modelling, Prediction and Control.”

REFERENCES

1. G. Aronsson and I. Mellander, *A deterministic model in biomathematics, asymptotic behavior and threshold conditions*, Math. Biosci. **49** (1980), 207–222.
2. E. Beretta and V. Capasso, *Global stability results for a multigroup SIR epidemic model*, in: (T. G. Hallam, L. J. Gross and S. A. Levin, eds.), *Mathematical Ecology*, World Scientific, Singapore, 1986, 317–342.
3. F. Bergeron, G. Labelle and P. Leroux, *Combinatorial Species and Tree-Like Structures*, Cambridge University Press, Cambridge, 1998.
4. A. Berman and R. J. Plemmons, *Nonnegative Matrices in the Mathematical Sciences*, Academic Press, New York, 1979.
5. N. P. Bhatia and G. P. Szegő, *Dynamical Systems: Stability Theory and Applications*, Lecture Notes in Mathematics **35**, Springer, Berlin, 1967.
6. G. J. Butler, H. I. Freedman and P. Waltman, *Uniformly persistent systems*, Proc. Amer. Math. Soc. **96** (1986), 425–430.
7. 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), 365–382.
8. H. I. Freedman and J. W. -H. So, *Global stability and persistence of simple food chains*, Math. Biosci. **76** (1985), 69–86.
9. H. I. Freedman, M. X. Tang and S. G. Ruan, *Uniform persistence and flows near a closed positively invariant set*, J. Dynam. Diff. Equat. **6** (1994), 583–600.
10. B. S. Goh, *Global stability in many-species systems*, Amer. Natur. **111** (1977), 135–143.
11. H. Guo and M. Y. Li, *Global dynamics of a staged progression model for infectious diseases*, Math. Biosci. Eng. **3** (2006), 513–525.
12. K. P. Hadeler and P. van den Driessche, *Backward bifurcation in epidemic control*, Math. Biosci. **146** (1997), 15–35.
13. H. W. Hethcote, *Mathematical models for the spread of infectious diseases*, in: (D. Ludwig and K. L. Cooke, eds.), *Epidemiology*, SIAM, Philadelphia, 1975, 122–131.
14. H. W. Hethcote, *Qualitative analyses of communicable disease models*, Math. Biosci. **28** (1976), 335–356.
15. H. W. Hethcote, *An immunization model for a heterogeneous population*, Theor. Popu. Biol. **14** (1978), 338–349.
16. H. W. Hethcote, *The mathematics of infectious diseases*, SIAM Review, **42** (2000), 599–653.

17. H. W. Hethcote and H. R. Thieme, *Stability of the endemic equilibrium in epidemic models with subpopulations*, Math. Biosci. **75** (1985), 205–227.
18. J. Hofbauer and K. Sigmund, *The Theory of Evolution and Dynamical Systems: Mathematical Aspects of Selection*, Cambridge University Press, Cambridge, 1988.
19. W. Huang, K. L. Cooke and C. Castillo-Chavez, *Stability and bifurcation for a multiple-group model for the dynamics of HIV/AIDS transmission*, SIAM J. Appl. Math. **52** (1992), 835–854.
20. A. Korobeinikov, *A Lyapunov function for Leslie-Gower predator-prey models*, Appl. Math. Lett. **14** (2001), 697–699.
21. A. Korobeinikov and P. K. Maini, *A Lyapunov function and global properties for SIR and SEIR epidemiological models with nonlinear incidence*, Math. Biosci. Eng. **1** (2004), 57–60.
22. A. Korobeinikov and G. C. Wake, *Lyapunov functions and global stability for SIR, SIRS, and SIS epidemiological models*, Appl. Math. Lett. **15** (2002), 955–960.
23. D. E. Knuth, *The Art of Computer Programming, Vol 1: Fundamental Algorithms*, 3rd edition, Addison-Wesley, Boston, 1997.
24. A. Lajmanovich and J. A. York, *A deterministic model for gonorrhoea in a nonhomogeneous population*, Math. Biosci. **28** (1976), 221–236.
25. J. P. LaSalle, *The Stability of Dynamical Systems*, Regional Conference Series in Applied Mathematics, SIAM, Philadelphia, 1976.
26. M. Y. Li, J. R. Graef, L. Wang and J. Karsai, *Global dynamics of a SEIR model with varying total population size*, Math. Biosci. **160** (1999), 191–213.
27. X. Lin and J. W.-H. So, *Global stability of the endemic equilibrium and uniform persistence in epidemic models with subpopulations*, J. Austral. Math. Soc. Ser. B **34** (1993), 282–295.
28. A. L. Lloyd and R. M. May, *Spatial heterogeneity in epidemic models*, J. Theor. Biol. **179** (1996), 1–11.
29. J. W. Moon, *Counting Labelled Trees*, William Clowes and Sons, London, 1970.
30. P. Pinsky and R. Shonkwiler, *A gonorrhoea model treating sensitive and resistant strains in a multigroup population*, Math. Biosci. **98** (1990), 103–126.
31. L. Rass and J. Radcliffe, *Global asymptotic convergence results for multitype models*, Int. J. Appl. Math. Comput. Sci. **10** (2000), 63–79.
32. H. L. Smith and P. Waltman, *The Theory of the Chemostat: Dynamics of Microbial Competition*, Cambridge University Press, Cambridge, 1995.
33. H. R. Thieme, *Local stability in epidemic models for heterogeneous populations*, in: (V. Capasso, E. Grosso and S.L. Paveri-Fontana, eds.), Mathematics in Biology and Medicine, Lecture Notes in Biomathematics **57**, Springer 1985, 185–189.
34. H. R. Thieme, *Mathematics in Population Biology*, Princeton University Press, Princeton, 2003.
35. P. van den Driessche and J. Watmough, *Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission*, Math. Biosci. **180** (2002), 29–48.
36. P. Waltman, *A brief survey of persistence in dynamical systems*, in: (S. Busenberg and M. Martelli, eds.), Delay Differential Equations and Dynamical Systems, Lecture Notes in Mathematics **1475**, Springer, Berlin, 1991, 31–40.

DEPARTMENT OF MATHEMATICAL AND STATISTICAL SCIENCES,
 UNIVERSITY OF ALBERTA, EDMONTON, ALBERTA, CANADA T6G 2G1
E-mail address: hguo@math.ualberta.ca, mli@math.ualberta.ca
E-mail address: zshuai@math.ualberta.ca