Research article

Modeling and analysis of COVID-19 based on a time delay dynamic model

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Abstract: The new type of coronavirus pneumonia is caused by the new type of coronavirus which appeared at the end of 2019. Because of its strong contagiousness, rapid spread and great harm, it has already given countries around the world serious effects. So far there is no clear specific drug. Scientifically grasping the development law of epidemics is extremely important for preventing and controlling epidemics. Since the latent of this epidemic are also highly contagious, traditional infectious disease models cannot accurately describe the regularity of this epidemic transmission. Based on the traditional infectious disease model, an infectious disease model with a time delay is proposed. The time difference is used to characterize the cycle of viral infection and treatment time. Using the epidemic data released in real time, firstly, through the numerical simulation parameter inversion, the minimum error is obtained; then we simulate the development trend of the epidemic according to the dynamics system; finally, we compare and analyze the effectiveness of isolation measures. This article has simulated COVID-19 and analyzed the development of the epidemic in Beijing and Wuhan. By comparing the severity of the epidemic in the two regions, early detection and isolation are still the top priority of epidemic prevention and control.

Keywords: COVID-19; time delay dynamics system; parameter inversion

1. Introduction

At the beginning of 2020, the new coronary pneumonia epidemic rapidly broke out on a global scale, which had a huge impact on the lives of people all over the world [1, 2]. As the outbreak point of the first round of the epidemic , the number of infections in Wuhan rose sharply in a short period of time. After several months of quarantine, the epidemic was stably controlled and the confirmed cases were cleared. On June 10, 2020, with no new local cases for several months, a new round of new coronary pneumonia broke out in Beijing. This new coronavirus pneumonia epidemic is caused by a covered positive-stranded single-stranded RNA virus. According to scientists, compared with SARS and MERS, COVID-19 is more contagious which has more routes of transmission and a large number

of susceptible people. Controlling the epidemic is difficult and expensive. The risk of another outbreak is likely still high.

Due to the significant differences between governments and residents on the understanding and response strategies of novel coronavirus, central and local governments in many countries still ignored the warning of WHO to restart the economy and relax restrictions even before the epidemic situation is effectively contained. These practices increase the risk of another outbreak. Because the relationship between epidemic prevention and control and restarting the economy is not easy to balance, in addition, human awareness of the new coronavirus is relatively limited, antiviral drugs and vaccines have not yet been born, normalization of epidemic prevention and control is extremely important, and we always pay attention to epidemic prevention and control.

The use of mathematical models to solve infectious disease problems has a long history. In the 18th century, mathematician Bernoulli used mathematical models to characterize the spread of smallpox and study the effectiveness of immunization. Through a simple mathematical analysis of the SIR model, the calculation formula for the risk technical indicators related to disease transmission can be obtained, including the basic reproductive number of infectious diseases, the peak and peak time of infectious disease peaks, and the final scale of infection [3, 4]. At the beginning of the SARS outbreak in 2003, the infectious disease modeling team of Xi'an Jiaotong University has established a discrete infectious disease model to more accurately predict the development trend of SARS, (epidemiological) elimination time and final infection scale and other key technical indicators [5–9]. This provides an important decision basis for the input and allocation of medical resources and the decision-making departments to formulate corresponding prevention and control measures [10]. In the early stage of the COVID-19 outbreak, based on mathematical models and a small amount of real-time updated data, many domestic and foreign teams analyzed the transmission capacity and risk of COVID-19 and have given key technical indicators including basic reproduction numbers. It is helpful for the disease prevention and control department to quickly understand its transmission power, so as to take corresponding prevention and control measures. With the development of the epidemic and the strengthening of control measures, the effectiveness and timeliness of containment and mitigation strategies are key factors for systematic research and prevention and control through the constant updating of models and the complex evolution of the epidemic, influencing the determined severity of the epidemic and providing an important basis for decision-making. At the same time, based on the model, using sensitivity and uncertainty analysis to evaluate the impact of resumption of work and school, local cluster outbreaks and other events on the second outbreak of the epidemic also provided theoretical support for important decisions such as resumption of work and production [11, 12].

