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ASSESSING THE EFFECT OF NON-PHARMACEUTICAL INTERVENTIONS ON CONTAINING AN EMERGING DISEASE

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Abstract. Non-pharmaceutical interventions, such as quarantine, isolation and entry screening, are usually the primary public health measures to control the spread of an emerging infectious disease through a human population. This paper proposes a multi-regional deterministic compartmental model to assess the effectiveness and implications of non-pharmaceutical interventions. The reproduction number is determined as the spectral radius of a nonnegative matrix product. Comparisons are made using the reproduction number, epidemic peaks and cumulative number of infections and mortality as indexes. Simulation results show that quarantine of suspected cases and isolation of cases with symptom are effective in reducing disease burden for multiple regions. Using entry screening strategy leads to a moderate time delay for epidemic peaks, but is of no help for preventing an epidemic breaking out. The study further shows that isolation strategy is always the best choice in the presence or absence of stringent hygiene precautions and should be given priority in combating an emerging epidemic.

1. **Introduction.** Since global availability of effective vaccine and antiviral agents is insufficient in response to a newly emerging infectious disease, such as SARS, the non-pharmaceutical interventions seem especially important. Hence, assessing the effectiveness and implications of the non-pharmaceutical interventions can potentially help us globally eliminate the emerging infectious diseases. In the non-pharmaceutical interventions, quarantine, isolation and entry and exit control are deemed to be three effective approaches for containing infectious diseases. Thus, it is significant to evaluate the effectiveness and implications of quarantine, isolation

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and entry and exit control on containing an emerging infectious disease. In this paper, quarantine means the removal of individuals suspected of being infected for the general population. Isolation means the removal of infected individuals exhibiting clinical symptoms. Entry and exit control refers to the entry and exit screenings.

Mathematical models have become important tools in assessing the effectiveness of different control measures [24]. There have been extensive published mathematical models focused on the effectiveness of different control measures, but the majority of such models have paid more attention to the influence of vaccination and antiviral use on containing infectious diseases. (see, for example, [12, 21, 18, 1, 22, 2, 16, 19] and references therein). Models assessing the effectiveness of the non-pharmaceutical measures are relatively less common. Several recent studies have focused on the effectiveness of quarantine and isolation for controlling SARS outbreaks [27, 10, 11, 13, 17, 8]. These models have provided useful insights into preventing and containing the spread of an emerging disease by using non-pharmaceutical interventions, but the aforementioned models have only considered transmission dynamics of the disease in an isolated community or city, ignoring the effect of the movement of individuals among communities or cities.

With the development of modern fast transportation, it is more convenient for people to move between communities, cities and countries frequently. Consequently, the movement of people is an important factor that leads to the worldwide spread of infectious diseases. Thus, it is necessary to incorporate spatial dynamics into the mathematical models for the spread of infectious diseases. In recent years, several studies have explored the transmission dynamics of infectious diseases in patchy environments by using deterministic metapopualtion epidemic models [5, 7, 26, 4, 23]. However, most of the above studies focused on the effect of population dispersal on transmission dynamics of an infectious disease, and there is little or no information on the effectiveness of strategies for migrating and preventing the spread of infectious diseases in the patchy environment. Up till now few papers have considered the issue.

In this paper, we adopt the approach of Arino and van den Driessche [4] and Ruan et al. [23] for modeling the spread of infectious diseases among discrete geographic regions. We extend their models by including a quarantined and isolated class. We focus only on assessing the effectiveness of quarantine, isolation and entry screening for preventing the spread of infectious diseases in the patchy environment. The paper is organized as follows: Section 2 introduces the new model which is an extension of the model in Arino et al. [4] by including a quarantine class class and an isolation class. The reproduction numbers are derived in section 3. In section 4, some numerical simulation results are presented to assess the effectiveness of the inventions on containing an emerging disease in both short and long terms. The paper ends with a brief discussion of the results in section 5.

2. **Model description.**

The model presented in this paper adopts a similar structure as that Arino and van den Driessche [4] and Ruan et al. [23]. As the main purpose of this paper is to look at the effectiveness and implications of quarantine, isolation and entry screening for preventing the spread of infectious diseases, we introduce a quarantined and isolated classes into the model.

Suppose that there are n geographical regions, and each region is mainly occupied by one community. Let $S_{ij}(t)$, $E_{ij}(t)$, $Q_{ij}(t)$, $I_{ij}(t)$, $J_{ij}(t)$ and $R_{ij}(t)$ denote the number of susceptible, asymptomatic, quarantined, symptomatic, isolated and

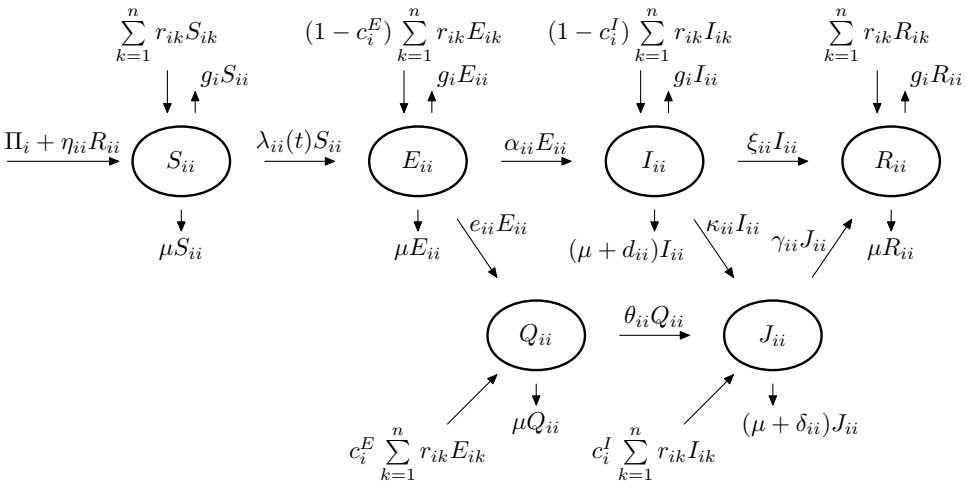


FIGURE 1. Schematic diagram of the model for each subpopulation from region i who are remain in this region.

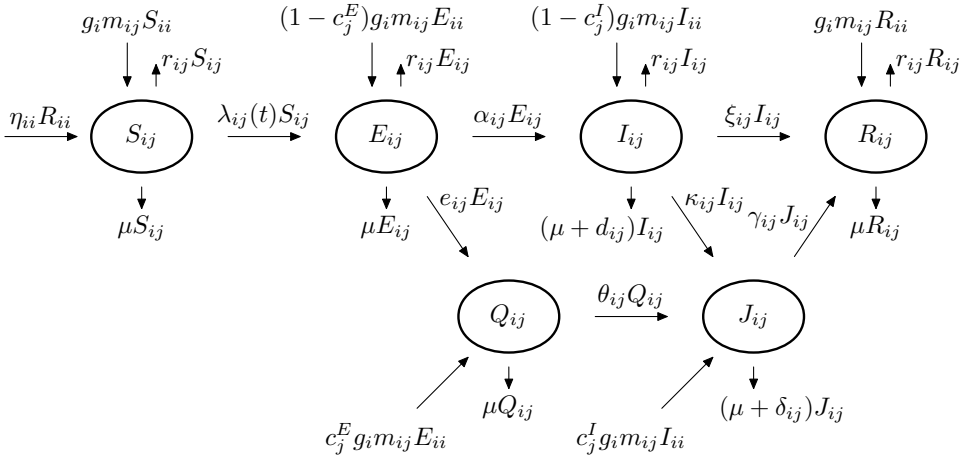


FIGURE 2. Schematic diagram of the model for each subpopulation from region i who are present in region j.

recovered individuals resident in region i who are present in region j at time t, respectively. The total number of residents of region i who are present in region j at time t is denoted by N_{ij}, i.e.,

$$N_{ij} = S_{ij} + E_{ij} + Q_{ij} + I_{ij} + J_{ij} + R_{ij}$$

for all $i, j = 1, \cdots, n$. Set

$$N_i^p = \sum_{j=1}^{n} N_{ji}, N_i^r = \sum_{j=1}^{n} N_{ij}.$$

Then, N_i^p is the total number of individuals who are physically present in region i at time t, and N_i^r is the total number of residents of region i at time t.

