A compartmental model for the analysis of SARS transmission patterns and outbreak control measures in China

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Abstract

We propose a compartmental model BloComp(2,7) that mimics the SARS control strategies implemented by the Chinese government after the middle of April 2003: the division of the whole population into two parallel blocks corresponding to the so-called free environment and the isolated environment and the partition of these blocks further into the compartments of susceptible, exposed, infective, possible, diagnosed, removed and the health care workers. We introduce a novel approach to calculate the transfer rate from the free environment to the isolated environment, and we incorporate into the model the fact that many individuals were misdiagnosed as SARS suspected and hence were mistakenly put in the isolated environment due to lack of fast and effective SARS diagnostic tests. We develop some methods for the parameter identification using the daily reported data from the Ministry of Health of China. Simulations based on these parameters agree with the accural data well, thus provide additional validation of the model. We then vary some parameters to assess the effectiveness of different control measures: these new parameters correspond to the situation when the quarantine measures in the free-environment were prematurely relaxed (we thus observe the second outbreak with the maximal number of daily SARS patients much higher than the first outbreak) or when the quarantine time of SARS patients is postponed (we observe

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delayed peak time but with much higher number of SARS patients at the peak). We also calculate the basic reproductive number and the basic adequate contact rate.
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1. Introduction

After the initial spread of severe acute respiratory syndrome (SARS) until the middle of April 2003, Chinese government started to implement a series of strict prevention and control measures. By the end of May of 2003, the number of SARS patients declined to single digit and this significant and rapid containment seems to suggest the effectiveness of these control measures. Since these measures unfortunately had significant negative impact on the daily life and the economic growth of the country, it becomes extremely important, for future control and prevention of possible outbreak of SARS and other infectious diseases, to determine whether relaxed measures might be able to yield similar results.

In addition to the unprecedented massive campaign involving newspapers, radios, televisions and posters to improve public awareness leading to some changes of daily life at both the individual and community levels (such as regular ventilation, reduction of social activities, increasing regular exercises), a national wide system of SARS checkpoints and health registrations [2] was quickly established, and the body temperature was measured at bus stations, train stations, airports, shipsides and major meeting facilities. The Chinese government also implemented a very strict quarantine and isolation policy, summarized in the Clinic Diagnostic Standard of SARS decreed by the Ministry of Health of China (MHC) [9]. Quarantine measures were implemented, with different strengths for three distinct environments: complete isolation, partial isolation and free environment [13]. In the hospital settings, complete isolation was strictly implemented. This included isolation and mandatory treatment of diagnosed and suspected cases, quarantining and close observation of individuals with fever, isolating areas and buildings hosted suspected and diagnosed SARS cases. Therefore, possible transmission links between the spreading sources in these areas and the outside were broken. In addition, all health care workers taking care of diagnosed and suspected SARS patients were fully isolated from the outside, in contrast to some other SARS affected regions [3,4,10]. Great restrictions were also imposed on the flow of individuals in many residential areas, villages, schools, universities, major companies and other partially isolated communities, and a very systematic recording system for the flow of individuals was developed. These helped to significantly reduce the basic reproductive number and also speed up the hospitalization time.

These communities were not fully isolated, so the tracking was effective but not perfect, and hence once some infective were identified, only a portion of exposed individuals could be tracked. In the free environment, there was no effective restriction for the movement and contact of individuals and the tracking was poor. Therefore, once an infective was identified, very few who had previous contact with the infective can be tracked. In summary, the quarantine measures implemented by the Chinese government involved the division of the whole population into two parallel blocks: one block corresponding to the so-called free environment where individuals can move and interact with each other without restrictions, and another block corresponding to the so-called isolated environment (mostly hospitals) that hosted all individuals with record of exposure to SARS virus or showing symptoms similar to those of SARS, in addition to the health care workers taking care of the SARS patients and suspected cases. The second block was relatively isolated from the first block except exposed and infective eventually enter to this isolated block and some misdiagnosed individuals were discharged and then entered the free environment.

One of the purposes of this paper is to develop a compartmental model that captures some of the essential features of the control measures aforementioned, some of which were unique among SARS affected regions. We divide the whole population into two interacting blocks, the isolated block and the free block. We further partition the isolated block into P-class (possible class), diagnosed class, and health-care worker class, and we subdivide the free block into susceptible, exposed, infective classes, and removed class.

