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DIFFERENTIAL SUSCEPTIBILITY AND INFECTIVITY EPIDEMIC MODELS

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Abstract. We formulate differential susceptibility and differential infectivity models for disease transmission in this paper. The susceptibles are divided into n groups based on their susceptibilities, and the infectives are divided into m groups according to their infectivities. Both the standard incidence and the bilinear incidence are considered for different diseases. We obtain explicit formulas for the reproductive number. We define the reproductive number for each subgroup. Then the reproductive number for the entire population is a weighted average of those reproductive numbers for the subgroups. The formulas for the reproductive number are derived from the local stability of the infection-free equilibrium. We show that the infection-free equilibrium is globally stable as the reproductive number is less than one for the models with the bilinear incidence or with the standard incidence but no disease-induced death. We then show that if the reproductive number is greater than one, there exists a unique endemic equilibrium for these models. For the general cases of the models with the standard incidence and death, conditions are derived to ensure the uniqueness of the endemic equilibrium. We also provide numerical examples to demonstrate that the unique endemic equilibrium is asymptotically stable if it exists.

In honor of Professor Zhien Ma's 70th birthday

1. **Introduction.** Genetic variation of susceptible individuals may lead to their differentiation of susceptibility on infection. The efficacy of available vaccinations for infectious diseases, such as rubeola, more commonly known as the "red measles", and hepatitis B (HB), is not perfect. Vaccinated individuals may still contract the disease and the susceptibility varies from individual to individual [1, 2].

Through their surface expression of CD38, $CD4^+$ T cells have shown differential susceptibility to M- and T-tropic HIV-1 infection. The $CD4^+CD38^-$ and $CD4^+CD45RA^-$ subsets have higher susceptibility to infection with the M-tropic Ba-L strain of HIV-1, and the $CD4^+CD38^+$ subset has higher susceptibility to

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infection with the T-tropic (LAI) strain of HIV-1 [3]. For the spread of Chagas disease, uninfected individuals are found in all reported studies of endemic areas, and more than half of the variation in seropositivity is attributable to genetic factors, which influences the differential outcomes of T. *cruzi* infection [4, 5].

On the other hand, couples studies for HIV transmissions have found that some individuals transfer the infection to their sexual partners after only a few contacts, but other couples have had thousands of unprotected contacts without transferring infection [6–9]. A few epidemiological studies for small cohorts have found that a partner either transferred the virus early in the course of infection, or did not transferr at all [10]. Some researchers have found evidence for increased transmission late in infection [11, 12], although others have not [9, 10]. Sometimes late-stage transmission does not occur because of the increased use of protective methods among couples; however, late-stage transmission occurred infrequently in one study even when the use of protective methods was controlled for in the data analysis [9].

These couples studies support that there is variability in the infectivity among infected individuals, variability in the susceptibility of their partners, or both. The HIV-1 RNA data support the idea of variations in infectiousness and suggest that there may be orders of magnitude differences in the viral shedding rates both over time and between individuals.

In previous studies [13, 14], we separated the issues of differential susceptibility (DS) and differential infectivity (DI) by proposing different mathematical models to investigate each effect independently. We assumed differential susceptibilities of susceptibles but homogeneous infectivity of infectives in the DS model [14], and homogeneous susceptibility of susceptibles but differential infectivities of infectives in the DI model [13].

These studies provided insight into the transmission dynamics of diseases with differential susceptibility or differential infectivity but not both. For many disease transmissions, the susceptibility and infectivity factors are coupled and cannot be completely separated. Findings in the couples studies for HIV transmissions may be due to variability in both susceptibility and infectivity. To further understand these phenomena, we propose a combined differential susceptibility and differential infectivity (DSDI) model in this paper.

2. **The Model Formulation.**

We consider the spread of a disease in a randomly mixing population that approaches a steady state, S^0, if there is no disease infection. We assume that infected individuals become fully immune or are removed from the susceptible population after they recover from the infection. We approximate the transmission dynamics with an SIR (Susceptible $\rightarrow$ Infective $\rightarrow$ Recovered) model. We assume that susceptibles may have different susceptibility and divide them into n groups, $S_1, S_2, \ldots, S_n$. Here, the individuals in each group have homogeneous susceptibility, but the susceptibilities of individuals from different groups are distinct. The susceptibles are distributed into the n susceptible subgroups, based on their inherent susceptibility, in such a way that the input flow into group S_i is $p_i \mu S^0$ with $\sum_{i=1}^{n} p_i = 1$. The infectives are divided into m groups, $I_1, I_2, \ldots, I_m$, such that upon infection, a susceptible individual in group S_i enters group I_j with probability q_{ij} and stays in this group until becoming recovered or removed, where $\sum_{j=1}^{m} q_{ij} = 1$, for $i = 1, 2, \ldots, n$.

