MODELING THE SECOND OUTBREAK OF COVID-19 WITH ISOLATION AND CONTACT TRACING

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Abstract. The first case of Corona Virus Disease 2019 (COVID-19) was reported in Wuhan, China in December 2019. Since then, COVID-19 has quickly spread out to all provinces in China and over 150 countries or territories in the world. With the first level response to public health emergencies (FLRPHE) launched over the country, the outbreak of COVID-19 in China is achieving under control in China. We develop a mathematical model based on the epidemiology of COVID-19, incorporating the isolation of healthy people, confirmed cases and contact tracing measures. We calculate the basic reproduction numbers $2.5$ in China (excluding Hubei province) and $2.9$ in Hubei province with the initial time on January 30 which shows the severe infectivity of COVID-19, and verify that the current isolation method effectively contains the transmission of COVID-19. Under the isolation of healthy people, confirmed cases and contact tracing measures, we find a noteworthy phenomenon that is the second epidemic of COVID-19 and estimate the peak time and value and the cumulative number of cases. Simulations show that the contact tracing measures can efficiently contain the transmission of the second epidemic of COVID-19. With the isolation of all susceptible people or all infectious people or both, there is no second epidemic of COVID-19. Furthermore, resumption of work and study can increase the transmission risk of the second epidemic of COVID-19.

1. Introduction. In December 2019, the novel coronavirus pneumonia case was reported in Wuhan, China. On January 7, 2020, the novel coronavirus was first isolated by Chinese authorities [4, 42]. Subsequently, the disease was named officially as Corona Virus Disease 2019 (COVID-19) by World Health Organization (WHO) [5, 42]. The most important routes of transmission of COVID-19 are respiratory droplets and contact transmission, and the incubation is 2-14 days [13, 18, 1]. From the confirmed cases of COVID-19, the symptoms range from fever, cough, and shortness of breath to severely ill and dying [1]. By June 30, 2021, 181,824,475 confirmed cases and 3,938,068 deaths have been reported in the world, where 118,561 confirmed cases and 5,495 deaths are in China [2]. The COVID-19 is now threatening public health all over the world.

China has made extraordinary efforts to contain the transmission of COVID-19 [11]. On January 20, COVID-19 is subordinated to a Class B notifiable disease by China’s National Infectious Diseases Law and Frontier Health and Quarantine Law. On January 23, the Chinese government started to limit the movement of people in and out of Wuhan. Since January 23, the first level response to public health emergencies (FLRPHE) was gradually launched in all provinces over the country.
During the FLRPHE, the government participated to deal with the public health emergency and implemented the control strategies such as limiting or stopping crowds, stopping work, class suspension, no business, management of the floating people and quarantine of transportation, adopting the emergency control methods by health administrative departments, releasing information and notification and disseminating hygienic knowledge, medical institution’s quarantine or treatment on the confirmed and suspected cases, and isolation of close contact traced people at home. Enormous efforts have been implemented by the Chinese government to prevent the spread of COVID-19. Four categories of people including confirmed cases, suspected cases, patients with fever, and contact tracing with the confirmed case are quarantined. All confirmed cases were treated and close contacts were traced, and then confirmed cases and close contact traced people were quarantined [35]. Besides, China has great strengths such as community mobilization. Building and community isolation were implemented and home isolation was encouraged to prevent the transmission of COVID-19. The intervention methods implemented by China have provided a 1-2 month time window for other countries to prevent their possible outbreaks.

Mathematical modelling could help us understand and control the transmission of infectious diseases [9, 34, 37, 40, 28, 29, 33]. Chen et al. [7] established a novel coronavirus transmission model and obtained the formula of basic reproduction number. Imai et al. [19] estimated the potential total number of COVID-19 in Wuhan. Shen et al. [26] built an ordinary differential equations (ODE) model and explored the transmission ability of diseases. Read et al. [25] used an SEIR model to assess the effect of early control methods and predict disease development. Tang et al. [32] established an ODE model with quarantine and obtained the basic reproduction number 6.47. Zhao et al. [41] estimated the basic reproduction number of a novel coronavirus in China using a data-driven analysis in the early phase of the outbreak. Gilbert et al. [12] evaluated the preparedness and vulnerability of African countries against their risk of importation of COVID-19 by a modeling study. Song et al. [30] used traveller-derived cases in Henan Province to quantify the spread of COVID-19 in Wuhan. Subsequently, Song et al. [31] investigated the outbreak of COVID-19 in Harbin and estimates the outbreak size of COVID-19 in Harbin. However, only a few studies have focused on the second epidemic of COVID-19 in China.

To assess the effect of isolation of healthy people, confirmed cases and contact tracing measure on the transmission of COVID-19 in China, and estimate the second epidemic of COVID-19, we propose a SIHR (Susceptible-Infectious-Hospitalized-Removed) model incorporating the isolation of healthy people, confirmed cases and contact tracing measures. We compute the basic reproduction number, assess the effectiveness of the isolation strategy, investigate whether there is a second epidemic or multiple epidemics of COVID-19, estimate the peak time and value, duration, and the cumulative number of cases in the second epidemic of COVID-19 and evaluate the effects of resumption of work and study on the second epidemic of COVID-19.

2. **Mathematical modeling of COVID-19 transmission with isolation and contact tracing.**

2.1. **Model.** According to the 6th edition treatment of novel coronavirus pneumonia [2] and report of the WHO-China Joint Mission on COVID-19 [6], we knew that most people are susceptible to COVID-19 and the patients in the incubation period
can infect healthy people. Susceptible people are infected by infectious people and become infected. After the incubation period, the symptom onset and infected people become infectious. The patients are found out and go to the hospital. After the treatment, people are removed from the hospital. We denote the susceptible people by $S$, unfound infectious people by $I$, patients in hospital by $H$, removed people by $R$, respectively. The total population is denoted as $N$.

