POPULATION DYNAMICS MODELS ON THE RELATION OF SOCIAL NATURE TO THE EPIDEMICS

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DECLARATION

I, Ying Xie, declare that this thesis titled, "Population dynamics models on the relation of social nature to the epidemics " and the work presented in it are my own. I confirm that:

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- Where any part of this thesis has previously been submitted for a degree or any other qualification at this University or any other institution, this has been clearly stated.
- Where I have consulted the published work of others, this is always clearly attributed.
- Where I have quoted from the work of others, the source is always given. With the exception of such quotations, this thesis is entirely my own work.
- I have acknowledged all main sources of help.
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Ying Xie
Sendai, March 2024

SUMMARY

Social nature could have a significant influence on the patterns and trends in the spread of infectious disease. Although it is difficult to quantify the social characteristics, mathematical models have become useful tools for understanding the relation of social nature to disease transmission. In this work, we consider three mathematical models incorporating social nature from the aspects of social response, community's policy, and detectability of the disease infection, respectively. The analysis of the model with the incorporation of social response, especially assuming that the infection rate is affected by such a response to the disease spread, shows that the social response could become a cause of recurring outbreaks whilst it must suppress the prevalence. From the model on the spread of a reinfectious disease in a community with the acceptance of visitors, particularly under the assumption that a certain proportion of visitors are immune, we find that the acceptance of visitors could have a significant influence on the disease's endemicity in the community, either suppressive or supportive. Furthermore, we consider a mathematical model on the disease spread by multiple strains with a competitive dominance, assuming the superinfection occurs when a more dominant strain takes over a host infected by a less dominant strain. This model shows that, strains could coexist with the existence of superinfection. Otherwise, the disease becomes eliminated or alternatively the endemic state arises with only the strain which has the largest strain-specific basic reproduction number while all the other strains get eliminated. Such theoretical/mathematical researches could provide better understanding of the complex interplay between social nature and the disease transmission.

Keywords: Epidemic dynamics, Social response, Public health, Recurring outbreaks, Reinfection, Multiple strains, Superinfection, Ordinary differential equations

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CONTENTS

1 INTRODUCTION

1.1 CHARACTERISTICS OF INFECTIOUS DISEASE SPREAD

1.1.1 *Recurring epidemic outbreaks*

Recurring outbreaks of transmissible diseases such as measles, chickenpox, mumps, and COVID-19 have been observed in our epidemic history[1–6]. Such recurring outbreaks could have a significant impact on the society, including people's mental health, public health care costs, economies, and development[7,8]. Observed in the Hong Kong influenza data and other related data, the influenza could show both seasonally periodic and non-periodic outbreaks[9]. Not only by the seasonal variation of temperature, humidity, and resource availability, such a seasonality of epidemic outbreak could be caused also by a seasonal change in people's social behavior and contact rate[10–13]. It has been indicated that the oscillation in epidemic dynamics could be induced by the feedback of the social behavior such as the ignorance when the disease prevalence decreases and the enforcement of containment measurements when the prevalence becomes cautious[14–19].

1.1.2 *Reinfectivity*

The reinfectivity of disease in this paper means that the immunity gained by either vaccination or recovery is imperfect. For a spreading transmissible disease accompanied with a reinfectivity, the acceptance of visitors must influence the endemicity of such a disease in the community. Then the community's policy must take account of the risk of reinfection for both residents and visitors. Actually there are transmissible diseases with a reinfectivity, including influenza[20–24], pertussis[25,26], Lyme disease[27], hand, foot and mouth disease[28], malaria[29,30], tuberculosis[31–33], Ebola virus disease[34,35], chronic lung diseases[36], invasive pneumococcal disease[37], meningococcal disease[38], and COVID-19[39–47], although the reinfectivity has been still requiring scientific researches to understand its kinetics and other nature.

1.1.3 *Superinfection*

Competition within a host individual for the limited resources between strains from the same species or from different species has been found in various transmissible diseases[48,49]. Gupta *et al.*[50] considered the competition between antigenically diverse strains through cross-reacting host immune response, a form of apparent competition, and showed that the competition for nonimmune hosts can shape the frequencies of strains. Le *et al.*[51] analyzed a coinfection system with n strains from the strains characteristics including transmissibility, clearance rates of single infection and coinfection, and transmission probability from mixed coinfection. Both of Gupta *et al.*[50] and Le *et al.*[51] excluded the possibility of superinfection and focused on coinfection models which assume that hosts can be infected by multiple strains simultaneously.

Superinfection implies a two-step process: a host individual previously infected by one strain becomes infected with another strain, after a time t, the second strain takes over the infected individual. Such a "takeover" of hosts by the second strain is assumed to be immediate[52]. Different from the concept of coinfection with multiple strains, superinfection refers to the infection with only one strain at a time or the coexistence duration of two strains is relatively short and one of them is instantaneously excluded by another. Nowak and May[53] proposed an SIS model with n strains following an order of virulence and assumed that a more virulent strain can superinfect a host who is already infected by a less virulent strain. Wu *et al.*[54] considered two-strain models in a heterogenous population represented by scale-free networks, incorporating competing interaction between these two strains by superinfection.

1.2 SOCIAL NATURES ON EPIDEMICS

1.2.1 *Social response*

Protective measures such as vaccination and medicine are available to control the disease spreading[55,56]. In some scientific works, the social behavior has been considered as a key factor to understand the epidemic dynamics [57–61]. When people become aware of the spread of a transmissible disease in a community, various media (e.g., TV, newspaper, and SNS) may provide information to alert the presence of a disease spreading over the community[62]. Then the community may promote or control some behaviors of its members, for instance, wearing a mask, limiting the number of contacts with others, and taking medication or vaccination[63–65]. Such information could induce some qualitative or quantitative changes in the quotidian behavior, which in turn may reduce the susceptibility to the disease[66]. Especially the report broadcasted by the media on a significant number of infected individuals is very likely to urge people's caution to take such preventive behaviors[67]. One of the typical behaviors is the social distancing, which is particularly useful and little costly to slow down the epidemic until a vaccine or medicine becomes widely available[68]. In this paper, we shall call the collective effect of such people's cautious behaviors on the epidemic dynamics by *social response*.

On the other hand, even when a disease has been spread in a community, people may not respond to the disease due to, for example, the cost or inconvenience to fight the disease spread[69–71]. We describe here that such a community is *insensitive* if the community is unaware or unresponsive to the disease spread. Even in such a case, a sufficiently large number of infectives, or severe symptoms by the disease may lead the community to show a social response about the disease spread.

1.2.2 *Community's policy*

Since the globalization in business and tourism becomes crucial more and more for the economical sustainability of local communities, the condition about the acceptance of visitors would be an important part of the community's policy for the public health about a spreading transmissible disease in and out of it. There must be such a decision on the policy by the host community as whether to accept visitors or not, the number of acceptable visitors, and the condition for acceptable visitors. Actually the importance of such a

policy on the tourism regulation has been recognized more and more in the post-COVID-19 period[72–76].

1.2.3 *Detectability of strains*

Genetic changes in strains can affect the virus's characteristics, such as transmissibility, virulence, antigenicity, and in some cases, the efficacy of vaccines and treatments. For some viruses, like the influenza virus, genetic variations are common and can lead to the emergence of new seasonal flu strains each year[77,78]. Although the characterization of multiple genotypes strains could contribute to identifying the disease infection, the emergence of mutant or novel strains of infectious diseases has provided a challenge to clinical diagnosis due to the lack of knowledge about the novel strains or the limitation of testing techniques[79,80].

1.3 CLASSIC EPIDEMIC DYNAMICS MODELS INCORPORATING SOCIAL NATURES

1.3.1 *Models incorporating social behaviors*

Funk *et al.*[82] quantified the impact on the endemicity of a disease in a well-mixed population under the variation of different disease parameters as a consequence of growing awareness in the population. They consider the spread of the awareness in response to the spread of an infectious disease and divide the population into two compartments: aware and unaware. Cabrera *et al.*[81] incorporated the social distancing behavior into an SIR model and argued that an effective social distancing could reduce the disease transmission and its effectiveness depends on the nature of the society. Agaba *et al.*[83] considered how the dissemination of private awareness arising from direct contact between unaware/aware individuals and that of public awareness through population-wide campaigns affect the disease spread. Both works focused on a substantial fraction of the population, while the effect of social response was not taken into account. Misra *et al.*[84] proposed a nonlinear mathematical model to discuss the effect of awareness about a disease spread. Their results indicate that the awareness programs through the media campaign can decrease the disease spread by isolating a fraction of susceptibles from infectives. Basir *et al.*[85] assumed the rate of becoming aware (resp. unaware) depends on the media campaign, and showed that increasing the rate of implementation of awareness program through the media could reduce the number of infectives.

1.3.2 *Models incorporating people's displacement*

There have been many investigations concerning the effect of a people's displacement due to social and political unrest as well as the natural migration of disease vectors to new areas on the epidemic outbreak, and especially conducted have been many theoretical/mathematical studies taking into account the possibility of individuals becoming infective during transportation and contributing significantly to transport-related infection (see Wilson[86] and references therein; especially for the SARS virus transmission, see Wang[87]). Not only the particular transportation with a long travel, but also the human quotidian mobility as a common phase of the human activity

can be considered as one of relevant factors that could cause the spread of a transmissible disease such as influenza[88,89]. So is the case of today's pandemic of COVID-19 in local regions of every country[90–92]. In the work presented by Parikh *et al.*[93], a synthetic population model of the Washington DC metro area was extended to include leisure and business travelers classified as transients. The final size of the epidemic among residents was found to be remarkably higher when transients were included in the simulation of a flu-like disease outbreak. In considering the emerging diseases of wildlife, Tompkins *et al.*[94] show that the key drivers of such diseases are agents from domestic sources and human-assisted exposure to infectious agents from wild populations. Talking about swine fever otherwise known as hog cholera, wild boar populations are known to serve as reservoir for the disease thereby constituting a great challenge for domestic pig farmers, veterinarians and other stakeholders[95,96].

2 SOCIAL RESPONSE BECOMES A CAUSE FOR RECURRING EPIDEMIC OUTBREAKS?

2.1 ASSUMPTIONS AND MODELING

2.1.1 *Assumptions*

When a transmissible disease spreads in a community, the behavioral change of the members in response to the outbreak may affect the course of its spread. For our mathematical modeling about the epidemic dynamics considered here under the social response, we set up the following assumptions:

- The spreading disease is non-fatal, and the disease-induced death can be negligible (for example, the common cold).
- The recovered individual cannot acquire a long-lasting effective immunity and becomes susceptible again in a sufficiently short period after the recovery.
- The demographic change about the community is negligible in the time scale of considered epidemic dynamics.
- The stronger social response makes the infection rate smaller, for example, with a decrease of individual contact rate.
- The social response follows a natural decay, while the fact of disease spread in the community tends to arouse the response.
- The disease spread may not cause the social response unless the number of infectives becomes enough to concern the people about it. Such a situation defines the social insensitivity. It may depend on the educational or cultural backgrounds of the community members.

2.1.2 *Modeling*

Let $S(t)$ and $I(t)$ be the susceptible and infective population densities in the community at time t, while $M(t)$ represents the strength of the social

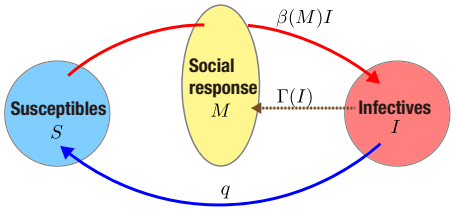

Figure 1: The epidemic state transition and the social response about our model (1).

response at time t. With the above assumptions, we shall consider the following model with ordinary differential equations (Figure 1):

$$\begin{aligned} \frac{dS}{dt} &= -\beta(M)IS + qI \\ \frac{dI}{dt} &= \beta(M)IS - qI \\ \frac{dM}{dt} &= \Gamma(I) - \mu M, \end{aligned} \tag{1}$$

where q is the recovery rate and μ is the natural decay rate of the social response. The coefficient of disease transmission $\beta = \beta(M)$ is given by a decreasing, positive, and differentiable function of $M \in [0, \infty)$. The initial condition is given by $S(0) > 0$, $I(0) > 0$, and $M(0) = 0$, which means that there is no social response at the beginning of the disease spread. Then people are unconcern about the disease spread. Thus $\beta_0 := \beta(0)$ denotes the coefficient of disease transmission in such a situation of the community with no social response.

The social sensitivity function $\Gamma(I)$ represents the nature of the social response according to its sensitivity to the disease spread.

we assume that the social response does not arise as long as the infective population density is not beyond a threshold value I_c:

$$\Gamma(I) := \begin{cases} 0 & \text{for } I \leqslant I_c; \\ \gamma(I - I_c) & \text{for } I > I_c. \end{cases} \tag{2}$$

Positive parameter γ is the social sensitivity coefficient, and I_c is the threshold value for infective population density to raise the social response. The threshold value I_c can be regarded as representing the social insensitivity to characterize the community. Parameter γ characterizes the responsiveness of the community that becomes aware of the epidemic situation. As γ gets larger, the strength of social response more sensitively increases with the increase of infectives in the community.

This kind of a switch-off change in the social collective behavior depending on the epidemic situation has been taken into account for the mathematical modeling also in some previous works with somewhat different contexts (for example,[97–101]), while we introduce it here as the nature of social insensitivity as described above. On the other hand, like our model (1) with (2) for $I_c \in (0, N)$, the system with a state-dependent switch in the dynamical nature may be regarded as a *piecewise smooth system* (PSS), or what is sometimes called *Filippov system* or *switching system*[102–107] and references therein, while we will not need to use any specific mathematical technique or knowledge for such a piecewise smooth system in the following analysis.

According to our assumptions, we have $S(t) + I(t) = N$ with a positive constant N for any $t \geqslant 0$. Then the system (1) can be reduced to the following two-dimensional one:

$$\begin{aligned} \frac{dI}{dt} &= \beta(M)(N - I)I - qI \\ \frac{dM}{dt} &= \Gamma(I) - \mu M \end{aligned} \tag{3}$$

with the initial condition given by $I(0) \in (0, N)$ and $M(0) = 0$. Note that $I(t) \in (0, N)$ for any $t \geqslant 0$.

We have a special case with $I_c \geqslant N$. This is the case where $\Gamma(I)$ is always zero for any $I \in (0, N)$ in the epidemic dynamics given by the system (1).

The alternative special case is such that $\gamma = 0$, which makes $\Gamma(I)$ always zero as well. These special cases correspond to the model with no social response which can be regarded as a reference model to our full model (1) with (2).

We have the other special case with $I_c = 0$. In this case, the social response arises for any number of infectives, so that it is regarded as the model for an epidemic dynamics in a community with no insensitivity about the disease spread. This case is mathematically equivalent to a particular case of the model analytically investigated in[108,109]. There are some other works[110–120] related to[108,109], and in part to this work.

2.2 BASIC REPRODUCTION NUMBER

The basic reproduction number $\mathscr{R}_0$ is defined as the expected number of secondary infectives generated by a single infective individual in a community consisting only of susceptible individuals in the duration of the infectivity of the initial infective individual [52,121–123]. To derive $\mathscr{R}_0$ for the model (1), we use the condition that $dI/dt|_{t=0} > 0$ for $I(0) \ll 1$ and $S(0) \approx N$. This condition corresponds to the situation in which the basic reproduction number $\mathscr{R}_0$ could be defined as the supremum for the number of secondary infectives[124]. From $M(0) = 0$, we can easily obtain the following condition with the definition of $\mathscr{R}_0$ for the model (1):

$$\mathscr{R}_0 = \frac{\beta_0 N}{q} > 1,$$

when the number of infectives increases in an early period after the disease invasion. If $\mathscr{R}_0 < 1$, the number of infectives decreases after the invasion. If $\mathscr{R}_0 > 1$, the disease is able to spread in the community at least for a while after its invasion.

2.3 MATHEMATICAL RESULTS ON THE MODEL

2.3.1 *Non-dimensionalization*

Since the total population size N is constant for our model (3) independently of time, we introduce the following non-dimensional transformation of variables and parameters:

$$u = \frac{S}{N};\ v = \frac{I}{N};\ \tau = qt;\ \mathscr{R}_0 = \frac{\beta_0 N}{q};\ \eta = \frac{\gamma N}{q};\ \theta_c = \frac{I_c}{N};\ \delta = \frac{\mu}{q},$$

and $u = 1 - v$. Then the system (3) can be rewritten as

$$\begin{aligned} \frac{dv}{d\tau} &= \frac{\beta(M)}{\beta_0}\mathscr{R}_0 v(1-v) - v \\ \frac{dM}{d\tau} &= G(v) - \delta M \end{aligned} \tag{4}$$

with

$$G(v) := \begin{cases} 0 & \text{for } v \leqslant \theta_c; \\ \eta(v - \theta_c) & \text{for } v > \theta_c. \end{cases} \tag{5}$$

In the subsequent sections, we investigate the dynamical nature of the non-dimensionalized system (4) with (5).

2.3.2 *Model with no social response*

We consider the system (4) when no social response arises, that is, when $M(t) \equiv 0$ for any $t \geqslant 0$. This corresponds to the case where $\eta = 0$ or $\theta_c \geqslant 1$ in (5) with $M(0) = 0$ as mentioned in Section 2.1. From (4), we have

$$\frac{dv}{d\tau} = \mathscr{R}_0 v(1-v) - v \tag{6}$$

which mathematically corresponds to the Verhulst model[125], being well-known today as the logistic equation. The ordinary equation (6) with the initial condition $v(0) = v_0 > 0$ is given as

$$v(\tau) = \begin{cases} \left(1 - \dfrac{1}{\mathscr{R}_0}\right) \dfrac{v_0}{v_0 + \{(1 - 1/\mathscr{R}_0) - v_0\} e^{-\tau/(\mathscr{R}_0 - 1)}} & \text{for } \mathscr{R}_0 \neq 1; \\ \dfrac{1}{\tau + 1/v_0} & \text{for } \mathscr{R}_0 = 1. \end{cases}$$

When $\mathscr{R}_0 \leqslant 1$, $v(\tau)$ is monotonically decreasing and approaches the disease-free equilibrium with $v = 0$. When $\mathscr{R}_0 > 1$, $v(\tau)$ monotonically approaches the endemic equilibrium with $v = v^* = 1 - 1/\mathscr{R}_0 > 0$.

2.3.3 *Model without social insensitivity*

In this section, we consider the system (4) without the social insensitivity, that is, with $\theta_c = 0$. This is the case where the community always has a social response whenever a transmissible disease exists in it. From (4) and (5), the model now becomes

$$\begin{aligned} \frac{dv}{d\tau} &= \frac{\beta(M)}{\beta_0} \mathscr{R}_0 v(1-v) - v \\ \frac{dM}{d\tau} &= \eta v - \delta M. \end{aligned} \tag{7}$$

This system has been analytically investigated also in[108,109], as already mentioned about the full model(1) with $I_c = 0$ for (2) at the end of Section 2.1.

The model (7) always has the disease-free equilibrium $E_0(0,0)$ and may have an endemic equilibrium $E_+(v^*, M^*)$ which satisfies that

$$\frac{\beta(M^*)}{\beta_0} \mathscr{R}_0 (1 - v^*) - 1 = 0; \quad \eta v^* - \delta M^* = 0. \tag{8}$$

Then we can get the following result on the existence of equilibria E_0 and E_+ (Appendix A.1):

Lemma 2.1. *For the model (4) without the social insensitivity, that is, for the system (7),*

(i) if and only if $\mathscr{R}_0 \leqslant 1$, there is only the disease-free equilibrium E_0;

(ii) if and only if $\mathscr{R}_0 > 1$, there are the disease-free equilibrium E_0 and the endemic equilibrium E_+ uniquely determined by (8), where $0 < v^* < 1 - 1/\mathscr{R}_0$.

With this lemma, we can obtain the following result on the stability of existing equilibrium:

Theorem 2.1. *For the model (4) without the social insensitivity,*

(i) if and only if $\mathscr{R}_0 \leqslant 1$, *the unique equilibrium* E_0 *is globally asymptotically stable;*

(ii) if and only if $\mathscr{R}_0 > 1$, *there are two equilibria* E_0 *and* E_+, *where* E_0 *is unstable and* E_+ *is globally asymptotically stable.*

This result corresponds to Theorem 5.1 in[108] or Theorem 5.2 in[109], which is on the SIS model with the recruitment of susceptibles to balance the death in the population. Thus our Theorem 2.1 can be proved by the arguments corresponding to their proof with a Lyapunov function for their model with their parameter $\mu = 0$.

2.3.4 *Model with social insensitivity*

In this section, we consider the model (4) with a social insensitivity, that is, with $\theta_c \in (0, 1)$. The model (4) always has the disease-free equilibrium $E_0(0, 0)$ and may have an endemic equilibrium (v^*, M^*) which satisfies that

$$\frac{\beta(M^*)}{\beta_0}\mathscr{R}_0(1 - v^*) - 1 = 0; \quad G(v^*) - \delta M^* = 0. \tag{9}$$

We can get the following result on the existence of equilibria (Appendix A.2):

Lemma 2.2. *For the model* (4) *with a social insensitivity,*

(i) if and only if $\mathscr{R}_0 \leqslant 1$, *there is only the disease-free equilibrium* $E_0(0, 0)$;

(ii) if and only if $1 < \mathscr{R}_0 \leqslant (1 - \theta_c)^{-1}$, *there are the disease-free equilibrium* $E_0(0, 0)$ *and the endemic equilibrium* $E_{+0}(1 - 1/\mathscr{R}_0, 0)$;

(iii) if and only if $\mathscr{R}_0 > (1 - \theta_c)^{-1}$, *there are the disease-free equilibrium* $E_0(0, 0)$ *and the endemic equilibrium* $E_{++}(v^*, M^*)$ *uniquely determined by*

$$v^* = 1 - \frac{1}{\mathscr{R}_0}\frac{\beta_0}{\beta(M^*)}; \quad M^* = \frac{\eta}{\delta}(v^* - \theta_c), \tag{10}$$

where $\theta_c < v^* < 1 - 1/\mathscr{R}_0$.

(iv) $E_{++} \to E_{+0}$ *as* $\mathscr{R}_0 \to (1 - \theta_c)^{-1} + 0$.

The equilibrium E_{+0} is the endemic state that people are unconcerned about the disease persisting in the community, while E_{++} is the endemic state that the persisting disease concerns people in the community.

With Lemma 2.2, we can obtain the following result on the stability of existing equilibrium (Appendix A.3):

Theorem 2.2. *For the model* (4) *with a social insensitivity,*

(i) if and only if $\mathscr{R}_0 \leqslant 1$, *the unique equilibrium* E_0 *is globally asymptotically stable;*

(ii) if and only if $1 < \mathscr{R}_0 \leqslant (1 - \theta_c)^{-1}$, *there are two equilibria* E_0 *and* E_{+0}, *where* E_0 *is unstable and* E_{+0} *is globally asymptotically stable;*

(iii) if and only if $\mathscr{R}_0 > (1 - \theta_c)^{-1}$, *there are two equilibria* E_0 *and* E_{++}, *where* E_0 *is unstable and* E_{++} *is globally asymptotically stable.*

Independently of whether the social insensitivity exists or not, the model (4) has an endemic equilibrium when and only when $\mathscr{R}_0 > 1$ while it always has the disease-free equilibrium E_0. Then there exists the endemic equilibrium E_{+0} or E_{++}, depending on the social insensitivity. In the absence of the social insensitivity (formally, $\theta_c = 0$), the disease and social response coexist when people keep a response to the disease ($M > 0$). In the presence of a social insensitivity ($0 < \theta_c < 1$), there is a critical condition for $\mathscr{R}_0$. If $1 < \mathscr{R}_0 \leqslant (1-\theta_c)^{-1}$, the disease persists in the community whereas people do not take care of it at the endemic equilibrium. If $\mathscr{R}_0 > (1-\theta_c)^{-1}$, the disease and social response coexist at the endemic equilibrium.

From Theorem 2.2, we find that, when $1 < \mathscr{R}_0 \leqslant (1-\theta_c)^{-1}$, the model (4) approaches the endemic equilibrium $E_{+0}(1-1/\mathscr{R}_0, 0)$. In this case, the endemic size of infectives is determined only by the basic reproduction number $\mathscr{R}_0$, that is, $1-1/\mathscr{R}_0$, while there is no social response at the endemic equilibrium. In contrast, for the case where $\mathscr{R}_0 > (1-\theta_c)^{-1}$, we can obtain the following result on the parameter dependence of the endemic size v^* and the strength of social response M^* at the endemic equilibrium E_{++} which the system approaches:

Corollary 2.2.1. *The endemic size v^* at the endemic equilibrium E_{++} is increasing in terms of $\mathscr{R}_0$, δ and θ_c, while it is decreasing in terms of η. The strength of social response M^* at E_{++} is increasing in terms of $\mathscr{R}_0$ and η, while it is decreasing in terms of δ and θ_c.*

The proof of this corollary can be obtained straightforwardly from the sign of the partial derivatives of v^* and M^* with respect to each parameter, where we used $d\beta(M)/dM < 0$ from the assumption for $\beta(M)$.

For a disease with high transmissibility (i.e., large $\mathscr{R}_0$), although people show a strong social response to the disease spread, there is a large number of infectives at the endemic equilibrium state due to the high transmissibility of the disease. As for a community of people more sensitive to the disease spread (i.e., small θ_c or large η), or more persistently keeping the social response (i.e., small δ), people show a stronger social response to the disease spread, and such a response can reduce the number of infectives at the endemic equilibrium state.

Furthermore as shown in Appendix A.3, we can obtain the following result on the behavior of the system to approach the equilibrium:

Corollary 2.2.2. *The system (4) approaches*

(i) the equilibrium E_0 in a monotonic manner when $\mathscr{R}_0 \leqslant 1$;

(ii) the equilibrium E_{+0} in a monotonic manner when $1 < \mathscr{R}_0 \leqslant (1-\theta_c)^{-1}$;

(iii) the equilibrium E_{++} in the following manner when $\mathscr{R}_0 > (1-\theta_c)^{-1}$:

$$\begin{cases} \text{a monotonic manner if } \Delta \geqslant 0; \\ \text{an oscillatory manner if } \Delta < 0, \end{cases}$$

where

$$\Delta := \left\{ \frac{\beta(M^*)}{\beta_0} \mathscr{R}_0 v^* + \delta \right\}^2 + 4\eta v^* \left. \frac{d \ln \beta(M)}{dM} \right|_{M=M^*}. \tag{11}$$

The behavior of the system (4) to approach E_{++} could have two different manners: monotonic or oscillatory. This is because the second term of (11) is

negative and its absolute value is determined by the derivative of β. Hence the sign of Δ essentially depends on the detailed features of function $\beta(M)$.

As a consequence, we have found the possibility that the social sensitivity could induce a damped oscillation in the epidemic dynamics. The emergence of a damped oscillation caused by the social response has been shown also in some literatures on the epidemic dynamics model (for example,[14,19], and references therein). Generally, independent of which an epidemic dynamics is approaching a disease-free or endemic state, an oscillatory variation in the infective population size must concern the public health in the community since it appears as recurring outbreaks. In the following part, we shall focus on the condition for the occurrence of such an oscillatory behavior of the system (4) with a social insensitivity.

2.3.5 *Extremely fast/slow social response*

To understand further the nature of epidemic dynamics by the model (1), we consider here a specific case where the strength of social response changes extremely faster or slower than the epidemic dynamics, and vice versa. Then we mathematically apply the quasi-stationary state approximation (QSSA) for the temporal change in M or ν, that is to use $dM/d\tau \approx 0$ or $d\nu/d\tau \approx 0$ respectively for the system (4)[124,126,127]. As proved in Appendix A.4, we can find the following nature of the epidemic dynamics with such an extremely fast/slow social response:

Theorem 2.3. *In the case of extremely fast/slow social response, Theorem 2.2 holds, and the system (4) necessarily approaches an equilibrium in a monotonic manner.*

Theorem 2.3 indicates that the system (4) does not approach the equilibrium in any oscillatory manner with the extremely fast/slow social response. In other mathematical words, any damped oscillation toward the equilibrium does not occur for the system (4) with the parameter value η and δ sufficiently larger/smaller than any other parameter values. Therefore it is implied that a damped oscillation toward the endemic equilibrium E_{++} could occur only for a finite range of parameter value η or δ when $\mathscr{R}_0 > (1-\theta_c)^{-1}$, following Corollary 2.2.2. We will consider the relation of social response and insensitivity to the occurrence of such a damped oscillation in more detail for the model (1) with a specific function $\beta(M)$ in the next section.

2.3.6 *A specific model*

We consider the model (1) with the following specific function $\beta(M)$:

$$\beta(M) = \frac{\beta_0}{1+aM}. \tag{12}$$

Positive constant a is the efficiency coefficient of the social response with respect to the transmission rate. The larger a means that the social response has the higher efficiency to reduce the risk of infection. The same relation of the social response to the infection coefficient was introduced also in the modified SIR and SEIQR models of[14,19,113,118,119].

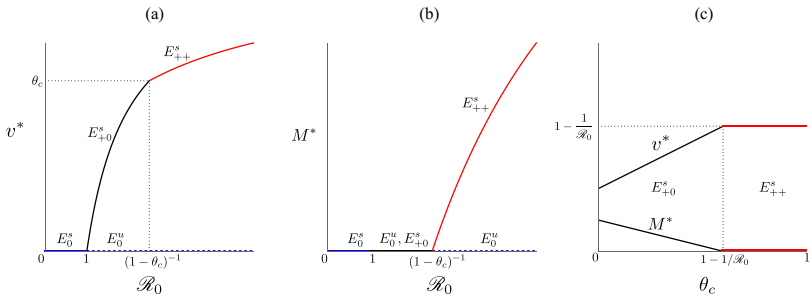

Figure 2: Bifurcation diagrams about v^* and M^* for the system (13). Solid curves are for stable equilibria E^s_0, E^s_{+0} and E^s_{++} in (a) and (b), for E^s_{++} when $\theta_c < 1 - 1/\mathscr{R}_0$ and E^s_{+0} when $\theta_c > 1 - 1/\mathscr{R}_0$ in (c). Dashed lines in (a) and (b) are for the unstable equilibrium E^u_0. Numerically drawn with (a) and (b) $\theta_c = 0.6$; (c) $\mathscr{R}_0 = 2.5$, and $\alpha = 5.0$; $\delta = 10.0$; $\eta = 5.0$.

