A Discrete Epidemic Model for SARS Transmission and Control in China

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Abstract—Severe acute respiratory syndrome (SARS) is a rapidly spreading infectious disease which was transmitted in late 2002 and early 2003 to more than 28 countries through the medium of international travel. The evolution and spread of SARS has resulted in an international effort coordinated by the World Health Organization (WHO).

We have formulated a discrete mathematical model to investigate the transmission of SARS and determined the basic reproductive number for this model to use as a threshold to determine the asymptotic behavior of the model. The dependence of the basic reproductive number on epidemic parameters has been studied. The parameters of the model have been estimated on the basis of statistical data and numerical simulations have been carried out to describe the transmission process for SARS in China. The simulation results matches the statistical data well and indicate that early quarantine and a high quarantine rate are crucial to the control of SARS. © 2005 Elsevier Ltd. All rights reserved.

1. INTRODUCTION

Severe acute respiratory syndrome (SARS) is a newly discovered infectious disease with a high potential for transmission to close contacts. SARS is an acute respiratory illness caused by infection by the SARS virus whose key signs and symptoms are fever, respiratory compromise, chills, muscle aches, headache, and loss of appetite. The etiological agent of SARS is a coronavirus which was identified in March 2003 [1]. The virus is spread predominantly by droplet and by direct or indirect contacts.

It is believed that SARS first appeared in China, in Guangdong province, on November 16, 2002. There were 305 SARS cases and five deaths between November 16 and February 9, 2003, reported in the Weekly Epidemiologic Record. On February 26, new reports of SARS outbreak came in from Hong Kong and Vietnam. More and more cases were reported worldwide since March and WHO has been reporting the daily SARS infection data. Since March 17, 2002, complete data has been collected and various kinds of research have been carried out. A new coronavirus has been isolated from patients with SARS [2], and the sequence of the complete genome of SARS-CoV was determined [3,4].

SARS is a highly contagious and rapidly spreading disease. It has taken advantage of the ease of international travel and as of June 13, 2003, the cumulative number of probable SARS cases worldwide has reached 8,454 with 792 deaths [5]. On the basis of detailed data, WHO estimates that the case fatality ratio of SARS ranges from 0% to 50% depending on the age group affected, with an overall estimate of case fatality of 14% to 15% [6].

Though much effort has been devoted to understanding this new health threat, and much successful research has been done on the disease, there are still no effective drugs or vaccines for SARS. Control has relied mainly on the rapid identification of cases and on effective isolation of probable cases and their contacts.

China is one of the countries most severely influenced by SARS. The cumulative number of diagnosed SARS cases is 5,327 with 343 deaths [7]. The diagnosed SARS cases were distributed over most provinces and special districts, and the number of SARS cases in China account for almost two-thirds of all reported cases worldwide. China was regarded as the epicentre of the SARS outbreak. A report of a WHO assessment team reached the following conclusion [8]. "If SARS is not brought under control in China, there will be no chance of controlling the global threat of SARS. Achieving control of SARS is a major challenge especially in a country as large and diverse as China."

SARS was transmitted mainly in Guangdong province in the southern part of China, before March 2003. The reported total of SARS cases was 305 with five deaths by February 9, 2003. Updated data on SARS cases and deaths in China has reached a total of 792 cases and 31 deaths as of February 28 [9]. On March 31, 2003, the diagnosed SARS case accumulated to 1,190 with 46 deaths [10]. There was a rapid spread of SARS in China beginning in April. Especially in late April and early May, the number of daily new diagnosed SARS cases was over 100.

The rapid growth in number of SARS cases set up a strong alarm to government and people, and public health authorities, physicians, and scientists all over the country began a campaign to cope with a severe and rapidly spreading infectious disease. Drastic measures and actions were taken to bring SARS under control since April 20 [11]. Newspapers, radio, TV stations, and posters campaigned to educate the public on SARS prevention. Disinfectant was sprayed in many public places, including streets, shopping centers, airports, railways, bus terminals, classrooms, offices, and transportation vehicles. Individuals who have had direct or indirect contact with probable SARS-infected cases have been quarantined in their homes, hospitals, or campuses. Stern travel advisories were issued to students and workers, and the Golden week holiday (International Labour Day) was shortened from seven days to five days. A body temperature check is done for all air passengers and passengers who fail a therm-imaging check at the entrance are checked by nurses and doctors at the station's quarantine center. Many stock exchanges, cinemas, theaters, and internet cafes were closed temporarily. Quarantine outpatient departments were set up for fever patients in many large hospitals. Special hospitals for SARS treatment were specified in every large city. For example, the emergency quarantine center in Xiaotangshan, with a 1000-bed facility, was constructed within eight days. The number of daily reported new diagnosed SARS cases were large in late April and early May, but the control measures taken were adequate and effective. SARS infections began to decline after the middle of May, and the downward trend has continued until now. The daily number of reported new probable cases of SARS in mainland China declined considerably from an average of 166 cases during the first week of May to 90

cases during the second week, 27 cases in the third week, and 16 in the fourth week. The daily number of reported new cases dropped to an average of 2.5 [12] and has decreased to zero more recently [13].

However, SARS transmission and all the measures to combat SARS have had strong negative side effects on daily life and development of the economy. Can these strict control measures be relaxed, and when is a suitable time to begin the relaxation? Any change in control measures will have effects on the spread of SARS. The present zero infection situation was not easy to achieve and any relaxation of control measures must be done carefully to avoid a recurrence of infections. Therefore, it is important to know what will happen if some of the quarantine measures are cancelled.

There are many questions about SARS transmission, which are, in fact, questions of importance for any disease outbreak. How many further infections will be produced by each infected person per day? How many people will become infected in the future? When will the infection peak arrives? How long does the infection peak last and how high is the peak? Will the current public health measures be enough to bring SARS under control? Mathematical modelling and analysis can help to give some answers to these questions.

In this paper, we formulate a discrete mathematical model to investigate the transmission of the SARS. A comparison theorem for the model has been established. The basic reproductive number for the comparison model has been calculated and used as a threshold to determine the asymptotic behavior of the model. We have used the data for SARS between April 20 and June 10, 2003 in China to estimate the epidemic parameters in the models. Numerical simulations have been carried out to show the transmission process for SARS in China and the simulation results match the statistical data well. The rapid decrease of the infected number per day per unquarantined SARS infection show that a high quarantine rate and early quarantine are crucial to the control of SARS. Our results in this paper give partial answers to the questions mentioned above, and can help to make assessments of control measures.

