

TRANSMISSION DYNAMICS AND CONTROL STRATEGIES OF COVID-19 IN WUHAN, CHINA

LIUYONG PANG*, SANHONG LIU^{†,¶}, XINAN ZHANG[‡],
TIANHAI TIAN[§] and ZHONG ZHAO*

**School of Mathematics and Statistics
Huanghuai University, Zhumadian 463000, P. R. China*

*†School of Mathematics and Statistics
Hubei University of Science and Technology
Xianning, Hubei 437100, P. R. China*

*‡School of Mathematics and Statistics
Central China Normal University
Wuhan 430079, P. R. China*

*§School of Mathematical Sciences
Monash University, Melbourne, Vic 3800, Australia*

¶jerrylish@163.com

Received 23 February 2020

Accepted 14 April 2020

Published 30 April 2020

In December 2019, a novel coronavirus, SARS-COV-2, was identified among patients in Wuhan, China. Two strict control measures, i.e., putting Wuhan on lockdown and taking strict quarantine rule, were carried out to contain the spread of COVID-19. Based on the different control measures, we divided the transmission process of COVID-19 into three stages. An SEIHR model was established to describe the transmission dynamics and was applied to fit the published data on the confirmed cases of Wuhan city from December 31, 2019 to March 25, 2020 to deduce the time when the first patient with COVID-19 appeared. The basic reproduction number was estimated in the first stage to demonstrate the number of secondary infectious cases generated by an average infectious case in the absence of policy intervention. The effective reproduction numbers in second and third stages were estimated to evaluate the effects of the two strict control measures. In addition, sensitivity analysis of the reproduction number according to model parameters was executed to demonstrate the effect of the control measures for containing the spread of COVID-19. Finally, the numerical calculation method was applied to investigate the influence of the different control measures on the spread of COVID-19. The results indicated that following the strict quarantine rule was very effective, and reducing the effective contact rates and improving the diagnosis rate were crucial in reducing the effective reproduction number, and taking control measures as soon as possible can effectively contain a larger outbreak of COVID-19. But a bigger challenge for us to contain the spread of COVID-19 was the transmission from the

[¶]Corresponding author.

asymptomatic carriers, which required to raising the public awareness of self-protection and keeping a good physical protection.

Keywords: COVID-19; Transmission Dynamics; Basic Reproduction Number; Control Measures; Numerical Simulation.

1. Introduction

In December 2019, a new respiratory virus named SARS-CoV-2 was identified first in Wuhan, Hubei Province, China.¹ The virus is the seventh member of the coronavirus family which includes other viruses such as 229E, NL63, OC43, HKU1, SARS-CoV and MERS-CoV.² It has caused coronavirus disease 2019 (COVID-19). The early confirmed cases were linked to the illegal sale of wild animals in Huanan Seafood Wholesale Market in Wuhan, China, which showed SARS-CoV-2 might cross the species barrier and spread from animals to humans. However, a growing number of cases proved that even those that had not been exposed to the market had contracted the disease, which indicated person-to-person transmission.³⁻⁶ COVID-19 turned out to be highly contagious⁷ and spread quickly to other areas. Increasing evidences have shown that COVID-19 is contagious during its incubation period, which makes it more difficult to contain the spread of COVID-19.^{8,9} In mainland China, a total of 81,960 cases had been confirmed as of March 25, 2020, including 50,006 cases in Wuhan. The panic caused by the disease forced many cases with flu into hospitals and exacerbated the shortage of medical resources. At present, the number of the confirmed cases with COVID-19 is increasing rapidly worldwide, especially in the United States, Italy and Spain. The COVID-19 pandemic has aroused deep concern around the world. A common measure for most countries to implement is to resort to strict quarantine. But it is not yet known to what extent the quarantine measures have been effective in containing the spread of COVID-19 and which factors have influence on their effectiveness. This study is to investigate these problems by applying a mathematical model to examine the quarantine measures in Wuhan city so as to provide enlightenment for the fighting against the COVID-19 in other places.

Mathematical modeling is a very useful and important tool to study the transmission dynamics of infectious diseases. Effective control measures can be designed and evaluated via mathematical analysis and numerical simulations of the model.¹⁰ Recently, there were some interesting studies on modeling the outbreak of COVID-19 in mainland China. Based on the clinical progression of the epidemic, epidemiological status of the individuals and intervention measures, Tang *et al.* devised a deterministic compartmental model to describe the transmission dynamics of COVID-19. Sensitivity analysis showed that interventions such as quarantine and isolation of those persons in close contact with the infected cases could effectively reduce the basic reproduction number and control the risk of transmission.¹¹ Joseph *et al.* used a SEIR metapopulation model to simulate the epidemics across all of the major cities in China, estimated the basic reproductive number, and inferred

that epidemics were already growing exponentially in multiple major cities of China with one to two weeks lag behind the Wuhan outbreak.¹² In the early phase of the outbreak, Zhao *et al.* applied the exponential growth model to estimate the basic reproduction number of COVID-19, and found it fell between 2.24 and 3.58.¹³ Lai *et al.* used the de-identified and aggregated domestic population movement data from 2013 to 2015 and international air travel data in 2018 to explore patterns of mobility of travelers from Wuhan to other cities in China, and informed the risk of COVID-19 spreading.¹⁴ Based on the data on the confirmed cases before January 23, 2020, Liu *et al.* applied an exponential growth model and maximum likelihood estimation to estimate the basic reproductive number, and found it fell between 2.32 and 3.63. Results showed that COVID-19 might have a higher pandemic risk than SARS in 2003, and suggested more rigorous control measures and prevention strategies to contain its further spread.¹⁵ Li *et al.* developed a mathematical model to simulate the spatiotemporal dynamics of epidemics among 375 Chinese cities and divided the infective individuals into two classes: (i) the documented infected individuals with severe symptoms; and (ii) the undocumented infected individuals.¹⁶ Kiesha *et al.* divided the population into the susceptible (S), the exposed (E), the infected (I) and the removed (R) individuals according to the infection status and constructed a deterministic stage-structured SEIR model to simulate the outbreak in Wuhan. Results indicated that restrictions on activities in Wuhan, if maintained until April, would probably help to delay the epidemic peak.¹⁷ Roda *et al.* found that an SIR model performs much better than an SEIR model in representing the information contained in the confirmed-case data based on the Akaike Information Criterion for model selection and used an SIR model to predict the COVID-19 epidemic in Wuhan after the lockdown and quarantine of the city and reported the results of modeling the impacts of the strict quarantine measures and the potential of a second outbreak after the return-to-work in the city.¹⁸