The model (1) with (12) becomes

$$\begin{aligned} \frac{dS}{dt} &= -\frac{\beta_0}{1+\alpha M} IS + qI \\ \frac{dI}{dt} &= \frac{\beta_0}{1+\alpha M} IS - qI \\ \frac{dM}{dt} &= \Gamma(I) - \mu M, \end{aligned}$$

with $\Gamma(I)$ defined by (2). The non-dimensionalized system (4) becomes

$$\begin{aligned} \frac{dv}{d\tau} &= \frac{\mathscr{R}_0}{1+\alpha M}(1-v)v - v \\ \frac{dM}{d\tau} &= G(v) - \delta M, \end{aligned} \tag{13}$$

with $G(v)$ given by (5). From Theorem 2.2, if $\mathscr{R}_0 > (1-\theta_c)^{-1}$, there is a globally asymptotically stable endemic equilibrium E_{++} with

$$v^* = \frac{(\mathscr{R}_0 - 1)\delta + \alpha\eta\theta_c}{\mathscr{R}_0\delta + \alpha\eta}; \quad M^* = \frac{(\mathscr{R}_0 - 1 - \mathscr{R}_0\theta_c)\eta}{\mathscr{R}_0\delta + \alpha\eta}. \tag{14}$$

We can obtain the bifurcation diagrams as shown in Figure 2 for the system (13) (refer to Corollary 2.2.1). From (14), we can find that v^* is monotonically decreasing in term of $\alpha\eta$. Since α is the efficiency coefficient of the social response with respect to the transmission rate, the endemic size v^* must become smaller as the social response more efficiently works to reduce the infection risk (see Figure 3).

From Corollary 2.2.2, only when E_{++} exists, the system (13) may approach it in an oscillatory manner (see Figure 4). Since the temporal oscillation of infective population size means recurring outbreaks of the disease spread as already mentioned before, it is worthwhile investigating what condition causes such an oscillatory behavior in the epidemic dynamics by the system (13).

The discriminant (11) of the characteristic equation for the endemic equilibrium E_{++} of the system (13) becomes

$$\Delta = \left(\frac{v^*}{1-v^*}\right)^2 - 2\left(\delta + \frac{2}{\mathscr{R}_0}\alpha\eta\right)\frac{v^*}{1-v^*} + \delta^2 \tag{15}$$

from (12) and (14). Then we derive the following result (Appendix A.5):

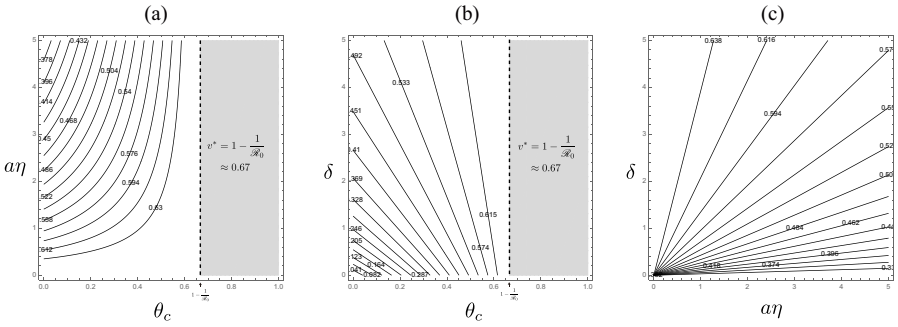

Figure 3: Parameter dependence of the endemic size v^* at the endemic equilibrium which is E_{++} if $\theta_c \leqslant 1 - 1/\mathscr{R}_0$, and E_{+0} if $\theta_c > 1 - 1/\mathscr{R}_0$ respectively. Numerically drawn with (a) $\delta = 2.0$; (b) $\alpha\eta = 5.0$; (c) $\theta_c = 0.3$, and $\mathscr{R}_0 = 3.0$.

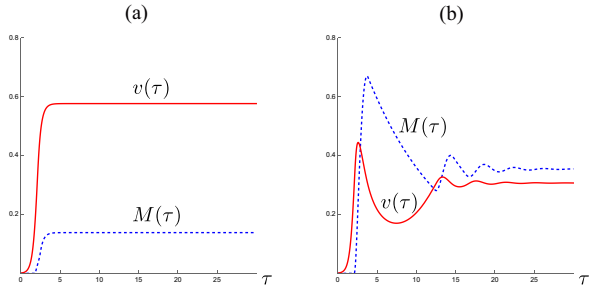

Figure 4: Temporal variations of v and M for the model (13) with $\alpha = 5.0$; $\mathscr{R}_0 = 4.0$; $\eta = 5.0$; $\theta_c = 0.3$; (a) $\delta = 10.0$; (b) $\delta = 0.1$. The initial condition is given as $(v(0), M(0)) = (0.001, 0.0)$.

Theorem 2.4. *When $\mathscr{R}_0 > (1-\theta_c)^{-1}$, the system (13) approaches E_{++} with a damped oscillation if and only if $\theta_-^c < \theta_c < \theta_+^c$, where*

$$\theta_\pm^c := \frac{(\delta + \alpha\eta)x_\pm - (\mathscr{R}_0 - 1)\delta}{\alpha\eta(1 + x_\pm)} \tag{16}$$

with

$$x_\pm := \left(\delta + \frac{2\alpha\eta}{\mathscr{R}_0}\right) \pm \sqrt{\left(\delta + \frac{2\alpha\eta}{\mathscr{R}_0}\right)^2 - \delta^2}. \tag{17}$$

If $\theta_c \leqslant \theta_-^c$ or $\theta_c \geqslant \theta_+^c$, the system approaches an equilibrium in a monotonic manner.

From Theorem 2.4, we can obtain the following detailed result of the condition about the occurrence of a damped oscillation for the system (13) (Appendix A.6):

Corollary 2.4.1. *For the system (13), a damped oscillation occurs*

(i) when $1 < \mathscr{R}_0^{\inf} < \mathscr{R}_0 < \mathscr{R}_0^c$ and $0 < \theta_-^c < \theta_c < 1 - 1/\mathscr{R}_0$;

(ii) when $1 < \mathscr{R}_0^{cc} < \mathscr{R}_0 < \mathscr{R}_0^{\sup}$ and $0 < \theta_c < \theta_+^c < 1 - 1/\mathscr{R}_0$;

(iii) when $\mathscr{R}_0^c < \mathscr{R}_0 < \mathscr{R}_0^{cc}$ and $0 < \theta_c < 1 - 1/\mathscr{R}_0$,

where $\mathscr{R}_0^{\inf}$, $\mathscr{R}_0^c$, $\mathscr{R}_0^{cc}$, and $\mathscr{R}_0^{\sup}$ are uniquely determined with $\alpha\eta$ and δ, satisfying that $\mathscr{R}_0^{\sup} > \mathscr{R}_0^{cc} > \mathscr{R}_0^c > \mathscr{R}_0^{\inf} > 1$. When $\mathscr{R}_0 < \mathscr{R}_0^{\inf}$, $\mathscr{R}_0 > \mathscr{R}_0^{\sup}$, or $\theta_c > 1 - 1/\mathscr{R}_0^{cc}$, the damped oscillation does not occur.

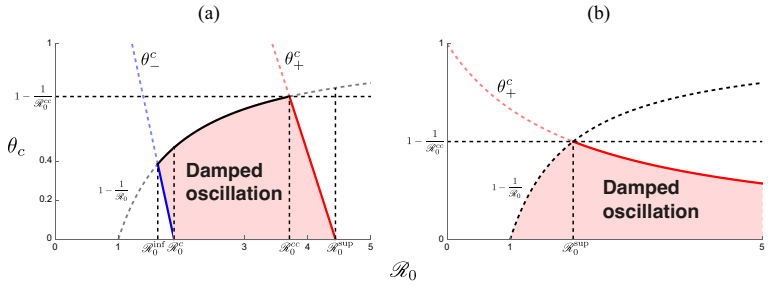

Figure 5: $(\mathscr{R}_0, \theta_c)$-dependence of the occurrence of a damped oscillation around the endemic equilibrium E_{++}. For the region out of the filled, the system (13) approaches an equilibrium (either disease-free or endemic) in a monotonic manner, as shown in Corollary 2.2.2. Numerically drawn with (a) $\delta = 1.5$; (b) $\delta = 0$, and $\alpha\eta = 0.5$.

Mathematical definitions of $\mathscr{R}_0^{\inf}$, $\mathscr{R}_0^{c}$, $\mathscr{R}_0^{cc}$ and $\mathscr{R}_0^{\sup}$ are given in Appendix A.6.

As indicated by Figure 5(a), the disease spread with sufficiently large or sufficiently small $\mathscr{R}_0$ does not show any damped oscillation, independently of the social sensitivity to it. Only if $\mathscr{R}_0$ is in a specific range greater than 1, a damped oscillation may occur. Moreover, if the community is insensitive so as to have $\theta_c > 1 - 1/\mathscr{R}_0^{cc}$, the recurring outbreaks do not occur for any $\mathscr{R}_0$. The community with sufficiently weak insensitivity (i.e., small θ_c) is very likely to have recurring outbreaks, even though such a community would have a relatively small endemic size at the equilibrium state as shown in Figure 2(c).

For a specific case where the social response never decays with $\delta = 0$, we can get the following simpler result (Appendix A.7):

Corollary 2.4.2. *For the system (13) with $\delta = 0$, a damped oscillation occurs*

(i) when $1 < \mathscr{R}_0 \leqslant \mathscr{R}_0^{cc} = (1 + \sqrt{1 + 16\alpha\eta})/2$ and $0 < \theta_c < 1 - 1/\mathscr{R}_0$;

(ii) when $\mathscr{R}_0 > \mathscr{R}_0^{cc}$ and $0 < \theta_c < \theta_+^c = 4\alpha\eta/(\mathscr{R}_0 + 4\alpha\eta) < 1 - 1/\mathscr{R}_0$.

Otherwise, the damped oscillation does not occur.

In such a specific case without the decay of the social response, a damped oscillation can occur for a sufficiently weak insensitivity for any $\mathscr{R}_0 > 1$, as indicated in Figure 5(b). Hence the community which keeps the social response longer would be more likely to show an oscillation in epidemic dynamics for a wide range of the basic reproduction number $\mathscr{R}_0$.

With a decay of the social response, that is, with $\delta > 0$, we can find the following result in the case of extremely poor/effective social response or the case of its extremely fast decay (Appendix A.8):

Corollary 2.4.3. *For $\alpha\eta \gg 1$, a damped oscillation occurs, while it does not for $\alpha\eta \ll 1$ or $\delta \gg 1$.*

In the extreme case where the community is sufficiently sensitive (i.e., large η) and the social response has sufficiently high efficiency in reducing the susceptibility (i.e., large α), recurring outbreaks necessarily occur. Recurring outbreaks do not occur in the opposite extreme case or in the case where the social response decays so fast (i.e., large δ).

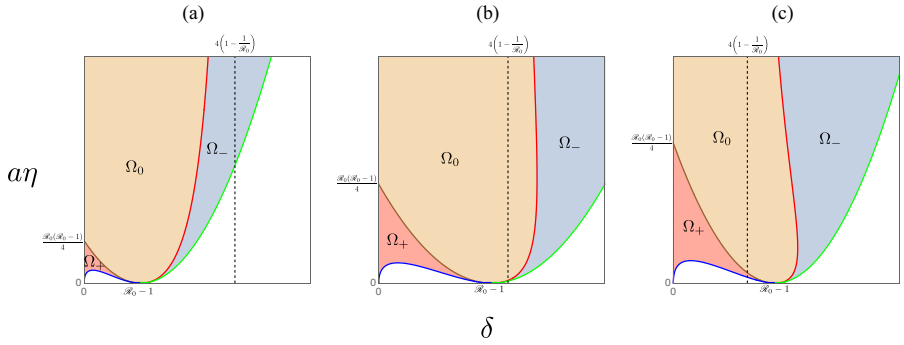

Figure 6: $(\delta, a\eta)$-dependence of the occurrence of a damped oscillation. (a) $1 < \mathscr{R}_0 \leqslant 2$; (b) $2 < \mathscr{R}_0 \leqslant 4$; (c) $\mathscr{R}_0 > 4$. A damped oscillation could occur only for the region $\Omega_0 \cup \Omega_+ \cup \Omega_-$, where the definitions of Ω_0, Ω_+, and Ω_- are given in the main text. For the blank region, the damped oscillation does not occur. Boundary curves between Ω_- and Ω_0, between Ω_0 and Ω_+, between Ω_+ and blank region, between blank region and Ω_- correspond to $\theta_-^c = 0$, $\theta_+^c = 1 - 1/\mathscr{R}_0$, $\theta_+^c = 0$ and $\theta_-^c = 1 - 1/\mathscr{R}_0$, respectively.

From Theorem 2.4 and Corollaries 2.4.1–2.4.3, we can get the result shown in Figure 6 on the $(\delta, a\eta)$-dependence of the occurrence of a damped oscillation (A.6), where the parameter region is classified into four subregions:

$$\begin{aligned}
\Omega_- &:= \{(\delta, a\eta) | 0 < \theta_-^c < 1 - 1/\mathscr{R}_0 < \theta_+^c\};\\
\Omega_+ &:= \{(\delta, a\eta) | \theta_-^c < 0 < \theta_+^c < 1 - 1/\mathscr{R}_0\};\\
\Omega_0 &:= \{(\delta, a\eta) | \theta_-^c < 0 < 1 - 1/\mathscr{R}_0 < \theta_+^c\},
\end{aligned}$$

and the rest. For parameter regions Ω_- and Ω_+, sufficiently large or small θ_c does not cause the damped oscillation. In contrast, for Ω_0, a damped oscillation occurs whenever E_{++} exists.

For the other specific case with no social insensitivity, that is, with $\theta_c = 0$, we can get the following result too (Appendix A.9):

Corollary 2.4.4. *For the system (13) with $\theta_c = 0$, a damped oscillation occurs when*

(i) $\delta = 4(1 - 1/\mathscr{R}_0)$ *with* $\mathscr{R}_0 > 2$ *and* $a\eta > (\mathscr{R}_0 - 4)^2(\mathscr{R}_0 - 1)/\{2\mathscr{R}_0(\mathscr{R}_0 - 2)\} > 0$;

(ii) $4(1 - 1/\mathscr{R}_0) < \delta < \min\{\mathscr{R}_0, (\mathscr{R}_0 + 2)(1 - 1/\mathscr{R}_0)\}$ *with* $\mathscr{R}_0 > 2$ *and* $0 < (a\eta)_-^c < a\eta < (a\eta)_+^c$;

(iii) $\delta < 4(1 - 1/\mathscr{R}_0)$ *and* $a\eta > (a\eta)_+^c > 0$,

where

$$(a\eta)_\pm^c = \frac{\mathscr{R}_0\delta(\mathscr{R}_0 - 1 - \delta) + 2(\mathscr{R}_0 - 1)\{\delta \pm \sqrt{\delta(\mathscr{R}_0 - 1)}\}}{\mathscr{R}_0\delta - 4(\mathscr{R}_0 - 1)}. \tag{18}$$

With no social insensitivity, a damped oscillation is more likely to occur for sufficiently small δ and sufficiently large $a\eta$. For a community in which people persistently keep the response to the disease spread and such a response can effectively work to reduce the infection risk, recurring outbreaks of epidemic dynamics would be more likely to occur. If people easily lose attention to the disease spread, recurring outbreaks would occur only if the efficiency of such a response is in a certain range.

With a social insensitivity, that is, with $\theta_c > 0$, the damped oscillation does not occur for sufficiently small $\alpha\eta$, while it must occur for sufficiently large $\alpha\eta$, as already shown in Corollary 2.4.3. If the effect of social response is persistent with sufficiently slow decay, recurring outbreaks occur only in the community with a sufficiently weak insensitivity, that is, with a sufficiently strong sensitivity for the disease spread.

As shown in Corollary 2.2.1 and in the early part of this section about the $\alpha\eta$-dependence of ν^*, it is certain that people's attention to disease and attempt to prevent its further spread necessarily suppress the endemicity to make the endemic size ν^* smaller: With the smaller δ or larger $\alpha\eta$, the endemic size ν^* becomes smaller. Hence the above-mentioned likeliness of recurring outbreaks indicates that a damped oscillation in the temporal variation in terms of the number of infectives would occur toward a relatively low level of endemicity. Since we use the word 'outbreaks' here as repeating peaks in the temporal variation about the number of infectives, someone may think the above arguments counter-intuitive. However note that it is not the case.

2.4 DISCUSSION

In this model, we focused on the relation of social response to the likeliness of recurring outbreaks of a spreading disease in a community. For our SIS model, recurring outbreaks may occur only when the system approaches an endemic equilibrium at which the social response remains active. In another endemic case where the social response disappears, the system approaches it in a monotonic manner, that is, the temporal variation of infective population size is monotonic around the endemic equilibrium.

Our model is based on the simplest SIS epidemic dynamics model. As shown in Section 2.3.2, the model with a constant infection coefficient β does not show any oscillatory behavior in the temporal variation of variables. Our modeling is to introduce the effect of social response only on the infection coefficient in the SIS model. Thus, the social response has an effect to vary only the velocity of the state transition from susceptible to infective. As a result of such our modeling, being seen with respect to the closed two dimensional system (3), the temporally varying social response can be regarded as a factor to lead to a temporal change of the intrinsic growth rate in a modified logistic equation with the constant carrying capacity N and the term of a proportional harvesting (qI), which is the ordinary differential equation to govern the temporal change of I. From this mathematical structure about our model, it has no sustained (non-decaying) periodic oscillations, whereas this result implies a possibility of the emergence of a sustained periodic oscillations in some similar models with different assumptions for the epidemic dynamics (for example, see [14,18,61,100,116–120,128,129]). As we have shown in our analysis on the model, the social response does not alter the endemicity of spreading disease although it can certainly suppress the endemic size. This is because it tends to fade out when the disease becomes about to be eliminated, which we could expect for any human community.

The social response could induce the recurring outbreaks in the epidemic dynamics, while it can suppress the endemic size. The results on our model implied that such recurring outbreaks hardly occur for a disease with sufficiently low or sufficiently high transmissibility. Only for a disease which has a certain intermediate range of transmissibility, such recurring outbreaks

may occur, the community approaching an endemic equilibrium at which the social response remains active. A community more sensitive to the disease spread is more likely to have such recurring outbreaks. Moreover, if the social response is more efficient to reduce the risk of infection, the recurring outbreaks are more likely to occur. In contrast, the recurring outbreaks hardly occur for the community much insensitive to the disease spread, while the endemic/epidemic size would become large.

Depending on the characteristics of the community and the nature of the transmissible disease, the social response could become a cause of recurring outbreaks whilst it must suppress the prevalence. Since the nature of actual social response for a disease spread must be one of interesting problems in social sciences, such a possibility that it could be an important factor to cause recurring outbreaks would become more important to our preparation for the future epidemic outbreaks after our experience of the recent pandemic of COVID-19.

3

THE ACCEPTANCE OF VISITORS PROMOTES THE DISEASE SPREAD?

3.1 ASSUMPTIONS AND MODELING

3.1.1 *Assumptions*

We consider the spread of a transmissible disease during a short-term period in time after the community starts to accept visitors from the outside, satisfying the following assumptions on the epidemic dynamics:

[H1] The demographic change in the resident population is negligible in the season.

[H2] The fatality of disease on the resident and visitor populations is negligible in the season.

[H3] The community starts the acceptance of a number of temporal visitors from the outside in the season after a transmissible disease has invaded in it.

[H4] The entry flow of visitors is constant, that is, the net entry rate is constant independently of time.

[H5] The exit of visitors from the community follows a constant per capita exit rate.

[H6] No infected visitor is accepted by the community (i.e., the perfect quarantine), so that every accepted visitor is susceptible or immune to the disease at the entry into the community.

[H7] A given proportion of visitors is immune at the entry into the community.

[H8] Only the susceptible residents can get the vaccination to become immune, and it is not available for any visitor staying in the community.

[H9] Every immune visitor or resident has a possibility to get reinfected (i.e., the *imperfect* or *partial* immunity) during its stay in the community.

[H10] Infected visitor has the same exit rate as the susceptible visitor, that is, we neglect any influence of the infection on the visitor during the stay in the community.

Assumption H1 indicates a time-independent constant size of resident population during the season in which the epidemic dynamics is going on. We then ignore the death due to the transmissible disease under consideration in the epidemic dynamics too, as indicated by the assumption H2. Assumption H3 indicates that the community accepts the visitors, even undergoing the spread of a transmissible disease, since the fatality of the disease is negligible with the assumption H2. No disease invasion with the visitors is assumed, as indicated by the assumption H6. From the assumptions H4

and H6, the community carries out the perfect regulation for the visitors at the entry according the entry number and the quarantine. Assumption H5 mathematically means that the exit of a visitor from the community follows the homogeneous Poisson process. In a model with ordinary differential equations, it can be introduced with a constant exit rate per visitor. Assumption H7 is to reflect the situation of public health out of the community, applying the mean-field approximation for the proportion of immune visitors at the entry.

Since we assume that the community undergoes the disease spread, the assumption H8 gives the existence of a vaccination program for the residents, while it is not applied to the visitors. However, since the disease is reinfectious as assumed by the assumption H9, the immunity obtained by the vaccination or the recovery of the infection works only to reduce the risk of reinfection. Hence the state transition in terms of the disease follows the susceptible–infective–recovered/immunized–infective (SIRI) structure in our modeling, as used for example in [130–143].

Remark that the assumed reinfection is not caused by the waning or loss of immunity, which must take a certain period after getting it by the infection or vaccination. As already mentioned in the introduction section, we assume instead the imperfectness of immunity obtained by the infection or vaccination. Hence we do not introduce any specific period or time scale to get reinfected after getting the immunity. Since the infection or vaccination generates an immunity against the disease, the assumption H9 indicates that the immunity is imperfect or partial against the infection, for example, due to the multiplicity of pathogen types (e.g., mutated variants) [24,132]. Because the cross-immunity is well-known for such similar pathogens by the antigen for a type of pathogen, the reinfection may be suppressed or fail to cause an effective symptom to reproduce and discharge the pathogen to the environment.

For a simplification, the assumption H10 indicates that the exit of visitor is independent of whether the visitor is infected or not during the stay in the community. This assumption would be appropriate when the expected duration of the visitor is sufficiently shorter than the latent period, whereas it may be less appropriate when it is long. As assumed by the assumption H2, we consider a transmissible disease with little serious symptom, so that the assumption H10 would be applicable for visitors infected by such a disease.

3.1.2 *Modeling*

Generic model

With these assumptions given in the previous section, we shall consider the following model of ordinary differential equations (Figure 7):

Dynamics for the visitor population:

$$\begin{cases} \dfrac{dS_v}{dt} = (1-\rho)\Lambda - \beta\dfrac{I_r + I_v}{N+m}S_v - qS_v; \\ \dfrac{dI_v}{dt} = \beta\dfrac{I_r + I_v}{N+m}S_v + \epsilon\beta\dfrac{I_r + I_v}{N+m}R_v - \gamma I_v - qI_v; \\ \dfrac{dR_v}{dt} = \rho\Lambda + \gamma I_v - \epsilon\beta\dfrac{I_r + I_v}{N+m}R_v - qR_v; \end{cases} \tag{19}$$

Dynamics for the resident population:

$$\begin{cases} \dfrac{dS_r}{dt} = -\beta\dfrac{I_r + I_v}{N+m}S_r - \sigma S_r; \\ \dfrac{dI_r}{dt} = \beta\dfrac{I_r + I_v}{N+m}S_r + \epsilon\beta\dfrac{I_r + I_v}{N+m}R_r - \gamma I_r; \\ \dfrac{dR_r}{dt} = \sigma S_r + \gamma I_r - \epsilon\beta\dfrac{I_r + I_v}{N+m}R_r, \end{cases} \tag{20}$$

where S_v, I_v, and R_v are the subpopulation sizes of susceptible, infective, and immune visitors respectively. Similarly S_r, I_r, and R_r are the corresponding subpopulation sizes about the residents. The population sizes of residents and visitors staying in the community are denoted by $N = S_r + I_r + R_r$ and $m = S_v + I_v + R_v$ respectively. The resident population size N is constant independently of time t, as seen from $d(S_r + I_r + R_r)/dt = 0$ for any t by the system (20). From Assumption H3 in Section 3.1.1, the community starts the acceptance of visitors from the outside in the considered season after a transmissible disease has already invaded in it. The visitor population size m could be reasonably assumed to be less than the population size of residents N: $m < N$, whereas we shall not specifically assume so but consider the mathematically general case of m in the subsequent sections without any constraint except for $m \geqslant 0$. On the other hand, as given in the following part, we will take an assumption on the visitor population size m accompanying with a confinement for the net entry rate of visitors Λ.

All parameters are positive. Parameter ρ is the proportion of immune visitors at the entry ($0 \leqslant \rho \leqslant 1$). Proportion $1-\rho$ of visitors is susceptible at the entry. Parameter q is the per capita exit rate of visitor. Thus the expected duration of a visitor's stay in the community is given by $1/q$.

Parameter $\epsilon\beta$ is the reinfection coefficient for immune resident and visitor, while β is the infection coefficient for susceptible ones. Then the infection forces for the susceptible individual and the immune individual are respectively given by $\beta(I_r + I_v)/(N+m)$ and by $\epsilon\beta(I_r + I_v)/(N+m)$ for both resident and visitor. Remark that, in the setup for our modeling, the visitors do not form any specific subcommunity distinct from the resident population. From Assumption H3, they are temporal visitors for tourism, business etc. For this setup, we could assume that most of visitors are independent of the others. Thus, for a mathematical simplification, the influence of their movement on the epidemic dynamics is introduced in the epidemic dynamics by the mean-field approximation. Further, although the visitors' contribution to the infection forces would be different from the residents' one because

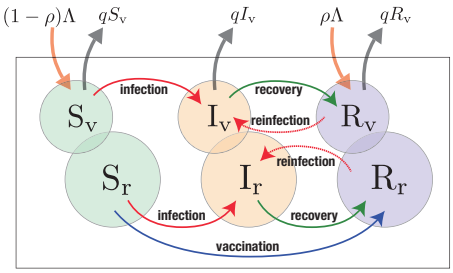

Figure 7: Scheme of the model for the epidemic dynamics in a community accepting temporal visitors, given by the system of (19) and (20).

of the difference in the mobility/behavioral pattern, the infection forces have their same contributions in our modeling here. This modeling may be regarded as an oversimplification, though we think that our modeling would still worth being considered to get a cue for the discussion about the influence of visitors on the epidemic dynamics within a community.

From Assumption H9 in Section 3.1.1, our modeling assumes that the immunity is imperfect or partial against the infection. Because of the cross-immunity by the obtained antigen, we reasonably assume that $0 \leqslant \epsilon \leqslant 1$ in our model, so that the reinfection coefficient $\epsilon\beta$ is not beyond the coefficient for susceptible β. That is, the reinfection after the vaccination or recovery from the disease generally has a smaller likelihood than that for the susceptible. For the extremal case of $\epsilon = 1$, the vaccination or recovery does not work at all to reduce the risk of reinfection. For $\epsilon = 0$, the recovery and vaccination give the perfect immunity so that there is no likelihood of reinfection. Thus the parameter ϵ means an index for the likelihood of reinfection after the recovery or vaccination, so that it can be regarded as an index for the risk of reinfection. Remark here again that the reinfection in our modeling is assumed to be not due to the waning of immunity (like for the SIRS models) but due to the imperfect immunity, and hence also the vaccinated individual has a risk to get infected, as introduced by Assumption H9.

Parameter γ is the recovery rate of an infective individual, and the recovered individual gets immunity, which is however imperfect. Only the susceptible residents can get the vaccination, with rate σ, and it is not available for any visitor staying in the community. Since the vaccination is imperfect from Assumption H9, it works to reduce the risk of infection but is unable to protect the vaccinated individual from the infection.

Assumption for the visitor population size in the community

According to the dynamics for the visitor population (19), we have

$$\frac{dm}{dt} = \Lambda - qm,$$

where $m = m(t) := S_v(t) + I_v(t) + R_v(t)$ is the visitor population size at time t, Λ the net entry rate of visitors, and q the per capita exit rate of visitor. Now let us consider the stationary situation with respect to the temporal change of visitor population size. This means that the number of visitors is assumed to be stationary, which may be regarded as a consequence of the regulation of their entry by the community, following the assumptions with H4 and H6 given in Section 3.1.1. Therefore we mathematically assume the

situation to satisfy that $dm/dt = 0$. Hence we put $\Lambda = qm$, and hereafter treat the visitor population size m as a positive constant.

