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AN ANALYSIS OF QUARANTINE AND ISOLATION IN AN SEQIJR MODEL

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Abstract

Three of the main strategies used in controlling the spread of infectious diseases are immunization, quarantine of exposed people who have been in contact with an infectious animal or person, and isolation of infected and infectious people. In this paper we analyze the effectiveness of quarantine and isolation strategies in an SEQIJR model originally proposed by Gumel et al. [1] for the SARS epidemics in 2003 in Beijing, Hong Kong, Canada and Singapore. Numerical simulations of the model are presented using parameter values for the SARS epidemics. The effects of strategies on the basic reproductive rate (R_0) are examined. The model includes changes of population due to natural births and deaths, and disease deaths. The numerical simulations show that a low level of nosocomial infection and a high level of isolation are required if isolation is to be an effective method for reducing the estimated numbers of deaths to acceptable levels. The simulations also show that quarantine is not expected to be an effective method for reducing the estimated numbers of deaths unless a high

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level of quarantine can be implemented. The results show that death rates can be reduced to reasonable levels even for values of R_0 greater than but close to 1.

1. Introduction

The SEQIJR model [1] of an infectious disease is a mathematical model which separates a population into the six categories of susceptible (S), exposed (E), quarantined (Q), infectious (I), isolated (J) and recovered (R). A susceptible person is a person who does not have the disease but can catch it, an exposed person is someone who has come into contact with an infectious person, an infectious person is a person who has the disease and can give it to another person, a recovered person is someone who has had the disease but no longer has it. A quarantined person is an exposed person who has been removed from contact with susceptible people and an isolated person is an infectious person who has been removed from contact with susceptible people. It is assumed that a recovered individual cannot become infected again, and that an exposed person has no disease symptoms (is asymptomatic).

Some of the strategies that can be used to control an infectious disease include immunization of susceptible people, quarantine of exposed people, isolation of infectious people, use of personal protective equipment by susceptible people, and closure of centers such as schools and shops where large numbers of susceptible people could become exposed to the disease. Each of these strategies has its limitations. For example, no effective vaccine may be available in sufficient quantities, there may be limited facilities available for quarantine and isolation, closure of shops can have significant economic effects etc. In addition, quarantined and isolated individuals can still infect other people because hospital staff are required to take care of these two groups and hospital-based (nosocomial) spread of a disease can be an important source of disease transmission [2, 3].

In the worldwide severe acute respiratory syndrome (SARS) epidemic of November 2002-July 2003 there were more than 8,000 infected people with

774 fatalities directly attributable to SARS [4]. It is believed that the transmission of SARS was effectively controlled by basic public health measures, including rapid case detection, case isolation, contact tracing, and good infection control through, e.g., hand-washing and use of personal protective equipment [5]. Another measure that was believed to be useful in preventing infections was the quarantine of asymptomatic but potentially infectious individuals [6, 7].

Many authors have developed mathematical models to analyze the SARS epidemic and to suggest effective methods of control. Gumel et al. [1] used an SEQIJR model to analyze the SARS epidemics in Beijing, Hong Kong, Singapore and Toronto (Canada). Models were also developed for China [8, 9], Hong Kong [10, 11, 12], Singapore [10, 13], Taiwan [9, 14] and Toronto [10]. Several authors [2, 3] showed that nosocomial spread was an important method of SARS transmission. Yan and Zou [15, 16] used optimal control theory to examine optimal quarantine and isolation policies for the SEQIJR model proposed by Gumel et al. [1] for the SARS epidemic in Beijing. They used two controls, a rate of quarantine of exposed individuals and a rate of isolation of infectious individuals. They used a cost function which included costs associated with numbers of exposed, quarantined, infectious and isolated individuals and costs of implementing the quarantine and isolation policies.

In this paper we examine the effectiveness of quarantine and isolation policies for an SEQIJR model. In particular, we are interested in analyzing conditions under which quarantine or isolation policies can reduce the numbers of people who contract the disease and the numbers of deaths in a given time period to a reasonable level. We examine two possible control methods for quarantine, namely, the rate of quarantine of exposed individuals and the rates of infection of susceptible individuals by quarantined individuals. Similarly, for isolation, we examine two possible controls for isolation, namely, the rate of isolation of infectious individuals and the rates of infection by isolated individuals. As stated above, the analysis is based on an SEQIJR model proposed by Gumel et al. [1] for the SARS epidemics of

2003. However, in the present paper, it is also assumed that the total population can change through births and deaths.

The outline of the paper is as follows. In Section 2 we describe the SEQIJR model and discuss possible strategies for controlling disease spread using quarantine and isolation. We also give analytical formulae for the two equilibrium points (disease-free and endemic) and define the basic reproductive rate R_0. In Section 3 we use Matlab to obtain numerical solutions of the differential equations for a range of values for the four control methods in order to find how the numbers of people with the disease and the numbers of disease deaths depend on these four methods. The numerical studies are carried out for parameter values suggested by Gumel et al. [1] for four regions affected by the SARS outbreaks of 2003, namely Beijing, Hong Kong, Singapore and Toronto. In the final section we give a discussion of results and conclusions.