In this paper, we construct an SEIHR mathematical model to simulate the data on the confirmed cases in Wuhan city to investigate the effectiveness of its quarantine measure and their factors influencing the effectiveness. The rest of this paper is arranged as follows. In Sec. 2, an SEIHR model is established to describe the transmission dynamics of COVID-19. In Sec. 3, the model is applied to fit the published data for numbers of the confirmed cases in Wuhan from December 31, 2019 to March 25, 2020 to deduce the time when the first patient with COVID-19 appeared, and to estimate the reproduction number at various stages. In Sec. 4, sensitivity analysis of the reproduction number in terms of model parameters is conducted to investigate their factors influencing the effect. In Sec 5, the transmission dynamics of COVID-19 is concluded.

2. The Transmission Model

Due to the high viral load observed in the patients with COVID-19,^{19–22} the patients are highly contagious. Recent research showed that some patients with COVID-19

had high level of the virus in throat swabs in the early stages of their disease, which means the pathogen could easily be emitted in a cough or sneeze — a process known as viral shedding — and spread to others.²³ When susceptible persons are in close contact with the infected persons, they will possibly get infected and become exposed ones. Note that the exposed persons are also contagious during the incubation period even if they are asymptomatic,^{24–26} and SARS-CoV-2 can be detected in their upper respiratory tracts, even early in the course of infection or before the disease onset.²¹ Therefore, when susceptible persons are in close contact with them, they will possibly get infected and also become exposed ones. The virus begins to multiply within cells when a person gets infected with COVID-19. After an incubation period of 1 to 14 days, early symptoms of infected cases begin to appear. We assume that all confirmed infected cases are taken into hospitals. For the sake of convenience, we divide the total population $N(t)$ into five categories: the susceptible, the exposed, the infected, the hospitalized and the recovered, with the size denoted by $S(t)$, $E(t)$, $I(t)$, $H(t)$ and $R(t)$ at time t , respectively. The flowchart of model is depicted in Fig. 1.

The transfer diagram leads to the following model:

$$\begin{cases} \frac{dS}{dt} = \Lambda - \frac{\beta_1 SI}{N} - \frac{\beta_2 SE}{N} - \mu S, \\ \frac{dE}{dt} = \frac{\beta_1 SI}{N} + \frac{\beta_2 SE}{N} - (\alpha + \mu)E, \\ \frac{dI}{dt} = \alpha E - (\mu + d + \gamma)I, \\ \frac{dH}{dt} = \gamma I - (\mu + d + \delta)H, \\ \frac{dR}{dt} = \delta H - \mu R, \end{cases} \quad (2.1)$$

where Λ is the recruitment rate, μ is the natural death rate, β_1 is the effective contact rate of susceptible individuals with infected individuals, β_2 is the effective contact rate of susceptible individuals with exposed individuals, $\frac{1}{\alpha}$ is the average incubation period of COVID-19, γ is the diagnosis rate of COVID-19, δ is the average recovery rate and d is the death rate of COVID-19.

Thus, the total population size $N(t)$ is given by $N = S(t) + E(t) + I(t) + H(t) + R(t)$ at time t . Note that there is always a unique disease-free equilibrium given by

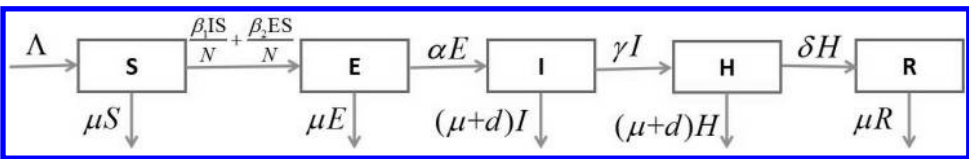


Fig. 1. Schematic diagram of model.

$E_0 = (\frac{\Lambda}{\mu}, 0, 0, 0, 0)$. The reproductive number of system (2.1) is as follows (see the appendix for details):

$$\mathcal{R} = \frac{\beta_2}{\alpha + \mu} + \frac{\beta_1 \alpha}{(\alpha + \mu)(\mu + d + \gamma)}. \quad (2.2)$$

By the results in Driessche and Watmough,²⁷ it follows that the disease-free equilibrium E_0 is stable if $\mathcal{R} < 1$, and unstable if $\mathcal{R} > 1$. Furthermore, a positive equilibrium exists when $\mathcal{R} > 1$. From the control point of view, COVID-19 can be controlled if $\mathcal{R} < 1$ and it becomes endemic in the population if $\mathcal{R} > 1$.

Remark: For the sake of distinction, thereafter we describe the basic reproductive number in the first stage as \mathcal{R}_0 , and the effective reproductive numbers in the second and third stages separately as \mathcal{R}_{e1} and \mathcal{R}_{e2} .

3. Results

3.1. Data

During the fight against COVID-19, Chinese authorities put Wuhan city on lockdown on January 23, 2020. With the use of the two specialized hospitals (Houshenshan and Leishenshan hospitals) and many mobile cabin hospitals, Chinese authorities imposed strict quarantine measures on February 11, 2020, and got almost all patients with pneumonia-related fever quarantined.²⁸ According to the change of the quarantine measures, we divide the process of fighting against COVID-19 into three different stages. The first stage, before January 23, 2020, is called as the early outbreak phase of COVID-19. In this stage, the transmission of COVID-19 was largely thought to be only from animals to humans, and it did not attract enough attention. The second stage, from January 23, 2020 to February 11, 2020, is called as the partial isolation phase. In this stage, only the confirmed cases were quarantined and hospitalized, mainly because too many suspected cases appeared and caused the grievous shortage of medical resources. The third stage, after February 11, 2020, is called as the rigorous isolation stage, in which almost all patients diagnosed with pneumonia-related fever were quarantined. Accordingly, this study uses three sets of data. The first set of data includes the number of the confirmed cases (accumulated hospitalized cases) from December 31, 2019 to January 23, 2020, in which a total of 496 confirmed cases were reported. The second set of data includes the number of the confirmed cases from January 24, 2020 to February 11, 2020, in which a total of 19,558 confirmed cases were reported. The third set of data includes the number of the confirmed cases from February 11, 2020 to March 25, 2020, in which a total of 50,006 confirmed cases were reported. All of those data were reported by Wuhan Municipal Health Commission. We use these published data to estimate the parameter values of model (2.1) in different stages, and execute chi-square test to verify how well our model actually reflects the published data.