The initial condition

Following the assumption of the stationary visitor population size with $\Lambda = qm$ as given in the above, we have the following dynamics for the visitor population at the disease-free state:

$$\begin{cases} \dfrac{dS_v}{dt} = (1-\rho)qm - qS_v; \\ \dfrac{dR_v}{dt} = \rho qm - qR_v, \end{cases}$$

where R_v means the subpopulation size of immune visitors when they enter in the disease-free community. It can be easily found that this dynamics results in an eventual approach to the equilibrium state such that $(S_v, R_v) \to ((1-\rho)m, \rho m)$ as $t \to \infty$ for any non-negative initial condition such that $S_v(0) \geqslant 0$ and $R_v(0) = m - S_v(0) \geqslant 0$. For this reason, let us assume the following initial condition for the epidemic dynamics with the model given by the system of (19) and (20):

$$(S_v, I_v, R_v, S_r, I_r, R_r) = \big((1-\rho)m, 0, \rho m, S_{r0}, I_{r0}, R_{r0}\big), \tag{21}$$

where $S_{r0} + I_{r0} + R_{r0} = N$ (a positive constant) with $S_{r0} > 0$, $I_{r0} > 0$ and $R_{r0} \geqslant 0$. This initial condition defines the situation when the community starts the acceptance of visitors from the outside, even under the existence of disease in it. The setup of this initial condition as our modeling follows Assumption H3 in Section 3.1.1.

3.2 BASIC REPRODUCTION NUMBER

For our model given by the system of (19) and (20), we can derive the following formula of the basic reproduction number $\mathscr{R}_0$ (Appendix B.1):

$$\begin{aligned} \mathscr{R}_0 &= \underbrace{\frac{1}{\gamma}}_{\substack{\text{the expected duration of infectivity.}}} \times \Bigg[\underbrace{\beta \frac{N}{N+m}}_{\substack{\text{the supremum of the expected new cases per unit time for the resident.}}} + \underbrace{\left\{ \beta \frac{(1-\rho)m}{N+m} + \epsilon\beta \frac{\rho m}{N+m} \right\}}_{\substack{\text{the supremum of the expected new cases per unit time for the visitor, given by the sum of secondary infections for susceptible and immune visitors.}}} \Bigg] \\ &= \mathscr{R}_{00} \left\{ 1 - (1-\epsilon)\rho \frac{\mu}{1+\mu} \right\}, \end{aligned} \tag{22}$$

where $\mu := m/N$, and for a convenience in the following arguments, we define $\mathscr{R}_{00} := \beta/\gamma$, which is the basic reproduction number for the community when no visitor comes in (i.e., $m = 0$). Note that this basic reproduction number is fundamentally for the epidemic dynamics in the community after it starts the acceptance of visitors.

From the formula (22), we can immediately find that the basic reproduction number $\mathscr{R}_0$ is less than 1 independently of the nature of accepted visitors if $\mathscr{R}_{00} < 1$. Hence, if the disease fails its invasion in the community with $\mathscr{R}_{00} < 1$ before starting the acceptance of visitors, the number of infectives in the community cannot turn to increase in the early period after the acceptance of visitors starts. As we will see in the later sections of the analysis on our model, this is valid only in the early period after the acceptance of visitors starts.

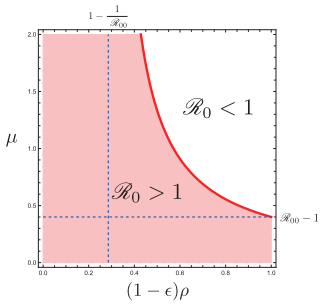

Figure 8: The dependence of the basic reproduction number $\mathscr{R}_0$ given by (22) on parameters $(1-\epsilon)\rho$ and $\mu := m/N$. Numerically drawn with $\mathscr{R}_{00} = 1.4$.

As for the dependence of $\mathscr{R}_0$ on the nature of accepted visitors, we note that $\mathscr{R}_0$ is monotonically decreasing in terms of μ when the visitors contain some immune ones (i.e., $\rho > 0$). Moreover, $\mathscr{R}_0$ becomes smaller as the proportion of immune visitors at the entry ρ gets larger. If any visitor is susceptible, that is, when $\rho = 0$, there is no contribution of the visitors to the basic reproduction number $\mathscr{R}_0$, that is, $\mathscr{R}_0 = \mathscr{R}_{00}$.

As an extremal case, if the immunity gained by the vaccination or recovery from the disease does not work at all to reduce the risk of reinfection, that is, if $\epsilon = 1$, the basic reproduction number $\mathscr{R}_0$ is independent of the acceptance of visitors. This is easily understandable, since the reinfection is regarded as the same as the infection for the susceptible so that the immune individual is regarded as equivalent to the susceptible according to the epidemic dynamics when $\epsilon = 1$. Such an extreme case may be regarded as corresponding to an SIS type of the epidemic dynamics, where the state transition in terms of the disease follows the susceptible–infective–susceptible structure.

As the other extremal case, if the immunity is perfectly effective to make the immune individual unable to be reinfected, that is, if $\epsilon = 0$, the entry of immune visitors works to reduce the value of $\mathscr{R}_0$ for the community. This extremal case may be regarded as corresponding to an SIR type of the epidemic dynamics, where the state transition in terms of the disease follows the susceptible–infective–removed structure.

From these arguments with the basic reproduction number $\mathscr{R}_0$ given by (22), We can get the following result on the influence of the acceptance of visitors at the early stage of the disease invasion in the community (Figure 8):

Theorem 3.1. *The acceptance of visitors influences the basic reproduction number $\mathscr{R}_0$ given by (22) for the epidemic dynamics with the system of (19) and (20) as follows:*

(i) The acceptance of visitors makes $\mathscr{R}_0$ smaller than $\mathscr{R}_{00}$ if and only if the visitors contain some immune, and its decrease becomes bigger as the number of accepted visitors gets larger;

(ii) When $\mathscr{R}_{00} > 1$, if

$$\rho \leqslant \rho^0_\infty := \frac{1}{1-\epsilon}\left(1 - \frac{1}{\mathscr{R}_{00}}\right),$$

then $\mathscr{R}_0 > 1$ independently of the number of accepted visitors;

(iii) When $\mathscr{R}_{00} > 1$, if and only if $\rho > \rho^0_\infty$, the acceptance of visitors so many as

$$\mu > \frac{1 - 1/\mathscr{R}_{00}}{(1-\epsilon)\rho - (1 - 1/\mathscr{R}_{00})}$$

makes $\mathscr{R}_0 < 1$.

The result (*i*) in Theorem 3.1 means that the acceptance of visitors does not help the invasion success of a transmissible disease as long as $\mathscr{R}_{00} \leqslant 1$, and instead it could work to suppress the invasion if the community accepts a sufficiently large number of visitors with a sufficiently large proportion of immune, as indicated by the results (*ii*) and (*iii*).

Note that these arguments and result are about the effect of the acceptance of visitors on the temporal change of the number of infectives only in the early period after the community starts the acceptance of visitors. They cannot be necessarily applied for its long-term temporal change. It may be possible that the number of infectives turns to increase in a later period, independently of what final state the epidemic dynamics approaches, as we will actually see in the later sections of the analysis on our model.

3.3 MATHEMATICAL RESULTS ON THE MODEL

3.3.1 *Non-dimensional transformation of the system*

Since the population sizes of visitors and residents are assumed constant independently of time, the above six dimensional system of (19) and (20) can be mathematically reduced to the following closed four dimensional one, making use of $S_v + I_v + R_v = m$ and $S_r + I_r + R_r = N$:

$$\begin{aligned}
\frac{dS_v}{dt} &= (1-\rho)qm - \beta\frac{I_r + I_v}{N+m}S_v - qS_v;\\
\frac{dI_v}{dt} &= \beta\frac{I_r + I_v}{N+m}S_v + \epsilon\beta\frac{I_r + I_v}{N+m}(m - S_v - I_v) - \gamma I_v - qI_v;\\
\frac{dS_r}{dt} &= -\beta\frac{I_r + I_v}{N+m}S_r - \sigma S_r;\\
\frac{dI_r}{dt} &= \beta\frac{I_r + I_v}{N+m}S_r + \epsilon\beta\frac{I_r + I_v}{N+m}(N - S_r - I_r) - \gamma I_r.
\end{aligned}$$

Now we apply the following transformation of variables and parameters for this four dimensional system:

$$\begin{aligned}
&\tau := \gamma t;\ x_v(t) := \frac{S_v(t)}{m};\ y_v(t) := \frac{I_v(t)}{m};\ x_r(t) := \frac{S_r(t)}{N};\ y_r(t) := \frac{I_r(t)}{N};\\
&\mu := \frac{m}{N};\ c := \frac{q}{\gamma};\ \omega := \frac{\sigma}{\gamma},
\end{aligned}$$

and then we can derive the following non-dimensinalized system:

$$\begin{aligned}
\frac{dx_v}{d\tau} &= (1-\rho)c - \mathscr{R}_{00}\frac{y_r + \mu y_v}{1+\mu}x_v - cx_v;\\
\frac{dy_v}{d\tau} &= \mathscr{R}_{00}\frac{y_r + \mu y_v}{1+\mu}x_v + \epsilon\mathscr{R}_{00}\frac{y_r + \mu y_v}{1+\mu}(1 - x_v - y_v) - (1+c)y_v;\\
\frac{dx_r}{d\tau} &= -\mathscr{R}_{00}\frac{y_r + \mu y_v}{1+\mu}x_r - \omega x_r;\\
\frac{dy_r}{d\tau} &= \mathscr{R}_{00}\frac{y_r + \mu y_v}{1+\mu}x_r + \epsilon\mathscr{R}_{00}\frac{y_r + \mu y_v}{1+\mu}(1 - x_r - y_r) - y_r,
\end{aligned} \tag{23}$$

where $\mathscr{R}_{00} := \beta/\gamma$ as before. Remark that the symbol $\mathscr{R}_{00}$ is formally introduced now as a dimensionless parameter for the non-dimensionalized system given by (23), while its meaning is given in Section 3.2 as the basic

reproduction number for the community when no visitor comes in. The initial condition (21) now becomes

$$(x_v(0), y_v(0), x_r(0), y_r(0)) = (1-\rho, 0, x_{r0}, y_{r0})$$

with $x_{r0} := S_{r0}/N = 1 - I_{r0}/N = 1 - y_{r0}$. In the following sections, we shall analyze the non-dimensionalized system (23) to investigate the nature of the epidemic dynamics by our model with the system of (19) and (20).

3.3.2 *Dynamics without reinfection*

In this section, we consider the system without reinfection, that is, with $\epsilon = 0$, while we will consider our model only with $\epsilon > 0$ in the subsequent sections. For the system (23) with $\epsilon = 0$, we can easily find that $x_r \to 0$ and $y_r \to 0$ as $\tau \to \infty$. In other words, since the epidemic dynamics for the resident population is governed by an SIR model with the continuous vaccination for the susceptibles, the disease eventually disappears in the resident population, and the residents come to make no contribution to the epidemic dynamics. This means that, for our model of (19) and (20) *without reinfection*, no endemic state can be established as long as the community does not accept any visitor from the outside. Thus we consider the case of $\mu > 0$ hereafter in this section, when the community accepts the visitors.

By the local stability analysis with the eigenvalues of Jacobi matrix at the equilibrium, we can easily find that the endemic equilibrium $E_{+0}(\widetilde{x}_v^*, \widetilde{y}_v^*, 0, 0)$ with

$$\widetilde{x}_v^* = \frac{(1+c)(1+\mu)}{\mathscr{R}_{00}\mu}; \quad \widetilde{y}_v^* = c\Big(\frac{1-\rho}{1+c} - \frac{1+\mu}{\mathscr{R}_{00}\mu}\Big) \tag{24}$$

is locally asymptotically stable when it exists. Then we can get the following theorem on the epidemic dynamics given by (23) with $\epsilon = 0$ (Appendix B.2):

Theorem 3.2. *For the system* (23) *with* $\epsilon = 0$*, if and only if the condition*

$$\mathscr{R}_{00} > \frac{1}{1-\rho}\Big(1 + \frac{1}{\mu}\Big)(1+c) \tag{25}$$

is satisfied, the endemic equilibrium $E_{+0}(\widetilde{x}_v^*, \widetilde{y}_v^*, 0, 0)$ *with* (24) *uniquely exists, and it is globally asymptotically stable. Otherwise, the disease-eliminated equilibrium* $E_{00}(1-\rho, 0, 0, 0)$ *is globally asymptotically stable.*

See Figure 9(a, b) for numerical examples.

From the basic reproduction number $\mathscr{R}_0$ given by (22) with $\epsilon = 0$, we can easily find that $\mathscr{R}_0 > 1$ if the condition (25) is satisfied, while the inverse does not necessarily hold. Hence we can get the following result:

Corollary 3.2.1. *Even when the disease successfully invades in the community with* $\mathscr{R}_0 > 1$*, the disease without reinfection eventually gets eliminated unless the condition* (25) *is satisfied.*

When the condition (25) is unsatisfied with $\mathscr{R}_0 > 1$, the number of infectives increases at the initial stage of disease spread in the community, and then it eventually turns to decrease toward zero, as numerically exemplified in Figure 9(a).

For $\rho = 1$, the condition (25) cannot be satisfied:

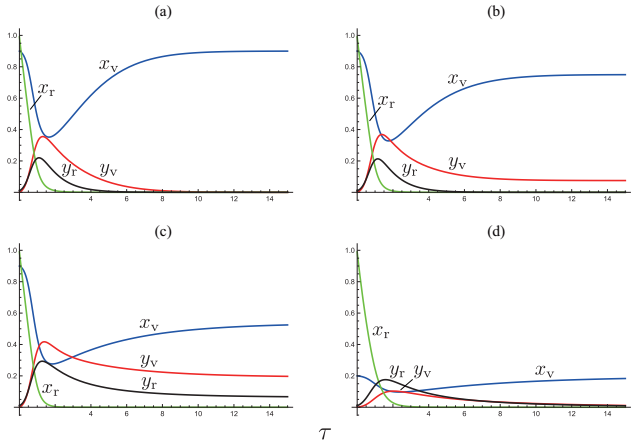

Figure 9: Temporal variations by the system (23). Numerically drawn with (a) $(\epsilon, \mu, \rho) = (0.0, 0.2, 0.1)$ ($\mathscr{R}_0 = 7.87$); (b) $(\epsilon, \mu, \rho) = (0.0, 0.5, 0.1)$ ($\mathscr{R}_0 = 7.73$); (c) $(\epsilon, \mu, \rho) = (0.1, 0.2, 0.1)$ ($\mathscr{R}_0 = 7.88$); (d) $(\epsilon, \mu, \rho) = (0.1, 0.5, 0.8)$ ($\mathscr{R}_0 = 6.08$); and commonly $\mathscr{R}_{00} = 8.0$; $c = 1.0$; $\omega = 1.0$; $(x_v(0), y_v(0), x_r(0), y_r(0)) = (1-\rho, 0.0, 0.99, 0.01)$. In (a, d), the system approaches the disease-eliminated equilibrium, and in (b, c), it approaches the endemic equilibrium.

Corollary 3.2.2. *If the community accepts only immune visitors, the epidemic dynamics without reinfection necessarily approaches the disease-eliminated equilibrium.*

Therefore, when the reinfection is impossible/negligible, the acceptance of visitors with a high immune proportion at the entry does not cause the endemicity of disease.

We must remark that the endemic equilibrium E_{+0} is sustained only by the visitor subpopulation, while no resident contributes to the epidemic dynamics at the equilibrium because all residents have eventually become immune by the past infection or vaccination (Figure 9(a, b)). From Theorem 3.2, for the disease with a sufficiently high infectivity, the acceptance of many visitors with a sufficiently small immune proportion at the entry can cause such an apparent endemicity in the community. Therefore, as seen in Figure 9(a, b), when the community successfully controls and reduces the number of visitors to make μ sufficiently small, or if the community suspends accepting the visitors, the endemic state can be disrupted, and then the disease gets eliminated in the community. However, as we will see in the subsequent sections, if the disease is accompanied by a reinfectivity, this could not be the case (Figure 9(c, d)).

3.3.3 *Dynamics with no visitor*

Next we consider the model of (19) and (20) with reinfection, that is, with $\varepsilon > 0$, when the community does not accept any visitor from the outside. Thus we analyze the following system derived from (23) with $x_v = y_v \equiv 0$ and $\mu = 0$:

$$\begin{aligned} \frac{dx_r}{d\tau} &= -\mathscr{R}_{00} y_r x_r - \omega x_r; \\ \frac{dy_r}{d\tau} &= (1-\epsilon)\mathscr{R}_{00} y_r x_r - \epsilon \mathscr{R}_{00} y_r^2 - \left(1 - \epsilon \mathscr{R}_{00}\right) y_r. \end{aligned} \tag{26}$$

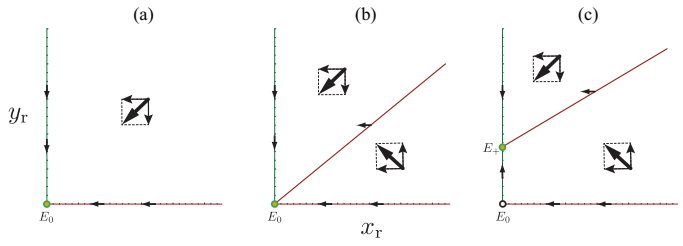

Figure 10: Application of the isocline method for the system with no visitor (26) when (a) $\epsilon\mathscr{R}_{00} < 1$; (b) $\epsilon\mathscr{R}_{00} = 1$; (c) $\epsilon\mathscr{R}_{00} > 1$.

As already mentioned in Section 3.2, tthe basic reproduction number for this epidemic dynamics is defined as $\mathscr{R}_0 = \mathscr{R}_{00} = \beta/\gamma$. It is easy to find that there are two feasible equilibria for this system of (x_r, y_r): the disease-eliminated equilibtium $E_0(0,0)$ and the endemic equilibrium $E_+\big(0, 1 - 1/(\epsilon\mathscr{R}_{00})\big)$. The endemic equilibrium E_+ exists when and only when $\epsilon\mathscr{R}_{00} > 1$.

Making use of the local stability analysis for the equilibrium of the system (26), we can easily find that the equilibrium E_0 is locally asymptotically stable if $\epsilon\mathscr{R}_{00} < 1$, and unstable if $\epsilon\mathscr{R}_{00} > 1$. The endemic equilibrium E_+ is locally asymptotically stable whenever it exists. Taking account of the result on the local stability of equilibria, the isocline method for the two dimensional system (26) can further give the following result (see Figure 10):

Theorem 3.3. *For the system* (26) *with no visitor,*

(i) if and only if $\epsilon\mathscr{R}_{00} \leqslant 1$, *the disease-eliminated equilibrium* E_0 *is globally asymptotically stable;*

(ii) if and only if $\epsilon\mathscr{R}_{00} > 1$, *the endemic equilibrium* E_+ *exists and is globally asymptotically stable, while* E_0 *is unstable.*

This result was shown for a mathematically equivalent SIRI model in[131].

From this result, we find that, even with the basic reproduction number $\mathscr{R}_{00} > 1$, the community approaches the disease-eliminated equilibrium E_0 if $\mathscr{R}_{00} \leqslant 1/\epsilon$ with $0 < \epsilon < 1$. In such a case, the number of infectives increases at the initial stage of disease spread in the community, and then it eventually turns to decrease toward zero. If and only if the basic reproduction number is sufficiently large as $\mathscr{R}_{00} > 1/\epsilon$, the disease becomes endemic in the community.

As shown in the previous section, no endemicity arises in the community with a non-reinfectious disease when no visitor is accepted. Now the result obtained in this section indicates that the endemicity of a disease can arise in the community even with no visitor if the disease has both sufficiently high infectivity ($\mathscr{R}_{00} > 1$) and sufficiently high reinfectivity ($\epsilon > 1/\mathscr{R}_{00}$).

3.3.4 *Dynamics with visitors*

Disease-eliminated equilibrium

For the system (23) with visitors, we can get the following result on the local stability of the disease-eliminated equilibrium $E_{00}(1-\rho, 0, 0, 0)$ (Appendix B.3):

Theorem 3.4. *The disease-eliminated equilibrium* E_{00} *is unstable if*

$$\epsilon\mathscr{R}_{00} > G(\mu, \rho) := \left[\left\{\frac{1}{\epsilon}(1-\rho) + \rho\right\}\frac{1}{1+c}\frac{\mu}{1+\mu} + \frac{1}{1+\mu}\right]^{-1}, \qquad (27)$$

while it is locally asymptotically stable if the inverse inequality of (27) *is satisfied.*

It can be easily seen that the condition (27) becomes equivalent to (25) as $\epsilon \to 0$. This shows a mathematical consistency of Theorem 3.4 to Theorem 3.2.

Moreover we can prove the following result about the relation of the basic reproduction number $\mathscr{R}_0$ defined by (22) to the condition (27) (Appendix B.4):

Corollary 3.4.1. *When $\mathscr{R}_0 \leqslant 1$, the disease-eliminated equilibrium E_{00} is locally asymptotically stable.*

This result is consistent with the biological/epidemiological meaning of the basic reproduction number with respect to the invasion success of a disease in a population, which was described in Section 3.2 and references therein. Under the condition that $\mathscr{R}_0 < 1$ at the initial stage of a disease invasion in a population, the number of infectives is expected to decrease toward the disease elimination. In a sense of epidemic dynamics, such a decline of the infective subpopulation toward the elimination must follow the locally asymptotic stability of the disease-free equilibrium (as referred in most literatures), which corresponds here to the disease-eliminated equilibrium E_{00}. The result of Corollary 3.4.1 shows this consistency.

Endemic equilibrium

From the equations of (23), if the endemic equilibrium $E_{++}(x_v^*, y_v^*, x_r^*, y_r^*)$ with $y_v^* > 0$ and $y_r^* > 0$ exists for $\rho < 1$, it must satisfy that

$$\begin{aligned} \mathscr{R}_{00}\frac{y_r^* + \mu y_v^*}{1+\mu} &= c\frac{1-\rho-x_v^*}{x_v^*}, \\ y_v^* &= \frac{1-\rho-x_v^*}{x_v^*}\,\frac{(1-\epsilon)x_v^* + \epsilon}{1 + 1/c + \epsilon(1-\rho-x_v^*)/x_v^*}, \\ y_r^* &= \frac{1-\rho-x_v^*}{x_v^*}\,\frac{\epsilon}{1/c + \epsilon(1-\rho-x_v^*)/x_v^*}, \end{aligned} \tag{28}$$

and $x_r^* = 0$. In contrast, at the endemic equilibrium E_{++} for $\rho = 1$, we have

$$\begin{aligned} \epsilon\mathscr{R}_{00}\frac{y_r^* + \mu y_v^*}{1+\mu}(1-y_v^*) - (1+c)y_v^* &= 0, \\ \epsilon\mathscr{R}_{00}\frac{y_r^* + \mu y_v^*}{1+\mu}(1-y_r^*) - y_r^* &= 0, \end{aligned} \tag{29}$$

and $x_v^* = 0$, $x_r^* = 0$, instead of (28). We can obtain the following result on the existence of E_{++} (Appendix B.5):

Theorem 3.5. *The endemic equilibrium E_{++} uniquely exists if and only if the condition* (27) *is satisfied.*

Hence, when the disease-eliminated equilibrium E_{00} is locally asymptotically stable, the endemic equilibrium E_{++} does not exist, and when E_{00} is unstable, E_{++} uniquely exists.

For the local stability of the endemic equilibrium E_{++} for (23), we can get the following result:

Theorem 3.6. *When the endemic equilibrium E_{++} exists, it is locally asymptotically stable.*

This theorem can be proved by the eigenvalue analysis on the Jacobi matrix for (23) at the endemic equilibrium E_{++}, applying the Routh-Hurwitz

criterion (Appendix B.6). Although we could not get any analytical result on the global stability of the endemic equilibrium E_{++}, our numerical calculations imply that it is globally asymptotically stable when it exists. We then have the mathematical consistency of Theorems 3.4, 3.5, and 3.6 to Theorem 3.2 as for the case with no reinfection, $\epsilon = 0$.

3.3.5 *Influence of the acceptance of visitors*

Shift in endemicity

First we can easily find the following features of $G(\mu, \rho)$ defined in (27):

- $G(0, \rho) = 1$.
- $G(\mu, \rho)$ is monotonically increasing in terms of ρ for any $\mu > 0$.
- $G(\mu, \rho)$ is $\begin{cases} \text{monotonically increasing in terms of } \mu \text{ if } \rho > \rho_s := 1 - \dfrac{c}{1/\epsilon - 1}; \\ \text{constant } (\equiv 1) \text{ independently of } \mu \text{ if } \rho = \rho_s; \\ \text{monotonically decreasing in terms of } \mu \text{ if } \rho < \rho_s. \end{cases}$
- $G(\mu, \rho) < 1$ for any positive μ and $\rho < \rho_s$ if and only if $\epsilon < 1/(1+c)$.
- $G(\mu, 0)$ is $\begin{cases} \text{monotonically increasing in terms of } \mu \text{ if } \rho_s < 0, \text{ that is, } \epsilon > \dfrac{1}{1+c}; \\ \text{constant } (\equiv 1) \text{ independently of } \mu \text{ if } \rho_s = 0, \text{ that is, } \epsilon = \dfrac{1}{1+c}; \\ \text{monotonically decreasing in terms of } \mu \text{ if } \rho_s > 0, \text{ that is, } \epsilon < \dfrac{1}{1+c}. \end{cases}$
- $G(\mu, 0)$ $\begin{cases} > 1 \text{ for any } \mu > 0 \text{ and } \epsilon > \dfrac{1}{1+c}; \\ > 1 \text{ for any } \mu > 0 \text{ and } \epsilon < \dfrac{1}{1+c}. \end{cases}$
- $\inf\limits_{\mu \in (0,\infty)} G(\mu, \rho) = \begin{cases} G(0, \rho) = 1 \text{ for } \epsilon \geqslant \dfrac{1}{1+c}; \\ \lim\limits_{\mu \to \infty} G(\mu, \rho) = G_\infty(\rho) := \dfrac{1+c}{(1-\rho)/\epsilon + \rho} < 1 \text{ for } \epsilon < \dfrac{1}{1+c}. \end{cases}$
- $\sup\limits_{\mu \in (0,\infty)} G(\mu, \rho) = \begin{cases} G_\infty(\rho) \geqslant 1 \text{ for } \rho \geqslant \rho_s; \\ G(0, \rho) = 1 \text{ for } \rho < \rho_s. \end{cases}$
- $\inf\limits_{(0,\infty)\times(0,1)} G(\mu, \rho) = \begin{cases} G(0, 0) = 1 \text{ for } \epsilon \geqslant \dfrac{1}{1+c}; \\ \lim\limits_{\mu \to \infty} G(\mu, 0) = \epsilon(1+c) < 1 \text{ for } \epsilon < \dfrac{1}{1+c}. \end{cases}$
- $\sup\limits_{(0,\infty)\times(0,1)} G(\mu, \rho) = \lim\limits_{\mu \to \infty} G(\mu, 1) = 1 + c.$

Then from these mathematical features of $G(\rho, \mu)$, and Theorems 3.4, 3.5, and 3.6, we can get the following result on the disease endemicity in the community accepting the visitors (see Figures 11 and 12):

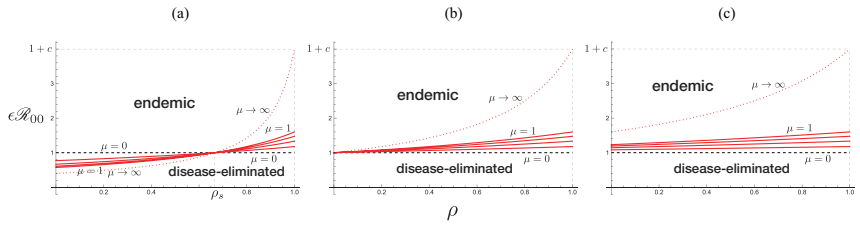

Figure 11: Parameter region and boundary indicated by the condition (27). The boundary curve is given by $G(\mu, \rho)$. (a) $\epsilon < 1/(1+c)$; (b) $\epsilon = 1/(1+c)$; (c) $\epsilon > 1/(1+c)$. Numerically drawn with (a) $\epsilon = 0.10$; (b) $\epsilon = 0.25$; (c) $\epsilon = 0.40$, commonly for $c = 3.0$. Solid curves are for $\mu = 0.25, 0.5, 0.75, 1.0$ in each figure. Dotted curve indicates $G_\infty(\rho)$.

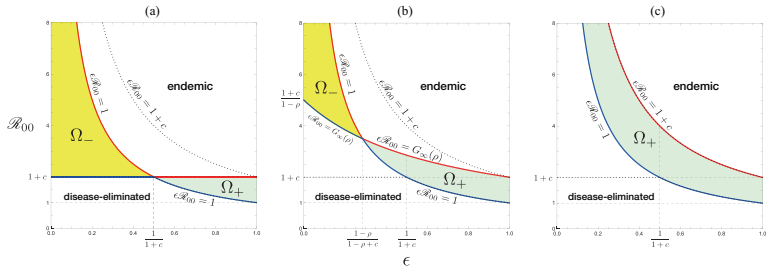

Figure 12: $(\epsilon, \mathscr{R}_{00})$-dependence of the endemicity, derived from the condition (30) in Theorem 3.7. Numerically drawn for (a) $\rho = 0.0$; (b) $\rho = 0.6$; (c) $\rho = 1.0$, commonly with $c = 1.0$. For the region Ω_+, the acceptance of visitors may change the endemic situation of the community for the disease-eliminated equilibrium as described in Theorem 3.8, while, for the region Ω_-, it may drive the situation of the community approaching the disease-eliminated equilibrium toward the endemic equilibrium as described in Theorem 3.9. For the region out of Ω_- and Ω_+, the endemicity is independent of whether the community accepts visitors or not.

Theorem 3.7. *Independently of whether the community accepts the visitors or not, it necessarily approaches an endemic equilibrium if* $\epsilon\mathscr{R}_{00} \geqslant \max\left[1, G_\infty(\rho)\right]$, *while it necessarily approaches the disease-eliminated equilibrium if* $\epsilon\mathscr{R}_{00} \leqslant \min\left[G_\infty(\rho), 1\right]$, *where*

$$G_\infty(\rho) := \lim_{\mu\to\infty} G(\mu, \rho) = \frac{1+c}{(1-\rho)/\epsilon + \rho}.$$

Only when

$$\min\left[G_\infty(\rho), 1\right] < \epsilon\mathscr{R}_{00} < \max\left[1, G_\infty(\rho)\right], \tag{30}$$

the endemicity could significantly depend on the acceptance of visitors.