We assume full immunity of recovered individuals or complete isolation after individuals are infected and diagnosed, and we group all these individuals to group R. The transmission dynamics of infection are governed by the system of differential equations

$$\begin{aligned}\frac{dS_i}{dt} =&\mu(p_iS^0 - S_i) - \lambda_i S_i, \qquad i = 1, \dots, n,\\ \frac{dI_j}{dt} =&\sum_{i=1}^{n} q_{ij}\lambda_i S_i - (\mu + \nu_j)I_j, \qquad j = 1, \dots, m,\\ \frac{dR}{dt} =&\sum_{j=1}^{m} \nu_j I_j - (\mu + \delta)R,\end{aligned} \tag{2.1}$$

where μ is the natural death rate in the absence of infection, ν_j is the recovery rate for infectives in group I_j, and δ is the death rate of recovered or removed individuals. The rate of infection for susceptibles in group S_i is given by

$$\lambda_i = c(N)\sum_{j=1}^{m} \alpha_i\beta_j\frac{I_j}{N} = \frac{c(N)}{N}\alpha_i\sum_{j=1}^{m}\beta_j I_j, \tag{2.2}$$

where $c(N)$ is the average number of contacts per individual with $N = \sum_{i=1}^{n} S_i + \sum_{j=1}^{m} I_j + R$, α_i is the susceptibility of susceptible individuals in group S_i, and β_j is the infectiousness of infected individuals in group I_j.

As was pointed out in [14–16], the number of contacts per person, in general, is a function of the population size. The choice of the function $c(N)$ depends on the modeled disease or situations investigated. For certain diseases, such as influenza and measles, or in certain ranges of population sizes, it is appropriate to assume that the number of contacts is proportional to the population size. Let $C(N) := c_0N$ in this case. Then the rate of infection in group S_i has a bilinear form given by

$$\lambda_i = c_0\alpha_i\sum_{j=1}^{m}\beta_j I_j. \tag{2.3}$$

For some other diseases, such as sexually transmitted diseases, or in different situations where contacts are saturated, the number of contacts are approximately constant. If we write $c(N) := r$, then the rate of infection in group S_i has a standard form given by

$$\lambda_i = \frac{r\alpha_i}{N}\sum_{j=1}^{m}\beta_j I_j. \tag{2.4}$$

3. **The Reproductive Number and Global Stability of the Infection-free Equilibrium.**

A key character in classic epidemiological models is the reproductive number, denoted by R_0, such that if $R_0 \le 1$, the modeled disease dies out, and if $R_0 > 1$, the disease spreads. The reproductive number is usually defined by the spectral radius of the next-generation operator [17–20]. It can also be determined by the local stability of the infection-free equilibrium, that is, the dominant eigenvalue of the Jacobian matrix at the infection-free equilibrium for models in a finite dimensional space [21, 22].

3.1. **The Reproductive Number.** We derive an explicit formula for R_0 by investigating the local stability of the infection-free equilibrium as follows.

Define $I := (I_1, \ldots, I_m)^T$, and note that the partial derivatives of λ_i with respect to I_j at the infection-free equilibrium with $I = 0$ and $R = 0$, are

$$\left.\frac{\partial \lambda_i}{\partial I_j}\right|_{(I,R)=(0,0)} = \frac{c(S^0)}{S^0}\alpha_i\beta_j, \qquad i = 1, \ldots, n, \quad j = 1, \cdot, m.$$

