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Research article

An SIHR epidemic model of the COVID-19 with general population-size dependent contact rate

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Abstract: Corona Virus Disease 2019 (COVID-19) which was firstly reported in Wuhan city last December, and then spread throughout the country rapidly. In this paper, we propose an SIHR model that predicts the course of the epidemic to help plan an effective control strategy. The values of parameters in the model are estimated on the basis of fitting to the reported data of COVID-19 from February 5 to March 17, 2020, in Hubei province. The results showed that (i) the peak of total confirmed cases will arrive around late February of 2020, (ii) the cumulative number of confirmed cases to be around 68,000 cases, (iii) the disease will end in mid-May of 2020. All these findings are consistent with the actual situation of Hubei province. Based on the empirical results, it is recommended to strengthen community closures and increase medical resources, which is the key to controlling the spread of COVID-19 in Hubei province.

Keywords: COVID-19; generalized SIHR model; infection prevention and control; parameter estimation; expected peak date
Mathematics Subject Classification: 92D30, 34D05

1. Introduction

COVID-19 is an emerging infectious disease caused by a novel coronavirus. Since its strong infectivity has caused serious problems on the lives and economy in all over the world. For instance, it has caused an epidemic outbreak with more than 7,742,900 confirmed cases and 427,400 reported deaths worldwide, as of June 13 2020 [1], and during the outbreak of COVID-19, China is imposing a more massive quarantine [2,3], such as, limiting or stopping crowds, closing schools, remote working, lockdown, isolation of close contacts tracked people at home, and so on. Consequently, the spread mechanisms and control strategies of COVID-19 have become a worldwide problem to be solved. During this anti-epidemic battle, besides medical and biological research, theoretical studies based

on either statistics or mathematical modeling may also play a non-negligible role in understanding the epidemic characteristics of the outbreak, in forecasting the inflection point and ending time, and in deciding the measures to curb the spreading. For instance, Alberti and Faranda [4] focused on statistical predictions of COVID-19 infections performed by fitting asymptotic distributions to actual data. By taking as a case-study the epidemic evolution of total COVID-19 infections in Chinese provinces and Italian regions, they found that there was a very large uncertainty in predictions the trend of disease spread at the early stages of the epidemic growth, however those uncertainties significantly reduce after the peak of the epidemic is reached. Bertozzi et al. [5] proposed that three regional scale models to fit and forecast the trend of COVID-19, moreover they evaluated the risk of relaxing nonpharmaceutical public health interventions in the absence of a vaccine or antiviral therapies. In addition, Faranda et al. [6] discussed the statistical and dynamical sensitivity of asymptotic estimates of COVID-19 infections when performed at the early stages of the epidemics, showed that dynamical and statistical modeling should focus on limited stages of the epidemics and restrict the analysis to specific regions. We also refer the readers to Tang et al. [7,8], He et al. [9], Lin et al. [10] and the references therein for the studying of the spread of COVID-19.

In modelling of the COVID-19, the incidence of the disease is the number of new cases per unit time and plays a crucial role in the study of the diseases, in most of the literature [11–15], the adequate contact rate frequently takes two forms, the bilinear incidence rate βIS and standard incidence rate $\beta\frac{S}{N}I$, respectively, where I, S and N represent respectively the numbers of susceptible, infective and the total population, β is the transmission rate. In fact, both of which adequate contact rates respectively be suitable for two extreme cases for the numbers of total population N being very small and very large. Since the number of contacts made by an infective within a given unit of time should increase as N increases, when N is not too large. But when N is quite large, the number of contacts made by an infective within a given unit of time should be limited as N increases. To improve such limitation, Zhang et al. in [16] formulated a general incidence rate $\beta(N)SI$, where $\beta(N)$ satisfies the following assumptions:

(H1) $\beta(\cdot) : \mathbb{R}_+ \to \mathbb{R}_+$.

(H2) $\beta'(x) \leq 0$ and $(\beta(x)x)' \geq 0$, where $\beta'(x)$ and $(\beta(x)x)'$ represent respectively the derivative of the function $\beta(x)$ and $(\beta(x)x)'$.

