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Impact of group mixing on disease dynamics

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ABSTRACT

A general mathematical model is proposed to study the impact of group mixing in a heterogeneous host population on the spread of a disease that confers temporary immunity upon recovery. The model contains general distribution functions that account for the probabilities that individuals remain in the recovered class after recovery. For this model, the basic reproduction number $\mathcal{R}_0$ is identified. It is shown that if $\mathcal{R}_0 < 1$, then the disease dies out in the sense that the disease free equilibrium is globally asymptotically stable; whereas if $\mathcal{R}_0 > 1$, this equilibrium becomes unstable. In this latter case, depending on the distribution functions and the group mixing strengths, the disease either persists at a constant endemic level or exhibits sustained oscillatory behavior.

1. Introduction

We formulate a model for diseases that confer temporary immunity upon recovery, for example, the common cold (primarily caused by rhinoviruses), pertussis, human respiratory syncytial virus, and some sexually transmitted diseases such as syphilis. We assume that the disease does not cause death and that the time scale is sufficiently fast so that vital dynamics can be ignored. Thus the total population remains constant. The diagram for the flow in the model is shown in Fig. 1.1. Here S, I, R are the numbers of individuals in the susceptible, infectious, and recovered classes, respectively, with $S + I + R = N$ a constant, $\beta > 0$ is the disease transmission coefficient, $\gamma > 0$ is the rate at which infectious individuals recover and move from the infectious class to the recovered class. In addition, $P(t)$ is the probability of remaining in the recovered class t time units after recovery, that is

$$R(t) = \int_0^t \gamma I(u) P(t-u)\, du$$

with the assumption that no individuals are in the recovered class at $t = 0$. We assume throughout that $P(t)$ satisfies the following biologically reasonable properties:

(A) $P : [0,\infty) \to [0,1]$ is nonincreasing, piecewise continuous with possibly finitely many jumps and satisfies $P(0+) = 1$, $\lim_{t\to\infty} P(t) = 0$ with $\int_0^\infty P(u)du$ positive and finite.

Assuming that the force of infection is given by mass action and that initially a small number of infectious individuals is introduced into an otherwise susceptible population, thus $S(0) > 0$, $I(0) > 0$, $R(0) = 0$ with $S(0) + I(0) = N$ a constant, the equations governing the SIRS model are

$$\begin{aligned} S(t) &= N - I(t) - R(t), \\ I'(t) &= \beta S(t) I(t) - \gamma I(t), \\ R(t) &= \int_0^t \gamma I(u) P(t-u)\, du. \end{aligned} \tag{1.1}$$

Here and in the sequel, integrals are in the sense of Riemann–Stieltjes integrals and prime means the derivative with respect to time t.

For a constant period of temporary immunity ω, $P(t)$ is the step function given by

$$P(t) = \begin{cases} 1 & t \in [0,\omega], \\ 0 & t \in (\omega,\infty), \end{cases} \tag{1.2}$$

with ω positive and finite. Then the model breaks into two parts: for $t \in [0,\omega]$ it is governed by the following ordinary differential equation (ODE) system

$$\begin{aligned} S'(t) &= -\beta I(t) S(t), \\ I'(t) &= \beta I(t) S(t) - \gamma I(t), \\ R'(t) &= \gamma I(t), \end{aligned} \tag{1.3}$$

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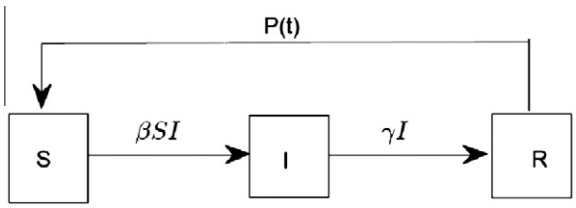

Fig. 1.1. Flow diagram of an SIRS model.

where $S(0) > 0$, $I(0) > 0$, $R(0) = 0$; whereas for $t > \omega$, the disease dynamics is described by the following system of delay differential equations (DDEs)

$$\begin{aligned} S'(t) &= -\beta I(t)S(t) + \gamma I(t-\omega), \\ I'(t) &= \beta I(t)S(t) - \gamma I(t), \\ R'(t) &= \gamma I(t) - \gamma I(t-\omega), \end{aligned} \tag{1.4}$$

with initial condition given by the solution of (1.3) in the interval $[0,\omega]$. Obviously, the long term behavior of the model solutions is determined by the second part. By Hopf bifurcation analysis, Hethcote et al. [3] showed that for some parameter values the system (1.4) can have periodic solutions. A similar model but including constant recruitment into the susceptible class and natural death was analyzed by Brauer et al. [1, Sections 2, 3].

In this paper, we extend model (1.1) to the situation in which the population is divided into n groups. Here the groups can be formed in terms of, for example, education levels, ethnic background, gender ($n = 2$), age, depending on the disease under consideration. We include heterogeneity by assuming that each group can transmit to the others (as in Lloyd and May [5]), rather than explicit spatial heterogeneity as in patch models (see, for example, Brauer et al. [1, Sections 4, 5]). For such a heterogenous host population consisting of n groups, the model (1.1) is extended in a straightforward way to the following system

$$\begin{aligned} S_i(t) &= N_i - I_i(t) - R_i(t), \\ I_i'(t) &= \sum_{j=1}^{n} \beta_{ij} I_j(t) S_i(t) - \gamma_i I_i(t), \\ R_i(t) &= \int_0^t \gamma_i I_i(u) P_i(t-u)\,du, \quad i = 1,2,\ldots,n, \end{aligned} \tag{1.5}$$

with $S_i(0) > 0$, $I_i(0) \geqslant 0$, $R_i(0) = 0$, $\sum_{i=1}^{n} I_i(0) > 0$ and N_i constant. Here γ_i is assumed to be positive with $\frac{1}{\gamma_i}$ being the average infectious period for group i, and $P_i(t)$ satisfies properties (A). The terms $\beta_{ii} I_i S_i$ refer to the infections within the same group i, while the terms $\beta_{ij} I_j S_i$, $j \neq i$ refer to the infections between group i and group j. The nonnegative matrix of disease transmission coefficients $B = (\beta_{ij})$ is assumed to be irreducible (i.e., every group has direct or indirect disease transmission to every other group). In this case the system is fully coupled and cannot be decomposed into two or more decoupled subsystems.

