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The introduction of population migration to SEIAR for COVID-19 epidemic modeling with an efficient intervention strategy

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ABSTRACT

In this paper, we present a mathematical model of an infectious disease according to the characteristics of the COVID-19 pandemic. The proposed enhanced model, which will be referred to as the SEIR (Susceptible–Exposed–Infectious–Recovered) model with population migration, is inspired by the role that asymptomatic infected individuals, as well as population movements can play a crucial role in spreading the virus. In the model, the infected and the basic reproduction numbers are compared under the influence of intervention policies. The experimental simulation results show the impact of social distancing and migration-in rates on reducing the total number of infections and the basic reproductions. And then, the importance of controlling the number of migration-in people and the policy of restricting residents' movements in preventing the spread of COVID-19 pandemic are verified.

1. Introduction

The outbreak of novel coronavirus (COVID-19) pneumonia continues to increase worldwide, causing a large number of casualties and global economic crises. The outbreak has put many countries in an emergency response phase. At present, research on developing a vaccine for coronavirus is still in preliminary stages and there are no specific drugs for efficient treatment of infected patients. The ones that are available can only assist a patient's self-autoimmunity. Under these conditions and based on the characteristics of COVID-19 pandemic, it is vital to develop a new mathematical model according to the characteristics of the COVID-19. It would be possible to analyze the pathology and dynamic transmission of infectious diseases, and also find an optimal decision for preventing spread of the virus with such a model.

However, well-established models, such as the Susceptible–Exposed–Infectious–Recovered (SEIR) model [1], cannot be considered for COVID-19 due to the unique characteristics of the virus. More importantly, the spread of COVID-19 is not limited to symptomatic individuals, but also to those who do not show any symptoms (i.e., asymptomatic). More specifically, unlike previous SEIR models, a new model has to take into consideration COVID-19 exposure characteristics that consist of two types: symptomatic and asymptomatic. By incorporating both types in a new model, it would then be possible to analyze the pathology and dynamic transmission of infectious diseases and then find an optimal solution to prevent spread of the virus.

Thus, in this paper, we incorporate asymptomatic infections and population migration into SEIR and introduce a new model, which will be referred to as the SEIAR (Susceptible–Exposed–Infectious–Asymptomatic–Recovered) model with population migration. Based on the proposed SEIAR model with the unique epidemiological characteristics of COVID-19, we evaluate differences in the asymptotic stability of the model with and without intervention. We then present our experimental results, which include verifying the effectiveness of interventions (e.g., social distancing and migration control) in mitigating the spread of COVID-19.

In summary, the main contributions of this paper include:

- By establishing a mathematical model of an infectious disease based on the characteristics of COVID-19 (such as the effect of asymptomatic infected patients in spreading the virus), the applicability of the modified model is proved.
- By calculating the curve of the number of infections based on the Euler numerical method, we then analyze and compare the effects of different anti-epidemic policies on reducing the number of infections.

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- By calculating the basic reproduction number of the model, We verify that reducing mobility rates based on the basic reproduction number again, i.e., the migration ban, can indeed slow down virus transmission.

The rest of the paper is organized as follows. The related works are introduced in Section 2. We develop a mathematical model to describe the transmission of COVID-19 and calculate the basic reproduction number for this model in Section 3. Then, we use a simulation to calculate the impact of quarantine measures and migration restrictions on the transmission of infectious diseases in Section 4. We also discuss our future work in Section 5. Finally, Section 6 concludes this paper.

2. Related work

The traditional model of infectious diseases is based on the population classification of infectious diseases. Presently, well-established mathematical models have been widely used to project the propagation of various epidemics, such as Susceptible–Infectious–Recovered (SIR) and SEIR [2]. Kermack et al. proposed an SIR-based model to project the expected epidemic scenarios for the plague [3]. In the case of Influenza, Hethcote et al. introduced a so-called fourth population classification (i.e. exposed person) [4]. This type of population is a potential infection population, it does not have the ability to infect others. The extended epidemic model is called the SEIR model [3].