As already observed in [7], modelling based simulations of the transmission patterns of SARS suffer a serious drawback in terms of the sensitivity on certain parameters due to the fact that the number of susceptible is extremely large comparing with the number of SARS patients. One of the contribution of this article is to lump several parameters together and use only the statistical data reported by MHC as the basis to calculate the basic adequate contact rate and the basic reproductive number. These two calculated numbers, together with other parameters describing the epidemiological features of SARS virus that have been determined in the two recent articles [16,17], allow us to use the model to generate the infectious curves that are in excellent agreement with the daily reported data from MHC. This agreement thus provides a convincing validation for the model and our identified parameters. We then vary parameters related to different control strategies and carry out intensive simulations to compare the influence and effectiveness of these control measures including the influence of different quarantine intensity, speed and duration. Our simulations based on the model show that the rapid decrease of the SARS patients is attributed to the high successful quarantine rate and timely implementation of the quarantine measures, and indeed all of the prevention and control measures implemented in China seem to be necessary, adequate and effective:

premature relaxation of some quarantine measures would lead to a second outbreak, and delayed implementation of these quarantine measures by one or two days would lead to much larger number of infected individuals.

2. The BloComp(2,7) model

We divide the total population into two blocks: Block F in which individuals can move freely and contact each other without restrictions, and Block Q where free movements of individuals are restricted. We assume the Block Q is fully isolated from the Block F in terms of the SARS spread in the sense to be explained later.

We further divide the Block F into four distinct epidemic classes: susceptible, exposed, infectious, and recovered, and we will denote the number of individuals at time t in the above classes by $S(t)$, $E(t)$, $I(t)$ and $R(t)$, respectively. We also divide the Block Q into three distinct classes: P-class, diagnosed, and health-care workers who take care of both suspected and diagnosed individuals. We shall use $P(t)$, $D(t)$ and $H(t)$ to denote the total numbers of individuals in the above three classes at time t. Note that the health-care workers dealing with suspected and diagnosed individuals are isolated from the community.

The susceptible class consists of individuals not exposed to the SARS virus, and individuals in the exposed class are exposed to the SARS virus, but in latent period (these are asymptomatic but possibly infective). The individuals in the infectious class show definitive symptoms and have high infectivity. These individuals have not yet been isolated/quarantined, and thus are capable of transmitting the disease to susceptible individuals in Block F. Individuals in the removed class are those who have recovered from SARS with acquired immunity. The individuals in the P-class are either individuals carrying SARS virus (but not yet diagnosed) or individuals without SARS virus but misdiagnosed as possible SARS patients, the second group will return to the susceptible class in Block F after further medical examinations fully explaining their illness. Individuals in the diagnosed class are carriers of SARS virus, and they have been quarantined and diagnosed. These individuals are fully isolated, they will either die of SARS or recover with acquired immunity.

The introduction of P-class in the Block Q is necessary as this class is neither the quarantine class nor the class of probable cases defined by WHO, but more in line with the Clinic Diagnostic Standard of SAR decreed by the Ministry of Health of China. As there is no validated, widely and consistently available test for infection with the SARS virus and as antibody tests may not become positive for three or more weeks after the onset of symptoms, SARS infection is tested by diagnosis of exclusion. Due to the fact that the outbreak occurred during the winter and spring that happened to be the fastigium of atypical

pneumonia, influenza, and other respiratory tract diseases with clinic symptoms similar to those of SARS such as fever, chills, muscular pain, and shortness of breath et al., [14,15] there were indeed a substantial amount of individuals in the P-class without SARS virus but misdiagnosed as possible SARS patients.

As shown in Fig. 1, When there is an adequate contact of a susceptible with an infectious individual, the susceptible individual becomes infected and enters the class E with no or low infectivity but without symptoms; once becoming symptomatic, a part of exposed individual is isolated and enter the P-class due to the stringent preventive measures, the remaining part that has not yet been isolated then enter the infectious class I. Infectious and a part of individuals in the P-class enter the diagnosed class D after they show obvious symptoms of SARS and diagnosed definitely. The diagnosed cases can get recovered to enter the recovered class with immunity [1,5,6].