2. The SEQIJR Model

2.1. The model equations

The system of equations for the SEQIJR model that we use is given in equations (1)-(8). Definitions of the parameters used in the model are given in Table 1 and the values for the four regions are shown in Table 2. The equations for *S*, *E*, *Q*, *I*, *J*, *R* and the parameter definitions and values are adapted from Gumel et al. [1]. We have added two extra equations to allow the total population $N = S + E + Q + I + J + R$ to be a function of time and to compute the total number of disease deaths $D(t)$. These extra equations are for the total population size $N(t)$ at time *t* and the total number of deaths due to disease $D(t)$ at time *t*:

$$\frac{dS}{dt} = \Pi - \frac{\beta S(I + \varepsilon_E E + \varepsilon_Q Q + \varepsilon_J J)}{N} - \mu S, \tag{1}$$

$$\frac{dE}{dt} = P + \frac{\beta S(I + \varepsilon_E E + \varepsilon_Q Q + \varepsilon_J J)}{N} - (\gamma_1 + k_1 + \mu)E, \tag{2}$$

$$\frac{dQ}{dt} = \gamma_1 E - (k_2 + \mu)Q, \tag{3}$$

$$\frac{dI}{dt} = k_1 E - (\gamma_2 + d_1 + \sigma_1 + \mu)I, \tag{4}$$

$$\frac{dJ}{dt} = \gamma_2 I + k_2 Q - (\sigma_2 + d_2 + \mu)J, \tag{5}$$

$$\frac{dR}{dt} = \sigma_1 I + \sigma_2 J - \mu R, \tag{6}$$

$$\frac{dN}{dt} = \Pi + P - d_1 I - d_2 J - \mu N, \tag{7}$$

$$\frac{dD}{dt} = d_1 I + d_2 J. \tag{8}$$

Table 1. Parameters for the SEQIJR model (rates are per day)

Parameters	Definition
Π	Rate of inflow of susceptible individuals into a region or community
μ	The natural death rate
P	Rate of inflow of asymptomatic individuals
β	Infectiousness and contact rate between a susceptible and an infectious individual
ε_E	Modification parameter associated with infection from an exposed individual
ε_Q	Modification parameter associated with infection from a quarantined individual
ε_J	Modification parameter associated with infection from an isolated individual
γ_1	Rate of quarantine of exposed asymptomatic individuals
γ_2	Rate of isolation of infectious symptomatic individuals

σ_1	Rate of recovery of symptomatic individuals
σ_2	Rate of recovery of isolated individuals
k_1	Rate of development of symptoms in asymptomatic individuals
k_2	Rate of development of symptoms in quarantined individuals
d_1	Rate of disease-induced deaths for symptomatic individuals
d_2	Rate of disease-induced deaths for isolated individuals

Source: Adapted from Gumel et al. [1].

Table 2. Parameter values for four regions (rates are per day)

Parameters	Beijing	Hong Kong	Singapore	Toronto
Π	408	221	136	136
P	0	0	0	0
μ	0.000034	0.000034	0.000034	0.000034
β	0.15	0.1	0.21	0.2
ε_E	0	0	0	0
ε_Q	0	0	0	0
ε_J	0.82	0.84	0.2	0.36
γ_1	0.1	0.1	0.1	0.1
γ_2	0.5	0.5	0.5	0.5
σ_1	0.0413	0.0337	0.0337	0.0337
σ_2	0.0431	0.0386	0.0386	0.0386
k_1	0.1	0.1	0.1	0.1
k_2	0.125	0.125	0.125	0.125
d_1	0.0055	0.0079	0.0079	0.0079
d_2	0.0041	0.0068	0.0068	0.0068

Source: Adapted from Gumel et al. [1].

2.2. Disease control strategies

An examination of the SEQIJR model shows that strategies for reducing the epidemic could include the following types of approach:

1. Reducing the number of susceptible people. This could be achieved by an effective vaccine. If the vaccine is 100% effective, then this could be included in the model by an extra term representing a direct transfer rate of individuals from the *S* population into the *R* population.

2. Reducing the infection rate of susceptible individuals by infected individuals (reducing the value of the parameter β). A reduction in β could be achieved by immunization by a vaccine that is not 100% effective or by reducing the amount of contact between susceptible and infected individuals, e.g., by closing centers of congregation such as schools, shopping centers, factories etc.