The classic mathematical models describing the spread of infectious diseases include SIR model, SEIR model and SEIJR model [13]. The main idea is to divide the population into susceptible persons S, latent persons E, and infectious persons I. Groups such as the diagnosed J and the recovered R, and through the communication mechanism of one group to another group, establish a system of ordinary differential equations to reveal the law of epidemic transmission. These models (and their variants) are used to study the spread of various infectious diseases such as measles, smallpox, rabies, Ebola virus, and population dynamics. After the SARS epidemic in 2003, mathematical models for the spread of SARS and MERS coronaviruses have gradually become abundant.

Most traditional models do not consider the time delay effect of the incubation period on transmission. Though latency has been considered in some SEIR and SEIRJ models, the latent E is assumed to

be weakly contagious. Thus these models cannot describe the characteristics of the new coronavirus that can be transmitted during the incubation period. In addition, when inverting the model parameters, the above models hardly consider the data lag caused by the time required to confirm the diagnosis before the data is released. To sum up, a model with time delay effect [14] is needed to better describe the spread of COVID-19. Compared with traditional models such as SIJR, we characterize the impact of time delay on epidemic prevention and control. MCMC algorithm is widely used in parameter inversion. Gatto et al. researched the spread and dynamics of the COVID-19 epidemic in Italy [15] and Wu et al. researched the model of nowcasting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China [16]. They all used MCMC for parameter inversion.

The infectious disease dynamics model proposed in this paper is based on the time delay dynamics system. Kucharski et al. have taken time delay into consideration when studying early dynamics of transmission and control of COVID-19 [17]. The parameters in the model are inverted through known historical data, and the parameters effectively show the effectiveness of epidemic prevention and control. Based on the inverted parameters, the trend of the epidemic was reasonably and accurately simulated. Wallinga et al. emphasized the importance of time for action during researching the Severe Acute Respiratory Syndrome Reveal [18]. In response to this epidemic, in the absence of a vaccine, early detection, isolation, and treatment are currently the most effective measures [19]. The stronger the measures, the faster the epidemic can be controlled.

The other sections of this paper are arranged as follows: The second section mainly introduces the new time delay dynamic model. The third section gives the algorithm of parameter inversion and epidemic analysis of the model. The fourth section mainly verifies the trend of the model analysis based on real-time updated data. Finally, the fifth section draws conclusions and gives recommendations.

2. A time delay dynamics system model

In this section, we shall introduce a new time delay dynamic model based on the traditional infectious disease model. Based on the progress of the disease, the epidemiological situation, and the control measures taken by the government, we divide the total population into susceptible, latent, infected, hospitalized and recovered. We use the following notation to represent the number of people in each group:

$S(t)$: the real-time total number of susceptible persons at time t ;

$E(t)$: the real-time total number of the latent at time t ;

$I(t)$: the real-time total number of infected persons at time t ;

$H(t)$: the real-time total of inpatient isolation at time t ;

$R(t)$: the cumulative total of recovered at time t .

Considering that the virus has an incubation period and other effects, we make the following assumptions for the model:

1) From a susceptible person being exposed to the virus to being infected, it takes τ_1 days to experience the virus transmission period, so after being spread, it will change from a susceptible person to a latent person.

2) Because the virus is extremely contagious, those without symptoms can also be contagious. Moreover, there will be a τ_2-days delay between the onset of symptoms and the diagnosis and isolation

and medical treatment. Once diagnosed, they will be treated in isolation and converted into hospitalized isolation.

3) Due to the difference in human immunity to viruses, the proportion of γ has strong immunity to viruses and can recover without isolation and hospitalization.

4) Due to the strengthening of government control measures, the infection rate of infected persons will continue to decline.

5) We assume that if the inpatients who are in quarantine finish treatment after τ_3 days, the proportion of r will be cured, while the proportion $1 - r$ will die. Because of the medical conditions, the degree of understanding of the virus will be to a large extent the cure rate.