Then the Jacobian at the infection-free equilibrium for model (2.1), with the standard or bilinear incidence, has the form

$$D = \begin{pmatrix} D_{11} & \cdot & 0 \\ 0 & D_{22} & 0 \\ 0 & \cdot & -(\mu+\delta) \end{pmatrix}, \tag{3.1}$$

where

$$D_{11} = \operatorname{diag}(-\mu, \ldots, -\mu)$$

and

$$D_{22} = \begin{pmatrix} -\sigma_1 + L_1\beta_1 & L_1\beta_2 & \ldots & L_1\beta_m \\ L_2\beta_1 & -\sigma_2 + L_2\beta_2 & \ldots & L_2\beta_m \\ \vdots & \vdots & \ddots & \vdots \\ L_m\beta_1 & L_m\beta_2 & \ldots & -\sigma_m + L_m\beta_m \end{pmatrix}. \tag{3.2}$$

Here we define $\sigma_j := \mu + \nu_j$, and $L_j = c(S^0)\sum_{i=1}^{n} q_{ij}\alpha_i p_i, j = 1, \ldots, m$. Then the local stability of the infection-free equilibrium is determined by D_{22}.

Consider matrix $-D_{22}$. It has all off-diagonal elements negative. Let $V := (L_1/\sigma_1, \ldots, L_m/\sigma_m)^T$, then

$$-D_{22}\, V = \left(1 - \sum_{j=1}^{m} \frac{L_j\beta_j}{\sigma_j}\right) (L_1, \ldots, L_m)^T.$$

Since $L_j > 0$, $j = 1, \ldots, m$, if we define $R_0 := \sum_{j=1}^{m} \frac{L_j\beta_j}{\sigma_j}$, then it follows from M-matrix theory that each eigenvalue of D_{22} has negative real part, and hence the infection-free equilibrium is locally asymptotically stable if $R_0 < 1$.

By mathematical induction, we can show that

$$\det D_{22} = (-1)^{m+1} \prod_{j=1}^{m} \sigma_j (R_0 - 1).$$

Then if $R_0 > 1$, D_{22} has at least one positive eigenvalue. Hence, the reproductive number for model (2.1) can be defined by R_0, which is expressed as

$$R_0 = \sum_{j=1}^{m} \frac{c(S^0)\left(\sum_{i=1}^{n} q_{ij}\alpha_i p_i\right)\beta_j}{\mu + \nu_j} = \sum_{i=1}^{n} p_i c(S^0)\alpha_i \sum_{j=1}^{m} \frac{q_{ij}\beta_j}{\mu + \nu_j}. \tag{3.3}$$

In particular, the reproductive number for model (2.1) with the bilinear incidence is

$$R_0 = \sum_{i=1}^{n} p_i c_0 S^0 \alpha_i \sum_{j=1}^{m} \frac{q_{ij}\beta_j}{\mu + \nu_j} \tag{3.4}$$

and with the standard incidence is

$$R_0 = \sum_{i=1}^{n} p_i r \alpha_i \sum_{j=1}^{m} \frac{q_{ij}\beta_j}{\mu + \nu_j}. \tag{3.5}$$

In summary, we have the following theorem.

Theorem 3.1. *Define the reproductive number of infection, R_0, for model* (2.1) *by* (3.3). *Then the infection-free equilibrium is locally asymptotically stable if $R_0 < 1$, and unstable if $R_0 > 1$.*

Notice that $1/(\mu+\nu_j)$ is the duration of infection of infectives in group I_j. Then

$$\sum_{j=1}^{m} \frac{q_{ij}}{\mu + \nu_j} := \bar{\tau}_i$$

is the mean duration of infection from all infectives to susceptibles in group S_i, and

$$\alpha_i \frac{1}{\bar{\tau}_i} \sum_{j=1}^{m} \frac{q_{ij}\beta_j}{\mu + \nu_j} := \bar{\beta}_i$$

is the mean transmission probability from all infectives to susceptibles in group S_i [13, 14].

Define the reproductive number of infection in the susceptible group S_i from all infectives to be

$$R_{0i} = c(S^0)\bar{\beta}_i \bar{\tau}_i,$$

for the standard and bilinear incidence models. Then the reproductive number for the entire population can be expressed as the weighted average of those group reproductive numbers such that

$$R_0 = \sum_{i=1}^{n} p_i R_{0i}. \tag{3.6}$$

3.2. **Global Stability of the Infection-free Equilibrium.** As $R_0 < 1$, we have shown the local stability of the infection-free equilibrium. Now we show that the infection-free equilibrium is also globally asymptotically stable if $R_0 < 1$ for the bilinear incidence case and for the case where the incidence is standard, but there is no disease-induced death. Therefore, the possibility of a backward bifurcation from the infection-free equilibrium in these cases is excluded.