TABLE 1. Definitions of frequently used parameters.

Symbol	Description
g_i	Transfer rate of residents in region i leaving their home region
m_{ij}	Proportion of outgoing individuals traveling from region i to region j
r_{ij}	Transfer rate of outgoing individuals from region i present in region j returning their home
Π_i	Recruitment rate of individuals in region i
$1/\mu$	Average life-span
$1/\eta_{ij}$	Average period of immunity for recovered individuals from region i present in region j
δ_i	Average number of contacts per unit time in region i
φ_{ikj}	Proportion of adequate contacts between a susceptible from region i and an infective from region k in region j
ε^E_{ikj}	Reduction factor in the transmission rate of asymptomatic individuals
ε^Q_{ikj}	Reduction factor in the transmission rate of quarantined individuals
ε^J_{ikj}	Reduction factor in the transmission rate of isolated individuals
$1/e_{ij}$	Average time before quarantine for asymptomatic individuals from region i present in region j
$1/\kappa_{ij}$	Average time before isolation for symptomatic individuals from region i present in region j
c^E_i	Probability of successfully detecting asymptomatic individuals for entry screening at the border of region i
c^I_i	Probability of successfully detecting symptomatic individuals for entry screening at the border of region i
$1/\alpha_{ij}$	Average time before the onset of symptom for asymptomatic individuals from region i present in region j
$1/\theta_{ij}$	Average time before the onset of symptom for quarantined individuals from region i present in region j
$1/\xi_{ij}$	Infectious period for symptomatic individuals from region i present in region j
$1/\gamma_{ij}$	Infectious period for isolated individuals from region i present in region j
d_{ij}	Death rate induced by disease for symptomatic individuals from region i present in region j
σ_{ij}	Death rate induced by disease for isolated individuals from region i present in region j

We assume that the individuals who are in the quarantined and isolated class cannot travel. As in [4, 3], residents of region i leave the region at a per capita rate $g_i \geq 0$ per unit time. A fraction of $m_{ij} \geq 0$ of these outgoing individuals go to region j, where m_{ii}=0. Thus, $g_i m_{ij}$ represents the travel rate from region i to region j, and we have $\sum_{j=1}^{n} m_{ij} = 1$ if $g_i > 0$. Residents of region i who are in region j return to region i with a per capita rate of $r_{ij} \geq 0$ with $r_{ii} = 0$. According to the paper [4], the outgoing matrix $(g_i m_{ji})_{n\times n}$ and the return matrix $(r_{ij})_{n\times n}$ are assumed to have the same zero/nonzero pattern.

We further assume that a population from the same region and living in the same region have the same biological parameters. Transition diagrams between epidemic classes for the population N_{ij} are shown in Figure 1 and 2. In this study, the

recruitment rate captures the input of individuals only by birth for simplicity. In addition, we suppose that individuals do not give birth when they are out of home and there is no vertical transmission. Therefore, recruitment for residents of region i occurs only in their home region at a per capita rate Π_i. μ is a per-capita natural death rate. The function $\lambda_{ij}(t)$ represents the rate at which a susceptible individual in class S_{ij} becomes asymptomatic infected case. An asymptomatic individual in class E_{ij} is quarantined at the rate e_{ij} and develops into a symptomatic case at the rate α_{ij}. For simplicity, we assume that all quarantined individuals in class Q_{ij} are asymptotic infected cases who will go on developing symptoms and move to the isolated class J_{ij} at the rate θ_{ij}. It is also assumed that the symptomatic individuals in class I_{ij} are put into the isolated class at the rate κ_{ii}. An symptomatic individual in class I_{ij} and an isolated individual in class J_{ij} recover at the rate ξ_{ij} and γ_{ij} and the disease-induced death rate for the symptomatic individual and isolated individual are d_{ij} and σ_{ij}, respectively. A recovered individual in class R_{ij} may lose immunity at the rate η_{ij} ($\eta_{ij} = 0$ represents the case of permanent immunity).

Let c_i^E, c_i^I denote the probability of successfully detecting an asymptomatic individual and an symptomatic individual for entry screening at the border of region i, respectively. We assume that susceptible and recovered individual are never wrongly identified as being asymptomatically or symptomatically infected. Once the asymptomatic and symptomatic individuals are identified, we assume that they will be quarantined and isolated immediately, respectively.

Based on the above assumptions, we arrive at the following equations for each subpopulation from region i who are remain in this region as

$$\begin{aligned}
\frac{dS_{ii}}{dt} &= \Pi_i + \sum_{k=1}^{n} r_{ik} S_{ik} - \lambda_{ii}(t) S_{ii} - (g_i + \mu)\, S_{ii} + \eta_{ii} R_{ii},\\
\frac{dE_{ii}}{dt} &= (1 - c_i^E) \sum_{k=1}^{n} r_{ik} E_{ik} + \lambda_{ii}(t) S_{ii} - (g_i + \mu + e_{ii} + \alpha_{ii})\, E_{ii},\\
\frac{dQ_{ii}}{dt} &= c_i^E \sum_{k=1}^{n} r_{ik} E_{ik} + e_{ii} E_{ii} - (\mu + \theta_{ii})\, Q_{ii},\\
\frac{dI_{ii}}{dt} &= (1 - c_i^I) \sum_{k=1}^{n} r_{ik} I_{ik} + \alpha_{ii} E_{ii} - (g_i + \mu + d_{ii} + \xi_{ii} + \kappa_{ii})\, I_{ii},\\
\frac{dJ_{ii}}{dt} &= c_i^I \sum_{k=1}^{n} r_{ik} I_{ik} + \kappa_{ii} I_{ii} + \theta_{ii} Q_{ii} - (\mu + \gamma_{ii} + \sigma_{ii})\, J_{ii},\\
\frac{dR_{ii}}{dt} &= \sum_{k=1}^{n} r_{ik} R_{ik} + \xi_{ii} I_{ii} + \gamma_{ii} J_{ii} - (g_i + \mu + \eta_{ii})\, R_{ii},
\end{aligned} \tag{1}$$

and the dynamical equations for each subpopulation from region i who are present in region j at time t as

$$\begin{aligned}
\frac{dS_{ij}}{dt} &= g_i m_{ij} S_{ii} - \lambda_{ij}(t) S_{ij} - (r_{ij} + \mu) S_{ij} + \eta_{ij} R_{ij},\\
\frac{dE_{ij}}{dt} &= (1 - c_j^E) g_i m_{ij} E_{ii} + \lambda_{ij}(t) S_{ij} - (r_{ij} + \mu + e_{ij} + \alpha_{ij}) E_{ij},\\
\frac{dQ_{ij}}{dt} &= c_j^E g_i m_{ij} E_{ii} + e_{ij} E_{ij} - (\mu + \theta_{ij}) Q_{ij},\\
\frac{dI_{ij}}{dt} &= (1 - c_j^I) g_i m_{ij} I_{ii} + \alpha_{ij} E_{ij} - (r_{ij} + \mu + d_{ij} + \xi_{ij} + \kappa_{ij}) I_{ij},\\
\frac{dJ_{ij}}{dt} &= c_j^I g_i m_{ij} I_{ii} + \kappa_{ij} I_{ij} + \theta_{ij} Q_{ij} - (\mu + \gamma_{ij} + \sigma_{ij}) J_{ij},\\
\frac{dR_{ij}}{dt} &= g_i m_{ij} R_{ii} + \xi_{ij} I_{ij} + \gamma_{ij} J_{ij} - (r_{ij} + \mu + \eta_{ij}) R_{ij}.
\end{aligned} \tag{2}$$

