# Modeling and Reviewing Study to the COVID-19 Epidemic in PR China

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## Abstract

**Background:** COVID-19 epidemic has been widely spread all over the world. During it appears in China, Chinese government quickly put forward and implement prevention and control measures to keep its spread within limits. This study aims to investigate the impacts of the prevention and control measures in controlling COVID-19 epidemic in China, so as to give a clue to control its spread in the world.

**Methods:** We establish a two-stage dynamics transmission model with "lockdown of Wuhan city" as the time line. The first stage is the SEIR derived model that considers the contagious of the exposed. It simulates the COVID-19 epidemic in Hubei Province before "lockdown of Wuhan city". The second stage is a novel transmission dynamics model named SEIRQH. It takes into account the influence on the COVID-19 epidemic from the series of measures such as travel restriction, contact tracing, centralized treatment, the asymptomatic infected patients, hospitalized patients and so on. It simulates the COVID-19 epidemic in China after "lockdown of Wuhan city". The least square method is used to estimate the parameters of SEIR derived model and the proposed SEIRQH model based on the collected epidemic data of COVID-19 from Hubei Province and the mainland of China.

**Results:** The SEIR derived model fits the actual data in Hubei Province before "lockdown of Wuhan city". The basic reproduction number of COVID-19 epidemic in Hubei Province is 3.2035 before "lockdown of Wuhan city". The SEIRQH model fits the number of the hospitalized persons of COVID-19 in Hubei Province and the mainland of China perfectly. The control reproductive number are 0.11428 and 0.09796 in Hubei Province and the mainland of China, respectively. The prevention and control measures taken by Chinese government play the significant role against the COVID-19 spread in China.

**Conclusions:** Our two-stage dynamics transmission model simulates the COVID-19 in China, especially our SEIRQH model fits the actual data very well. The prevention and control measures implemented by Chinese government are effective in preventing the wide spread of COVID-19 epidemic in China. These measures give the reference to World Health Organization and other countries in controlling COVID-19 epidemic.

**Keywords:** Novel coronavirus, COVID-19, Dynamics model, Control reproduction number

## Background

In December 2019, an atypical pneumonia caused by a new type of coronavirus appeared in Wuhan city, Hubei Province, China [1, 2]. On January 20, 2020, this new type of coronavirus was named as 2019-nCoV (2019 novel coronavirus) by the WHO (World health organization) for the first time. The atypical pneumonia caused by 2019-nCoV was subsequently named as COVID-19 (Coronavirus disease 2019) on February 11, 2020. It has been reported that the natural host of 2019-nCoV may be the bat [3-4], but the intermediate host is still controversial [5]. Although the origin of 2019-nCoV is still disputed, the infectious disease COVID-19 caused by 2019-nCoV has spread globally and has become an infectious disease that threatens all of humankind. It is report by WHO that, as of August 13, 2020, the cumulative number of infected people around the world had exceeded 20 million and the number of deaths had reached to 742,878.

In the early and middle stages of the COVID-19 spread in China, there are many researchers who devoted themselves to study the trend of the COVID-19 epidemic using the differential equations of infectious disease transmission dynamics. The traditional transmission dynamic models comprise SI (Susceptible-Infectious), SIR (Susceptible-Infectious-Recovered), SEIR (Susceptible-Exposed-Infectious-Recovered) and its derived models. The SIR and SEIR models were widely adopted in the studies of COVID-19 epidemic at the early stage of COVID-19. The transmission mechanism of COVID-19 was not clear and the epidemic prevention and control measures were not explicitly published at that time. For example, Yang *et al*. [6] used the SIR model to predict the epidemic trend in Chongqing, and estimated that Chongqing would come to its inflection point on February 25. Fang *et al*. [7] used the SEIR model considering the incubation period to predict and analyze the specific time of inflection point of COVID-19 in Wuhan under the

condition of different incubation periods. Geng *et al*. [8] studied the impact of travel restriction measures on the trend of COVID-19 epidemic based on SEIR model.

To restraint the spread of COVID-19 epidemic in China, Chinese government took several policies, such as travel restriction, close contact tracing, centralized treatment, and so on. Therefore the traditional SIR and SEIR models are no longer suitable to simulate the trend of COVID-19 in China. Such that many derived models are proposed on the basis of the traditional SEIR model by adding some compartments, so as to investigate the impact of the prevention and control measures taken by Chinese government on the COVID-19 epidemic. For example, Tang *et al*. [9] proposed a SEIR derived model based on the epidemic prevention and control measures in China, which comprises some appropriate compartments such as quarantine, isolation and treatment. Their follow-up study [10] described the contact and diagnose rates as the time-dependent functions in their model, which effectively evaluated the trend of the COVID-19 epidemic in China under the gradually strengthening epidemic prevention and control measures. Cao *et al*. [11] established a SEIR derived model that considers the infectivity of latent patients and the measures of contact tracing. The SEI model established by Li *et al*. [12] studied the impact of unrecorded infected patients on the COVID-19 epidemic in China. They estimated that there were about 86% (95%CI: 82-90%) infected patients which had not been recorded before January 23, 2020, and about 79% recorded infected patients come from unrecorded infected patients. Chen *et al*. [13] proposed a BHRP (Bats-Hosts-Reservoir-People) transmission network model based on traditional SEIR model, and used its simplified model RP (Reservoir-People) to simulate the transmission mechanism of the early 2019-nCoV outbreak. They estimated that the $R_0$ (Basic reproduction number) of COVID-19 was 3.58 in China. Wei *et al*. [14] established the SEIR$^{+CAQ}$ model based on the transmission

mechanism, infection spectrum and prevention and control measures of COVID-19, so as to provide the basis for decision making about the development, prevention and control of COVID-19 epidemic. Li *et al*. [15] proposed a derived SEIR model to analyze the impact on the COVID-19 epidemic of the prevention measures and the people's compliance and the resumption of work and production. Wang *et al*. [16] proposed a SEIR derived network model by integrated multi-source data. They did a detailed analysis of when the resumption work and production should be done in Wuhan and other places in Hubei Province according to the $R_c$ (Control reproductive number), and whether it would or not cause the second outbreak of the COVID-19 epidemic.

The aforementioned transmission dynamic models of infectious disease provide important base to predict COVID-19 epidemic and make related prevention and control measures in China. These studies play positive theoretical and practical significance in analyzing the impact on the later stage of COVID-19 epidemic from the resumption of work, production and schooling. Now the COVID-19 epidemic is under control in China, though there are still trifle outbreaks. However, the COVID-19 epidemic are still serious abroad. In order to investigate the impact on the COVID-19 epidemic from the prevention and control measures taken by Chinese government over the past few months, we put forward an epidemic dynamics model named SEIRQH (Susceptible-Exposed-Infectious-Recovered-Quarantined-Hospitalized) based on the prevention and control measures adopted by Chinese government, such as considering the influence from travel restriction, contact tracing, centralized treatment, and the asymptomatic patients. Then a two-stage model is established. This two-stage model takes the "lockdown of Wuhan city" as the time line. The SEIR derived model comprises the first stage. It considers the infectivity of latent patients. It is used to investigate the trend of COVID-19 epidemic in the early stage, that is, before the "lockdown of Wuhan city" on

January 23, 2020. The second stage is our proposed SEIRQH model. It is used to study the COVID-19 epidemic trend after the "lockdown of Wuhan city" on January 23, 2020 under the implementation of prevention and control measures to COVID-19. The least square method is used to estimate the parameters of the SEIR derived model and our SEIRQH model. The basic reproduction number $R_0$ and control reproduction number $R_c$ of COVID-19 epidemic are calculated according to SEIR derived model and our SEIRQH model and their estimated parameters.