Since the total population satisfies the equation

$$\frac{dN}{dt} = \mu S^0 - \mu N - \delta R,$$

we have $0 \le N \le S^0$. Let $S := (S_1, \ldots, S_n)^T$ and define the region $G := \{(S, I, R) \,|\, 0 \le N \le S^0\}$. Then G is a positively time-invariant set for system (2.1).

Moreover, it follows from (2.1) that

$$\frac{dS_i}{dt} \le \mu(p_i S^0 - S_i), \qquad i = 1, \ldots, n,$$

in set G. Since the solutions of the equations

$$\frac{dS_i}{dt} = \mu(p_i S^0 - S_i), \qquad i = 1, \ldots, n,$$

approach $p_i S^0$, by the comparison principle we have

$$S_i(t) \le p_i S^0 \tag{3.7}$$

in set G.

3.2.1. *The Bilinear Incidence Case.* Assume the infection rate follows the bilinear incidence. Define vectors $P := (p_1, \ldots, p_n)^T$ and $B := (\beta_1, \ldots, \beta_m)^T$, and define matrices $A := \text{diag}(\alpha_1, \ldots, \alpha_n)$, $D := \text{diag}(\sigma_1, \ldots, \sigma_m)$, and

$$Q := \begin{pmatrix} q_{11} & q_{12} & \cdots & q_{1m} \\ q_{21} & q_{22} & \cdots & q_{2m} \\ \vdots & \vdots & \ddots & \vdots \\ q_{n1} & q_{n2} & \cdots & q_{nm} \end{pmatrix}.$$

Then system (2.1), in the bilinear incidence case, can be written as

$$\begin{aligned} \frac{dS}{dt} =& \mu(S^0 P - S) - c_0 B^T I A S, \\ \frac{dI}{dt} =& c_0 B^T I Q^T A S - D I, \\ \frac{dR}{dt} =& v I - (\mu + \delta) R, \end{aligned} \tag{3.8}$$

where $v := (\nu_1, \ldots, \nu_n)^T$, and the reproductive number in (3.4) can be expressed as

$$R_0 = c_0 S^0 B^T D^{-1} Q^T A P. \tag{3.9}$$

Define function $V = B^T D^{-1} I$ for $I_j \geq 0$. Then V is positive definite. It follows from (3.8) that

$$\begin{aligned} \frac{dV}{dt} =& B^T D^{-1} \left(c_0 B^T I Q^T A S - D I \right) = c_0 B^T D^{-1} Q^T A S B^T I - B^T I \\ \leq& c_0 S^0 B^T D^{-1} Q^T A P B^T I - B^T I = (R_0 - 1) B^T I. \end{aligned} \tag{3.10}$$

Then $dV/dt \leq 0$ for t sufficiently large, if $R_0 < 1$. Notice that $dV/dt = 0$ only if $I = 0$. Hence the infection-free equilibrium is the only point in the set $\{(S, I, R) \mid dV/dt = 0\}$. Therefore, by Liapunov stability theory, the infection-free equilibrium is globally asymptotically stable for the bilinear incidence case.

Theorem 3.2. *The infection-free equilibrium of system* (2.1) *with bilinear incidence is always globally asymptotically stable if* $R_0 < 1$.

3.2.2. *The Standard Incidence Case without Disease-Induced Death.* We assume that the incidence of infection has the standard form. By using the matrix notation, the equation for the infectives has the form

$$\frac{dI}{dt} = \frac{r}{N} Q^T A S B^T I - D I.$$

It follows from

$$\frac{dN}{dt} = \mu S^0 - \mu N - \delta R > \mu S^0 - (\mu + \delta) N$$

that

$$N \geq \frac{\mu S^0}{\mu + \delta},$$

in set G, again from the comparison principle. Then the infection rate satisfies

$$\lambda_i = \frac{r \alpha_i}{S^0} \sum_{j=1}^{m} \beta_j I_j \leq \frac{(\mu + \delta) r \alpha_i}{\mu S^0} B^T I. \tag{3.11}$$