The paper is organized as follows. The discrete mathematical model for SARS transmission is formulated in Section 2 and the asymptotic behavior of the model is analyzed in Section 3. The simulations for different epidemic parameters are done to show SARS transmission and the influence of the parameters in Section 4. The dependence of the the basic reproductive number on the epidemic parameters is discussed, and suggestions on the interpretation of our simulations are given in Section 4.

2. MODEL FORMULATION

While epidemiologists are still working to understand SARS and to develop a treatment, mathematical models have been formulated and analyzed in order to help formulate control strategies until a treatment can be developed. By piecing together preliminary data on the infections and making use of accumulating case notifications, the quantitative assessment of the epidemic potential of SARS, and the effectiveness of control measures have been analyzed by Lipsitch *et al.* and Riley *et al.* [14,15]. Their main conclusion is that this new coronavirus is sufficiently transmissible to cause a very large epidemic if unchecked, but not so contagious as to be uncontrollable with good, basic public health measures. On the basis of several sources containing information on epidemiological, demographic, and clinical variables in Hong Kong, the key epidemiological time distributions from infection to onset, onset to admission, admission to death, and admission to discharge, and the relations between the SARS case fatality rate and patients' age have been estimated by Donnelly *et al.* [16]. By using global and regional data from the SARS epidemic a mathematical model on SARS transmission was set up, and the average properties extracted by Chowell *et al.* [17].

We formulate a discrete mathematical model to estimate the epidemic parameters, to predict the transmission of the disease, and to give assessment of the effect of the control measures. We

follow the basic idea and structure of mathematical modelling in epidemiology [18,19]. We divide the population into the following six classes, as follows.

(1) Susceptibles $S(t)$: members of the population who may become infected.
(2) Exposed $E(t)$: members of population infected by the SARS virus, in the incubation period, asymptomatic, possibly infectious (without infectivity or with very low infectivity).
(3) Infectives $I(t)$: members of the population who are infective with strong infectivity, but have not yet been quarantined.
(4) Quarantined $Q(t)$: members of the population who have been infected, and have not been diagnosed, but have been quarantined.
(5) Diagnosed $J(t)$: members of the population who are infective, have been diagnosed and have been quarantined.
(6) Recovered $R(t)$: members of the population who have recovered from the disease with full immunity against reinfection.

The variables $S(t)$, $E(t)$, $I(t)$, $Q(t)$, $J(t)$, and $R(t)$ are the numbers of the individuals in the six classes at time t, respectively. Since all the data of the SARS infection are now announced daily, it is natural for us to use a discrete epidemic model to describe the dynamics of the spread of SARS. We assume that the epidemic process operates on a much faster time scale than natural deaths, and assume that the only deaths are due to disease.

The number of exposed, infective, quarantined, diagnosed, and recovered members is very small compared to the number of susceptibles. For example, the population size of China is over 1.3 billion, while the cumulative number of diagnosed SARS cases is under 6000. We assume that all contacts sufficient to transmit infection by infectious members of the population are with susceptibles, neglecting contacts with exposed, infective, quarantined, recovered, and diagnosed members. Thus, all these contacts produce new infections, and we concentrate our modelling and analysis on exposed, infective, quarantined, diagnosed, and recovered members. This will have the effect of leading to a linear system model.

An individual infected by SARS virus enters the exposed class and is in the incubation period. The incubation period lasts two to 12 days [20]. Although it is not yet known whether individuals in the incubation period are able to transmit SARS, we suppose that they have some infectivity, but a lower infectivity than infectives. Some exposed individuals will enter the quarantined class as a result of prevention measures. The remaining exposed individuals will enter the infective class. Individuals in the quarantined and infective classes will enter the diagnosed class after obvious symptoms of SARS appear and they are diagnosed definitely. Diagnosed individuals either recover and enter the recovered class or die of the infection. The schematic representation of the individual flow between the different classes is shown in Figure 1.
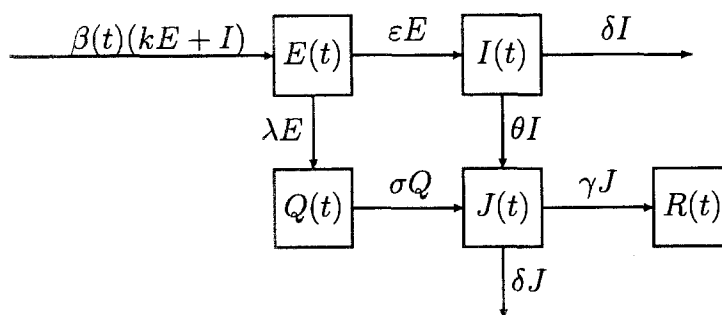

Figure 1. The flow of individuals among different classes. The new infected exposed is proportional to the sum $kE(t) + I(t)$. E-individuals move into the infective class and quarantined class at the rate ε and λ, respectively. Q-individuals moves to diagnosed class J at the rate σ. I-individuals moves to the diagnosed class J at the rate θ. J-individuals moves to the recovered class R at the rate γ. The individuals in I and J classes die at the rate δ.

From the transmission mechanics and the schematic representation in Figure 1, we obtain recurrence relations for the numbers of individuals in the five classes. The number of exposed members at time $t + 1$ is equal to the number of the exposed members at time t plus the newly infected members minus the individuals who move to the quarantined and infective classes. Similar arguments can be used to obtain the recurrence relations for the infectives, quarantined, diagnosed, and recovered members.

Therefore, we can formulate the following system of linear difference equations as a mathematical model using the general principles of epidemiological modelling [21,22].

$$
\begin{aligned}
E(t+1) &= E(t) + \beta(t)(kE(t) + I(t)) - (\varepsilon + \lambda)E(t), \\
I(t+1) &= I(t) + \varepsilon E(t) - (\delta + \theta)I(t), \\
Q(t+1) &= Q(t) + \lambda E(t) - \sigma Q(t), \\
J(t+1) &= J(t) + \theta I(t) + \sigma Q(t) - (\delta + \gamma)J(t), \\
R(t+1) &= R(t) + \gamma J(t),
\end{aligned}
\tag{1}
$$

$$
E(0) > 0, \qquad I(0) > 0, \qquad Q(0) > 0, \qquad J(0) > 0, \qquad R(0) > 0,
$$

where δ is the SARS induced death rate, γ is the recovery rate, ε is the transfer rate from exposed to infective class, λ is the transfer rate from exposed to quarantined class, σ is the transfer rate from quarantined to diagnosed class, θ is the transfer rate from infective to diagnosed class, k is the infectivity fraction for the exposed individuals compared with individuals in the infective class, and $\beta(t)$ is the transmission rate per day.