Clearly, the incidence function $\beta(N)$ generalizes many common forms such as $\beta(N) = \beta$, $\beta(N) = \frac{\beta}{N}$, $\beta(N) = N^\alpha$ in [17], where $\alpha \in (-1, 0)$, $\beta(N) = \frac{\beta}{1+bN}$ in [18], $\beta(N) = \frac{\beta}{1+bN+\sqrt{1+2bN}}$ in [19,20].

Since the inability to quickly produce highly effective vaccines, quarantine or treatment on the confirmed and suspected cases was considered as the most effective method in controlling the spread of COVID-19 and as soon as possible eliminate epidemic disease. In generally, the infectious cases are divided into two subpopulations: non-confirmed cases and confirmed cases. The non-confirmed refer to groups that have been infected and infectious but have not been confirmed by medical institutions. Once the non-confirmed cases after taking Nucleic acid test positive, then the cases become confirmed cases and will be treated in hospital and isolate from the infection of the epidemic. In this paper, we

will consider the following SIHR compartment model

$$\begin{cases} \frac{dS}{dt} = A - \beta(N)SI - \mu S, \\ \frac{dI}{dt} = \beta(N)SI - (\gamma + \delta + \mu + \mu_1)I, \\ \frac{dH}{dt} = \delta I - (m + \mu + \mu_2)H, \\ \frac{dR}{dt} = \gamma I + mH - \mu R, \end{cases} \tag{1.1}$$

where H and R represent respectively the numbers of hospitalized (confirmed) and recovered individuals, A is the recruitment rate of the population, μ is the natural death rate, γ is the natural recovery rate. δ is the confirmation rate from the infected population to confirmed case. μ_1, μ_2 are the extra disease-related death rate constant in compartments I and H respectively. m is transform rate from the confirmed population to removed population.

The main focus of this article is to study the dynamics of the general SIHR model with general population-size dependent contact rate, in model (1.1). The rest of this article is organized as follows: In Section 2, we present a qualitative analysis to model (1.1). Specifically, we show that the disease-free equilibrium is globally asymptotically stable if the basic reproduction number is less than unity; and if the basic reproduction number is greater than unity, the model admits a unique endemic equilibrium which is locally asymptotically stable. In Section 3, we make full use of the existing reported data of COVID-19 cases from February 5 to March 17, 2020, in Hubei province, to estimate the parameters of model (1.1) by least square method. Finally, in Section 4, we give a brief discussion and the summary of the main results.

2. The dynamics of model (1.1)

In this section we study the dynamics of model (1.1), and the proof of all the theorems are shown in Appendix A. A straightforward computation shows that model (1.1) is continuous and Lipschizian in $\mathbb{R}^4_+$. From the existence and uniqueness of the solution of the ordinary differential equation, there exists a unique solution of model (1.1) for any initial value $(S(0), I(0), H(0), R(0)) \in \mathbb{R}^4_+$. From the second equation in (1.1) we have $\frac{dI}{dt} = \beta(N)SI - (\gamma + \delta + \mu + \mu_1)I$, then we can get

$$I(t) = I(0) \exp\left(\int_0^t \Big(\beta(N(\tau))S(\tau) - (\gamma + \delta + \mu + \mu_1)\Big) d\tau \right),$$

therefore $I(t) \geq 0$ for all $t \geq 0$ and $I(0) > 0$. Then we have $\frac{dH}{dt} \geq -(m + \mu + \mu_2)H$, similarly, we have $H(t) \geq 0$ for all $t \geq 0$ and $H(0) > 0$. In the same way, one can get that $R(t) \geq 0$ and $S(t) \geq 0$ for all $t \geq 0$, $R(0) > 0$ and $S(0) > 0$.