The results of this retrospective study based on the actual COVID-19 epidemic data before and after "lockdown of Wuhan city" show that the COVID-19 epidemic prevention and control measures taken by Chinese government, such as travel restriction, contact tracing, centralized treatment and so on, have effectively blocked the spread of the COVID-19 epidemic in China. The Huoshenshan, Leishenshan, and mobile cabin hospitals, built for centralized treatment to the COVID-19 patients, and medical workers from all over country rushed to support Hubei Province, provide a solid base for the success in struggling COVID-19 epidemic. All measures guarantee the recovery of the infected patients in Hubei Province. Those COVID-19 epidemic prevention and control measures taken by Chinese government have provided useful references for WHO and other countries to defeat the COVID-19 epidemic.

## Methods

We collect the COVID-19 epidemic data in the mainland of China from the official website of National Health Commission of the People's Republic of China (http://www.nhc.gov.cn/), and the COVID-19 epidemic data in Hubei Province from the official website of the Health Commission of Hubei Province (http://wjw.hubei.gov.cn/). The COVID-19 epidemic data about Hubei Province is from January 10, 2020 to April 30, 2020, and about the mainland of China is from January 23, 2020

to April 30, 2020. We take the "lockdown of Wuhan city" on January 23, 2020 as the borderline, such that the process against the COVID-19 epidemic is divided into two stages. The first stage is the SEIR derived model considering the latent patient infectivity. We use the epidemic data of Hubei Province from January 10, 2020 to January 22, 2020 and the least square method to estimate the parameters of SEIR derived model. Then we simulate the transmission trend of COVID-19 after January 23, 2020 in Hubei Province using this SEIR derived model. The second stage is a novel model proposed in this paper. We name it as SEIRQH (Susceptible-Exposed-Infectious-Recovered-Quarantined-Hospitalized) model. We adopt the least square method to estimate the parameters of the SEIRQH model in Hubei Province and in the mainland of China, respectively, by using the epidemic data of Hubei Province and the mainland of China from January 23, 2020 to April 30, 2020, respectively. It is the period when the prevention and control measures are taken by Chinese government. We analyze the impact of these measures, such as travel restrictions, contact tracing and the efforts of medical screening, on the development trend of COVID-19 epidemic in Hubei Province and in the mainland of China. All experiments are implemented in MATLAB.

**Datasets**

The COVID-19 epidemic data used in this paper are the actual data about COVID-19 in Hubei Province from January 10, 2020 to April 30, 2020, and about the COVID-19 in the mainland of China from January 23, 2020 to April 30, 2020. These datasets include the newly confirmed, deaths and cured cases of each day; and the cumulative confirmed, deaths and cured cases; and the number of hospitalized cases and the number of quarantined cases with medical observation. Fig. 1 shows the daily changes of some key attributes of the COVID-19 epidemic data in Hubei Province and in the mainland of China.
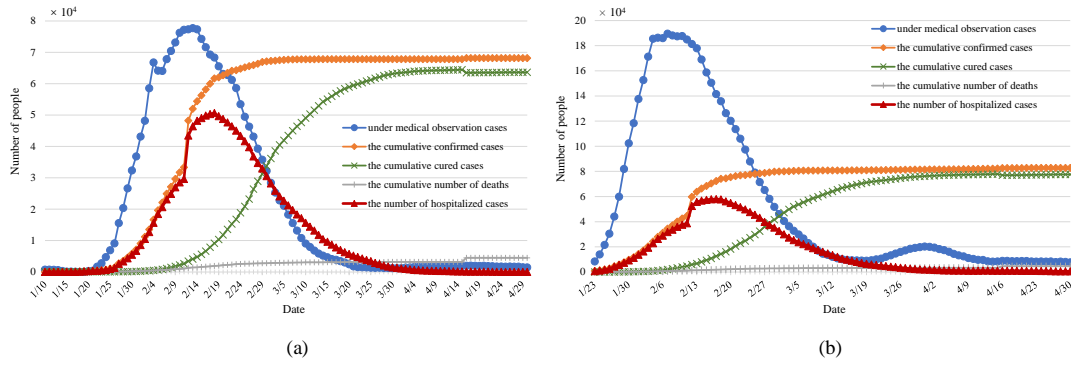
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Fig. 1. The actual trend of COVID-19 in Hubei Province (from January 10, 2020 to April 30, 2020) and in the

mainland of China (from January 23, 2020 to April 30, 2020). (a) Hubei Province, (b) the mainland of China.

## Infectious disease dynamic model

SEIR model is a widely used classical infectious disease transmission dynamics model. It assumes

that all individuals are at the risk of being infected and divides populations into four compartments,

which are susceptible (S), exposed (E), infected (I) and recovered (R). Compared to the SI and SIR

model, SEIR model takes into account the incubation period properties of infectious diseases. It has

evolved to several derived models [8, 9, 11] according to some factors such as whether the patients

in incubation period will infect others, whether the cured patients will be infected again, and whether

some prevention and control measures are taken. These derived models have been widely used in

preventing, controlling, and predicting the trend of many major epidemics, such as MERS (Middle

east respiratory syndrome) [17], HIV (Human immuno-deficiency virus) [18-19], SARS (Severe

acute respiratory syndrome) [20-21], COVID-19 [7, 9-11, 15, 22-26], and so on.

### The SEIR derived model considering the infectivity of latent patients

The SEIR model is a common SEIR derived model that considers the infectiousness of patients in

incubation period, as shown in Fig. 2. This SEIR derived model partitions the populations into

susceptible (S), exposed (E), infected (I), and recovered (R) parts. The individuals in incubation

(exposed) and infected periods have got the same infective capability. Assume that the infectious

probability is $\beta$, and the average contact number of individuals is $c$ between the susceptible and

the infected, and the contact factor is $\xi$ between the exposed, relative to the infected, and

susceptible individuals, then the dynamics differential equations of this SEIR derived model at time
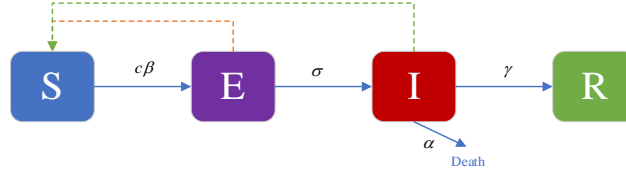
$t$ are shown in formula (1).