After the outbreak of COVID-19 in China, FLRPHE was gradually launched in all provinces over the country since January 23. During FLRPHE, susceptible people were also advised to isolate themselves at home by isolating communities, and all close contact traced people were quarantined. Therefore, we divide susceptible people into susceptible people ($S_1$), the quarantined susceptible people ($S_2$) by contact tracing measure, and isolated susceptible people ($S_3$) due to the isolation of their communities. Infectious people are divided into unfound infectious people ($I_1$), quarantined infectious people ($I_2$) by contact tracing measure and found infectious people in hospital ($H$).

In this study, the following assumptions are considered. We assume that all susceptible people of isolation at home cannot be infected and all infectious people of isolation at home cannot infect healthy people. The infectivity of the patients in the incubation period and the patients without being diagnosed are assumed to be the same. The isolation of healthy people and confirmed cases, and contact tracing measures are investigated. The experience gained from the first epidemic of COVID-19 is not considered. The effect of vaccines on the second epidemic of COVID-19 is not also analyzed.

Liu et al. [22] considered the isolation of reported cases in the model, and Wu et al. [38] investigated the effect of contact tracing on the transmission of COVID-19 in Ontario, Canada. In this study, the isolation of confirmed cases and contact tracing are considered, and the isolation of healthy people in high-risk areas are also investigated. Based on the epidemiological pattern of COVID-19 and intervention methods [23, 39], we establish the transmission dynamics of COVID-19 governed by the following equations:

$$\begin{align*}
\frac{dS_1(t)}{dt} &= \alpha_1 S_2(t) - \frac{\beta S_1(t) I_1(t)}{N - S_2(t) - S_3(t) - I_2(t) - H(t)} - q_1(t) S_1(t) + \alpha_2 S_3(t), \\
\frac{dS_2(t)}{dt} &= q_1(t) - \alpha_1 S_2(t), \\
\frac{dS_3(t)}{dt} &= \mu S_1(t) - \alpha_2 S_3(t), \\
\frac{dI_1(t)}{dt} &= \frac{\beta S_1(t) I_1(t)}{N - S_2(t) - S_3(t) - I_2(t) - H(t)} - q_2(t) I_1(t) - \gamma I_1(t), \\
\frac{dI_2(t)}{dt} &= q_2(t) - \gamma I_2(t), \\
\frac{dH(t)}{dt} &= \gamma I_1(t) + \gamma I_2(t) - \delta H(t), \\
\frac{dR(t)}{dt} &= \delta H(t),
\end{align*}$$

where $q_1 = \min\{S_1, \gamma b \frac{S_1}{S_1 + I_1} (I_1 + I_2)\}$, $q_2 = \min\{I_1, \gamma b \frac{I_1}{S_2 + I_2} (I_1 + I_2)\}$. The found infectious people ($\gamma (I_1 + I_2)$) per day move to the hospital compartment ($H$).
According to the contact tracing measure, the certain number of people \((\gamma(I_1 + I_2)b)\) were quarantined per day by the average number \((b)\) of close contact traced from found infectious people, where the certain number of susceptible people \((q_1)\) and infectious people \((q_2)\) were quarantined per day, respectively. Here \(q_1\) and \(q_2\) denote the number of quarantined susceptible people and infectious people per day, respectively. In theory, the number of quarantined susceptible people per day should be the proportion of susceptible people among susceptible \((S_1)\) and unfound infectious people \((I_1)\) multiplied by \(\gamma(I_1 + I_2)b\). Most of the infectious people are found out, and then we choose that the number of quarantined susceptible people per day is the proportion of quarantined susceptible people among quarantined susceptible \((S_2)\) and quarantined infectious people \((I_2)\) multiplied by \(\gamma(I_1 + I_2)b\). Due to that the number of quarantined susceptible people and infectious people per day are less than the number of susceptible people and infectious people at time \(t\), then we choose \(q_1 = \min\{S_1, \gamma b\frac{S_2}{S_2 + I_2}(I_1 + I_2)\}\) and \(q_2 = \min\{I_1, \gamma b\frac{I_2}{S_2 + I_2}(I_1 + I_2)\}\).

After the time of isolation for 14 days \((1/\alpha_1)\), the quarantined susceptible people move to susceptible compartment. When quarantined infectious people have symptoms, they are diagnosed, and found infectious people per day \((\gamma I_1)\) and \((\gamma I_2)\) move to the hospitalized compartment \((H)\). After treatment \((\text{the time of treatment } 1/\delta)\), they remove from the hospital. The communities are isolated and healthy people are also advised to isolate themselves at home unless they have something urgent to deal with. Then \(\mu S_1\) and \(\alpha_2 S_3\) denote the weak movements of people from susceptible to isolated susceptible and from isolated susceptible to susceptible, respectively. Parameters and variables are defined in Table 1. The flow diagram is shown in Fig. 1.

![Flow diagram of COVID-19 in SIHR model](image)

**Figure 1.** The flow diagram of COVID-19 in SIHR model.

The basic reproduction number is defined as the expected number of secondary cases produced by a single infection in a completely susceptible people and varies as time goes on. Using the next-generation matrix theory [8, 36], the basic reproduction number is computed as

\[
R_0 = \frac{\beta S_1(0)}{\gamma(N - S_2(0) - S_3(0) - I_2(0) - H(0))}
\]

with the initial time on January 30.