We note that in the modelling of SARS outbreak, the number of the susceptible individuals is extremely large, comparing with the number of actual infected population. Consequently, the in-flow from S-class to P-class should not be proportional to the total number of susceptible individuals. We note that some statistical analysis from Chinese CDC shows strong correlation between the daily number of the new SARS suspected cases and the daily number of the new SARS diagnosed cases, with the mean ratio 1:1.3 (see [11,12]). Thus, we shall assume that during one unit time, the number of individuals misdiagnosed as SARS patients and entering the P-class is $d_{sp}D$, with d_{sp} being a constant/parameter to be identified later.
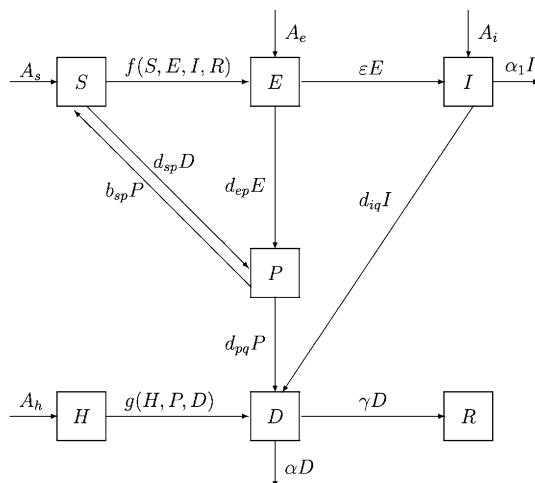

Fig. 1. Transmission diagram for the model involving two blocks and seven compartments.

We also note that health workers dealing with P-class and diagnosed SARS patients are strictly isolated from contact with the Block F and are closely observed for any possible SARS symptoms, they might become infected only by contacts with individuals from the P-class and the diagnosed patients, and once they are infected they move to the diagnosed class.

The incidence is the number of new cases per unit time. The general form of the incidence is $\beta C \frac{S}{N} I$, with β being the probability per unit time of transmitting the virus effectively between a carrier and a susceptible (this measures the toxicity of the virus), and C being the contact rate: the average number of contacts of an individual with other individuals per unit time. This contact can give birth to new cases if and only if a contact occurs between a carrier of SARS and a susceptible. So, the total number of new cases per unit time generated by an SARS virus carrier is

$$\beta C = \frac{S}{S+E+I+R} \triangleq \lambda(t).$$

Let C_E and C_I denote the contact rates, and let β_E and β_I denote the probabilities of transmission, of exposed individuals and infective individuals. It is still unclear whether contact with individuals in the E-class can lead to infection, but it is certain that $\beta_E \leqslant \beta_I$. The incidence in Block F is given by

$$f(S,E,I,R) = (\beta_E C_E E + \beta_I C_I I) \frac{S}{S+E+I+R}.$$

Similarly, the incidence in Block Q is

$$g(H,P,D) = (\beta_P C_P P + \beta_D C_D D) \frac{H}{H+P+D},$$

where C_P and C_D are the contact rates, and β_P and β_D are the probabilities of transmission, of individuals in the P-class and D-class, respectively. These parameters are related to the hospital infection control measures.

We can now formulate our compartmental model as follows:

$$\begin{cases} S' = A_s - f(S,E,I,R) - d_{sp}D + b_{sp}P, \\ E' = A_e + f(S,E,I,R) - \varepsilon E - d_{ep}E, \\ I' = A_i + \varepsilon E - d_{iq}I - \alpha I, \\ P' = d_{ep}E + d_{sp}D - b_{sp}P - d_{pq}P, \\ D' = g(H,P,D) + d_{pq}P + d_{iq}I - \alpha D - \gamma D, \\ H' = A_h - g(H,P,D), \\ R' = \gamma D. \end{cases} \tag{2.1}$$

We will refer this to BloCom (2,7) model to reflect the nature of 2 blocks and 7 compartments for the SARS transmission pattern. In the aforementioned model, α is the SARS-induced death rate, $\frac{1}{\gamma}$ is the mean recover period, ε is the transfer rate from the E-class to the I-class, d_{ep} is the transfer rate from the E-

class to the P-class, $\frac{1}{\varepsilon + d_{ep}}$ is the mean latent period, d_{iq} is the transfer rate from the I-class to the P-class, d_{pq} is the transfer rate from the P-class to the D-class, b_{sp} is the exclusion rate from the P-class, d_{sp} is the misdiagnosis rate, A_s, A_e, A_i, and A_h are the inflow rates to the S-, E-, I-, H-class, respectively.

3. The reproductive number and the outbreak control

For the simplicity of presentation, we rewrite the incidence term $f(S, E, I, R)$ as

$$f(S, E, I, R) = \frac{\beta_I C_I S}{S + E + I + R}(\delta_f E + I)$$

and we call $\frac{\beta_I C_I S}{S+E+I+R}$ the *basic adequate contact rate* in the Block F. This basic adequate contact rate is the average number of adequate contacts with susceptible of a typical SARS virus carrier in the Block F per unit time. Then $\delta_f = \frac{\beta_E C_E}{\beta_I C_I}$ is the ratio of the infectivity between an individual in the E-class and an individual in the I-class, and this ratio is clearly less than 1 and is believed to be small.