6) Recovered people will not be infected again and will not be infectious.

$$\begin{cases} \dfrac{dS}{dt} = -\dfrac{\beta S(t)I(t)}{N(t)}, \\[2mm] \dfrac{dE}{dt} = \dfrac{\beta S(t)I(t)}{N(t)} - \dfrac{\beta S(t-\tau_1)I(t-\tau_1)}{N(t-\tau_1)}, \\[2mm] \dfrac{dI}{dt} = \dfrac{\beta S(t-\tau_1)I(t-\tau_1)}{N(t-\tau_1)} - \gamma I(t) - \dfrac{\beta p S(t-\tau_2)I(t-\tau_2)}{N(t-\tau_2)}, \\[2mm] \dfrac{dH}{dt} = \dfrac{\beta p S(t-\tau_2)I(t-\tau_2)}{N(t-\tau_2)} - \dfrac{r\beta p S(t-\tau_3)H(t-\tau_3)}{N(t-\tau_3)}, \\[2mm] \dfrac{dR}{dt} = \gamma I(t) + \dfrac{r\beta p S(t-\tau_3)H(t-\tau_3)}{N(t-\tau_3)}. \end{cases} \tag{2.1}$$
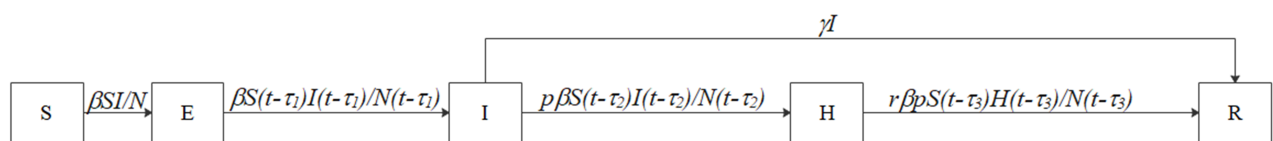

Figure 1. Schematic diagram of the model (2.1).

Model explanation:

1) β is the infection rate, the number of people infected by each infected person per unit time. Due to the implementation of government control measures, assuming that the infection rate will change over time, it is expressed $\beta(t) = (\beta_0 - \beta_m)e^{-kt} + \beta_m$ to describe the control effect. Among them, β_0 represents the initial infection rate, and β_m represents the minimum infection rate under the control measures. That is $\lim_{t\to\infty}\beta(t) = \beta_m$.

2) The latent person has spread the virus for τ_1 days with no symptoms. But after the time, he/she will be already contagious and turn into an infected person.

3) p represents the success rate of isolation and identification, which is mainly used to measure the identification ability of the infected person. The parameters that affect the infected person mainly include the local medical level (mainly the virus detection ability), the severity of symptoms and asymptomatic infected persons.

4) γ means self-healing rate, the proportion of infected people who do not need to go through isolation treatment and recover health on their own.

5) $H(t)$ represents the cumulative number of isolated hospitalizations, all from the number of infected persons after the onset of obvious symptoms; Once transferred to an isolated inpatient, treatment begins.

6) The change of restorers $R(t)$ is determined by two factors:

(I) Due to the body's autoimmune ability, some infected people do not need to go through isolation and hospitalization and recover directly.

(II) Isolation and hospitalization will end after τ_3 days of treatment.

3. Parameter inversion and epidemic prediction

In this section, we first estimate the optimal dynamics system based on the known official data and use the fitted optimal dynamics system to predict the development of COVID-19.

Knowing the initial values of the parameters $\{\beta, N, \gamma, r, \tau_1, \tau_2, \tau_3\}$ and $\{S(t), E(t), I(t), H(t), R(t)\}$, the numerical solution of system dynamics is obtained. In practical application, we suggest using *matlab* embedded program DDE23 to solve the new dynamics system.

In practical applications, make the following parameter assumptions:

Initial value hypothesis: At the initial time t_0, suppose that there are five infected persons as the first batch of infected persons, and no one was isolated and hospitalized and recovered that day, namely $S(t_0) = N - 5$, $E(t_0) = 0$, $I(t_0) = 5$, $H(t_0) = R(t_0) = 0$. It is also assumed that at $T = t_0 + t_1$, the government did not take measures such as intervention and isolation on the day. For Beijing, $t_1 = 10$, for Wuhan, $t_1 = 25$.