2.2. Dynamical analysis. For model (1), we assume that the initial conditions

\[
\begin{align*}
S_1(0) &= S_{10} \in \mathbb{R}_+, S_2(0) = S_{20} \in \mathbb{R}_+, S_3(0) = S_{30} \in \mathbb{R}_+, I_1(0) = I_{10} \in \mathbb{R}_+, \\
I_2(0) &= I_{20} \in \mathbb{R}_+, H(0) = H_0 \in \mathbb{R}_+, R(0) = R_0 \in \mathbb{R}_+.
\end{align*}
\]
Table 1. Related parameters and initial values in China (excluding Hubei province) and Hubei province.

| Parameter | Description | Mean value | 95% CI | Source |
|-----------|-------------|------------|--------|--------|
| $\alpha_1$ | The time of isolation at home for susceptible people | 1/14 | | [3] |
| $\beta$ | The transmission rate of COVID-19 | 0.3567 | (0.3291, 0.3815) | Estimated |
| $b$ | The average number of contact tracing | | | |
| $\gamma$ | The hospitalization rate of infectious people | 0.1429 | (0.1396, 0.1538) | Estimated |
| $\delta$ | The discharged rate from hospital | 0.0949 | | Calculated |
| $\mu$ | The transfer rate from susceptible to isolated susceptible people | $1.76 \times 10^{-4}$ | (1.66 x 10^{-4}, 1.86 x 10^{-4}) | Estimated |
| $\alpha_2$ | The transfer rate from isolated susceptible to susceptible people | $5.05 \times 10^{-6}$ | (4.95 x 10^{-6}, 5.15 x 10^{-6}) | Estimated |

Initial Values

| Parameter | Description | Mean value | 95% CI | Source |
|-----------|-------------|------------|--------|--------|
| $N$ | Total population of China (excluding Hubei province) | $1.3462 \times 10^9$ | | [3] |
| $S_1(0)$ | The number of initial susceptible people | $2.6723 \times 10^8$ | (2.6723 x 10^8, 2.6723 x 10^8) | Estimated |
| $S_2(0)$ | The number of initial quarantined susceptible people | 3762 | | Estimated |
| $H(0)$ | The number of initial hospitalized people | 3886 | | Data |
| $R(0)$ | The number of initial removed people | 64 | | Data |

| Parameter | Description | Mean value | 95% CI | Source |
|-----------|-------------|------------|--------|--------|
| $\alpha_3$ | The time of isolation at home for susceptible people | 1/18 | | [3] |
| $\alpha_4$ | The transmission rate of COVID-19 | 0.3999 | (0.3845, 0.4045) | Estimated |
| $b$ | The average number of contact tracing | 5 | (4.968, 5.1203) | Estimated |
| $\gamma$ | The hospitalization rate of infectious people | 0.1379 | (0.1289, 0.1460) | Estimated |
| $\delta$ | The discharged rate from hospital | 1/18 | | Calculated |
| $\mu$ | The transfer rate from susceptible to isolated susceptible people | $9.983 \times 10^{-6}$ | (9.56 x 10^{-6}, 1.02 x 10^{-5}) | Estimated |
| $\alpha_5$ | The transfer rate from isolated susceptible to susceptible people | $4.825 \times 10^{-5}$ | (4.7506 x 10^{-5}, 4.9615 x 10^{-5}) | Estimated |

Initial Values

| Parameter | Description | Mean value | 95% CI | Source |
|-----------|-------------|------------|--------|--------|
| $N$ | Total population of Hubei province | $5.317 \times 10^9$ | | [3] |
| $S_1(0)$ | The number of initial susceptible people | $1.18 \times 10^9$ | (1.18 x 10^9, 1.18 x 10^9) | Estimated |
| $S_2(0)$ | The number of initial quarantined susceptible people | 5367 | (5352, 5382) | Estimated |
| $S_3(0)$ | The number of initial isolated susceptible people | $4.7336 \times 10^7$ | (4.7336 x 10^7, 4.7336 x 10^7) | Estimated |
| $I_0(0)$ | The number of initial initial infectious people | 12973 | (12963, 12985) | Estimated |
| $H(0)$ | The number of initial hospitalized people | 2023 | (2014, 2029) | Estimated |
| $R(0)$ | The number of initial removed people | 5806 | | Data |

Notes: 95% CI: 95% highest posterior density interval.

Following the Theorem 5.2.1 in [27], the nonnegativeness of solutions of model (1) with initial conditions (2) is obtained immediately.

From model (1), we have

$$
\frac{d(S_1 + S_2 + S_3 + I_1 + I_2 + H + R)}{dt} = 0,
$$

which means that the total population keeps constant $N$. Then the solutions of model (1) are bounded.

Due to $q_1 = \min\{S_1, \gamma b S_2 S_3 I_1 I_2, I_1 + I_2\}$, $q_2 = \min\{I_1, \gamma b S_2 I_1 I_2, I_1 + I_2\}$, model (1) will be analyzed in terms of four cases:

**Case (i):** $\gamma b S_2 S_3 I_1 I_2 (I_1 + I_2) \leq S_1, \gamma b S_2 I_1 I_2 (I_1 + I_2) \leq I_1$;

**Case (ii):** $\gamma b S_2 S_3 I_1 I_2 (I_1 + I_2) \leq S_1, \gamma b S_2 I_1 I_2 (I_1 + I_2) > I_1$;

**Case (iii):** $\gamma b S_2 S_3 I_1 I_2 (I_1 + I_2) > S_1, \gamma b S_2 I_1 I_2 (I_1 + I_2) \leq I_1$;

**Case (iv):** $\gamma b S_2 S_3 I_1 I_2 (I_1 + I_2) > S_1, \gamma b S_2 I_1 I_2 (I_1 + I_2) > I_1$. 


For the model (1) with four cases, we compute the disease free equilibrium and basic reproduction number, and prove the global stability of the disease free equilibrium.