Our main goal is to investigate the impact of the inter-group infections on the disease dynamics. To this end, the rest of this paper is organized as follows. In Section 2, it is proved that the model is well-posed, the basic reproduction number is identified and it is shown that the disease free equilibrium is globally stable. The existence of the endemic equilibrium is given in Section 3 for two typical special forms of $P_i(t)$. The case of two groups is studied in detail with simulations in Section 4. A discussion is given in Section 5.

2. Well-posedness and global stability of the disease free equilibrium

The Volterra integro-differential equation system (1.5) satisfies the hypotheses stated by Miller [6, p. 338] that are sufficient to ensure the existence, uniqueness and continuity of solutions. Let

$$D_i = \{(S_i, I_i, R_i) \in \mathbb{R}^3 : S_i, I_i, R_i \geqslant 0, S_i + I_i + R_i = N_i\}.$$

Then system (1.5) is positively invariant in $D = \prod_{i=1}^{n} D_i$.

System (1.5) always allows a disease free equilibrium (DFE) E_0 that has $S_i = N_i$, $I_i = R_i = 0$ for $i = 1,2,\ldots,n$. Substituting

$$S_i(t) = N_i - I_i(t) - \gamma_i \int_0^t I_i(u) P_i(t-u)\,du,$$

$i = 1,2,\ldots,n$, into the I_i equations in (1.5) gives the equivalent system

$$I_i'(t) = \sum_{j=1}^{n} \beta_{ij} I_j(t) \left(N_i - I_i(t) - \gamma_i \int_0^t I_i(u) P_i(t-u)\,du \right) - \gamma_i I_i(t). \tag{2.1}$$

Then the stability of the DFE of (1.5) is equivalent to the stability of the trivial solution of (2.1). The characteristic equation of (2.1) at $I_i = 0$, $i = 1,2,\ldots,n$, is

$$\det(F - V - I_d z) = 0,$$

where I_d is the $n \times n$ identity matrix, $F = (\beta_{ij} N_i)$ and $V = diag(\gamma_i)$. Since this is a polynomial equation, the DFE is locally asymptotically stable (LAS) if the stability modulus of matrix $F - V$ is negative, that is, $s(F - V) = \max\{Re(\lambda)\colon \lambda \text{ is an eigenvalue of } F - V\} < 0$. Then FV^{-1} is the next generation matrix of the model (1.5) (see, e.g., [8]) and the DFE is LAS if the basic reproduction number $\mathcal{R}_0 = \rho(FV^{-1}) < 1$ and unstable if $\mathcal{R}_0 > 1$, where ρ denotes the spectral radius. Note that FV^{-1} is entrywise nonnegative, thus $\rho(FV^{-1})$ is attained at the largest real positive eigenvalue of FV^{-1}. For the matrices F and V given above,

$$\mathcal{R}_0 = \rho\left(\left(\frac{\beta_{ij} N_i}{\gamma_j} \right) \right). \tag{2.2}$$

Moreover, defining the basic reproduction number of each group by

$$\mathcal{R}_0^{(i)} = \frac{\beta_{ii} N_i}{\gamma_i} \quad \text{for } i = 1,2,\ldots,n, \tag{2.3}$$

the monotonicity of $\rho(FV^{-1})$ with respect to the entries gives

$$\mathcal{R}_0 \geqslant \max\left\{ \mathcal{R}_0^{(i)}, i = 1,2,\ldots,n \right\}.$$

This indicates that if one group in isolation has high prevalence (the associated basic reproduction number is greater than one), then the disease will become endemic in the whole population in the presence of inter-group transmission. A more interesting observation is that due to group mixing, even if $\mathcal{R}_0^{(i)} < 1$ for all $i = 1,2,\ldots,n$, it is still possible to have $\mathcal{R}_0 > 1$, as illustrated in Figs. 4.4 and 4.5 in Section 4 below.

Next we show that when $\mathcal{R}_0 < 1$, E_0 is indeed globally asymptotically stable (GAS). To this end, notice from (1.5) as $S_i \leqslant N_i$ that

$$I_i'(t) \leqslant \sum_{j=1}^{n} \beta_{ij} I_j(t) N_i - \gamma_i I_i(t).$$

Since $\mathcal{R}_0 < 1$, the trivial solution of the linear system

$$I_i'(t) = \sum_{j=1}^{n} \beta_{ij} I_j(t) N_i - \gamma_i I_i(t) \tag{2.4}$$

is LAS and thus is GAS. Since (2.4) is a cooperative system, by a comparison theorem [7, Theorem 1.1.3,p.78], it follows that $I_i(t) \to 0$ as

$t \to \infty$ for $i = 1,2,\ldots,n$. Thus for $\epsilon > 0$, there exists $T_1 > 0$ such that $I_i(t) \leqslant \epsilon$ for $t \geqslant T_1$, and we show that this implies that $R_i(t) \to 0$ as $t \to \infty$. Recall that $P_i(t)$ satisfies properties (A), thus $M_i = \int_0^\infty P_i(u)du > 0$ is finite. Then for the same $\epsilon > 0$, there exists $T_2 > 0$ such that $\int_{t-T_1}^{t} P_i(u)du < \epsilon$ for $t \geqslant T_2$. Therefore it follows from (1.5) that for $t \geqslant T_1 + T_2$,

$$\begin{aligned} R_i(t) &= \int_0^t \gamma_i I_i(u) P_i(t-u)du \\ &= \int_0^{T_1} \gamma_i I_i(u) P_i(t-u)du + \int_{T_1}^t \gamma_i I_i(u) P_i(t-u)du \\ &\leqslant \gamma_i N_i \int_0^{T_1} P_i(t-u)du + \gamma_i \epsilon \int_{T_1}^t P_i(t-u)du \\ &\leqslant \gamma_i N_i \int_{t-T_1}^t P_i(u)du + \gamma_i \epsilon \int_0^\infty P_i(u)du \\ &\leqslant \gamma_i N_i \epsilon + \gamma_i M_i \epsilon = (N_i + M_i)\gamma_i \epsilon. \end{aligned}$$

This shows that $R_i(t) \to 0$ as $t \to \infty$ and hence $S_i(t) \to N_i$ as $t \to \infty$.

Summarizing the above gives the following theorem.