The precise value of β_I is still unknown, and C_I depends heavily on the intensity of control measures and the precise value of C_I is also difficult to estimate. Fortunately, the basic adequate contact rate $\frac{\beta_I C_I S}{S+E+I+R}$ can be calculated from the daily report of MHC, as discussed below. Therefore, we will denote

$$\lambda_f(t) = \frac{\beta_I C_I S}{S + E + I + R}$$

and regard it as a known function of time t. The same discussions above apply to the term $g(H, P, D)$, and we write

$$g(H, P, D) = \lambda_q(t)(\delta_q P + D).$$

Then, (2.1) becomes a linear non-autonomous system with the following subsystem:

$$\begin{cases} E' = \lambda_f(t)(\delta_f E + I) - (\varepsilon + d_{ep})E, \\ I' = \varepsilon E - d_{iq}I - \alpha I, \\ P' = d_{ep}E + d_{sp}D - b_{sp}P - d_{pq}P, \\ D' = \lambda_q(t)(\delta_q P + D) + d_{pq}P + d_{iq}I - (\alpha + \gamma)D. \end{cases} \tag{3.2}$$

This subsystem is obviously of fundamental importance for the prevention and control of SARS outbreak. In this section, we consider the long-term behaviours of the above subsystem under the assumption that the basic adequate contact rates in both blocks change continuously and are bounded, thus $\lambda_f(t)$ is a continuous function bounded below by λ_f^0 and above by λ_f^*, $\lambda_q(t)$ is also a continuous function bounded below by λ_q^0 and above by λ_q^*.

We now define the (maximal) basic reproductive number in Block F as

$$R_{0f}^{M} = \frac{\lambda_{f}^{*}(\varepsilon + \delta_{f}(\alpha + d_{iq}))}{(\alpha + d_{iq})(\varepsilon + d_{ep})}$$

and this can be written as

$$R_{0f}^{M} = \lambda_{f}^{*}\delta_{f} \times \frac{1}{\varepsilon + d_{ep}} + \lambda_{f}^{*} \times \frac{\varepsilon}{\varepsilon + d_{ep}} \times \frac{1}{\alpha + d_{iq}},$$

where λ_{f}^{*} is the maximal number of new infective produced by a typical infective individual per unit time during the entire course of the outbreak, δ_{f} is the infectivity ratio of the individuals in exposed class relative to the individuals in the infective class, $\frac{1}{\varepsilon + d_{ep}}$ is the mean time of an individual staying in the exposed class, $\frac{\varepsilon}{\varepsilon + d_{ep}}$ is the fraction of the exposed individuals which move to the I-class, $\frac{1}{\alpha + d_{iq}}$ is the average time that the infectious individuals stay in the I-class. Thus the basic reproductive number R_{0f}^{M} in Block F is the maximal number of secondary infections generated by an average infectious individual during the mean time staying in the I-class in an entirely susceptible population. This quantity thus determines the potential for the SARS virus to start an outbreak, or the extent of transmission in the absence of control measures. Similarly, we can define the minimal reproductive number in Block F as

$$R_{0f}^{m} = \frac{\lambda_{f}^{0}(\varepsilon + \delta_{f}(\alpha + d_{iq}))}{(\alpha + d_{iq})(\varepsilon + d_{ep})}$$

and the maximal and minimal basic reproductive numbers in Block Q as

$$R_{0q}^{M} = \frac{\lambda_{q}^{*}(\delta_{q}d_{sp} + b_{sp} + d_{pq})}{(b_{sp} + d_{pq})(\alpha + \gamma) - d_{sp}d_{pq}}$$

and

$$R_{0q}^{m} = \frac{\lambda_{q}^{*}(\delta_{q}d_{sp} + b_{sp} + d_{pq})}{(b_{sp} + d_{pq})(\alpha + \gamma) - d_{sp}d_{pq}}.$$

The following theorem, standard in mathematical epidemiology, shows that the basic reproduction numbers determine the long-term outcome of the SARS outbreak.

Theorem 3.1. *The trivial solution of the model* (3.2) *is globally asymptotically stable if* $R_{0f}^{M} \leqslant 1$ *and* $R_{0q}^{M} \leqslant 1$, *and unstable if* $R_{0f}^{m} > 1$ *or* $R_{0q}^{m} > 1$.