Currently, the SEIR model is applicable to influenza, AIDS, and other epidemics. For example, in [5], Syafruddin et al. studied the differential equations of transmission dynamics of dengue fever in Selangor Malaysia. They finally proved that the SEIR model has certain applicability between theoretical calculation and practical calculation. In terms of the global stability of the SIR and SEIR models, Abtae. et al. applied Lyapunov function to determine the global asymptotical stability conditions of disease-free and endemic free equilibrium and concluded that the stability of SEIR is better than SIR [6]. Moreover, Li et al. proposed an infectious disease model where individuals in the exposed state and those in the recovered state are infectious [6]. However, according to the infectivity characteristics of COVID-19, the SEIR model is not applicable to describe the actual infectious process of COVID-19.

Currently, based on a simple mathematical model and limited data, Zhong et al. [7] used the epidemic data of COVID-19 in Wuhan (at the initial stage) to estimate the infection rate, mortality, and other parameters. These parameters were then fed into the SIR model to predict the outbreak of COVID-19 in China. The authors did not consider the difference between the infection rate and mortality rate among various cities. For instance, patients in the exposed period were omitted. They also ignored the impact of population migration. In [8], Iwata et al. investigated the possibility of potential outbreak caused by imported cases in a community outside China. Moreover, the authors in this paper put different coefficients into the mathematical model and got sets of results which were not representative.

However, there are many deficiencies in recent studies [9]. Firstly, there were not enough data to know the origin, the rule of infection, and the mode of infection of COVID-19 with certainty, while it is still in the early stage of the outbreak. Secondly, the migration of population and the dynamic change of parameters have been ignored.

Thus, based on the above analysis, previous SEIR-based models cannot be directly applied to COVID-19. This is due to the fact that while individuals in the exposed state of COVID-19 are infectious, there is no evidence to prove that individuals in the recovered state cannot still be infectious. So, we need to enhance the SEIR model by considering only the exposed state as being infectious and not the recovered state. In order to build such a model, we set up two infection rates; one is the infection rate of the exposed person and the other is the infection rate of the infected person. In addition, after establishing the model, we consider the impact of the exposed period of COVID-19 on the spread of the epidemic. In the next section, we will describe the specific SEIAR model.

3. Methods

In this paper, we propose a new epidemic model that tasks asymptomatic cases and migration into consideration. Because of the change of contact and migration rates, we incorporate these two parameters as a function of time in our model.

3.1. The SEIAR model

According to the known characteristics of COVID-19, we can divide the regional population into the following five categories: susceptible group (S), exposed group (E), infected (symptomatic infection) group (I), asymptomatic infected group(A), or recovered group (R), as illustrated in Fig. 1.

Furthermore, according to the report of the World Health Organization, the general transmission process is as follows:

- If susceptible persons contact asymptomatic and symptomatic infected people, their status will change to exposed.
- Most of the exposed people are transformed into infected or asymptomatic infected after the exposed period. It should be noted that the exposed of COVID-19 is 5.2 days.
- Infected and asymptomatic people will be moved into convalescence after rehabilitation, because they are expected to develop a certain immunity within an unknown period of time.

Thus, we introduce the transformation relationship between these five groups as shown in Fig. 1. Here, we consider the existence of asymptomatic infected people and migration. Note that asymptomatic infected people will not die of the COVID-19 infection, but infected people may.

Moreover, the population density of these categories is denoted by $S(t)$, $E(t)$, $I(t)$, $A(t)$ and $R(t)$ at time t, respectively. Let $N(t)$ denote the total number of people at time t, then, we can obtain

$$N(t) = S(t) + E(t) + I(t) + A(t) + R(t) \tag{1}$$

We set the parameters within the SEIAR model as follows: the contact rate of susceptible individuals contacting symptomatic and asymptomatic infected persons is defined as α, i.e , the number of susceptible patients who are exposed every day. We denote the derivative of recorded exposed time as ρ. After the exposed period, the probability of an exposed person entering into infected status is χ, among which the probability of symptomatic infected is β_1, and the probability of exposed into asymptomatic infected is β_2, and $\beta_1 + \beta_2 = 1$. Moreover, ω is the proportion of people who are infected before symptoms relative to those who have symptoms. Furthermore, the probability of symptomatic patient recovering is δ_1 and the recovery probability of asymptomatic patients is δ_2. We set the probability of mortality due to COVID-19 to η and the natural mortality rate to θ.