3.2. Parameter estimation

Assume that the life expectancy of people is 70 years old,¹⁰ then the natural death rate is estimated as $\mu = 1/(70 \times 365) \approx 3.9139 \times 10^{-5}$. Based on the fact that the population of permanent residents in Wuhan approximates 12 million people, i.e., $N = 1.2 \times 10^7$, the recruitment rate of humans is estimated as $\Lambda = \mu \times N \approx 4.6967 \times 10^2$. Since control strategies are different in every spread stage of COVID-19, parameter estimations will be carried out step by step.

In the first stage, the initial values of model (2.1) are assumed to be $S(0) = 1.2 \times 10^7$, $E(0) = 0$, $I(0) = 1$, $H(0) = 0$ and $R(0) = 0$, respectively. There are seven undetermined parameters, i.e., the time span from the day when the first patient with COVID-19 appeared to December 31, 2019 (d_1), the effective contact rates (β_1 and β_2), the rate of progression to infectious (α), the diagnosis rate (γ), the average recovery rate (δ) and the death rate by disease (d). We estimate those parameter values by calculating the minimum sum of square (MSS)^{29–31}

$$\text{MSS} = \sum_i (\log_2(\text{the confirmed cases of the } i\text{th day}) - \log_2(\text{the simulated data of the } i\text{th day}))^2,$$

with Matlab tool `fminsearch`, which is a part of the optimization toolbox.

We first apply the confirmed cases of Wuhan from December 31, 2019 to January 23, 2020 to estimate all unknown parameters and list their values in Table 1. In addition, in order to obtain optimal parameters, we apply the monte carlo method to run 2000 trials and select 400 best results. If we regard every parameter as normal distribution, the 95% confidence intervals (CI) are calculated in Table 1.

From Table 1, we can infer that the infectivity of the infected persons is stronger than that of the exposed persons. The average incubation period of COVID-19 is assessed as $\frac{1}{\alpha} = \frac{1}{0.1700} \approx 5.8824$ days, which is consistent with the reports from World Health Organization and some other literatures.^{32–34} The diagnosis rate of COVID-19 (γ) is estimated as 0.0315, which indicates that only 3.15% of the infected cases are confirmed. The main reason may be that the hospitals are in the serious shortage of the confirmatory test kits. It implies that the number of the confirmed cases is underreported at this point.³⁵ The recovery rate is estimated as 0.1396, which indicates that it takes eight days to cure a confirmed case on average. The death rate of COVID-19 is assessed as 5%. In addition, we deduce that the

Table 1. Estimation of parameters with 95% confidence interval.

Pars	β_1	β_2	α	γ
Values	0.2983	0.1706	0.1700	0.0315
95% CI	[0.2389, 0.3540]	[0.1287, 0.2025]	[0.1342, 0.2088]	[0.0265, 0.0393]
Pars	δ	d	d_1	\mathcal{R}_0
Values	0.1396	0.0500	28.0000	4.6355
95% CI	[0.1092, 0.1724]	[0.0384, 0.0611]	[26.8614, 29.8036]	[3.7552, 5.4153]

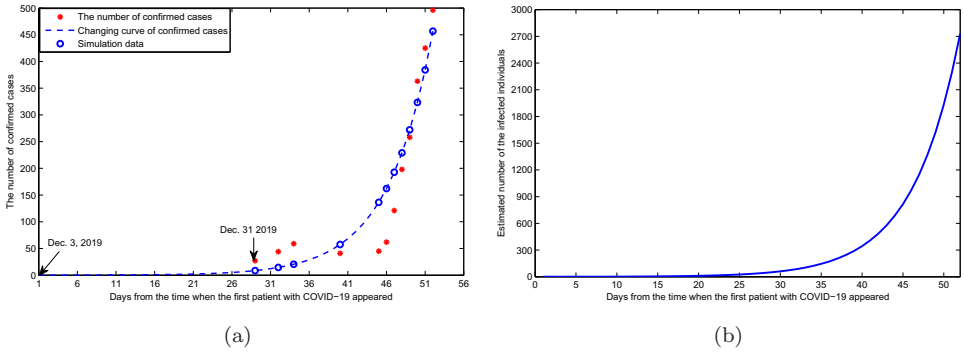


Fig. 2. (a) Comparison of the daily numbers of confirmed cases simulated in the model and the numbers from the report from December 31, 2019 and January 23, 2020. (b) Estimated number of the infected persons from the time when the first patient with COVID-19 appeared to January 23, 2020.

first infected patient with COVID-19 appeared nearly on December 3, 2019 (see Fig. 2). We also infer that there are about 2731 infected cases before January 24, 2020, which means that only 18.16% of total infections in Wuhan were reported. The number 18.16% is close to 14% estimated by Li *et al.*¹⁶ The reason for the underreporting of the number of the infected cases is that the diagnosis rate is low.

According to the simulated results of the first phase, initial values of model (2.1) in the second phase are given as $S(0) = 8.9938 \times 10^6$, $E(0) = 3.2513 \times 10^3$, $I(0) = 2,731$, $H(0) = 228$ and $R(0) = 126$, respectively. We assume the average incubation period remain unchanged, then we fix the conversion ratio from the exposed persons to the infected persons as $\alpha = 0.1700$. In addition, we also fix the natural death rate as $\mu = 3.9139 \times 10^{-5}$. Note the fact that about 3 million people (about 25% of people in Wuhan) departed from Wuhan on January 23, 2020 when Wuhan was put on lockdown. Then we recalculate the recruitment rate of humans in the second stage as $\Lambda \approx 9 \times 10^6 \times \mu \approx 3.5225 \times 10^2$. The effective contact rates β_1 and β_2 , the diagnosis rate γ , the recovery rate δ and the death rate of COVID-19 d are regarded as undetermined parameters. We use the reported confirmed cases from January 24, 2020 to February 11, 2020 to assess all unknown parameters and list all new estimated parameter values with 95% CI in Table 2. The numerical simulation of the cumulative hospitalized cases against the number of the confirmed cases is illustrated in Fig. 3a.