3. Quarantine of exposed individuals or isolation of infected individuals. These effects are included in the model through the parameters γ_1, ε_Q, γ_2 and ε_J. We will look at the effects of these parameters in this paper.

4. Reducing death rates from the disease by appropriate medical treatment, i.e., reducing the parameters d_1 and d_2.

5. Preventing the entry of exposed people from outside, i.e., reducing the value of the parameter *P*. However, it is unlikely that it is possible to make $P = 0$ due to the large amount of travel between countries and the difficulty of detecting exposed individuals who are assumed to be asymptomatic.

In this paper, we will look at the effects of controlling the values of the quarantine and isolation rate parameters γ_1 and γ_2 and the quarantine and isolation infection rate parameters ε_Q and ε_J. In practice, each of these parameters will have lower and upper bounds. The upper bounds on γ_1 and

γ_2 will mainly be due to the limitations on the facilities available for first identifying exposed and infectious individuals and then housing them in appropriate quarantine and isolation facilities. The infection rate parameters ε_Q and ε_J are a measure of the effectiveness of quarantine and isolation in preventing infection of susceptible individuals through nocosomial infection in the isolation hospitals and quarantine facilities.

We will aim to minimize the number of people who contract the disease in a given period, e.g., 1000 days, by selecting optimal values for γ_1, γ_2, ε_Q and ε_J subject to upper and lower bounds on each of the four control parameters. In addition, we will not accept a solution if the numbers of isolated and quarantined individuals exceeds reasonable limits on the facilities available for quarantine and isolation. The mathematical problem can then be stated as:

$$\text{For given } T, \min_{\gamma_1, \gamma_2, \varepsilon_Q, \varepsilon_J} F(T) = E(T) + Q(T) + I(T) + J(T) + R(T) + D(T)$$

$$\text{subject to } L_1 \le \gamma_1 \le U_1,\ L_2 \le \gamma_2 \le U_2,\ L_Q \le \varepsilon_Q \le U_Q,\ L_J \le \varepsilon_J \le U_J,$$

$$0 \le Q(t) \le V_Q,\ 0 \le J(t) \le V_J,$$

$$\text{where } 0 \le t \le T \tag{9}$$

and where the SEQIJR model differential equations in equations (1)-(8) are satisfied and where U_Q and U_J are upper limits on the maximum numbers of quarantined and isolated individuals, respectively, at any given time.

We note that, if the disease death rates d_1 and d_2 remain constant, then minimizing the total number of people who contract the disease is effectively the same as minimizing the death rate.

2.3. Equilibrium solutions and the basic reproductive rate (R_0)

There are two equilibrium solutions for the above model which can be identified as a “disease-free” equilibrium and an “endemic” equilibrium. If we introduce “decay” parameters for the *E*, *Q*, *I* and *J* populations defined

by:

$$D_E = \gamma_1 + k_1 + \mu, \quad D_Q = k_2 + \mu, \quad D_I = \gamma_2 + \sigma_1 + d_1 + \mu,$$

$$D_J = \sigma_2 + d_2 + \mu, \tag{10}$$

and consider the special case $P = 0$ (no incoming exposed individuals), the equilibrium solutions can be written in the form:

$$S^* = \frac{1}{\mu}(\Pi - \alpha_S I^*), \text{ where } \alpha_S = D_E \alpha_E, \tag{11}$$

$$E^* = \alpha_E I^*, \text{ where } \alpha_E = \frac{D_I}{k_1}, \tag{12}$$

$$Q^* = \alpha_Q I^*, \text{ where } \alpha_Q = \frac{\gamma_1}{D_Q}\alpha_E, \tag{13}$$

$$J^* = \alpha_J I^*, \text{ where } \alpha_J = \frac{\gamma_2 + k_2 \alpha_Q}{D_J}, \tag{14}$$

$$R^* = \alpha_R I^*, \text{ where } \alpha_R = \sigma_1 + \sigma_2 \alpha_J, \tag{15}$$

$$N^* = \frac{1}{\mu}(\Pi - \alpha_N I^*), \text{ where } \alpha_N = d_1 + d_2 \alpha_J, \tag{16}$$

where there are two possible values for I^* given by:

$$I_1^* = 0, \quad I_2^* = \frac{\Pi}{(B_I - \alpha_N)}(R_0 - 1). \tag{17}$$

The constant R_0 in equation (17) can be identified as the basic reproductive rate, which gives the number of secondary infections that occur when an infected person enters a disease-free population, i.e., if $R_0 < 1$, then the number of infected people decreases and if $R_0 > 1$, then the number of infected people increases. It is defined by:

$$R_0 = \frac{B_I}{\alpha_S}, \text{ where } B_I = \beta(\varepsilon_E \alpha_E + 1 + \varepsilon_Q \alpha_Q + \varepsilon_J) \tag{18}$$

can be identified as the equilibrium rate of new infections per infectious

individual. Note that from equation (16), α_N is the death rate due to disease at equilibrium. It is clear that an endemic equilibrium can only occur if $B_I > \alpha_N$, i.e., if the rate of new infections is greater than the death rate from the disease at equilibrium. Since it is also necessary that S^* and N^* are non-negative, it can be seen from equation (11) that the endemic equilibrium can only occur if the birth rate $\Pi > \alpha_S I_2^*$. Note that, since $S + E + Q + I + J + R = N$, non-negative S, E, Q, I, J, R imply non-negative N.

It can be shown by the usual method of analyzing the eigenvalues of the Jacobian of the linearized model that the two equilibrium points have the following properties:

1. The first solution is a disease-free equilibrium. For $R_0 < 1$, it is asymptotically stable. The other solution has negative populations and therefore does not exist.

2. For $R_0 > 1$, the disease-free equilibrium is not asymptotically stable. For $B_I > \alpha_N$ and $\Pi > \alpha_S I_2^*$, the second solution has positive S, E, Q, I, J, R populations and is asymptotically stable. This solution is an endemic disease equilibrium.

In analyzing strategies for eliminating diseases, some authors concentrate on the value of R_0 and the equilibrium solutions and their asymptotic stability. However, the fact that the disease eventually disappears is not always acceptable in practice as the number of disease deaths might become excessive even though the disease eventually disappears. An examination of the dynamic behavior of the solution when the endemic equilibrium exists shows that the endemic equilibrium solution is often attained only after an extremely long time, e.g., 100,000 days, and after a sequence of recurring epidemics [17]. Therefore, we believe that it is usually necessary to examine the detailed dynamical behavior of a disease model as well as the equilibrium solutions and the value of R_0.

3. Numerical Solutions

3.1. Optimal solutions

We have used Matlab to numerically integrate the equations (1)-(8) using the *ode45* solver. From the numerical solutions we can compute the objective function $F(T)$ in equations (9) for given *T*, γ_1, γ_2, ε_Q and ε_J for parameter values for the four regions given in Table 2. We then used the Matlab nonlinear optimization function *fminbnd* to solve the optimization problem in equations (9) but without the state variable constraints on $Q(t)$ and $I(t)$, i.e., to minimize $F(T)$ subject to upper and lower bounds on the four control parameters. We found that in all cases examined the results were the same, namely that γ_1 and γ_2 must be at their upper limits and ε_Q and ε_J at their lower limits, i.e., the maximum possible number of individuals should be quarantined and isolated and the infection rates from the quarantined and isolated individuals must be kept as low as possible. We next looked at the sensitivity of $F(T)$ and the disease deaths $D(T)$ and the basic reproductive rate R_0 to variations in each of the four parameters.

3.2. Effectiveness of isolation

In order to study the effectiveness of isolation, we assumed that values for all other parameters in the equations were as given in Table 2. We then calculated the numbers of people contracting the disease and the disease deaths in a given period (typically 1000 days) and the values of R_0 for a range of the γ_2 and ε_J values subject to upper and lower bounds on the two parameters. As in Section 3.1, we found that the minima for people who had the disease and for disease deaths always occurred when γ_2 was at the upper limit and ε_J at the lower limit. We therefore decided to look at the effects of the two parameters separately.