Proof. We first consider the equilibrium $O(0,0,0,0)$ of the following linear autonomous system:

$$\begin{cases} E' = \lambda_f^*(\delta_f E + I) - (\varepsilon + d_{ep})E, \\ I' = \varepsilon E - (d_{iq} + \alpha)I, \\ P' = d_{ep}E + d_{sp}D - (b_{sp} + d_{pq})P, \\ D' = \lambda_q^*(\delta_q P + D) + d_{pq}P + d_{iq}I - (\alpha + \gamma)D. \end{cases} \tag{3.3}$$

The coefficient matrix is

$$J = \begin{pmatrix} \lambda_f^*\delta_f - \varepsilon - d_{ep} & \lambda_f^* & 0 & 0 \\ \varepsilon & -(\alpha + d_{iq}) & 0 & 0 \\ d_{ep} & 0 & -(b_{sp} + d_{pq}) & d_{sp} \\ 0 & d_{iq} & \lambda_q^*\delta_q + d_{pq} & \lambda_q^* - (\alpha + \gamma) \end{pmatrix}.$$

The characteristic polynomial of the matrix J is the product of $\det(J_1)$ and $\det(J_2)$, where

$$J_1 = \begin{pmatrix} \rho - \lambda_f^*\delta_f + \varepsilon + d_{ep} & -\lambda_f^* \\ -\varepsilon & \rho + \alpha + d_{iq} \end{pmatrix},$$

$$J_2 = \begin{pmatrix} \rho + b_{sp} + d_{pq} & -d_{sp} \\ -\lambda_q^*\delta_q - d_{pq} & \rho - \lambda_q^* + \alpha + \gamma \end{pmatrix}.$$

It is easy to see that all the four eigenvalues of the matrix J are real. Furthermore, when

$$\lambda_f^* \leqslant \frac{(\alpha + d_{iq})(\varepsilon + d_{ep})}{\varepsilon + \delta_f(\alpha + d_{iq})} \quad \text{and} \quad \lambda_q^* \leqslant \frac{(b_{sp} + d_{pq})(\alpha + \gamma) - d_{sp}d_{pq}}{\delta_q d_{sp} + b_{sp} + d_{pq}},$$

these eigenvalues are all negative so that the equilibrium O is globally asymptotically stable.
When

$$\lambda_f^m > \frac{(\alpha + d_{iq})(\varepsilon + d_{ep})}{\varepsilon + \delta_f(\alpha + d_{iq})} \quad \text{or} \quad \lambda_q^m > \frac{(b_{sp} + d_{pq})(\alpha + \gamma) - d_{sp}d_{pq}}{\delta_q d_{sp} + b_{sp} + d_{pq}},$$

the matrix J has at least one positive eigenvalue.

The standard comparison argument can then be used to obtain the stated results of the theorem. □

From the theorem above, long-term containment of SARS can be achieved if R_{0f}^M and R_{0q}^M are all less than 1. It becomes evident that in order to control SARS outbreak, control measures in both Blocks must be implemented and strictly enforced.

4. Numerical simulations: assessment of the effectiveness of control measures

We start with some discussions about parameter identification. Unfortunately, there is insufficient experimental data for the SARS transmission that we can use to determine all model parameters. In addition, some parameters involved in our model are related to the control measures implemented by the Chinese government that can hardly be quantified and identification of these parameters should be part of the purpose of reliable mathematical models. Nevertheless, significant amount of data have been collected during the course of SARS outbreak in China after the middle of April 2003, we are going to use the back tracking method and these limited data to estimate most parameters and the basic adequate contact rate. We mention that there is one related work [18] in this aspect.

We take the unit time as one day, and we are going to assume that the average latent period is 5 days [1,8], or the first symptom appears in the sixth day after being infected. So, we also assume the time interval between being infected by SARS virus and being diagnosed as a SARS case is 8 days, with the first 5 days in the E-class (with low infectivity) and the last 3 days in the I-class (high infectivity), or in the P-class if promptly isolated as a result of the effective control measures. We take the fraction δ_f as 0.1, the exact value of this number should not change much of the discussions below if it is small.

The still poor understanding of the SARS virus toxicities and the transmission mechanisms does not give us direct estimation of C_E, C_I, β_E and β_I. On the other hand, what we need for the purpose of simulations, according to the expression $\lambda_f(t)(\delta_f E + I)$ and $\lambda_q(t)(\delta_q P + D)$ for the incidences in two blocks, is the estimation of the basic adequate contact rate $\lambda_f(t)$ and $\lambda_q(t)$. The key in our parameter identification is that the above incidences can be estimated from the data released daily by MHC as follows.