Case (i) When \( \gamma_1 \frac{\beta}{\gamma b} (I_1 + I_2) \leq S_1, \gamma_2 \frac{I_2}{\gamma b} (I_1 + I_2) \leq I_1 \), model (1) becomes

\[
\begin{align*}
\frac{dS_1(t)}{dt} &= \alpha_1 S_2(t) - \frac{\beta S_1(t) I_1(t)}{N - S_2(t) - S_3(t) - I_2(t) - H(t)} - \gamma b \frac{S_2}{S_2 + I_2} (I_1 + I_2) - \mu S_1(t) + \alpha_2 S_3(t), \\
\frac{dS_2(t)}{dt} &= \gamma b \frac{S_2}{S_2 + I_2} (I_1 + I_2) - \alpha S_2(t), \\
\frac{dS_3(t)}{dt} &= \mu S_1(t) - \alpha_2 S_3(t), \\
\frac{dI_1(t)}{dt} &= \beta S_1(t) I_1(t) - \gamma b \frac{I_2}{S_2 + I_2} (I_1 + I_2) - \gamma I_1(t), \\
\frac{dI_2(t)}{dt} &= \gamma b \frac{I_2}{S_2 + I_2} (I_1 + I_2) - \gamma I_2(t), \\
\frac{dH(t)}{dt} &= \gamma I_1(t) + \gamma I_2(t) - \delta H(t), \\
\frac{dR(t)}{dt} &= \delta H(t),
\end{align*}
\]

(3)

Thus, the characteristic equation of (4) at \( E_{01} = (S_1^0, 0, \mu S_1^0/\alpha_2, 0, 0, 0, R^*) \), where constants \( S_1^0 < N \) and \( R^* < N \). Using the next-generation matrix theory \([8, 36]\), the basic reproduction number is computed as

\[
R_{01} = \frac{\beta S_1^0}{\gamma (N - \mu S_1^0/\alpha_2)}.
\]

In what follows, we first analyze the local stability of the disease free equilibrium \( E_{01} \), and prove the global stability of \( E_{01} \) using the fluctuation lemma \([16]\). For the bounded function \( f \) on \( \mathbb{R}_+ \), define

\[
f^\infty = \limsup_{t \to \infty} f(t) \quad \text{and} \quad f_\infty = \liminf_{t \to \infty} f(t).
\]

**Theorem 2.1.** If \( R_{01} < 1 \), then the disease free equilibrium \( E_{01} \) is globally asymptotically stable.

**Proof.** First, we prove that \( E_{01} \) is locally asymptotically stable. Then we only consider the following equations

\[
\begin{align*}
\frac{dI_1(t)}{dt} &= \beta S_1(t) I_1(t) - \gamma b \frac{I_2}{S_2 + I_2} (I_1 + I_2) - \gamma I_1(t), \\
\frac{dI_2(t)}{dt} &= \gamma b \frac{I_2}{S_2 + I_2} (I_1 + I_2) - \gamma I_2(t),
\end{align*}
\]

(4)

Thus, the characteristic equation of (4) at \( E_{01} \) is

\[
[\lambda - \left( \frac{\beta S_1^0}{(N - \mu S_1^0/\alpha_2)} - \gamma \right)](\lambda + \gamma) = 0.
\]

Obviously, \( \lambda = -\gamma \) and \( \lambda = \frac{\beta S_1^0}{(N - \mu S_1^0/\alpha_2)} - \gamma \) are negative roots when \( R_{01} < 1 \). Therefore, \( E_{01} \) is locally asymptotically stable.
In the following, we prove that $E_{01}$ is globally attractive. According to the fluctuation lemma [16], there is a sequence $\{\tau_n\}$ such that $\tau_n \to \infty$, $I_1(\tau_n) + I_2(\tau_n) \to I_1^\infty + I_2^\infty$ and $\frac{d(I_1(\tau_n) + I_2(\tau_n))}{dt} \to 0$ as $n \to \infty$. Then
\[
\frac{d(I_1(\tau_n) + I_2(\tau_n))}{dt} = \frac{\beta S_1(\tau_n) I_1(\tau_n)}{N - S_2(\tau_n) - S_3(\tau_n) - I_2(\tau_n) - H(\tau_n)} - \gamma(I_1(\tau_n) + I_2(\tau_n))
\leq \frac{\beta S_1(\tau_n) I_1(\tau_n)}{N - \mu S_1^0/\alpha_2} - \gamma(I_1(\tau_n) + I_2(\tau_n))
= \gamma(R_{01} - 1)(I_1(\tau_n) + I_2(\tau_n)).
\]

Thus,
\[
1 \leq \gamma(R_{01} - 1)(I_1^\infty + I_2^\infty).
\]

Then $I_1^\infty = I_2^\infty = 0$ when $R_{01} < 1$.