In the third stage, thanks to the sufficient coronavirus-testing kits, it is possible to finish checking all of the suspected cases in time and distinguish the patient with COVID-19 from the rest.³⁶ In addition, according to the simulated results of the second phase, we fix the parameters $\gamma = 1$, $d = 0.0417$ and $\delta = 0.1134$. We select the contact rates, β_1 and β_2 , as undermined parameters. Based on the published data from February 12, 2020 to March 25, 2020, we estimated all of the unknown parameters and listed all of the new estimated parameter values with 95%

Table 2. Estimation of parameters for the second set of data.

Pars	β_1	β_2	γ
Values	0.2625	0.1279	0.2200
95% CI	[0.2298, 0.3002]	[0.1103, 0.1498]	[0.1953, 0.2258]
Pars	δ	d	\mathcal{R}_{e1}
Values	0.1134	0.0417	1.7549
95% CI	[0.0996, 0.1386]	[0.0372, 0.0512]	[1.6908, 1.9206]

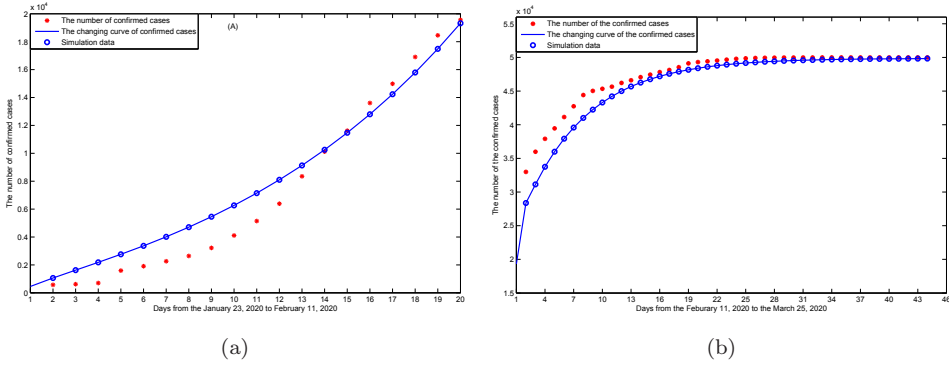


Fig. 3. (a) Comparison of the daily numbers of confirmed cases simulated in the model and the numbers from the report from January 23, 2020 to February 11, 2020. (b) Comparison of the daily numbers of confirmed cases simulated in the model and the numbers from the report from February 12, 2020 and March 25, 2020.

CI in Table 3. The numerical simulation of cumulative hospitalized cases against the number of the confirmed cases is illustrated in Fig. 3b.

From Figs. 2 and 3, we find that simulation data are in good agreement with the number of the confirmed cases reported in Wuhan. From the comparison of Tables 1 and 2, we note that the effective contact rates of the second phase are less than that of the first phase, which shows that the serious epidemic situation has aroused the public vigilance and the control measures have been effective in containing the spread of disease. We also find that the diagnosis rate γ of the second phase is greater than that of the first phase, which is connected with the great efforts undertaken by many medical workers from all over the country, and a large amount of medical materials provided by many people at home and abroad.³⁷ On February 2, 2020, China announced that all patients diagnosed with pneumonia-related fever were to be quarantined.³⁸ Most of the suspected cases were quarantined before February 11,

Table 3. Estimation of parameters for the third set of data.

Pars	β_1	β_2	\mathcal{R}_{e2}
Values	0.0227	0.0242	0.1636
95% CI	[0.0202, 0.0277]	[0.0212, 0.0294]	[0.1471, 0.1963]

2020. Hence, the effective contact rates of the susceptible persons with the infected persons β_1 and the effective contact rates of the susceptible individuals with the exposed persons β_2 significantly reduced. From Table 3, we see that the result of simulation is consistent with the reality. In addition, we also find that the death rate of COVID-19 is about 4.17%, which approximates the true value reported by Wuhan Municipal Health Commission.

3.3. Chi-square test of goodness of fit

In order to test how well our model reflects the data actually, we consider the following hypotheses:

(H0) Null hypothesis: The estimated parameters are equal to actual values.

(H1) Alternative hypothesis: The estimated parameters are not equal to actual values.

The chi-square values and degrees of freedom for each stage between the data and the simulated results are listed in Table 4, where DF denotes degree of freedom and AV denotes the accepting value at 5% significant level. By Pearson's criterion of Chi-square test, the null hypothesis at the 5% significant level cannot be rejected.³⁹

3.4. Estimations of the reproduction numbers

From expression (5) and the parameter values estimated in the first stage (see Table 1), the basic reproduction number of the first stage is calculated as 4.6355. The basic reproduction number of COVID-19 is obviously higher than that of SARS, which indicates that COVID-19 has a greater epidemic risk than the SARS breakout in 2003.

In the first stage, if all infected cases were confirmed and quarantined timely, i.e., the diagnosis rate was raised to 100%, the effective reproduction number would quickly decrease to 1.2841, which shows improving the diagnosis rate is crucial to slow the spread of COVID-19. In addition, the partial derivative of \mathcal{R} with respect to the contact rate β_1 and β_2 are calculated as $\frac{\partial \mathcal{R}}{\partial \beta_1} = \frac{\alpha}{(\alpha + \mu)(\mu + d + \gamma)}$ and $\frac{\partial \mathcal{R}}{\partial \beta_2} = \frac{1}{\alpha + \mu}$, respectively. Obviously, $\frac{\partial \mathcal{R}}{\partial \beta_1} > 0$, $\frac{\partial \mathcal{R}}{\partial \beta_2} > 0$, which means that reducing the effective contact rates can help to reduce the value of the reproduction number and thus slow the spread of COVID-19. Meanwhile, $\frac{\partial \mathcal{R}}{\partial \beta_2} > 0$ means that the asymptomatic

Table 4. Chi-square values and degrees of freedom for every stage.

	Chi-square value	DF	AV
The first stage	2.3532	3	7.815
The second stage	0.9375	13	22.362
The third stage	0.0142	40	55.758

transmission increases the difficulty of slowing the spread of COVID-19. Even if all of the infected cases and suspected cases were strictly quarantined, i.e., $\beta_1 = 0$, the effective reproduction number would still be as high as 1.0012, which indicates that the asymptomatic transmission is also an important factor affecting the spread of COVID-19. As Qiu warned, covert coronavirus infections could be seeding new outbreaks.¹⁹ For this reason, people must improve their awareness of health and safety.