We make the following assumptions on the parameters of the discrete SARS model (1).

(A1) All the parameters are positive, and the following inequalities hold,

$$
0 < d + \varepsilon + \lambda < 1, \qquad 0 < \delta + \theta < 1, \qquad 0 < \sigma < 1, \qquad 0 < \delta + \gamma < 1.
$$

The epidemiological interpretation of these inequalities is that the transfer rates of individuals in classes E, I, Q, J, and R from time t to $t + 1$ is between 0 and 1.

(A2) The transmission rate function $\beta(t)$ is a continuous function bounded by β_0 and β^*, $\beta_0 \leq \beta(t) \leq \beta^*$. This inequality says that the transmission rate of an infective individual per day is bounded.

Define the vector,

$$
\vec{x}(t) = (E(t), I(t), Q(t), J(t), R(t))^\mathsf{T},
$$

and the matrix $A(\beta(t))$,

$$
\begin{bmatrix}
1 + k\beta(t) - (\varepsilon + \lambda) & \beta(t) & 0 & 0 \\
\varepsilon & 1 - (\delta + \theta) & 0 & 0 \\
\lambda & 0 & 1 - (\sigma) & 0 \\
0 & \theta & \sigma & 1 - (\delta + \gamma)
\end{bmatrix},
$$

where, T stands for the transpose of a vector. The vector form of the SARS model (1) is

$$
\vec{x}(t+1) = A(\beta(t))\,\vec{x}(t), \qquad \vec{x}(0) = \vec{x}_0 > \vec{0}.
\tag{2}
$$

From the recurrence relations of model (2), we can get obtain an explicit expression for the solution of the SARS model (2),

$$
\vec{x}(t) = A(\beta(t-1))\,A(\beta(t-2))\ldots A(\beta(1))\,A(\beta(0))\,\vec{x}(0)
\tag{3}
$$

and this gives the numbers of individuals in each class at each time once the parameters and initial values are determined.

3. THE DISEASE-FREE EQUILIBRIUM AND ITS STABILITY

There are many results for continuous epidemic models, but there has been little analysis of discrete epidemic models. Allen has studied the discrete SI, SIS, SIR epidemic models and found that the SI and SIR models are similar in behavior to their continuous analogues under some natural restrictions, but the SIS model can have more diverse behaviour [23]. Castillo-Chavez and Yakubu have studied discrete time SIS models which exhibit bistability over a wide range of parameter values [24,25]. Méndez and Fort investigated the dynamical evolution of discrete epidemic models by taking into account an intermediate population [26]. Allen and Thrasher formulated an age-dependent model for varicella and herpes zoster and the effects of various control strategies [27]. Hethcote and van Ark formulated discrete epidemic models to study HIV transmission in the United States [28]. Lesnoff *et al.* developed a seasonal population-dynamics Leslie matrix model to account for seasonal changes in demographics rates and to assess the effects of preventive medicine programs on the productivity of sheep flocks [29].

In this section, we give a brief analysis of the asymptotic behavior of the discrete SARS model (1). Because system (1) is linear, its stability properties are global.

There is only one equilibrium of the SARS model (1), namely, the disease-free equilibrium $P^0(0,0,0,0,0)$. From the expression for solution (3), we see that asymptotic stability of the disease free equilibrium is completely determined by the product of the matrices

$$A\left(\beta\left(t-1\right)\right)A\left(\beta\left(t-2\right)\right)\ldots A\left(\beta\left(1\right)\right)A\left(\beta\left(0\right)\right).$$

To analyze the product of matrices with time dependent elements, we need to establish the following comparison theorem.

THEOREM 1. *Assume that Hypotheses (A1) and (A2) hold. Let $\vec{u}(t)$, $\vec{x}(t)$, and $\vec{v}(t)$ be the solutions of the difference equations,*

$$\vec{u}\left(t+1\right)=A\left(\beta_0\right)\vec{u}\left(t\right),\qquad\vec{x}\left(t+1\right)=A\left(\beta\left(t\right)\right)\vec{x}\left(t\right),\qquad\text{and}\qquad\vec{v}\left(t+1\right)=A\left(\beta^*\right)\vec{v}\left(t\right),$$

with the same positive initial value $\vec{u}(0)=\vec{x}(0)=\vec{v}(0)\geq0$. Then, for any $t>0$,

$$\vec{u}\left(t\right)\leq\vec{x}\left(t\right)\leq\vec{v}\left(t\right).$$

PROOF. Let $\vec{u}(t)$, $\vec{x}(t)$, and $\vec{v}(t)$ be the solution of the difference equations with the same initial value

$$\begin{aligned}
\vec{u}\left(t+1\right)&=A\left(\beta_0\right)\vec{u}\left(t\right), & \vec{u}\left(0\right)&=\vec{x}_0>\vec{0},\\
\vec{x}\left(t+1\right)&=A\left(\beta\left(t\right)\right)\vec{x}\left(t\right), & \vec{x}\left(0\right)&=\vec{x}_0>\vec{0}, & (4)\\
\vec{v}\left(t+1\right)&=A\left(\beta^*\right)\vec{v}\left(t\right), & \vec{v}\left(0\right)&=\vec{x}_0>\vec{0}.
\end{aligned}$$

Hypotheses (A1) and (A2) imply that the solutions $\vec{u}(t)$, $\vec{x}(t)$, and $\vec{v}(t)$ are nonnegative, for all $t>0$, that is,

$$\vec{u}\left(t\right)\geq\vec{0},\qquad\vec{x}\left(t\right)\geq\vec{0},\qquad\vec{v}\left(t\right)\geq\vec{0}.$$

From the equations in (4), it follows that

$$\begin{aligned}
\vec{x}\left(1\right)-\vec{u}\left(1\right)&=\left[A\left(\beta\left(0\right)\right)-A\left(\beta_0\right)\right]\vec{x}_0\geq\vec{0},\\
\vec{v}\left(1\right)-\vec{x}\left(1\right)&=\left[A\left(\beta^*\right)-A\left(\beta\left(0\right)\right)\right]\vec{x}_0\geq\vec{0}.
\end{aligned}$$

That is,

$$\vec{u}\left(1\right)\leq\vec{x}\left(1\right)\leq\vec{v}\left(1\right).$$

Assume that $\vec{u}(t) \leq \vec{x}(t) \leq \vec{v}(t)$. By defining $\vec{\xi}(t) = \vec{x}(t) - \vec{u}(t) \geq \vec{0}$ and $\vec{\eta}(t) = \vec{v}(t) - \vec{x}(t) \geq \vec{0}$, we have

$$\vec{x}(t+1) - \vec{u}(t+1) = [A(\beta(t)) - A(\beta_0)]\vec{u}(t) + A(\beta(t))\vec{\xi}(t) \geq \vec{0},$$
$$\vec{v}(t+1) - \vec{x}(t+1) = [A(\beta^*) - A(\beta(t))]\vec{x}(t) + A(\beta^*)\vec{\eta}(t) \geq \vec{0}.$$

Hence, the theorem is proved by induction.