Using the same Liapunov function $V = B^T D^{-1} I$ and inequalities (3.7) and (3.11), we have

$$\begin{aligned}\frac{dV}{dt} =& B^T D^{-1}\left(\frac{r}{N} B^T I Q^T A S - D I\right)\\ \leq& \frac{(\mu+\delta)}{\mu} r B^T D^{-1} Q^T A P B^T I - B^T I = \left(\frac{\mu+\delta}{\mu} R_0 - 1\right) B^T I.\end{aligned} \tag{3.12}$$

Then, it follows again from Liapunov stability theory that the infection-free equilibrium is globally asymptotically stable if

$$R_0 \leq \frac{\mu}{\mu+\delta} \leq 1. \tag{3.13}$$

Here we use the fact that if $dV/dt = 0$, then since all the components of A, B, D, and Q are nonnegative, the omega-set of system (2.1) in this case contains only the infection-free equilibrium, which implies its global asymptotic stability.

In summary we have the following theorem.

Theorem 3.3. *The infection-free equilibrium of system* (2.1) *with standard incidence is globally asymptotically stable if* $R_0 < \dfrac{\mu}{\mu+\delta} \leq 1$.

As was discussed in section 2, the disease-induced death can be relatively small for some diseases, and then δ is eligible. In those cases, the infection-free equilibrium is globally asymptotically stable if $R_0 < 1$.

4. **Endemic Equilibrium.** We have shown in section 3 that if $R_0 > 1$, the infection-free equilibrium is unstable, and then the disease spreads if a small infection is introduced into the population. Now we assume $R_0 > 1$ and show that there exists an endemic equilibrium all of whose components are positive.

For system (2.1), an endemic equilibrium needs to satisfy the equations

$$\begin{aligned}&\mu(p_i S^0 - S_i) - \lambda_i S_i = 0, \qquad i = 1, \ldots, n,\\ &\sum_{i=1}^{n} q_{ij}\lambda_i S_i - (\mu+\nu_j) I_j = 0, \qquad j = 1, \ldots, m,\\ &\sum_{j=1}^{m} \nu_j I_j = (\mu+\delta) R.\end{aligned} \tag{4.1}$$

We first assume that the infection follows bilinear incidence. Then we let $W := c_0 \sum_{j=1}^{m} \beta_j I_j$, such that $\lambda_i = W\alpha_i$. Solving (4.1) for S_i and then for I_i yields

$$\begin{aligned}S_i =& \frac{\mu p_i S^0}{\mu + \alpha_i W}, \qquad i = 1, \ldots, n,\\ I_j =& \frac{\mu W S^0}{\sigma_j} \sum_{i=1}^{n} \frac{q_{ij}\alpha_i p_i}{\mu + \alpha_i W}, \qquad j = 1, \ldots, m.\end{aligned} \tag{4.2}$$

Hence

$$W = c_0 \sum_{j=1}^{m} \beta_j I_j = c_0 \mu W S^0 \sum_{j=1}^{m}\sum_{i=1}^{n} \frac{\beta_j q_{ij}\alpha_i p_i}{\sigma_j(\mu + \alpha_i W)}.$$

Define

$$H_1(W) := c_0 \mu S^0 \sum_{j=1}^{m}\sum_{i=1}^{n} \frac{\beta_j q_{ij}\alpha_i p_i}{\sigma_j(\mu + \alpha_i W)} - 1.$$

Then there exists an endemic equilibrium for system (2.1) with bilinear incidence if and only if there exists a positive root for $H_1(W) = 0$.

Note that

$$H_1'(W) = -c_0\mu S^0 \sum_{j=1}^{m}\sum_{i=1}^{n} \frac{\beta_j q_{ij}\alpha_i^2 p_i}{\sigma_j(\mu+\alpha_i W)^2} < 0,$$

$\lim_{W\to\infty} H_1(W) = -1$, and

$$H_1(0) = R_0 - 1.$$

Hence there exists a unique endemic equilibrium if and only if $R_0 > 1$.