In this paper, we adopt a standard incidence rate for disease transmission which is believed more accurate for many human diseases [15], then the function $\lambda_{ij}(t)$ can be expressed by

$$\lambda_{ij}(t) = \sum_{k=1}^{n} \beta_{ikj} \frac{\varepsilon_{ikj}^E E_{kj} + \varepsilon_{ikj}^Q Q_{kj} + I_{kj} + \varepsilon_{ikj}^J J_{kj}}{N_j^p}.$$

where $\beta_{ikj} = \delta_j \varphi_{ikj}$. Here δ_k is the average number of contacts per unit time in region k; φ_{ikj} is the proportion of adequate contacts between a susceptible from region i and an infective from region k in region j. ε_{ikj}^E is the modification parameters which accounts for the fraction of reduction in the transmission rate of asymptomatic individuals. The fact that poor sanitation increases the risk of transmission by quarantined or isolated individuals can not be ruled out. In this paper, the levels of hygiene precautions during quarantine and isolation are denoted by two modification parameters ε_{ikj}^Q and ε_{ikj}^J, respectively. All involved parameters are nonnegative constants, and their definitions are listed in Table 1.

3. **Threshold dynamics.** One of the important subjects in epidemiological modeling studies is to obtain the reproduction number. It is generally defined as the average number of secondary cases (infections) produced by a typical infected individual during the entire period of infection when introduced into a completely susceptible population [9]. In most cases, it is the reproduction number that may determine the persistence and eradication of the disease [6, 14]. Generally, if the basic reproduction number is less than unity, the disease can not break out, and otherwise the disease will be endemic. Thus, in the section we mainly derive the important parameter, and then investigate the local stabilities of the disease free equilibrium (DFE) and the permanence of (1)-(2).

For ease of notation, we arrange the order of the variables in the system (1)-(2). We sort them by the index of regions, then by the number of sites, and finally by epidemiological class: susceptible, asymptomatic, quarantined, infected, isolated and recovered. Let

$$S_i = (S_{i1}, S_{i2}, \cdots, S_{in}), E_i = (E_{i1}, E_{i2}, \cdots, E_{in}), Q_i = (Q_{i1}, Q_{i2}, \cdots, Q_{in}),$$

$$I_i = (I_{i1}, I_{i2}, \cdots, I_{in}), J_i = (J_{i1}, J_{i2}, \cdots, J_{in}), R_i = (R_{i1}, R_{i2}, \cdots, R_{in}).$$

In order to find disease free equilibrium, we now consider the following system

$$\begin{aligned} \frac{dS_{ii}}{dt} &= \Pi_i + \sum_{k=1,k\neq i}^{n} r_{ik} S_{ik} - (g_i + \mu) S_{ii}, \\ \frac{dS_{ij}}{dt} &= g_i m_{ij} S_{ii} - (r_{ij} + \mu) S_{ij}, j = 1, 2, \quad \cdots, n. \end{aligned} \tag{3}$$

We can easily see that system (3) admits a unique positive equilibrium $S_i^0(S_{i1}^0, S_{i2}^0, \cdots, S_{in}^0)$ which is globally asymptotically stable, where

$$S_{ii}^0 = \frac{\Pi_i}{g_i(1 - \sum_{j=1,j\neq i}^{n} \frac{r_{ij} m_{ij}}{r_{ij} + \mu}) + \mu}, S_{ij}^0 = \frac{g_i m_{ij}}{r_{ij} + \mu} S_{ii}^0, j = 1, 2, \cdots, n, j \neq i.$$

It then follows that $E_0(S_1^0, S_2^0, \cdots, S_n^0, 0, 0 \cdots, 0)$ is the disease free equilibrium of system (1)-(2).

We now derive the reproduction number for the system (1)-(2). For convenience, let us set

$$\begin{aligned} &\phi_{ii}^E = g_i + \mu + e_{ii} + \alpha_{ii}; && \phi_{ij}^E = r_{ij} + \mu + e_{ij} + \alpha_{ij}; \\ &\phi_{ii}^Q = \mu + \theta_{ii}; && \phi_{ij}^Q = \mu + \theta_{ij}; \\ &\phi_{ii}^I = g_i + \mu + d_{ii} + \xi_{ii} + \kappa_{ii}; && \phi_{ij}^I = r_{ij} + \mu + d_{ij} + \xi_{ij} + \kappa_{ij}; \\ &\phi_{ii}^J = \mu + \gamma_{ii} + \sigma_{ii}; && \phi_{ij}^J = \mu + \gamma_{ij} + \sigma_{ij}, \end{aligned} \quad i \neq j,$$

and define

$$M_i^E = -\begin{pmatrix} -\phi_{i1}^E & 0 & \cdots & (1-c_1^E) g_i m_{i1} & \cdots & 0 \\ 0 & -\phi_{i2}^E & \cdots & (1-c_2^E) g_i m_{i2} & \cdots & 0 \\ \cdots & \cdots & \cdots & \cdots & \cdots & \cdots \\ (1-c_i^E) r_{i1} & (1-c_i^E) r_{i2} & \cdots & -\phi_{ii}^E & \cdots & (1-c_i^E) r_{in} \\ \cdots & \cdots & \cdots & \cdots & \cdots & \cdots \\ 0 & 0 & \cdots & (1-c_n^E) g_i m_{in} & \cdots & -\phi_{in}^E \end{pmatrix},$$

$$M_i^I = -\begin{pmatrix} -\phi_{i1}^I & 0 & \cdots & (1-c_1^I) g_i m_{i1} & \cdots & 0 \\ 0 & -\phi_{i2}^I & \cdots & (1-c_2^I) g_i m_{i2} & \cdots & 0 \\ \cdots & \cdots & \cdots & \cdots & \cdots & \cdots \\ (1-c_i^I) r_{i1} & (1-c_i^I) r_{i2} & \cdots & -\phi_{ii}^I & \cdots & (1-c_i^I) r_{in} \\ \cdots & \cdots & \cdots & \cdots & \cdots & \cdots \\ 0 & 0 & \cdots & (1-c_n^I) g_i m_{in} & \cdots & -\phi_{in}^I \end{pmatrix},$$

$$M_i^{EQ} = \begin{pmatrix} e_{i1} & 0 & \cdots & c_1^E g_i m_{i1} & \cdots & 0 \\ 0 & e_{i2} & \cdots & c_2^E g_i m_{i2} & \cdots & 0 \\ \cdots & \cdots & \cdots & \cdots & \cdots & \cdots \\ c_i^E r_{i1} & c_i^E r_{i2} & \cdots & e_{ii} & \cdots & c_i^E r_{in} \\ \cdots & \cdots & \cdots & \cdots & \cdots & \cdots \\ 0 & 0 & \cdots & c_n^E g_i m_{in} & \cdots & e_{in} \end{pmatrix},$$

$$M_i^{IJ} = \begin{pmatrix} \kappa_{i1} & 0 & \cdots & c_1^I g_i m_{i1} & \cdots & 0 \\ 0 & \kappa_{i2} & \cdots & c_2^I g_i m_{i2} & \cdots & 0 \\ \cdots & \cdots & \cdots & \cdots & \cdots & \cdots \\ c_i^I r_{i1} & c_i^I r_{i2} & \cdots & \kappa_{ii} & \cdots & c_i^I r_{in} \\ \cdots & \cdots & \cdots & \cdots & \cdots & \cdots \\ 0 & 0 & \cdots & c_n^I g_i m_{in} & \cdots & \kappa_{in} \end{pmatrix},$$

$$M_i^Q = diag(\phi_{i1}^Q, \phi_{i2}^Q, \cdots, \phi_{in}^Q); M_i^J = diag(\phi_{i1}^J, \phi_{i2}^J, \cdots, \phi_{in}^J);$$

$$M_i^{EI} = diag(\alpha_{i1}, \alpha_{i2}, \cdots, \alpha_{in}); M_i^{QJ} = diag(\theta_{i1}, \theta_{i2}, \cdots, \theta_{in}).$$