Theorem 2.1. *Consider the n-group model (1.5) with $\mathcal{R}_0$ defined in (2.2). If $\mathcal{R}_0 < 1$, then the DFE is GAS; if $\mathcal{R}_0 > 1$, then the DFE is unstable.*

Remark 2.1. There is a special case in which each group has the same total population, the same average infectious period, the same transmission within its group and the same (usually smaller) transmission between groups. Writing $N_i = N$, $\gamma_i = \gamma$, $\beta_{ii} = \beta$, $\beta_{ij} = \delta\beta$ with $0 < \delta \leqslant 1$ for $i \neq j$, gives $\mathcal{R}_0 = \beta N((n-1)\delta + 1)/\gamma$, which is similar to the formula found by Lloyd and May [5, Eq. (36)].

3. Special forms of $P_i(t)$

The basic reproduction number $\mathcal{R}_0$ given by (2.2) is independent of $P_i(t)$, and we now examine whether different forms of $P_i(t)$ yield different dynamic behavior when $\mathcal{R}_0 > 1$.

3.1. $P_i(t)$ is negatively exponentially distributed

Assume that $P_i(t) = e^{-\alpha_i t}$ with $\alpha_i > 0$ for $i = 1,2,\ldots,n$, thus $\alpha_i > 0$ is the rate at which individuals of group i in the recovered class lose immunity and return to the susceptible class, so $1/\alpha_i$ is the average time of immunity. Then system (1.5) reduces to the ODE system

$$\begin{aligned} S_i'(t) &= -\sum_{j=1}^n \beta_{ij} I_j(t) S_i(t) + \alpha_i R_i(t), \\ I_i'(t) &= \sum_{j=1}^n \beta_{ij} I_j(t) S_i(t) - \gamma_i I_i(t), \\ R_i'(t) &= \gamma_i I_i(t) - \alpha_i R_i(t), \quad i = 1,2,\ldots,n. \end{aligned} \tag{3.1}$$

The basic reproduction number is as in (2.2) and the DFE is GAS if the basic reproduction number is less than one and is unstable if it is greater than one. Next we are concerned with the existence and stability of an EE of system (3.1), which is a solution to the following algebraic system

$$0 = -\sum_{j=1}^n \beta_{ij} I_j S_i + \alpha_i R_i, \tag{3.2}$$

$$0 = \sum_{j=1}^n \beta_{ij} I_j S_i - \gamma_i I_i, \tag{3.3}$$

$$0 = \gamma_i I_i - \alpha_i R_i, \quad i = 1,2,\ldots,n. \tag{3.4}$$

An EE, denoted by $E^* = (S_1^*, I_1^*, R_1^*, \ldots, S_n^*, I_n^*, R_n^*)^T$, is thus a solution of (3.2)–(3.4) with $S_i^* > 0$, $I_i^* > 0$, $R_i^* > 0$. It follows from (3.3) and (3.4) that for $i = 1,2,\ldots,n$,

$$\begin{aligned} &\sum_{j=1}^n \beta_{ij} I_j^* S_i^* = \gamma_i I_i^*, \\ &\gamma_i I_i^* = \alpha_i R_i^*. \end{aligned} \tag{3.5}$$

Using $N_i = S_i^* + I_i^* + R_i^*$ and eliminating S_i^* and R_i^*, an EE can be found by solving the following equations

$$\gamma_i I_i^* = \left(N_i - \frac{\alpha_i + \gamma_i}{\alpha_i} I_i^*\right) \sum_{j=1}^n \beta_{ij} I_j^*, \quad i = 1,2,\ldots,n. \tag{3.6}$$

If $I^* = (I_1^*, \ldots, I_n^*)^T$ is a positive solution of Eq. (3.6) with $I_i^* \in (0, \frac{\alpha_i}{\alpha_i+\gamma_i} N_i)$, then an EE is determined by $R_i^* = \frac{\gamma_i}{\alpha_i} I_i^*$ and $S_i^* = N_i - I_i^* - R_i^*$. The following theorem shows there exists a unique EE provided $\mathcal{R}_0 > 1$.

Theorem 3.1. *For the ODE epidemiological model (3.1), the basic reproduction number $\mathcal{R}_0$ is given by (2.2). If $\mathcal{R}_0 < 1$, then the DFE is GAS and if $\mathcal{R}_0 > 1$, then the DFE is unstable and there exists a unique EE.*

Proof. We need only to show the existence and uniqueness of an EE under the condition $\mathcal{R}_0 > 1$. Set $y_i = \frac{\alpha_i+\gamma_i}{\alpha_i} I_i^*$ for $i = 1,2,\ldots,n$. Then (3.6) becomes

$$\frac{\alpha_i \gamma_i}{\alpha_i + \gamma_i} y_i = (N_i - y_i) \sum_{j=1}^n \frac{\beta_{ij}\alpha_j}{\alpha_j + \gamma_j} y_j, \quad i = 1,2,\ldots,n.$$

Consider a related system of differential equations

$$y' = Ay + f(y), \tag{3.7}$$

where $y = (y_1, y_2, \ldots, y_n)^T$, $A = F_1 - V_1$ with

$$F_1 = \left(\frac{\beta_{ij}\alpha_j N_i}{\alpha_j + \gamma_j}\right), \quad V_1 = diag\left(\frac{\alpha_i \gamma_i}{\alpha_i + \gamma_i}\right)$$

and

$$f(y) = \left(-\sum_{j=1}^n \frac{\beta_{1j}\alpha_j}{\alpha_j + \gamma_j} y_j y_1, \ldots, -\sum_{j=1}^n \frac{\beta_{nj}\alpha_j}{\alpha_j + \gamma_j} y_j y_n\right)^T.$$

Note that I^* is a positive solution of (3.6) if and only if y is a positive equilibrium of system (3.7). By [4, Theorem 3.1], system (3.7) has a unique positive equilibrium provided that $s(A) > 0$. From the proof of Theorem 2 in [8], $s(A) > 0$ is equivalent to $\mathcal{R}_0 = \rho(F_1 V_1^{-1}) > 1$, completing the proof. □

In the special case of Remark 2.1, if $\mathcal{R}_0 > 1$, then in each group $S_i^* = \frac{N}{\mathcal{R}_0}$, $I_i^* = \frac{\alpha}{\alpha+\gamma}(1 - \frac{1}{\mathcal{R}_0})N$, $R_i^* = \frac{\gamma I_i^*}{\alpha}$ and solutions approach the EE.