Theoretically, the asymptotic behavior of the nonautonomous linear SARS model (1) is completely determined by the product $A(\beta(t-1))A(\beta(t-2))\ldots A(\beta(1))A(\beta(0))$. In practice, the explicit expression of the product $A(\beta(t-1))A(\beta(t-2))\ldots A(\beta(1))A(\beta(0))$ is not easy to obtain. We use the following two comparison systems to control the solutions of the SARS model (1),

$$\vec{v}(t+1) = A(\beta^*)\vec{v}(t), \qquad \vec{v}(0) = \vec{x}_0 > \vec{0}, \tag{5}$$
$$\vec{u}(t+1) = A(\beta_0)\vec{u}(t), \qquad \vec{u}(0) = \vec{x}_0 > \vec{0}. \tag{6}$$

It follows from Theorem 1 that the solution of (5) provides an upper bound for the solution of SARS model (1), and the solution of (6) provides a lower bound for the solution of the SARS model (1). Since the two comparison systems (5) and (6) are linear systems with constant coefficients, their asymptotic behavior is much easier to determine than that of (1). The zero vector is the equilibrium solution of the two comparison systems.

Let us first determine the asymptotic behavior of the comparison model (5). The solution of the comparison model (5) is

$$\vec{v}(t) = [A(\beta^*)]^t \vec{x}_0 \geq \vec{0}. \tag{7}$$

The asymptotic behavior of solutions of the comparison model (5) is determined by the magnitude of the eigenvalues of the matrix $A(\beta^*)$. The eigenpolynomial of the matrix $A(\beta^*)$ is

$$f(\rho) = |A(\beta^*) - \rho I| = [\rho^2 - b\rho + c][\rho - (1 - \delta - \gamma)][\rho - (1 - \sigma)], \tag{8}$$

where

$$b = 2 + k\beta^* - (\varepsilon + \lambda + \delta + \theta),$$
$$c = (1 - \delta - \theta)(1 + k\beta^* - \varepsilon - \lambda) - \varepsilon\beta^*.$$

All four eigenvalues of $A(\beta^*)$ are real, and they are given by

$$\begin{aligned}
\rho_1 &= 1 - \sigma, \\
\rho_2 &= 1 - (\delta + \gamma), \\
\rho_3 &= \frac{1}{2}\left(b + \sqrt{b^2 - 4c}\right), \\
\rho_4 &= \frac{1}{2}\left(b - \sqrt{b^2 - 4c}\right),
\end{aligned} \tag{9}$$

where

$$b^2 - 4c = (k\beta^* + \delta + \theta - \varepsilon - \lambda)^2 + 4\varepsilon\beta^* > 0.$$

It is obvious that $0 < \rho_j < 1$ $(j = 1, 2)$. The stability of the disease free equilibrium is determined by the magnitude of the eigenvalues ρ_3 and ρ_4. We focus on the critical eigenvalues $\rho_3 = 1$ and $\rho_4 = -1$, where ρ_3 and ρ_4 are the solutions of the quadratic equation,

$$\rho^2 - b\rho + c = 0.$$

From the explicit expressions of ρ_3 and ρ_4, we see that they are continuous function of β^*. When $\beta^* = 0$, we obtain the roots

$$0 < \rho_3 = 1 - (\varepsilon + \lambda) < 1, \qquad \text{if } \delta + \theta \geq \varepsilon + \lambda,$$
$$0 < \rho_3 = 1 - (\delta + \theta) < 1, \qquad \text{if } \delta + \theta < \varepsilon + \lambda,$$
$$0 < \rho_4 = 1 - (\varepsilon + \lambda) < 1, \qquad \text{if } \delta + \theta < \varepsilon + \lambda,$$
$$0 < \rho_4 = 1 - (\delta + \theta) < 1, \qquad \text{if } \delta + \theta \geq \varepsilon + \lambda.$$

The fact $b^2 - 4c > 0$ implies that ρ_3 and ρ_4 are simple roots of the quadratic equation (10), and $2\rho_j = b \pm \sqrt{b^2 - 4c} \neq b(j = 3, 4)$. Differentiation of both sides of equation (10) with respect to β^* yields that

$$\frac{\partial \rho}{\partial \beta^*} = \frac{k\rho - k(1 - \delta - \theta) + \epsilon}{2\rho - b}.$$

In the critical cases $\rho_3 = 1$ and $\rho_4 = -1$, we have

$$\left. \frac{\partial \rho_3}{\partial \beta^*} \right|_{\rho_3 = 1} = \frac{k(\delta + \theta) + \epsilon}{\sqrt{b^2 - 4c}}, \qquad \left. \frac{\partial \rho_4}{\partial \beta^*} \right|_{\rho_4 = -1} = \frac{-k(2 - \delta - \theta) + \epsilon}{-\sqrt{b^2 - 4c}}.$$