We then assume that the infection follows standard incidence. By letting $W = \frac{r}{N}\sum_{j=1}^{m}\beta_j I_j$, components S_i and I_j are still given by formulas (4.2), and component R satisfies

$$R = \frac{1}{\mu+\delta}\sum_{j=1}^{m}\nu_j I_j = \frac{\mu W S^0}{\mu+\delta}\sum_{j=1}^{m}\frac{\nu_j}{\sigma_j}\sum_{i=1}^{n}\frac{q_{ij}\alpha_i p_i}{\mu+\alpha_i W}, \tag{4.3}$$

at an endemic equilibrium. Hence we have

$$N = S^0 - \frac{\delta}{\mu}R = S^0\left(1 - \frac{\delta W}{\mu+\delta}\sum_{j=1}^{m}\frac{\nu_j}{\sigma_j}\sum_{i=1}^{n}\frac{q_{ij}\alpha_i p_i}{\mu+\alpha_i W}\right). \tag{4.4}$$

Substituting (4.2) and (4.4) into $W = \frac{r}{N}\sum_{j=1}^{m}\beta_j I_j$, we have

$$r\mu W S^0 \sum_{j=1}^{m}\sum_{i=1}^{n}\frac{\beta_j q_{ij}\alpha_i p_i}{\sigma_j(\mu+\alpha_i W)} = W S^0\left(1 - \frac{\delta W}{\mu+\delta}\sum_{j=1}^{m}\frac{\nu_j}{\sigma_j}\sum_{i=1}^{n}\frac{q_{ij}\alpha_i p_i}{\mu+\alpha_i W}\right).$$

Define function $H_2(W)$ by

$$\begin{aligned} H_2(W) :=& r\mu\sum_{j=1}^{m}\sum_{i=1}^{n}\frac{q_{ij}\alpha_i p_i\beta_j}{\sigma_j(\mu+\alpha_i W)} + \frac{\delta}{\mu+\delta}\sum_{j=1}^{m}\sum_{i=1}^{n}\frac{\nu_j q_{ij}\alpha_i p_i W}{\sigma_j(\mu+\alpha_i W)} - 1 \\ =& \sum_{i=1}^{n}\frac{\mu p_i}{\mu+\alpha_i W}\left(R_{0i} + \frac{\delta\alpha_i}{\mu(\mu+\delta)}\sum_{j=1}^{m}\frac{q_{ij}\nu_j}{\sigma_j}W\right) - 1. \end{aligned} \tag{4.5}$$

Then, there exists a positive endemic equilibrium if and only if there exists a positive solution to $H_2(W) = 0$.

Since $H_2(0) = \sum_{i=1}^{n} p_i R_{0i} - 1 = R_0 - 1$, and

$$\lim_{W\to\infty} H_2(W) = \sum_{i=1}^{n}\frac{\delta p_i}{\mu+\delta}\sum_{j=1}^{m}\frac{q_{ij}\nu_j}{\mu+\nu_j} - 1 < \sum_{i=1}^{n} p_i\sum_{j=1}^{m} q_{ij} - 1 = 0,$$

there exists at least one positive solution of $H_2(W) = 0$, that is, an endemic equilibrium of system (2.1), if $R_0 > 1$.

Simple calculation shows that

$$\begin{aligned} H_2'(W) &= -\sum_{i=1}^{n} \frac{\mu p_i \alpha_i}{(\mu+\alpha_i W)^2} \left(R_{0i} + \frac{\delta \alpha_i}{\mu(\mu+\delta)} \sum_{j=1}^{m} \frac{q_{ij}\nu_j}{\sigma_j} \left(W - \frac{\mu+\alpha_i W}{\alpha_i} \right) \right) \\ &= -\sum_{i=1}^{n} \frac{\mu p_i \alpha_i}{(\mu+\alpha_i W)^2} \left(R_{0i} - \frac{\delta}{\mu+\delta} \sum_{j=1}^{m} \frac{q_{ij}\nu_j}{\sigma_j} \right) \\ &= -\sum_{i=1}^{n} \frac{\mu p_i \alpha_i}{(\mu+\alpha_i W)^2} \sum_{j=1}^{m} \frac{q_{ij}}{\sigma_j} \left(r\alpha_i\beta_j - \frac{\delta\nu_j}{\mu+\delta} \right). \end{aligned} \tag{4.6}$$

For the case of no disease-induced death, $\delta = 0$. Then $H_2'(W) < 0$ for all $W \geq 0$. Hence the endemic equilibrium is unique. If $\delta > 0$, we notice that

$$\frac{\delta}{\mu+\delta} \sum_{j=1}^{m} \frac{q_{ij}\nu_j}{\sigma_j} = \frac{\delta}{\mu+\delta} \sum_{j=1}^{m} \frac{q_{ij}\nu_j}{\mu+\nu_j} < 1.$$