Fig. 2. The SEIR derived transmission dynamics model considering the infectivity of latent patients.

$$\begin{cases} dS/dt = -c\beta(S/N)I - c\beta\xi(S/N)E \\ dE/dt = c\beta(S/N)I + c\beta\xi(S/N)E - \sigma E \\ dI/dt = \sigma E - \gamma I - \alpha I \\ dR/dt = \gamma I \end{cases} \tag{1}$$

Where, $N(N = S + E + I + R)$ is the total number of individuals. Parameter $\sigma$ represents the

transition probability from the exposed to the infected. Its value is the reciprocal of the incubation

period, such as $\sigma = 1/5$ in [16, 27]. Parameters $\gamma$ and $\alpha$ are the recovery rate and death rate

of the infected, respectively. In the early stage of COVID-19, due to the insufficient awareness and

the poor prevention and control measures for the epidemic, we assume that the average contact

number between the exposed and the susceptible individuals is the same as that between the infected

and susceptible individuals, that is $\xi = 1$. The specific definitions of each parameter in formula (1)

are given in Table 1.

**The SEIRQH model**

With the increasing awareness of the transmission mechanism and clinical symptoms of COVID-

19, Chinese government has adopted a series of mandatory epidemic prevention and control

measures, such as restricting travel, contact tracing, centralized treatment and so on. To further

simulate the trend of COVID-19 in Hubei Province and the mainland of China after 23 January

2020, a new transmission dynamics model, named SEIRQH (Susceptible-Exposed-Infectious-

Recovered-Quarantined-Hospitalized) is proposed in this paper based on the epidemic prevention and control measures taken by Chinese government, as shown in Fig. 3.
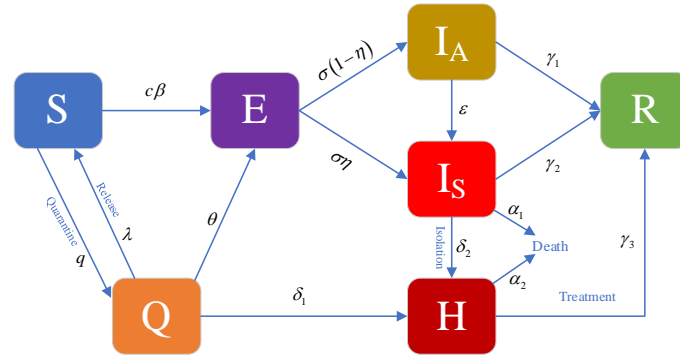


Fig. 3. The transmission dynamics model of our SEIRQH.

This SEIRQH model partitions the populations into seven compartments. They are susceptible (S), exposed (E), asymptomatic infected ($I_A$), symptomatic infected ($I_S$), recovered (R), quarantined (Q), and hospitalized (H). It takes into account the contact tracing measures in China. Once the susceptible individuals closely contact the individuals infected by the coronavirus (including the exposed, asymptomatic infected, or the symptomatic infected) in their daily life, then the susceptible individuals are moved into the quarantined compartment Q to accept the medical observation in probability $q$. The other 1-$q$ proportional individuals exposed to the virus are missed from the contact tracing and transformed into the compartment E. The quarantined individuals are then transformed into the compartment H in probability $\delta_1$, or into the compartment E in probability $\theta$, or into the susceptible compartment S in probability $\lambda$ ( $\lambda = 1/14$, the reciprocal of the quarantined period [9, 10, 16]) by the medical screening. The individuals in compartment E are then transformed into the infected in probability $\sigma$, where the proportions of the asymptomatic infection individuals $I_A$ and the symptomatic infection individuals $I_S$ are $1-\eta$ and $\eta$, respectively. Furthermore, there are $\varepsilon$ proportion of asymptomatic infections will be transformed into symptomatic infections. Through clinical diagnosis or nucleic acid testing, etc., the symptomatic

infections are converted into the hospitalized H with the probability $\delta_2$ and are sent to the

designated hospitals for isolation treatment quickly. The mortality of the symptomatic infectious

and of the hospitalized are $\alpha_1$ and $\alpha_2$, respectively. The recovery rates of the asymptomatic

infected individuals, the symptomatic infected individuals, and of the hospitalized individuals are

$\gamma_1$, $\gamma_2$, and $\gamma_3$, respectively. The dynamics differential equations of our SEIRQH model are shown

in formula (2).

$$
\begin{cases}
dS/dt = -cS\left(I_S + \mu I_A + \xi E\right)\left[\beta(1-q)+q\right] + \lambda Q \\
dE/dt = c\beta(1-q)S\left(I_S + \mu I_A + \xi E\right) + \theta Q - \sigma E \\
dI_A/dt = \sigma(1-\eta)E - (\gamma_1 + \varepsilon)I_A \\
dI_S/dt = \sigma\eta E + \varepsilon I_A - (\delta_2 + \gamma_2 + \alpha_1)I_S \\
dQ/dt = cqS\left[I_S + \mu I_A + \xi E\right] - (\lambda + \theta + \delta_1)Q \\
dH/dt = \delta_1 Q + \delta_2 I_S - (\gamma_3 + \alpha_2)H \\
dR/dt = \gamma_1 I_A + \gamma_2 I_S + \gamma_3 H
\end{cases}
\tag{2}
$$

Where, $c$ represents the average contact number between the infected and the susceptible persons,

$\beta$ is the probability of infection. The parameter $\mu$ is the contact factor between the asymptomatic

infected, relative to the symptomatic infected, and the susceptible. The parameter $\xi$ is the contact

factor between the exposed, relative to the symptomatic infected, and the susceptible. The specific

definitions of each parameter in formula (2) are given in Table 2.

**Basic reproduction number**

The basic reproduction number, $R_0$ [28-30], refers to the number of secondary infections produced

by an infected person through the entire duration of the infectious period when all individuals in a

certain area have no immunity to infectious diseases and there is not external control in

epidemiology. The $R_0$ is used to measure the spread capability of an infectious disease. It is the

quantitative base to judge the propagation and extinction of an infectious disease in the populations.

The control reproduction number, $R_c$ [16, 18], is the number of secondary infections by an infected

individual during the entire infectious duration with the control and intervention existing.

During the process of transmission of an infectious disease, if $R_0$ or $R_c$ is greater than 1, then the number of infected people will increase exponentially, and the infectious disease will eventually spread throughout the whole populations. However, the infectious disease tends to disappear with the decreasing number of infected people when $R_0$ or $R_c$ is less than 1. COVID-19 is an infectious disease that has never appeared before. $R_0$ and $R_c$ are of great significance in studying its spread trend, prevention, and control.