The inequality (30) gives a necessary condition for which the acceptance of visitors could change the epidemic situation in the community from the endemic equilibrium to the disease-eliminated equilibrium or vice versa. The corresponding parameter regions are shown as Ω_- and Ω_+ in Figure 11. Numerical examples of such a change of endemicity by the acceptance of visitors are given in Figure 13(a, c).

Further from the monotonicity of $G(\mu, \rho)$ in terms of μ and ρ as described in the above, we find the following result on the condition with respect to the influence of the acceptance of visitors on the endemicity in the community:

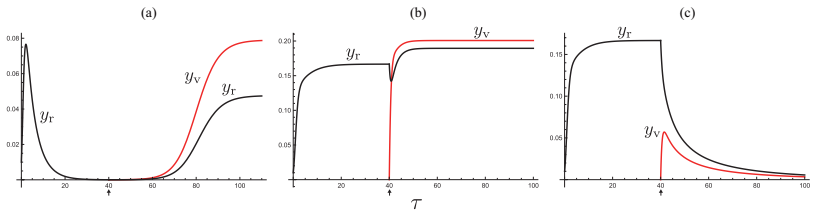

Figure 13: Temporal variations of infective subpopulations y_r and y_v by the systems (23) and (26). Numerically drawn for the model (26) until $\tau = 40$ until $\tau = 40$ and model (23) for $\tau > 40$, with (a) $(\epsilon, \mu, \rho) = (0.2, 0.9, 0.3)$ ($\mathscr{R}_0 = 3.55$; $\epsilon\mathscr{R}_{00} = 0.8$); (b) $(\epsilon, \mu, \rho) = (0.3, 0.9, 0.3)$ ($\mathscr{R}_0 = 3.60$; $\epsilon\mathscr{R}_{00} = 1.2$); (c) $(\epsilon, \mu, \rho) = (0.3, 0.9, 0.9)$ ($\mathscr{R}_0 = 2.81$; $\epsilon\mathscr{R}_{00} = 1.2$); and commonly $\mathscr{R}_{00} = 4.0$; $c = 1.0$; $\omega = 1.0$; $(x_r(0), y_r(0)) = (0.99, 0.01)$; $(x_v(40), y_v(40)) = (1-\rho, 0.0)$. In (a) and (c), the endemicity is changed before and after starting the acceptance of visitors, while in (b) the system remains at an endemic state before and after it.

Corollary 3.7.1. *Independently of whether the community accepts the visitors or not, it necessarily approaches an endemic equilibrium if*

$$\epsilon\mathscr{R}_{00} \geqslant \sup_{(0,\infty)\times(0,1)} G(\mu, \rho) = 1 + c,$$

while it necessarily approaches the disease-eliminated equilibrium if

$$\epsilon\mathscr{R}_{00} \leqslant \inf_{(0,\infty)\times(0,1)} G(\mu, \rho) = \min\left[1,\ \epsilon(1+c)\right].$$

Only when

$$\min\left[1,\ \epsilon(1+c)\right] < \epsilon\mathscr{R}_{00} < 1 + c, \tag{31}$$

the endemicity could significantly depend on the acceptance of visitors.

As seen in Figures 11 and 12, such an influence to cause a change of endemicity depends on the nature of accepted visitors (i.e., the number, the immune proportion, and the duration of stay).

Moreover, from the features of $G(\mu, \rho)$ described in the above, we find that, if $\epsilon\mathscr{R}_{00} \geqslant G_\infty(\rho) \geqslant 1$, the disease is endemic independently of how many visitors the community accepts even under the condition (31), as seen in Figure 11. Thus, in comparison to the result for the community with no visitor (i.e., $\mu = 0$) given by Theorem 3.3, we can get the following result (see Figure 12):

Theorem 3.8. *Suppose that the disease was endemic under the condition that $1 < \epsilon\mathscr{R}_{00} < 1 + c$ before the community accepts visitors. If the community accepts visitors with an immune proportion*

$$\rho \leqslant \rho_\infty := \frac{1}{1-\epsilon}\left(1 - \frac{1+c}{\mathscr{R}_{00}}\right), \tag{32}$$

the disease remains endemic independently of how many visitors are accepted. If the community accepts visitors with an immune proportion $\rho > \rho_\infty$, then the acceptance of visitors so many as

$$\mu > \mu_c := \frac{1 - 1/(\epsilon\mathscr{R}_{00})}{1/(\epsilon\mathscr{R}_{00}) - \{(1-\rho)/\epsilon + \rho\}/(1+c)} \tag{33}$$

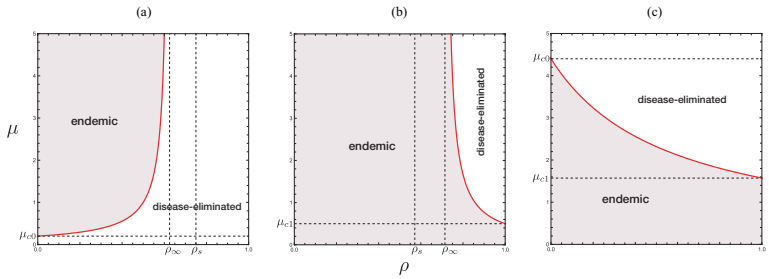

Figure 14: (ρ, μ)-dependence of the endemicity, derived from the condition (27) with the results given by Theorems 3.4, 3.5, and 3.6: (a, b) $\epsilon < 1/(1+c)$; (c) $\epsilon > 1/(1+c)$. Numerically drawn for (a) $(\mathscr{R}_{00}, \epsilon, c) = (4.0, 0.2, 1.0)$ $(\epsilon\mathscr{R}_{00} = 0.8)$; (b) $(\mathscr{R}_{00}, \epsilon, c) = (4.0, 0.3, 1.0)$ $(\epsilon\mathscr{R}_{00} = 1.2)$; (c) $(\mathscr{R}_{00}, \epsilon, c) = (1.8, 0.8, 1.0)$ $(\epsilon\mathscr{R}_{00} = 1.44)$, each of which satisfies the condition (31) in Corollary 3.7.1.

makes the community approach the disease-eliminated equilibrium. Even if $\rho > \rho_\infty$, the acceptance of visitors with $\mu \leqslant \mu_c$ does not sufficiently shift the endemicity, and the disease remains endemic.

The critical value ρ_∞ satisfies the equation $\epsilon\mathscr{R}_{00} = G_\infty(\rho_\infty)$. The latter case of $\rho > \rho_\infty$ in Theorem 3.8 corresponds to the parameter region Ω_+ in Figure 12. Figure 14(b) shows a numerical example of the (ρ, μ)-dependence in such a case when $\epsilon\mathscr{R}_{00} > 1$.

Since μ_c defined by (33) is monotonically decreasing in terms of ρ when $\epsilon\mathscr{R}_{00} > 1$, we note that

$$\mu_c \geqslant \mu_c\big|_{\rho=1} = \mu_{c1} := \frac{1 - 1/(\epsilon\mathscr{R}_{00})}{1/(\epsilon\mathscr{R}_{00}) - 1/(1+c)}, \tag{34}$$

where $\mu_{c1} > 0$ for $1 < \epsilon\mathscr{R}_{00} < 1 + c$. Hence we get the following corollary:

Corollary 3.8.1. *When $1 < \epsilon\mathscr{R}_{00} < 1 + c$, if the community accepts visitors few enough to have $\mu < \mu_{c1}$, the disease remains endemic independently of how much proportion of visitors is immune at the entry.*

This result is numerically pointed out in Figure 14(b, c).

Moreover we note that, when ρ_∞ defined by (32) is negative, that is, when $\mathscr{R}_{00} < 1 + c$, the first case in Theorem 3.8 does not occur. Then the (ρ, μ)-dependence becomes as shown by Figure 14(c), where there is a finite value of μ beyond which the community approaches the disease-eliminated equilibrium, independently of the immune proportion in the visitors at the entry:

$$\mu_{c0} := \mu_c\big|_{\rho=0} = \frac{1 - 1/(\epsilon\mathscr{R}_{00})}{1/(\epsilon\mathscr{R}_{00}) - 1/\{\epsilon(1+c)\}}. \tag{35}$$

Corollary 3.8.2. *When $1 < \epsilon\mathscr{R}_{00} < \epsilon(1+c)$, if the community accepts visitors so many as $\mu > \mu_{c0}$, the disease goes eliminated independently of how much proportion of visitors is immune at the moment of their immigration. When $\epsilon(1+c) \leqslant \epsilon\mathscr{R}_{00} < 1 + c$, only the acceptance of visitors with $\rho > \rho_\infty$ and $\mu > \mu_c$ can change the endemicity and lead the community to the disease-eliminated equilibrium.*

Hence the value μ_{c0} gives a sufficient number of accepted visitors which is effective to suppress the spread of disease in the community when $1 < \epsilon\mathscr{R}_{00} < \epsilon(1+c)$. See the numerical examples in Figure 13(b, c).

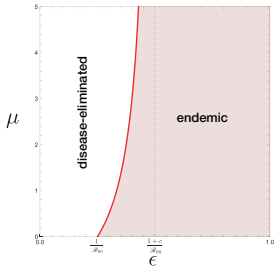

Figure 15: Parameter region and boundary indicated by the condition (27) with the results given by Theorems 3.4, 3.5, and 3.6 when the community accepts only immune visitors with $\rho = 1$. Numerically drawn with $\mathscr{R}_{00} = 4.0$ and $c = 1.0$.

In contrast, when the risk of reinfection is so weak as $\epsilon < 1/(1+c)$, the acceptance of visitors may cause the inverse influence on the epidemic dynamics, as numerically indicated by Figure 14(a):

Theorem 3.9. *Suppose that the disease was getting eliminated under the condition that* $\epsilon(1+c) < \epsilon\mathscr{R}_{00} < 1$ *before the community accepts visitors. If the community accepts visitors with an immune proportion* $\rho \geqslant \rho_\infty$*, the disease keeps getting eliminated independently of how many visitors are accepted. If the community accepts visitors with an immune proportion* $\rho < \rho_\infty$*, then the acceptance of visitors so many as* $\mu > \mu_c$ *induces the endemicity, and the disease becomes endemic. Even if* $\rho < \rho_\infty$*, the acceptance of visitors so few as* $\mu \leqslant \mu_c$ *does not induce the endemicity, and the disease keeps getting eliminated.*

The situation considered in this theorem corresponds to the parameter region Ω_- in Figure 12, and is numerically exemplified by Figure 13(a). Theorem 3.9 indicates that, if the proportion of immune visitors is so low as $\rho < \rho_\infty$, there exists the upper threshold μ_c for the number of accepted visitors to suppress the revival of the disease spread after starting the acceptance of visitors in the community where the disease was getting eliminated.

Acceptance of only immune visitors

When the community accepts only immune visitors, that is, when $\mu > 0$ with $\rho = 1$, $G(\mu, 1)$ is necessarily greater than 1 and monotonically increasing in terms of μ. Then, from Theorem 3.8, we can find that only the acceptance of visitors so many as $\mu > \mu_{c1}$ can induce the disease-eliminated equilibrium in the community where the disease was endemic before starting the acceptance of visitors. As defined by (34), the critical value μ_{c1} depends on the risk of reinfection, and then, from Theorems 3.7 and 3.8, we can find the following result (see Figures 14 and 15):

Corollary 3.8.3. *Suppose that the disease was endemic under the condition that* $\epsilon\mathscr{R}_{00} > 1$ *before the community accepts only immune visitors. If* $\epsilon\mathscr{R}_{00} \geqslant 1+c$*, the endemicity remains independently of how many visitors the community accepts. If* $1 < \epsilon\mathscr{R}_{00} < 1+c$*, the acceptance of visitors so many as* $\mu > \mu_{c1}$ *is effective to make the disease eliminated.*

Therefore the community under an endemic situation could have a preferable influence to suppress the endemicity by accepting only immune visitors only when the reinfectivity is sufficiently low as indicated by Figure 15.

If the community was approaching the disease-eliminated equilibrium with the risk of reinfection so low as $\epsilon\mathscr{R}_{00} \leqslant 1$, the community keeps

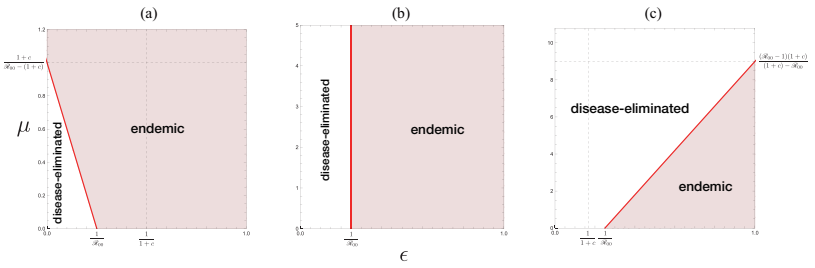

Figure 16: Parameter region and boundary indicated by the condition the condition (27) with the results given by Theorems 3.4, 3.5, and 3.6 when all visitors accepted by the community is susceptible with $\rho = 0$: (a) $\mathscr{R}_{00} > 1 + c$; (b) $\mathscr{R}_{00} = 1 + c$; (c) $\mathscr{R}_{00} < 1 + c$. Numerically drawn with (a) $c = 1.0$; (b) $c = 3.0$; (c) $c = 5.0$, and commonly $\mathscr{R}_{00} = 4.0$.

approaching the disease-eliminated equilibrium even after starting the acceptance of only immune visitors, independently of how many visitors the community accepts.

Acceptance of only susceptible visitors

Now let us consider the case where all visitors accepted by the community are susceptible, that is, when $\mu > 0$ with $\rho = 0$. Then, from Theorem 3.9, we find three different cases according to the influence of the acceptance of visitors as shown in Figure 16, taking account of the features of $G(\mu, 0)$ given at the beginning of this section. For this case, we can get the following result:

Corollary 3.9.1. *When the disease was getting eliminated under the condition that* $\epsilon\mathscr{R}_{00} \leqslant 1$, *the acceptance of only susceptible visitors induces*

$$\begin{cases} \text{no endemicity if } \epsilon\mathscr{R}_{00} \leqslant \epsilon(1+c); \\ \text{no endemicity if } \epsilon\mathscr{R}_{00} > \epsilon(1+c) \text{ and } \mu \leqslant \mu_{c0}; \\ \text{the endemicity if } \epsilon\mathscr{R}_{00} > \epsilon(1+c) \text{ and } \mu > \mu_{c0}. \end{cases}$$

In contrast, when the disease was endemic under the condition that $\epsilon\mathscr{R}_{00} > 1$, *the acceptance of only susceptible visitors induces*

$$\begin{cases} \text{no change in the endemicity if } \epsilon\mathscr{R}_{00} \geqslant \epsilon(1+c); \\ \text{no change in the endemicity if } \epsilon\mathscr{R}_{00} < \epsilon(1+c) \text{ and } \mu \leqslant \mu_{c0}; \\ \text{the elimination of disease if } \epsilon\mathscr{R}_{00} < \epsilon(1+c) \text{ and } \mu > \mu_{c0}. \end{cases}$$

The critical value μ_{c0} is defined by (35).

Therefore the acceptance of only susceptible visitors could have the counter effect according to the endemicity, depending on the infectivity of disease. Only for a moderately high infectious disease such that $1/\epsilon < \mathscr{R}_{00} < 1 + c$, the acceptance of only susceptible visitors so many as $\mu > \mu_{c0}$ can lead the community to the disease-eliminated equilibrium. For the disease with a low reinfectivity such that $1 + c < \mathscr{R}_{00} \leqslant 1/\epsilon$, the acceptance of only susceptible visitors so many as $\mu > \mu_{c0}$ can lead the community to the endemic equilibrium.

Further, as indicated by Figure 16, we find that there is a sufficient value of μ which determines the epidemic situation in the community:

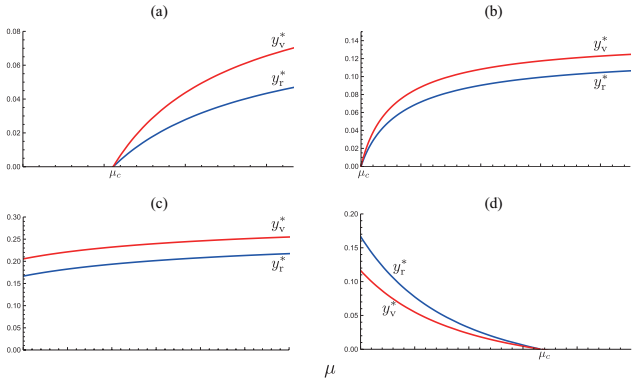

Figure 17: The μ-dependence of endemic sizes. Numerically drawn by (28) with (a) $(\epsilon, \rho) = (0.2, 0.4)$ ($\epsilon\mathscr{R}_{00} = 0.8$, $\mu_c = 0.56$); (b) $(\epsilon, \rho) = (0.25, 0.4)$ ($\epsilon\mathscr{R}_{00} = 1.0$, $\mu_c = 0.0$, $\rho_c = 0.67$), (c) $(\epsilon, \rho) = (0.3, 0.1)$ ($\epsilon\mathscr{R}_{00} = 1.2$, $\mu_c < 0$, $\rho_c = 0.40$), (d) $(\epsilon, \rho) = (0.3, 0.8)$ ($\epsilon\mathscr{R}_{00} = 1.2$, $\mu_c = 1.67$, $\rho_c = 0.40$), and commonly $\mathscr{R}_{00} = 4.0$; $c = 1.0$.

Corollary 3.9.2. *If $\mathscr{R}_{00} > 1 + c$, the acceptance of only susceptible visitors so many as*

$$\mu \geqslant \frac{1+c}{\mathscr{R}_{00} - (1+c)}$$

necessarily makes the disease endemic. In contrast, if $\mathscr{R}_{00} < 1 + c$, the acceptance of only susceptible visitors so many as

$$\mu \geqslant \frac{(\mathscr{R}_{00} - 1)(1+c)}{(1+c) - \mathscr{R}_{00}}$$

necessarily makes the disease eliminated.

The former case means an unpreferable influence of the sufficiently large number of visitors for the community with the spread of a highly infectious disease, while the latter does a preferable influence for the community with the spread of a moderately infectious disease.

Change in endemic size

Figure 17 shows the numerically drawn μ-dependence of endemic sizes y_r^* and y_v^* at the endemic equilibrium given by (28). As the figure implies, the endemic size necessarily has a monotonic dependence on the number of accepted visitors, represented now by μ, about which we can get the following analytical result (Appendix B.7):

Theorem 3.10. *The endemic sizes y_r^*, y_v^*, and the total endemic size*

$$z^* := \frac{y_r^* + \mu y_v^*}{1+\mu} = \frac{I_r^* + I_v^*}{N+m} \tag{36}$$

are monotonically increasing in terms of μ if and only if $\epsilon\mathscr{R}_{00} \leqslant 1$ or

$$\begin{cases} \epsilon\mathscr{R}_{00} > 1; \\ \rho < \rho_c := \dfrac{1 - \epsilon^2\mathscr{R}_{00} - \epsilon c}{(1-\epsilon)\epsilon\mathscr{R}_{00}}. \end{cases} \tag{37}$$

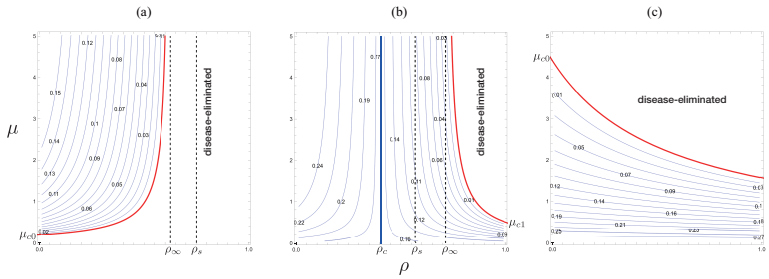

Figure 18: (ρ, μ)-dependence of the endemic size y_r^*. Numerically drawn contour maps for three cases correspond to those in Figure 14: (a) $\epsilon\mathscr{R}_{00} = 0.8$; (b) $\epsilon\mathscr{R}_{00} = 1.2$ and $\rho_c = 0.40$; (c) $\epsilon\mathscr{R}_{00} = 1.44$ and $\rho_c = -3.31$, where the parameter values are respectively the same as in Figure 14.

It can be easily found that $\rho_c < 1$ when $\epsilon\mathscr{R}_{00} > 1$. See the numerically drawn (ρ, μ)-dependence of the endemic size y_r^* in Figure 18.

We remark that, as shown in this section, the endemic equilibrium for $\rho = 1$ exists only when $\epsilon\mathscr{R}_{00} > 1$. Then we can find the following result too (Appendix B.8):

Corollary 3.10.1. *When the community accepts only immune visitors (i.e., $\rho = 1$), the endemic size is monotonically decreasing in terms of μ.*

This result could be regarded as included in Theorem 3.10 because any condition given in Theorem 3.10 cannot be applicable when $\rho = 1$. We can see the numerical examples in Figure 18(b, c).

When ρ_c defined by (37) is non-positive with $\epsilon\mathscr{R}_{00} > 1$, any ρ cannot be smaller than ρ_c, so that the endemic size is necessarily monotonically decreasing in terms of μ:

Corollary 3.10.2. *If $\epsilon\mathscr{R}_{00} > \max\left[1, 1/\epsilon - c\right]$, the endemic size is necessarily monotonically decreasing in terms of μ.*

The numerical example of Figure 18(c) illustrates the case.

For the critical case of $\rho = \rho_c > 0$ with $\epsilon\mathscr{R}_{00} > 1$, we can derive the explicit values at the endemic equilibrium E_{00} from (28) (Appendix B.7):

$$x_v^* = \frac{c}{(1-\epsilon)\mathscr{R}_{00}};\ y_v^* = y_r^* = z^* = 1 - \frac{1}{\epsilon\mathscr{R}_{00}}. \tag{38}$$

Hence the endemic sizes are independent of the number of accepted visitors in this case:

Corollary 3.10.3. *For $\rho = \rho_c > 0$ with $\epsilon\mathscr{R}_{00} > 1$, the endemic sizes y_r^*, y_v^*, and the total endemic size z^* are determined independently of μ.*

A numerical example is given in Figure 18(b). We note it necessary for $\rho_c > 0$ with $\epsilon\mathscr{R}_{00} > 1$ that $1/\epsilon - c > 1$, that is, $\epsilon(1+c) < 1$. Moreover the case of Corollary 3.10.3 can appear only when $1 < \epsilon\mathscr{R}_{00} < 1/\epsilon - c$.

Additionally we can find the following relations among the specific values ρ_s, ρ_∞, and ρ_c for the immune proportion of accepted visitors at the entry:

Corollary 3.10.4. *It holds that $\rho_c < \rho_\infty$ and $\rho_c < \rho_s$.*

The proof is easy by calculating the differences $\rho_\infty - \rho_c$ and $\rho_s - \rho_c$ and showing them positive. Numerical calculation of Figure 18(b) demonstrates this result.

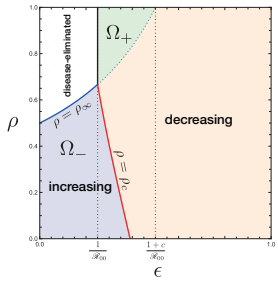

Figure 19: Classification of the parameter region of (ϵ, ρ) according to the μ-dependence of the change in the endemic size. Numerically drawn with $\mathscr{R}_{00} = 4.0$ and $c = 1.0$. Regions $\Omega_\pm$ correspond to those in Figure 12.

Consequently, as indicated by Figure 19, the larger number of accepted visitors makes the endemic size bigger only when the immune proportion of accepted visitors at the entry is sufficiently small under the epidemic situation with a sufficiently low risk of infection.

3.4 DISCUSSION

The results of our model imply that the acceptance of temporal visitors from the outside may induce a significant change of the epidemic state in the community. Contrary to an intuitive expectation, the acceptance of visitors does not necessarily make the epidemic situation worse in the community. Only when the reinfectivity of the disease is sufficiently weak, the acceptance of visitors may induce the endemicity if the community accepts the visitors only with a sufficiently low immune proportion. Furthermore, when the reinfectivity is high, the acceptance of a sufficiently large number of visitors may induce the elimination of the disease if the community can regulate to accept the visitors with a sufficiently high immune proportion.

The visitors certainly play a role of recruitment of hosts for the disease spread in the community. The visitors with a higher susceptible proportion could be regarded as a larger supply of highly susceptible individuals in the community, and they provide a fast recruitment of new infectives. In contrast, the visitors with a high immune proportion cause only a slow recruitment of new infectives with the reinfection. For these reasons, the influence of the visitor acceptance on the epidemic dynamics with a reinfectious disease must depend on the immune proportion in the visitors at the entry. On the other hand, the entry of many visitors could induce a dilution of the infective density in the community at the same time, which is regarded as an advantageous influence of the visitor acceptance against the disease spread. In the epidemic dynamics with our model, a balance of these counteractive factors of the visitor acceptance with respect to the disease spread could significantly affect the consequence of epidemic dynamics in the community.

As a result, a preferable acceptance of visitors must be regulated to have a sufficiently large immune proportion according to the public health in the community. In this sense, the best policy for the visitor acceptance would be to allow the entry only for the immune visitors. From the results on our model, such an acceptance of only immune visitors may lower the endemic size, and further suppress the endemicity to induce the elimination of the disease spread in the community.

In contrast, when the community was on the way to the disease-eliminated equilibrium before starting the acceptance of visitors, the acceptance of

visitors without any epidemiological regulation may cause the revival of the disease spread in the community. Such a case would occur by reduced cautiousness of the disease before starting the acceptance of visitors, which is caused by the reason that the number of infective residents became rather small in comparison to that at the outbreak.

Our model could be regarded as a consideration on the epidemic dynamics in a season. In this sense, the number of visitors may be beyond the number of residents in the community (i.e., $\mu > 1$), as some popular touristic local places like Venice in the vacation season, or a certain place attracting visitors like a newly found gold mine. As another example, we could consider a community accepting many evacuees from a certain calamity. Even though the number of visitors would be smaller than the number of residents in most cases (i.e., $\mu < 1$), our results imply that the influence of the visitor acceptance could depend on the infectivity and reinfectivity in the epidemic dynamics, and the regulation on the epidemiological nature of accepted visitors.

Since the infectivity and reinfectivity are not only determined by the nature of disease itself but also by social custom, the sanitary condition, and the people's behavior [57–59,144–148], the influence of the visitor acceptance could depend also on social factors in the community which accepts the visitors under the epidemic dynamics. Such social factors could be affected by the situation of disease spread during the epidemic dynamics in the community. For example, some strategic/non-strategic transmission of information about the disease spread or a public health campaign to prevent the further disease spread could alter people's social behavior, and subsequently the risk of infection/reinfection. Hence if the infectivity and reinfectivity would be changeable in the epidemic dynamics, the influence of the visitor acceptance would be qualitatively changed.

The results from our model imply such a possibility that a shift of the infectivity and/or reinfectivity to the weaker would induce an epidemic situation in which the acceptance of visitors causes the increase in the epidemic size or the revival of disease spread even with the endemicity. If so, there would be repetitive revivals of disease spread in the community, driven by a temporal shift of the infectivity and/or reinfectivity which could bring a feedback influence on the policy to control the disease spread in the community. Such theoretical/mathematical researches on the relation between the disease spread and the nature of hosts are interesting and require further development.

4 MULTIPLE STRAINS SUPPORT THE ENDEMICITY?

4.1 ASSUMPTIONS AND MODELING

4.1.1 *Assumptions*

The strains from the same species or different species interact with competition. They compete not only for the host population by infecting as many healthy individuals as possible, but also for the growth-limiting resources within the host individual[149–151]. For example, they compete for the healthy cells, which could be one of the identical resources within the host individual, and only one strain can persist. We consider the superinfection as one of the results of strains competition within the host individual. For our mathematical modeling, we set up the following assumptions:

- Strains compete for the host population. We assume that the infection force of infectives with strain k for the healthy individuals is given by $\beta_k I_k$.
- Strains compete for the resources within a host following a strict hierarchy order of competitive dominance.
- Superinfection occurs when a more dominant strain j takes over a host infected by a less dominant strain k. For the infectives who hold strain k, we assume that the infection force of infectives I_j with strain j is given by $\epsilon_{jk}\beta_j I_j$ under the possibility ϵ_{jk}.
- The quarantine efficiency is determined by the detectability of strain.
- The recovered individual gets immunity lasting in the epidemic season under consideration.
- The influence of disease in demographic change is negligible in the time scale of considered epidemic dynamics.

Although there are some studies have shown that the more virulent strains of rodent malaria, the more competitive advantage within the hosts[152], there is no necessary relationship between the competitive dominance, the transmissibility, and the virulence[153,154]. We shall focus on the distribution of detectability and consider that the transmissibility and the possibility of superinfection are independent of strains (i.e., $b_k = b$ and $\epsilon_{jk} = \epsilon$ for all k and $j < k$).

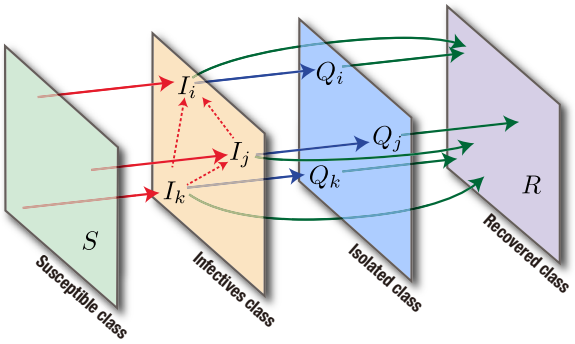

Figure 20: The state transition in the epidemic dynamics of our model. S, I_k, Q_k, and R ($k = 1, 2, \ldots, n$) are population densities of susceptibles, infectives who hold strain k as the strain of the highest dominance, corresponding isolated and recovered individuals respectively, where $1 \leqslant i < j < k$.