By summing all the equations in model (1.1) we can get that the total population $N(t) = S(t) + I(t) + H(t) + R(t)$ which satisfies $\frac{dN}{dt} = A - \mu N - \mu_1 I - \mu_2 H$. Let

$$\Gamma = \left\{ (S, I, H, R) : \frac{A}{\mu + \mu_1 + \mu_2} \leq S + I + H + R \leq \frac{A}{\mu},\ S \geq 0, I \geq 0, H \geq 0, \text{ and } R \geq 0 \right\}. \tag{2.1}$$

It is obvious that Γ is positively invariant of model (1.1). Now we consider the following model:

$$\begin{cases} \frac{dN}{dt} = A - \mu N - \mu_1 I - \mu_2 H, \\ \frac{dI}{dt} = \beta(N)(N - I - H - R)I - (\gamma + \delta + \mu + \mu_1)I, \\ \frac{dH}{dt} = \delta I - (m + \mu + \mu_2)H \\ \frac{dR}{dt} = \gamma I + mH - \mu R. \end{cases} \tag{2.2}$$

It is easy to see that model (2.2) is equivalent to model (1.1). One can get that the positively invariant region of model (2.2)

$$\widehat{\Gamma} = \left\{(N, I, H, R) : \frac{A}{\mu + \mu_1 + \mu_2} \leq N \leq \frac{A}{\mu},\ 0 \leq I, 0 \leq H, 0 \leq R \text{ and } 0 \leq I + H + R \leq N\right\}. \tag{2.3}$$

Hence, in this section, we will analyze model (2.2) in the positively invariant $\widehat{\Gamma}$.

First, we compute that the basic reproduction number

$$R_0 = \frac{A\beta(\frac{A}{\mu})}{\mu(\gamma + \delta + \mu + \mu_1)}. \tag{2.4}$$

by using the next generation matrix theory [11, 21]. Then we immediately get a standard result for model (2.2).

Theorem 2.1. *The disease-free equilibrium $E_0 = (\frac{A}{\mu}, 0, 0, 0)$ of model* (2.2) *always exits. Moreover, it is locally asymptotically stable if $R_0 < 1$.*

Next, we will investigate the existence and the uniqueness of the positive equilibrium of model (2.2). For convenience, let us introduce some notations as follows:

$$\ell_1 = \frac{\delta}{m + \mu + \mu_2} > 0,\ \ell_2 = \frac{\gamma + m\ell_1}{\mu} > 0,\ \ell_3 = \frac{1}{\mu_1 + \mu_2\ell_4} > 0. \tag{2.5}$$

Theorem 2.2. *If $R_0 > 1$, then model* (2.2) *has a unique endemic equilibrium $E^* = (N^*, I^*, H^*, R^*)$, where $I^* = \ell_3(A - \mu N^*)$, $H^* = \ell_1\ell_3(A - \mu N^*)$ $R^* = \ell_2\ell_3(A - \mu N^*)$.*

Theorem 2.1 show that the disease-free equilibrium of model (2.2) is local stability if $R_0 < 1$. And then, we will focus on that the disease-free equilibrium is globally asymptotically stable under the same condition.

Theorem 2.3. *If $R_0 < 1$, the disease-free equilibrium $E_0 = (\frac{A}{\mu}, 0, 0, 0)$ of model* (2.2) *is globally asymptotically stable.*

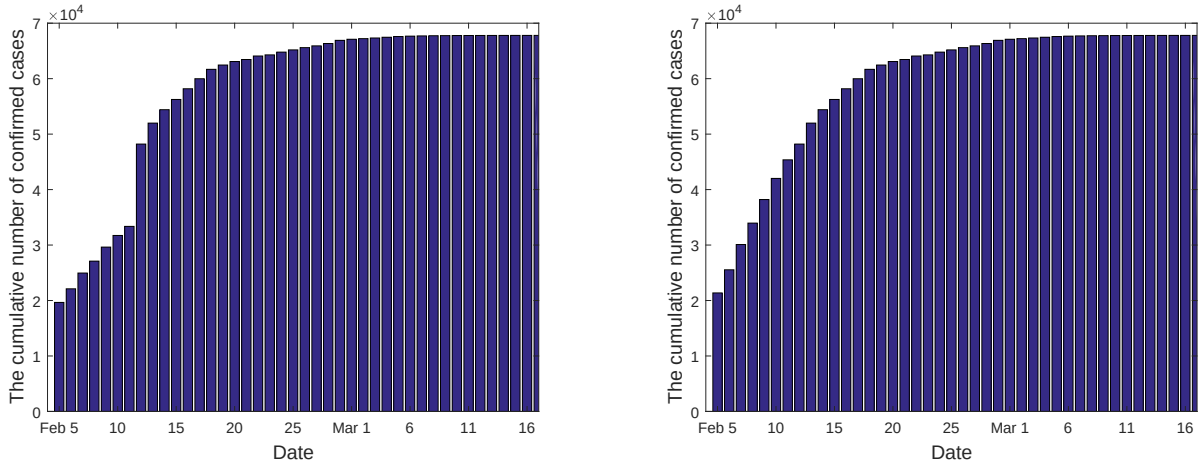
In the following theorem, we show that the stability of endemic equilibrium E^*.