Let $\hat{f}(t)$ denote the number of new diagnosed SARS cases (released by MHC) minus the number of new diagnosed SARS cases in the H-class. Then, $\bar{f}(t)$, the new infective at time t in the Block F should be $\hat{f}(t+8)$ because the average number of days from exposure to the SARS virus to the definite diagnosis is 8 days. That is, $\bar{f} = \hat{f}(t+8)$. In the case where δ_f is small, $\delta_f E(t) + I(t)$ should be $\sum_{k=1}^{7} \bar{f}(t-k)$. As $\sum_{k=1}^{7} \bar{f}(t-k) = \sum_{k=1}^{7} \hat{f}(t+k)$, we then conclude that

$$\bar{\lambda}_f(t) = \frac{\hat{f}(t+8)}{\sum_{k=1}^{7} \hat{f}(t+k)}. \tag{4.4}$$

Fig. 2 gives the above $\bar{\lambda}_f(t)$ ($t = 1, 2, \ldots, 25$) from April 21, 2003 to May 16, 2003 according to the expressions (4.4), the continuous curve is the basic adequate contact rate $\lambda_f(t)$ in the Block F obtained from $\bar{\lambda}_f(t)$, here the hori-
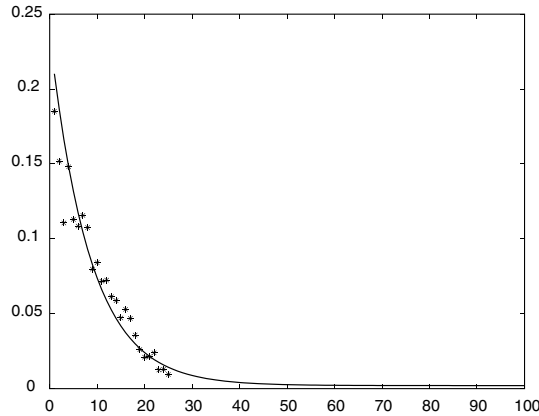
Fig. 2. The basic adequate contact rate $\bar{\lambda}_f(t)$ and $\lambda_f(t)$: the continuous curve is the smooth approximation of the actual data reported by MHC.

zontal axis is the time starting from April 21, 2003. Analogously, we can obtain the basic adequate contact rate $\lambda_q(t)$ in the Block Q.

From the statistic data at MHC [11,12], 80% of the diagnosed SARS cases come from the P-class (the so-called SARS suspected individuals who have been quarantined and treated in hospitals), and the remaining 20% come from the I-class in the Block F. So, we let

$$\varepsilon = \frac{1}{5} \times \frac{20}{100}, \quad d_{ep} = \frac{1}{5} \times \frac{80}{100}, \quad d_{iq} = 1/3.$$

Let P_s and P_q denote respectively the number of the individuals in the P-class who are later negatively diagnosed and thus return the S-class S at time t, and the number of the individuals in the P-class who are positively diagnosed as SARS patients and enter the D-class at time t. We found the average $\frac{P_s}{P_s+P_q}$ is 0.6341 using the above data. Recall that the statistical analysis from MHC shows strong correlation between the the daily number of the new SARS suspected cases and the daily number of the new SARS diagnosed cases, with the mean ratio 1:1.3. Therefore, d_{sp} is $1.3 \times 0.6341 \times \frac{1}{30}$. It takes about 10 days for an individual who was misdiagnose as a SARS patient to leave the P-class, therefore, $b_{sp} = 0.6341 \times \frac{1}{10}$. We also use the assumption that the average transition time from the P-class to the D-class is 3 days to get $d_{pq} = (1 - 0.6341) \times \frac{1}{3}$. Finally, the the period of recovery for a SARS patient is about 30 days, so we choose $\gamma = \frac{1}{30}$; and the average SARS-induced death rate is 14% and hence $\alpha = \frac{1}{30} \times 0.14$.

With the above preparation, we can now carry out some numerical simulations to validate our model, to discuss the effectiveness of control measures, and to see if alternatives are permitted.

Simulation 1. Comparison with daily reported data

In Fig. 3, the curve in stars is the daily SARS patient number reported by MHC, and the continuous curve is the results simulated by our model with the aforementioned identified parameters. The simulated result shows that the number of the SARS patients increases rapidly during the first week, reaches the peak between May 11 and May 18, 2003, and with the maximal number between 3164 cases and 3220 cases. The reported data is 3068. This simulation suggests very good agreement with real data, serving as a validation of the model.