Using the fluctuation lemma [16], there is a sequence $\{\sigma_n\}$ such that $\sigma_n \to \infty$, $H(\sigma_n) \to H^\infty$ and $\frac{dH(\sigma_n)}{dt} \to 0$ as $n \to \infty$. Then
\[
\frac{dH(\sigma_n)}{dt} = \gamma I_1(\sigma_n) + \gamma I_2(\sigma_n) - \delta H(\sigma_n)
\leq -\delta H(\sigma_n).
\]

Thus, $H^\infty = 0$. Using the fluctuation lemma and similar discussion, we immediately obtain $\lim_{t \to \infty} S_1(t) = S_1^0$, $\lim_{t \to \infty} S_2(t) = 0$, $\lim_{t \to \infty} S_3(t) = \mu S_1^0/\alpha_2$ and $\lim_{t \to \infty} R(t) = R^*$.

Based on the above discussion, we obtain that $\lim_{t \to \infty} (S_1(t), S_2(t), S_3(t), I_1(t), I_2(t), H(t), R(t)) = E_{01}$. Therefore, $E_{01}$ is globally asymptotically stable.

Case (ii) When $\gamma b \frac{S_1}{S_2 + I_2} (I_1 + I_2) \leq S_1$, $\gamma b \frac{I_2}{S_2 + I_2} (I_1 + I_2) > I_1$, model (1) becomes
\[
\begin{align*}
\frac{dS_1(t)}{dt} &= \alpha S_2(t) - \frac{\beta S_1(t) I_1(t)}{N - S_2(t) - S_3(t) - I_2(t) - H(t)} - \gamma b \frac{S_2}{S_2 + I_2} (I_1 + I_2) - \mu S_1(t) + \alpha_2 S_3(t), \\
\frac{dS_2(t)}{dt} &= \gamma b \frac{S_2}{S_2 + I_2} (I_1 + I_2) - \alpha_1 S_2(t), \\
\frac{dS_3(t)}{dt} &= \mu S_1(t) - \alpha_2 S_3(t), \\
\frac{dI_1(t)}{dt} &= \frac{\beta S_1(t) I_1(t)}{N - S_2(t) - S_3(t) - I_2(t) - H(t)} - I_1 - \gamma I_1(t), \\
\frac{dI_2(t)}{dt} &= I_1 - \gamma I_2(t), \\
\frac{dH(t)}{dt} &= \gamma I_1(t) + \gamma I_2(t) - \delta H(t), \\
\frac{dR(t)}{dt} &= \delta H(t), 
\end{align*}
\]

Note that model (5) always has the disease free equilibrium $E_{02} = (S_1^0, 0, \mu S_1^0/\alpha_2, 0, 0, 0, R^*)$, where constants $S_1^0 < N$ and $R^* < N$. Using the next-generation matrix theory [8, 36], the basic reproduction number is computed as
\[
R_{02} = \frac{\beta S_1^0}{(\gamma + 1)(N - \mu S_1^0/\alpha_2)}. 
\]
Using the similar arguments with Theorem 2.1, we have the following result.

**Theorem 2.2.** If \( R_{02} < 1 \), then the disease free equilibrium \( E_{02} \) is globally asymptotically stable.

**Case (iii)** When \( \gamma b \frac{S_2}{S_2 + I_2} (I_1 + I_2) > S_1, \gamma b \frac{I_2}{S_2 + I_2} (I_1 + I_2) \leq I_1 \), model (1) becomes

\[
\begin{aligned}
\frac{dS_1(t)}{dt} &= \alpha_1 S_2(t) - \frac{\beta S_1(t)I_1(t)}{N - S_2(t) - S_3(t) - I_2(t) - H(t)} - S_1(t) - \mu S_1(t) + \alpha_2 S_3(t), \\
\frac{dS_2(t)}{dt} &= S_1(t) - \alpha_1 S_2(t), \\
\frac{dS_3(t)}{dt} &= \mu S_1(t) - \alpha_3 S_3(t), \\
\frac{dI_1(t)}{dt} &= \frac{\beta S_1(t)I_1(t)}{N - S_2(t) - S_3(t) - I_2(t) - H(t)} - \gamma b \frac{I_2}{S_2 + I_2} (I_1 + I_2) - \gamma I_1(t), \\
\frac{dI_2(t)}{dt} &= \gamma b \frac{I_2}{S_2 + I_2} (I_1 + I_2) - \gamma I_2(t), \\
\frac{dH(t)}{dt} &= \gamma I_1(t) + \gamma I_2(t) - \delta H(t), \\
\frac{dR(t)}{dt} &= \delta H(t).
\end{aligned}
\]

Note that model (6) always has the disease free equilibrium \( E_{03} = (S_1^0, S_2^0/\alpha_1, \mu S_3^0/\alpha_2, 0, 0, 0, R^*) \), where constants \( S_1^0 < N \) and \( R^* < N \). Using the next-generation matrix theory [8, 36], the basic reproduction number is computed as

\[
R_{03} = \frac{\beta S_1^0}{\gamma(N - S_1^0/\alpha_1 - \mu S_1^0/\alpha_2)}.
\]

Using the similar arguments with Theorem 2.1, we have the following result.