4.1.2 *Modeling*

With the assumptions in Section 4.1.1, our model is given by the following system of ordinary differential equations (Figure 20):

$$
\begin{aligned}
\frac{dS}{dt} &= \mu N - \sum_{k=1}^{n} \beta I_k S - \mu S; \\
\frac{dI_1}{dt} &= \beta I_1 S + \sum_{k=2}^{n} \epsilon\beta I_1 I_k - \sigma_1 I_1 - \rho_1 I_1 - \mu I_1; \\
\frac{dI_j}{dt} &= \beta I_j S + \sum_{k=j+1}^{n} \epsilon\beta I_k I_j - \sum_{k=1}^{j-1} \epsilon\beta I_j I_k \\
&\quad -\sigma_j I_j - \rho_j I_j - \mu I_j \quad (1 < j < n); \\
\frac{dI_n}{dt} &= \beta I_n S - \sum_{k=1}^{n-1} \epsilon\beta I_k I_n - \sigma_n I_n - \rho_n I_n - \mu I_n; \\
\frac{dQ_k}{dt} &= \sigma_k I_k - \alpha_k Q_k - \mu Q_k \quad (k = 1, 2, \ldots, n); \\
\frac{dR}{dt} &= \sum_{k=1}^{n} \rho_k I_k + \sum_{k=1}^{n} \alpha_k Q_k - \mu R,
\end{aligned}
\tag{39}
$$

where S, I_k, Q_k, and R are population densities of susceptibles, infectives who hold strain k, corresponding isolated and recovered individuals respectively, The total population size is denoted by $N = S + \sum_{k=1}^{n} I_k + \sum_{k=1}^{n} Q_k + R$. βI_k gives the infection force of strain k for the susceptible with the coefficient β, and $\epsilon\beta I_j$ gives that for the infective with strain j of the lower dominance. Parameter σ_k is the quarantine rate for the infective who holds strain k, which reflects the detectability of strain k. Parameters α_k and ρ_k are the recovery rates for the infective with strain k under and out of the isolation, respectively. μ is the natural death rate.

4.2 BASIC REPRODUCTION NUMBER

To derive the basic reproduction number for the model (39), we use the next-generation method. The model (39) has the disease-free equilibrium

$E_0 = (N, 0, \dots, 0)$. We can derive the next-generation matrix $G = FV^{-1}$, where F and G are diagonal matrices given by

$$F = \mathrm{diag}(\beta N, \beta N, \cdots, \beta N);$$
$$V = \mathrm{diag}(\sigma_1 + \rho_1 + \mu, \sigma_2 + \rho_2 + \mu, \cdots, \sigma_n + \rho_n + \mu).$$

Thus we have

$$FV^{-1} = \mathrm{diag}(\mathscr{R}_{0,1}, \mathscr{R}_{0,2}, \cdots, \mathscr{R}_{0,n}),$$

where

$$\mathscr{R}_{0,k} := \frac{\beta N}{\sigma_k + \rho_k + \mu} \quad (k = 1, 2, \cdots, n). \tag{40}$$

The basic reproduction number for the system (39) mathematically given by

$$\mathscr{R}_0 = \max\{\mathscr{R}_{0,1}, \mathscr{R}_{0,2}, \cdots, \mathscr{R}_{0,n}\}.$$

The basic reproduction number $\mathscr{R}_0$ for the system (39) is given by the maximum of the expected number of new cases. This $\mathscr{R}_0$ is meaningful only if we consider all strains are included in the initial stage with $0 < I_k(0) \ll 1$ $(k = 1, 2, \dots, n)$. The number of new cases infected by per infective individual is defined for each strain, which is given by $\mathscr{R}_{0,k}$ $(k = 1, 2, \dots, n)$. At the initial stage, if the initial invasion includes only strain k, we have $dI_k(t)/dt > 0$ with $I_k(0) > 0$, $I_k(0) \ll 1$, and $I_j(0) = 0$ $(j \neq k)$. In such a case, we have the basic reproduction number given by $\mathscr{R}_{0,k}$. Let us call $\mathscr{R}_{0,k}$ the *strain-specific basic reproduction number*.

For the mathematical convenience, we define a set $\Omega := \{k \mid \mathscr{R}_{0,k} > 1\}$, which represents the strain with $\mathscr{R}_{0,k} > 1$. The set Ω is empty when $\mathscr{R}_0 \leqslant 1$.

4.3 MATHEMATICAL RESULTS ON THE MODEL

4.3.1 *Non-dimensionalization*

We apply the following parameter transformation to non-dimensionalize the model (39) $(k = 1, 2, \cdots, n)$:

$$\begin{aligned} &\tau := \mu t;\ u := \frac{S}{N};\ v_k := \frac{I_k}{N};\ q_k := \frac{Q_k}{N};\ w := \frac{R}{N};\\ &b := \frac{\beta N}{\mu};\ \gamma_k := \frac{\sigma_k}{\mu};\ a_k := \frac{\alpha_k}{\mu};\ \eta_k := \frac{\rho_k}{\mu}, \end{aligned} \tag{41}$$

then our model can be rewritten as:

$$\begin{aligned} \frac{du}{d\tau} &= 1 - b\Big(\sum_{k=1}^{n} v_k\Big)u - u;\\ \frac{dv_1}{d\tau} &= bv_1 u + \epsilon b\Big(\sum_{k=2}^{n} v_k\Big)v_1 - (1 + \gamma_1 + \eta_1)v_1;\\ \frac{dv_j}{d\tau} &= bv_j u + \epsilon b\Big(\sum_{k=j+1}^{n} v_k\Big)v_j - \epsilon b\Big(\sum_{k=1}^{j-1} v_k\Big)v_j\\ &\quad -(1 + \gamma_j + \eta_j)v_j \quad (1 < j < n);\\ \frac{dv_n}{d\tau} &= bv_n u - \epsilon b\Big(\sum_{k=1}^{n-1} v_k\Big)v_n - (1 + \gamma_n + \eta_n)v_n;\\ \frac{dq_k}{d\tau} &= \gamma_k v_k - a_k q_k - q_k \quad (k = 1, 2, \dots, n);\\ \frac{dw}{d\tau} &= \sum_{k=1}^{n} \eta_k v_k + \sum_{k=1}^{n} a_k q_k - w \end{aligned} \tag{42}$$

with the initial condition that $u(0) = u^0 > 0$, $v_1(0) = v_1^0 > 0$, $v_j(0) = v_j^0 > 0$, $v_n(0) = v_n^0 > 0$, $q_k(0) = 0$, $w(0) = 0$ $(1 < j < n)$, and $u^0 + \sum_{k=1}^{n} v_k^0 = 1$. From (40), the strain-specific reproduction number is given by

$$\mathscr{R}_{0,k} = \frac{b}{1+\gamma_k+\eta_k} \quad (k = 1, 2, \ldots, n). \tag{43}$$

Hereafter, we assume that $\mathscr{R}_{0,j} \neq \mathscr{R}_{0,k}$ for $j \neq k$.

4.3.2 *Model without superinfection*

In this section, we consider that superinfection never happens ($\epsilon = 0$). This is the case when there is no such order of competition dominance among strains. Once a host is infected with a strain, such strain is considered as completely owning that host. From (41), model (39) without superinfection can be nondimensionalized as:

$$\begin{aligned}
\frac{du}{d\tau} &= 1 - b\Big(\sum_{k=1}^{n} v_k\Big)u - u; \\
\frac{dv_k}{d\tau} &= bv_k u - (1+\gamma_k+\eta_k)v_k \quad (k = 1, 2, \ldots, n); \\
\frac{dq_k}{d\tau} &= \gamma_k v_k - a_k q_k - q_k; \\
\frac{dw}{d\tau} &= \sum_{k=1}^{n} \eta_k v_k + \sum_{k=1}^{n} a_k q_k - w.
\end{aligned} \tag{44}$$

We can obtain the following result on the stability of the equilibrium for the model without superinfection (Appendix C.1):

Theorem 4.1. *For the model without superinfection ($\epsilon = 0$), that is, for the model (44),*

(i) if Ω is empty, E_0 is is globally asymptotically stable. Otherwise, E_0 is unstable;

(ii) if Ω is not empty, we have a unique locally asymptotically stable single strain endemic equilibrium E_ℓ given by

$$u^* = \frac{1}{\mathscr{R}_{0,\ell}}; \; v_\ell^* = \frac{\mathscr{R}_{0,\ell} - 1}{b}; \; v_k^* = 0; \; q_\ell^* = \frac{\gamma_\ell v_\ell^*}{a_\ell + 1}; \; q_k^* = 0, \tag{45}$$

where ℓ such that $\mathscr{R}_{0,\ell} = \mathscr{R}_0$.

When Ω is empty, that is, when $\mathscr{R}_{0,k} \leqslant 1$ for any k, the system (44) necessarily approaches the disease-free equilibrium. When Ω is not empty, that is, when there exists ℓ such that $\mathscr{R}_{0,\ell} > 1$, if the system (44) approaches the endemic equilibrium, it consists of the infectives with the strain which has the largest strain-specific basic reproduction number. Therefore, If and only if Ω is not empty, when there is a single strain ℓ which has the basic reproduction number $\mathscr{R}_{0,\ell} > 1$ or when all strains with the basic reproduction number greater than one have the same basic reproduction number, there is a single endemic equilibrium.

On the other hand, if we consider that there exist some j such that $\mathscr{R}_{0,j} = \mathscr{R}_{0,k} > 1$ $(j \neq k)$, we have an endemic equilibrium consisting of both infectives with strain j and infectives with strain k, while v_j^* and v_k^* are alternatively positive or zero at the equilibrium.

From (45), we have the equilibrium endemic size z^* at E_ℓ is given by

$$z^* := v_\ell^* + q_\ell^* = \frac{1+\gamma_\ell/(a_\ell+1)}{1+\gamma_\ell+\eta_\ell}\left(1-\frac{1}{\mathscr{R}_{0,\ell}}\right) = \frac{1+\gamma_\ell/(a_\ell+1)}{1+\gamma_\ell+\eta_\ell}\left(1-\frac{1+\gamma_\ell+\eta_\ell}{b}\right). \tag{46}$$

It is easy to see that the endemic size z^* at E_ℓ is monotonically decreasing in terms of $1/\mathscr{R}_{0,\ell}$. We can also have the following results about the γ_ℓ-dependence on the equilibrium endemic size z^* at E_ℓ (Appendix C.2):

Theorem 4.2. *For the model without superinfection ($\epsilon = 0$), that is, for the model (44) with $\mathscr{R}_{0,\ell} = \mathscr{R}_0 > 1$,*

(i) if $b(\eta_\ell - a_\ell) \leqslant (1+\eta_\ell)^2$, the equilibrium endemic size z^* at E_ℓ is monotonically decreasing in terms of γ_ℓ;

(ii) if $b(\eta_\ell - a_\ell) > (1+\eta_\ell)^2$, the equilibrium endemic size z^* at E_ℓ takes a maximum value for a specific value of γ_ℓ which is given by $-(1+\eta_\ell) + \sqrt{b(\eta_\ell - a_\ell)}$.

Moreover, the results shown in Theorems 4.1 and 4.2 hold even if the transmissibility depends on strains (i.e., $b_j \neq b_k$ for $j \neq k$).

4.3.3 *Model with superinfection*

Boundedness for the solution

Since the first $(n+1)$ equations in the model (42) is closed, it is sufficient to consider the stability with the reduced closed system of model (42). We set the following mathematical results on the boundedness for the solution of the reduced system of model (42) (Appendix C.3):

Lemma 4.1. *For the initial condition such that $u(0) = u^0 > 0$, $v_1(0) = v_1^0 > 0$, $v_j(0) = v_j^0 > 0$ $(j = 2, 3, \ldots, n-1)$, $v_n(0) = v_n^0 > 0$, and $u(0) + \sum_{k=1}^n v_k(0) = u^0 + \sum_{k=1}^n v_k^0 = 1$, the solution of the reduced closed system of model (42) belongs to the region D for any $\tau > 0$, where*

$$D := \left\{(u, v_1, \ldots, v_n) \,\middle|\, u > 0, v_k > 0\,(k = 1, 2, \ldots, n), u + \sum_{k=1}^n v_k < 1\right\}. \tag{47}$$

Feasible equilibrium

First we can get the following result on the reduced closed system of model (42) (Appendix C.4):

Lemma 4.2. *If $\mathscr{R}_{0,k} \leqslant 1$, the strain necessarily die out as $\tau \to \infty$.*

If the strain with the strain-specific reproduction number less than or equal to 1, such a strain can not persist in the population. On the other hand, it is necessary to have the strain-specific reproduction number greater than 1 to persist such a strain. For model (42), we have the disease-free equilibrium E_0 always exists. Making use of the eigenvalue analysis, we can easily get the following result about the local stability of E_0 (Appendix C.5):

Lemma 4.3. *The disease-free equilibrium E_0 is locally asymptotically stable if Ω is empty. If Ω is not empty, it is unstable.*

Making use of the result in Lemmas 4.1, 4.2, and 4.3, we can get the following result about the stability of E_0:

Theorem 4.3. *The disease-free equilibrium E_0 is globally asymptotically stable in D if Ω is empty, where D is given in (47). Otherwise, if Ω is not empty, it is unstable.*

When Ω is not empty, that is, when there are some strain k such that $\mathscr{R}_{0,k} > 1$, we have some endemic equilibria where at least one strain persists. If there exists a strain ℓ such that $\mathscr{R}_{0,\ell} > 1$, we have a single strain endemic equilibrium E_ℓ given by

$$u^* = \frac{1}{\mathscr{R}_{0,\ell}};\ v_\ell^* = \frac{\mathscr{R}_{0,\ell} - 1}{b_\ell};\ v_k^* = 0;\ q_\ell^* = \frac{\gamma_\ell v_\ell^*}{a_\ell + 1};\ q_k^* = 0;\ w^* = \eta_\ell v_\ell^* + a_\ell q_\ell^*, \tag{48}$$

where $k = 1, 2, \ldots, n$ and $k \neq \ell$.

Single strain endemic equilibrium

We can get the following result about the stability of E_ℓ given in (48) (Appendix C.6):

Theorem 4.4. *When the equilibrium E_ℓ exists with $\mathscr{R}_{0,\ell} > 1$ and satisfies*

$$\min_{k<\ell}\left\{\frac{1}{\mathscr{R}_{0,k}}\right\} > \frac{1}{\mathscr{R}_{0,\ell}} + \frac{\epsilon}{b}(\mathscr{R}_{0,\ell} - 1); \tag{49}$$

$$\min_{k>\ell}\left\{\frac{1}{\mathscr{R}_{0,k}}\right\} > \frac{1}{\mathscr{R}_{0,\ell}} - \frac{\epsilon}{b}(\mathscr{R}_{0,\ell} - 1), \tag{50}$$

it is globally asymptotically stable in D given in (47). Otherwise, if the condition (49) or (50) is unsatisfied, E_ℓ is unstable even when it exists.

When $\mathscr{R}_{0,k} > 1$ for all $k = 1, 2, \ldots, n$, if there exists a globally asymptotically stable single strain endemic equilibrium E_ℓ, all the other single strain endemic equilibria E_k ($k \neq \ell$) are unstable even they exist.

From Theorem 4.4, we have the following results:

Corollary 4.4.1. *For the strain which has $\mathscr{R}_{0,j} = \min\{\mathscr{R}_{0,k}\}$ with $\mathscr{R}_{0,j} > 1$ ($k = 1, 2, \ldots, n$), the single strain endemic equilibrium E_j is necessarily unstable.*

From Theorems 4.3 and 4.4, when there is more than one strain with strain-specific reproduction number greater than 1, if the system does not approach a single strain endemic equilibrium, it will approach an endemic state persisting more than one strains.

4.3.4 *Dependence on the distribution of strain-specific basic reproduction number*

From Corollary 4.2, we know that a strain k may persist only if it has the strain-specific reproduction number $\mathscr{R}_{0,k} > 1$. In this section, we assume that $\mathscr{R}_{0,k} > 1$ for any $k = 1, 2, \ldots, n$.

Monotonically decreasing

If the strain-specific basic reproduction number is monotonically decreasing following the strain's order of competitive dominance (i.e., $\mathscr{R}_{0,k+1} < \mathscr{R}_k$ for all k), we have the single strain endemic equilibrium E_1 is necessarily globally asymptotically stable since the condition (50) with $\ell = 1$ is always satisfied. From Corollary 4.4.1, we have E_k are unstable for all $k > 1$. Therefore, we can get the following result:

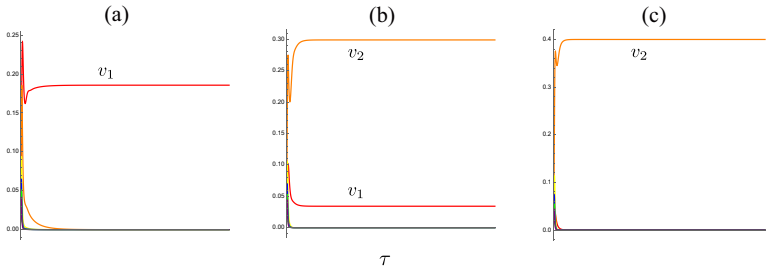

Figure 21: Temporal variations for n strain model with $n = 6$. Numerically drawn with (a) $\gamma_1 = 1.5$; (b) $\gamma_1 = 3.0$; (c) $\gamma_1 = 4.5$. Commonly, $b = 10.0$; $\gamma_k = 0.8$; $\eta_k = 1.0$ $(k = 2, 3, \ldots, 6)$; $\epsilon = 0.6$; $(u(0), v_1(0), v_2(0), v_3(0), v_4(0), v_5(0), v_6(0)) = (0.94, 0.01, 0.01, 0.01, 0.01, 0.01, 0.01)$.

Theorem 4.5. *If $\mathscr{R}_{0,k+1} > \mathscr{R}_k$ with $\mathscr{R}_{0,k} > 1$ for all $k = 1, 2, \ldots, n$, the system (42) necessarily approaches the single strain endemic equilibrium E_1.*

If the more dominant strain has a lower strain-specific basic reproduction number, only the most dominant strain (i.e., strain 1) can persist while any other subordinate strains disappear. In this case, it is impossible to have more than one strains at the endemic state.

Monotonically increasing

If the strain-specific basic reproduction number is monotonically decreasing following the strain's order of competitive dominance (i.e., $\mathscr{R}_{0,k+1} > \mathscr{R}_k$ for all k), we have the system (42) may approach a single strain endemic equilibrium, depending on the conditions (49) and (50). When the condition (49) or (49) is unsatisfied for any $\ell = 1, 2, \ldots, n$, we have the system (42) approaches an endemic state where more than one strains persist.

Let us assume that $\gamma_1 > 0$, $\gamma_k = 0$, $\eta_1 = \eta_k = \eta$ for $k \neq 1$, then we have $\mathscr{R}_{0,1} < \mathscr{R}_{0,k}$ for $k \neq 1$. We can obtain the following result:

Theorem 4.6. *When $\gamma_1 > 0$, $\gamma_k = 0$, and $\eta_1 = \eta_k = \eta$ with $\mathscr{R}_{0,k} > 1$ for any $k \neq 1$, the system (42) approaches an endemic state where more than one strains persist if*

$$\frac{1}{2}\left\{-(1+\eta+\epsilon)+\sqrt{(1+\eta-\epsilon)^2+4\epsilon b}\right\} < \gamma_1 < \epsilon\left(\frac{b}{1+\eta}-1\right).$$

When the recovery rate is independent of strains, if the most dominant strain (i.e., strain 1) is the only detectable strain while any other subordinate strains are undetectable, the system may approach an endemic equilibrium at which the infectives holding different strains persist. If the detectability for the infection with strain 1 is sufficiently low, the system approaches the endemic equilibrium E_1 (see Figure 21(a)). On the other hand, if the detectability for the infection with strain 1 is sufficiently high, the system approaches the endemic equilibrium E_2 (see Figure 21(c)). Only if the detectability for the infection with strain 1 is in an intermediate range, the system approaches an endemic equilibrium where strain 1 and strain 2 persist, while the other strains get eliminated (see Figure 21(b)).

If $\gamma_j > 0$ and $\gamma_k = 0$ for $j \neq 1$ and $k \neq j$, we have the endemic equilibrium E_1 is necessarily locally asymptotically stable, while other endemic equilibria E_k $(k \neq 1)$ are unstable. If there is the only detectable strain j which is not the

most dominant strain ($j \neq 1$), while other strains k ($k \neq j$) are undetectable, the system approaches an endemic equilibrium where there are only the infectives with strain 1, and no infectives with strain k ($k \neq 1$) exists.

4.3.5 *Two strain model*

In this section, we shall consider the model (42) of two strains ($n = 2$):

$$\begin{aligned}
\frac{du}{d\tau} &= 1 - bv_1u - bv_2u - u;\\
\frac{dv_1}{d\tau} &= bv_1u + \epsilon bv_1v_2 - (1+\gamma_1+\eta_1)v_1;\\
\frac{dv_2}{d\tau} &= bv_2u - \epsilon bv_1v_2 - (1+\gamma_2+\eta_2)v_2;\\
\frac{dq_1}{d\tau} &= \gamma_1v_1 - a_1q_1 - q_1;\\
\frac{dq_2}{d\tau} &= \gamma_2v_2 - a_2q_2 - q_2;\\
\frac{dw}{d\tau} &= \eta_1v_1 + \eta_2v_2 + a_1q_1 + a_2q_2 - w,
\end{aligned} \tag{51}$$

with $u + v_1 + v_2 + q_1 + q_2 + w = 1$ and the initial condition that

$$(u(0), v_1(0), v_2(0), q_1(0), q_2(0), w(0)) = (u^0, v_1^0, v_1^0, 0, 0, 0).$$

where $u^0 > 0$, $v_1^0 > 0$, $v_2^0 > 0$, and $u^0 + v_1^0 + v_2^0 = 1$. We suppose that $\mathscr{R}_{0,1} \neq \mathscr{R}_{0,2}$, where $\mathscr{R}_{0,1}$ and $\mathscr{R}_{0,2}$ are defined by (43). The system (51) has the disease-free equilibrium $E_0 = (1, 0, 0, 0, 0, 0)$ and may have the endemic equilibria $E_1 = (u^*, v_1^*, 0, q_1^*, 0, w^*)$, $E_2 = (u^*, 0, v_2^*, 0, q_2^*, w^*)$, and $E_{12} = (u^*, v_1^*, v_2^*, q_1^*, q_2^*, w^*)$ where $u^* > 0$, $v_1^* > 0$, $v_2^* > 0$, $q_1^* > 0$, $q_2^* > 0$, and $w^* > 0$.

In the absent of superinfection (i.e., $\epsilon = 0$), from the results derived in Section 4.3.2, we know that, if and only if $\mathscr{R}_{0,1} \leqslant 1$ and $\mathscr{R}_{0,2} \leqslant 1$, the system (51) necessarily approaches the disease-free equilibrium E_0. If $\mathscr{R}_{0,1} > 1$ and $\mathscr{R}_{0,2} \leqslant 1$, the system (51) approaches the single strain endemic equilibrium E_1. If $\mathscr{R}_{0,1} \leqslant 1$ and $\mathscr{R}_{0,2} > 1$, it approaches the single strain endemic equilibrium E_2. If $\mathscr{R}_{0,1} > 1$ and $\mathscr{R}_{0,2} > 1$, the system (51) approaches E_1 when $\mathscr{R}_{0,1} > \mathscr{R}_{0,2}$, while it approaches E_2 when $\mathscr{R}_{0,2} > \mathscr{R}_{0,1}$.

With the presence of superinfection where $0 < \epsilon < 1$, we can get the following result on the existence of the equilibrium for the system (51) (Appendix C.7):

Lemma 4.4. *For the system* (51),

(i) the disease-free equilibrium E_0 *always exists;*

(ii) the endemic equilibrium E_1 *exists if* $\mathscr{R}_{0,1} > 1$, *where*

$$u^* = \frac{1}{\mathscr{R}_{0,1}};\ v_1^* = \frac{\mathscr{R}_{0,1} - 1}{b};\ v_2^* = 0;\ q_1^* = \frac{\gamma_1 v_1^*}{a_1 + 1};\ q_2^* = 0;\ w^* = \eta_1 v_1^* + a_1 q_1^*;$$

(iii) the endemic equilibrium E_2 *exists if* $\mathscr{R}_{0,2} > 1$, *where*

$$u^* = \frac{1}{\mathscr{R}_{0,2}};\ v_1^* = 0;\ v_2^* = \frac{\mathscr{R}_{0,2} - 1}{b};\ q_1^* = 0;\ q_2^* = \frac{\gamma_2 v_2^*}{a_2 + 1};\ w^* = \eta_2 v_2^* + a_2 q_2^*;$$

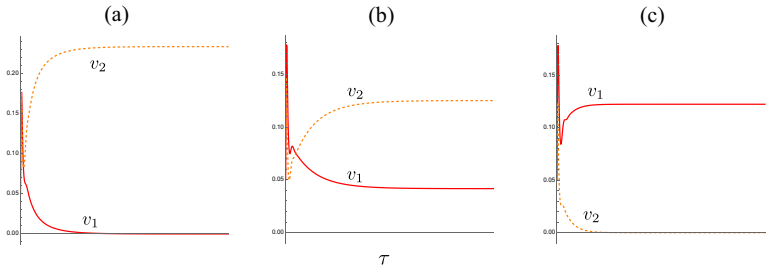

Figure 22: Temporal variations for the two strain model. Numerically drawn with (a) $\gamma_2 = 0.9$; (b) $\gamma_2 = 0.5$; (c) $\gamma_2 = 0.2$. Commonly, $\gamma_1 = 0.8$; $\eta_1 = 0.6$; $a_1 = 2.0$; $\eta_2 = 0.6$; $a_2 = 3.0$; $b = 3.0$; $\epsilon = 0.8$; $(u(0), v_1(0), v_2(0), q_1(0), q_2(0), w(0)) = (0.9, 0.05, 0.05, 0, 0, 0)$.

(iv) the endemic equilibrium E_{12} *exists if and only if* $\mathscr{R}_{0,2} > \mathscr{R}_{0,1} > 1$ *and*

$$\frac{1}{1-\hat{\epsilon}}\left(\frac{1}{\mathscr{R}_{0,1}} - \hat{\epsilon}\right) < \frac{1}{\mathscr{R}_{0,2}} \tag{52}$$

$$\frac{1}{\mathscr{R}_{0,2}} < \frac{1}{(1-\hat{\epsilon}) + \hat{\epsilon}\mathscr{R}_{0,1}} \cdot \frac{1}{\mathscr{R}_{0,1}} \tag{53}$$

are satisfied, where

$$\hat{\epsilon} := \frac{\epsilon}{1+\gamma_2+\eta_2}. \tag{54}$$

and

$$u^* = \left\{1 + \frac{b}{\epsilon}\left(\frac{1}{\mathscr{R}_{0,1}} - \frac{1}{\mathscr{R}_{0,2}}\right)\right\}^{-1};\ v_1^* = \frac{1}{\epsilon}\left(u^* - \frac{1}{\mathscr{R}_{0,2}}\right);\ v_2^* = \frac{1}{\epsilon}\left(\frac{1}{\mathscr{R}_{0,1}} - u^*\right);$$

$$q_1^* = \frac{\gamma_1 v_1^*}{a_1+1};\ q_2^* = \frac{\gamma_2 v_2^*}{a_2+1};\ w^* = \eta_1 v_1^* + \eta_2 v_2^* + a_1 q_1^* + a_2 q_2^*. \tag{55}$$

If $\mathscr{R}_{0,1} \leqslant 1$ and $\mathscr{R}_{0,2} \leqslant 1$, there is not any equilibrium other than the disease-free equilibrium E_0. If $\mathscr{R}_{0,1} > 1$ or $\mathscr{R}_{0,2} > 1$, we may have three endemic equilibria with the persistence of a single strain or the coexistence of two strains (Figure 22).

From Theorem 4.3, we have the disease-free equilibrium E_0 is globally asymptotically stable if and only if $\mathscr{R}_{01} \leqslant 1$ and $\mathscr{R}_{02} \leqslant 1$. We can also obtain the following result about the stability of E_1, E_2, and E_{12} for the two strain model (51) (Appendix C.8):

Theorem 4.7. *For the two strain model* (51),

(i) E_1 *is globally asymptotically stable only if the condition given by the inverse inequality in* (53) *is satisfied;*

(ii) E_2 *is globally asymptotically stable only if the condition given by the inverse inequality in* (52) *is satisfied;*

(iii) E_{12} *is always globally asymptotically stable whenever it exists.*

From the results in Theorem 4.7, when E_1 or E_2 is globally asymptotically stable, we have E_{12} does not exists. When E_{12} exists, we have E_1 and E_2 are unstable. We can also get the following results from Theorem 4.7:

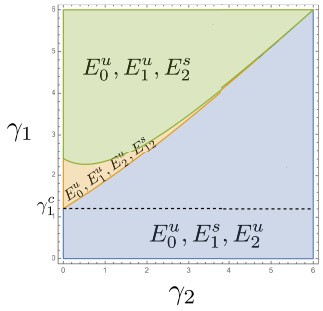

Figure 23: (γ_1, γ_2)-dependence of the existence and stability of equilibria for the two strain model. Numerically drawn for $b = 8.0$. $\eta_1 = \eta_2 = 1.0$; $\epsilon = 0.8$, where $\gamma_1^c := -(1+\eta_1) + \{(1+\eta_1-\epsilon) + \sqrt{(1+\eta_1-\epsilon)^2 + 4\epsilon b}\})/2 \approx 1.2$.