Based on the above parameters, we propose the SEIAR model population migration using the following ordinary differential equations (ODEs):

$$\begin{aligned}
\frac{\partial S}{\partial t} &= \lambda_1 S(t) - \frac{\alpha\rho S(t)\,(I(t) + \omega E(t))}{N} - \lambda_2 S(t) - \theta S(t) \\
\frac{\partial E}{\partial t} &= \lambda_1 E(t) + \frac{\alpha\rho S(t)(I(t) + \omega E(t))}{N} - (\chi + \lambda_2 + \theta)E(t) \\
\frac{\partial I}{\partial t} &= \lambda_1 I(t) + \chi\beta_1 E(t) - (\eta + \delta_1 + \lambda_2 + \theta)I(t) \\
\frac{\partial A}{\partial t} &= \lambda_1 A(t) + \beta_2 E(t) - (\delta_2 + \lambda_2 + \theta)A(t) \\
\frac{\partial R}{\partial t} &= \lambda_1 R(t) + \delta_1 I(t) + \delta_2 A(t) - (\lambda_2 + \theta)R(t)
\end{aligned} \tag{2}$$

where λ_1 denotes the migration-in rate, and λ_2 denotes the migration-out rate.

For the above parameters $(\alpha, \rho, \chi, \theta, \beta_1, \beta_2, \delta_1, \delta_2, \eta, \lambda_1, \lambda_2)$, we can solve it by the machine learning algorithm. In this paper, for the sake of simplicity, we use existing work to estimate the parameters. Furthermore, we utilize the Euler numerical method to solve the ODEs (2).

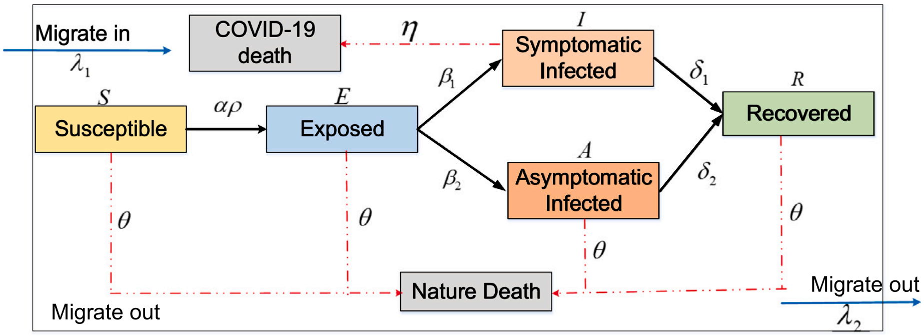


Fig. 1. The transformation of Susceptible, Exposed, Infectious, Asymptomatic, and Recovered individuals of COVID-19 in SEIAR model with population migration.

3.2. Computation of the basic reproduction number

The basic reproduction number R_0 is an important indicator to describe the epidemic dynamics. It refers to the number of the expected cases directly generated by one case in which all individuals in a population are susceptible to infection. In this paper, we use the next generation matrix [10,11] to derive a formula for the control reproduction number when control measures are in force.

To be specific, firstly, we divide the population into five categories according to the state of infection. Then, we denote matrix $\mathcal{J}_i(x)$ as the new infection rate in category i. Let $x = (x_1, x_2, x_3, x_4, x_5)$ be the combination of crowd categories, x_i represents the number of people in each category. $\mathcal{J}(x)$ is the vector of $\mathcal{J}_i(x)$. Moreover, we denote by $v_i(x)$ is the rate where other categories are converted to category i. $\mathcal{V}(x)$ is the vector of $v_i(x)$. According to the mathematical model of infectious diseases, we can obtain $\mathcal{J}(x)$ and $\mathcal{V}(x)$ as follows:

$$\mathcal{J}(x) = \begin{bmatrix} \lambda_1 E + \frac{\alpha\rho S(I+\omega E)}{N} \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} \tag{3}$$

and

$$\mathcal{V}(x) = \begin{bmatrix} (\chi + \lambda_2 + \theta)E \\ -\lambda_1 S + \frac{\alpha\rho S(t)(I(t)+\omega E(t))}{N} + (\lambda_2 + \theta)S \\ -\lambda_1 I - \chi\beta_1 E + (\eta + \delta_1 + \lambda_2 + \theta)I(t) \\ \lambda_1 A(t) + \beta_2 E(t) - (\delta_2 + \lambda_2 + \theta)A(t) \\ \lambda_1 R(t) + \delta_1 I(t) + \delta_2 A(t) - (\lambda_2 + \theta)R(t) \end{bmatrix} \tag{4}$$