3.2.1. Effectiveness of isolation infective rate ε_J as a control

We looked at the changes in the numbers of diseased people in 1000

days as the value of ε_J was varied from 0.1-0.5. Typical results of the computations are shown in Figures 1-5 and Table 3. We have only shown results for Beijing and Hong Kong as the results for Singapore and Toronto were similar to Beijing. Figure 1 shows how the numbers of diseased individuals and disease deaths in 1000 days in Beijing vary as the isolation infective rate ε_J is changed for a fixed isolation rate $\gamma_2 = 0.5$. The values for the quarantine parameters were taken as $\gamma_1 = 0.1$ and $\varepsilon_Q = 0.15\varepsilon_E$ with $\varepsilon_E = 0.3$ [15, 16]. All other parameters were assumed to have values given for Beijing in Table 2. Figure 3(a) shows the variation in the basic reproductive rate values R_0 under the same conditions. The actual values computed for disease deaths $(D(1000))$, total disease $(F(1000))$ and R_0 are shown in Table 3 for $\gamma_2 = 0.3, 0.5, 0.7$. This table also includes maximum values for exposed $(E(t))$, quarantined $(Q(t))$, infectious $(I(t))$ and isolated $(J(t))$ for $t \in [0, 1000]$ days. It can be seen that the disease numbers become "reasonable" (hundreds or thousands) only for $\varepsilon_J < 0.11$ for $\gamma_2 = 0.5, 0.7$. For higher values the model predicts disease population numbers of the order of hundreds of thousands or millions. For the actual values estimated by Gumel et al. [1] of $\varepsilon_J = 0.82$ for Beijing, the numbers of deaths predicted by the model would be of the order of millions if isolation was the only policy used to control the disease. A value of $\varepsilon_J < 0.11$ requires that nosocomial (hospital-based) infections must be strictly controlled. The results for Hong Kong are shown in Figures 2 and 3(b). The behaviour of the results are similar to those for Beijing but with one major difference. For Beijing there is a sharp decrease in the disease for $\varepsilon_J \approx 0.15$. For Hong Kong this sharp decrease occurs for $\varepsilon_J \approx 0.3$. An examination of the parameter values in Table 2 shows that the most likely cause of the difference is that the infective rate from infectious individuals β has the value 0.15 in Beijing and 0.1 in Hong Kong. This change means that the R_0 value for Hong Kong would be approximately two thirds of the value for Beijing.

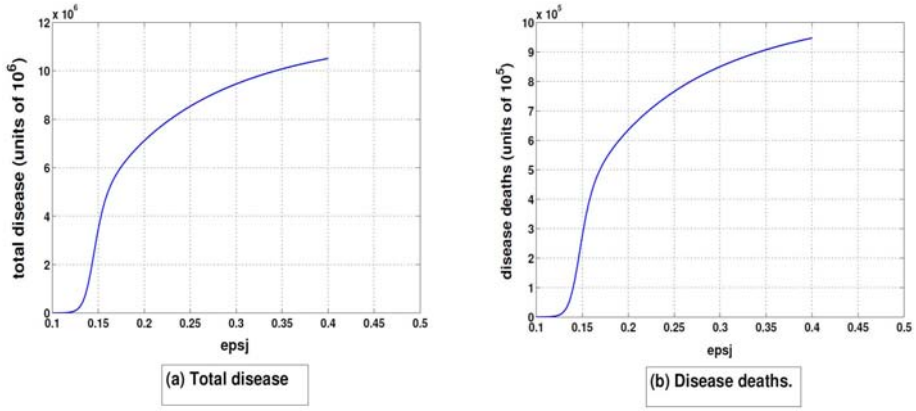

Figure 1. Beijing Total Diseased People and Disease Deaths in 1000 Days as Function of Isolation Infective Rate ε_J. $\gamma_2 = 0.5$, $\gamma_1 = 0.1$, $\varepsilon_E = 0.3$, $\varepsilon_Q = 0.15\varepsilon_E = 0.045$.

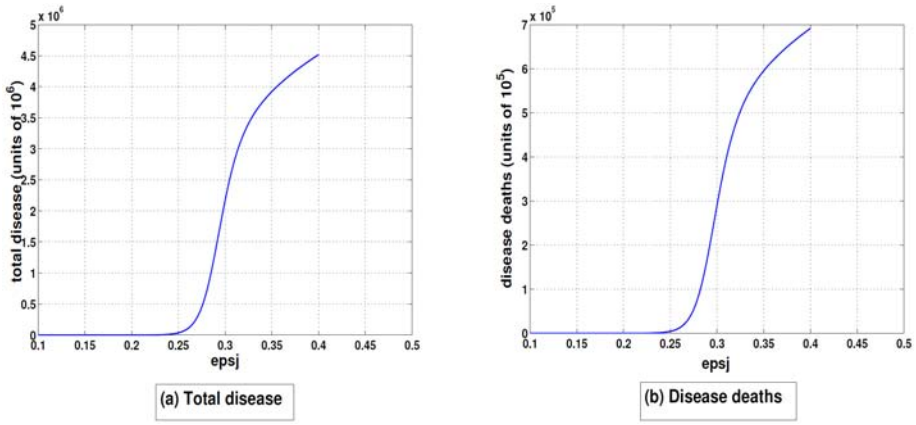

Figure 2. Hong Kong Total Diseased People and Disease Deaths in 1000 Days as Functions of Isolation Infective Rate ε_J. $\gamma_2 = 0.5$, $\gamma_1 = 0.1$, $\varepsilon_E = 0.3$, $\varepsilon_Q = 0.15\varepsilon_E = 0.045$.