Corollary 4.7.1. *When* E_1 *is globally asymptotically stable,* E_2 *is unstable and vice versa.*

Corollary 4.7.2. *When* E_{12} *exists, both of* E_1 *and* E_2 *exist, and they are unstable.*

From Theorem 4.7 with (52) and (53), we can draw the (γ_1, γ_2)-dependence of the existence and stability of equilibria for the two strain model (Figure 23). As shown by Figure 23, strain 2 can persist only if strain 1 has a sufficiently high detectability. The harder the strain 2 is to detect, the more likely it can persist. Moreover, strain 1 and strain 2 can coexist only for certain intermediate ranges of γ_1 and γ_2. If both strains have sufficiently high detectabilities, it is less likely to have both strains coexist.

4.4 DISCUSSION

In this work, we consider a mathematical model on the epidemic dynamics of a disease transmission with n strains which follows an order of the competitive dominance according to the infection success in the host. In our model, when no superinfection occurs, the disease becomes eliminated or alternatively the endemic state arises with only the strain which has the largest basic reproduction number while all the other strains get eliminated. For the persisting strain with a sufficiently low transmissibility, the detectability of the infection with such a strain can reduce the endemic size. On the other hand, for the persisting strain with a sufficiently high transmissibility, the endemic size takes maximum value for a specific value of the detectability of the infection with such a strain.

For the two strain model with superinfection, we show a possibility that the system goes to the endemic equilibrium where there are infectives with strain 1 and infectives strain 2. If the transmissibility of strain 1 (or strain 2) is sufficiently large, the system approaches the endemic equilibrium which consists of infectives with only strain 1 (or strain 2). Only if the transmissibilities of strain 1 and strain 2 are under an intermediate ranges with $\mathscr{R}_{0,2} > \mathscr{R}_{0,1}$, these two strain can co-exist at the endemic equilibrium, that is, there exist infectives with strain 1 and infectives with strain 2 at the endemic equilibrium.

For the n strain model with superinfection, we find it is possible that there are more than one strain persisting at the endemic equilibrium. The model with n strain which have the same transmissibility to the susceptible and the possibility of superinfection to the infectives with subordinate strain shows that, if there is no detectable strain other than the most dominate

strain (i.e., strain 1) with $\mathscr{R}_{0,1} > 1$, it is likely to persist more than one strain at the endemic equilibrium state. If the unique detectable strain is not the most dominate strain but a subordinate strain k ($k > 1$) with $\mathscr{R}_{0,k} > 1$, the system approaches the endemic equilibrium where there are the infectives with only strain 1.

With the presence of superinfection, the subordinate may persist at the endemic equilibrium. If the system approaches the endemic equilibrium at which not only one strain persists, surprisingly, the endemic size is not necessarily reduced by the superinfection possibility. Depending on the characteristics of the strains, superinfection could either support or suppress the endemic size.

5

CONLUSION

The emergence and spread of infectious diseases have posed significant challenges to public health concerns, and the social nature including social response, social sensitivity, community's policy, and detectability of infection has been considered as playing a critical role in the disease transmission.

Social behavior changes triggered by risk perception such as wearing masks, taking medication, vaccination, and keeping social distance can further alter the evolution of an epidemic outbreak. Especially, the social response with sensitivity and insensitivity could cause the emergence of recurring epidemic outbreaks, and the strong social insensitivity would stabilize the temporal variation of the infective size, certainly raising the endemic size.

People's displacement due to social and political unrest as well as the natural migration of disease vectors to new areas on the epidemic outbreak could have a significant influence on the spread of infectious diseases. The acceptance of visitors under such an epidemic dynamics with the risk of reinfection could not only support the endemicity but also suppress it by either shifting the endemicity or reducing the endemic size, depending on the nature of infectious disease. It is therefore essential to develop effective measures to mitigate the spread of an infectious disease, taking into account the characteristics of such a disease.

Moreover, the emergence of mutant or novel strains of infectious diseases could provide a challenge to clinical diagnosis due to the lack of knowledge about the strains or the limitation of testing techniques. Such strains are clearly under the exploitative competition for the host and for the reproduction in the host. Even when an individual is infected by a hardly detectable novel or mutant strain, the superinfection of another detectable strain could serve the infected individual to be diagnosed and quarantined, which in turn may help to suppress the disease spread.

The spread of transmissible diseases is a major public health concern that can result in significant morbidity and mortality, as seen in recent pandemics like COVID-19. Understanding of the complex relation between social nature and disease transmission could enable policymakers and healthcare professionals to develop targeted interventions to mitigate the spread of transmissible diseases and minimize the occurrence of repeated epidemic outbreaks. Such a kind of theoretical/mathematical works on the relation of social nature to the epidemics would also be valuable for reducing the burden of infectious diseases on global health.

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APPENDIX FOR CHAPTER 2

A.1 PROOF OF LEMMA 2.1 IN SECTION 2.3.3

From (8), it is necessary for the existence of E_+ that the following equation in terms of M has a positive root $M = M^*$:

$$\frac{\delta}{\eta} M = 1 - \frac{1}{\mathscr{R}_0} \frac{\beta_0}{\beta(M)}. \tag{A.1}$$

Since $\beta(M)$ is continuous, positive, and decreasing in terms of $M \in [0, \infty)$ from the assumption introduced in Section 2.1 and $\beta(0) = \beta_0$, the right side of (A.1) is a decreasing function of M and its supremum value is given by $1 - 1/\mathscr{R}_0$ for $M = 0$. Hence, if $1 - 1/\mathscr{R}_0 \leqslant 0$, the right side of (A.1) is non-positive for any $M > 0$, so that we do not have any positive root $M = M^*$ for the equation (A.1). Inversely, if $1 - 1/\mathscr{R}_0 > 0$, the right side of (A.1) is continuously decreasing from $1 - 1/\mathscr{R}_0 > 0$ at $M = 0$, while the left side of (A.1) is linearly increasing from 0 at $M = 0$. Thus we find that the equation (A.1) necessarily has a unique positive root $M = M^*$ in this case. Consequently, if and only if $1 - 1/\mathscr{R}_0 > 0$, that is, $\mathscr{R}_0 > 1$, the equation (A.1) has a unique positive root $M = M^*$.

When $M^* > 0$ exists with $\mathscr{R}_0 > 1$, it is satisfied from (8) that

$$0 < \nu^* = 1 - \frac{1}{\mathscr{R}_0} \frac{\beta_0}{\beta(M^*)} < 1 - \frac{1}{\mathscr{R}_0} \frac{\beta_0}{\beta(0)} = 1 - \frac{1}{\mathscr{R}_0} < 1.$$

Therefore, with a positive root $M = M^*$ for (A.1) with $\mathscr{R}_{01} > 1$, we have a reasonable value $\nu^* \in (0, 1)$ at the endemic equilibrium E_+. These arguments prove Lemma 2.1.

A.2 PROOF OF LEMMA 2.2 IN SECTION 2.3.4

First, it is easily seen from the system (4) that the disease-free equilibrium always exists. Next, suppose that an endemic equilibrium with $M^* = 0$ exists. From (9), we have $\nu^* = 1 - 1/\mathscr{R}_0$ and $G(\nu^*) = 0$. Therefore, for $\nu^* > 0$, it is necessary that $\mathscr{R}_0 > 1$. Besides, from $G(\nu^*) = 0$, it is necessary that $\nu^* = 1 - 1/\mathscr{R}_0 \leqslant \theta_c$, that is, $\mathscr{R}_0 \leqslant (1 - \theta_c)^{-1}$. Inversely, consider the case where $1 < \mathscr{R}_0 \leqslant (1 - \theta_c)^{-1}$. From (9), we have

$$\nu^* = 1 - \frac{1}{\mathscr{R}_0} \frac{\beta_0}{\beta(M^*)} \leqslant 1 - \frac{1}{\mathscr{R}_0} \frac{\beta_0}{\beta(0)} = 1 - \frac{1}{\mathscr{R}_0},$$

since $\beta(M)$ is a decreasing function of M with $\beta(0) = \beta_0$. Then, from $\mathscr{R}_0 \leqslant (1 - \theta_c)^{-1}$, we have $1 - 1/\mathscr{R}_0 \leqslant \theta_c$, so that $\nu^* \leqslant \theta_c$. This means that $G(\nu^*) = 0$, and subsequently $M^* = G(\nu^*)/\delta = 0$ from (9). These arguments prove (ii) of Lemma 2.2.

Now suppose that an endemic equilibrium with ν^* and $M^* > 0$ exists. From $M^* = G(\nu^*)/\delta > 0$ in (9), ν^* must be larger than θ_c to satisfy that $G(\nu^*) > 0$. Then, $G(\nu^*) = \eta(\nu^* - \theta_c) > 0$ from (5), and $\nu^* = \eta M^*/\delta + \theta_c$ from (9). Therefore, from (9), the following equation in terms of M must have a positive root $M = M^*$:

$$\frac{\delta}{\eta} M + \theta_c = 1 - \frac{1}{\mathscr{R}_0} \frac{\beta_0}{\beta(M)}. \tag{A.2}$$

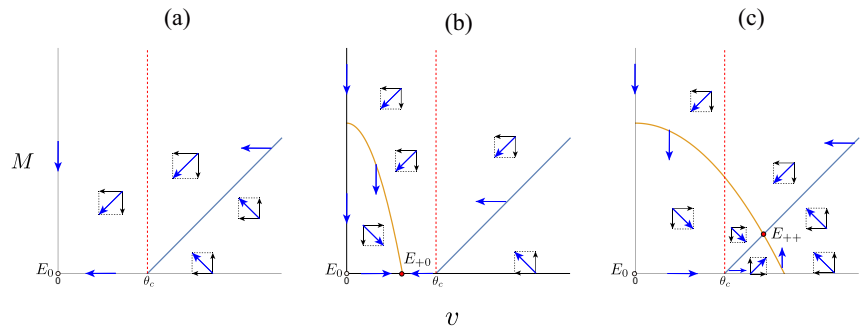

Figure 24: Sketches of the vector flow in the (v, M)-phase plane for the system (4) with the nullclines. (a) $\mathscr{R}_0 \leqslant 1$; (b) $1 < \mathscr{R}_0 \leqslant (1-\theta_c)^{-1}$; (c) $\mathscr{R}_0 > (1-\theta_c)^{-1}$.

Since the right side of (A.2) is monotonically decreasing in terms of M while the left side is linearly increasing, we find that a positive root $M = M^*$ uniquely exists if and only if

$$\theta_c < 1 - \frac{1}{\mathscr{R}_0}\frac{\beta_0}{\beta(0)} = 1 - \frac{1}{\mathscr{R}_0},$$

that is, $\mathscr{R}_0 > (1-\theta_c)^{-1}$. From the former equation in (9) and $v^* = \eta M^*/\delta + \theta_c$, we have

$$\theta_c < v^* = 1 - \frac{1}{\mathscr{R}_0}\frac{\beta_0}{\beta(M^*)} < 1 - \frac{1}{\mathscr{R}_0} \tag{A.3}$$

for all $M^* > 0$. Hence, when a positive root $M = M^*$ for the equation (A.2) exists, we have $v^* \in (\theta_c, 1 - 1/\mathscr{R}_0)$ at the same time. Hence (iii) of Lemma 2.2 is proved.

Since $1 - 1/\mathscr{R}_0 \to \theta_c$ as $\mathscr{R}_0 \to (1-\theta_c)^{-1} + 0$, we find from (A.3) that $v^* \to \theta_c$ as $\mathscr{R}_0 \to (1-\theta_c)^{-1} + 0$ Then, from (A.2), we have $M^* \to 0$ as $\mathscr{R}_0 \to (1-\theta_c)^{-1} + 0$. These arguments prove (iv) of Lemma 2.2.

A.3 PROOF OF THEOREM 2.2 AND COROLLARY 2.2.2 IN SECTION 2.3.4

When $\mathscr{R}_0 \leqslant 1$, the vector flow in the (v, M)-phase plane indicates that $(v(\tau), M(\tau))$ necessarily approaches the unique equilibrium E_0, and then E_0 is globally asymptotically stable (Figure 24(a)). When $1 < \mathscr{R}_0 \leqslant (1-\theta_c)^{-1}$, the vector flow in the phase plane shows that $(v(\tau), M(\tau))$ goes far away from the equilibrium E_0 and approaches the equilibrium E_{+0}, where E_0 is unstable while E_{+0} is globally asymptotically stable (Figure 24(b)).

Next let us consider the case of $\mathscr{R}_0 > (1-\theta_c)^{-1}$ (Figure 24). From (4), we have

$$\frac{dv}{d\tau} = \mathscr{R}_0 v\Big\{\frac{\beta(M)}{\beta_0}(1-v) - \frac{1}{\mathscr{R}_0}\Big\} < \mathscr{R}_0 v\Big(1 - v - \frac{1}{\mathscr{R}_0}\Big),$$

for any $M > 0$ and $v \in (0,1)$ since $\beta(M)$ is monotonically decreasing in terms of M and $\beta(0) = \beta_0$. Thus we have $dv/d\tau < 0$ for $v \geqslant 1 - 1/\mathscr{R}_0$, so that the trajectory must go to the left direction in the (v, M)-phase plane as long as $v > 1 - 1/\mathscr{R}_0$. Thus the trajectory with $v(0) \geqslant 1 - 1/\mathscr{R}_0$ must enter the region where $v < 1 - 1/\mathscr{R}_0$ at a certain moment. If $v(\tau_1) < 1 - 1/\mathscr{R}_0$ at a $\tau_1 > 0$, $v(\tau)$ is always less than $1 - 1/\mathscr{R}_0$ for any $\tau \geqslant \tau_1$, because $v(\tau)$ cannot become larger than $1 - 1/\mathscr{R}_0$ again.

In the region where $\nu \leqslant \theta_c$, we have $dM/d\tau = -\delta M < 0$ for any $M > 0$. In the region where $\theta_c < \nu < 1 - 1/\mathscr{R}_0$ and $M \geqslant (1 - 1/\mathscr{R}_0 - \theta_c)\eta/\delta$, we have

$$\begin{aligned}\frac{dM}{d\tau} &= \eta(\nu - \theta_c) - \delta M \leqslant \eta(\nu - \theta_c) - \Big(1 - \frac{1}{\mathscr{R}_0} - \theta_c\Big)\eta \\ &= \eta\Big(\nu - 1 + \frac{1}{\mathscr{R}_0}\Big) < 0\end{aligned}$$

from (4), so that the trajectory must go down in the region of the (ν, M)-phase plane where $0 < \nu < 1 - 1/\mathscr{R}_0$ and $M \geqslant (1 - 1/\mathscr{R}_0 - \theta_c)\eta/\delta$. Thus the trajectory with $M(0) \geqslant (1 - 1/\mathscr{R}_0 - \theta_c)\eta/\delta$ must enter the region where $M < (1 - 1/\mathscr{R}_0 - \theta_c)\eta/\delta$. Consequently we find that the trajectory from any initial condition $(\nu(0), M(0)) \in U = (0, 1 - 1/\mathscr{R}_0) \times [0, (1 - 1/\mathscr{R}_0 - \theta_c)\eta/\delta)$ must remain in U for any $\tau \geqslant 0$. From Lemma 2.2. there is only the equilibrium E_{++} in the domain U when $\mathscr{R}_0 > (1 - \theta_c)^{-1}$. Further, making use of the standard eigenvalue analysis on the Jacobi matrix $J(E_{++})$ for E_{++}, we can show that, if the equilibrium E_{++} exists, it is locally asymptotically stable.

As a result of these arguments with Lemma 2.2, the unique equilibrium E_{++} in the domain U is locally asymptotically stable when $\mathscr{R}_0 > (1 - \theta_c)^{-1}$. Therefore, from Poincaré–Bendixson Theorem, the equilibrium E_{++} for the system (4) is globally asymptotically stable when $\mathscr{R}_0 > (1 - \theta_c)^{-1}$ for any $M(0) \geqslant 0$ and $\nu(0) > 0$. This proves Theorem 2.2.

When $\mathscr{R}_0 \leqslant (1 - \theta_c)^{-1}$, from the vector flow in the (ν, M)-phase plane shown in Figure 24(a, b), it is easily seen that the trajectory must monotonically approach the equilibrium E_0 when $\mathscr{R}_0 \leqslant 1$, and the equilibrium E_{+0} when $1 < \mathscr{R}_0 \leqslant (1 - \theta_c)^{-1}$.

Further, when $\mathscr{R}_0 > (1 - \theta_c)^{-1}$, we have the discriminant of the characteristic equation for the Jacobi matrix $J(E_{++})$, Δ given by (11). If $\Delta > 0$, the eigenvalues λ_1 and λ_2 are both negative as shown in the above. Then the system (4) monotonically approaches E_{++}. If $\Delta < 0$, the eigenvalues λ_1 and λ_2 are imaginary with a negative real part. In this case, the system (4) approaches E_{++} with a damped oscillation. This proves Corollary 2.2.2.

A.4 PROOF OF THEOREM 2.3 IN SECTION 2.3.5

First let us consider the case where the social response changes much faster than the epidemic dynamics. Then we apply the QSSA to put $dM/d\tau \approx 0$. Thus we assume

$$M(\tau) \approx \frac{G(\nu(\tau))}{\delta} \tag{A.4}$$

for any $\tau \geqslant 0$. Substituting (A.4) for (4), we get the approximated dynamics about ν:

$$\frac{d\nu}{d\tau} = \varphi(\nu)\nu := \left\{\frac{\mathscr{R}_0}{\beta_0}\beta\Big(\frac{G(\nu)}{\delta}\Big)(1 - \nu) - 1\right\}\nu. \tag{A.5}$$

When $\nu \leqslant \theta_c$, we have $G(\nu) = 0$, and then the equation (A.5) becomes a logistic equation same as (6). When $\nu > \theta_c$, we have $G(\nu) = \eta(\nu - \theta_c)$. In this case, we can easily find that $d\varphi/d\nu < 0$ for any $\nu > 0$ because of $\beta'(M) < 0$ for any $M > 0$. Since $\varphi(\theta_c) = \mathscr{R}_0(1 - \theta_c) - 1$, we have $\varphi(\nu) < 0$ for any $\nu > \theta_c$ if $\varphi(\theta_c) \leqslant 0$, that is, if $\mathscr{R}_0 \leqslant (1 - \theta_c)^{-1}$. On the other hand, we have $\varphi(1) = -1 < 0$. Hence, if $\varphi(\theta_c) > 0$, that is, if $\mathscr{R}_0 > (1 - \theta_c)^{-1}$, there is a unique value of ν, $\nu = \nu^* \in (\theta_c, 1)$ such that $\varphi(\nu^*) = 0$, $\varphi(\nu) > 0$ for $\nu < \nu^*$, and $\varphi(\nu) < 0$ for $\nu > \nu^*$.

As a result, we find that, if $\mathscr{R}_0 \leqslant 1$, $dv/d\tau < 0$ for any $\tau > 0$. Then $v \to 0$ as $\tau \to \infty$ in a monotonic manner. If $1 < \mathscr{R}_0 \leqslant (1-\theta_c)^{-1}$, v must reach θ_c at a certain finite time for any $v(0) > \theta_c$ because $dv/d\tau < 0$ for any $v > \theta_c$. For $v(0) \leqslant \theta_c$, the equation (A.5) becomes the logistic equation (6) as mentioned above. Then v monotonically approaches $1 - 1/\mathscr{R}_0 < \theta_c$ when $1 < \mathscr{R}_0 < (1-\theta_c)^{-1}$. When $\mathscr{R}_0 = (1-\theta_c)^{-1}$, we have $dv/d\tau = 0$ for $v = \theta_c = 1 - 1/\mathscr{R}_0$. This means that $v = \theta_c$ is the equilibrium for (A.5). Hence we find that $v \to \theta_c = 1 - 1/\mathscr{R}_0$ as $\tau \to \infty$ when $\mathscr{R}_0 = (1-\theta_c)^{-1}$.

In contrast, if $\mathscr{R}_0 > (1-\theta_c)^{-1}$, we have $dv/d\tau > 0$ in (6) for any positive $v \leqslant \theta_c$. Hence v must necessarily become greater than θ_c from any positive $v(0) < \theta_c$. Once v becomes greater than θ_c, $v \to v^*$ as $\tau \to \infty$ in a monotonic manner because of the sign of $\varphi(v)$ and $\varphi(v^*) = 0$ as shown above. Consequently, these arguments prove Theorem 2.4 for the case where the social response changes extremely fast.

Next let us consider the case where the social response changes much slower than the epidemic dynamics. Then we apply the QSSA to put $dv/d\tau \approx 0$ with $v \in [0, 1)$. Thus we have

$$v(\tau) \approx 0 \quad \text{or} \quad v(\tau) \approx 1 - \frac{1}{\mathscr{R}_0}\frac{\beta_0}{\beta(M(\tau))} \leqslant 1 - \frac{1}{\mathscr{R}_0} \tag{A.6}$$

for any $\tau \geqslant 0$. Since we have the initial value $M(0) = 0$, we find that $v(\tau) \approx 0$ if $\mathscr{R}_0 \leqslant 1$, while $v(\tau)$ is approximated by the latter in (A.6) if $\mathscr{R}_0 > 1$. Thus, when $\mathscr{R}_0 \leqslant 1$, we have $M \approx 0$ for any $\tau > 0$, because $G(v) = 0$ so that $dM/dt \approx 0$ for any $\tau > 0$ with $M(0) = 0$. Let us consider hereafter the case of $\mathscr{R}_0 > 1$. When $v \leqslant \theta_c$, we have $G(v) = 0$, and $dM/d\tau = -\delta M < 0$ for any $M > 0$. When $v > \theta_c$, substituting the latter approximation in (A.6) for (4), we get the approximated dynamics about M:

$$\frac{dM}{d\tau} = \psi(M) := \eta\left(1 - \frac{1}{\mathscr{R}_0}\frac{\beta_0}{\beta(M)} - \theta_c\right) - \delta M.$$

We can easily find that $d\psi(M)/\tau < 0$ for any $M > 0$ because $\beta'(M) < 0$ for any $M > 0$. Since $\psi(0) = \eta(1 - 1/\mathscr{R}_0 - \theta_c)$, if $\psi(0) \leqslant 0$, that is, if $\mathscr{R}_0 \leqslant (1-\theta_c)^{-1}$, we have $\psi(M) < 0$ for any $M > 0$. On the other hand, we have $\psi(M) \to -\infty$ as $M \to \infty$. Hence, if $\psi(0) > 0$, that is, if $\mathscr{R}_0 > (1-\theta_c)^{-1}$, there is a unique value of M, $M = M^* > 0$ such that $\psi(M^*) = 0$, $\psi(M) > 0$ for $M < M^*$, and $\psi(M) < 0$ for $M > M^*$.

As a result, we find that, if $\mathscr{R}_0 \leqslant 1$, $M \to 0$ as $\tau \to \infty$ in a monotonic manner. If $1 < \mathscr{R}_0 \leqslant (1-\theta_c)^{-1}$, we have $v < 1 - 1/\mathscr{R}_0 < \theta_c$ for any $\tau > 0$ from (A.6). Then we have $dM/d\tau < 0$ for any $M > 0$. Thus, we have $M \to 0$ as $\tau \to \infty$ in a monotonic manner for any positive $M(0)$. If $\mathscr{R}_0 > (1-\theta_c)^{-1}$, we also have $v < 1 - 1/\mathscr{R}_0 < \theta_c$ for any $\tau > 0$ from (A.6). Then we have $dM/d\tau > 0$ for any $M < M^*$, and $dM/d\tau < 0$ for any $M > M^*$. Thus $M \to M^*$ as $\tau \to \infty$ in a monotonic manner. Finally we have Theorem 2.4.

A.5 PROOF OF THEOREM 2.4 IN SECTION 2.3.6

The discriminant Δ given by (15) can be rewritten as

$$\Delta = f(x) := x^2 - 2\left(\delta + \frac{2}{\mathscr{R}_0}\alpha\eta\right)x + \delta^2 \tag{A.7}$$

with

$$x = \frac{v^*}{1-v^*} = \frac{(\mathscr{R}_0 - 1)\delta + \alpha\eta\theta_c}{\delta + \alpha\eta(1-\theta_c)}. \tag{A.8}$$

There are two distinct positive roots x_- and x_+ ($x_- < x_+$) of the equation $f(x) = 0$ as given by (17). We have $f(x) < 0$ for and only for $x \in (x_-, x_+)$. Hence, from the inequality $x_- < x < x_+$ with (A.8), we can derive the condition $\theta_-^c < \theta_c < \theta_+^c$ with (16), since $f(x) < 0$ means the negative discriminant (15) so that the eigenvalue for E_{++} is imaginary. Therefore, a damped oscillation occurs if (16) is satisfied, These arguments prove Theorem 2.4.

A.6 PROOF OF COROLLARY 2.4.1 IN SECTION 2.3.6

When $\theta_\pm^c = 1 - 1/\mathscr{R}_0$, we have $x_\pm = \mathscr{R}_0 - 1$ from (16) and (17), where $x_\pm$ is defined by the roots of the equation $f(x) = 0$ given by (A.7) in A.5. We have $dx_-/d\mathscr{R}_0 > 0$ and $dx_+/d\mathscr{R}_0 < 0$ from (17). Then there are uniquely determined positive roots $\mathscr{R}_0^{\inf}$ and $\mathscr{R}_0^{cc}$ of equations $x_\pm = \mathscr{R}_0 - 1$ with respect to $\mathscr{R}_0$, where $\mathscr{R}_0^{cc} > \mathscr{R}_0^{\inf} > 1$. We have $\mathscr{R}_0 - 1 < x_-$ for $\mathscr{R}_0 < \mathscr{R}_0^{\inf}$, $x_- < \mathscr{R}_0 - 1 < x_+$ for $\mathscr{R}_0^{\inf} < \mathscr{R}_0 < \mathscr{R}_0^{cc}$, and $\mathscr{R}_0 - 1 > x_+$ for $\mathscr{R}_0 > \mathscr{R}_0^{cc}$. Therefore, we have $\theta_-^c > 1 - 1/\mathscr{R}_0$ for $\mathscr{R}_0 < \mathscr{R}_0^{\inf}$, $\theta_-^c < 1 - 1/\mathscr{R}_0 < \theta_+^c$ for $\mathscr{R}_0^{\inf} < \mathscr{R}_0 < \mathscr{R}_0^{cc}$, and $\theta_+^c < 1 - 1/\mathscr{R}_0$ for $\mathscr{R}_0 > \mathscr{R}_0^{cc}$. The damped oscillation does not occur for $\mathscr{R}_0 < \mathscr{R}_0^{\inf}$ independently of θ_c.

For $\theta_\pm^c = 0$, we have $x_\pm = (\mathscr{R}_0 - 1)\delta/(\delta + \alpha\eta)$ from (16) and (17). There are uniquely determined positive roots $\mathscr{R}_0^c$ and $\mathscr{R}_0^{\sup}$ of equations $x_\pm = (\mathscr{R}_0 - 1)\delta/(\delta + \alpha\eta)$ with respect to $\mathscr{R}_0$, where $\mathscr{R}_0^{\sup} > \mathscr{R}_0^c > 1$. We have $(\mathscr{R}_0 - 1)\delta/(\delta + \alpha\eta) < x_-$ for $\mathscr{R}_0 < \mathscr{R}_0^c$, $x_- < (\mathscr{R}_0 - 1)\delta/(\delta + \alpha\eta) < x_+$ for $\mathscr{R}_0^c < \mathscr{R}_0 < \mathscr{R}_0^{\sup}$, and $(\mathscr{R}_0 - 1)\delta/(\delta + \alpha\eta) > x_+$ for $\mathscr{R}_0 > \mathscr{R}_0^{\sup}$. Therefore we have $\theta_-^c > 0$ for $\mathscr{R}_0 < \mathscr{R}_0^c$, $\theta_-^c < 0 < \theta_+^c$ for $\mathscr{R}_0^{cc} < \mathscr{R}_0 < \mathscr{R}_0^{\sup}$, and $\theta_+^c < 0$ for $\mathscr{R}_0 > \mathscr{R}_0^{\sup}$. The damped oscillation does not occur for $\mathscr{R}_0 > \mathscr{R}_0^{\sup}$ independently of θ_c.

We note that there is no case where $0 < \theta_-^c < \theta_+^c < 1 - 1/\mathscr{R}_0$ from the definition of $\theta_\pm^c$. Therefore, we can subsequently find it not valid that $\mathscr{R}_0^{cc} \leqslant \mathscr{R}_0^c$. Hence, as a consequence, $\mathscr{R}_0^{\sup} > \mathscr{R}_0^{cc} > \mathscr{R}_0^c > \mathscr{R}_0^{\inf} > 1$. Further, we have $1 - \mathscr{R}_0 < \theta_-^c$ for $\mathscr{R}_0 < \mathscr{R}_0^{\inf}$, $1 - \mathscr{R}_0 > \theta_-^c > 0$ for $\mathscr{R}_0^{\inf} < \mathscr{R}_0 < \mathscr{R}_0^c$, and $\theta_-^c < 0$ for $\mathscr{R}_0 > \mathscr{R}_0^c$. On the other hand, we have $1 - \mathscr{R}_0 < \theta_+^c$ for $\mathscr{R}_0 < \mathscr{R}_0^{cc}$, $1 - \mathscr{R}_0 > \theta_+^c > 0$ for $\mathscr{R}_0^{cc} < \mathscr{R}_0 < \mathscr{R}_0^{\sup}$, and $\theta_+^c < 0$ for $\mathscr{R}_0 > \mathscr{R}_0^{\sup}$. When $\theta_c \geqslant 1 - 1/\mathscr{R}_0^{cc}$, if $\mathscr{R}_0 \leqslant \mathscr{R}_0^{cc}$, then E_{++} does not exist since $\mathscr{R}_0 \leqslant \mathscr{R}_0^{cc} \leqslant (1 - \theta_c)^{-1}$. If $\mathscr{R}_0 > \mathscr{R}_0^{cc}$, we have $\mathscr{R}_0 - 1 > x_+$, that is, $\theta_+^c < 1 - 1/\mathscr{R}_0$. There is no damped oscillation since $\theta_c \geqslant 1 - 1/\mathscr{R}_0^{cc} > 1 - 1/\mathscr{R}_0 > \theta_+^c$. Therefore the damped oscillation does not occur for $\theta_c \geqslant 1 - 1/\mathscr{R}_0^{cc}$ independently of $\mathscr{R}_0$. These arguments prove the Corollary 2.4.1.