Furthermore, we define **J** and **V** as the Jacobian matrices of function $\mathcal{J}(x)$ and $\mathcal{V}(x)$. Then, we can obtain the Jacobian matrixes of (3) and (4) with respect to x which can be expressed as follows:

$$\mathbf{J} = \begin{bmatrix} F & 0 \\ 0 & 0 \end{bmatrix} \tag{5}$$

and

$$\mathbf{V} = \begin{bmatrix} V & 0 \\ J_3 & J_4 \end{bmatrix} \tag{6}$$

where F and V is a 3×3 matrices. We define $F = \left[\frac{\partial J_i}{\partial x_j}(x_0)\right]$, $V = \left[\frac{\partial V_i}{\partial x_j}(x_0)\right]$,where $1 \le i, j \le 3$, and the disease free equilibrium $x_0 = (0, s_0, 0, 0, 0)$. x_0 is a locally asymptotically or stable equilibrium solution of (2). It is clear that $(0, 1, 0, 0, 0)$ is a disease free equilibrium of (2) [12]. Then

$$F = \begin{bmatrix} 1 + \lambda_1 & \alpha\rho & \alpha\rho \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \tag{7}$$

and

$$V = \begin{bmatrix} \chi + \lambda_2 + \theta & 0 & 0 \\ -\chi\beta & \eta + \delta_1 + \lambda_2 + \theta - \lambda_1 & 0 \\ -\chi\beta_2 & 0 & \delta_2 + \lambda_2 + \theta - \lambda_1 \end{bmatrix} \tag{8}$$

Thus, we obtain the next generation matrix of COVID-19 as $\mathbf{G} = FV^{-1}$. Therefore, the basic reproduction number R_0 of the SEIAR model can be obtained by calculating the spectrum radius of **G** as follows:

$$R_0 = \frac{1}{\chi + \lambda_2 + \theta}\left[(\lambda + \delta_1 + \lambda_2 + \theta) + \frac{\alpha\rho\chi\beta_1}{(\delta_2 + \lambda_2 + \theta) - \lambda_1}\right] \tag{9}$$

In epidemiology, the basic reproduction number is the average number of people who are infected with an infectious disease. The basic reproduction number can be used to determine how easy it is to control an epidemic. If $R_0 < 1$, infectious diseases will gradually disappear. If $R_0 > 1$, infection can spread exponentially, but it generally does not last forever as the number of people likely to be infected slowly declines. Some people may die of the infection, while others may recover and develop immunity. If $R_0 = 1$, the infectious disease can become endemic to populations.

4. Performance evaluation

In this paper, we mainly study the impact of different effective epidemic prevention measures on controlling the epidemic situation. Currently, research of COVID-19 in Wuhan has been well investigated. Thus, we use the research parameters used by Tang, et al. in [13,14] directly. We mainly analyze the infection data of Wuhan, China, which is consistent with the infection direction of our early experimental area, so we can use the parameters in this study directly.

Specifically, we set the total number of people in the experimental area to 10,000. The contact rate of susceptible individuals and infected people is $\alpha = 140$. The disease incidence probability of each contact transmission is $\rho = 2.1011 \times 10^{-5}$. The exposed period is $\gamma = 1/\chi = 5.2$ [15].

After the exposed period, the probability of the exposed people becoming infected is $\beta_1 = 0.86834$, and the probability of exposed infection to asymptomatic infection is $\beta_2 = 1 - 0.86834$. The probability of recovery is $\delta_1 = 0.13029$, and the recovery probability of asymptomatic patients with infection is $\delta_2 = 0.1$. The probability of death due to COVID-19 is $\eta = 0.2$. The natural mortality rate is $\theta = 7.14 \times 10^{-3}$. Furthermore, we set initial $S = 9999, E = 0, I = 1, A = 0, R = 0$.