Let $S_i^{0p} = \sum_{j=1}^n S_{ji}^0$ and $\omega_{ijq} = \beta_{ijq}\frac{S_{iq}^0}{S_q^{0p}}$. Then we define

$$M_{ij}^{EE} = diag(\varepsilon_{ij1}^E\omega_{ij1}, \varepsilon_{ij2}^E\omega_{ij2}, \cdots, \varepsilon_{ijn}^E\omega_{ijn});$$

$$M_{ij}^{QE} = diag(\varepsilon_{ij1}^Q\omega_{ij1}, \varepsilon_{ij2}^Q\omega_{ij2}, \cdots, \varepsilon_{ijn}^Q\omega_{ijn});$$

$$M_{ij}^{IE} = diag(\omega_{ij1}, \omega_{ij2}, \cdots, \omega_{ijn});$$

$$M_{ij}^{JE} = diag(\varepsilon_{ij1}^J\omega_{ij1}, \varepsilon_{ij2}^J\omega_{ij2}, \cdots, \varepsilon_{ijn}^J\omega_{ijn}).$$

Noting that the system (1)-(2) has $4n^2$ infected variables, namely, $E_1, \cdots, E_n$, $Q_1, \cdots, Q_n$, $I_1, \cdots, I_n$ and $J_1, \cdots, J_n$, it follows that, using the notation of Driessche and Watmough [25], the lower triangular block matrix V for the remaining transfer terms and the non-negative matrix F for the new infection terms are respectively given by

$$V = \begin{pmatrix} M^E & 0 & 0 & 0 \\ -M^{EQ} & M^Q & 0 & 0 \\ -M^{EI} & 0 & M^I & 0 \\ 0 & -M^{QJ} & -M^{IJ} & M^J \end{pmatrix},$$

$$F = \begin{pmatrix} M^{EE} & M^{QE} & M^{IE} & M^{JE} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix},$$

where

$$M^E = diag\left(M_1^E, M_2^E, \cdots, M_n^E\right); \qquad M^Q = diag\left(M_1^Q, M_2^Q, \cdots, M_n^Q\right);$$

$$M^I = diag\left(M_1^I, M_2^I, \cdots, M_n^I\right); \qquad M^J = diag\left(M_1^J, M_2^J, \cdots, M_n^J\right);$$

$$M^{EQ} = diag\left(M_1^{EQ}, M_2^{EQ}, \cdots, M_n^{EQ}\right); \quad M^{EI} = diag\left(M_1^{EI}, M_2^{EI}, \cdots, M_n^{EI}\right);$$

$$M^{QJ} = diag\left(M_1^{QJ}, M_2^{QJ}, \cdots, M_n^{QJ}\right); \quad M^{IJ} = diag\left(M_1^{IJ}, M_2^{IJ}, \cdots, M_n^{IJ}\right);$$

$$M^{EE} = \begin{pmatrix} M_{11}^{EE} & \cdots & M_{1n}^{EE} \\ \cdots & \cdots & \cdots \\ M_{n1}^{EE} & \cdots & M_{nn}^{EE} \end{pmatrix}; \qquad M^{QE} = \begin{pmatrix} M_{11}^{QE} & \cdots & M_{1n}^{QE} \\ \cdots & \cdots & \cdots \\ M_{n1}^{QE} & \cdots & M_{nn}^{QE} \end{pmatrix};$$

$$M^{IE} = \begin{pmatrix} M_{11}^{IE} & \cdots & M_{1n}^{IE} \\ \cdots & \cdots & \cdots \\ M_{n1}^{IE} & \cdots & M_{nn}^{IE} \end{pmatrix}; \qquad M^{JE} = \begin{pmatrix} M_{11}^{JE} & \cdots & M_{1n}^{JE} \\ \cdots & \cdots & \cdots \\ M_{n1}^{JE} & \cdots & M_{nn}^{JE} \end{pmatrix}.$$

According to the paper[25], the reproduction number of the model (1)-(2) is denoted by

$$\begin{aligned} \mathcal{R}_c : &= \rho(FV^{-1}) \\ &= \rho\left(\hat{M}^E + \hat{M}^Q + \hat{M}^I + \hat{M}^J\right) \end{aligned} \tag{4}$$

where $\rho(M)$ represents the spectral radius of the matrix M, and

$$\hat{M}^E = M^{EE}\left(M^E\right)^{-1};$$

$$\hat{M}^Q = M^{QE}\left(M^Q\right)^{-1} M^{EQ}\left(M^E\right)^{-1};$$

$$\hat{M}^I = M^{IE}\left(M^I\right)^{-1} M^{EI}\left(M^E\right)^{-1};$$

$$\hat{M}^J = M^{JE}\left(M^J\right)^{-1}\left(M^{QJ}\left(M^Q\right)^{-1} M^{EQ} + M^{IJ}\left(M^I\right)^{-1} M^{EI}\right)\left(M^E\right)^{-1}.$$

Using the results in [25], we have the following stability result.

Theorem 3.1. *The disease free equilibrium E_0 of system (1)-(2) is locally asymptotically stable if $\mathcal{R}_c < 1$, and unstable if $\mathcal{R}_c > 1$.*

4. **Numerical simulations.** In this section, we present some numerical results for SARS epidemics. The purpose is to determine the impacts of non-pharmaceutical measures (quarantine, isolation and entry screening) as single interventions and find out which one is more beneficial in decreasing disease burden by comparing their effects in the absence or presence of transmission caused by quarantined and isolated individuals. In this study, we focus on the reproduction number, epidemic peaks and cumulative number of infections and mortality as indexes to judge the impact of non-pharmaceutical measures. Here, we consider the situation in two regions and assume both regions are identical for simplicity. Parameter values used in the simulation are assumed as in the current literatures: $\mu = 0.000034$, $\beta_{ikj} = 0.2$, $d_{ij} = 0.0079$, $\sigma_{ij} = 0.0068$, $\alpha_{ij} = 0.1$, $\theta_{ij} = 0.125$, $\xi_{ij} = 0.0337$, $\gamma_{ij} = 0.0386$, $\eta_{ij} = 0$, for $i, j = 1, 2$, which are summarized in Table 2. In addition, it is assumed that the epidemic starts at region 1 and there is a 30-day delay before implementation of these interventions since the index case in each region, unless otherwise stated. And travelers with symptoms are assumed to be completely successfully detected and timely isolated soon after in the border of each region. Thus, entry screening measure concerned here is entirely for the detection of asymptomatically-infected individuals.

TABLE 2. Parameter values used in the simulations.