In the second stage, thanks to a great deal of medical supplies from home and aboard and medical workers from all over the country, the diagnosis rate γ increased. On the other hand, medical supplies and hospital beds were still unable to meet the needs of all of the suspected case.⁴⁰ and a large number of suspected cases and infected cases could not be hospitalized and strictly quarantined. As a result, the effective contract rates did not decrease much. Thus, the decline of the effective reproduction number was not particularly large. The effective reproduction number in the second stage is estimated as 1.7549 (see Table 2).

In the third stage, the coronavirus-testing kits were sufficiently supplied and stricter quarantine measures were carried out which requires that everyone must stay at home except for shopping for basic necessities. These measures ensured that the effective contact rates between the susceptible persons and the exposed cases or the infected cases significantly decreased. It is bound to result in the observable decrease of the effective reproduction number. Hence, the effective reproduction number in the third stage is estimated as 0.1636 (see Table 3).

We compare the reproduction numbers of three stages and list our findings as follows: (1) The diagnosis rate and the public awareness of health and safety are key factors. A low diagnosis rate and weak awareness of health and safety led to a large outbreak of COVID-19 in the first stage. (2) In the second stage, despite the lockdown of the city effectively containing the spread of COVID-19 to other areas outside of Wuhan, it was still unable to contain the spread of COVID-19 in Wuhan. However, a great deal of medical supplies and medical assistance from all over the country sped the detection for COVID-19 and slowed down the spread of COVID-19. (3) In the third stage, the rigorous quarantine measure and the improvement of the diagnosis rate can contain the spread of COVID-19 in Wuhan.

4. Sensitivity Analysis of \mathcal{R} and Discussion

In this section, we conduct the sensitivity analysis of the reproduction number on some parameters and discuss the influence of the different factors in the quarantine measures on the spread of COVID-19.

4.1. Sensitivity analysis of \mathcal{R}

Based on the expression (5) of the reproduction number \mathcal{R} , we, respectively, calculate the partial derivatives of \mathcal{R} with respect to the natural death rate μ and the

death rate of COVID-19 d as

$$\frac{\partial \mathcal{R}}{\partial \mu} = \frac{-\beta_1 \alpha (2\mu + d + \gamma + \alpha) - \beta_2 (\mu + d + \gamma)^2}{(\alpha + \mu)^2 (\mu + d + \gamma)^2} < 0 \quad \text{and}$$

$$\frac{\partial \mathcal{R}}{\partial d} = \frac{-\beta_1 \alpha}{(\alpha + \mu)(\mu + d + \gamma)^2} < 0,$$

from which we easily know that \mathcal{R} will decrease with the death rates μ and d increasing.

Next, we first fix all parameters (as shown in Table 1) except β_1 and β_2 , the reproduction number \mathcal{R} increases as either β_1 or β_2 increases (see Fig. 4a). Moreover, to make sure that $\mathcal{R} < 1$, we need to decrease the values of the effective contact rates (β_1 and β_2). It implies that reducing the effective contact rates is very effective to contain the spread of COVID-19.

Second, we fix all parameters (as shown in Table 1) except α and γ , the reproduction number \mathcal{R} increases as either α or γ decreases (see Fig. 4b). It indicates that the longer the incubation period is, the harder it is to prevent the spread of COVID-19. It also shows that the improving the diagnosis rate of COVID-19 is very beneficial to contain the spread of COVID-19.

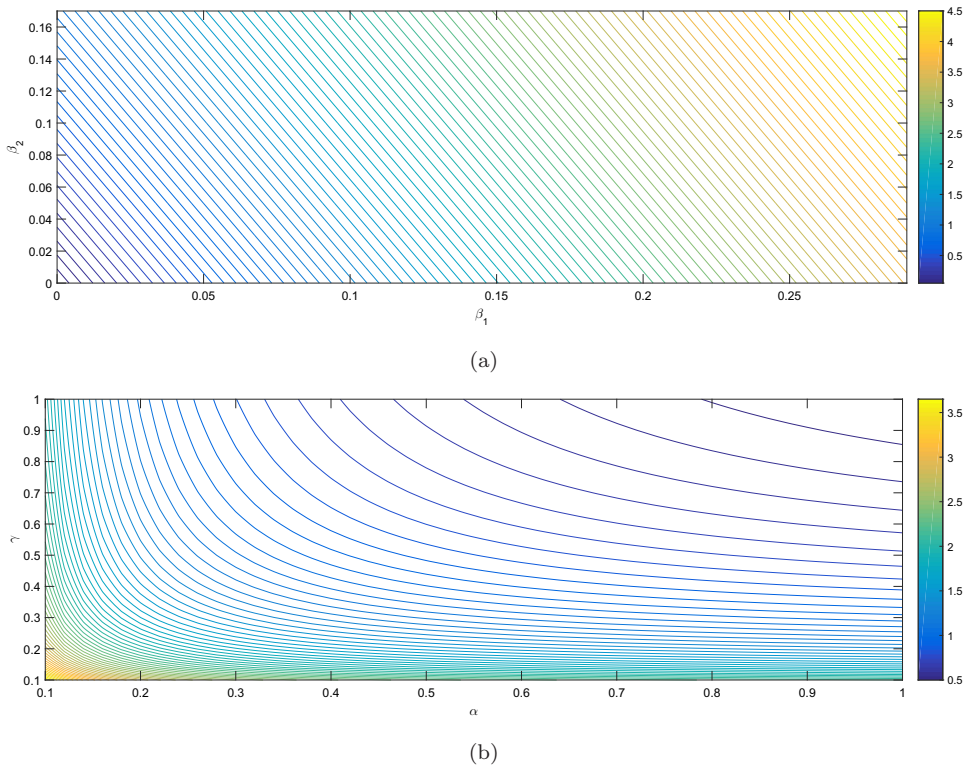


Fig. 4. \mathcal{R} in terms of (a) β_1 and β_2 ; (b) δ and γ . The color bar reflects the value of \mathcal{R} .

4.2. The influences of different measures on spread dynamics

Four situations are analyzed to investigate the influences of different control strategies on the spread of COVID-19.