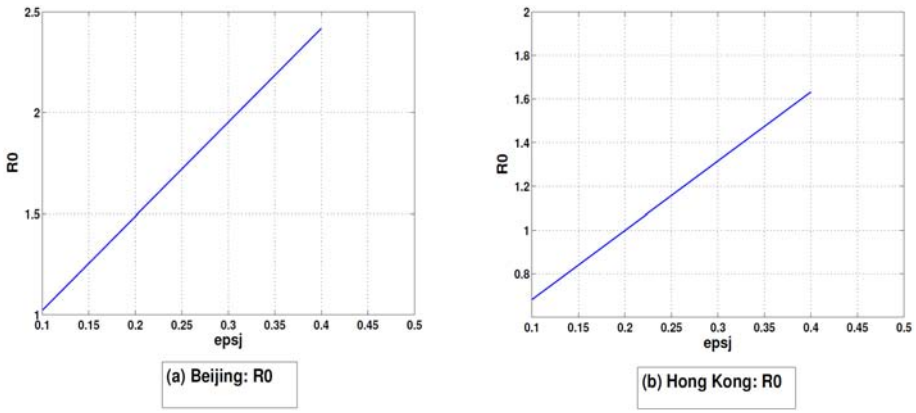

Figure 3. Basic Reproductive Rates (R_0) for Beijing and Hong Kong as Functions of Isolation Infective Rate ε_J. $\gamma_2 = 0.5$, $\gamma_1 = 0.1$, $\varepsilon_E = 0.3$, $\varepsilon_Q = 0.15\varepsilon_E = 0.045$.

A comparison of the R_0 values in Figures 1, 2 and 3 shows that the marked declines in death rates occur for $R_0 > 1$. $R_0 > 1$ implies that the number of infections initially increases. However, as the number of susceptible people becoming infected increases, the infection rate will reach a maximum and then begin to decline. For R_0 close to 1, this decline occurs early enough for the total number of infected people to remain low.

3.2.2. Effectiveness of isolation rate (γ_2) as a control

We looked at the changes in the total numbers of diseased people in 1000 days in Beijing and Hong Kong as the value of γ_2 was varied from 0.3-0.7. Typical results of the computations are shown in Figures 4 and 5 and in Table 3. In the figures, the values of other quarantine and isolation parameters were taken as $\varepsilon_J = 0.2$, $\gamma_1 = 0.1$ and $\varepsilon_Q = 0.15\varepsilon_E$ with $\varepsilon_E = 0.3$. All other parameters were assumed to have the values in Table 2. For Beijing the number of diseased people is always in the hundreds of thousands for $\varepsilon_J = 0.2$. For Hong Kong the value of $\varepsilon_J = 0.2$ gives a number of diseased people less than 500 for $\gamma_2 > 0.4$. It can be seen that the numbers of diseased people vary much more slowly with γ_2 than they do

with ε_J. This suggests that reducing the infection rate from isolated people will be a more effective method of reducing the disease than increasing the rate of isolation of infectious people.

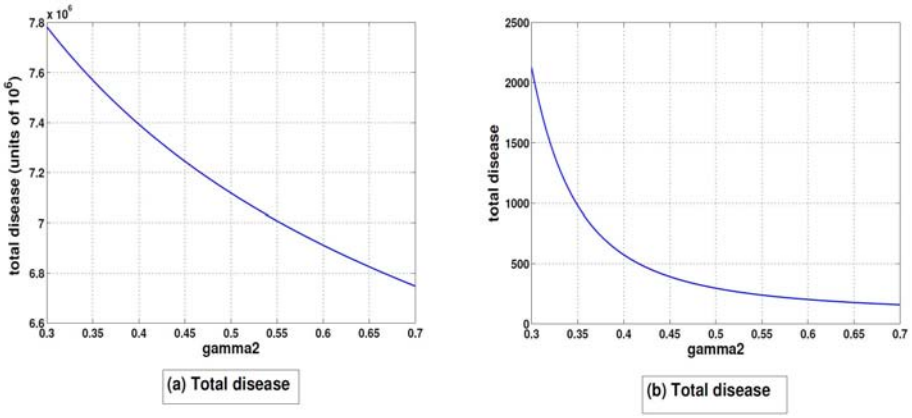

Figure 4. Beijing and Hong Kong Total Diseased People in 1000 Days as Functions of Isolation Rate γ_2. $\varepsilon_J = 0.2$, $\gamma_1 = 0.1$, $\varepsilon_E = 0.3$, $\varepsilon_Q = 0.15\varepsilon_E = 0.045$.