Parameter hypothesis: According to the data released by the National Health commission at all levels, due to the effect of time delay, we choose the data of Beijing since June 16, 2020. Because Wuhan only began to implement the lockdown strategy in the early morning of January 23, 2020, we select the data of Wuhan after January 21, 2020, as well as the information such as clinical symptoms were analyzed, the initial infection rate β_0, the lowest infection rate β_m and the average length of time τ_1 from exposure to the virus to infectiousness can be obtained. According to official reports, some people do not need to go through isolation treatment and directly recover their health and have a self-healing rate $\gamma = 0.15$ [20]. The specific parameter values are shown in Table 1.

Table 1. Parameter values.

Areas	β_0	β_m	N	γ	r	τ_1	τ_2	τ_3
Beijing	1.651	0.0012	2.51×10^7	0.15	0.99	5	4.5	18
Wuhan	2.145	0.0012	1.11×10^7	0.15	0.97	5	4.5	14

Finally, the exponential decline coefficient of the infection rate and the isolation recognition rate are determined according to the daily cumulative number of diagnoses announced in real time every day, and the inversion of these two parameters is transformed into a least square problem:

$$\min_{k,p} \|H(k, p) - H\|_2 \tag{3.1}$$

In this paper, we consider the following Cauchy problem for the Laplace equation in a strip domain:

$$\begin{cases} \Delta u(k, p) = 0, k \in (0, 1) \\ u = (0, p), y \in R \\ u_k(0, p) = H(p), y \in R \end{cases} \tag{3.2}$$

The method of parameter inversion and epidemic prediction is divided into the following two steps:

1) Firstly, Levenbery-Marquad (LM) method or Markov Chain Monte Carlo (MCMC) method was used to solve the above least square problem, and the coefficient of decline of infection rate index and the success rate of isolation identification were inverted by using data parameters.

2) Secondly, substituting the value $\{\beta, N, \gamma, r, \tau_1, \tau_2, \tau_3\}$ into the time delay dynamics system and solving numerically $\{S(t), E(t), I(t), H(t), R(t)\}$ to obtain the historical and future evolution values.

4. Model demonstration and epidemic analysis

4.1. Model parameter inversion

Use the parameter inversion and epidemic prediction in the previous section. We use the cumulative number of confirmed diagnoses in Beijing from June 20 to July 1, 2020 to fit the exponential decline coefficient of the inferred infection rate k and the optimal value of the isolation recognition success rate p . For Wuhan, we use the cumulative number of cases from January 23 to March 5, 2020. The estimated parameters of the corresponding regions are shown in Table 2.

The accuracy of parameter estimation is verified by bringing the obtained inversion parameters into the dynamics system. The parameters are estimated through official published data, and the resulting model is used to verify the next day's situation. The model simulates the development of the epidemic with published data very well, and successfully predicts the data of Beijing and Wuhan the next day. This shows that the inversion parameters are scientific and also shows that the time delay dynamics model is effective.

Table 2. Inversion parameter values.

Areas	k	p
Beijing	0.1444	0.75
Wuhan	0.1091	0.55

4.2. Epidemic analysis

According to the epidemic development curve shown in the figure, we draw the following conclusions:

Trend of the epidemic: According to the evolution curve of the cumulative number of confirmed cases in Figure 2, it can be seen that compared with Wuhan, the spread of the epidemic in Beijing was controlled at the source and large-scale infection was avoided. The spread of the epidemic is very fast, with a large number of people infected in a short period of time. However, with the increasing intervention of the government, the epidemic has been effectively controlled in a relatively short time. At

present, the prevention and control of COVID-19 in Beijing is at a normal stage. Therefore, intervention measures were taken in a timely manner than in Wuhan, and large-scale infections were avoided at the source. The Beijing epidemic can be suppressed in a relatively short period of time. Due to the outbreak in Wuhan, we did not know enough about the virus and did not have enough ability to detect the virus. However, this outbreak in Beijing has greatly improved the ability to detect the virus as soon as possible and greatly improved the success rate of isolation and identification. Taking into account the continuous development of Beijing's quarantine measures, the number of infected patients will gradually drop to zero after reaching a peak (See Figure 3).