The next generation matrix method is the one that calculates the basic reproduction number $R_0$ by the spectral radius of the next generation matrix. The next generation matrix is obtained at the disease-free equilibrium point of the model [28-29]. Given an infectious disease model containing $n$ compartments, this model can be divided into infected class with $m(1 \leq m \leq n)$ compartments and uninfected class with $n-m$ compartments according to the biological significances of the infectious disease. We define vector $X = (x_1, \cdots x_i, \cdots x_m)$ for the infected class containing $m$ compartments, where $x_i(i=1,\cdots,m)$ represents the number of individuals in the compartment $i$. Let $f_i(X)$ represent the rate of newly-added individuals in the compartment $i$ via infection, then $v_i(X) = v_i^-(X) - v_i^+(X)$ is the rate of newly-added individuals in the compartment $i$ by any other means except for infection, where $v_i^-(X)$ and $v_i^+(X)$ are, respectively, the output and input rate of individuals of the compartment $i$ by any other means except for infection. Given the disease-free equilibrium point $x_0$, then we can obtain the next generation matrix $FV^{-1}$ by calculating the partial derivative matrices $F = \left[ \dfrac{\partial f_i(x_0)}{\partial x_j} \right]$ and $V = \left[ \dfrac{\partial v_i(x_0)}{\partial x_j} \right]$, where $i, j = 1, 2, \cdots, m$. The basic reproduction number $R_0$ is defined as the spectral radius of matrix $FV^{-1}$, shown in formula (3).

$$R_0 = \rho\left(FV^{-1}\right) \tag{3}$$

For SEIR derived model that considers the infectiousness of patients in incubation period, the $m = 2$ holds according to the biological significances of the infectious disease, that is, the infected class includes two compartments E and I. Therefore, the basic reproduction number $R_0$ of SEIR derived model can be calculated by formula (4).

$$R_0 = \rho\left(FV^{-1}\right) = \rho\left(\begin{bmatrix} c\xi\beta & c\beta \\ 0 & 0 \end{bmatrix}\begin{bmatrix} \dfrac{1}{\sigma} & 0 \\ \dfrac{1}{\gamma+\alpha} & \dfrac{1}{\gamma+\alpha} \end{bmatrix}\right) = \frac{c\xi\beta}{\sigma} + \frac{c\beta}{\gamma+\alpha} \tag{4}$$

where, $V = \begin{bmatrix} \sigma & 0 \\ -\sigma & \gamma+\alpha \end{bmatrix}$.

For our proposed SEIRQH model, we can see that there are four compartments in the infected class. They are E, $I_A$, $I_S$ and H, that is, $m = 4$ holds. Therefore, the control reproduction number $R_c$ of our SEIRQH model can be calculated by formula (5).

$$R_c = \rho\left(FV^{-1}\right) \times S(0) = \left[\frac{c\beta\mu(1-\eta)(1-q)}{\gamma_{I_A}+\varepsilon} + \frac{\eta\gamma_{I_A}+\varepsilon}{\varepsilon+\gamma_{I_A}} \times \frac{c\beta(1-q)}{\delta_I+\gamma_{I_S}+\alpha_1} + \frac{c\beta\xi(1-q)}{\sigma}\right] S(0) \tag{5}$$

Where, $S(0)$ is the initial value of the susceptible individual. The matrices $F$, $V$ and its inverse matrix $V^{-1}$ are shown in formulas (6), (7), and (8), respectively.

$$F = \begin{bmatrix} c\xi\beta(1-q) & c\mu\beta(1-q) & c\beta(1-q) & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \tag{6}$$

$$V = \begin{bmatrix} \sigma & 0 & 0 & 0 \\ \sigma(\eta-1) & \gamma_{I_A}+\varepsilon & 0 & 0 \\ -\sigma\eta & -\varepsilon & \delta_I+\gamma_{I_S}+\alpha_1 & 0 \\ 0 & 0 & -\delta_I & \gamma_H+\alpha_2 \end{bmatrix} \tag{7}$$

$$\boldsymbol{V}^{-1} = \begin{bmatrix} \dfrac{1}{\sigma} & 0 & 0 & 0 \\[2ex] \dfrac{1-\eta}{\gamma_{I_A}+\varepsilon} & \dfrac{1}{\gamma_{I_A}+\varepsilon} & 0 & 0 \\[2ex] \dfrac{\eta\gamma_{I_A}+\varepsilon}{\left(\gamma_{I_A}+\varepsilon\right)\left(\delta_I+\gamma_{I_S}+\alpha_1\right)} & \dfrac{\varepsilon}{\left(\gamma_{I_A}+\varepsilon\right)\left(\delta_I+\gamma_{I_S}+\alpha_1\right)} & \dfrac{1}{\delta_I+\gamma_{I_S}+\alpha_1} & 0 \\[2ex] \dfrac{\delta_I\left(\eta\gamma_{I_A}+\varepsilon\right)}{\left(\gamma_{I_A}+\varepsilon\right)\left(\delta_I+\gamma_{I_S}+\alpha_1\right)\left(\gamma_H+\alpha_2\right)} & \dfrac{\varepsilon\delta_I}{\left(\gamma_{I_A}+\varepsilon\right)\left(\delta_I+\gamma_{I_S}+\alpha_1\right)\left(\gamma_H+\alpha_2\right)} & \dfrac{1}{\left(\delta_I+\gamma_{I_S}+\alpha_1\right)\left(\gamma_H+\alpha_2\right)} & \dfrac{1}{\gamma_H+\alpha_2} \end{bmatrix} \tag{8}$$

# Results

## Experimental results of SEIR derived model

Based on the COVID-19 epidemic data of Hubei Province from January 10, 2020 to January 22, 2020, the parameters of SEIR derived model are calculated by using the least square method. All the parameters estimated are shown in Table 1. Fig. 4(a) shows the fitting result of SEIR derived model to the number of infected cases in Hubei Province from January 10, 2020 to January 22, 2020. Fig. 4 (b) shows the simulation results of the SEIR derived model for the trend of COVID-19 epidemic within 100 days after January 10, 2020, that is, from January 10, 2020 to April 19, 2020, based on the parameters shown in Table 1.

Table 1. Parameter definitions and their estimated values of the SEIR derived model

| Parameters | Definitions | Estimated values | Source |
|---|---|---|---|
| $c$ | The average number of contacts | 18.53002 | Parameter estimation |
| $\beta$ | Effective probability of infection | 0.01727 | Parameter estimation |
| $\sigma$ | Transition rate of exposed persons to the infected class | 1/5 | [16, 26] |
| $\gamma$ | Recovery rate of the infected | 0.19571 | Parameter estimation |
| $\alpha$ | Mortality rate of the infected | 0.00374 | Parameter estimation |
| $\xi$ | The contact factor between the exposed and susceptible persons relative to the infected | 1 | Assumed value |
| Initial values | Definitions | Estimated values | Source |
| $S(0)$ | Initial value of susceptible population | 252600.21 | Parameter estimation |
| $E(0)$ | Initial value of exposed population | 26 | Parameter estimation |
| $I(0)$ | Initial value of infected population | 38 | [31] |
| $R(0)$ | Initial value of recovered population | 2 | [31] |
| $R_0$ | Basic reproduction number | 3.2035 | -- |
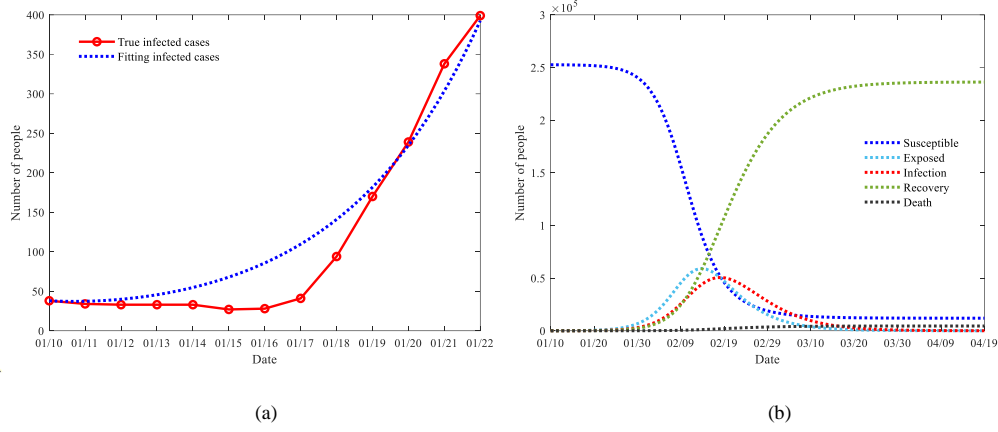
Fig.4. Experimental results of the SEIR derived model on COVID-19 epidemic data of Hubei Province.