Table 3. Deaths, Total Diseased, R_0, Maximum Values of *E*, *Q*, *I*, *J* in 1000 days as Functions of Isolation Rate γ_2 and Isolation Infective Rate ε_J for Beijing Parameters

γ_2	ϵ_J	Deaths	TotalDisease	R_0	Max E	Max Q	Max I	Max J
0.30	0.30	8.918e+005	9.823e+006	2.08	5.037e+005	3.928e+005	1.447e+005	1.731e+006
	0.20	7.26e+005	8.028e+006	1.63	2.765e+005	2.185e+005	7.96e+004	1.013e+006
	0.15	5.714e+005	6.353e+006	1.4	1.561e+005	1.24e+005	4.496e+004	5.908e+005
	0.13	4.774e+005	5.361e+006	1.31	1.089e+005	8.676e+004	3.139e+004	4.176e+005
	0.11	2.744e+005	3.353e+006	1.22	6.471e+004	5.163e+004	1.865e+004	2.511e+005
	0.10	9.687e+004	1.319e+006	1.17	4.194e+004	3.278e+004	1.2e+004	1.511e+005
0.50	0.30	8.624e+005	9.591e+006	1.99	4.419e+005	3.462e+005	8.071e+004	1.592e+006
	0.20	6.632e+005	7.418e+006	1.53	2.094e+005	1.661e+005	3.828e+004	8.046e+005
	0.15	4.266e+005	4.964e+006	1.3	9.332e+004	7.439e+004	1.706e+004	3.696e+005
	0.13	1.072e+005	1.483e+006	1.2	4.857e+004	3.791e+004	8837	1.792e+005
	0.11	2651	3.567e+004	1.11	1071	817.1	193.8	3733
	0.10	358.5	4502	1.06	83.72	65.06	15.21	309.2
0.70	0.30	8.478e+005	9.472e+006	1.95	4.135e+005	3.246e+005	5.534e+004	1.522e+006
	0.20	6.298e+005	7.089e+006	1.48	1.801e+005	1.431e+005	2.411e+004	7.065e+005
	0.15	2.27e+005	2.965e+006	1.25	6.82e+004	5.442e+004	9131	2.753e+005
	0.13	1.126e+004	1.588e+005	1.15	5885	4447	780.4	2.018e+004
	0.11	245.5	3062	1.06	51.31	40	6.841	193.9
	0.10	47.45	555.3	1.01	6	3.017	1	15.29

Quarantine parameters: Quarantine rate $\gamma_1 = 0.1$, Exposed infection rate $\varepsilon_E = 0.3$, Quarantine infection rate $\varepsilon_Q = 0.045$.

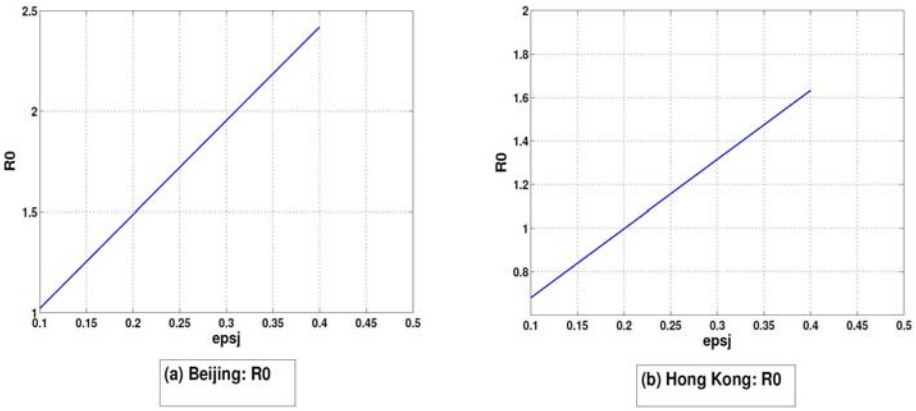

Figure 5. Beijing and Hong Kong Basic Reproductive Rates (R_0) as Functions of Isolation Rate γ_2. $\varepsilon_J = 0.2$, $\gamma_1 = 0.1$, $\varepsilon_E = 0.3$, $\varepsilon_Q = 0.15\varepsilon_E = 0.045$.

Table 4. Deaths, Total Diseased, R_0, Maximum Values of *E*, *Q*, *I*, *J* in 1000 days as Functions of Quarantine Rate γ_1 and Quarantine Infection Rate ε_Q for Beijing Parameters

γ_1	ϵ_Q	Deaths	TotalDisease	R_0	Max E	Max Q	Max I	Max J
0.10	0.09	1.049e+006	1.16e+007	4.46	1.346e+006	2.445e+005	9.811e+005	3.751e+006
	0.06	1.049e+006	1.159e+007	4.43	1.331e+006	2.417e+005	9.718e+005	3.726e+006
	0.03	1.048e+006	1.159e+007	4.4	1.316e+006	2.391e+005	9.621e+005	3.701e+006
0.02	0.09	1.042e+006	1.159e+007	4.36	8.859e+005	1.609e+005	1.294e+006	3.748e+006
	0.06	1.042e+006	1.158e+007	4.32	8.709e+005	1.582e+005	1.275e+006	3.71e+006
	0.03	1.042e+006	1.158e+007	4.28	8.559e+005	1.555e+005	1.256e+006	3.673e+006
0.30	0.09	1.039e+006	1.158e+007	4.31	6.566e+005	1.193e+005	1.441e+006	3.736e+006
	0.06	1.039e+006	1.157e+007	4.27	6.433e+005	1.169e+005	1.416e+006	3.692e+006
	0.03	1.038e+006	1.157e+007	4.23	6.301e+005	1.145e+005	1.391e+006	3.647e+006