Parameter analysis: According to the obtained inversion parameters, simulated epidemic trends in Beijing and Wuhan, the analysis is as follows:

1) Initial infection rate β_0 . It is because the Wuhan epidemic broke out without people's awareness of prevention, and people do not know enough about the new coronavirus, resulting in a high initial infection rate. The epidemic in Beijing this time is a local epidemic which has rebounded under the normalization of epidemic prevention and control. People have put in place basic precautions against new coronary pneumonia, so the initial infection rate has been significantly lower than that in Wuhan.

2) Exponential drop coefficient of infection rate. Under the normalization of epidemic prevention and control, due to the need to resume work and production, the large-scale personnel movement has not stopped, so the isolation is not high. The size of the index decline coefficient of the infection rate has a huge impact on the development trend of the epidemic. Figure 4 shows the prediction results of the epidemic situation in Beijing .When Figure 4 (b) compared to Figure 4 (a), the number of patients and the number of people cured have increased significantly. In Wuhan, due to the little knowledge of COVID-19 at that time, the lack of knowledge of virus increased the difficulty of epidemic prevention. Under the normalization of epidemic prevention and control, as soon as a confirmed case appeared in Beijing, the response was initiated, and hence the response was faster than that in Wuhan. This decreased the difficulty of tracing the root cause. Therefore, the development of the epidemic was controlled in a relatively short period of time, and the index of the infection rate decreased largely.

3) The government compulsory intervention time. Comparing Beijing and Wuhan outbreak, found early, in the absence of a wide range of communication, is to take strong tracking isolation measures and the source to control the infection. The time for taking measures has a significant impact on the development of the epidemic. Figure 5 shows the prediction results of the epidemic situation in Beijing with $T = t_0 + 15$ and $T = t_0 + 7$. Figure 5(b) compared to Figure 5(a) indicates that the earlier the government intervened, the number of confirmed cases decreased more significantly. Figure 5(d) compared with Figure 5(c) shows that the peak number of real-time infections decreased significantly. Therefore, early detection and early isolation are still the key to epidemic prevention and control.

4) Identify the success rate of isolation. By the detection means, the detection ability has been greatly improved from Wuhan's insufficient testing capabilities to Beijing's ability to perform all inspections. Compared with Wuhan, Beijing detected the epidemic earlier and had fewer infected people, which facilitates timely tracking.