(a) fitting results of the infected from 10 January, 2020 to 22 January, 2020, (b) simulation results of the trend of

COVID-19 epidemic within 100 days after January 10, 2020.

## Experimental results of SEIRQH model

Based on the official published data of the COVID-19 epidemic in Hubei Province and in the mainland of China from Jan. 23, 2020 to April 30, 2020, the parameters of the SEIRQH models in Hubei Province and in the mainland of China are estimated, respectively, using the least square method. These parameters are shown in Table 2. The fitting results of the SEIRQH model to the number of hospitalized patients in Hubei Province and the mainland of China are shown in Fig. 5.

Table 2. Parameter definitions and estimated values of the SEIRQH model

| Parameters | Definitions | Estimated values of Hubei Province | Estimated values of the mainland of China | Source |
|---|---|---|---|---|
| $c$ | The average number of contacts | 11.98513 | 11.97384 | Parameter estimation |
| $\beta$ | Effective probability of infection | $1.8 \times 10^{-9}$ | $1 \times 10^{-9}$ | Parameter estimation |
| $q$ | Quarantined rate of medical observation | $1.53 \times 10^{-7}$ | $1.25 \times 10^{-7}$ | Parameter estimation |
| $\lambda$ | Rate of uninfected quarantine individuals released to susceptible population | 1/14 | 1/14 | [9, 10, 16] |
| $\sigma$ | Transition rate of exposed persons to the infected | 1/5 | 1/5 | [16, 27] |
| $\eta$ | Probability of symptoms among infected persons | 0.68914 | 0.70395 | Parameter estimation |
| $\varepsilon$ | Transition rate of asymptomatic infected individuals to the symptomatic infected population | 0.09358 | 0.04488 | Parameter estimation |
| $\theta$ | Transition rate of quarantined persons to the exposed population | 0.10735 | 0.12363 | Parameter estimation |
| $\delta_1$ | Transition rate of quarantined persons to the hospitalized population | 0.03410 | 0.02317 | Parameter estimation |
| $\delta_2$ | Transition rate of symptomatic infected persons to the hospitalized population | 0.79477 | 0.70026 | Parameter estimation |
| $\gamma_1$ | Recovery rate of asymptomatic infected individuals | 0.09127 | 0.03745 | Parameter estimation |
| $\gamma_2$ | Recovery rate of symptomatic infected individuals | 0.01005 | 0.00429 | Parameter estimation |

| | | Estimated values of Hubei Province | Estimated values of the mainland of China | |
|---|---|---|---|---|
| $\gamma_3$ | Recovery rate of hospitalized individuals | 0.29934 | 0.34425 | Parameter estimation |
| $\alpha_1$ | Mortality rate of symptomatic infected individuals | 0.00701 | 0.00135 | Parameter estimation |
| $\alpha_2$ | Mortality rate of hospitalized individuals | 0.00140 | 0.00346 | Parameter estimation |
| $\xi$ | The contact factor between the exposed and susceptible persons relative to the symptomatic infected | 1.40569 | 1.17993 | Parameter estimation |
| $\mu$ | The contact factor between the asymptomatic infected and susceptible persons relative to the symptomatic infected | 1.50055 | 1.46045 | Parameter estimation |
| Initial values | Definitions | Estimated values of Hubei Province | Estimated values of the mainland of China | Source |
| $S(0)$ | Initial value of susceptible population | 500000.00 | 641000.00 | Parameter estimation |
| $E(0)$ | Initial value of exposed population | 4142.00 | 6126.98 | Parameter estimation |
| $I_A(0)$ | Initial value of asymptomatic infected population | 608.00 | 807.91 | Parameter estimation |
| $I_S(0)$ | Initial value of symptomatic infected population | 220.00 | 289.56 | Parameter estimation |
| $R(0)$ | Initial value of recovered population | 31 | 34 | [32, 33] |
| $Q(0)$ | Initial value of quarantined population | 2776 | 8420 | [32, 33] |
| $H(0)$ | Initial value of hospitalized population | 494 | 771 | [32, 33] |
| $R_c$ | Control reproductive number | 0.11428 | 0.09796 | -- |
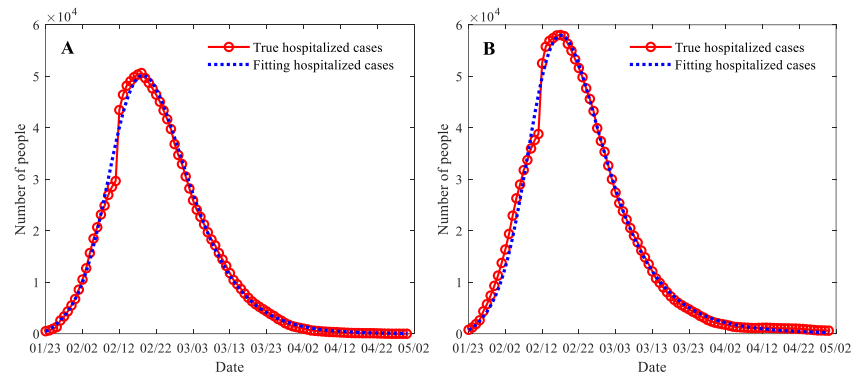


Fig. 5. Fitting results of our SEIRQH model for the hospitalized individuals of COVID-19.

(a) Hubei Province, (b) the mainland of China.

## Effects of prevention and control measures on COVID-19

The proposed SEIRQH model fits the trend of COVID-19 epidemic in Hubei Province and in the

mainland of China from January 23, 2020 to April 30, 2020 very well. This demonstrates that the

prevention and control measures taken by Chinese government prevent the large-scale transmission

of the COVID-19 epidemic effectively. How the parameters of SEIRQH model, such as the average

number of contacts $c$, the quarantined rate $q$, the transition rates $\delta_1$ of the quarantined to the

hospitalized individuals, and the probability $\delta_2$ of symptomatic infected patients transforming to

the hospitalized ones, will influence the trend of COVID-19? Here are the simulation results of the

SEIRQH model parameters on the COVID-19.