The above equalities show that the root ρ_3 always increases with respect to β^* whenever $\rho_3 = 1$. This fact implies that there is only one critical value,

$$\beta^* = \frac{(\varepsilon + \lambda)(\delta + \theta)}{\varepsilon + k(\delta + \theta)} \triangleq \beta_1^*,$$

such that $0 < \rho_3 < 1$, if $\beta^* < \beta_1^*$, and $\rho_3 > 1$, if $\beta^* > \beta_1^*$. A similar argument implies that there is no critical value of β^* if $\varepsilon \leq k(2 - \delta - \theta)$, and there is only one critical value of β^* if $\varepsilon > k(2 - \delta - \theta)$,

$$\beta^* = \frac{4 + (1 - \delta - \theta)(1 - \varepsilon - \lambda) - (\varepsilon + \lambda + \delta + \theta)}{\varepsilon - k(2 - \delta - \theta)} \triangleq \beta_2^*,$$

such that $\rho_4 > -1$ if $\beta^* < \beta_2^*$, and $\rho_4 < -1$ if $\beta^* > \beta_2^*$. Under the condition, $\varepsilon > k(2 - \delta - \theta)$, an algebraic calculation gives

$$\beta_2^* - \beta_1^* = \frac{[4 - 2(\varepsilon + \lambda + \delta + \theta)][\varepsilon + k(\delta + \theta)] + 2k(\varepsilon + \lambda)(\delta + \theta)}{[\varepsilon + k(\delta + \theta)][\varepsilon + k(\delta + \theta) - 2k]} > 0.$$

The above inequality, $\beta_2^* > \beta_1^*$, implies that the root ρ_3 will increases to 1 before the root ρ_4 decreases to -1 as the transmission rate β^* increases from 0 to infinity, that is, the disease-free equilibrium will lose its stability when $\rho_3 = 1$.

Define the basic reproductive number

$$R_0 = \frac{\beta^*(\varepsilon + k(\delta + \theta))}{(\varepsilon + \lambda)(\delta + \theta)}.$$

The basic reproductive number R_0 can be written as

$$R_0 = \beta^* \times \left(k \times \frac{1}{\varepsilon + \lambda} + \frac{\varepsilon}{\varepsilon + \lambda} \times \frac{1}{\delta + \theta} \right),$$

where β^* is the number of the new infections produced by an infective individual per day, k is the infectivity fraction of an individual in the exposed class compared with an individual in infective class, $1/(\varepsilon + \lambda)$ is the average time that an exposed member remains in that class, $\varepsilon/(\varepsilon + \lambda)$ is the fraction of exposed members who move to the infective class, and $1/(\delta + \theta)$ is the average time that an infective individual remains in the class I. The epidemiological interpretation of

the basic reproductive number is that R_0 is the expected number of secondary infectious cases generated by an average infected individual during the infective period in an entirely susceptible population. This quantity determines the potential for an infectious agent to start an outbreak, and the extent of transmission in the absence of control measures.

It follows from the expressions for the eigenvalues that $\rho_3 < 1$, if $R_0 < 1$, and $\rho_3 > 1$, if $R_0 > 1$. Since the four eigenvalues of the matrix $A(\beta^*)$ are real and simple (or double but with two independent eigenvectors), the four eigenvectors corresponding to the 4 eigenvalues form a basis of the four-dimensional Euclidean space $\mathbf{R}^4$. Any vector in $\mathbf{R}^4$ can be expressed as a linear combination of those eigenvectors.

In particular,

$$\vec{x}_0 = c_1 \vec{v}_1 + c_2 \vec{v}_2 + c_3 \vec{v}_3 + c_4 \vec{v}_4, \tag{11}$$

where $\vec{v}_j$ is the eigenvector corresponding to the eigenvalue,

$$\rho_j \qquad (j = 1, 2, 3, 4),$$

and

$$\vec{v}_3 = \begin{bmatrix} 1 \\ \dfrac{\varepsilon}{\delta + \theta - 1 + \rho_3} \\ \dfrac{\lambda}{\sigma - 1 + \rho_3} \\ \dfrac{1}{\delta + \gamma - 1 + \rho_3} \left(\dfrac{\theta \varepsilon}{\delta + \theta - 1 + \rho_3} + \dfrac{\sigma \lambda}{\sigma - 1 + \rho_3} \right) \end{bmatrix}.$$

By applying $A(\beta^*)$ to the expression for $\vec{x}_0$, it follows from (7) that

$$\vec{v}(t) = c_1 \rho_1^t \vec{v}_1 + c_2 \rho_2^t \vec{v}_2 + c_3 \rho_3^t \vec{v}_3 + c_4 \rho_4^t \vec{v}_4. \tag{12}$$

It follows from the expression $\vec{v}(t)$ in (12) that

$$\lim_{t \to \infty} \vec{v}(t) = \vec{0}, \qquad \text{if } \rho_3 < 1,$$
$$\lim_{t \to \infty} \vec{v}(t) = \infty, \qquad \text{if } \rho_3 > 1,$$
$$\lim_{t \to \infty} \vec{v}(t) = c_4 \vec{v}_4, \qquad \text{if } \rho_3 = 1,$$

where c_3 is found from the equation (11). The case $\beta^* = \beta_1^*$ is the critical value, for which the eigenvector $\vec{v}_3$ corresponds to the eigenvalue $\rho_3 = 1$.

The above analysis can be applied to the model (6) to obtain a similar result. By using the comparison theorem, we obtain the following stability theorem.

THEOREM 2. *The disease-free equilibrium of the SARS model (1) is globally asymptotically stable if $\beta^* < \beta_1^*$ and unstable if $\beta_0 > \beta_1^*$.*

The stability in Theorem 2 is easily proved using the comparison theorem and the fact that

$$\rho_3 < 1 \qquad (\rho_3 = 1, \rho_3 > 1)$$

is equivalent to

$$R_0 < 1 \qquad (R_0 = 1, R_0 > 1).$$

4. NUMERICAL SIMULATION

Although the disease is not yet well understood, much data has been collected during the SARS epidemic. We use statistical data for SARS in China to estimate the parameters and do numerical simulations on the basis of the discrete SARS model (1). The average incubation period is taken as six days, divided into two parts, the first three days in the exposed class with less infectivity, and the last three days with more infectivity. The fraction k is taken as 0.1. From the statistical data, we estimate that a fraction 3/5 of the diagnosed SARS cases came from SARS suspected individuals, who had been quarantined and treated in hospitals, and a fraction 2/5 of the diagnosed SARS cases came from unquarantined individuals. We assume that a fraction 3/5 of the exposed individuals have been quarantined after they left the exposed class due to the stringent control measures. The transfer rate from the exposed class to the quarantined class is taken as a fraction (1/3) (3/5), while 2/5 of the exposed individuals still have not been quarantined after they left the exposed class before obvious SARS symptoms appeared and they were diagnosed. The transfer rate from the exposed class to the infective class is taken as (1/3) (2/5). Individuals in the infective and quarantined classes will enter the diagnosed class after three days on average and individuals in the diagnosed class will recover or die after three weeks in hospital on average. The SARS induced death rate is taken to be (15/100) (1/21). Thus, the values of parameters are estimated as follows:

$$\epsilon = (1/3)(2/5), \qquad \lambda = (1/3)(3/5), \qquad \delta = (15/100)(1/21),$$
$$\theta = 1/3, \qquad \sigma = 1/3, \qquad \gamma = 1/21, \qquad k = 0.1.$$