5) Cure rate r. According to the clinical manifestations of COVID-19, most of the symptoms are mild. Most of the deaths in Wuhan are due to the lack of timely treatment, the majority of severe cases, and the lack of medical resources to keep up with the number of infections. Because the outbreak in Beijing was detected in time, the number of people infected was small. Therefore, the cure rate of Beijing is higher than that of Wuhan.
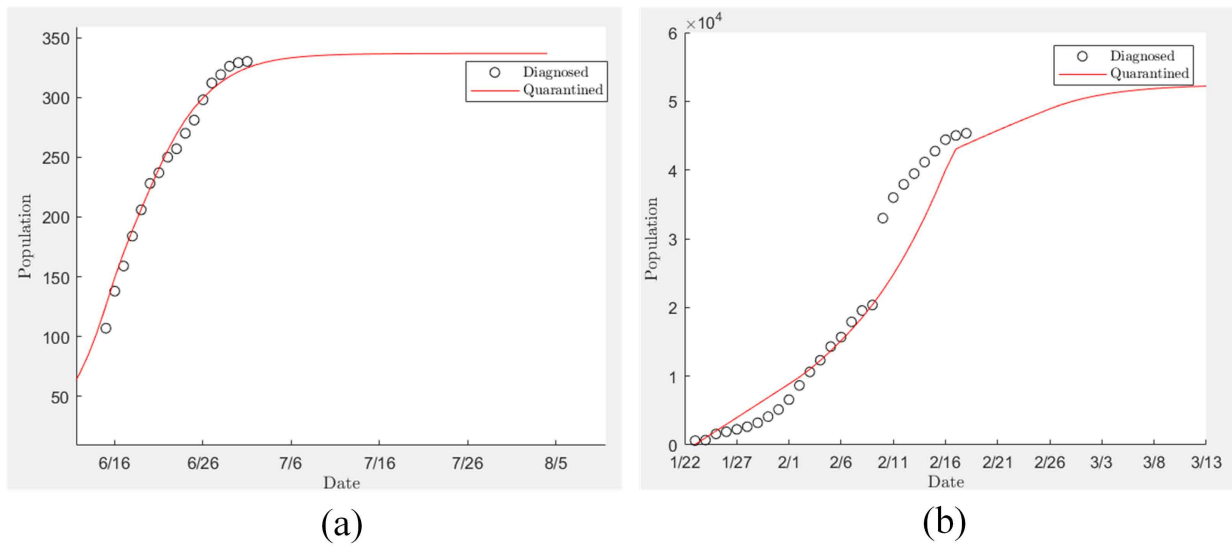
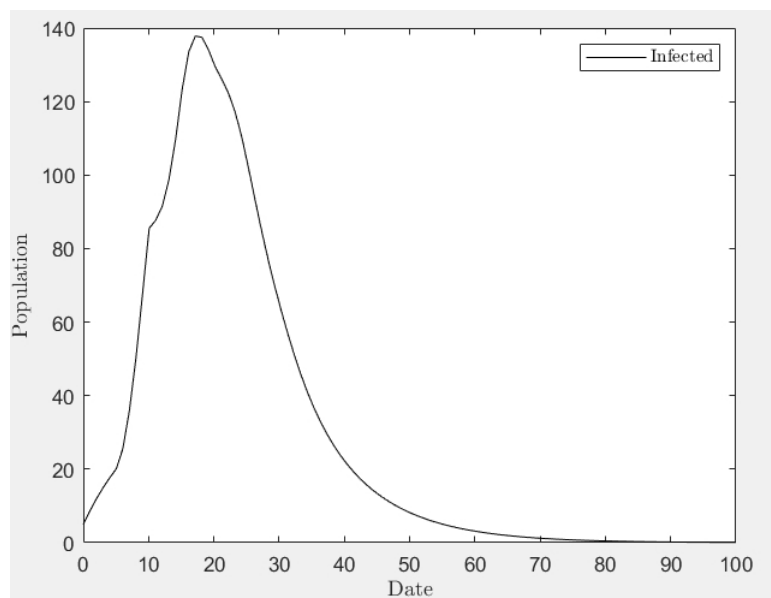**Figure 2.** Simulates the development trend of the epidemic. (a): Beijing, (b): Wuhan.

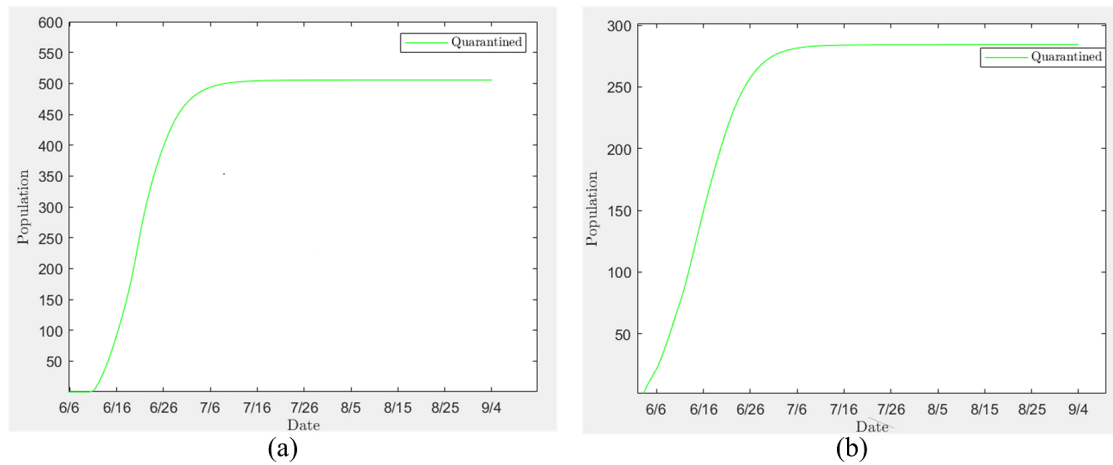**Figure 3.** The daily increment of the number of infected people in Beijing.