4.1. Real data for the SEIAR model

In order to verify the feasibility of the model, we used real data from Wuhan for simulation. We set the initial experimental data as: $S = 11081000, E = 0, I = 1, A = 0, R = 0$. The first case was detected on December 6, 2019, according to China's national health commission.

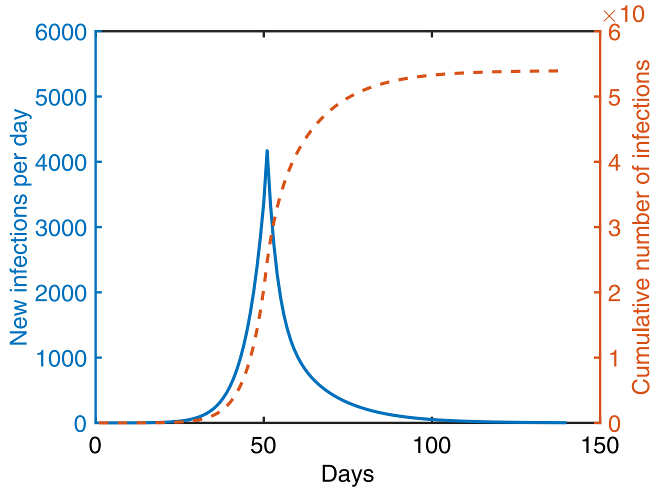


Fig. 2. The real data for SEIAR Model.

On January 24, 2020, Wuhan implemented a strict lock-down policy for the population. In this way, from case detection to day 50, the contact rate drops significantly. We set it to $\alpha_0 = 5$.

The experimental results are shown in Fig. 2. We found that the daily increase of infections was different from the actual report in Wuhan. Some patients were not detected due to the limited number of test reagents in the early stage of infection. The number of patients reported dramatically increases suddenly after the number of test reagents increased. Therefore, the daily increase number of infections is reasonable. According to the experimental results, the cumulative number of infections increases every day, and after about 80 days, the cumulative number of infections is basically unchanged. This phenomenon is consistent with the report of the Wuhan health and health commission, which fully proves the applicability of our model.

4.2. Contact rate control

In order to control the spread of COVID-19, measures such as staying home should be considered to reduce the contact rate. Thus, in this paper, we set three contact rates: (i) constant contact rate $\alpha = \alpha_0$, (ii) exponential decreasing contact rate $\alpha(t) = (\alpha_0 - \alpha_{\min} e^{-r_1 t}) + \alpha_{\min}$, and (iii) piecewise exponential function contact ratio, which is as follows:

$$F_1 = \begin{cases} \alpha_0 & 0 \le t < L \\ (\alpha - \alpha_0)e^{-r_1 t} + \alpha_{\min} & L \le t \end{cases} \tag{10}$$

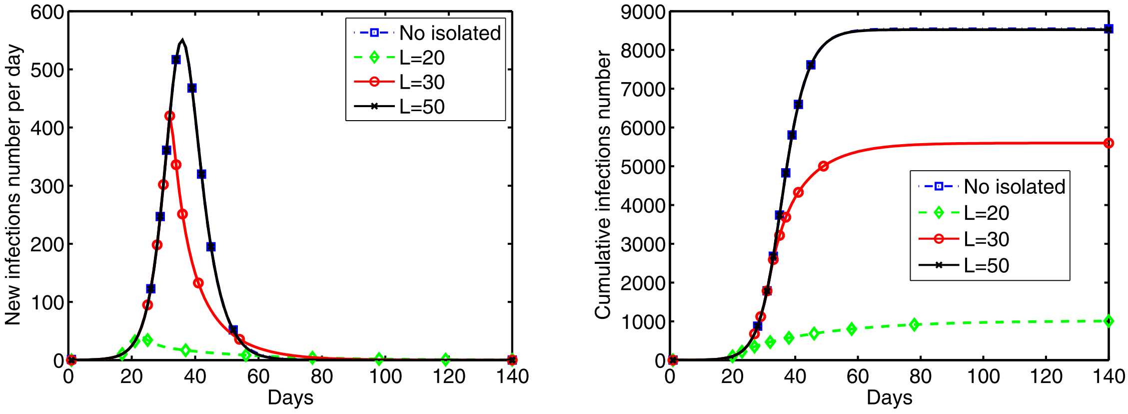
$$F_2 = \begin{cases} \alpha_0 & 0 \le t < L_0 \\ (\alpha - \alpha_0)e^{-r_1(t-L_0)} + \alpha_{\min} & L_0 \le t < L \\ -(\alpha - \alpha_0)e^{-r_1(t-L)+1} + \alpha_0 & L \le t \end{cases} \tag{11}$$