Parameter	Nominal values in region 1	Nominal values in region 2	Ranges	References
β_{ikj}	0.2	0.2	[0.2, 0.5]	(Podder et al. [20])
μ	0.000034	0.000034		(Gumel et al. [13])
d_{ij}	0.0079	0.0079		(Gumel et al. [13])
σ_{ij}	0.0068	0.0068		(Gumel et al. [13])
α_{ij}	0.1	0.1		(Gumel et al. [13])
θ_{ij}	0.125	0.125		(Gumel et al. [13])
ξ_{ij}	0.0337	0.0337		(Gumel et al. [13])
γ_{ij}	0.0386	0.0386		(Gumel et al. [13])
η_{ij}	0	0		(Ruan et al. [23])

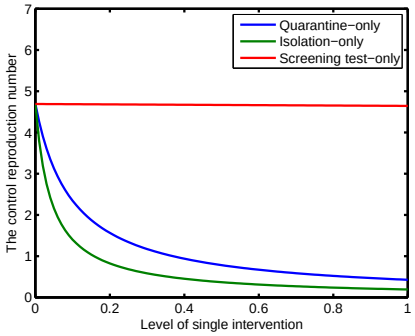


FIGURE 3. The reproduction number as a function of the level of single intervention. For the cases of quarantine-only and isolation-only, horizontal axis represents e_{ij} and κ_{ij}, respectively. For the case of screening test-only, it represents c_i^E and c_i^I.

4.1. **Effects on the reproduction number.** As described in theoretic analysis above, the reproduction number $\mathcal{R}_c$ is capable of determining whether an epidemic breaks out in a short term. However, due to the complexity of spatial dynamics, an explicit formula for $\mathcal{R}_c$ of this model is hardly derived from (4). Hence, studying the dependence of $\mathcal{R}_c$ on the relevant parameters from theoretical analysis is not practical in the general case. Numerical simulation can provide direct insight into this problem. In this situation, we apply numerical analysis to investigate the behavior of $\mathcal{R}_c$ here. Thus, the results are based on the graphs only.

In the presence of stringent hygiene precautions ($\varepsilon_{ikj}^Q = \varepsilon_{ikj}^J = 0$), simulation results show that both quarantine and isolation are generally effective compared with entry screening, according to their influence on $\mathcal{R}_c$ (Fig. 3). Under the implementation of quarantine and isolation, $\mathcal{R}_c$ will drop below 1 rapidly with the increase of quarantine rates and isolation rates. However, in the absence of quarantine or isolation, entry screening can not force $\mathcal{R}_c$ less than unity, for the reality that $\mathcal{R}_c$ decreases slightly with the increase of success rates of entry screening. And $\mathcal{R}_c$ is more sensitive to the changes of mean time before isolation than that of mean time before quarantine. It should be mentioned that SARS is a fulminating infectious disease. Gumel et al. [13] shows that the basic reproduction number is far more than 2 (more than 5 for some communities), when no control measures are carried out.

For the case where transmission by quarantined or isolated individuals occurs, isolating individuals with symptoms remains the first option to fight against epidemics, such as SARS, by calculating $\mathcal{R}_c$ under different levels of hygiene precautions (Fig. 4). And entry screening still performs unsatisfactorily, which means $\mathcal{R}_c$ hardly drops off with the increase of success rates of entry screening. It is worth noting that increasing ε_{ikj}^Q will not affect the effectiveness of isolation, when quarantine strategy or entry screening is absent, as shown in figure 4(a). The reason for this situation is that hygiene precautions during quarantine (ε_{ikj}^Q) are unnecessary if there are no quarantined individuals.

4.2. **Effects on epidemic peaks.** For a long period, as opposed to reproduction number, it is more suitable to investigate the process of an outbreak through peak

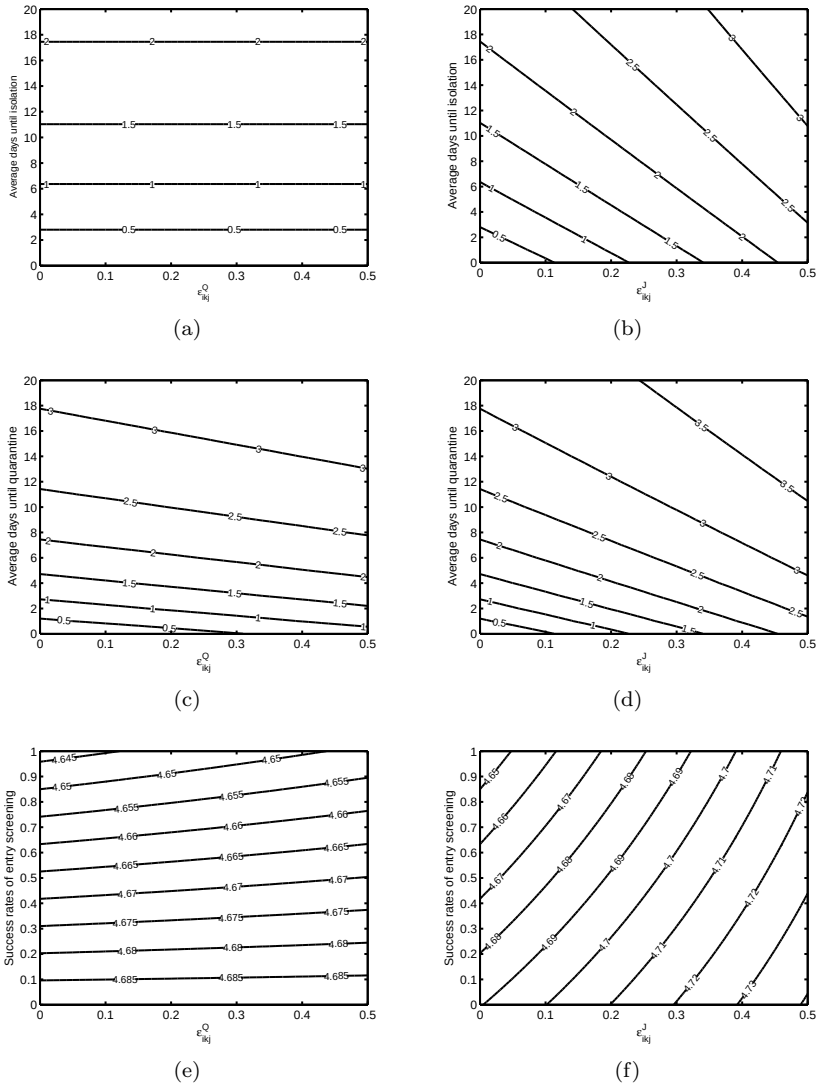
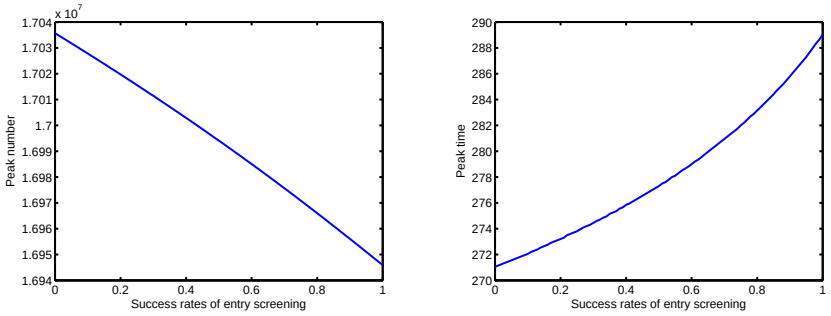