Figure 4. Decrease coefficient of different infection rate index in Beijing. (a) $k = 0.15$, (b) $k = 0.135$.
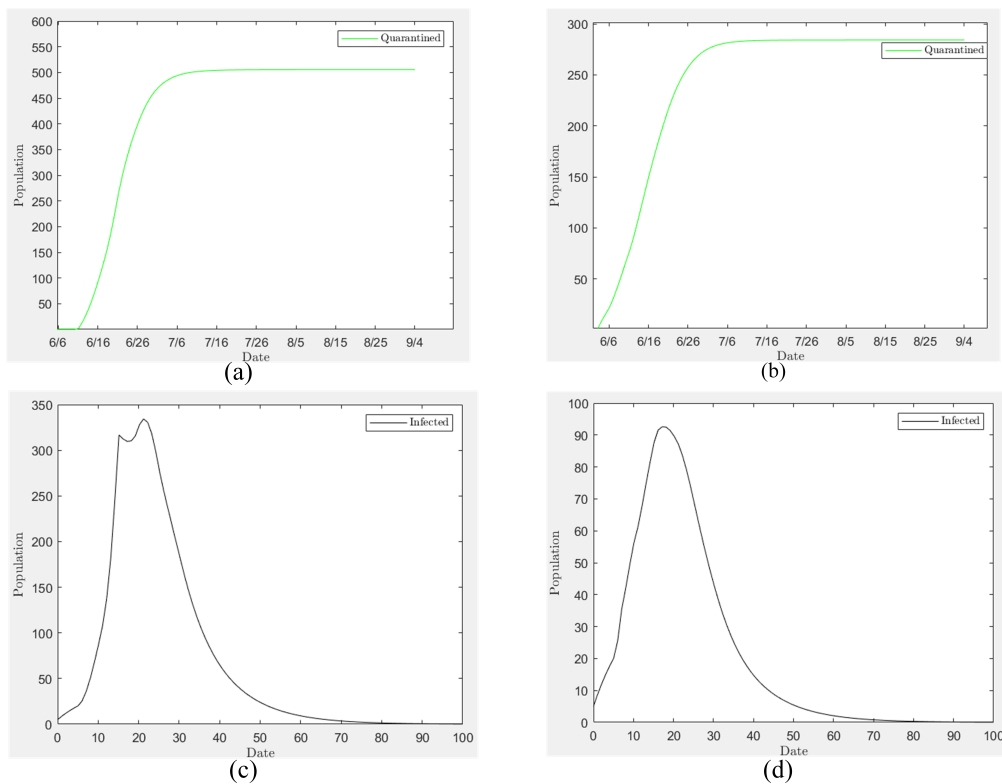

Figure 5. The development trend of the epidemic situation in Beijing under different initial control periods. (a) (c)$T = t_0 + 15$, (b) (d)$T = t_0 + 7$.

5. Conclusions

In response to the development of COVID-19, we have established a type of infectious disease model based on a time delay dynamics system. Based on the cumulative number of reported cases in Beijing and Wuhan, we fitted the estimates of unknown parameters of the model. Through this model, we can not only reverse the index decline coefficient of the infection rate and the success rate of isolation identification, but also accurately predict the development trend of the epidemic. Through curve numerical simulation, early detection and early control can largely prevent the spread of the epidemic.

There are some limitations to our analysis. We use parameters based on current scientific evidence for COVID-19, but these parameters are likely to improve with greater understanding. The existing single index cannot fully and intuitively measure the development of the epidemic. The introduction of a new index can directly analyze the epidemic and improve the efficiency of identification [21]. The research did not fully consider the influence of external factors such as geographic environment. Adding geographic environment and other factors can greatly improve the accuracy of model prediction [22]. The research lacked the virus transmission dynamics, geographical characteristics of positive incidences.

Acknowledgments

Conflict of interests

All authors declare no conflict of interests in this paper.

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