**Influence from the parameter *c***

During COVID-19 epidemic outbreaks in China, all levels of Chinese government have successively raised the emergency response level to public health emergencies, such as restricting public transportation, and closing restaurants and entertainment venues, and guiding residents to isolate themselves at home, and other preventive works as well. These measures reduced the person-to-person contact and the gathering infection. The average contact number in Hubei Province and in the mainland of China are estimated based on the actual data shown in Table 2, respectively, by using the least squares algorithm and MATLAB simulation experiments. These two average contact numbers are both 12. We study the impact from the average contact number *c* on the trend of COVID-19 by changing its values. Fig. 6 shows the simulation results of the hospitalized case variations in Hubei Province (Fig. 6(a)) and in the mainland of China (Fig. 6(b)) with the variations of parameter *c* within the 200 days after January 23, 2020, that is, from January 23, 2020 to August 10, 2020. The simulation results of peak time and the peak value of the hospitalized cases of COVID-19 are shown in Table 3.
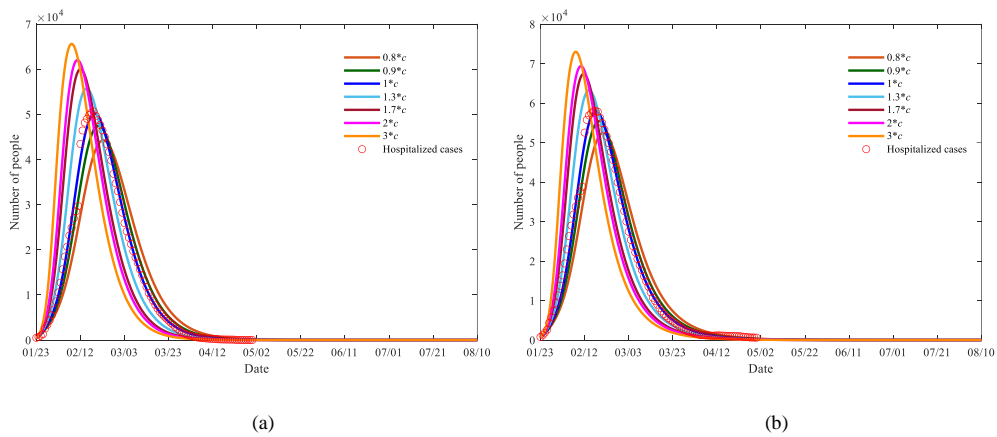


(a)                                              (b)

Fig. 6. The impact of the average contact number *c* on the hospitalized cases.

(a) Hubei Province, (b) the mainland of China.

Table 3. The simulation results of the peak time and peak value of the hospitalized cases in Hubei Province and in

the mainland of China with different values of $c$

| Hubei Province | 0.8*$c$ | 0.9*$c$ | 1*$c$ | 1.3*$c$ | 1.7*$c$ | 2*$c$ | 3*$c$ |
|---|---|---|---|---|---|---|---|
| Peak time (days) | 29.98 | 28.31 | 26.73 | 23.00 | 20.23 | 18.50 | 15.85 |
| Peak value | 44248 | 47519 | 50154 | 55722 | 59999 | 62022 | 65605 |
| the mainland of China | 0.8*$c$ | 0.9*$c$ | 1*$c$ | 1.3*$c$ | 1.7*$c$ | 2*$c$ | 3*$c$ |
| Peak time (days) | 28.32 | 26.65 | 24.99 | 21.81 | 19.43 | 18.20 | 15.92 |
| Peak value | 52425 | 55473 | 57951 | 63211 | 67371 | 69359 | 72995 |

Note: days refer to the days from January 23, 2020

**Influence from the quarantined rate $q$**

In order to prevent the transmission of the COVID-19 epidemic, the strict contact tracing measures have been taken throughout China. The susceptible individuals, who are in close contact with the exposed, asymptomatic infected and symptomatic infected persons of COVID-19, need to be quarantined with medical observation for 14 days. In SEIRQH model, the greater quarantined rate $q$ means the greater number of people need isolating. This means there are much more number of susceptible individuals who are in close contact with the exposed, infected, and asymptomatic infected persons. Therefore, the quarantined rate $q$ from the compartment S to the compartment Q reflects the people's awareness to abide by the measures reducing going out and isolating at home, also reflects the effectiveness of the measures guided by Chinese government.

This subsection studies the impact of measures such as reducing going out, isolating at home and not gathering on the trend of COVID-19 in Hubei Province and in the mainland of China by changing the quarantined rate $q$ for the susceptible population. The simulation results of the number of daily hospitalized cases in Hubei Province and in the mainland of China with the changes of $q$ values are shown in Fig. 7 during the 200 days from January 23, 2020 to August 10, 2020. The inflection point time and the peak value of the hospitalized cases with different values of $q$ are shown in Table 4.
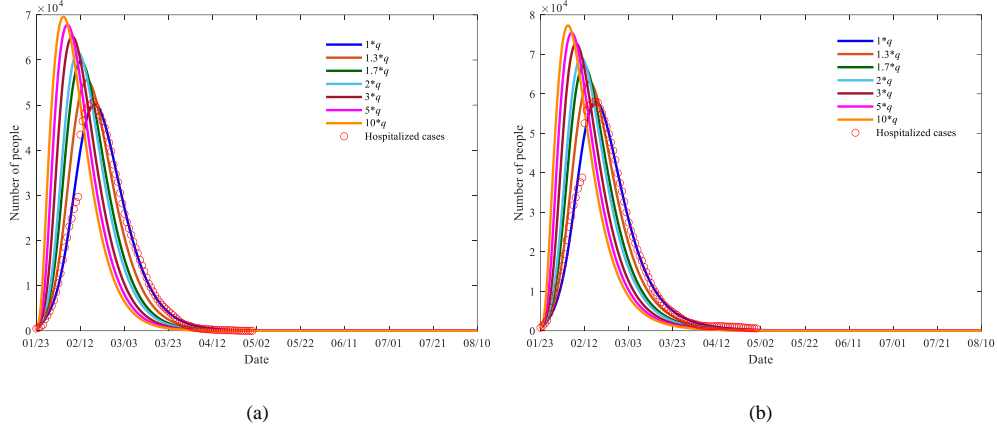
Fig. 7. The impact of the quarantined rate $q$ on the number of hospitalized cases.

(a) Hubei Province, (b) the mainland of China.

Table 4. The simulation results of peak time and the peak value of the hospitalized cases in Hubei Province and the

mainland of China with different value $q$

| Hubei Province | $1*q$ | $1.3*q$ | $1.7*q$ | $2*q$ | $3*q$ | $5*q$ | $10*q$ |
|---|---|---|---|---|---|---|---|
| Peak time (days) | 26.73 | 22.98 | 20.21 | 18.92 | 16.32 | 14.03 | 12.25 |
| Peak value | 50154 | 55532 | 59701 | 61677 | 65222 | 67806 | 69563 |
| the mainland of China | $1*q$ | $1.3*q$ | $1.7*q$ | $2*q$ | $3*q$ | $5*q$ | $10*q$ |
| Peak time (days) | 24.99 | 22.34 | 19.87 | 18.63 | 16.26 | 14.20 | 12.46 |
| Peak value | 57952 | 63086 | 67162 | 69127 | 72721 | 75429 | 77315 |

Note: days mean the days from January 23, 2020

**Influence from the medical screening**

Clinical imaging features are considered as the diagnostic criteria for COVID-19 in the Diagnosis

and Treatment Protocol for COVID-19 (Trial Version 5) [34] issued by the National Health

Commission of the People's Republic of China. Increasing the medical screening can enable the

infected persons diagnosed and treated timely. This will prevent the transmission of COVID-19 and

benefit the recovery rate of infected individuals, and shorten the period against the epidemic.