Simulation 2. The impact of the strict quarantine measure:

Case 1. The pattern of SARS transmission in China if there is no preventive and control measures.

Assuming that there is no preventive and control measures implemented, but the toxicity of SARS virus naturally declines at the rate of 0.01 per unit time, then our model simulation shows a completely different pattern as shown in Fig. 4: the outbreak will peak at the end of October of 2004, with the maximal number 4.5 million before it declines to 10,000 cases (about 19 months after the peak) and then eventually disappear slowly.

Case 2. The pattern of SARS transmission if the preventive and control measures are relaxed prematurely.

It is evident that preventive and control measures did play a significant role in the containment of SARS outbreak in China, these measures did have great negative impact to the daily life and economic development. It becomes nat-
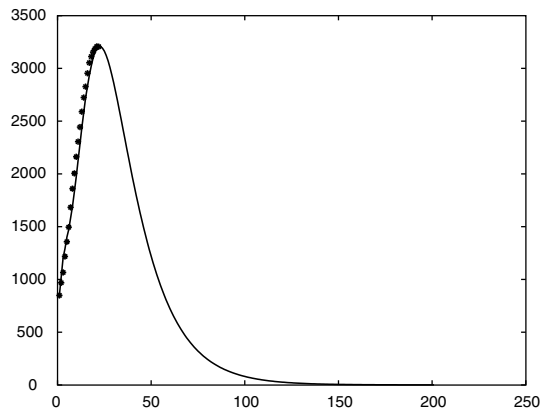

Fig. 3. The simulated curve (continuous) and the reported (by MHC, marked in stars) of the daily number of SARS patients.
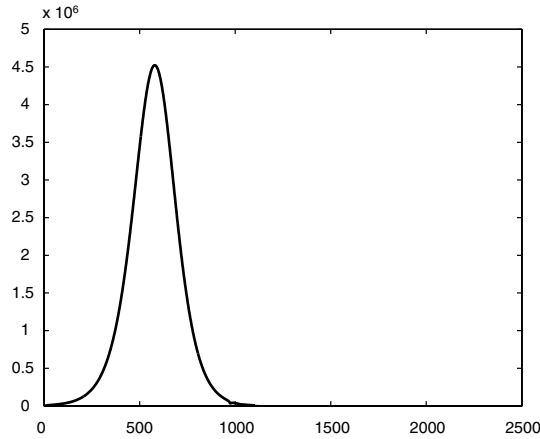
Fig. 4. The prediction for the transmission pattern in China without control measures after April of 2003. The outbreak will peak at the end of October of 2004 with over 4.5 million individuals infected, though the SARS toxicity declines exponentially.

ural, and also important for the control and prevention of the outbreak of SARS and other emerging infectious diseases, to ask whether those strict control measures could be relaxed and lifted earlier. To address this issue, we carried out some numerical simulations by taking $\lambda_f(t)$ to be $\lambda_{r0}(t)$, that is $\lambda_f(t)$ when $t \leqslant t_0$ and $\lambda_f(0)0.99^{t-t_0}$ when $t > t_0$, where t_0 represents the time when the prevention and control measures is relaxed in the Block F while the Block Q is still under complete control. Some of these simulation results with t_0 being 30 (corresponding to May 19), 37 (corresponding to May 26), and 44 (corresponding to June 3), respectively, are shown in Figs. 5–7. In Fig. 5, the stars is the reported data of SARS patients and the broken line is the simulation curve for the number of SARS patients, and our simulation shows that SARS would rebound and the second peak of SARS epidemic would appear in China and the number of SARS patients at the second peak could reach over 4000, higher than that of the first peak. In comparison, Fig. 6, shows that although the number of SARS patients could increase again and the second peak of SARS epidemic would appear, the number of SARS patients at the second peak would be only 730, much less than that at the first peak. Note also that the time when the number of SARS patients falls below 4 would be postponed. With $t_0 = 44$ shown in Fig. 7, however, the speed of the decrease of the number of SARS patients would be slightly slower (than the real data), there would be no second outbreak anymore.