3.2. $P_i(t)$ is a step function

Assume that the disease has the same constant period of temporary immunity ω in all groups. That is, $P_i(t)$, $i = 1,2,\ldots,n$, are identically given by (1.2). Then for $t \in [0,\omega]$, the model becomes

$$\begin{aligned} S_i'(t) &= -\sum_{j=1}^n \beta_{ij} I_j(t) S_i(t), \\ I_i'(t) &= \sum_{j=1}^n \beta_{ij} I_j(t) S_i(t) - \gamma_i I_i(t), \\ R_i(t) &= \int_0^t \gamma_i I_i(x)dx, \end{aligned} \tag{3.8}$$

with $S_i(0) > 0$, $I_i(0) > 0$, $R_i(0) = 0$, $i = 1,2,\ldots,n$; whereas for $t \in (\omega,\infty)$,

$$\begin{aligned} S_i'(t) &= \sum_{j=1}^{n} \beta_{ij} I_j(t) S_i(t) + \gamma_i I_i(t-\omega), \\ I_i'(t) &= \sum_{j=1}^{n} \beta_{ij} I_j(t) S_i(t) - \gamma_i I_i(t), \\ R_i(t) &= \int_{t-\omega}^{t} \gamma_i I_i(x)dx. \end{aligned} \tag{3.9}$$

From Theorem 2.1 and applying [4, Theorem 3.1] as in the proof of Theorem 3.1 gives the following result.

Theorem 3.2. *Consider the n-group model (3.8) and (3.9) with $\mathcal{R}_0$ defined by (2.2). If $\mathcal{R}_0 < 1$, then the DFE is the unique equilibrium and is GAS; whereas if $\mathcal{R}_0 > 1$, then the DFE is unstable and there is a unique EE denoted by $E^+ = (S_1^+, I_1^+, R_1^+, \ldots, S_n^+, I_n^+, R_n^+)^T$ where $(I_1^+, \ldots, I_n^+)^T$ is the unique positive solution to*

$$\gamma_i I_i^+ = \left(N_i - (1+\gamma_i\omega)I_i^+\right)\sum_{j=1}^{n}\beta_{ij}I_j^+, \quad i = 1,\ldots,n$$

and

$$R_i^+ = \gamma_i\omega I_i^+, \quad S_i^+ = N_i - (1+\gamma_i\omega)I_i^+, \quad i = 1,\ldots,n.$$

Remark 3.1. In the special case of Remark 2.1, if $\mathcal{R}_0 > 1$, then for each group $S_i^+ = N/\mathcal{R}_0$, $I_i^+ = (1 - 1/\mathcal{R}_0)N/(1+\gamma\omega)$, and $R_i^+ = \gamma\omega I_i^+$. Linear stability of this special case is the same as for the one group model with β replaced by $\beta((n-1)\delta + 1)$. Thus the results of [3, Section 3] on Hopf bifurcation apply and periodic solutions are possible for some parameter values. These can arise as the group mixing strengths, specified by δ, increase.

Remark 3.2. The limiting case of $\omega = 0$ corresponds to a model for a disease that confers no immunity, i.e., the SIRS model reduces to an SIS model. In this case, the result of [4, Theorem 3.1] shows that, if $\mathcal{R}_0 > 1$, then the unique EE is globally asymptotically stable.

Because of the high dimension of the system, it is not easy to determine the stability of the EE in the case of $\omega > 0$. In the next section, we explore this topic and the disease dynamics for the model with *two* groups.

4. The case of two groups

In this section, we consider the case with $n = 2$. It is easy to compute the matrices F and V from Section 2 as

$$F = \begin{pmatrix} \beta_{11}N_1 & \beta_{12}N_1 \\ \beta_{21}N_2 & \beta_{22}N_2 \end{pmatrix} \quad \text{and} \quad V = \begin{pmatrix} \gamma_1 & 0 \\ 0 & \gamma_2 \end{pmatrix}$$

and thus

$$\mathcal{R}_0 = \frac{1}{2}\left(\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)} + \sqrt{\left(\mathcal{R}_0^{(1)} - \mathcal{R}_0^{(2)}\right)^2 + 4\beta_{12}\beta_{21}\frac{N_1N_2}{\gamma_1\gamma_2}}\right), \tag{4.1}$$

with $\mathcal{R}_0^{(i)}$ as in (2.3) for $i = 1, 2$.

4.1. Two groups with negatively exponentially distributed function $P_i(t)$

For two groups with $P_i(t)$ being negatively exponentially distributed, (3.1) becomes

$$\begin{aligned} S_1'(t) &= -(\beta_{11}I_1(t) + \beta_{12}I_2(t))S_1(t) + \alpha_1 R_1(t), \\ I_1'(t) &= (\beta_{11}I_1(t) + \beta_{12}I_2(t))S_1(t) - \gamma_1 I_1(t), \\ R_1'(t) &= \gamma_1 I_1(t) - \alpha_1 R_1(t), \\ S_2'(t) &= -(\beta_{21}I_1(t) + \beta_{22}I_2(t))S_2(t) + \alpha_2 R_2(t), \\ I_2'(t) &= (\beta_{21}I_1(t) + \beta_{22}I_2(t))S_2(t) - \gamma_2 I_2(t), \\ R_2'(t) &= \gamma_2 I_2(t) - \alpha_2 R_2(t). \end{aligned}$$

Since (β_{ij}) is assumed irreducible, β_{12} and β_{21} are positive. If $\mathcal{R}_0 > 1$, then by Theorem 3.1, there exists a unique EE, denoted by $(S_1^*, I_1^*, R_1^*, S_2^*, I_2^*, R_2^*)^T$.

Using the fact that $N_i = S_i + I_i + R_i$ is constant for $i = 1, 2$, we only need to consider the following reduced system

$$\begin{aligned} I_1'(t) &= [\beta_{11}I_1(t) + \beta_{12}I_2(t)](N_1 - I_1(t) - R_1(t)) - \gamma_1 I_1(t), \\ I_2'(t) &= [\beta_{21}I_1(t) + \beta_{22}I_2(t)](N_2 - I_2(t) - R_2(t)) - \gamma_2 I_2(t), \\ R_1'(t) &= \gamma_1 I_1(t) - \alpha_1 R_1(t), \\ R_2'(t) &= \gamma_2 I_2(t) - \alpha_2 R_2(t). \end{aligned} \tag{4.2}$$

Linearizing about the EE gives a fourth degree characteristic polynomial, (A.1) in the Appendix. Calculations given in the Appendix show that by the Routh–Hurwitz Theorem, see for example [2], the EE is LAS since all eigenvalues of the characteristic Eq. (A.1) have negative real parts. Summarizing the above analysis gives the following result.