The transition rate $\delta_1$ from the quarantined to the hospitalized and the transition rate $\delta_2$ from

the symptomatic infected to the hospitalized are both proportional to the power of medical screening

in our SEIRQH model. Therefore, we investigate the impact of medical screening power to the

COVID-19 by changing the values of parameters $\delta_1$ and $\delta_2$.

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Fig. 8 shows the variations of the number of hospitalized cases in Hubei Province from January 23, 2020 to August 10, 2020 with different values of parameters $\delta_1$ and $\delta_2$. Fig. 9 displays the influence of parameters $\delta_1$ and $\delta_2$ on the number of hospitalized cases in the mainland of China from January 23, 2020 to August 10, 2020.



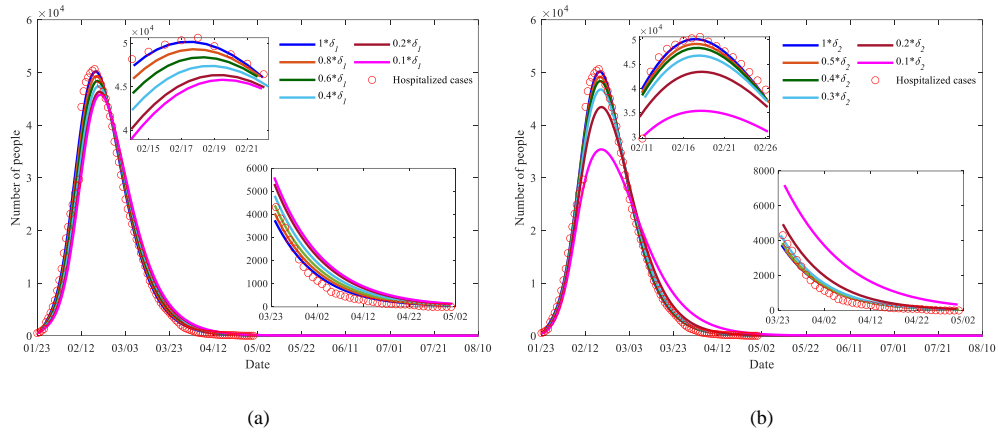(a)                                                                 (b)

Fig. 8. The impact of medical screening power on the trend of COVID-19 epidemic in Hubei Province.

(a) the number of the hospitalized cases with different values of parameter $\delta_1$, (b) the number of the hospitalized

cases with different values of parameter $\delta_2$



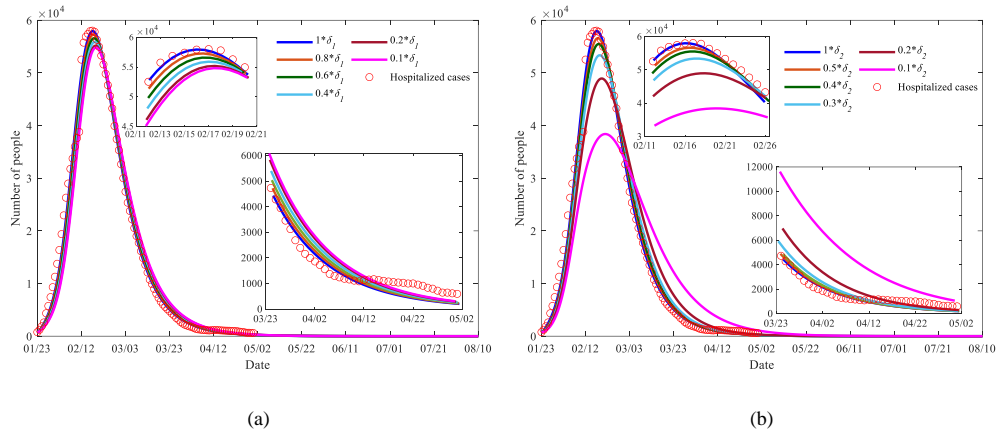(a)                                                                 (b)

Fig. 9. The impact of medical screening power on the trend of COVID-19 epidemic in the mainland of China.

(a) the number of the hospitalized cases with different values of parameter $\delta_1$, (b) the number of the hospitalized

cases with different values of parameter $\delta_2$

## Discussion

### SEIR derived model

It can be seen from the experimental results in Fig. 4(a) that the SEIR derived model fits the COVID-19 infection cases in Hubei Province from January 10, 2020 to January 22, 2020 to some extent. The simulation results in Fig. 4(b) show that the COVID-19 epidemic enters the outbreak phase in the late of January, and reaches its peak on February 18, 2020. The number of infections of the peak is 50,629. Subsequently, the number of COVID-19 infections gradually decreases, and disappears in the early of April. The number of deaths goes up slowly, and as of April 19, 2020, the death toll is 4,513. Comparing the simulation results in Fig. 4(b) to the actual data of COVID-19 in Hubei Province from January 10, 2020 to April 30, 2020 in Fig. 1(a), it can be found that the SEIR derived model can simulate the trend of COVID-19 epidemic in Hubei Province after January 23, 2020. This fact demonstrate that the first stage of our two-stage transmission dynamics model is effective in predicting the COVID-19 epidemic trend in Hubei province after January 23, 2020.

Although the basic reproduction number $R_0$ of the COVID-19 has not been known yet, its value in the early stage of COVID-19 outbreak in Hubei Province can be calculated by using the estimated parameters shown in Table 1 and the formula (4). It is 3.2035, slightly higher than the 1.4-2.5 released by the WHO [35]. But it is consistent with 2.3-3.58 published by Chen *et al*. [13], and is also consistent with 2.24-5.71 given by Zhao *et al*. in [36], and is also consistent with the 3.2 given by Huang *et al*. in [37] when they are considering the delay in treatment. It is lower than the 6.47 (95%CI: 5.71-7.23) given by Tang *et al*. [9].

### SEIRQH model

It can be seen from the results in Fig. 5 that the proposed SEIRQH model fits the number of the

hospitalized persons of COVID-19 in Hubei Province and in the mainland of China perfectly. This fact demonstrates that the proposed SEIRQH model can accurately predict the trend of the COVID-19 epidemic when the prevention and control measures are implemented by Chinese government. The control reproductive number $R_c$ of COVID-19 in Hubei Province and in the mainland of China are calculated based on formula (5) and the estimated values of the parameters of our SEIRQH model in Hubei Province and the mainland of China in Table 2. They are 0.11428 and 0.09796, respectively. They are both less than 1, indicating that the COVID-19 infectious disease will gradually disappear in China. This fact also demonstrates that the prevention and control measures against COVID-19 such as restricting travel, home quarantine, and contact tracing implemented by Chinese governments all over the China have effectively controlled the spread of COVID-19. The Huoshenshan, Leishenshan and mobile cabin hospitals in Wuhan and other places with severe epidemics for centralized treatment of infected patients not only effectively prevented the large-scale spread of the COVID-19, but also concentrated resources to treat infected patients, which has played a key role in rapidly decreasing the number of hospitalized cases and effectively controlling the COVID-19 epidemic in a short time.