Theorem 2.4. *If $R_0 > 1$, the endemic equilibrium $E^* = (N^*, I^*, H^*, R^*)$ of model* (2.2) *is locally asymptotically stable.*

3. Fitting results and control for the COVID-19 in Hubei province

In this section, model (1.1) with the incidence function $\beta(N) = \frac{\beta}{N}$ (which satisfies the assumptions (H1) and (H2)) is applied to analyze the characteristics of COVID-19 in Hubei province, China. Since Hubei government adopted the measure of lockdown on January 25 2020, the people can hardly leave or return Hubei. In this case, we assume the parameters $A = \mu = \mu_1 = \mu_2 = 0$ except for the other specification.

It is worth noting that, on February 12, 2020, Hubei province change the diagnosed approaches, which leads to the cumulative confirmed cases has increased 14840 on that day [1]. Compared with the increment of confirmed cases on February 11, the increment of confirmed cases on February 12 exceeded around 12000. This is mainly due to the fact that the early stage of the outbreak, the amounts of reagents used for the detection of nucleic acids in patients are insufficient, and many suspected cases are not included in the confirmed population in time. In order to better fit model (1.1) with the COVID-19 data in Hubei, we first need to revise the data for the data from February 5 to February 11 (the revised data are 21369, 25541, 30096, 33957, 38202, 42014, 45366 respectively), so that the calibrated data can be used to obtain the values of parameters in the model. Figure 1 gives the revised data and real data of the cumulative number of confirmed cases on February 5 to March 17.



(a) Raw data (b) Revised data

Figure 1. Comparison between reported data and revised data of cumulative confirmed cases of COVID-19 in Hubei province.

The total populations of Hubei province is about 59170000, therefore, the initial value of the susceptible population in model (1.1) is taken as 59170000. According to the reported cases about COVID-19 infection at February 5 and the revised data, one can see that $R(0) = 633$, $H(0) = 20736$. Then, based on the cumulative number of confirmed cases from February 5 to March 17, 2020, in Hubei province, using the least square method we estimate the initial values $S(0) = 59118631$, $I(0) = 30000$, and the parameter values

$$\beta = 0.0741,\ \gamma = 0.0185,\ \delta = 0.1836 \text{ and } m = 0.0667. \tag{3.1}$$

The model parameters fitted to the data of the cumulative number of confirmed cases is shown in Figure

2 (a). It is clear that the prediction is nearly full agreement with real data, which also well validates the accuracy of proposed model. As shown in Figure 2, the peak of total confirmed cases will reach around late February of 2020, the total number of confirmed cases is predicted to be around 68,000 cases, and the disease will end in mid-May of 2020, if the Hubei province government remains their control policy, such as city-wide lockdown and suspension of works and classes.