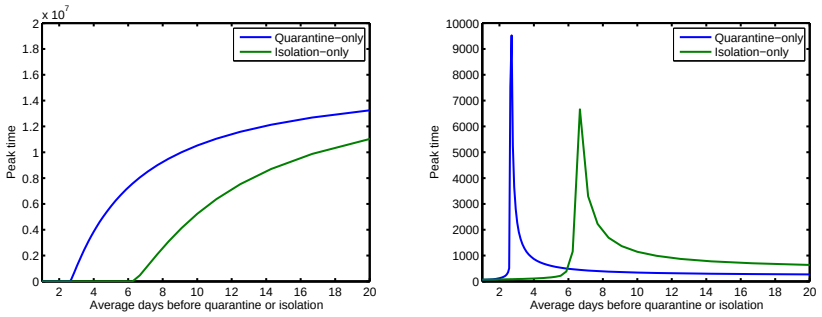
FIGURE 4. Contour plots of $\mathcal{R}_c$ for simulation. Plot (a) and (b) contours of $\mathcal{R}_c$ versus average days before isolation and levels of hygiene precautions. Contours for $\mathcal{R}_c$ versus average days before quarantine and levels of hygiene precautions are shown in (c) and (d). Then, (e) and (f) represent contours of $\mathcal{R}_c$ versus success rates of entry screening and levels of hygiene precautions.

number of infections and time of peak when an epidemic persists. Simulation results indicate that the positive effects of these non-pharmaceutical measures on decreasing the peak number of infected cases are noticeable. Concretely, high success rates of entry screening results a slightly decline on the peak number of infected individuals for both regions and a moderate delay in the time of epidemic peaks for only region 2 (Fig. 5). As an example, stringent entry screening (all asymptomatically and



(a) (b)

FIGURE 5. Peak number of infections and time of an epidemic peak in region 2 as a function of success rates of entry screening respectively in the absence of quarantine and isolation.



(a) (b)

FIGURE 6. Peak number of infections and time of an epidemic peak in the two regions as a function of average days before quarantine or isolation respectively in the absence of entry screening.

symptomatically-infected travelers are completely detected at the borders) results about 18 days delay compared with the case without entry screening (Fig. 5(b)). There is scarcely any time delay of epidemic peaks for region 1 due largely to the fact that intervention of entry screening affects only the migration, which is not plotted. By contrast, a great drop for the peak number of infections is observed, according to the improvement of quarantine or isolation program (Fig. 6(a)). An obvious time delay can be observed under implementation of quarantine or isolation measures in both regions when $\mathcal{R}_c > 1$ (Fig. 6(b)). For the case $\mathcal{R}_c < 1$, peak time will not continue to increase because the epidemic is extinct. By comparing quarantine strategy and isolation strategy, it is obvious that isolating symptomatic individuals is still better than quarantining asymptomatic individuals. As described before, poor hygiene precautions will counteract the effects of non-pharmaceutical interventions on the reproduction number and cumulative numbers of infections and deaths. However, it will not change the state that isolation measure is the best

TABLE 3. Comparison of epidemic peaks under single interventions for $\varepsilon_{ikj}^{Q} \neq 0$.

ε_{ikj}^{Q}	Isolation-only	Quarantine-only	Entry screening-only
0.1	$1/\kappa_{ij} = 20$: PT= 383, PK= 10,586,169.	$1/e_{ij} = 20$: PT= 321, PK= 12,070,860.	$c_i^E = 0.1$: PT= 264, PK= 14,437,966.
	$1/\kappa_{ij} = 10$: PT= 700, PK= 5,533,033.	$1/e_{ij} = 10$: PT= 398, PK= 9,821,720.	$c_i^E = 0.3$: PT= 266, PK= 14,154,775.
	$1/\kappa_{ij} = 5$: PT= 54, PK= 17.25.	$1/e_{ij} = 5$: PT= 644, PK= 6,044,739.	$c_i^E = 0.5$: PT= 269, PK= 13,823,832.
	$1/\kappa_{ij} = 3$: PT= 39, PK= 13.81.	$1/e_{ij} = 3$: PT= 1611, PK= 2,257,830.	$c_i^E = 0.9$: PT= 276, PK= 12,961,817.
0.3	$1/\kappa_{ij} = 20$: PT= 383, PK= 10,586,169.	$1/e_{ij} = 20$: PT= 305, PK= 12,373,273.	$c_i^E = 0.1$: PT= 264, PK= 14,465,575.
	$1/\kappa_{ij} = 10$: PT= 700, PK= 5,533,033.	$1/e_{ij} = 10$: PT= 354, PK= 10,476,444.	$c_i^E = 0.3$: PT= 265, PK= 14,250,025.
	$1/\kappa_{ij} = 5$: PT= 54, PK= 17.25.	$1/e_{ij} = 5$: PT= 480, PK= 7,405,505.	$c_i^E = 0.5$: PT= 267, PK= 14,008,770.
	$1/\kappa_{ij} = 3$: PT= 39, PK= 13.81.	$1/e_{ij} = 3$: PT= 740, PK= 4,442,051.	$c_i^E = 0.9$: PT= 272, PK= 13,442,502.
0.5	$1/\kappa_{ij} = 20$: PT= 383, PK= 10,586,169.	$1/e_{ij} = 20$: PT= 291, PK= 12,665,253.	$c_i^E = 0.1$: PT= 264, PK= 14,492,191.
	$1/\kappa_{ij} = 10$: PT= 700, PK= 5,533,033.	$1/e_{ij} = 10$: PT= 320, PK= 11,094,971.	$c_i^E = 0.3$: PT= 265, PK= 14,340,555.
	$1/\kappa_{ij} = 5$: PT= 54, PK= 17.25.	$1/e_{ij} = 5$: PT= 383, PK= 8,650,593.	$c_i^E = 0.5$: PT= 266, PK= 14,176,797.
	$1/\kappa_{ij} = 3$: PT= 39, PK= 13.81.	$1/e_{ij} = 3$: PT= 475, PK= 6,363,904.	$c_i^E = 0.9$: PT= 268, PK= 13,802,139.

Note: PT = peak time, PK = peak number of infections.

choice among these three interventions, especially for the case $\varepsilon_{ikj}^{Q} \neq 0$ only, which can be also found in table 3 and 4.

4.3. **Effects on cumulative numbers of infections and mortality.** The damage caused by an infectious disease could be displayed by cumulative numbers of infections and mortality directly. The "infections" here contains asymptomatically-infected individuals, symptomatically-infected individuals and those who have been quarantined and isolated. And the "mortality" here is completely derived from deaths induced by the disease. Thus, cumulative numbers of infections and mortality are expressed by

$$CI(t) = \sum_{i=1}^{n}\sum_{j=1}^{n}\int_0^t E_{ij}(t) + Q_{ij}(t) + I_{ij}(t) + J_{ij}(t)dt,$$
$$CD(t) = \sum_{i=1}^{n}\sum_{j=1}^{n}\int_0^t d_{ij}I_{ij}(t) + \sigma_{ij}J_{ij}(t)dt.$$

Table 5 depicts a comparison of quarantine, isolation and entry screening strategies as single interventions for their effects on cumulative numbers of deaths and

TABLE 4. Comparison of epidemic peaks under single interventions for $\varepsilon_{ikj}^{J} \neq 0$.