where $\alpha_{\min}$ represents the minimum exposure rate after implementation of the policy. In Eq. (10), L is the days the ban. In Eq. (11), L_0 is the days for beginning the ban. L is the days for ending the ban.

Quarantine can keep people at a social distance, and then change contact rate. Therefore, we can define different values for the contact rate according to different epidemic prevention measures. Firstly, if the authorities do not take any preventive measures, we assume that the contact is constant. Otherwise, we assume that the contact rate will exponentially decrease. Over time, when people become less alert or the authorities end the quarantine too early, we set the contact rate to increase exponentially. The contact rate meets Eq. (10).

In Fig. 3, in order to reduce the impact of the migration-in rate on the test area, we assume that no infected persons will migrate to that area within the next 140 days. Moreover, we set $\alpha_{\min} = 2$, $r_1 = 1.3768$. In Fig. 3, experimental results show that the number of new symptomatic infections per day increases with a fastest pace in areas without quarantine measures (i.e., no isolated), and the cumulative number of symptomatic infections is the largest. The larger the value of L, the larger the cumulative number of symptomatic infections. Because the sooner quarantine measures are made, the less contact people will have, i.e., the less contact rate. If these measures are implemented on day 50 (i.e., $L = 50$), the quarantine measures will have little effect. The results of this trial prove that if we want to mitigate the epidemic as soon as possible and reduce the number of infections during the epidemic, it is essential to implement strict guidelines as early as possible.

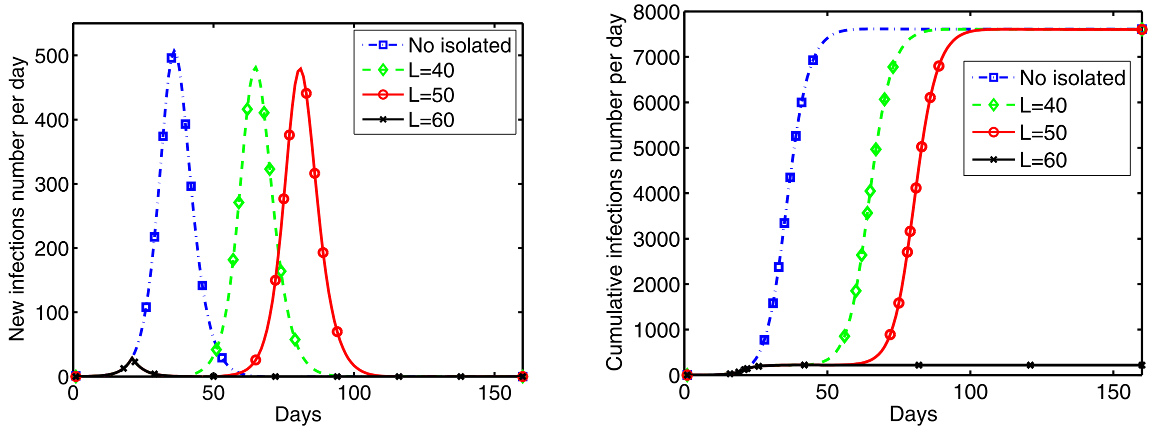
Secondly, as shown in Fig. 4, the contact rate meets equation (11). We begin quarantine measures 20 days after the case was found, i.e, $L_0 = 20$. The quarantine ended on the 40th (i.e., L=40), 50th (i.e., L=50), and 60th (i.e., L=60) days in the experimental area. When quarantine measures are ended, the contact rate increases exponentially. According to curves of No isolated, $L = 40$ and $L = 50$, there is no difference between the premature termination of the quarantine and the failure to take preventive measures. The daily number of new infections stopped rising after the quarantine is terminated on the 60th day. There is no significant difference between the effect of the quarantine and that of continuous implementation of the quarantine measures. The analysis showed that the government neither can end the quarantine measures prematurely, nor need to close dated measures too late. According to the infection data, it can be reasonably estimated the time needed of quarantine measures.