Theorem 4.1. *For the ODE epidemiological model (4.2), the basic reproduction number $\mathcal{R}_0$ is given by (4.1). If $\mathcal{R}_0 < 1$, then the DFE is GAS; if $\mathcal{R}_0 > 1$, then the DFE becomes unstable and there exists a unique EE that is LAS.*

Numerical simulations, see for example Fig. 4.2, indicate that if $\mathcal{R}_0 > 1$, then the EE is in fact GAS.

4.2. Two groups with $P_i(t)$ a step function

When $P_i(t)$ is a step function, it has been shown in [3] that Hopf bifurcation can occur when $n = 1$, implying that the disease can appear periodically. It is natural to expect that the cyclic behavior is also possible when $n \geqslant 2$. Here we are interested in whether or not the group mixing affects this type of cyclic behavior. The two group model with a common constant period of immunity ω is given by (3.8) and (3.9) with $n = 2$. Since R_1 and R_2 do not appear in the S and I equations, we can consider the reduced system for $t \in (\omega,\infty)$

$$\begin{aligned} S_1'(t) &= -[\beta_{11}I_1(t) + \beta_{12}I_2(t)]S_1(t) + \gamma_1 I_1(t-\omega), \\ I_1'(t) &= [\beta_{11}I_1(t) + \beta_{12}I_2(t)]S_1(t) - \gamma_1 I_1(t), \\ S_2'(t) &= -[\beta_{21}I_1(t) + \beta_{22}I_2(t)]S_2(t) + \gamma_2 I_2(t-\omega), \\ I_2'(t) &= [\beta_{21}I_1(t) + \beta_{22}I_2(t)]S_2(t) - \gamma_2 I_2(t). \end{aligned} \tag{4.3}$$

By Theorem 3.2, Remark 3.2, and the continuous dependence of eigenvalues of the characteristic equation on the parameter ω, we have the following result.

Theorem 4.2. *For the DDE epidemiological model (4.3), if $\mathcal{R}_0 < 1$, then the DFE is GAS; if $\mathcal{R}_0 > 1$, then the DFE is unstable and there exists a unique EE, which is LAS for small ω.*

The stability of the EE in the case of $\omega > 0$ is not easy to determine, because it involves analyzing a quasi-polynomial of degree 4 in which the coefficients depend on the delay ω and the EE is not explicitly known. In the rest of this section, we numerically investigate the impact of the cross transmission on the disease dynamics in both groups. To this end, we vary β_{ij} for $i, j = 1, 2$ and fix the other parameters. We take $\omega = 60$ days (on average, a recovered individual has 60 days of temporary immunity upon recovery), $\gamma_1 = 0.1$ per day (average infectious period in group one is 10 days), $\gamma_2 = 0.05$ per day (average infectious period in group two is

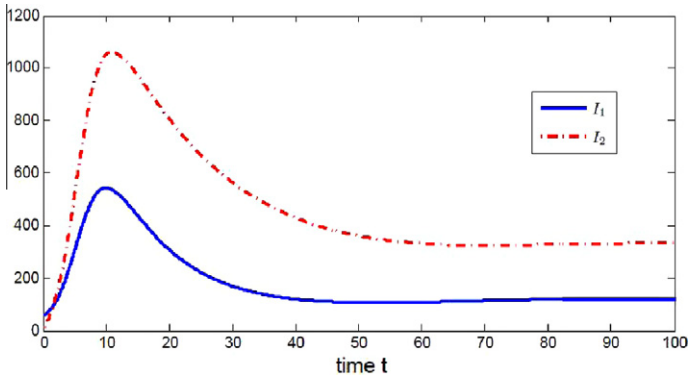

Fig. 4.2. Initial conditions: $S_1(0) = 950$, $I_1(0) = 50$, $R_1(0) = 0$ and $S_2(0) = 1495$, $I_2(0) = 5$, $R_2(0) = 0$; parameters: $\beta_{11} = 5 \times 10^{-4}$, $\beta_{22} = 1.0 \times 10^{-4}$, $\beta_{12} = 5 \times 10^{-5}$, $\beta_{21} = 5 \times 10^{-4}$, $\gamma_1 = 0.1$, $\gamma_2 = 0.05$, $\alpha_1 = \alpha_2 = 1/60$; $\mathcal{R}_0 \approx 6.92$: the EE is LAS.

20 days). We set as initial conditions $S_1(0) = 950$, $I_1(0) = 50$, $R_1(0) = 0$ and $S_2(0) = 1495$, $I_2(0) = 5$, $R_2(0) = 0$. Thus group one has a population of $N_1 = 1{,}000$; whereas group two has a population of $N_2 = 1{,}500$. Note that we assume individuals in different groups have different infectious periods, simulations show that the dynamics is very similar if we assume the same infectious period with $\gamma_1 = \gamma_2$.

We first choose $\beta_{11} = 1.5 \times 10^{-5}$ and $\beta_{22} = 1.0 \times 10^{-5}$, resulting in $\mathcal{R}_0^{(1)} = 0.15 < 1$ and $\mathcal{R}_0^{(2)} = 0.3 < 1$. Thus, in the absence of transmission between groups ($\beta_{12} = 0 = \beta_{21}$), the disease dies out in both groups, as demonstrated in Fig. 4.3. But disease may becomes endemic in both groups if there is cross transmission between the two groups. Fig. 4.4 corresponds to $\beta_{12} = 3 \times 10^{-4}$ and $\beta_{21} = 1 \times 10^{-4}$ giving $\mathcal{R}_0 \approx 3.23$; while Fig. 4.5 represents the simulations for $\beta_{12} = 3 \times 10^{-4}$ and $\beta_{21} = 5 \times 10^{-4}$ leading to $\mathcal{R}_0 \approx 6.93$. Notice that both Figs. 4.4 and 4.5 illustrate endemic disease, but the former shows convergence to the EE, whereas the latter shows convergence to a periodic solution implying that the disease will develop a periodic pattern in the long run. These simulation results show that the cross transmission not only can help an otherwise dying out disease to persist in both groups, but also can play a role in determining the patterns of persistence.