Then if $R_{0i} > 1$ for all $i = 1, \ldots, n$, $H_2'(W) < 0$ for all $W \geq 0$. Or if $r\alpha_i\beta_j > (\delta\nu_j)/(\mu+\delta)$, for all $i = 1, \ldots, n$, and $j = 1, \ldots, m$, $H_2'(W) < 0$ for all $W \geq 0$. Then we obtain the uniqueness of the endemic equilibrium. We summarize these results as follows.

Theorem 4.1. *There exists a unique endemic equilibrium, all of whose components are positive, for system* (2.1) *with bilinear incidence or with standard incidence and no disease-induced death if* $R_0 > 1$. *For system* (2.1) *with standard incidence and disease-induced death, if* (a) $R_{0i} > 1$ *for* $i = 1, \ldots, n$, *or* (b) $r\alpha_i\beta_j > (\delta\nu_j)/(\mu+\delta)$, *for* $i = 1, \ldots, n$, *and* $j = 1, \ldots, m$, *then there exists a unique endemic equilibrium as* $R_0 > 1$.

Remark. Condition (a) in Theorem 4.1 is a strong condition. There could be many groups with $R_{0i} \leq 1$, but we still have $R_0 > 1$. Condition (b) is much weaker. Suppose condition (b) holds. Then

$$R_{0i} = r\alpha_i \sum_{j=1}^{m} \frac{q_{ij}\beta_j}{\mu+\nu_j} > \frac{\delta}{\mu+\delta} \sum_{j=1}^{m} \frac{\nu_j}{\mu+\nu_j}.$$

Notice that $\sum_{j=1}^{m} q_{ij} = 1$. The qualities $\delta/(\mu+\delta)\sum_{j=1}^{m} \nu_j/(\mu+\nu_j)$ can be very small.

The stability analysis for the endemic equilibrium seems analytically untractable, but we believe that the unique endemic equilibrium is asymptotically stable. We provide a numerical example below to show that solutions approach a unique endemic equilibrium asymptotically.

Example 1. We assume there are four groups of susceptibles and four groups of infectives with standard incidence of infection. That is, our model equations are based on (2.1) with the infection rate given by (2.4). We assume that the natural death $\mu = 0.012$; the death rate of recovered individuals $\delta = 0.05$; the average number of contacts $r = 25$; the fractions of input flow into susceptible groups are $p_1 = 0.3$, $p_2 = 0.1$, $p_3 = 0.5$, and $p_4 = 0.1$; the recovery rates for infectives in the four groups are $\nu_1 = 0.5$, $\nu_2 = 0.6$, $\nu_3 = 0.5$, and $\nu_4 = 0.4$; the susceptibilities for the four susceptible groups are $\alpha_1 = 0.2$, $\alpha_2 = 0.05$, $\alpha_3 = 0.1$, and $\alpha_4 = 0.35$; and

the infectivities of the four infective groups are $\beta_1 = 0.3$, $\beta_2 = 0.25$, $\beta_3 = 0.15$, and $\beta_4 = 0.07$. We use the following probabilities, q_{ij}, for susceptibles entering the infective groups:

$$\begin{array}{llll} q_{11} = 0.3, & q_{12} = 0.2, & q_{13} = 0.4, & q_{14} = 0.1, \\ q_{21} = 0.2, & q_{22} = 0.15, & q_{23} = 0.4, & q_{24} = 0.25, \\ q_{31} = 0.1, & q_{32} = 0.1, & q_{33} = 0.3, & q_{34} = 0.5, \\ q_{41} = 0.3, & q_{42} = 0.3, & q_{43} = 0.1, & q_{44} = 0.3. \end{array}$$

The reproductive numbers for the four infective groups are

$$R_{01} = 1.9583, \quad R_{02} = 0.4227, \quad R_{03} = 0.6807, \quad R_{04} = 3.3127.$$