(a) The number of new symptomatic infections increased daily after the quarantine began on day L.

(b) The cumulative number of symptomatic infected persons after the quarantine began on day L.

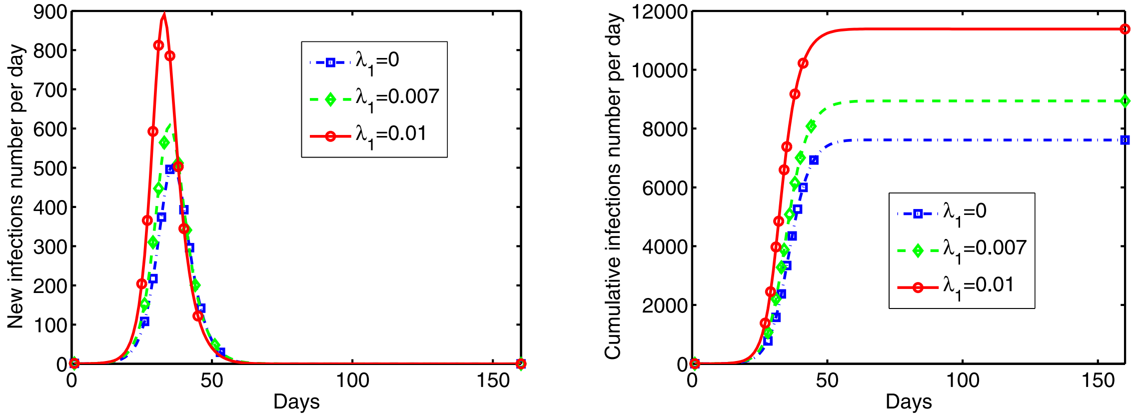
Fig. 3. The impact of the initiation time of quarantine measures on the spread of COVID-19.



(a) The number of symptomatic infections increased daily by taking different isolation time.

(b) The cumulative number of symptomatic infections increased daily by taking different isolation time.

Fig. 4. The impact of the end time of quarantine measures on the spread of COVID-19.



(a) The number of symptomatic infections increased daily by taking different migration-in rates.

(b) The cumulative number of infections increased daily by taking different migration-in rates.

Fig. 5. The impact of restrict migration-in on the spread of COVID-19.

4.3. The impact of migration-in rate on COVID-19

In our next experiment, we set different mobility-in rates. Firstly, $\lambda_1 = 0$ represents a blockage to entering or exiting the epidemic area. In addition, to compare the impact of the migration rate on our infection model, we set the migration-in rate to $\lambda_1 = 0.01$ and $\lambda_1 = 0.007$. The results, which are shown in Fig. 5 for symptomatic population, indicate that the total number of infected people in the experimental area decreases with a reduction in the migration-in rate. Additionally, the lower the migration-in rate, the faster it will reach the peak number of infected people.

4.4. Basic reproduction number of COVID-19

The base reproduction number R_0 can be used as a parameter to measure the rate of infection. As shown in Fig. 6, we set different mobility rates, i.e., $\lambda_1 = 0.00714$, $\lambda_1 = 0.001$ and $\lambda_1 = 0$. We make the contact rate of each curve decrease exponentially. According to Fig. 6, in the initial stage, the basic reproduction number is greater than 1. As time goes on, the contact rate decreases, which makes the basic reproduction decrease, and it ends up being less than 1. In addition, compared with the three curves, the smaller the different mobility