ε_{ikj}^{J}	Isolation-only	Quarantine-only	Entry screening-only
0.1	$1/\kappa_{ij} = 20$: PT= 358, PK= 11, 458, 451.	$1/e_{ij} = 20$: PT= 318, PK= 12, 423, 839.	$c_i^E = 0.1$: PT= 263, PK= 14, 648, 426.
	$1/\kappa_{ij} = 10$: PT= 526, PK= 8, 033, 451.	$1/e_{ij} = 10$: PT= 387, PK= 10, 418, 477.	$c_i^E = 0.3$: PT= 264, PK= 14, 401, 949.
	$1/\kappa_{ij} = 5$: PT= 1562, PK= 2, 683, 255.	$1/e_{ij} = 5$: PT= 575, PK= 7, 261, 966.	$c_i^E = 0.5$: PT= 266, PK= 14, 116, 100.
	$1/\kappa_{ij} = 3$: PT= 52, PK= 15.19.	$1/e_{ij} = 3$: PT= 998, PK= 4, 297, 115.	$c_i^E = 0.9$: PT= 272, PK= 13, 388, 750.
0.3	$1/\kappa_{ij} = 20$: PT= 323, PK= 12, 770, 094.	$1/e_{ij} = 20$: PT= 298, PK= 13, 257, 726.	$c_i^E = 0.1$: PT= 260, PK= 15, 028, 384.
	$1/\kappa_{ij} = 10$: PT= 393, PK= 10, 970, 260.	$1/e_{ij} = 10$: PT= 337, PK= 11, 847, 662.	$c_i^E = 0.3$: PT= 261, PK= 14, 888, 106.
	$1/\kappa_{ij} = 5$: PT= 531, PK= 8, 814, 900.	$1/e_{ij} = 5$: PT= 411, PK= 9, 880, 807.	$c_i^E = 0.5$: PT= 262, PK= 14, 719, 604.
	$1/\kappa_{ij} = 3$: PT= 685, PK= 7, 403, 483.	$1/e_{ij} = 3$: PT= 501, PK= 8, 259, 506.	$c_i^E = 0.9$: PT= 265, PK= 14, 343, 695.
0.5	$1/\kappa_{ij} = 20$: PT= 297, PK= 13, 722, 669.	$1/e_{ij} = 20$: PT= 282, PK= 13, 926, 285.	$c_i^E = 0.1$: PT= 258, PK= 15, 332, 710.
	$1/\kappa_{ij} = 10$: PT= 331, PK= 12, 677, 142.	$1/e_{ij} = 10$: PT= 303, PK= 12, 907, 758.	$c_i^E = 0.3$: PT= 258, PK= 15, 248, 871.
	$1/\kappa_{ij} = 5$: PT= 381, PK= 11, 563, 884.	$1/e_{ij} = 5$: PT= 337, PK= 11, 578, 317.	$c_i^E = 0.5$: PT= 259, PK= 15, 164, 125.
	$1/\kappa_{ij} = 3$: PT= 421, PK= 10, 883, 845.	$1/e_{ij} = 3$: PT= 369, PK= 10, 532, 613.	$c_i^E = 0.9$: PT= 260, PK= 14, 974, 976.

Note: PT = peak time, PK = peak number of infections.

infected individuals after 50 days, 100 days, 150 days in the absence of poor hygiene precautions. Results show that effect of quarantine or isolation on the number of cumulative deaths exceeds that of high levels of entry screening. In fact, increasing probability of successfully detecting asymptomatically-infected individuals for entry screening make a very little contribution to the decline of cumulative infections and mortality. In addition, isolation of individuals with symptoms is more beneficial in reducing the numbers of infected cases and mortality than quarantine of asymptomatic individuals.

Additional simulations for cumulative numbers on the 100th day after the index case in region 1 are carried out, when hygiene precautions are not stringent enough (Table 6 and 7). Comparisons among the three measures also indicate that isolation strategy is more beneficial than the other two interventions, although the effectiveness of these non-pharmaceutical measures are inevitably falling down under this situation. And entry screening at the borders of each region is of very little help to reducing the number of infections and deaths.

5. **Discussion.** To understand how quarantine, isolation and entry screening as non-pharmaceutical interventions take effect on the development of an emerging disease incorporated discrete geographical regions, a deterministic multi-regional

TABLE 5. Comparison of cumulative numbers under isolation-only, quarantine-only and entry screening-only strategies respectively for $\varepsilon_{ikj}^{Q} = \varepsilon_{ikj}^{J} = 0$.

Days	Isolation-only	Quarantine-only	Entry screening-only
50	$1/\kappa_{ij}$=20: CD=2.082, CI= 564.75.	$1/e_{ij}$=20: CD=2.253, CI= 615.30.	c_i^E=0.1: CD=2.318, CI= 649.15.
	$1/\kappa_{ij}$=10: CD=1.924, CI= 508.88.	$1/e_{ij}$=10: CD=2.202, CI= 590.27.	c_i^E=0.3: CD=2.318, CI= 648.99.
	$1/\kappa_{ij}$=5: CD=1.736, CI= 443.15.	$1/e_{ij}$=5: CD=2.130, CI= 556.59.	c_i^E=0.5: CD=2.318, CI= 648.83.
	$1/\kappa_{ij}$=3: CD=1.607, CI= 399.66.	$1/e_{ij}$=3: CD=2.070, CI= 530.20.	c_i^E=0.9: CD=2.317, CI= 648.52.
100	$1/\kappa_{ij}$=20: CD=28.15, CI= 7265.8.	$1/e_{ij}$=20: CD=46.66, CI= 12, 178.	c_i^E=0.1: CD=91.22, CI= 25, 720.
	$1/\kappa_{ij}$=10: CD=12.66, CI= 3021.2.	$1/e_{ij}$=10: CD=28.87, CI= 7097.8.	c_i^E=0.3: CD=90.94, CI= 25, 631.
	$1/\kappa_{ij}$=5: CD=5.560, CI= 1214.4.	$1/e_{ij}$=5: CD=16.047, CI= 3656.4.	c_i^E=0.5: CD=90.65, CI= 25, 542.
	$1/\kappa_{ij}$=3: CD=3.700, CI= 778.20.	$1/e_{ij}$=3: CD=10.88, CI= 2359.5.	c_i^E=0.9: CD=90.09, CI= 25, 365.
150	$1/\kappa_{ij}$=20: CD=278.53, CI= 71, 469.	$1/e_{ij}$=20: CD=742.47, CI= 192, 918.	c_i^E=0.1: CD=3493.3, CI= 984, 380.
	$1/\kappa_{ij}$=10: CD=45.39, CI= 10, 595.	$1/e_{ij}$=10: CD=234.32, CI= 56, 908.	c_i^E=0.3: CD=3468.5, CI= 977, 049.
	$1/\kappa_{ij}$=5: CD=8.032, CI= 1685.7.	$1/e_{ij}$=5: CD=55.952, CI= 12, 369.	c_i^E=0.5: CD=3443.9, CI= 969, 780.
	$1/\kappa_{ij}$=3: CD=4.235, CI= 865.51.	$1/e_{ij}$=3: CD=22.76, CI= 4730.9.	c_i^E=0.9: CD=3395.4, CI= 955, 423.

Note: CD = cumulative deaths, CI = cumulative infections.

model is formulated. An explicit calculation for the reproduction number $\mathcal{R}_c$ is made subsequently. In order to find out which is the best measure to lessen disease burden, comparisons among the effects of those measures on $\mathcal{R}_c$, epidemic peaks and number of infections or mortality are drawn. Results are shown as follows.

Quarantining asymptomatically infected individuals and isolating symptomatically infected individuals perform effective in reducing disease burden for multiple regions. Moderate quarantine or isolation can force an epidemic to extinct rapidly by making $\mathcal{R}_c$ less than 1. On the other hand, the outbreak of an epidemic will not be prevented by only implementing entry screening at the border of a community. Using isolation strategy only makes $\mathcal{R}_c$ fall much faster in contrast with quarantine program in the absence or presence of transmissions caused by quarantined and isolated individuals.