(a) We first discuss the influences of early isolation and early warning on the control effect of COVID-19. Because the outbreak of COVID-19 in Wuhan city was initially reported to WHO on December 31, 2019, we select December 31, 2019 as the starting time of executing rigorous isolation and warning measures. Therefore, before December 31, 2019, the parameter values of model (2.1) should be selected in Table 1. However, after December 31, 2019, parameter values of model (2.1) should be selected in Table 2, and the values of the effective contact rates β_1 and β_2 should be taken in Table 3. The changes in the numbers of the infected cases and the confirmed cases are shown in Fig. 5, from which we can see that COVID-19 will not lead to a larger outbreak in the case of early control and rigorous quarantine.

(b) Second, we investigate the dynamic behavior of COVID-19 when putting Wuhan city on lockdown and strict quarantine measures are delayed for five days to be executed. The variation trend of the number of the confirmed cases is shown in Fig. 6, from which we find that the real number of the total confirmed case is about 50,000 in Wuhan. However, the total number of the confirmed cases will increase to approximately 120,000 when the lockdown and strict quarantine are delayed for five days. As a matter of fact, a large number of the confirmed cases caused by the delay of putting Wuhan city on lockdown and quarantine measures can easily break down the medical system, and make the situation much worse.

(c) Furthermore, we investigate the influence of the diagnosis rate on the spread of COVID-19. We reduce the diagnosis rate to half of the estimated value in every stage. The variation trend of the confirmed cases is shown in Fig. 7, which indicates that the total number of the confirmed cases will increase to approximately 100,000.

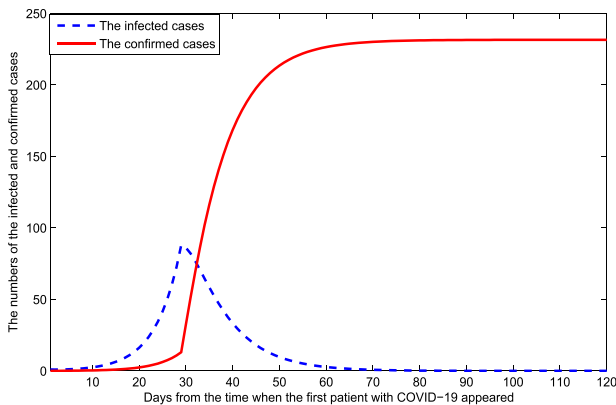


Fig. 5. The predicted variation trend of the number of infected individuals and confirmed cases in the case of early control and rigorous quarantine.

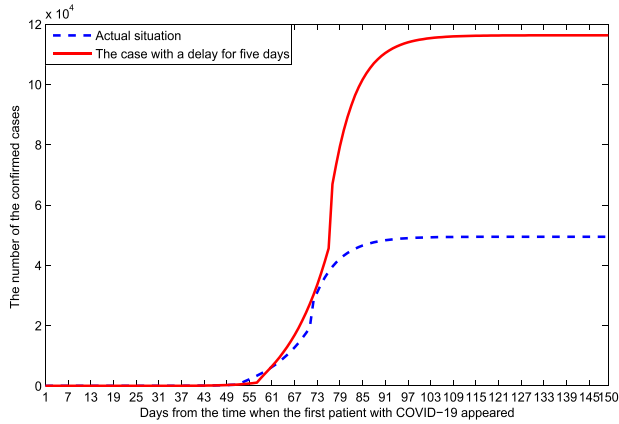


Fig. 6. The blue line denotes the actual changes of the confirmed cases in Wuhan. However, the red line represents the variations trend of the confirmed cases when two strict control measures are delayed for five days to be executed.

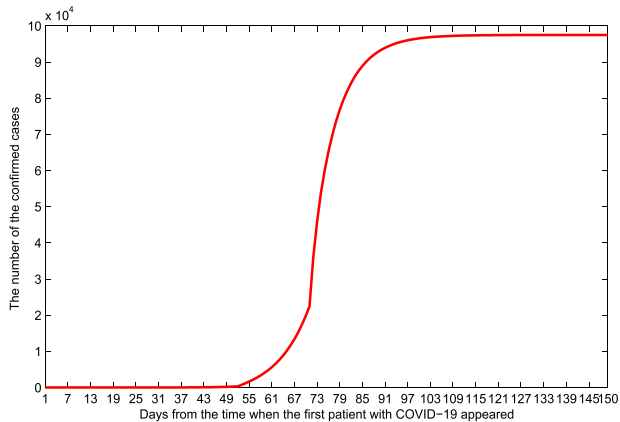


Fig. 7. The curve denotes the variation trend of the confirmed cases when the diagnosis rate reduces to half of the estimated value in every stage.

It shows that the increase of the diagnosis rate is conducive to contain the spread of COVID-19.

(d) Finally, we investigate the variation trend of the confirmed cases when two strict control measures, i.e., putting Wuhan city on lockdown and strict quarantine, are executed on January 23, 2020. The variation trend of the confirmed cases is shown in Fig. 8, from which we can find that the total confirmed cases are only about 6,500 in Wuhan. It verifies once again that rigorous quarantine can effectively control the spread of COVID-19.

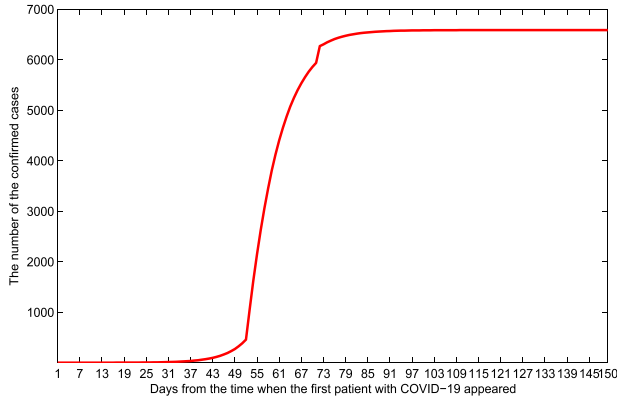


Fig. 8. The curve shows the variation trend of the confirmed cases when two strict control measures, i.e., putting Wuhan city on lockdown and strict quarantine, are executed concurrently on January 23, 2020.