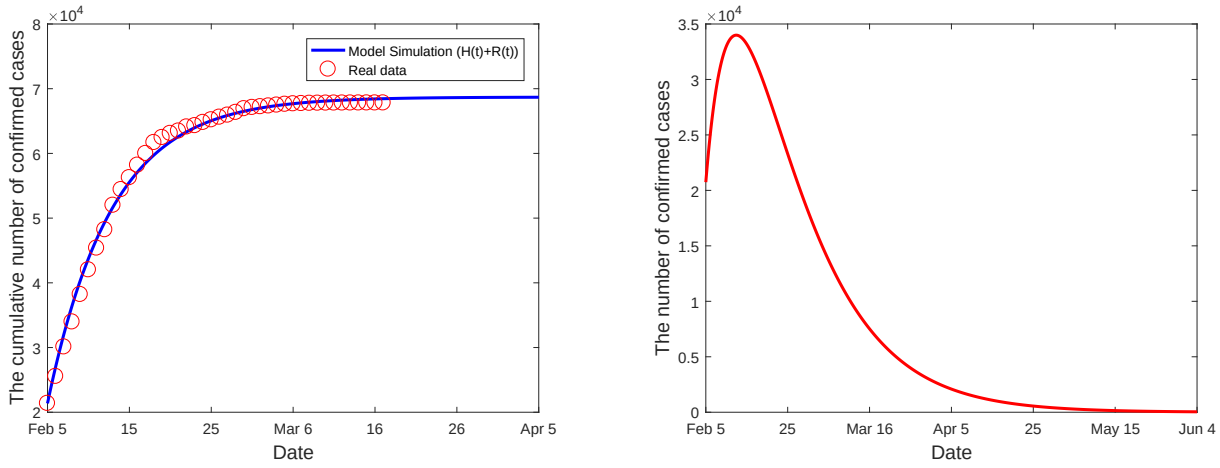


Figure 2. (a) The simulation time series and real data of the cumulative number of confirmed cases in Hubei province. (b) The evolution of the number of confirmed cases in Hubei province.

Next we focus on the effects of the choice of the time intervals to the fitting result.

- Based on the data from February 5 to February 11, the fitting result as shown in the green dotted line of Figure 3. The result shows that the cumulative number of confirmed cases is overestimated by around 109.4%.
- According to the data from February 12 to February 18, the fitting result as shown in the carmine dotted line of Figure 3. The result shows that the cumulative number of confirmed cases is overestimated by around 31.3%.
- On the basis of the data from February 5 to February 17, the fitting result as shown in the black dotted line of Figure 3. The result shows that the cumulative number of confirmed cases is overestimated by around 26.5%.

These results showed that the data from the mature stage of the epidemic growth could allow to obtain more stable fits.

In later December 2019, an outbreak of the novel COVID-19 began in Wuhan, and spread throughout the country rapidly. Then the Chinese government has taken many efficacious strategies (such as closing community, increasing medical resource) on January 23, 2020 to limit the spread of the epidemic. The closing community will decrease the transmission rate β of COVID-19, and the laboratory diagnosis rate δ will increase with the increase of medical resources, this is mainly due to the fact that more suspected cases will receive better medical care and have much lower chances to spread virus. To examine and evaluate the potential efficacy of these strategies, we conducted a sensitivity analysis of two vital model parameters β and δ.

- For the fixed $\beta = 0.0741$, the predicted cumulative number of confirmed cases will decrease and the expected peak date will be earlier as δ increases. For example, for $\beta = 0.0741$ and $\delta = 0.45$, the predicted cumulative number of confirmed cases are about 56,000, and the expected peak date is about Feb 15 (See Figure 4).
- For the fixed $\delta = 0.1836$, the total number of confirmed cases will increase and the expected peak date will delay as β increases. For example, for $\delta = 0.1836$ and $\beta = 0.15$, the predicted cumulative number of confirmed cases are about 138,000, and the expected peak will arrive in late April or early May of 2020 (See Figure 5).

The results show that the closing community and increasing medical resource be essential to control the spreading of the COVID-19.