The infection rate $\beta(t)$ is the most important parameter in the model and model predictions are very sensitive to changes in the infection rate. From the statistical data we know that the infection rate $\beta(t)$ is a decreasing function after stringent control measures went into effect and cut down the infection gradually. We try to fit the function $\beta(t)$ by repeated numerical simulation and choose a fractional function of t,

$$\beta(t) = \frac{31 + t}{22 + 5t}.$$

From the statistical data we estimate the initial values as of April 21, 2003,

$$E(0) = 477, \qquad I(0) = 286, \qquad Q(0) = 191, \qquad J(0) = 848, \qquad R(0) = 1213.$$

Using MATLAB, we obtain the simulation result shown in Figure 2[1].

In Figure 2, the dotted line is the statistical data [30], the continuous curve is the prediction of the model. The infection rate is estimated from the actual statistical data to be

$$\beta(t) = \frac{31 + t}{22 + 5t}.$$

We see that the number of the diagnosed SARS individuals (who are staying in hospitals) increases rapidly for the first three weeks and reaches a peak on May 11. The predicted number on May 11 is 3,083. After May 11, the number decreases rapidly. This shows the effectiveness of the stringent control measures adopted in China. The prediction curve matches the actual data well.

In order to investigate the influence of the infection rate $\beta(t)$, we do numerical simulation by taking $\beta(t)$ to be three different constants. In Figure 3, $\beta(t)$ is taken to be 0.7, slightly above the critical value $\beta_1^* = 0.6781$. The simulation results shows that the number of diagnosed SARS cases was below the actual data before May 15, but it continues to increase and reaches 28,060 one year later. In Figure 4, $\beta(t)$ is taken to be critical value, $\beta_1^* = 0.6781$. The simulation results

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[1]In the figures, from Figures 2–10, the horizontal axis is the time measured in days starting from April 21, 2003.
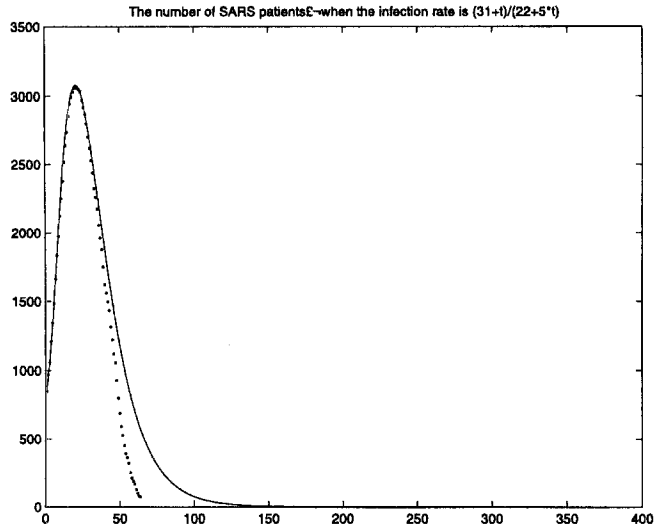
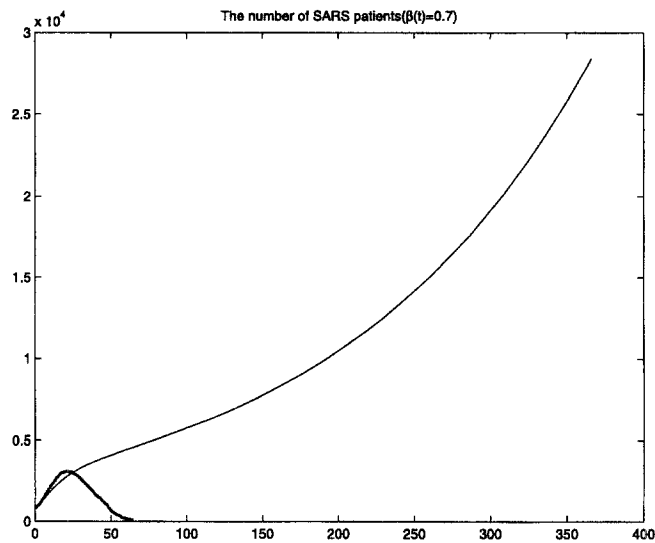Figure 2. The prediction and actual diagnosed SARS cases in China.

Figure 3. The prediction and actual diagnosed SARS cases in China $\beta(t) = 0.7$.
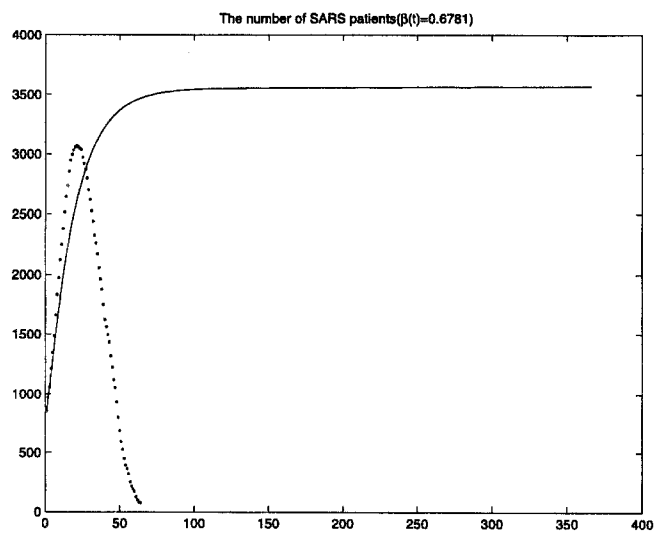