A.7 PROOF OF COROLLARY 2.4.2 IN SECTION 2.3

If $\delta = 0$, we have $\nu^* = \theta_c$ and the discriminant (11) as

$$\Delta = \frac{\theta_c}{1 - \theta_c}\left(\frac{\theta_c}{1 - \theta_c} - \frac{4\alpha\eta}{\mathscr{R}_0}\right).$$

The discriminant Δ becomes negative if and only if

$$\theta_c < \theta_+^c = \frac{4\alpha\eta}{\mathscr{R}_0 + 4\alpha\eta}. \tag{A.9}$$

We have $\theta_+^c \geqslant 1 - 1/\mathscr{R}_0$ if and only if

$$\mathscr{R}_0 \leqslant \mathscr{R}_0^{cc} = \frac{1}{2}(1 + \sqrt{1 + 16\alpha\eta}). \tag{A.10}$$

Hence, when the condition (A.10) is satisfied for $\mathscr{R}_0 > 1$, the condition (A.9) holds for any $\theta_c < 1 - 1/\mathscr{R}_0$. That is, $\Delta < 0$ whenever E_{++} exists with $\theta_c \in (0, 1 - 1/\mathscr{R}_0)$. From Corollary 2.2.2, the damped oscillation does not occur for $\theta_c \geqslant 1 - 1/\mathscr{R}_0$. This proves Corollary 2.4.2(i). Unless (A.10) is not satisfied, that is, if $\mathscr{R}_0 > \mathscr{R}_0^{cc}$, then we have $\theta_+^c < 1 - 1/\mathscr{R}_0$. Hence in this case, from Corollary 2.2.2, we obtain the result of Corollary 2.4.2(ii). For the other case, we have $\theta_c \geqslant 1 - 1/\mathscr{R}_0$ or $\theta_c \geqslant \theta_+^c$, that is, E_{++} does not exist or it exists with $\Delta \geqslant 0$. Therefore a damped oscillation occurs only in the cases described in Corollary 2.4.2.

A.8 PROOF OF COROLLARY 2.4.3 IN SECTION 2.3

From (A.8) as $a\eta \to \infty$, we have $x \to \theta_c/(1-\theta_c)$ and

$$\Delta \to \left(\frac{\theta_c}{1-\theta_c}\right) + \delta^2 - \left(\frac{\theta_c}{1-\theta_c}\right) \lim_{a\eta\to\infty} \left(\delta + \frac{1}{\mathscr{R}_0} a\eta\right) < 0.$$

Besides, $x \to \mathscr{R}_0 - 1$ and

$$\Delta \to (\mathscr{R}_0 - 1 - \delta)^2 \geqslant 0$$

as $a\eta \to +0$ or $\delta \to \infty$. These results prove Corollary 2.4.3.

A.9 PROOF OF COROLLARY 2.4.4 IN SECTION 2.3.6

With $\theta_c = 0$, the discriminant (15) becomes

$$\Delta|_{\theta_c=0} = \frac{\delta}{{\mathscr{R}_0}^2 (a\eta + \delta)^2} g(a\eta),$$

where

$$\begin{aligned} g(a\eta) := &\left\{\delta - 4\left(1 - \frac{1}{\mathscr{R}_0}\right)\right\}(a\eta)^2 \\ &- 2\delta\left\{2\left(1 - \frac{1}{\mathscr{R}_0}\right) + (\mathscr{R}_0 - 1 - \delta)\right\} a\eta + \delta(\mathscr{R}_0 - 1 - \delta)^2 \end{aligned}$$

with (14). For $\delta \neq 4(1 - 1/\mathscr{R}_0)$, we have $g(a\eta) < 0$ when $4(1 - 1/\mathscr{R}_0) < \delta < \min\{\mathscr{R}_0, (\mathscr{R}_0 + 2)(1 - 1/\mathscr{R}_0)\}$ with $\mathscr{R}_0 > 2$ and $(a\eta)_-^c < a\eta < (a\eta)_+^c$, or when $\delta < 4(1 - 1/\mathscr{R}_0)$ and $a\eta > (a\eta)_+^c$, where $(a\eta)_\pm^c$ are given in (18). For $\delta = 4(1 - 1/\mathscr{R}_0)$, we have

$$g(a\eta) = 4\left(1 - \frac{1}{\mathscr{R}_0}\right)^2 \left\{(\mathscr{R}_0 - 4)^2 \left(1 - \frac{1}{\mathscr{R}_0}\right) - 2(\mathscr{R}_0 - 2) a\eta\right\}.$$

Then $g(a\eta) < 0$ for $a\eta > (\mathscr{R}_0 - 4)^2(\mathscr{R}_0 - 1)/\{2\mathscr{R}_0(\mathscr{R}_0 - 2)\} > 0$ with $\mathscr{R}_0 > 2$. These prove Corollary 2.4.4.

B

APPENDIX FOR CHAPTER 3

B.1 DERIVATION OF $\mathscr{R}_0$ IN SECTION 3.2

In our model, the new cases consist of residents and visitors. Therefore, from the conceptual definition and the mathematical feature of the basic reproduction number, we shall derive it here from the following conditions:

$$\left.\frac{d(I_v+I_r)}{dt}\right|_{0<I_v+I_r\ll 1} > 0 \text{ for } \mathscr{R}_0 > 1; \quad \left.\frac{d(I_v+I_r)}{dt}\right|_{0<I_v+I_r\ll 1} < 0 \text{ for } \mathscr{R}_0 < 1,$$

for the initial condition (21) with $0 < I_v(0) + I_r(0) = 0 + I_{r0} \ll 1$. This is because the basic reproduction number is defined as the expected number of new infectives produces by one infective individual in an environment consisting of only susceptibles. Following Assumption H3 in Section 3.1.1, we shall adopt the initial condition (21) in order to define the basic reproduction number. Then, in place of the above conditions, we can use the followings:

$$\left.\frac{d(I_v+I_r)}{dt}\right|_{t=0} > 0 \text{ for } \mathscr{R}_0 > 1; \quad \left.\frac{d(I_v+I_r)}{dt}\right|_{t=0} < 0 \text{ for } \mathscr{R}_0 < 1$$

for the initial condition (21) with $0 < I_v(0) + I_r(0) = 0 + I_{r0} \ll 1$. Remark that, in this context about the situation to define the basic reproduction number of our model, the initial infective must be a resident, which matches Assumption H3 in Section 3.1.1. Then, making use of (21), we have

$$\left.\frac{d(I_v+I_r)}{dt}\right|_{t=0} = \left\{\beta\frac{(1-\rho)m+S_{r0}}{N+m} + \epsilon\beta\frac{\rho m+R_{r0}}{N+m} - \gamma\right\}I_{r0}.$$

Thus we find that

$$\left.\frac{d(I_v+I_r)}{dt}\right|_{t=0} > 0 \text{ if and only if } \frac{\beta}{\gamma}\frac{(1-\rho)m+S_{r0}}{N+m} + \frac{\epsilon\beta}{\gamma}\frac{\rho m+R_{r0}}{N+m} > 1.$$

Consequently we can define the basic reproduction number $\mathscr{R}_0$ as follows:

$$\begin{aligned}
\mathscr{R}_0 &= \sup_{(S_{r0},R_{r0})}\left\{\frac{\beta}{\gamma}\frac{(1-\rho)m+S_{r0}}{N+m} + \frac{\epsilon\beta}{\gamma}\frac{\rho m+R_{r0}}{N+m}\right\}\\
&= \sup_{S_{r0}}\left\{\frac{\beta}{\gamma}\frac{(1-\rho)m+S_{r0}}{N+m} + \frac{\epsilon\beta}{\gamma}\frac{\rho m+N-S_{r0}}{N+m}\right\}\\
&= \sup_{S_{r0}}\left\{\frac{\beta}{\gamma}\frac{(1-\rho)m}{N+m} + \frac{\epsilon\beta}{\gamma}\frac{\rho m+N}{N+m} + \frac{(1-\epsilon)\beta}{\gamma}\frac{S_{r0}}{N+m}\right\}\\
&= \frac{\beta}{\gamma}\frac{(1-\rho)m+N}{N+m} + \frac{\epsilon\beta}{\gamma}\frac{\rho m}{N+m}.
\end{aligned}$$

This formula can be rewritten as given by (22) to clarify the meaning.

B.2 PROOF OF THEOREM 3.2 IN SECTION 3.3.2

From the arguments in the first paragraph of Section 3.3.2, we find that the dynamics given by (23) with $\epsilon = 0$ necessarily approaches the dynamics with the following limiting system in terms of the visitor population:

$$\begin{aligned} \frac{d\widetilde{x}_v}{d\tau} &= (1-\rho)c - \mathscr{R}_{00}\frac{\mu}{1+\mu}\widetilde{y}_v\widetilde{x}_v - c\widetilde{x}_v; \\ \frac{d\widetilde{y}_v}{d\tau} &= \mathscr{R}_{00}\frac{\mu}{1+\mu}\widetilde{y}_v\widetilde{x}_v - (1+c)\widetilde{y}_v. \end{aligned} \tag{B.1}$$

The feasible equilibria are $\widetilde{E}_0(1-\rho, 0)$ and $\widetilde{E}_+(\widetilde{x}_v^*, \widetilde{y}_v^*)$ with (24). The former $\widetilde{E}_0$ corresponds to the disease-eliminated equilibrium for the system (23), $E_{00}(1-\rho, 0, 0, 0)$, and so does the latter $\widetilde{E}_+$ to the endemic equilibrium $E_{+0}(\widetilde{x}_v^*, \widetilde{y}_v^*, 0, 0)$. The endemic equilibrium E_{+0} can exist when and only when the condition (25) is satisfied. By the local stability analysis with the eigenvalues of the Jacobi matrix at the equilibrium, we can easily find that the endemic equilibrium E_{+0} is locally asymptotically stable when it exists. In the following part, we shall consider its global stability.

First we set the following mathematical result on the boundedness for the solution of the system (B.1):

Lemma B.1. *For any initial condition* $\big(\widetilde{x}_v(0), \widetilde{y}_v(0)\big)$ *in the domain*

$$D := \Big\{ (\widetilde{x}_v, \widetilde{y}_v) \mid \widetilde{x}_v > 0,\ \widetilde{y}_v > 0,\ \widetilde{x}_v + \widetilde{y}_v < 1-\rho \Big\}, \tag{B.2}$$

the solution $\big(\widetilde{x}_v(\tau), \widetilde{y}_v(\tau)\big)$ *of* (B.1) *stays in* D *for any* $\tau > 0$.

Proof. We can obtain the following features from (B.1) for the initial condition $\big(\widetilde{x}_v(0), \widetilde{y}_v(0)\big) \in D$:

$$\left.\frac{d\widetilde{x}_v}{d\tau}\right|_{x_v=0} = 1-\rho > 0;\ \widetilde{y}_v(\tau) = \widetilde{y}_v(0)\exp\left[\int_0^\tau \left\{\mathscr{R}_{00}\frac{\mu}{1+\mu}\widetilde{x}_v(s) - (1+c)\right\}ds\right] > 0.$$

The first inequality indicates that $\widetilde{x}_v$ cannot reach o from the initial value $\widetilde{x}_v(0) > 0$. The second equation indicates that $\widetilde{y}_v$ is necessarily positive for any $\tau > 0$ and $\widetilde{y}_v(0) > 0$. Then, from

$$\left.\frac{d\big(\widetilde{x}_v + \widetilde{y}_v\big)}{d\tau}\right|_{\widetilde{x}_v+\widetilde{y}_v=1-\rho} = -\widetilde{y}_v < 0$$

for $\widetilde{y}_v > 0$, we can find that $\widetilde{x}_v + \widetilde{y}_v$ cannot become $\widetilde{x}_v + \widetilde{y}_v = 1-\rho$ for any $\tau > 0$ and initial condition in D. □

Lemma B.1 means that the domain D is invariant for the dynamics given by (B.1). Further, when the endemic equilibrium $\widetilde{E}_+$ exists, satisfying the condition (25), we find from (24) that

$$\begin{aligned} \widetilde{x}_v^* + \widetilde{y}_v^* &= (1-\rho)\frac{c}{c+1} + \frac{1+\mu}{\mu}\frac{1}{\mathscr{R}_{00}} \\ &< (1-\rho)\frac{c}{c+1} + \frac{1+\mu}{\mu}\frac{1}{c+1}(1-\rho)\frac{\mu}{1+\mu} = 1-\rho. \end{aligned}$$

Hence we have the following result:

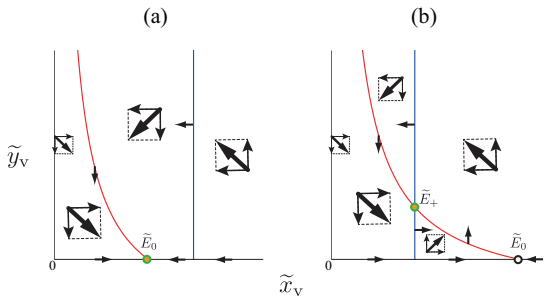

Figure 25: Application of the isocline method for the system (B.1) when the condition (25) is (a) not satisfied; (b) satisfied.

Lemma B.2. *When* $\widetilde{E}_+(\widetilde{x}_v^*, \widetilde{y}_v^*)$ *exists, it must belong to the domain* D *defined by* (B.2).

When the condition (25) is not satisfied, that is, when the endemic equilibrium does not exist, we can easily find that the disease-eliminated equilibrium is globally asymptotically stable, making use of the isocline method shown by Figure 25(a). In contrast, as seen from Figure 25(b), when the condition (25) is satisfied and the endemic equilibrium $\widetilde{E}_+$ exists, the stability cannot be determined only by the isocline method.

When the endemic equilibrium $\widetilde{E}_+$ exists, let us consider the following function of $(\widetilde{x}_v, \widetilde{y}_v)$ in the domain D defined by Lemma B.1:

$$V(\widetilde{x}_v, \widetilde{y}_v) := \frac{1}{2}\{(\widetilde{x}_v^* - \widetilde{x}_v) + (\widetilde{y}_v^* - \widetilde{y}_v)\}^2 + \left(\widetilde{x}_v^* + c\frac{1+\mu}{\mathscr{R}_{00}\mu}\right)\left(\widetilde{y}_v - \widetilde{y}_v^* - \widetilde{y}_v^* \ln\frac{\widetilde{y}_v}{\widetilde{y}_v^*}\right). \tag{B.3}$$

It can be easily found that $V(\widetilde{x}_v^*, \widetilde{y}_v^*) = 0$ and $V(\widetilde{x}_v, \widetilde{y}_v) > 0$ for any $(\widetilde{x}_v, \widetilde{y}_v) \neq (\widetilde{x}_v^*, \widetilde{y}_v^*)$ in D. Further, making use of (B.1), we can derive

$$\frac{dV}{d\tau} = -(\widetilde{x}_v^* - \widetilde{x}_v)^2 - \frac{\mu}{1+\mu}\widetilde{x}_v^*(\widetilde{y}_v^* - \widetilde{y}_v)^2,$$

which becomes zero only for $(\widetilde{x}_v, \widetilde{y}_v) = (\widetilde{x}_v^*, \widetilde{y}_v^*)$, and negative for any $(\widetilde{x}_v, \widetilde{y}_v) \neq (\widetilde{x}_v^*, \widetilde{y}_v^*)$ in D. These features of V indicates that it is a Lyapunov function according to the endemic equilibrium $\widetilde{E}_+$ for the system (B.1). Therefore, when the endemic equilibrium $\widetilde{E}_+$ exists for the system (B.1), it is globally asymptotically stable with respect to the dynamics given by (B.1) with the initial condition in D. Since the dynamics of (23) with $\epsilon = 0$ must eventually approach that of (B.1), this result shows the global stability of the endemic equilibrium for (23).

B.3 PROOF OF THEOREM 3.4 IN SECTION 3.3.4

The characteristic equation $\det(J_{00} - \lambda E) = 0$ with the Jacobian matrix J_{00} according to the disease-eliminated equilibrium $E_{00}(1-\rho, 0, 0, 0)$ for the system (23) becomes

$$(-1-\lambda)(-\omega-\lambda)\begin{vmatrix} \{1-(1-\epsilon)\rho\}\mathscr{R}_{00}\dfrac{\mu}{1+\mu} - (1+c) - \lambda & \{1-(1-\epsilon)\rho\}\mathscr{R}_{00}\dfrac{\mu}{1+\mu} \\ \epsilon\mathscr{R}_{00}\dfrac{\mu}{1+\mu} & \epsilon\mathscr{R}_{00}\dfrac{1}{1+\mu} - 1 - \lambda \end{vmatrix} = 0.$$

Hence we have two negative eigenvalues -1 and $-\omega$ with the other two given by the roots of the equation that the above 2×2 determinant is equal to zero. Both of them have negative real parts if and only if

$$\begin{cases} \{1-(1-\epsilon)\rho\}\mathscr{R}_{00}\dfrac{\mu}{1+\mu} - (1+c) + \epsilon\mathscr{R}_{00}\dfrac{1}{1+\mu} - 1 < 0; \\ \left[\{1-(1-\epsilon)\rho\}\mathscr{R}_{00}\dfrac{\mu}{1+\mu} - (1+c)\right]\left(\epsilon\mathscr{R}_{00}\dfrac{1}{1+\mu} - 1\right) \\ \qquad\qquad - \{1-(1-\epsilon)\rho\}\mathscr{R}_{00}\dfrac{\mu}{1+\mu}\cdot\epsilon\mathscr{R}_{00}\dfrac{\mu}{1+\mu} > 0, \end{cases}$$

that is,

$$\begin{cases} \{1-(1-\epsilon)\rho\}\mathscr{R}_{00}\dfrac{\mu}{1+\mu} - (1+c) + \epsilon\mathscr{R}_{00}\dfrac{1}{1+\mu} - 1 < 0; \\ \{1-(1-\epsilon)\rho\}\mathscr{R}_{00}\dfrac{\mu}{1+\mu} - (1+c) + (1+c)\epsilon\mathscr{R}_{00}\dfrac{1}{1+\mu} < 0. \end{cases}$$

Therefore we find that the second inequality gives the necessary and sufficient condition that every eigenvalue has a negative real part. It can be expressed as the inverse inequality of (27). At the same time, we can find that, if the inverse of the above second inequality is satisfied, there exists an eigenvalue with a positive real part. Then the disease eliminated equilibrium E_{00} is unstable.

B.4 PROOF OF COROLLARY 3.4.1 IN SECTION 3.3.4

It is sufficient to show that $\{G(\mu,\rho)\}^{-1} < 1/(\epsilon\mathscr{R}_{00})$ when $\mathscr{R}_0 \leqslant 1$. From the definition of $\mathscr{R}_0$ defined by (22), we have $\mathscr{R}_0 \leqslant 1$ if and only if

$$\frac{1}{\epsilon\mathscr{R}_{00}} \geqslant \frac{1}{\epsilon}\left\{1-(1-\epsilon)\rho\frac{\mu}{1+\mu}\right\}.$$

Then we can derive

$$\begin{aligned} &\frac{1}{\epsilon}\left\{1-(1-\epsilon)\rho\frac{\mu}{1+\mu}\right\} - \{G(\mu,\rho)\}^{-1} \\ &\quad= \frac{1-\epsilon}{\epsilon} + \frac{\mu}{1+\mu}\left\{1-\frac{1}{\epsilon}\frac{1}{1+c} - \rho\frac{1-\epsilon}{\epsilon}\left(1-\frac{1}{1+c}\right)\right\} \\ &\quad> \frac{1-\epsilon}{\epsilon} + \frac{\mu}{1+\mu}\left(1-\frac{1}{\epsilon} - \rho\frac{1-\epsilon}{\epsilon}\right) = \frac{1-\epsilon}{\epsilon}\left\{1-(1-\rho)\frac{\mu}{1+\mu}\right\} \geqslant 0. \end{aligned}$$

Therefore, we find that $\{G(\mu,\rho)\}^{-1} < 1/(\epsilon\mathscr{R}_{00})$ when $\mathscr{R}_0 \leqslant 1$, and then the inverse equality of (27) is satisfied.

B.5 PROOF OF THEOREM 3.5 IN SECTION 3.3.4

First we consider the case of $\rho = 1$. From (29), we can derive the following equations about y_v^* and y_r^*:

$$y_r^* = \frac{(1+c)y_v^*}{1+cy_v^*};\ \varphi(y_v^*) := \frac{\epsilon\mathscr{R}_{00}}{1+\mu}\left(\frac{1+c}{1+cy_v^*} + \mu\right)(1-y_v^*) - (1+c) = 0. \quad \text{(B.4)}$$

The function $\varphi(y)$ is monotonically decreasing in terms of $y > 0$, and $\varphi(1) = -(1+c) < 0$. Hence, if and only if $\varphi(0) > 0$, the equation $\varphi(y) = 0$ has a unique positive root $y = y_v^* < 1$. We remark from the first equation

of (B.4) that y_r^* is uniquely determined for each positive $y_v^* < 1$ such that $0 < y_r^* < 1$. Therefore, if and only if $\varphi(0) > 0$, the endemic equilibrium E_{++} exists when $\rho = 1$. It is easy to show that the condition that $\varphi(0) > 0$ is necessary and sufficient to make (27) hold with $\rho = 1$.

Next, from (28) in the case of $\mu > 0$ and $\rho < 1$, we can derive an equation $\psi(\zeta^*) = 0$ in terms of $\zeta^* := (1-\rho-x_v^*)/x_v^*$ with

$$\psi(\zeta) := \frac{c(1+\mu)}{\mathscr{R}_{00}} - \frac{\epsilon}{1/c+\epsilon\zeta} - \frac{\mu}{1/c+1-\epsilon}\left\{\epsilon\frac{1/c+\rho(1-\epsilon)}{1/c+1+\epsilon\zeta} + \frac{(1-\epsilon)(1-\rho)}{1+\zeta}\right\}. \tag{B.5}$$

Since $x_v^* \in (0, 1-\rho)$ for the endemic equilibrium, we have $\zeta^* \in (0,\infty)$. We can easily find that $\psi(\zeta)$ is monotonically increasing in terms of $\zeta > 0$. Further $\psi(\zeta) \to c(1+\mu)/\mathscr{R}_{00}$ as $\zeta \to \infty$. Hence the equation $\psi(\zeta) = 0$ necessarily has a unique positive root ζ^* if and only if $\psi(0) < 0$, which can be easily proved to be equivalent to the condition (27). With $\zeta^* > 0$, the equilibrium value x_v^* is uniquely determined by $x_v^* = (1-\rho)/(1+\zeta^*)$.

On the other hand, with the second equation of (28), we can derive

$$\begin{aligned} x_v^* + y_v^* = g(x_v^*) := \frac{1/c}{1+1/c-\epsilon}x_v^* + \frac{1-\epsilon}{1+1/c-\epsilon}\left\{\frac{(1-\rho)(1+1/c)}{1+1/c-\epsilon} - \frac{\epsilon}{1-\epsilon}\right\} \\ + \frac{\epsilon(1-\rho)(1+1/c)}{(1+1/c-\epsilon)^2}\frac{1/c+(1-\epsilon)\rho}{(1+1/c-\epsilon)x_v^* + \epsilon(1-\rho)}. \end{aligned}$$

Then we can easily find that $g(x)$ is concave with $g(0) = 1$ and $g(1-\rho) = 1-\rho < 1$, so that $g(x) < 1$ for $x \in (0, 1-\rho)$. This result indicates that, if the equation $\psi(x) = 0$ has a unique positive root x_v^* such that $0 < x_v^* < 1-\rho$, the value y_v^* is reasonably determined by the second equation of (28) such that $x_v^* + y_v^* < 1$. Moreover, by the third equation of (28), the value y_r^* is reasonably determined at the same time such that $0 < y_r^* < 1$. Finally, from these arguments, if and only if $\psi(0) < 0$, which is equivalent to the condition (27), the endemic equilibrium E_{++} uniquely exists when $\rho < 1$.

B.6 PROOF OF THEOREM 3.6 IN SECTION 3.3.4

The Jacobian matrix about the endemic equilibrium E_{++} becomes

$$J(E_{++}) := \begin{pmatrix} -(B+c) & -\dfrac{\mu}{1+\mu}\mathscr{R}_{00}x_v^* & 0 & -\dfrac{1}{1+\mu}\mathscr{R}_{00}x_v^* \\ (1-\epsilon)B & \mu\Xi - (\epsilon B + 1 + c) & 0 & \Xi \\ 0 & 0 & -(B+\omega) & 0 \\ 0 & \mu\Phi & (1-\epsilon)B & \Phi - \epsilon B - 1 \end{pmatrix},$$

where

$$B := \mathscr{R}_{00}\frac{y_r^* + \mu y_v^*}{1+\mu};\ \Phi := \frac{y_r^*}{y_r^* + \mu y_v^*};$$
$$\Xi := \frac{1+c}{\mu}\frac{\mu y_v^*}{y_r^* + \mu y_v^*} = \frac{1+c}{\mu}\left(1 - \frac{y_r^*}{y_r^* + \mu y_v^*}\right) = \frac{1+c}{\mu}(1-\Phi).$$

Then the characteristic polynomial for the eigenvalue λ about E_{++} can be obtained as $\left|J(E_{++}) - \lambda E\right| = (B + \omega + \lambda)h(\lambda)$ with

$$h(\lambda) := -\begin{vmatrix} -(B+c+\lambda) & 0 & -\frac{1}{1+\mu}\mathscr{R}_{00}x_v^* \\ (1-\epsilon)B & -(\epsilon B + 1 + c + \lambda) & \Xi \\ 0 & \mu(\epsilon B + 1 + \lambda) & \Phi - \epsilon B - 1 - \lambda \end{vmatrix}$$
$$= \lambda^3 + a_2\lambda^2 + a_1\lambda + a_0, \tag{B.6}$$

where

$$a_2 = c\Phi + 1 + c + B + 2\epsilon B;$$
$$a_1 = (c + B + \epsilon B)c\Phi + (B+c)(2\epsilon B + 1) + \epsilon B(\epsilon B + 1) + \frac{(1-\epsilon)\mu}{1+\mu}\mathscr{R}_{00}x_v^* B;$$
$$a_0 = \epsilon B(B+c)(\epsilon B + 1 + c\Phi) + \frac{(1-\epsilon)\mu}{1+\mu}\mathscr{R}_{00}x_v^* B(\epsilon B + 1).$$

Thus we have a negative eigenvalue $\lambda = -(B+\omega)$ and the cubic equation $h(\lambda) = 0$ given by (B.6) to determine the other three eigenvalues for E_{++}.

Every coefficient of $h(\lambda)$ is positive: $a_2 > 0$, $a_1 > 0$, and $a_0 > 0$. Since $0 < \Phi < 1$, we have

$$a_2 > a_2' := 1 + c + B + 2\epsilon B > 0;$$
$$a_1 > a_1' := (B+c)(2\epsilon B + 1) + \epsilon B(\epsilon B + 1) + \frac{(1-\epsilon)\mu}{1+\mu}\mathscr{R}_{00}x_v^* B > 0;$$
$$a_0 < a_0' := \epsilon B(B+c)(\epsilon B + 1 + c) + \frac{(1-\epsilon)\mu}{1+\mu}\mathscr{R}_{00}x_v^* B(\epsilon B + c),$$

and subsequently find that

$$\begin{aligned} a_2a_1 - a_0 > a_2'a_1' - a_0' = {} & (\epsilon B + 1 + c)(\epsilon B + 1)(c + B + \epsilon B) \\ & + (1+\epsilon)B\{(B+c)(2\epsilon B + 1) + \epsilon B(\epsilon B + 1)\} \\ & + \frac{(1-\epsilon)\mu}{1+\mu}\{1 + (1+\epsilon)B\}\mathscr{R}_{00}x_v^* B > 0. \end{aligned} \tag{B.7}$$

Consequently from the Routh-Hurwitz criterion, we can find that all roots of $h(\lambda) = 0$ have negative real parts. Therefore it has been proved that every eigenvalue for E_{++} has negative real part. This result shows Theorem 3.6 about the local stability of E_{++} when it exists.