The simulation results seem to indicate strongly that all of the prevention and control measures implemented in China are necessary, adequate and effective, and that the time to relax prevention and control measures has
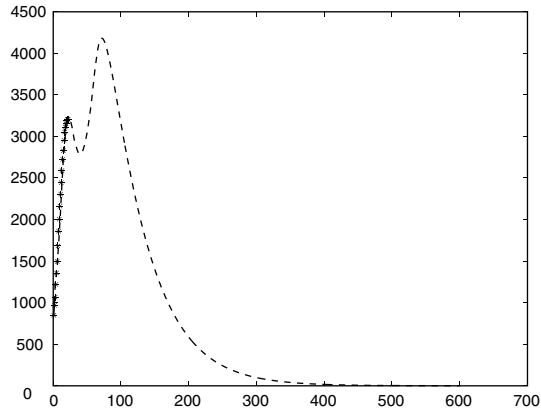
Fig. 5. The pattern of SARS transmission if the preventive and control measures were relaxed from May 19, though the toxicity of SARS virus naturally declines at the rate of 0.01 per unit time: there would be a second outbreak with the maximum number of SARS patients higher than that of the first outbreak.
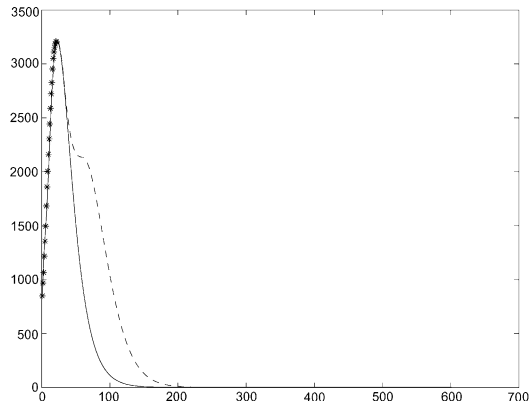

Fig. 6. The pattern of SARS transmission if the preventive and control measures were relaxed from May 26, though the toxicity of SARS virus naturally declines at the rate of 0.01 per unit time: there would still be the second outbreak but the maximal number of SARS patients will be much smaller than that of the first outbreak.

significant impact not only on the rate at which the disease dies out but also on the transmission pattern.

Simulation 3. The influence of the delayed quarantine

In order to investigate the impact on the pattern of SARS epidemic of implementing the quarantine measure with different speed, we carried out our
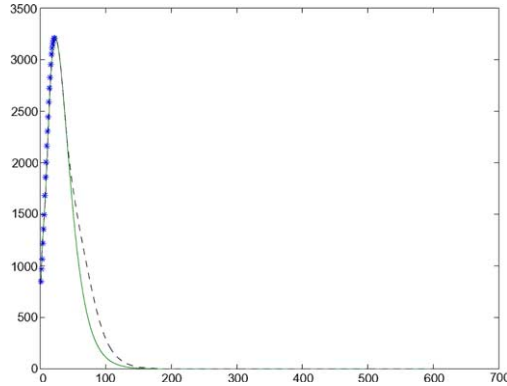
Fig. 7. The pattern of SARS transmission if the preventive and control measures were relaxed from June 3, though the toxicity of SARS virus naturally declines at the rate of 0.01 per unit time: there would be no second outbreak but the speed of decline in SARS patients would be slightly smaller than the real data.

simulations with varying transfer rate d_{iq}. In Fig. 8, the stars and real lines are the same as that in Fig. 7. The bottom broken line at the bottom shows the daily number of SARS patients when all infective stay in the I-class for one additional day since April 21: the peak would be postponed for about 2 days and the number of SARS patients at the peak would increase by about 880 cases. The top broken line presents the daily number of SARS patients when all infective stay in I-class for two more days since April 21: the peak would be postponed for about 4 days but the number of SARS patients at the peak would increase by about 1900.
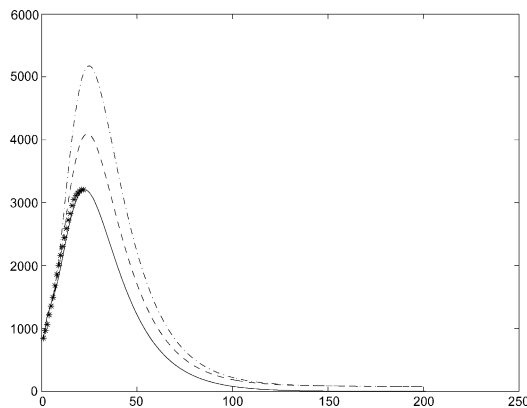

Fig. 8. The influence of the slow quarantine speed: the top and bottom lines show the number of daily SARS patients when the infective stay in the I-class for 2 and 1 more days, respectively. The peak would be postponed by 4 or 2 days, but the numbers at the peak would be much higher.

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