Hence the reproductive number for the entire population is $R_0 = 1.3014$, and there exists a unique endemic equilibrium given by

$$\begin{array}{lllll} S_1 = 0.1960, & S_2 = 0.1005, & S_3 = 0.4007, & S_4 = 0.0510, & \\ I_1 = 0.0029, & I_2 = 0.0019, & I_3 = 0.0041, & I_4 = 0.0049, & R = 0.1063. \end{array}$$

This unique endemic equilibrium is asymptotically stable. With various initial sizes for the susceptible, infective, and removed groups, susceptibles and infectives approach this endemic equilibrium asymptotically. The numerical simulations with initial sizes $(1, 1, 1, 1, 0.1, 0.1, 0.1, 0.1, 0)$ and $(0.5, 0.5, 0.5, 0.17, 0.17, 0.17, 0.17, 0.17, 0.5)$ are illustrated in Figure 1 where only infectives are shown. While early temporal oscillations are exhibited, solutions approach the endemic equilibrium eventually.

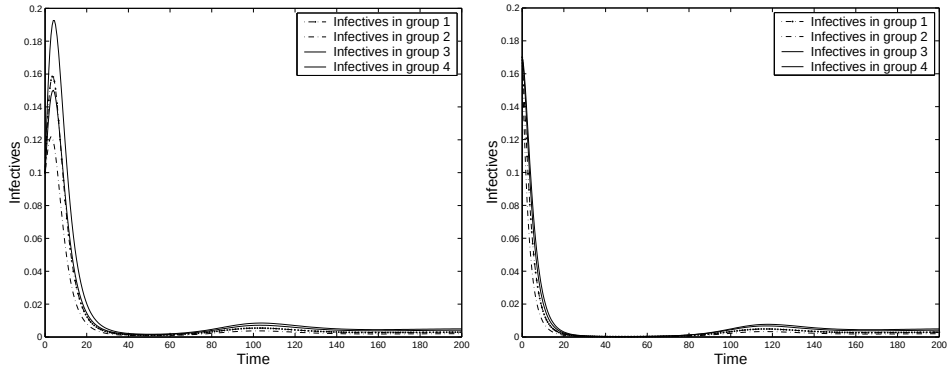

FIGURE 4.1. The model parameters are given in Example 1. Only infectives are shown in these figures. Initial sizes for the left- and right-hand figures are $(1, 1, 1, 1, 0.1, 0.1, 0.1, 0.1, 0)$ and $(0.5, 0.5, 0.5, 0.17, 0.17, 0.17, 0.17, 0.17, 0.5)$, respectively. While there are early temporal oscillations, the susceptible, infectives, and removeds asymptotically approach the unique endemic equilibrium, the values of whose components are given in Example 1.

5. **Concluding Remarks.** We have formulated compartmental differential susceptibility and differential models in various settings. The susceptibles and infectives are divided into n and m subgroups based on their susceptibilities and infectivities, respectively. We considered the situations where the number of contacts is either proportional to the total population size or a constant. We then

considered the cases where the disease-induced mortality is negligible or needs to be included.

We derived an explicit formula for the reproductive number, R_0, for all models. We then showed that the infection-free equilibrium, whose component of infectives is zero, is globally asymptotically stable if $R_0 < 1$ and is unstable if $R_0 > 1$ for the models with bilinear incidence of infection or for the models with standard incidence of infection but with no disease-induced mortality.

If $R_0 > 1$, we further proved that there exists a unique endemic equilibrium with all components positive for the models with bilinear incidence. For the models with standard incidence, we showed that there exists at least one endemic equilibrium and obtained sufficient conditions under which the endemic equilibrium is unique.

The transmission dynamics of the DSDI models 2.1 are similar to the dynamics of the DS models studied in [14]. Neither backward bifurcation nor multiple endemic equilibria appear.

Similarly as in [14], the explicit formulas of R_0 for the models in this paper fit well in the calculations of R_0 for a variety of epidemiological models in the literature [19, 22–24]. That is, the reproductive number for each subgroup, R_{0i}, is defined as a product of the mean number of contacts, the mean infectivity, and the mean duration of infection. Then, the reproductive number for the whole population, R_0, is defined as a weighted average of those R_{0i}, weighted by the distribution of the influx into the susceptible subgroups.

The DSDI models can be also applied to predation interaction with either the principle of mass action or ratio dependence. The n susceptible subgroups can be used for n prey populations, and the m infective subgroups can be used for m predator populations [14].

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