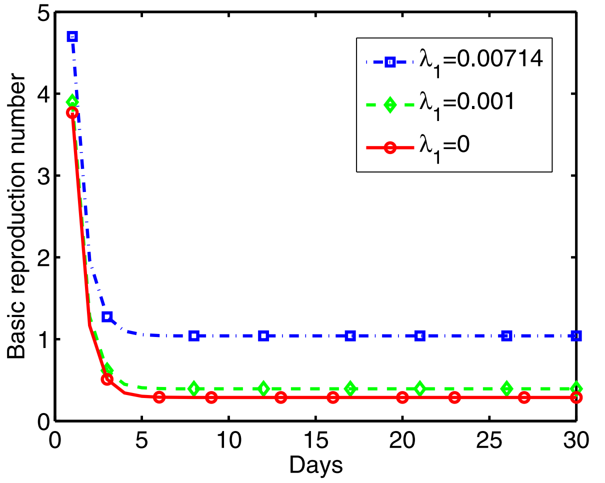


Fig. 6. The influence of mobility and contact rate on basic reproduction number.

rates are, the smaller the migration rate. These experimental results indicate that quarantine measures are conducive to control the spread of infectious diseases.

5. Discussion and future research directions

In this paper, according to the characteristics of COVID-19, considering the asymptomatic infected and the migration and emigration of users, we propose the this model and evaluate the validity of SEIAR model by experimentation. In the future, there remain several interesting topics which are as follows:

Medical Resource Allocation: Due to different severities of the COVID-19 epidemic in different areas, utilization of medical resources in different regions is also different. For example, in severe areas, doctors, nurses, protective materials and drugs are in serious shortage. However, there is a surplus of medical supplies in areas with less severe outbreaks. Therefore, we need to establish a scheduling scheme to transfer the remaining medical materials from the slight epidemic area to areas with serious epidemic.

In order to make an optimal scheduling scheme, we need to establish a multi-objective optimization problem: the objective function is to minimize mortality of the infected patients in the experimental area, and to minimize the cost of deployment. The constraint is that cities should share medical resources with other cities and ensure that medical resources of its own city can be self-sufficient. The allocated materials accepted by the city receiving the medical resources cannot exceed the amount of medical resources it needs. Thus, we need to build a scheduling model of hospital to hospital.

User Mobility Control for Economic Recovery: The epidemic has seriously affected the economies of all countries. Achieve economic recovery on the basis of controlling the COVID-19 epidemic situation is a challenging problem. From the perspective of existing research, user mobility is an important factor affecting epidemic prevention and economic recovery. Thus, we plan to give user mobility control to achieve economic recovery on the basis of epidemic control. In particular, some novel approaches based on edge intelligence could be considered [16], especially advanced mobile networking and healthcare systems [17].

For example, we take the income of the hospitality industry and the number of people infected by the virus as the target, and establish a multi-objective optimization problem. The objective function is to maximize the income of the catering industry and minimize the number of people infected. There exists a trade-off, because an increase in the number of infected people will restrict people from going out, so the income of the hospitality industry will decrease. In order to improve the income of this industry, we will increase the number of people going out, but at the expense of increasing the number of infected people. Thus, we can give an appropriate mobility of users, and realize the profit of the catering industry on the basis of controlling the epidemic.

Deep Learning for Population Migration: In order to get the dynamic mobility of population in an experimental region, we can divide the movement of a population into two parts, i.e., the number of people moving into the area, called the migrate in, and those moving out as migrate out. According to previous studies, the amount of migration in any region is continuous from a time perspective. For example, the amount of migrate in has a strong correlation with the amount of migrate in at the previous moment.

Moreover, population movement is affected by the COVID-19. In this paper, we give simple parameters to describe the influence of migration and emigration on COVID-19. In future work, we will use the deep learning [18,19] approach to build a spatial and temporal population migration model, to better predict the impact of population migration on the COVID-19 epidemic.

6. Conclusion

Based on the results of our simulations, some interventions are needed to control the spread of COVID-19. Home confinement reduces person-to-person contact and can effectively reduce the rate of transmission and the number of people infected. In addition, if earlier measures to control person-to-person contact are implemented, the faster the spread of the virus is controlled. Moreover, these measures must not be terminated prematurely. The experimental results of the study on migration rates also prove the importance of implementing migration control.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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