Figure 4. The prediction and actual diagnosed SARS cases in China $\beta(t) = 0.6781$.
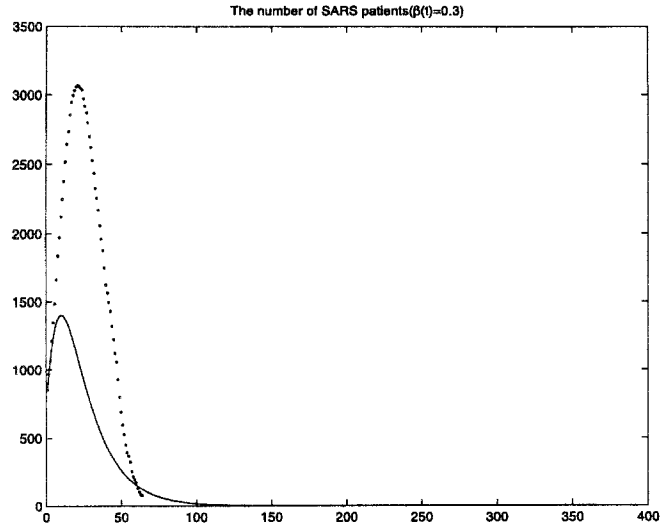
Figure 5. The prediction and actual diagnosed SARS cases in China $\beta(t) = 0.3$.
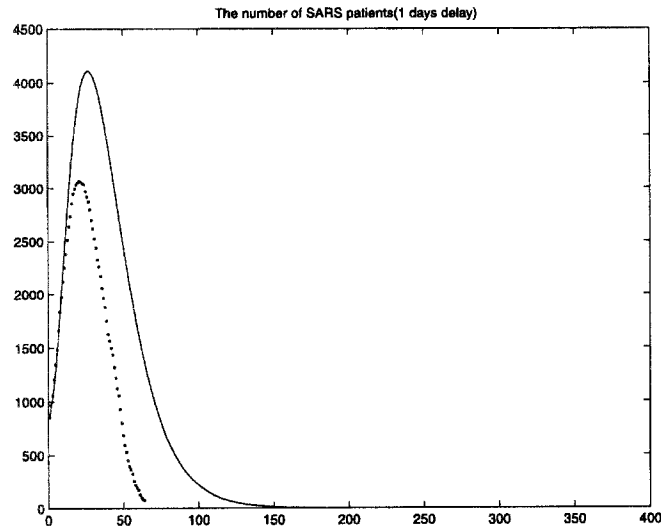

Figure 6. The prediction and actual diagnosed SARS cases in China $\theta(t) = 1/4$.
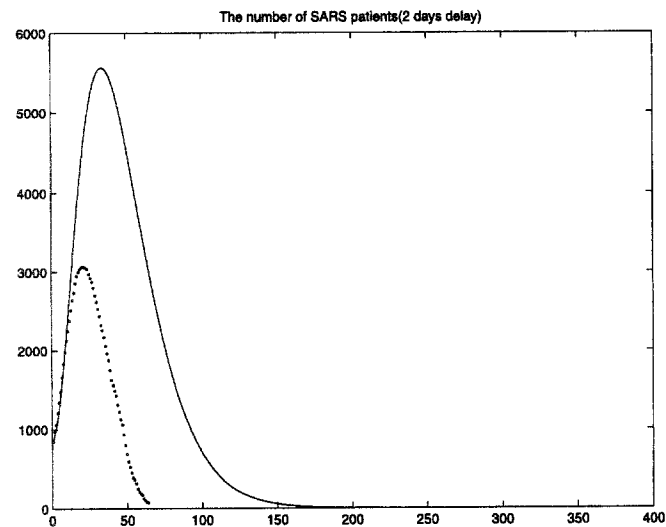

Figure 7. The prediction and actual diagnosed SARS cases in China $\theta(t) = 1/5$.
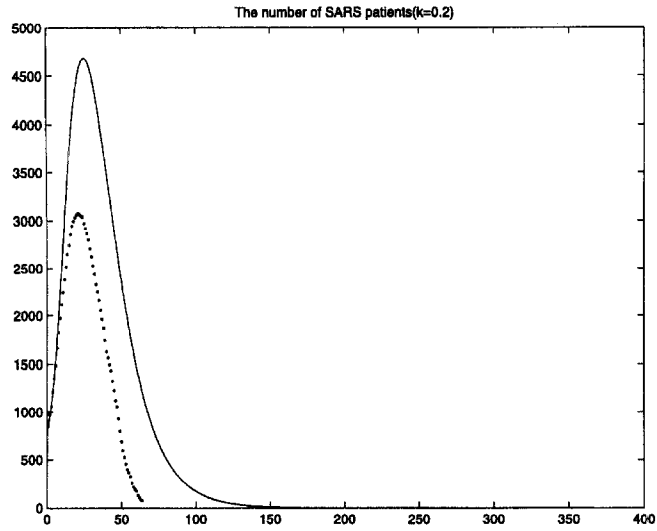
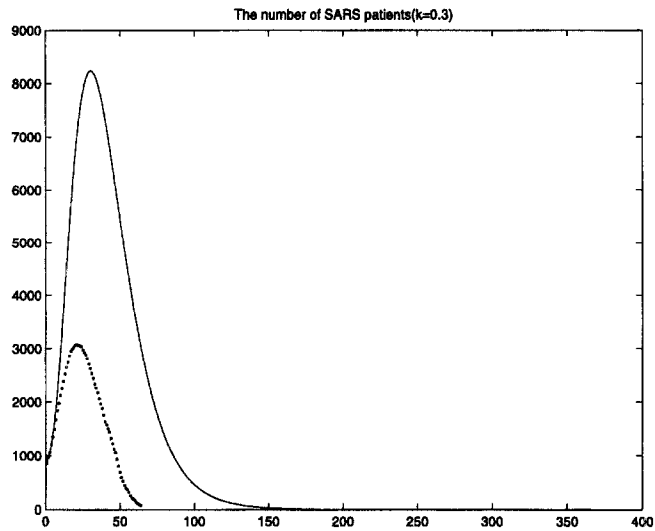Figure 8. The prediction and actual diagnosed SARS cases in China $k = 0.2$.