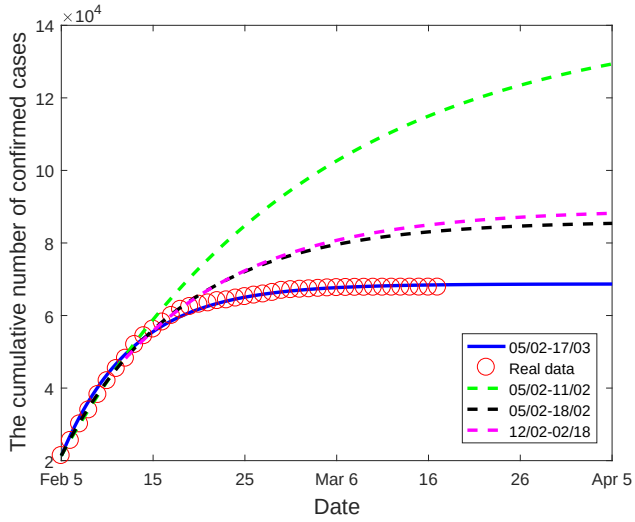


Figure 3. Data fits during the different time intervals of epidemic in Hubei province.

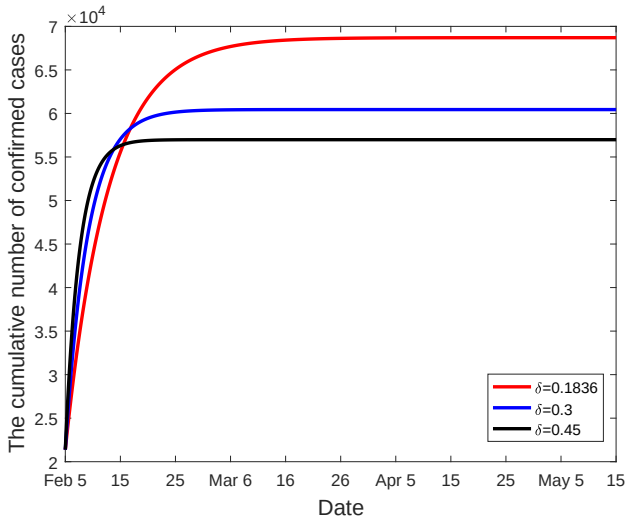


Figure 4. The evolution of the cumulative numbers of confirmed of model (1.1) is graphed for different values of δ : $0.1836, 0.3, 0.45$. All other parameters are given in (3.1).

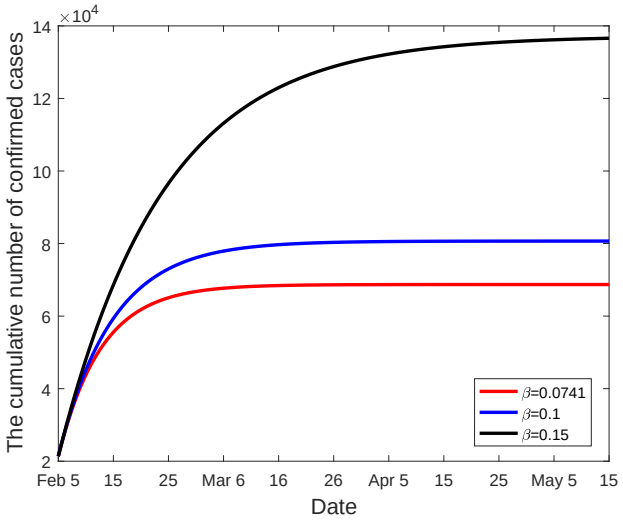


Figure 5. (a) The evolution of the numbers of confirmed cases of model (1.1) is graphed for different values of β : $0.0741, 0.1, 0.15$. All other parameters are given in (3.1).