Next, we choose $\beta_{11} = 5 \times 10^{-4}$ giving $\mathcal{R}_0^{(1)} = 5 > 1$, and $\beta_{22} = 1.0 \times 10^{-4}$ giving $\mathcal{R}_0^{(2)} = 3 > 1$. Then, in the absence of cross transmission ($\beta_{12} = 0 = \beta_{21}$), $I_1(t)$ demonstrates periodic behavior (see Fig. 4.6 and [3, Fig. 2]) and $I_2(t)$ tends to a positive constant corresponding to the EE for this group (see Fig. 4.7). Interestingly, by simulations, we find that some appropriately chosen positive values of β_{12} and β_{21} may make the EE stable, while some other positive values of β_{12} and β_{21} may drive the EE unstable and lead to the periodic disease dynamics in both groups. For example, $\beta_{12} = 4 \times 10^{-4}$ and $\beta_{21} = 5 \times 10^{-5}$ (giving $\mathcal{R}_0 \approx 6.65$) result in a stable EE as is shown in Fig. 4.8; and $\beta_{12} = 5 \times 10^{-5}$, $\beta_{21} = 5 \times 10^{-4}$ (giving $\mathcal{R}_0 \approx 6.92$) result in an unstable EE and cause sustained oscillations in both groups, as is shown in Fig. 4.9.

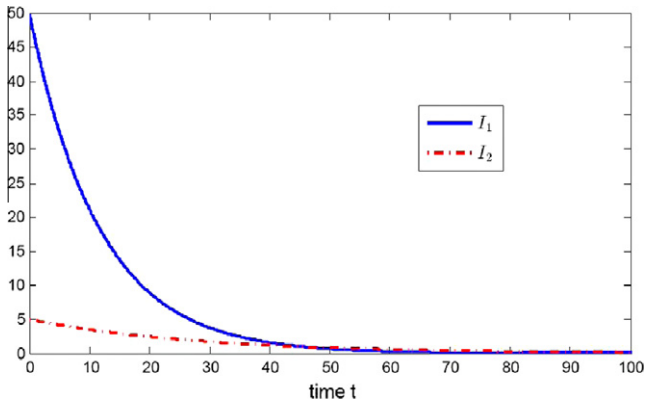

Fig. 4.3. $\beta_{11} = 1.5 \times 10^{-5}$, $\beta_{22} = 1.0 \times 10^{-5}$, $\beta_{12} = \beta_{21} = 0$, $\mathcal{R}_0^{(1)} = 0.15$, $\mathcal{R}_0^{(2)} = 0.3$: DFE is stable in isolated two groups.

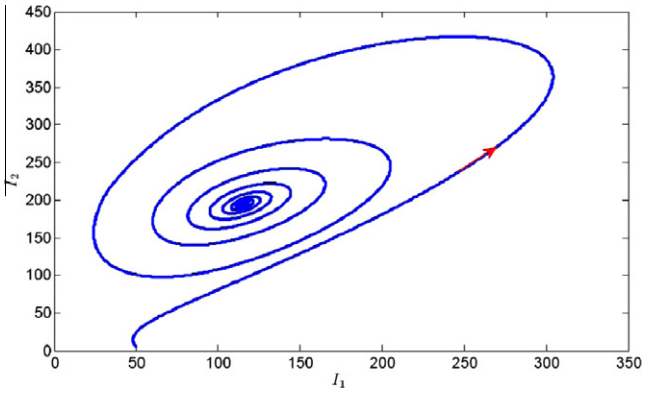

Fig. 4.4. $\beta_{11} = 1.5 \times 10^{-5}$, $\beta_{22} = 1.0 \times 10^{-5}$, $\beta_{12} = 3 \times 10^{-4}$, $\beta_{21} = 1 \times 10^{-4}$, $\mathcal{R}_0^{(1)} = 0.15 < 1$, $\mathcal{R}_0^{(2)} = 0.3 < 1$, $\mathcal{R}_0 \approx 3.23$: EE is stable.

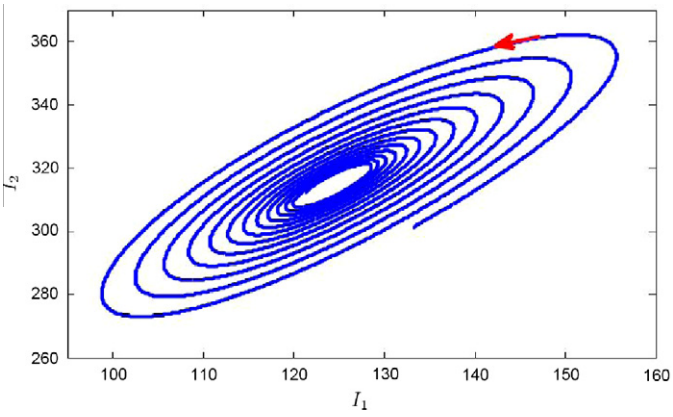

Fig. 4.5. $\beta_{11} = 1.5 \times 10^{-5}$, $\beta_{22} = 1.0 \times 10^{-5}$, $\beta_{12} = 3 \times 10^{-4}$, $\beta_{21} = 5 \times 10^{-4}$, $\mathcal{R}_0^{(1)} = 0.15 < 1$, $\mathcal{R}_0^{(2)} = 0.3 < 1$, $\mathcal{R}_0 \approx 6.93$: oscillations appear in two groups.

5. Discussion

Based on the work [3,5], we have proposed a general model, given by (1.5), for diseases that confer temporary immunity upon

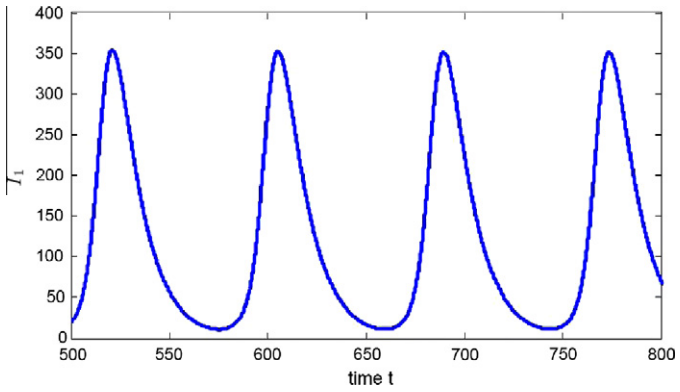

Fig. 4.6. $\beta_{11} = 5 \times 10^{-4}$, $\mathcal{R}_0^{(1)} = 5$: oscillations appear in isolated group one (transient oscillations are omitted).