5. Conclusions

In this paper, a set of ordinary differential equations is applied to describe the transmission dynamics of COVID-19 in Wuhan City. The total population is divided into five subclasses: the susceptible persons, the exposed persons, the infected persons, the hospitalized persons and the recovered persons.

First, we apply our model to simulate the published data for the confirmed cases of Wuhan from December 31, 2019 to March 25, 2020 to deduce the time when the first patient with COVID-19 appeared. Results indicate that the first infected patient with COVID-19 may have appeared around December 3, 2019, and about 2731 infected cases and 4335 exposed persons may have appeared before the lockdown in Wuhan City, i.e., January 23, 2020.

Second, we estimate the reproduction number \mathcal{R} in different developmental stages of COVID-19. In the first stage, the basic reproduction number \mathcal{R}_0 is estimated as 4.6355, which means that COVID-19 is highly contagious. In the second stage, the effective reproduction number \mathcal{R}_{e1} is estimated as 1.7549, which means that reducing the effective contact rates and improving the diagnosis rate are very important to contain the spread of COVID-19. The upturn occurred in the third stage. Since the rigorous quarantine measures are implemented and the sufficient coronavirus-testing kits are supplied, the effective reproduction number \mathcal{R}_{e2} quickly descends to 0.1636, which illustrates that rigorous quarantine and improving the diagnosis rate are very important to contain the spread of COVID-19. In addition, sensitivity analysis of \mathcal{R} in terms of model parameters also demonstrates that the quarantine and the improvement of the diagnosis rate are two critical factors in fighting against COVID-19.

Finally, four situations are analyzed to investigate the influences of different control strategies on the spread of COVID-19. The results indicate once again that

the rigorous quarantine measures and improving the diagnosis rate are crucial to contain the spread of COVID-19, and early control measures can also effectively prevent a larger outbreak of COVID-19.

Although improving the diagnosis rate can be realized by providing efficient confirmatory test kits, doctors and other medical resource and reducing the effective contact rate can be realized by quarantining the confirmed, suspected and exposed persons, how to effectively find out the asymptomatic exposed persons or asymptomatic infected cases and quarantine them is a big challenge that we have to face in the future.

Acknowledgments

The authors are very grateful to the reviewers for their constructive suggestions and comments which helped us to improve the paper significantly. This research is partially supported by the National Natural Science Foundation of China (Nos. 11871238, 61973177 and 11871060), the Natural Science Foundation of Henan Province of China under Grants 182102410021 and 182102410067, the young backbone teacher of Henan Province (2018GGJS148), Henan International Joint Laboratory of Behavior Optimization Control for Smart Robots, file No. [2018]19, the programme of Henan Innovative Research Team of Cooperative Control in Swarm-based Robotics, and the self-determined research funds of CCNU from the colleges basic research and operation of MOE (Grant No. CCNU16JCZX10).

References

1. WHO, Naming the coronavirus disease (COVID-19) and the virus that causes it, [https://www.who.int/emergencies/diseases/novel-coronavirus-2019/technical-guidance/naming-the-coronavirus-disease-\(covid-2019\)-and-the-virus-that-causes-it](https://www.who.int/emergencies/diseases/novel-coronavirus-2019/technical-guidance/naming-the-coronavirus-disease-(covid-2019)-and-the-virus-that-causes-it).
2. Zhu N *et al.*, A novel coronavirus from patients with pneumonia in China, 2019, *N Engl J Med* **382**:727–733, 2020.
3. CDC, About 2019 novel coronavirus (2019-nCoV), <https://www.cdc.gov/coronavirus/2019-nCoV/about/index.html>.
4. CDC, Coronavirus disease 2019 (COVID-19), https://www.cdc.gov/coronavirus/2019-ncov/prevent-getting-sick/how-covid-spreads.html?CDC_AA_refVal=https%3A%2F%2Fwww.cdc.gov%2Fcoronavirus%2F2019-ncov%2Fprepare%2Ftransmission.html.
5. Chan JFW *et al.*, A familial cluster of pneumonia associated with the 2019 novel coronavirus indicating person-to-person transmission: A study of a family cluster, *Lancet* **395**:514–523, 2020, doi:10.1016/S0140-6736(20)30154-9.
6. Kang M *et al.*, Evidence and characteristics of human-to-human transmission of SARS-CoV-2, medRxiv Preprint, 2020, doi:10.1101/2020.02.03.20019141v3.
7. CNN, Chinese CDC study finds Covid-19 virus to be more contagious than SARS or MERS, <https://edition.cnn.com/2020/02/19/health/coronavirus-china-sars-mers-intl-hnk/index.html>.
8. BBC, China coronavirus 'spreads before symptoms show', <https://www.bbc.co.uk/news/world-asia-china-51254523>.