4. Discussion and conclusion

In this study, we propose a generalized SIHR model to analyze the epidemic of COVID-19 which was firstly reported in Wuhan last December and then spread throughout the country rapidly. In this model, a new quarantined state H takes replace of the original Q state in the classical SIQR model and correctly accounts for the daily reported the numbers of confirmed cases. Based on detailed analysis of the public data of Health Commission of Hubei province from February 5 to March 17, we estimate the parameter values of model (1.1) according to the least square method [22], and the fitting result shows that a good fitting between the solution of the model and the real data (see Figure 2). In addition, We also find that some parameters affect the predicted cumulative number of confirmed cases and the expected peak date, for instance, the laboratory diagnosis rate δ will increase with the increase of medical resources, and the closure of the community will reduce the transmission rate β of COVID-19. As shown in Figures 4 and 5, the predicted cumulative infectious cases will decrease and reach peak quickly as the laboratory diagnosis rate δ increases; when β increases, the predicted peak cumulative infectious cases will also increase meanwhile the expected peak date will postpone. This means that it is urgent, necessary and effective to implement strong household quarantine measures and increase medical resources to control the COVID-19 transmission. And the earlier these measures are implemented, the stronger the effect will be. Moreover, we showed that the data from the mature stage of the epidemic growth could allow to obtain more stable fits (see Figure 3), which is consistent with the results in Alberti and Faranda [4].

Our findings provide policymakers with a tool to assess the consequences of possible strategies, including lockdown and the increase of medical resources. We believe these indications can be useful to understand the epidemic characteristics of the COVID-19 outbreak, and other countries may acquire useful information for COVID-19 from the perspective of transmission.

Some interesting questions deserve further investigation, such as one may consider the influence of delay [12–14], and spatial heterogeneity [15] on the spread of infectious diseases, which will be the focus of the future study.

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Conflict of interest

The authors declare no conflicts of interest in this paper.

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Appendix

A. The proof of Theorem 2.2

Proof. Notice that the endemic equilibrium $E^*(N^*, I^*, H^*, R^*)$ of model (2.2) satisfies the following equations:

$$\begin{cases} A - \mu N^* - \mu_1 I^* - \mu_2 H^* = 0, \\ \beta(N^*)(N^* - I^* - H^* - R^*)I^* - (\gamma + \delta + \mu + \mu_1)I^* = 0, \\ \delta I^* - (m + \mu + \mu_2)H^* = 0 \\ \gamma I^* + mH^* - \mu R^* = 0. \end{cases} \tag{A.1}$$

Direct calculation, one can see that

$$I^* = \ell_3(A - \mu N^*), \quad H^* = \ell_1\ell_3(A - \mu N^*) \quad R^* = \ell_2\ell_3(A - \mu N^*), \tag{A.2}$$

where ℓ_1, ℓ_2, ℓ_3 are defined as in (A.2). Notice that $I^* \neq 0$, and then substituting (A.2) into (A.1), one can get that

$$\beta(N^*)\Big(N^* - \ell_3(A - \mu N^*) - \ell_1\ell_3(A - \mu N^*) - \ell_2\ell_3(A - \mu N^*)\Big) - (\gamma + \delta + \mu + \mu_1) = 0. \tag{A.3}$$

Define

$$f(x) = \beta(x)\Big(x - \ell_3(A - \mu x) - \ell_1\ell_3(A - \mu x) - \ell_2\ell_3(A - \mu x)\Big) - (\gamma + \delta + \mu + \mu_1).$$

From the assumption (H2), one can see that $f(x)$ is a increasing function in $x \in (0, \frac{A}{\mu})$. Clearly

$$\lim_{x\to 0^+} f(x) = -(\gamma + \delta + \mu + \mu_1) < 0, \quad f(\frac{A}{\mu}) = (\gamma + \delta + \mu + \mu_1)(R_0 - 1) > 0.$$

Hence, $f(x) = 0$ has a unique positive solution $N^* \in (0, \frac{A}{\mu})$. That is to say, if $R_0 > 1$, then model (2.2) has a unique endemic equilibrium $E^* = (N^*, I^*, H^*, R^*)$. This completes the proof. □

B. The proof of Theorem 2.3

Proof. Define the Lyapunov function $V = I$ in $\mathbb{R}^4_+$ with the Lyapunov derivative

$$\begin{aligned}\frac{dV}{dt} =& (\beta(N)(N - I - H - R) - (\gamma + \delta + \mu + \mu_1))\, I\\ \leq& (\beta(N)N - (\gamma + \delta + \mu + \mu_1))\, I\\ \leq& \left(\beta(\frac{A}{\mu})\frac{A}{\mu} - (\gamma + \delta + \mu + \mu_1)\right) I\\ <& 0.\end{aligned}$$