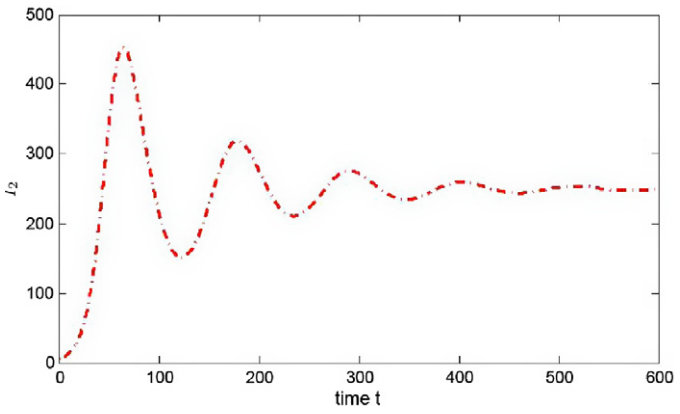

Fig. 4.7. $\beta_{22} = 1.0 \times 10^{-4}$, $\mathcal{R}_0^{(2)} = 3$: stable EE appears in isolated group two.

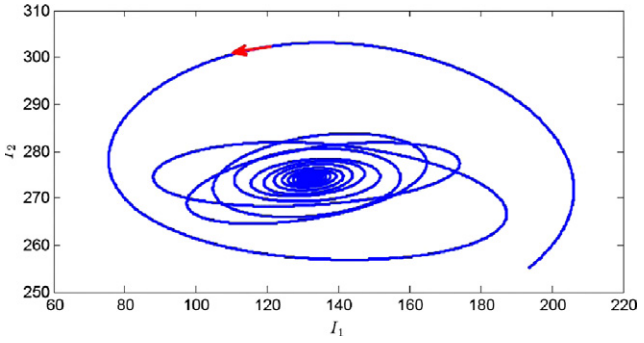

Fig. 4.8. $\beta_{11} = 5 \times 10^{-4}$, $\beta_{22} = 1.0 \times 10^{-4}$, $\beta_{12} = 4 \times 10^{-4}$, $\beta_{21} = 5 \times 10^{-5}$, $\mathcal{R}_0 \approx 6.65$: stable EE appears in two groups.

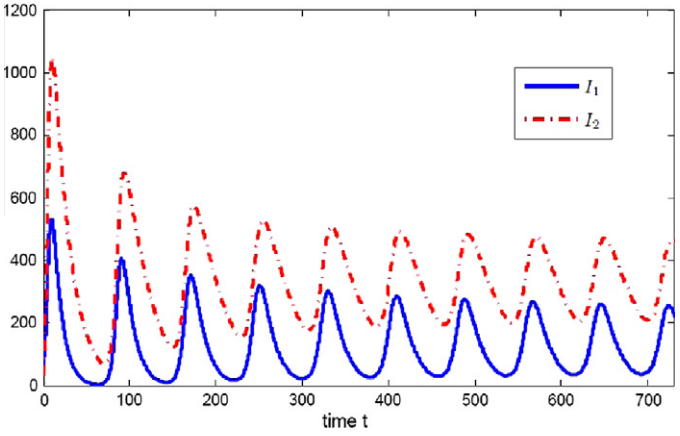

Fig. 4.9. $\beta_{11} = 5 \times 10^{-4}$, $\beta_{22} = 1.0 \times 10^{-4}$, $\beta_{12} = 5 \times 10^{-5}$, $\beta_{21} = 5 \times 10^{-4}$, $\mathcal{R}_0 \approx 6.92$: oscillations appear in two groups.

recovery and that spread in a heterogeneous host population. The model contains general distribution functions $P_i(t)$, $i = 1,2,\ldots,n$, which account for the probabilities that recovered individuals remain in the recovered class t time units after recovery. For this model, we have identified the basic reproduction number $\mathcal{R}_0$, and have shown that if $\mathcal{R}_0 < 1$, then the disease dies out in the sense that the DFE is GAS; and if $\mathcal{R}_0 > 1$, the DFE becomes unstable.

When $P_i(t)$, $i = 1,2,\ldots,n$, are negatively exponentially distributed functions, we have shown that the model allows a unique EE when $\mathcal{R}_0 > 1$. Stability of the EE is a difficult mathematical problem, and we obtained some results only for the two group case, for which we have shown that the EE is LAS. In this case, although the cross transmission rates do affect the value of the basic reproduction number $\mathcal{R}_0$, they do not cause sustained oscillations; see Fig. 4.2.

When $P_i(t)$, $i = 1,2,\ldots,n$, are the same step function, we have also proved that there is a unique EE when $\mathcal{R}_0 > 1$. The stability of the EE is much more difficult, even in the two group case. This forces us to seek numerical simulations, and the simulation results show a variety of possibilities. A comparison of Figs. 4.2 and 4.9, which have the same mean period of temporary immunity, the same disease parameters and $\mathcal{R}_0$, shows that the choice of distribution functions $P_i(t)$ influences the qualitative nature of the time evolution of the disease. The strengths of group mixing not only affect $\mathcal{R}_0$ and hence determine whether or not the disease becomes endemic, they also affect the patterns of disease persistence: they can prevent oscillations and they can also enhance oscillations, as observed in the simulations shown in Figs. 4.3–4.9. A similar variety of possibilities was found numerically by Brauer et al. [1, Section 5] in a two patch model. Theoretically identifying the ranges of the cross transmission rates for the above phenomena is an important but challenging mathematical problem.

Figs. 4.2 and 4.9 have demonstrated that different distribution functions may result in different outcomes. When the distribution functions are taken as step functions, simulations in Section 4.2 show that the impacts of the cross transmission on the disease dynamics can be complicated. We point out that such impacts depend on the magnitude of the delay. To see this, we keep all parameter values the same as in the simulation for Fig. 4.9 but reduce the value of ω from 60 to 30. Then, as can be seen from Fig. 5.10, the oscillations disappear. This shows that, besides the mixing pattern, the length of temporary immunity can also cause oscillatory behavior in disease dynamics. The simulation results in Figs. 4.9 and 5.10, together with Theorem 4.2, also suggest that when all other parameters are fixed, there is a critical value for $\omega = \omega_c$ (numerical simulations suggest that $\omega_c \approx 50$ for parameter values in Figs. 4.9 and 5.10) distinguishing stability ($0 \leqslant \omega < \omega_c$) and instability ($\omega > \omega_c$) of the EE. The value of ω_c could be obtained more accurately by Hopf bifurcation analysis, but would involve lengthy computations.