**Theorem 2.3.** If \( R_{03} < 1 \), then the disease free equilibrium \( E_{03} \) is globally asymptotically stable.

**Case (iv)** When \( \gamma b \frac{S_1}{S_1 + I_2} (I_1 + I_2) > S_1, \gamma b \frac{I_1}{S_1 + I_2} (I_1 + I_2) > I_1 \), model (1) becomes

\[
\begin{aligned}
\frac{dS_1(t)}{dt} &= \alpha_1 S_2(t) - \frac{\beta S_1(t)I_1(t)}{N - S_2(t) - S_3(t) - I_2(t) - H(t)} - S_1(t) - \mu S_1(t) + \alpha_2 S_3(t), \\
\frac{dS_2(t)}{dt} &= S_1(t) - \alpha_1 S_2(t), \\
\frac{dS_3(t)}{dt} &= \mu S_1(t) - \alpha_3 S_3(t), \\
\frac{dI_1(t)}{dt} &= \frac{\beta S_1(t)I_1(t)}{N - S_2(t) - S_3(t) - I_2(t) - H(t)} - I_1 - \gamma I_1(t), \\
\frac{dI_2(t)}{dt} &= I_1 - \gamma I_2(t), \\
\frac{dH(t)}{dt} &= \gamma I_1(t) + \gamma I_2(t) - \delta H(t), \\
\frac{dR(t)}{dt} &= \delta H(t).
\end{aligned}
\]
Note that model (7) always has the disease free equilibrium $E_{04} = (S_0^0, S_1^0/\alpha_1, \mu S_1^0/\alpha_2, 0, 0, 0, 0, 0, 0, R^*)$, where constants $S_1^0 < N$ and $R^* < N$. Using the next-generation matrix theory [8, 36], the basic reproduction number is computed as

$$R_{04} = \frac{\beta S_0^0}{(\gamma + 1)(N - S_1^0/\alpha_1 - \mu S_1^0/\alpha_2)}.$$  

Using the similar arguments with Theorem 2.1, we have the following result.

**Theorem 2.4.** If $R_{04} < 1$, then the disease free equilibrium $E_{04}$ is globally asymptotically stable.

3. Parameter estimation.

3.1. Data source. Since the medical resources corresponding to patients are very different between China (excluding Hubei province) and Hubei province, then the transmission of COVID-19 in China (excluding Hubei province) and Hubei province is studied, respectively. Data of COVID-19 cases were obtained in China from the National Health Commission of the People’s Republic of China and Coronavirus disease (COVID-19) situation reports in WHO [5, 3]. After the emergent closure of Wuhan city on January 23 and the whole Hubei province later, it is almost impossible to travel from Hubei province to other places. Then data were collected from January 30, 2019, to March 18, 2020, in China and Hubei province. The data set includes the cumulative and new numbers of confirmed cases, suspected cases, death cases, and cured cases, and the cumulative number of contact tracing and hospitalization time.

The total populations of China and Hubei province are 1.3954 billion and 59.17 million, respectively. All close contact traced people are advised to isolate themselves at home for 14 days, then $\alpha_1 = 1/14$. According to the data statistics of treatment time in the provinces, we obtain that the time of treatment is about 10.534 days outside Hubei province and 18 days inside Hubei province, then $\delta = 1/10.534$ on provinces outside Hubei and $\delta = 1/18$ in Hubei province. We choose the cumulative number of confirmed cases from January 30 to March 18 in China (excluding Hubei province). The cumulative number of confirmed cases from January 30 to February 4 and from February 12 to March 18 are chosen in Hubei province since comprehensive troubleshooting was carried out from February 8 to February 11 in Wuhan and caused the exception data. By January 30, 2020 in China (excluding Hubei province), 3886 confirmed cases were reported leading to $H(0) = 3886$, and 65 patients were removed from hospital leading to $R(0) = 65$. By January 30, 2020 in Hubei province, 5806 confirmed cases were reported leading to $H(0) = 5806$, and 320 patients were removed from hospital leading to $R(0) = 320$. We estimate other parameters and initial values using the least square method in Table 1. All numerical simulations are carried out using Matlab programs.

Using Bayesian methods, we estimated the parameter values $\beta, b, \gamma, \mu, \alpha_2$ and initial values $S_1(0), S_2(0), S_3(0), I_1(0), I_2(0)$. We chose multivariate Gaussian as the prior distribution of five unknown parameters, and took the mean of the posterior distribution as the estimated value of the initial values and parameters, which were estimated by the Markov Chain Monte Carlo (MCMC) method. Based on the SIHR model and the cumulative number of confirmed cases, using Markov Chain Monte Carlo (MCMC) methods employing the adaptive Metropolis-Hasting algorithm with 10000 iterations and a 5000 iteration burn-in period [15], we estimate
the parameter values $\beta, b, \gamma, \mu, \alpha_2$ and initial values $S_1(0), S_2(0), S_3(0), I_1(0), I_2(0)$ which are shown in Table 1.

3.2. Fitting results. Based on the SIHR model and cumulative confirmed cases, using Markov Chain Monte Carlo (MCMC) methods, we estimate the parameter values $\beta, b, \gamma, \mu, \alpha_2$ and initial values $S_1(0), S_2(0), S_3(0), I_1(0), I_2(0)$ which are shown in Table 1. Here the mean absolute percentage errors (MAPE) are 0.0126 and 0.02 when the cumulative confirmed cases in China (excluding Hubei province) and Hubei province are fitted, respectively. With the initial time on January 30, the basic reproduction numbers are 2.5 in China (excluding Hubei province) and 2.9 in Hubei province.

Under the current isolation of healthy people, confirmed cases and contact tracing measures, the peak time of confirmed cases occurs around February 6 with the peak value of 5814 and prevalence seems to be vanishing around April 5 with the cumulative number of confirmed cases of 13,340 in China (excluding Hubei province), and the peak time of confirmed cases occurs around February 15 with the peak value of 34,688 and prevalence seems to be vanishing around May 23 with the cumulative number of confirmed cases of 69,196 in Hubei province (Fig. 2). Hence, our simulations are consistent with the real data of cumulative number of confirmed cases.