In a long term, isolating symptomatic individuals is more beneficial in reducing peak number of infections and postponing peak time than other interventions if the epidemic persists. Although entry screening for infected travelers leads to a slightly decrease on peak number of infections, a moderate time delay for epidemic peaks is observed, which can buy public health authorities time to devise more effective interventions, such as quarantine and isolation in each region.

TABLE 6. Comparison of cumulative numbers under single interventions for $\varepsilon_{ikj}^{Q} \neq 0$ on the 100th day after epidemic's start.

ε_{ikj}^{Q}	Isolation-only	Quarantine-only	Entry screening-only
0.1	$1/\kappa_{ij} = 20$: CD= 28.15, CI= 7265.8.	$1/e_{ij} = 20$: CD= 50.42, CI= 13,278.	$c_i^E = 0.1$: CD= 91.24, CI= 25,726.
	$1/\kappa_{ij} = 10$: CD= 12.66, CI= 3021.2.	$1/e_{ij} = 10$: CD= 32.69, CI= 8158.5.	$c_i^E = 0.3$: CD= 90.99, CI= 25,647.
	$1/\kappa_{ij} = 5$: CD= 5.560, CI= 1214.4.	$1/e_{ij} = 5$: CD= 18.86, CI= 4384.2.	$c_i^E = 0.5$: CD= 90.74, CI= 25,569.
	$1/\kappa_{ij} = 3$: CD= 3.700, CI= 778.20.	$1/e_{ij} = 3$: CD= 12.85, CI= 2842.4.	$c_i^E = 0.9$: CD= 90.24, CI= 25,413.
0.3	$1/\kappa_{ij} = 20$: CD= 28.15, CI= 7265.8.	$1/e_{ij} = 20$: CD= 59.04, CI= 15,832.	$c_i^E = 0.1$: CD= 91.27, CI= 25,737.
	$1/\kappa_{ij} = 10$: CD= 12.66, CI= 3021.2.	$1/e_{ij} = 10$: CD= 42.40, CI= 10,918.	$c_i^E = 0.3$: CD= 91.09, CI= 25,679.
	$1/\kappa_{ij} = 5$: CD= 5.560, CI= 1214.4.	$1/e_{ij} = 5$: CD= 27.06, CI= 6573.7.	$c_i^E = 0.5$: CD= 90.91, CI= 25,622.
	$1/\kappa_{ij} = 3$: CD= 3.700, CI= 778.20.	$1/e_{ij} = 3$: CD= 19.13, CI= 4436.4.	$c_i^E = 0.9$: CD= 90.55, CI= 25,509.
0.5	$1/\kappa_{ij} = 20$: CD= 28.15, CI= 7265.8.	$1/e_{ij} = 20$: CD= 69.38, CI= 18,945.	$c_i^E = 0.1$: CD= 91.31, CI= 25,747.
	$1/\kappa_{ij} = 10$: CD= 12.66, CI= 3021.2.	$1/e_{ij} = 10$: CD= 55.81, CI= 14,838.	$c_i^E = 0.3$: CD= 91.20, CI= 25,712.
	$1/\kappa_{ij} = 5$: CD= 5.560, CI= 1214.4.	$1/e_{ij} = 5$: CD= 40.75, CI= 10,400.	$c_i^E = 0.5$: CD= 91.08, CI= 25,677.
	$1/\kappa_{ij} = 3$: CD= 3.700, CI= 778.20.	$1/e_{ij} = 3$: CD= 31.21, CI= 7680.7.	$c_i^E = 0.9$: CD= 90.86, CI= 25,606.

Note: CD = cumulative deaths, CI = cumulative infections.

Similar results are obtained by exploring the effects of non-pharmaceutical programs on cumulative numbers of infections and mortality. Isolation program is the best one to prevent damage by disease from rising too high. In spite of the fact that an epidemic could not be terminated by entry screening alone, it is undoubted that effective entry screening is more or less helpful in reductions in cumulative numbers of disease.

Overall, this study assesses the effectiveness of non-pharmaceutical interventions in fighting against the global spreading of an emerging epidemic. Simulation results suggest that isolation strategy is a much better choice in reducing disease burden than quarantine strategy and entry screening program, by comparing their effects on the reproduction number, epidemic peaks and cumulative number of infections and mortality. In other words, isolating individuals with symptom timely should be a top priority. This may be helpful to establish a more effective control strategy for such an epidemic. It should be emphasized that the conclusions are derived from simulations for two regions. But the reality is that there must be a plenty of regions need to be considered when an epidemic break out, which is much more complex. Therefore, the effects of topological structure for migration among regions on control measures need to be taken into account after this work.

TABLE 7. Comparison of cumulative numbers under single interventions for $\varepsilon^J_{ikj} \neq 0$ on the 100th day after epidemic's start.

ε^J_{ikj}	Isolation-only	Quarantine-only	Entry screening-only
0.1	$1/\kappa_{ij} = 20$: CD= 32.06, CI= 8424.0.	$1/e_{ij} = 20$: CD= 50.41, CI= 13,299.	$c^E_i = 0.1$: CD= 90.54, CI= 25,819.
	$1/\kappa_{ij} = 10$: CD= 15.94, CI= 3947.8.	$1/e_{ij} = 10$: CD= 32.95, CI= 8266.7.	$c^E_i = 0.3$: CD= 91.47, CI= 25,799.
	$1/\kappa_{ij} = 5$: CD= 7.638, CI= 1763.2.	$1/e_{ij} = 5$: CD= 19.48, CI= 4580.2.	$c^E_i = 0.5$: CD= 91.34, CI= 25,759.
	$1/\kappa_{ij} = 3$: CD= 5.135, CI= 1142.9.	$1/e_{ij} = 3$: CD= 13.58, CI= 3056.9.	$c^E_i = 0.9$: CD= 91.17, CI= 25,705.
0.3	$1/\kappa_{ij} = 20$: CD= 41.01, CI= 11,123.	$1/e_{ij} = 20$: CD= 58.64, CI= 15,797.	$c^E_i = 0.1$: CD= 91.97, CI= 25,956.
	$1/\kappa_{ij} = 10$: CD= 24.40, CI= 6418.0.	$1/e_{ij} = 10$: CD= 42.68, CI= 11,115.	$c^E_i = 0.3$: CD= 91.77, CI= 25,895.
	$1/\kappa_{ij} = 5$: CD= 13.91, CI= 3524.9.	$1/e_{ij} = 5$: CD= 28.63, CI= 7143.0.	$c^E_i = 0.5$: CD= 91.58, CI= 25,834.
	$1/\kappa_{ij} = 3$: CD= 9.949, CI= 2462.3.	$1/e_{ij} = 3$: CD= 21.49, CI= 5199.6.	$c^E_i = 0.9$: CD= 91.19, CI= 25,712.
0.5	$1/\kappa_{ij} = 20$: CD= 51.62, CI= 14,395.	$1/e_{ij} = 20$: CD= 67.97, CI= 18,671.	$c^E_i = 0.1$: CD= 92.47, CI= 26,114.
	$1/\kappa_{ij} = 10$: CD= 35.90, CI= 9913.1.	$1/e_{ij} = 10$: CD= 54.82, CI= 14,772.	$c^E_i = 0.3$: CD= 92.34, CI= 26,072.
	$1/\kappa_{ij} = 5$: CD= 24.11, CI= 6573.5.	$1/e_{ij} = 5$: CD= 41.76, CI= 10,985.	$c^E_i = 0.5$: CD= 92.20, CI= 26,030.
	$1/\kappa_{ij} = 3$: CD= 18.77, CI= 5071.6.	$1/e_{ij} = 3$: CD= 34.15, CI= 8828.7.	$c^E_i = 0.9$: CD= 91.93, CI= 25,946.

Note: CD = cumulative deaths, CI = cumulative infections.

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