**Prevention and control measures on COVID-19**

The SEIRQH model fits the actual data of COVID-19 epidemic in Hubei Province and in the mainland of China from January 23, 2020 to April 30, 2020 very well. This demonstrates that the prevention and control measures taken by Chinese government are effective in preventing the wide spread of COVID-19 epidemic in China. Here are sensitivity analyses to the parameters of SEIRQH model, so as to further investigate the impact of prevention and control measures on the trend of COVID-19.

**Sensitivity analyses to the parameter *c***

It can be seen from Fig. 6 that the number of hospitalized cases in Hubei Province and in the mainland of China both increase with the increasing of average contact number. The peak time of the number of hospitalized cases comes earlier when the average contact number increases. That is to say, if the Chinese government reduces or fails to adopt strict control measures, such as home quarantine and travel restrictions, the COVID-19 epidemic may become aggravated, and the hospitalized cases may have got a higher peak value, and the epidemic inflection point will be earlier.

The experimental results in Table 3 show that the inflection point of the hospitalized cases in Hubei Province and in the mainland of China comes earlier and the peak value of the hospitalized cases becomes bigger with the increasing of parameter *c*. When the average contact number *c* is doubled, the peak value of hospitalized cases in Hubei Province will increase by 11,868 (=62022-50154), and the peak time, that is the time of inflection point in Hubei Province, will come 8.23 (=26.73-18.5) days earlier; while the peak value of hospitalized cases in the mainland of China will increase by 11,408 (=69359-57951), and the inflection point of it will come 6.79 (=24.99-18.20) days earlier. Therefore we can say that the prevention and control measures are effective taken by Chinese government. They not only prevent the large-scale spread of the COVID-19 epidemic in China, but also minimize its harm to humankind.

Although the results in Fig. 6 and Table 3 show that the peak value of the hospitalized cases in Hubei Province and in the mainland of China will be reduced by taking more stricter prevention and control efforts, and the inflection point time will be delayed as well, that is, the peak time of the number of hospitalized cases in Hubei Province and the mainland of China comes later. But the stricter measures may cause unnecessary social panic. Therefore, the prevention and control

measures need to be formulated according to the actual situation of COVID-19 epidemic, so as to prevent its widespread transmission and minimize its harm maximally.

**Sensitivity analyses to the quarantined rate $q$**

The experimental results in Fig. 7 show that the peak value of the hospitalized cases in Hubei Province and the mainland of China becomes larger as the value of $q$ increases, and the inflection point of the hospitalized case number comes earlier. The number of hospitalized cases in Hubei Province and the mainland of China rises with the increasing $q$ value. It can be concluded that people will be in the risk to be infected if they do not abide by the guidance from the government, because going out and gathering will increase the probability to contact the exposed, the infected, and the asymptomatic infected. This may cause the more severe COVID-19 epidemic than current.

It can also be seen from the results in Table 4 that both the peak values of hospitalized cases in Hubei Province and in the mainland of China increases with the increasing $q$ value, and the inflection point time appears earlier as well. The peak value of hospitalized cases in Hubei Province or in the mainland of China will be increased by about 20,000 individuals if $q$ is increased to its 10 times. The inflection point may appear around February 4, 2020, with 14.48 (=26.73-12.25) and 12.53 (=24.99-12.46) days earlier as well in Hubei Province and the mainland of China, respectively.

The theoretical analyses in Table 4 and Fig. 7 reveal that stricter measures of isolation at home and prohibition of gathering can further decrease the quarantine probability, so as to reduce the risk to be infected for susceptible persons. Therefore, citizens can do a favor against COVID-19 epidemic by abiding by the prevention and control measures.

**Sensitivity analyses to the medical screening**

It can be seen from Fig. 8(a) that the peak value of the hospitalized cases drops when the value of

parameter $\delta_1$ decreases. This will lead to more pressure on the later period of the epidemic and make the epidemic last more time. In other words, decreasing of the medical screening strength for the quarantined people will increase the later pressure against COVID-19 and will increase the risk of the epidemic spreading further and increasing the death numbers as well. Fig. 8(b) shows that the transition rate $\delta_2$ has the similar impact on the trend of COVID-19 in Hubei Province as that of the rate $\delta_1$ does. But the influence from $\delta_2$ is bigger than that from $\delta_1$.

From the experimental results in Fig. 9, we can see that the impact of parameters $\delta_1$ and $\delta_2$ on the COVID-19 in the mainland of China is similar to that in Hubei Province. The transition rate $\delta_2$ has a more significant impact on the trend of COVID-19 in the mainland of China. The number of the hospitalized decreases very slowly in the later period of COVID-19 with the decreasing of parameters $\delta_1$ and $\delta_2$. Consequently the end of COVID-19 is postponed, even become uncontrollable, especially the decreasing of parameter $\delta_2$ can make stronger influence on COVID-19 than parameter $\delta_1$ can.

The above sensitivity analyses of the average contact number $c$, the quarantined rate $q$, and the transition rates $\delta_1$ and $\delta_2$ in the proposed SEIRQH model on the trend of COVID-19 show that the proposed SEIRQH model can simulate the actual trend of COVID-19 in PR China. The prevention and control measures taken by Chinese government play significant role against the COVID-19 spreading in PR China.

## Conclusions

COVID-19 epidemic caused by 2019-nCoV has been controlled in PR China. We propose a two-stage transmission dynamics model to conduct reviewing study to the COVID-19 in PR China. This model uses the "lockdown of Wuhan city" as the time line. The first stage is the SEIR derived model

considering the infectivity of latent patients. The second stage is our proposed novel infectious disease transmission dynamics model named as SEIRQH. The SEIRQH is based on the prevention and control measures taken by Chinese government.

The extensive reviewing study show that proposed two-stage model, especially the proposed SEIRQH model simulates the actual data perfectly in Hubei Province and in the mainland of China from January 23, 2020 to August 10, 2020. This demonstrates that the strategies are very effective taken by Chinese government against COIVD-19. It also provides references to WHO and other countries again the COIVID-19 epidemic.

## List of abbreviations

2019-nCoV: 2019 novel coronavirus;

WHO: World health organization;

COVID-19: Coronavirus disease 2019;

SI: Susceptible-Infectious;

SIR: Susceptible-Infectious-Recovered;

SEIR: Susceptible-Exposed-Infectious-Recovered;

SEIRQH: Susceptible-Exposed-Infectious-Recovered-Quarantined-Hospitalized;

$R_0$: Basic reproduction number;

$R_c$: Control reproductive number;

MERS: Middle east respiratory syndrome;

HIV: Human immuno-deficiency virus;

SARS: Severe acute respiratory syndrome;

## Declarations

### Ethics approval and consent to participate

Not applicable

### Consent for publication

Not applicable

### Availability of data and materials

Not applicable

### Competing interests

The authors declare no conflict of interest.

### Funding

### Authors' contributions

MW, JX, and SX discussed and designed this study. MW implemented all algorithms and wrote the experimental results. JX wrote this paper. SX revised the paper. All authors read and approved the final manuscript.

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Not applicable

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