4. The effect of interventions on COVID-19 and second outbreak of COVID-19.

4.1. The effect of interventions on COVID-19. When isolation of healthy people, confirmed cases and contact tracing measures are not implemented (the related parameter values and initial values are defined in Table 1), the peak time of confirmed cases is expected to appear around April 7 with the peak value of $4.099 \times 10^8$, and the cumulative number of confirmed cases reaches $1.271 \times 10^9$ in China (excluding Hubei province) (Fig. 3). This illustrates that the current isolation strategy makes the peak in advance by 60 days, and the peak value and cumulative confirmed cases are reduced by over 99%. Similar results are obtained for Hubei province.

4.2. The second outbreak of COVID-19. Under the current isolation of healthy people, confirmed cases, and contact tracing measures (the related parameter values and initial values are defined in Table 1), we perform simulations and find a noteworthy phenomenon which is the second epidemic of COVID-19 (Fig. 4). Here we take the measures implemented by the government during the first epidemic of COVID-19 into account and ignore the experience gained from the first epidemic. In China (excluding Hubei province), the second epidemic of COVID-19 will start around July 27, 2020, and persist for several years with cumulative confirmed cases of $1.58 \times 10^8$, and the peak time of infectious people will occur around October 25, 2020, with the peak value of $2.29 \times 10^7$. In Hubei province, the second outbreak will start around July 29, 2020, and persist for several years with cumulative confirmed cases of $4.5785 \times 10^7$, and the peak time of infectious people will occur around October 12, 2020, with the peak value of $1.1845 \times 10^7$. When all susceptible people or all infectious people or both groups are isolated (Fig. 5), there is no second epidemic of COVID-19 in China (excluding Hubei province). To prevent and control the second epidemic of COVID-19, we investigate the effect of the isolation strategy including the average number of contact tracing and the time of isolation on the
Figure 2. The cumulative number of confirmed cases and unfound infectious cases in China (excluding Hubei province) and Hubei province are shown under the current intervention methods. Where $CumH$ denotes the cumulative number of confirmed cases, $CumI$ is the cumulative number of infectious people, $I_1 + I_2$ is the unfound infectious people and $H$ represents the confirmed cases. Other parameter values and initial values are defined in Table 1.

Second epidemic of COVID-19 (Fig. 6). When the time of isolation for 14 days and the average number of contact tracing $b = 45$, the disease arrives at the peak of $1.428 \times 10^7$ around November 4. The average number of contact tracing $b = 45$ delays the peak by 10 days, and the peak value is reduced by 37% in contrast with $b = 12$. When the average number of contact tracing $b = 12$, the epidemic arrives at the peak of $1.876 \times 10^7$ around October 29 for the time of isolation of 33 days, and the disease arrives at the peak of $1.738 \times 10^7$ around October 5 for the time of isolation of 61 days which makes the peak in advance for 24 days and the peak value is reduced by 7%. Similar results are obtained for Hubei province. Therefore, the isolation strategy can effectively contain the transmission of the second epidemic of COVID-19 by making the peak in advance and reducing the peak value.
Figure 3. The effect of the isolation of healthy people, confirmed cases and contact tracing measures on the transmission of COVID-19 in China (excluding Hubei province). The top figure shows the cumulative number of confirmed cases and confirmed cases under the current intervention methods. The bottom figure shows the cumulative number of confirmed cases and confirmed cases when the current isolation strategy is not carried out. Where CumH denotes the cumulative number of confirmed cases, CumI is the cumulative number of infectious people, $S_2 + I_2$ is the quarantined susceptible and infectious people, $I_1 + I_2$ is the unfound infectious people and $H$ represents the confirmed cases. Other parameter values and initial values are defined in Table 1.
The predicted cumulative number of confirmed cases and infectious cases of the potential second epidemic of COVID-19 in China (excluding Hubei province) and Hubei province are shown under the current intervention methods. The embedded figures are the thumbnail of Fig. 2. Where $CumH$ denotes the cumulative number of confirmed cases, $CumI$ is the cumulative number of infectious people, $I_1 + I_2$ is the unfound infectious people and $H$ represents the confirmed cases. Other parameter values and initial values are defined in Table 1.

4.3. The effects of resumption of work and study on the second epidemic of COVID-19. The effects of resumption of work and study on the second epidemic of COVID-19 in China (excluding Hubei province) are also investigated (Figs. 7 and 8). When there is no resumption of work, the disease of the second epidemic of COVID-19 arrives at the peak of $2.461 \times 10^7$ around October 18, and the cumulative
Figure 5. There is no second epidemic in China (excluding Hubei province) when all susceptible people (top) or all infectious people (middle) or all susceptible people and infectious people (bottom) are isolated. Where CumH denotes the cumulative number of confirmed cases, CumI is the cumulative number of infectious people, $S_2 + I_2$ is the quarantined susceptible and infectious people, $I_1 + I_2$ is the unfound infectious people and $H$ represents the confirmed cases. Parameter values and initial values are defined in Table 1.
Figure 6. Under the current intervention methods, the top figure shows the effect of the average number of contact tracing $b$ on the second epidemic of COVID-19 when the time of isolation is 14 days, and the bottom figure shows the effect of the time of isolation on the second epidemic of COVID-19 when the average number of contact tracing $b$ is 12. Here we assumed that 80% of the susceptible people are isolated in China (excluding Hubei province) on January 30. Where $CumH$ denotes the cumulative number of confirmed cases, $CumI$ is the cumulative number of infectious people, $S_2 + I_2$ is the quarantined susceptible and infectious people, $I_1 + I_2$ is the unfound infectious people and $H$ represents the confirmed cases. Parameter values and initial values are defined in Table 1.
number of confirmed cases is $1.579 \times 10^8$. When all workers return to work and no resumption of study, the disease of the second epidemic of COVID-19 arrives at the peak of $7.067 \times 10^7$ around October 31, and the cumulative number of confirmed cases is $4.84 \times 10^8$. The resumption of work delays the peak by 13 days, and the peak value and cumulative confirmed cases are increased by more than twice. When there is no school, the disease of the second epidemic of COVID-19 arrives at a peak of $7.037 \times 10^7$ around November 1. When all students return to school on March 30, the disease of the second epidemic of COVID-19 arrives at the peak of $1.192 \times 10^8$ around November 24. The resumption of the study delays the peak by 23 days, and the peak value is increased by nearly quadruple. Similar results are obtained for Hubei province. Therefore, the resumptions of work and study increase the transmission risk of the second epidemic of COVID-19 by delaying the peak and dramatically increasing the peak value.