From the results on this general model and in terms of the perspective of controlling a disease, weakening or even cutting the mixing between groups is an effective measure. However, to reach conclusions for public health recommendations, a more detailed, specific model is required.

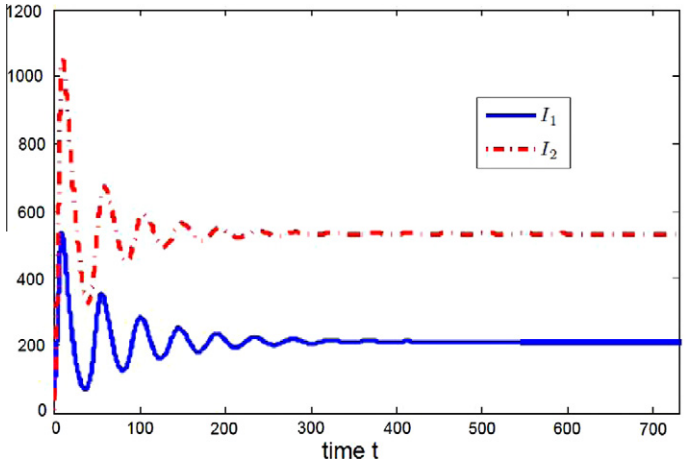

Fig. 5.10. $\omega = 30, \beta_{11} = 5 \times 10^{-4}, \beta_{22} = 1.0 \times 10^{-4}, \beta_{12} = 5 \times 10^{-5}, \beta_{21} = 5 \times 10^{-4}, \mathcal{R}_0 \approx 6.92$: oscillations disappear in both groups as ω is decreased from 60 in Fig. 4.9 to 30.

Acknowledgments

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Appendix A

To investigate the linear stability of the EE of (4.2), Let $b_1 = \beta_{11}I_1^* + \beta_{12}I_2^*, b_2 = \beta_{21}I_1^* + \beta_{22}I_2^*$, $c_1 = \beta_{12}S_1^*, c_2 = \beta_{21}S_2^*$ and $a_1 = \beta_{11}S_1^* - \gamma_1 - b_1$, $a_2 = \beta_{22}S_2^* - \gamma_2 - b_2$ and define $p := a_1a_2 - c_1c_2$. Using (3.5) with $n = 2$, it follows from $(\beta_{11}I_1^* + \beta_{12}I_2^*)S_1^* = \gamma_1 I_1^*$ that $\beta_{11}S_1^* - \gamma_1 = -\beta_{12}S_1^*\frac{I_2^*}{I_1^*} < 0$. Similarly, $\beta_{22}S_2^* - \gamma_2 = -\beta_{21}S_2^*\frac{I_1^*}{I_2^*} < 0$. This shows that $a_1 < 0$, $a_2 < 0$. Note that

$$\begin{aligned} p &= (\beta_{11}S_1^* - \gamma_1 - b_1)(\beta_{22}S_2^* - \gamma_2 - b_2) - \beta_{12}S_1^*\beta_{21}S_2^* \\ &= -(\beta_{11}S_1^* - \gamma_1)b_2 - (\beta_{22}S_2^*s - \gamma_2)b_1 + b_1b_2 > 0. \end{aligned}$$

Linearizing system (4.2) at the EE gives the characteristic equation

$$z^4 + Az^3 + Bz^2 + Cz + D = 0, \tag{A.1}$$

where

$$\begin{aligned} A &= \alpha_1 + \alpha_2 - (a_1 + a_2), \\ B &= p + b_1\gamma_1 + b_2\gamma_2 + \alpha_1\alpha_2 - (\alpha_1 + \alpha_2)(a_1 + a_2), \\ C &= (\alpha_1 + \alpha_2)p - \alpha_1\alpha_2(a_1 + a_2) + b_1\gamma_1(\alpha_2 - a_2) + b_2\gamma_2(\alpha_1 - a_1), \\ D &= b_1b_2\gamma_1\gamma_2 + \alpha_1\alpha_2p - b_1\gamma_1a_2\alpha_2 - b_2\gamma_2a_1\alpha_1. \end{aligned}$$

Note that $p > 0$ and $a_i < 0$, $\alpha_i > 0$, $\gamma_i > 0$ for $i = 1, 2$, implying

$$A > 0,\ B > 0,\ C > 0,\ D > 0.$$

Direct calculations show that

$$\begin{aligned} AB - C = &-(a_1 + a_2)p + b_1\gamma_1(\alpha_1 - a_1) + b_2\gamma_2(\alpha_2 - a_2) \\ &+ \alpha_1\alpha_2(\alpha_1 + \alpha_2) - (\alpha_1 + \alpha_2)(a_1 + a_2)A > 0 \end{aligned}$$

and

$$\begin{aligned} ABC - A^2D - C^2 = &-(\alpha_1 + \alpha_2)(a_1 + a_2)p^2 \\ &+ p[b_1\gamma_1((\alpha_1 + \alpha_2)(\alpha_1 - a_1) - (\alpha_2 - a_2)(a_1 + a_2)) \\ &+ b_2\gamma_2((\alpha_1 + \alpha_2)(\alpha_2 - a_2) - (\alpha_1 - a_1)(a_1 + a_2)) \\ &+ (\alpha_1 + \alpha_2)^2(a_1 + a_2)^2 \\ &- (\alpha_1 + \alpha_2)(\alpha_1^2 + \alpha_2^2)(a_1 + a_2)] \\ &+ (\alpha_1 - a_1)(\alpha_2 - a_2)(b_1\gamma_1 - b_2\gamma_2)^2 \\ &+ (\alpha_1 + \alpha_2)\alpha_1\alpha_2A(a_1 + a_2)^2 \\ &- (\alpha_1 + \alpha_2)\alpha_1^2\alpha_2^2(a_1 + a_2) \\ &+ b_1\gamma_1[A(\alpha_1a_1a_2 + \alpha_1a_2^2 - \alpha_2^2a_1 + \alpha_1\alpha_2^2) \\ &- 2\alpha_1\alpha_2(\alpha_1 - a_1)(a_1 + a_2)] \\ &+ b_2\gamma_2[A(\alpha_2a_1a_2 + \alpha_2a_1^2 - \alpha_1^2a_2 + \alpha_1^2\alpha_2) \\ &- 2\alpha_1\alpha_2(\alpha_2 - a_2)(a_1 + a_2)] > 0. \end{aligned}$$

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