Isolation parameters: Isolation rate $\gamma_2 = 0.5$, isolation infection rate $\varepsilon_J = 0.2$,
Exposed infection rate $\varepsilon_E = 0.3$.

3.3. Effectiveness of quarantine

To study quarantine we followed a similar procedure to that for isolation. We first did an optimization including both parameters γ_1 and ε_Q. As expected, the minimum numbers of diseased people and disease deaths occurred when γ_1 was at its upper limit and ε_Q at its lower limit. We then

looked at the separate effects of the two parameters. Typical results obtained for Beijing by varying the quarantine infective rate ε_Q and the quarantine rate γ_1 are shown in Table 4. The results show clearly that for the SEQIJR model considered in this paper, quarantine would not be an effective method of controlling the disease.

4. Discussion and Conclusions

The results in Section 3 show clearly that isolation is a more effective method of reducing the number of disease cases than quarantine. For the parameters used in this analysis, quarantine appears to have little practical value. If anything, our analysis may overestimate the usefulness of quarantine because we have assumed a value of $\varepsilon_E = 0.3$ (following [15, 16]) instead of $\varepsilon_E = 0$ (Gumel et al. [1]). Clearly, if $\varepsilon_E = 0$, then quarantine cannot directly affect the infection rate, although it can indirectly because quarantined people are likely to be closely monitored for appearance of the disease with a consequent earlier transfer to isolation if they become symptomatic. In the analysis of the SEQIJR model in this paper, we have assumed that $P = 0$, i.e., no exposed people are entering the population from outside. If the population is initially disease-free, then quarantine could be useful if all entering exposed people could be quarantined. In earlier times, quarantine was a useful strategy because the number of travellers was small and everyone from a suspect origin could be quarantined until they were found to be disease free. In modern times, quarantine of exposed people is much more difficult because of the greatly increased mobility of people and the economic importance of tourism and international trade. However, a selective quarantine involving an aggressive searching of contacts of infectious people or of people from infectious regions is a useful method for reducing the spread of a disease, especially in its early stages.

The results for isolation show that, for the parameter values used, the deaths from the disease and the total number of people contracting the disease can only be reduced to acceptable levels by very strict control of

infection in isolation wards ($\varepsilon_J < 0.11$ for Beijing parameter values) and by a very active identification and isolation of infectious individuals ($\gamma_2 > 0.5$). If these policies are implemented early in the disease cycle, then the model suggests that isolation can keep the disease at a very low level even for a highly infectious disease. However, once a sizeable number of individuals become infected, then isolation facilities are likely to be swamped and a large number of deaths might be expected unless other measures are taken. For example, if the values of $\gamma_2 = 0.5$ and $\varepsilon_J \approx 0.8$ for Beijing and Hong Kong and $\varepsilon_J = 0.36$ for Toronto given by Gumel et al. [1] are correct, then the model suggests that in all 3 regions the numbers of people dying from the disease would reach hundreds of thousands in 1000 days. These death rates are clearly unacceptable and fortunately did not occur. Of the four regions, only Singapore had a sufficiently low value of $\varepsilon_J = 0.2$ for isolation to help keep disease rates at acceptable levels. If the model and parameter values are correct, then it is clear that factors other than quarantine and isolation must have been the main factors in controlling the disease in the four regions. Looking at the formula (equation (18)) for the basic reproductive rate R_0 it is clear that reduction of the parameter β is likely to be a major weapon in controlling a disease. As stated earlier, factors such as immunization, basic hygiene, closure of centres of concentration of people can all be used to reduce the value of β. Although it is not included in the SEQIJR model of this paper, an effective vaccine can be used to directly transfer people from the susceptible to the recovered class.

The results suggest that a study of the actual dynamics of the disease is important, i.e., that the equilibrium solutions and the basic reproductive rate (R_0) only give partial information. Our results show that disease death rates can be kept to reasonable levels even when $R_0 > 1$. However, this is only possible for values of R_0 close to 1. We have also found [17] that the dynamic approach to the endemic equilibrium of the model can take a long time and can show a sequence of recurring epidemics before the equilibrium is reached.

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