5. **Discussion and conclusion.** Since the first case of COVID-19 was reported in Wuhan in December 2019, COVID-19 has spread rapidly over all provinces in China and over 200 countries and caused 118,561 confirmed cases and 5,495 deaths in China by June 30, 2021. According to the cumulative number of confirmed cases and the SIHR model, we estimate the related parameters value and initial values using the data fitting, and then we obtain the basic reproduction numbers 2.5 in China (excluding Hubei province) and 2.9 in Hubei province with the initial
Figure 8. Under the isolation strategy, the effect of resumption of study on the second epidemic of COVID-19 in China (excluding Hubei province) is assessed in case of no school, resumption of study on March 30 and April 20. We assume that 38% of the susceptible people is isolated before school. Here, $CumH$ denotes the cumulative number of confirmed cases, $CumI$ is the cumulative number of infectious people, $S_2 + I_2$ is the quarantined susceptible and infectious people, $I_1 + I_2$ is the unfound infectious people and $H$ represents the confirmed cases. Other parameter values and initial values are defined in Table 1.

time on January 30 in contrast with the basic reproduction numbers of SARS in Beijing ($R_0 = 4.91$) and Hongkong ($R_0 = 3.6$) in 2003 [14], and MERS in Jeddah ($R_0 = 3.5 - 6.7$) in 2014 [24]. This direct comparison implies that COVID-19 is highly contagious and causes a serious threat to public health around the world.

The main contribution of our study is that the isolation of healthy people, confirmed cases and contact tracing measures implemented by China are highly effective to prevent and control the transmission of COVID-19. This method used in China (excluding Hubei province) makes the peak in advance by 60 days and diminishes the peak value and cumulative confirmed cases by over 99% in contrast with the situation of no isolation. Similar results are obtained for Hubei province. The current isolation of healthy people, confirmed cases and contact tracing measures effectively contain the transmission of COVID-19 in China and protect public health all over the world.

One major finding of our quantitative study is that there is a second epidemic of COVID-19 in China under the isolation strategy. The reasons are as follows. On the one hand, the contact tracing measure has a weak effect on the transmission of COVID-19 when prevalence seems to be vanishing, which causes an increase of unfound infectious people. On the other hand, people have weak awareness of prevention and control at the moment and relax their vigilance, and then unfound infectious people get back to their normal work and life. Then unfound infectious people mix evenly with healthy people, which will cause the transmission of COVID-19 and thereupon then lead to the second epidemic of COVID-19 [21, 10]. In our
model, the multiple of found infectious people is the number of quarantined people by contact tracing measure, and then the second epidemic of COVID-19 appears. While in [38], the certain proposition of susceptible and infected people is the number of quarantined people by contact tracing measure, and then there is no second epidemic of COVID-19. When all susceptible people or all infectious people or both groups are isolated, there is no second epidemic of COVID-19. Simulations show that strengthening isolation of contact tracing by increasing the average number of contact tracing and the time of isolation makes the peak in advance and reduces the peak value and the cumulative number of confirmed cases during the second epidemic of COVID-19. Numerical simulations reveal that resumptions of work and study delay the peak and increase the peak value and the cumulative number of confirmed cases.

Based on the isolation of healthy people, confirmed cases and contact tracing measures, we establish the transmission dynamical model of COVID-19, calculate the basic reproduction numbers 2.5 in China (excluding Hubei province) and 2.9 in Hubei province with the initial time on January 30, which shows the severe infectivity of COVID-19 and the current isolation strategy effectively contains the transmission of COVID-19 by making the peak in advance and reducing the peak value and the cumulative number of confirmed cases. Under the isolation of healthy people, confirmed cases and contact tracing measures, we find that there may be a second epidemic of COVID-19, and the isolation of contact tracing measure efficiently lowers down the probability of a second epidemic of COVID-19. When all susceptible people or all infectious people or both groups are isolated, there is no second epidemic of COVID-19. Besides, resumptions of work and study delay the peak and increase the peak value and the cumulative number of confirmed cases of COVID-19.

Nevertheless, there are several limitations to this study. Firstly, we take the measures implemented by the government during the epidemic of COVID-19 into account and ignore the experience gained from the first epidemic and other measures, which could cause that the epidemic size of the second epidemic and the effect of contact tracing measure are overestimated. Secondly, we ignore the effect of vaccines [17] on the second epidemic of COVID-19. We may explore such work in the future. Finally, due to the increasing number of imported infected cases got into China and the emergence of new variants of SARS-CoV-2 [20], we must remain vigilant against the multiple epidemics of COVID-19 and the possibility that COVID-19 turns into a chronic epidemic disease.

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