9. Beijing Daily, The incubation period of novel coronavirus are 1-14 days, It is infectious in the incubation period, <https://baijiahao.baidu.com/s?id=1656777529300298714&wfr=spider&for=pc>.
10. Zhang X *et al.*, Avian influenza A H7N9 virus has been established in China, *J Biol Syst* **25**(4):605–623, 2017.
11. Tang B *et al.*, Estimation of the transmission risk of the 2019-nCoV and its implication for public health interventions, *J Clin Med* **9**:462, 2020, doi:10.2139/ssrn.3525558.
12. Joseph T, Leung K, Leung G, Nowcasting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China: A modelling study, *Lancet* **395**:689–697, 2020, doi:10.1016/S0140-6736(20)30260-9.
13. Zhao S *et al.*, Preliminary estimation of the basic reproduction number of novel coronavirus (2019-nCoV) in China, from 2019 to 2020: A data-driven analysis in the early phase of the outbreak, *Int J Infect Dis* **92**:214–217, 2020, <https://doi.org/10.1016/j.ijid.2020.01.050>.
14. Lai S *et al.*, Preliminary risk analysis of 2019 novel coronavirus spread within and beyond China, <https://www.worldpop.org/resources/docs/china/WorldPop-coronavirus-spread-risk-analysis-v1-25Jan.pdf>.
15. Liu T *et al.*, Transmission dynamics of 2019 novel coronavirus (2019-nCoV), bioRxiv Preprint, 2020, <http://dx.doi.org/10.1101/2020.01.25.919787>.
16. Li R *et al.*, Substantial undocumented infection facilitates the rapid dissemination of novel coronavirus (SARS-CoV2), *Science* 2020, doi:10.1126/science.abb3221.
17. Prem K *et al.*, The effect of control strategies to reduce social mixing on outcomes of the COVID-19 epidemic in Wuhan, China: A modelling study, *Lancet Public Health*, 2020, <https://www.sciencedirect.com/science/article/pii/S2468266720300736>.
18. Roda W, Varughese M, Han D and Li M, Why is it difficult to accurately predict the COVID-19 epidemic? *Infect Dis Model* **5**:271–281, 2020.
19. Qiu J, Covert coronavirus infections could be seeding new outbreaks, *Nature* 2020, doi:10.1038/d41586-020-00822-x.
20. Scitechdaily, Strains of coronavirus 2019-nCoV detected in France isolated, <https://scitechdaily.com/strains-of-coronavirus-2019-ncov-detected-in-france-isolated/>.
21. Van der Werf S, Peltékian C, Facing challenges with the novel coronavirus SARS-CoV-2 outbreak, *Virology* **24**(S1):E12–E15, 2020.
22. Zhou L *et al.*, SARS-CoV-2 viral load in upper respiratory specimens of infected patients, *N Engl J Med* **382**:1177–1179, 2020.
23. Woelfel R *et al.*, Clinical presentation and virological assessment of hospitalized cases of coronavirus disease 2019 in a travel-associated transmission cluster, medRxiv preprint, 2020, doi:10.1101/2020.03.05.20030502.
24. Bai Y *et al.*, Presumed asymptomatic carrier transmission of COVID-19, *JAMA* 2020, doi:10.1001/jama.2020.1585.
25. Rothe C *et al.*, Transmission of 2019-nCoV infection from an asymptomatic contact in Germany, *N Engl J Med* **382**:970–971, 2020, doi:10.1056/NEJMc2001468.
26. US and Global News, WHO aware of 2019-nCoV transmission from asymptomatic people, <https://usandglobal.com/world/who-aware-of-2019-nCoV-transmission-from-asymptomatic-people/>.
27. van den Driessche P, Watmough J, Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease Transmission, *Math Biosci* **180**:29–48, 2002.

28. Globaltimes, Wuhan imposes strictest quarantine measures amid fight against the novel coronavirus, <https://www.globaltimes.cn/content/1178250.shtml>.
29. Zhang X, Zhao Y, Neumann A, Partial immunity and vaccination for influenza, *J Comput Biol* **17**:1689–1696, 2009.
30. Pang L *et al.*, Transmission dynamics and optimal control of measles epidemics, *Appl Math Comput* **256**:131–147, 2015.
31. Li Y *et al.*, The data fitting and optimal control of a hand, foot and mouth disease (HFMD) model with stage structure, *Appl Math Comput* **276**:61–74, 2016.
32. WHO, Coronavirus disease (COVID-2019): Situation report – 30, https://www.who.int/docs/default-source/coronaviruse/situation-reports/20200219-sitrep-30-covid-19.pdf?sfvrsn=3346b04f_2.
33. Anderson R *et al.*, How will country-based mitigation measures influence the course of the COVID-19 epidemic? *Lancet* **395**:931–934, 2020.
34. Li Q *et al.*, Early transmission dynamics in Wuhan, China, of novel coronavirus-infected pneumonia, *New Engl J Med* **382**:1199–1207, 2020.
35. Reuters. Data suggests virus infections under-reported, exaggerating fatality rate, <https://www.reuters.com/article/us-china-health-deaths/data-suggests-virus-infections-under-reported-exaggerating-fatality-rate-idUSKBN1ZZ1AH>.
36. Li M, Liang X, Jiang Q, An update on the epidemiological characteristics of novel coronavirus pneumonia, *China J Epidemiol* **4**:139–144, 2020.
37. SinaEnglish, China beefs up action against novel coronavirus as cases increase, <http://english.sina.com/china/s/2020-01-27/detail-iihnzakh6536335.shtml>.
38. People, Hubei province notice: centralized isolation of all suspected cases, <http://society.people.com.cn/n1/2020/0202/c1008-31567326.html>.
39. Snedecor G, Cochran W, *Statistical Methods*, 8th edn., Iowa State University Press, Ames, 1989.
40. MSN, Coronavirus cases soar to 60,000-plus (Here’s why): Live updates on 2019-nCoV. <https://www.msn.com/en-us/health/medical/coronavirus-deaths-exceed-1000-live-updates-on-2019-nCoV/ar-BBZgiis>.

Appendix A.

Let $x = [E, I, H, S, R]$, system (2.1) be written as

$$\frac{dx}{dt} = \mathcal{F}(x) - \mathcal{V}(x),$$

where

$$\mathcal{F}(x) = \begin{bmatrix} \frac{\beta_1 SI}{N} + \frac{\beta_2 SE}{N} \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}, \quad \mathcal{V}(x) = \begin{bmatrix} (\alpha + \mu)E \\ (\mu + d + \gamma)I - \alpha E \\ (\mu + d + \delta)H - \gamma I \\ \frac{\beta_1 SI}{N} + \frac{\beta_2 SE}{N} + \mu S - \Lambda \\ \mu R - \delta H \end{bmatrix}.$$

The infective compartments are E , I and H . Following the method provided by van den Driessche and Watmough,²⁷ we obtain

$$F = \begin{bmatrix} \beta_2 & \beta_1 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}, \quad V = \begin{bmatrix} \alpha + \mu & 0 & 0 \\ -\alpha & \mu + d + \gamma & 0 \\ 0 & \gamma & \mu + d + \delta \end{bmatrix}.$$

A straightforward calculation yields

$$V^{-1} = \begin{bmatrix} \frac{1}{\mu + \alpha} & 0 & 0 \\ \frac{\alpha}{(\mu + d + \gamma)(\alpha + \mu)} & \frac{1}{\mu + d + \gamma} & 0 \\ \frac{-\gamma\alpha}{(\mu + d + \gamma)(\alpha + \mu)(\mu + d + \delta)} & \frac{-\gamma}{(\mu + d + \gamma)(\mu + d + \delta)} & \frac{1}{\mu + d + \gamma} \end{bmatrix}.$$

Hence, we obtain the reproduction number

$$\mathcal{R} = \frac{\beta_2}{\alpha + \mu} + \frac{\beta_1\alpha}{(\alpha + \mu)(\mu + d + \gamma)}.$$