Figure 9. The prediction and actual diagnosed SARS cases in China $k = 0.3$.
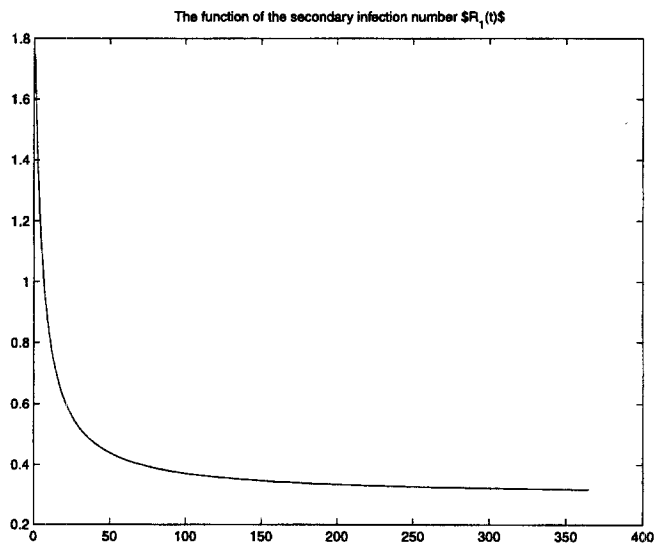

Figure 10. Decline of the secondary reproductive number R^*.

shows that the number of diagnosed SARS cases continues to increase and reaches a stable value, $J = 3548$. In Figure 5, $\beta(t)$ is taken to be 0.3, which is well below the critical value, $\beta_1^* = 0.6781$. The simulation result shows that the number of diagnosed SARS cases is always less than the actual data. The peak appears at the end of April with the maximum number,

$$J = 1403.$$

Next, we investigate the influence of delaying quarantine by fixing the infection rate,

$$\beta(t) = \frac{31 + t}{22 + 5t},$$

and taking the other parameters the same as above. We vary the transfer rate θ to obtain different results. In Figure 6, the transfer rate θ is taken to be $1/4$, that is, individuals stay in infective class one day longer. The simulation result shows that the peak will move to May 17, with maximum number 4,111. Compared with the result shown in Figure 2, the peak is six days later, and 1028 individuals higher. In Figure 7 the transfer rate θ is taken to be $1/5$, that is, individuals stay in infective class two days longer. The simulation result shows that the peak will move to May 24, with maximum number 5,561. Compared with the result shown in Figure 2, the peak is 13 days later, and 2,478 individuals. The simulation results indicate that timely quarantine is significant for the control of SARS transmission.

Finally, we investigate the influence of k, the infectivity fraction of individuals in the class E compared to individuals in class I on SARS transmission. In the prediction of Figure 2, the proportion is 0.1. Here, we vary the proportion to be 0.2 and 0.3 (See Figures 8 and 9), and leave the other parameters unchanged. In Figure 8, k is 0.2, and we see that the number of diagnosed SARS cases is higher than that in Figure 2. The peak is reached on May 15 with maximum number 4,682. The number of diagnosed SARS cases at the peak is 1,599 higher than that in Figure 2. In Figure 9, k is 0.3 and we see that the number of diagnosed SARS cases is much higher than that in Figure 2. The peak is reached on May 20, with maximum number 8,227. The number of diagnosed SARS cases at the peak is 5,144 more than that in Figure 2.

Similar ideas and further simulations can be used to study the influence of other factors on the SARS transmission.

The simulation results in Figures 8 and 9 shows that infections transmitted by individuals in the exposed class can have great influence on SARS transmission. This indicates that determination of the infectivity for exposed individuals is essential for making good predictions. Early identification, early tracing and early quarantine are key factors in coping with the spread of SARS.

5. DISCUSSION

We have formulated an EIQJR model to study the spread of SARS in China. The dynamical behavior of the model is analyzed, the basic reproductive number is determined and used as a threshold for the spread of the SARS epidemic. Numerical simulations have been done for our model of the transmission of SARS in China after the parameters and the initial values have been estimated and the prediction curve fits the actual data well. The modelling, analysis and simulations in this paper form a simple and rough approach to the complete research of SARS transmission.

Similar to other epidemic models the basic reproductive number R_0 plays a crucial rule in the spread of SARS. However, since we are using a time-dependent infection rate $\beta(t)$ in our model, we define a secondary reproductive number

$$R^* = \frac{\beta(t)(\varepsilon + k(d + \delta + \theta))}{(d + \varepsilon + \lambda)(d + \delta + \theta)},$$

which is time-dependent and which we use in place of R_0 in describing the course of the epidemic. From the estimates based on the data in China, we found that the secondary reproductive number R^* decreases with time due to the effect of the control measures. The simulated secondary reproductive number R^* is shown in Figure 10. From Figure 10, we see that this reproductive number is 1.7478 on April 20, 1.0493 on April 25, 0.9331 on April 26, 0.8044 on April 30, 0.5530 on May 15, 0.4640 on May 31, and 0.4227 on June 15. The secondary reproductive number R^* is quite large on April 20 since few prevention measures had been taken before that day. After April 20, various stringent and drastic preventive measures were taken across the nation. Those control measures took effect gradually and the secondary reproductive number R^* decreased rapidly in late April and early May, dropping to 0.9331 on April 26, and the number of daily reported SARS diagnosed cases began to decrease in early May.

From the expression for the basic reproductive number R_0, we see that R_0 increases with k and β, and decreases with θ. Thus, increases in β and k, and an increase of the period in the infective class all would contribute to an increase in the basic reproductive number. In a similar way, we can study the influence of changes in the other parameters on the basic reproductive number. In order to reduce the infection, it is necessary to bring the secondary reproductive number below 1 and the smaller the secondary reproductive number, the more rapid the decrease of the disease. Our suggestion is to identify and quarantine SARS infected persons as early as possible.

SARS transmission is a complicated problem and our analysis is based on a simple model. Many more factors should be take into account to develop a more accurate model, but our simple model is sufficiently accurate to point to suitable control measures.

We have not considered the fact that numerous cases of infections to health-care workers were reported in the early stages of the spread. Infected doctors and nurses account for roughly a quarter of the SARS cases in China before the middle of April. These health care workers have close contact with infectives and form a high risk groups. How to include SARS transmission in health care workers in our model is an important question and it would be important to learn what new phenomena might appear if this factor was considered.

Different quarantine and various stringent control measure have been used in coping with SARS transmission in China. How may we describe the effect and assess the effectiveness of these measures in a model? For example, if a person is diagnosed as SARS infected or suspected, how many directly or indirectly contacted people should be quarantined in their homes or in hospital?

China is a vast country with a huge population and SARS transmission is different from city to city and province to province. For most cities and provinces there are very few SARS cases. Should equally stringent control measures be taken over the entire nation or should the stringency of the measures taken depend on the severity of the outbreak? It would be valuable to formulate a mathematical model to describe SARS transmission for those cities or provinces with few reported cases? We hope that more practical and applicable models will be formulated for the prediction and understanding of the SARS transmission. The goal would be to develop a strategy for coping with any future serious infectious disease.

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