B.7 PROOF OF THEOREM 3.10 AND COROLLARY 3.10.3 IN SECTION 3.3.5

As shown in the proof for Theorem 3.5 (Appendix B.5), the endemic size can be determined by the unique positive root $\zeta = \zeta^*$ of the equation $\psi(\zeta) = 0$ with (B.5) for $\rho < 1$ under the condition (27). From the equation $\psi(\zeta^*) = 0$, we can derive

$$\frac{\partial \zeta^*}{\partial \mu} = \frac{1 + \epsilon c\zeta^* - \epsilon\mathscr{R}_{00}}{K\mu\mathscr{R}_{00}(1/c + \epsilon\zeta^*)} \tag{B.8}$$

with

$$K := \frac{\epsilon^2}{(1/c + \epsilon\zeta^*)^2} + \frac{\mu}{1/c + 1 - \epsilon}\left\{\epsilon^2\frac{1/c + (1-\epsilon)\rho}{(1/c + 1 + \epsilon\zeta^*)^2} + \frac{(1-\epsilon)(1-\rho)}{(1+\zeta^*)^2}\right\} > 0.$$

First for $\epsilon\mathscr{R}_{00} \leqslant 1$, we find from (B.8) that $\partial\zeta^*/\partial\mu > 0$ for any $\zeta^* > 0$ and $\mu > 0$. Since $x_v^* = (1-\rho)/(1+\zeta^*)$, we then have $\partial x_v^*/\partial\mu < 0$. Lastly we can get the following result:

Lemma B.3. *x_v^* is monotonically decreasing in terms of $\mu > 0$ when $\rho < 1$ and $\epsilon\mathscr{R}_{00} \leqslant 1$.*

Next for $\epsilon\mathscr{R}_{00} > 1$, the partial derivative (B.8) indicates that $\partial\zeta^*/\partial\mu > 0$ if and only if $\zeta^* > \zeta_c := (\epsilon\mathscr{R}_{00}-1)/(\epsilon c)$, while $\partial\zeta^*/\partial\mu < 0$ if and only if $\zeta^* < \zeta_c$. Since $\psi(\zeta)$ is monotonically increasing in terms of $\zeta > 0$, such that $\psi(\zeta) < 0$ for $\zeta < \zeta^*$ and $\psi(\zeta) > 0$ for $\zeta > \zeta^*$ under the condition (27), we find that $\partial\zeta^*/\partial\mu > 0$ if and only if $\psi(\zeta_c) < 0$, while $\partial\zeta^*/\partial\mu < 0$ if and only if $\psi(\zeta_c) > 0$. Since ζ_c is independent of μ, this result indicates that the sign of $\partial\zeta^*/\partial\mu$ is determined independently of μ. Hence we obtain the following lemma:

Lemma B.4. *$x_v^* > 0$ is monotonic in terms of $\mu > 0$ when $\rho < 1$.*

Now we can derive

$$\psi(\zeta_c) = \frac{\mu\{\epsilon c - 1 + \epsilon^2\mathscr{R}_{00} + \epsilon(1-\epsilon)\mathscr{R}_{00}\rho\}}{\epsilon\mathscr{R}_{00}(1+\epsilon\mathscr{R}_{00}/c)\{1+(\epsilon\mathscr{R}_{00}-1)/(\epsilon c)\}}. \tag{B.9}$$

Thus we can result that $\psi(\zeta_c) < 0$ if and only if $\rho < \rho_c$ where ρ_c is defined by (37). That is, $\partial\zeta^*/\partial\mu > 0$ if and only if $\rho < \rho_c$. Lastly we have

Lemma B.5. *$x_v^* > 0$ is monotonically decreasing in terms of $\mu > 0$ if and only if $\rho < \rho_c$ when $\rho < 1$ and $\epsilon\mathscr{R}_{00} > 1$.*

It can be easily found that $\rho_c < 1$ when $\epsilon\mathscr{R}_{00} > 1$.

In the critical case of $\rho = \rho_c > 0$ with $\epsilon\mathscr{R}_{00} > 1$, we have $\psi(\zeta_c) = 0$ in (B.9), which means that $\zeta^* = \zeta_c$ and subsequently $\partial\zeta^*/\partial\mu = 0$. Actually, from $\zeta^* = \zeta_c$, we find that $x_v^* = (1-\rho)/(1+\zeta_c)$, the endemic sizes y_r^*, y_v^*, and z^* defined by (36) are independent of μ, as given by (38) which are derived by (28). This result gives Corollary 3.10.3.

On the other hand, from (28), we can easily find that the endemic sizes y_r^*, y_v^*, and z^* are monotonically decreasing in terms of $x_v^* > 0$. Therefore, from Lemma B.4, we can get the following lemma:

Lemma B.6. *The endemic sizes y_r^*, y_v^*, and z^* are monotonic in terms of μ when $\rho < 1$.*

Consequently, from Lemmas B.3, B.4, B.5, and B.6, we can obtain the result of Theorem 3.10 for $\rho < 1$.

B.8 PROOF OF COROLLARY 3.10.1 IN SECTION 3.3.5

In case of $\rho = 1$, the unique positive root of $\varphi(y) = 0$ with (B.4) gives the endemic size y_v^* under the condition (27) with $\rho = 1$ (Appendix B.5). Then, from the equation $\varphi(y_v^*) = 0$, we can derive

$$\frac{\partial y_v^*}{\partial\mu} = \frac{1 - y_v^* - (1+c)/(\epsilon\mathscr{R}_{00})}{(1+c)^2/(1+cy_v^*)^2 + \mu}. \tag{B.10}$$

When $\epsilon\mathscr{R}_{00} \leqslant 1+c$, we have $\partial y_v^*/\partial\mu < 0$ for any $\mu > 0$. Therefore we obtain the following result:

Lemma B.7. *The endemic sizes y_r^* and y_v^* are monotonically decreasing in terms of μ when $\rho = 1$ and $\epsilon\mathscr{R}_{00} \leqslant 1+c$.*

From the first equation in (B.4), we note that the endemic size y_r^* is monotonically increasing in terms of y_v^*.

When $\epsilon\mathscr{R}_{00} > 1 + c$, $\partial y_v^*/\partial\mu > 0$ if and only if $y_v^* < y_v^c := 1 - (1 + c)/(\epsilon\mathscr{R}_{00})$, while $\partial y_v^*/\partial\mu < 0$ if and only if $y_v^* > y_v^c$. Since $\varphi(y)$ is monotonically decreasing in terms of $y > 0$, such that $\varphi(y) > 0$ for $y < y_v^*$ and $\varphi(y) < 0$ for $y > y_v^*$. Hence, $\partial y_v^*/\partial\mu > 0$ if and only if $\varphi(y_v^c) < 0$, while $\partial y_v^*/\partial\mu < 0$ if and only if $\varphi(y_v^c) > 0$. Now we can derive

$$\varphi(y_v^c) = \frac{c(1+c)}{(1+\mu)(\epsilon\mathscr{R}_{00} - c)} > 0$$

for $\epsilon\mathscr{R}_{00} > 1 + c$. Therefore we have the following result:

Lemma B.8. *The endemic sizes y_r^* and y_v^* are monotonically decreasing in terms of μ when $\rho = 1$ and $\epsilon\mathscr{R}_{00} > 1 + c$.*

Consequently, from Lemmas B.7 and B.8, the endemic sizes y_r^* and y_v^* are monotonically decreasing in terms of μ when $\rho = 1$.

C

APPENDIX FOR CHAPTER 4

C.1 PROOF OF THEOREM 4.1 IN SECTION 4.3.2

Since the first $(n+1)$ equations equation in the model (44) is closed, we shall consider the reduced system of the first $(n+1)$ equations in model (44). We can derive the Jacobi matrix $J(E_0)$ for the equilibrium E_0 is given by

$$J(E_0) = \begin{pmatrix} -1 & -b_1 & -b_2 & \cdots & -b_n \\ 0 & b_1\left(1-\frac{1}{\mathscr{R}_{0,1}}\right) & 0 & \cdots & 0 \\ \vdots & \vdots & \vdots & \ddots & \cdots \\ 0 & 0 & 0 & \cdots & b_n\left(1-\frac{1}{\mathscr{R}_{0,n}}\right) \end{pmatrix}.$$

It is clear that the eigenvalues of $J(E_0)$ are $\lambda_0 = -1 < 0$ and $\lambda_k = b(1 - 1/\mathscr{R}_{0,k})$ $(k = 1, 2, 3, \ldots, n)$. Thus E_0 is unstable if there exists ℓ where $\ell \in \Omega$, that is, $\mathscr{R}_0 > 1$. For $\mathscr{R}_0 \leqslant 1$, from $du/d\tau$, if $u \to 1$, we have $\sum_{k=1}^{n} bv_i \to 0$. Thus we have $v_k \to 0$ as $\tau \to \infty$ $(k = 1, 2, \ldots, n)$. If $u \to u^* < 1$, since

$$\sum_{k=1}^{n} \frac{dv_k}{d\tau} < \sum_{k=1}^{n} bv_k(u-1) < 0$$

for $\mathscr{R}_0 \leqslant 1$, then $v_k \to 0$ as $\tau \to \infty$ $(k = 1, 2, \ldots, n)$. Thus we have $u \to 1$ as $\tau \to \infty$ from $du/d\tau$. Therefore, we have shown that E_0 is globally asymptotically stable if and only if $\mathscr{R}_0 \leqslant 1$, while it is unstable when $\mathscr{R}_0 > 1$.

Next we consider the local stability of the endemic equilibrium E_ℓ for the model (44). Making use of (45), we derive the characteristic equation of the Jacobi matrix $J(E_\ell)$ for the equilibrium E_ℓ

$$\left\{\lambda^2 + \mathscr{R}_{0,\ell}\lambda + (1+\gamma_\ell+\eta_\ell)\left(1-\frac{1}{\mathscr{R}_{0,\ell}}\right)\right\}\prod_{k\neq\ell}\left\{(1+\gamma_k+\eta_k)\left(\frac{\mathscr{R}_{0,k}}{\mathscr{R}_{0,\ell}}-1\right)-\lambda\right\} = 0$$

There are two eigenvalues λ_1 and λ_2 satisfying

$$\lambda_1+\lambda_2 = -\mathscr{R}_{0,\ell} < 0 \quad \text{and} \quad \lambda_1\lambda_2 = (1+\gamma_\ell+\eta_\ell)\left(1-\frac{1}{\mathscr{R}_{0,\ell}}\right) > 0.$$

Thus λ_1 and λ_2 have negative real parts. The other eigenvalues are negative if and only if $\mathscr{R}_{0,\ell} > \mathscr{R}_{0,k}$ for any $k = 1, 2, \ldots, n$ and $k \neq \ell$. Thus the endemic equilibrium E_ℓ is locally asymptotically stable. If there exist some k such that $\mathscr{R}_{0,k} > \mathscr{R}_{0,\ell}$, there is a positive eigenvalue for the characteristic equation of the Jacobi matrix $J(E_\ell)$ for the endemic equilibrium E_ℓ. Thus we have E_ℓ is unstable. Therefore, there is a unique locally asymptotically stable endemic equilibrium E_ℓ with $\mathscr{R}_{0,\ell} = \mathscr{R}_0$. These arguments show the proof of Theorem 4.1.

C.2 PROOF OF THEOREM 4.2 IN SECTION 4.3.2

From (46), we can derive

$$\frac{\partial z^*}{\partial \gamma_\ell} = \frac{1}{b_\ell(a_\ell+1)(1+\gamma_\ell+\eta_\ell)^2}\{-(1+\gamma_\ell+\eta_\ell)^2 + b_\ell(\eta_\ell - a_\ell)\}.$$

If

$$b_\ell(\eta_\ell - a_\ell) \leqslant (1+\eta_\ell)^2,$$

we have $\partial z^*/\partial \gamma_\ell < 0$ for any $\gamma_\ell > 0$. Then z^* is monotonically decreasing in terms of γ_ℓ. If

$$b_\ell(\eta_\ell - a_\ell) > (1+\eta_\ell)^2,$$

since $1+\gamma_\ell+\eta_\ell < b_\ell$, we have

$$\begin{aligned}
\frac{\partial z^*}{\partial \gamma_\ell}\Big|_{\gamma_\ell \to b_\ell-(1+\eta_\ell)-0} &= \frac{1}{b_\ell(a_\ell+1)(1+\gamma_\ell+\eta_\ell)^2}\{-{b_\ell}^2 + b_\ell(\eta_\ell - a_\ell)\} \\
&= \frac{1}{(a_\ell+1)(1+\gamma_\ell+\eta_\ell)^2}\{-b_\ell + (\eta_\ell - a_\ell)\} \\
&< \frac{1}{(a_\ell+1)(1+\gamma_\ell+\eta_\ell)^2}\{-(1+\eta_\ell) + (\eta_\ell - a_\ell)\} \\
&= -\frac{1}{(1+\gamma_\ell+\eta_\ell)^2}.
\end{aligned}$$

Thus there exists a unique positive root of $\partial z^*/\partial \gamma_\ell = 0$ which is given by

$$\gamma_\ell = -(1+\eta_\ell) + \sqrt{b_\ell(\eta_\ell - a_\ell)}$$

where z^* takes a maximum value. We have shown the proof of Theorem 4.2.

C.3 PROOF OF LEMMA 4.1 IN SECTION 4.3.3

From the equations of v_1, v_j $(j = 2, 3, \ldots, n-1)$, and v_n in the reduced system of model (42), we have

$$v_1(\tau) = v_1(0)\exp\Big[b\int_0^\tau u(s) + \epsilon\Big\{\sum_{k=2}^{n} v_k(s)\Big\}\,ds - \frac{\tau}{\mathscr{R}_{0,1}}\Big];$$

$$v_j(\tau) = v_j(0)\exp\Big[b\int_0^\tau u(s) + \epsilon\Big\{\sum_{k=j+1}^{n} v_k(s) - \sum_{k=1}^{j-1} v_k(s)\Big\}\,ds - \frac{\tau}{\mathscr{R}_{0,j}}\Big];$$

$$v_n(\tau) = v_n(0)\exp\Big[b\int_0^\tau u(s) - \epsilon\Big\{\sum_{k=1}^{n-1} v_k(s)\Big\}\,ds - \frac{\tau}{\mathscr{R}_{0,n}}\Big].$$

Hence it holds that $v_1(\tau) > 0$, $v_j(\tau) > 0$, and $v_n(\tau) > 0$ for any $\tau > 0$ with $v_1(0) = v_1^0 > 0$, $v_j(0) = v_j^0 > 0$ $(j = 2, 3, \ldots, n-1)$, $v_n(0) = v_n^0 > 0$. Besides, since $\frac{du}{d\tau}\big|_{u=0} = 1 > 0$, we have $u(\tau) > 0$ for any $\tau > 0$ with $u(0) = u^0 > 0$.

Next, from (42), we have

$$\begin{aligned}
\frac{d}{d\tau}\Big(u + \sum_{k=1}^{n} v_k\Big)\Big|_{u+\sum_{k=1}^{n} v_k \geqslant 1} &= \Big[1 - u - \sum_{k=1}^{n}(1+\gamma_k+\eta_k)v_k\Big]_{u+\sum_{k=1}^{n} v_k \geqslant 1} \\
&= \Big[1 - u - \sum_{k=1}^{n} v_k - \sum_{k=1}^{n}(\gamma_k+\eta_k)v_k\Big]_{1-u-\sum_{k=1}^{n} v_k \leqslant 0} < 0,
\end{aligned}$$

so that $u + \sum_{k=1}^{n} v_k < 1$ for any $\tau > 0$ with $u(0) + \sum_{k=1}^{n} v_k(0) = u^0 + \sum_{k=1}^{n} v_k^0 = 1$. Consequently we have Lemma 4.1.

C.4 PROOF OF LEMMA 4.2 IN SECTION 4.3.3

From (42), we have

$$\frac{dv_1}{d\tau} < b\Big(u + \sum_{k=2}^{n} v_k - \frac{1}{\mathscr{R}_{0,1}}\Big)v_1 = b\Big(u + \sum_{k=1}^{n} v_k - v_1 - \frac{1}{\mathscr{R}_{0,1}}\Big)v_1 < b\Big(1 - v_1 - \frac{1}{\mathscr{R}_{0,1}}\Big)v_1; \tag{C.1}$$

$$\frac{dv_j}{d\tau} < b\Big(u + \sum_{\substack{k=1\\k\neq j}}^{n} v_k - \frac{1}{\mathscr{R}_{0,j}}\Big)v_j = b\Big(u + \sum_{k=1}^{n} v_k - v_j - \frac{1}{\mathscr{R}_{0,j}}\Big)v_j < b\Big(1 - v_j - \frac{1}{\mathscr{R}_{0,j}}\Big)v_j; \tag{C.2}$$

$$\frac{dv_n}{d\tau} < b\Big(u - \frac{1}{\mathscr{R}_{0,n}}\Big)v_n < b\Big(1 - \sum_{k=1}^{n} v_k - \frac{1}{\mathscr{R}_{0,n}}\Big)v_n < b\Big(1 - v_n - \frac{1}{\mathscr{R}_{0,n}}\Big)v_n \tag{C.3}$$

for any $\tau > 0$ because $u + \sum_{k=1}^{n} v_j < 1$ for any $\tau > 0$ from Lemma 4.1. Thus we find that the right sides of (C.1), (C.2), and (C.3) are always non-positive when $\mathscr{R}_{0,k} \leqslant 1$ for all k. Therefore, when $\mathscr{R}_{0,k} \leqslant 1$ for all k, we have $dv_k/d\tau < 0$ for all k and any $\tau > 0$. That is, $v_k \to 0$ as $\tau \to \infty$ for all k if $\mathscr{R}_{0,k} \leqslant 1$ for all k. We have shown the proof of Lemma 4.2.

C.5 PROOF OF LEMMA 4.3 IN SECTION 4.3.3

The Jacobi matrix $J(\bullet)$ for the reduced system of model (42) is given by

$$J(\bullet) = \begin{pmatrix} -\frac{1}{u^*} & -bu^* & -bu^* & -bu^* & \cdots & -bu^* & -bu^* \\ bv_1^* & \Delta_1(\bullet) & \epsilon bv_1^* & \epsilon bv_1^* & \cdots & \epsilon bv_1^* & \epsilon bv_1^* \\ bv_2^* & -\epsilon bv_2^* & \Delta_2(\bullet) & \epsilon bv_2^* & \cdots & \epsilon bv_2^* & \epsilon bv_2^* \\ bv_3^* & -\epsilon bv_3^* & -\epsilon bv_3^* & \Delta_3(\bullet) & \cdots & \epsilon bv_3^* & \epsilon bv_3^* \\ \vdots & \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ bv_n^* & -\epsilon bv_{n-1}^* & -\epsilon bv_{n-1}^* & -\epsilon bv_{n-1}^* & \cdots & \Delta_{n-1}(\bullet) & \epsilon bv_{n-1}^* \\ bv_n^* & -\epsilon bv_n^* & -\epsilon bv_n^* & -\epsilon bv_n^* & \cdots & -\epsilon bv_n^* & \Delta_n(\bullet) \end{pmatrix}, \tag{C.4}$$

where

$$\begin{aligned} \Delta_1(\bullet) &= bu^* + \epsilon b \sum_{k=2}^{n} v_k^* - (1 + \gamma_1 + \eta_1); \\ \Delta_j(\bullet) &= bu^* + \epsilon b\Big(\sum_{k=j+1}^{n} v_k^* - \sum_{k=1}^{j-1} v_k^*\Big) - (1 + \gamma_j + \eta_j) \quad (1 < j < n); \\ \Delta_n(\bullet) &= bu^* - \epsilon b \sum_{k=1}^{n-1} v_k^* - (1 + \gamma_n + \eta_n). \end{aligned} \tag{C.5}$$

The characteristic equation of the Jacobi matrix $J(E_0)$ for the disease-free equilibrium E_0 is given by

$$(\lambda+1)\prod_{k=1}^{n}\left\{b\left(1-\frac{1}{\mathscr{R}_{0,k}}\right)-\lambda\right\}=0.$$

If $\mathscr{R}_0<1$, all eigenvalues of $J(E_0)$ have negative real parts. Thus we have E_0 is locally asymptotically stable if $\mathscr{R}_0<1$. If $\mathscr{R}_0>1$, that is, if there exists k such that $\mathscr{R}_{0,k}>1$, there exists a positive eigenvalue $b(1-1/\mathscr{R}_{0,k})$ for the Jacobi matrix $J(E_0)$. Thus we have the disease-free equilibrium E_0 is unstable if $\mathscr{R}_0>1$. Taking account of Lemma 4.3, we have shown the proof of Theorem 4.3.

C.6 PROOF OF THEOREM 4.4 IN SECTION 4.3.3

We can get the following result of the local stability of E_ℓ:

Lemma C.1. *The single strain endemic equilibrium E_ℓ exists and is locally asymptotically stable if conditions (49) and (50) are satisfied with $\mathscr{R}_{0,\ell}>1$. If the condition with the inverse inequality of (49) or (50) is satisfied, it is unstable.*

Proof. For the endemic equilibrium E_ℓ where only the infectives with strain ℓ persist and there is no infectives with strain k ($k\neq\ell$), from (C.4) with (C.5), we have the characteristic equation of the Jacobi matrix $J(E_\ell)$ is given by

$$\left\{\lambda^2+\mathscr{R}_{0,\ell}\lambda+b\left(1-\frac{1}{\mathscr{R}_{0,\ell}}\right)\right\}\prod_{k\neq\ell}\left(\Delta_k(E_\ell)-\lambda\right)=0.$$

There exists two eigenvalues λ_1 and λ_2 satisfying

$$\lambda_1+\lambda_2=-\mathscr{R}_{0,\ell}<0\quad\text{and}\quad\lambda_1\lambda_2=b\left(1-\frac{1}{\mathscr{R}_{0,\ell}}\right)>0.$$

Thus λ_1 and λ_2 have negative real parts with $\mathscr{R}_{0,\ell}>1$. The other eigenvalues are negative if and only if $\Delta_k(E_\ell)<0$ for any $k\neq\ell$, that is,

Then we have the endemic equilibrium E_ℓ is locally asymptotically stable if the above conditions are satisfied. If there exists i where $k\neq\ell$ such that $\Delta_k(E_\ell)>0$, that is, if the inverse inequality of (49) or (50) is satisfied, the endemic equilibrium E_ℓ is unstable. □

Let us consider the following function of u, v_ℓ, and v_k when E_ℓ exists ($k=1,2,\dots,n$ and $k\neq\ell$):

$$V(u,v_1,\dots,v_\ell,\dots,v_n):=\frac{1}{2u^*}(u-u^*)^2+\left(v_\ell-v_\ell^*-v_\ell^*\ln\frac{v_\ell}{v_\ell^*}\right)+\sum_{k\neq\ell}v_k$$

with $u^*=1/\mathscr{R}_{0,\ell}$, $v_\ell^*=(\mathscr{R}_{0,\ell}-1)/b$. Taking account of Lemma 4.1, it holds that $V>0$ for any $(u,v_1,\dots,v_n)\in D\backslash\{E_\ell\}$ and $V=0$ for E_ℓ. Then, making use of the equations in (42) we can derive the following time-derivative:

$$\begin{aligned}\frac{dV}{d\tau}=&-\frac{1}{u^*}(u-u^*)^2\left(1+b\sum_{k=1}^{n}v_k\right)+\left\{\left(\frac{1}{\mathscr{R}_{0,\ell}}-\frac{1}{\mathscr{R}_{0,k}}\right)+\frac{\epsilon}{b}(\mathscr{R}_{0,\ell}-1)\right\}\sum_{k=1}^{\ell-1}\frac{bv_k}{v_\ell}\\&+\left\{\left(\frac{1}{\mathscr{R}_{0,\ell}}-\frac{1}{\mathscr{R}_{0,k}}\right)-\frac{\epsilon}{b}(\mathscr{R}_{0,\ell}-1)\right\}\sum_{k=\ell+1}^{n}\frac{bv_k}{v_\ell}.\end{aligned}\tag{C.6}$$

The second term of (C.6) is negative when the condition (49) is satisfied, while the third term of (C.6) is negative when the condition (50) is satisfied. Then the derivative $dV/d\tau$ is always negative under the conditions (49) and (50), taking account of Lemma 4.1. Besides, when the corresponding left and right sides of (49) and (50) are equal to each other, the second and third terms of (C.6) becomes zero, and the derivative $dV/d\tau$ is negative unless $u = u^*$. Since the value u temporally varies as long as $(u, v_1, \dots, v_\ell, \dots, v_n) \neq (u^*, 0, \dots, v_\ell^*, \dots, 0)$ even when $u = u^*$ at a certain finite moment, we note from (C.6) that the derivative $dV/d\tau$ is negative for almost every time $\tau > 0$ unless $(u, v_1, \dots, v_\ell, \dots, v_n) \neq (u^*, 0, \dots, v_\ell^*, \dots, 0)$.

As a result, the derivative $dV/d\tau$ is always negative under the conditions (49) and (50), and then the function V is always decreasing as time passes.

C.7 PROOF OF LEMMA 4.4 IN SECTION 4.3.5

Lemma 4.4 (i) and (ii) can be easily shown. Let us consider the existence of the endemic equilibrium E_{12}. Since the first three equations in the model (51) is closed, we can consider the endemic equilibrium $\overline{E}_{12}(u^*, v_1^*, v_2^*)$ for the system of the first three equations in the model (51), where u^*, v_1^*, and v_2^* are given in (55). Let us consider first the positiveness of u^*, v_1^*, and v_2^*. From (55), the positiveness holds if and only if

$$\frac{1}{\mathscr{R}_{0,2}} < u^* < \frac{1}{\mathscr{R}_{0,1}}. \tag{C.7}$$

We remark that, if the condition (C.7) is satisfied, then $\mathscr{R}_{0,1} < \mathscr{R}_{0,2}$, $0 < u^* < 1$, and $\mathscr{R}_{0,2} > 1$. We have the first inequality of the condition (C.7) can be rewritten as the inequality (52), and the second inequality of the condition (C.7) can be rewritten as the inequality (53) with (54). If the condition (52) is satisfied, since $\mathscr{R}_{0,2} > 1$, we have

$$\frac{1}{1-\hat{\varepsilon}}\left(\frac{1}{\mathscr{R}_{0,1}} - \hat{\varepsilon}\right) < \frac{1}{\mathscr{R}_{0,2}} < 1.$$

Thus it is necessary that $\mathscr{R}_{0,1} > 1$ to satisfy the condition (52). Since

$$\frac{1}{(1-\hat{\varepsilon}) + \hat{\varepsilon}\mathscr{R}_{0,1}} \cdot \frac{1}{\mathscr{R}_{0,1}} - \frac{1}{1-\hat{\varepsilon}}\left(\frac{1}{\mathscr{R}_{0,1}} - \hat{\varepsilon}\right) = \frac{1}{1-\hat{\varepsilon}} \cdot \frac{\hat{\varepsilon}(\mathscr{R}_{0,1} - 1)}{(1-\hat{\varepsilon}) + \hat{\varepsilon}\mathscr{R}_{0,1}} > 0$$

when $\mathscr{R}_{0,1} > 1$, we have the condition (C.7) is satisfied if and only if the inequalities (53) and (52) are satisfied with $\mathscr{R}_{0,2} > \mathscr{R}_{0,1} > 1$. Thus $\overline{E}_{12}$ exists only if the conditions (53) and (52) are satisfied. Since the corresponding equilibrium E_{12} for the system (51) satisfies that $u^* + v_1^* + v_2^* + q_1^* + q_2^* + w^* = 1$, we have the consistent equilibrium values for E_{12} exists if and only if u^*, v_1^*, and v_2^* are positive. Therefore, the endemic equilibrium $\overline{E}_2$ for the system of the first three equations in the model (51), and the corresponding endemic equilibrium E_2 for the system (51) exist if and only if the conditions (53) and (52) are satisfied with $\mathscr{R}_{0,2} > \mathscr{R}_{0,1} > 1$. When E_{12} exists, E_1 and E_2 is necessarily exist. We have shown the proof of Lemma 4.4 (iii).

C.8 PROOF OF THEOREM 4.7 IN SECTION 4.3.5

Theorem 4.7 (i) and (ii) can be shown by Theorem 4.4. As for the equilibrium E_{12}, we can derive the Jacobi matrix $J(E_{12})$

$$J(E_{12}) = \begin{pmatrix} -\frac{1}{u^*} & -bu^* & -bu^* \\ bv_1^* & 0 & \epsilon b_1 v_1^* \\ bv_2^* & -\epsilon b v_2^* & 0 \end{pmatrix}.$$

From (55), we can derive the characteristic equation given by

$$\lambda^3 + \frac{1}{u^*}\lambda^2 + b^2(u^*v_1^* + u^*v_2^* + \epsilon^2 v_1^* v_2^*)\lambda + \frac{1}{u^*}\epsilon^2 b^2 v_1^* v_2^* = 0. \tag{C.8}$$

Since all coefficients of equation (C.8) are positive and they satisfy that

$$\frac{b^2}{u^*}(u^*v_1^* + u^*v_2^* + \epsilon^2 v_1^* v_2^*) - \frac{b^2}{u^*}\epsilon^2 v_1^* v_2^* = b^2(v_1^* + v_2^*) > 0,$$

according to Routh-Hurwitz stability criterion, the endemic equilibrium E_{12} is locally asymptotically stable. Then we consider the following function of u, v_1, and v_2 when E_{12} exists:

$$V(u, v_1, v_2) := \frac{1}{2u^*}(u - u^*)^2 + \left(v_1 - v_1^* - v_1^* \ln \frac{v_1}{v_1^*}\right) + \left(v_2 - v_2^* - v_2^* \ln \frac{v_2}{v_2^*}\right).$$

It is easily found that $V > 0$ for any $(u, v_1, v_2) \in \overline{D}\backslash\{E_{12}\}$ and $V = 0$ for E_{12}, where $\overline{D} := \{(u, v_1, v_2) \mid u > 0, v_1 > 0, v_2 > 0, u + v_1 + v_2 < 1\}$. Then, making use of the first three equations in (51) we can derive the following time-derivative:

$$\frac{dV}{d\tau} = -\frac{1}{u^*}(u - u^*)^2(b_1 v_1 + b_2 v_2 + 1). \tag{C.9}$$

Since the value u temporally varies as long as $(u, v_1, v_2) \neq (u^*, v_1^*, v_2^*)$ even when $u = u^*$ at a certain finite moment, we note from (C.9) that the derivative $dV/d\tau$ is negative for almost every time $\tau > 0$ unless $(u, v_1, v_2) = (u^*, v_1^*, v_2^*)$. Hence the function V is always decreasing as time passes. Thus the function V defines a Lyapunov function for the equilibrium E_{12}. Finally we have that, whenever the two strain endemic equilibrium E_{12} exists, it is globally asymptotically stable. The above arguments show the proof of Theorem 4.7 (iii).