The Lyapunov-Lasalle theorem means that solutions in $\hat{\Gamma}$ approach the largest positively invariant subset of the set $\frac{dV}{dt} = 0$, i.e., the plane $I = 0$. In this plane, we have $\frac{dH}{dt} = -(m + \mu + \mu_2)H$, $\frac{dR}{dt} = mH - \mu R$ and $\frac{dN}{dt} = A - \mu N - \mu_2 H$ which implies $\lim_{t\to\infty} H(t) = 0$, $\lim_{t\to\infty} R(t) = 0$ and $\lim_{t\to\infty} N(t) = \frac{A}{\mu}$. Thus all solutions in the plane $I = 0$ go to the disease-free equilibrium E_0. Therefore E_0 is globally asymptotically stable. □

C. The proof of Theorem 2.4

Proof. When $R_0 > 1$, the Jacobian matrix of model (2.2) evaluated at $E^* \in \hat{\Gamma}$ is

$$J(E^*) = \begin{pmatrix} -\mu & -\mu_1 & -\mu_2 & 0\\ \beta'(N^*)I^*(N^* - I^* - H^* - R^*) + \beta(N^*)I^* & -\beta(N^*)I^* & -\beta(N^*)I^* & -\beta(N^*)I^*\\ 0 & \delta & -(m + \mu + \mu_2) & 0\\ 0 & \gamma & m & -mu \end{pmatrix},$$

where $\beta'(N^*) = \left.\frac{d\beta(N)}{dN}\right|_{N=N^*}$. One can verify $\lambda = -mu$ is always an eigenvalue, and the other three eigenvalues of $J(E^*)$ are the roots of

$$\lambda^3 + a_2\lambda^2 + a_1\lambda + a_0 = 0, \tag{C.1}$$

where

$$\begin{aligned}a_2 =& m + 2\mu + \mu_2 + \beta(N^*)I^* > 0,\\ a_1 =& (m + 2\mu + \mu_2 + \delta + \gamma)\beta(N^*)I^* + \mu(m + \mu + \mu_2)\\ &+ \mu_1(\beta'(N^*)I^*(N^* - I^* - H^* - R^*) + \beta(N^*)I^*) > 0,\\ a_0 =& \beta(N^*)I^*(\mu(m + \mu + \mu_2 + \delta) + \delta m + (m + \mu + \mu_2)\gamma))\\ &+ (\beta'(N^*)I^*(N^* - I^* - H^* - R^*) + \beta(N^*)I^*)(\mu_1(m + \mu + \mu_2) + \mu_2\delta) > 0.\end{aligned}$$

It would be noted that $(\beta'(N^*)I^*(N^* - I^* - H^* - R^*) + \beta(N^*)I^*) = \frac{\partial(\beta(N)I(N-I-H-R)+\beta(N)I)}{\partial N}\Big|_{N=N^*} > 0$. This is mainly due to the facts that $\frac{d(\beta(N)N)}{dN} \geq 0$ and $\frac{d\beta(N)}{dN} \leq 0$. Then

$$\begin{aligned}
&a_1a_2 - a_0\\
&= (m + 2\mu + \mu_2 + \beta(N^*)I^*)\Big((m + 2\mu + \mu_2 + \delta + \gamma)\beta(N^*)I^* + \mu(m + \mu + \mu_2)\\
&+ \mu_1[\beta'(N^*)I^*(N^* - I^* - H^* - R^*) + \beta(N^*)I^*]\Big)\\
&- \Big(\beta(N^*)I^*(\mu(m + \mu + \mu_2 + \delta) + \delta m + (m + \mu + \mu_2)\gamma)\Big)\\
&- [\beta'(N^*)I^*(N^* - I^* - H^* - R^*) + \beta(N^*)I^*](\mu_1(m + \mu + \mu_2) + \mu_2\delta))\\
&> 0.
\end{aligned}$$

Hence, it follows from the Routh-Hurwitz criteria that the endemic equilibrium E^* of model (2.2) is locally asymptotically stable if $R_0 > 1$. This concludes our proof. □

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