SIR Model of COVID-19 Epidemic Spread Between Two Regions

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Abstract. COVID-19, a worldwide pandemic, has had negative implications on the global economy and politics. Previous studies, based on the SIR Model and its variations, divided the population of a single area into the suspected, the infected and the recovered and other parts, and proposed corresponding dynamic systems to simulate the development of the epidemic. However, the movement of people from one region to another can lead to the spread of COVID-19 from one region to another. We establish SIR Model for the transmission of the epidemic between two regions, and theoretically derived the disease-free equilibrium point and the basic reproduction number of the proposed dynamic system. Next, we study the effect of population mobility rate between different regions on the basic reproduction number. Finally, we carry out numerical simulation of the model and analyze the development of the epidemic under the parameter hypothesis. These results have clinical and guiding implications for epidemic prevention and control in different regions.

Keywords: SIR Model, COVID-19, Population Movement

1. Introduction

Corona Virus Disease 2019(COVID-19), a worldwide epidemic, was first detected in Wuhan in 2019. The disease is caused by the SARS-CoV-2 virus and spreads from person to person. On 11 March 2020, WHO Director-General Tedros Adhanom Ghebreyesus announced that, based on the assessment, WHO believes the current COVID-19 outbreak can be called a pandemic. The COVID-19 outbreak has caused a large number of confirmed cases and deaths worldwide, and has had a profound impact on global healthcare, tourism, economy and politics.

Compartmental model is an important tool for mathematical modeling of infectious disease evolution. In the early 20th century, Kermack and McKendrick et al. started a systematic study on infectious disease modeling [1]. SIR Model has been widely used as one of the simplest Compartmental models [2]. Today, there are many different variations of the SIR Model as more and more influencing factors are taken into account. Hye Md. Abdul et al. developed an SIR Model to explore the transmission dynamics of coinfection of COVID-19 and dengue and to predict the outbreak [3]. Considering those who have been exposed to the virus, Thomas Reetha et al. explored four different SEIRS models and solved them with an effective homotopy perturbation method [4].Considering those who are hospitalized, Faizunnesa Khondaker et al. established the SEIHR model (Susceptible (S), Exposed (E), Infected (I),

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Hospitalized (H), Recovered (R)) and important optimal conditions were recovered using optimal control theory to control disease transmission [5]. Considering vaccination, Kammegne Brice et al. established the SEIRV model (Susceptible, Exposed, Infected, Recovered, and Vaccinated) using the reaction - diffusion equations [6]. Considering the unique modes of transmission of certain infectious diseases, Lan Zou et al. studied infectious diseases such as hepatitis B with characteristics of sexual and mother-to-child transmission, improved the SIR Model and calculated the basic reproduction number under the model [7]. Scientists have taken different factors into account and built different models based on the SIR Model. They use these models to analyze regional cases and try to predict and control the development of epidemics [8-14].

Nevertheless, previous work focused only on single region, ignoring the movement of people in different regions that causes outbreaks to spread between regions. When one region has a high incidence of infection and another is less severe, the movement of people between the two regions can significantly affect the development of the epidemic. In addition, if two regions have different quarantine policies, people in the region with stricter quarantine policies are more likely to wear masks and avoid gathering, which reduces the transmission rate of the disease. If two regions have different medical conditions, then in the region with higher medical conditions, people can have access to better medical equipment and drugs, which will lead to different cure rates of diseases. Under such conditions, in this paper, we study the influence of population movement rate between different regions on the epidemic situation and what factors influence the equilibrium point reached by the epidemic situation.

In this paper, to tackle the above issues, we first formulate SIR Models of population movements between two regions and modify the traditional SIR Model according to the actual situation. Next, we derived the disease-free equilibrium, calculated the basic reproduction number of the model and explored the monotonicity of the basic reproduction number with respect to the mobility rate of infected people. Then, we write a Matlab program to simulate the model, and study how the change of population movement rate affects the development of the epidemic. These results have guiding significance for studying the evolution and spread of the epidemic between regions and exploring the conditions under which inter-regional population movement should be encouraged or suppressed.

2. Modeling

2.1 Model Formulation

The SIR Model divides the population of each region into three parts: S for those who have never been infected, I for those who have been infected with the virus, and R for those who have recovered. If the susceptible is in contact with the infected, then the susceptible is likely to infect the virus. It is assumed that the number of susceptible people infected by a patient in unit time is proportional to the total number of susceptible people, with a proportional coefficient of β, so that the number of infected people infected by all patients in unit time at time t is $\beta S(t)I(t)/N(t)$. The infected may recover and lose infectivity. It is assumed that the recovery people in unit time is proportional to the number of infected people, denoted as $I(t)$, and the proportion coefficient is γ, so the number of patients recovered in unit time at time t is $\gamma I(t)$. Assume that the birth rate and death rate of a region do not change over time. The

number of births per unit time is denoted as $b(N)$, the death rate of the susceptible and the recovered is denoted as d, and the death rate of the infected is denoted as d'. Given that patients may die from the coronavirus, assume $d' > d$.

Let's consider the movement of people between the two regions, where S_1, I_1, R_1 represents the susceptible, the infected and the recovered in region 1 respectively and S_2, I_2, R_2 represents the susceptible, the infected and the recovered in region 2 respectively. We divide the population movement between regions 1 and 2 into three parts, where $\alpha_S, \alpha_I, \alpha_R$ represents the movement rate of the susceptible, the infected and the recovered from region 1 to region 2, and $\delta_S, \delta_I, \delta_R$ represents the movement rate of the susceptible, the infected and the recovered from region 2 to region 1. The dynamic system obtained by SIR Model is shown in Figure1, where the parameters are summarized in Table1.

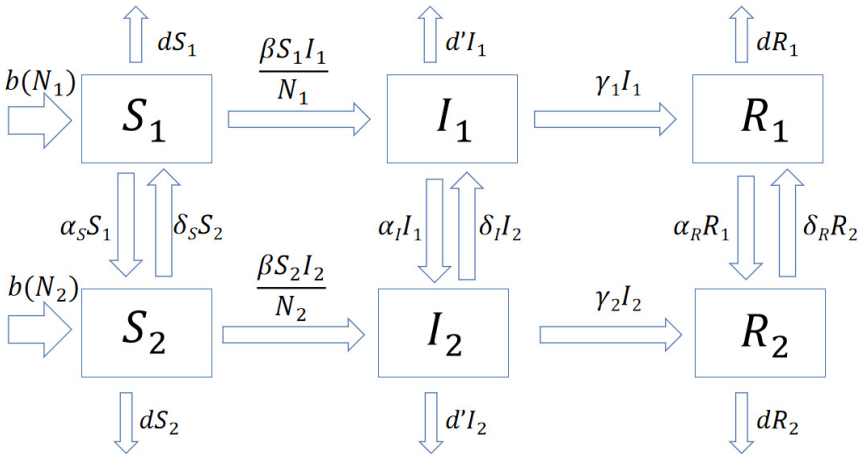

Figure 1. The SIR Model with Population Movements [Owner-draw]

However, the SIR Model obtained in this way does not completely accord with the reality, and we need to correct it. First, considering different policies on the prevention and treatment of infectious diseases in different regions, it is reasonable to believe that the contact rate between the uninfected and the infected is different, that is, β is different. Secondly, given that there is no lifelong immunity after infection, recovered persons may be reinfected with the virus, which is positively correlated with the contact rate between recovered persons and infected persons. The revised dynamic system is shown in Figure 2, where the parameters are summarized in Table1.

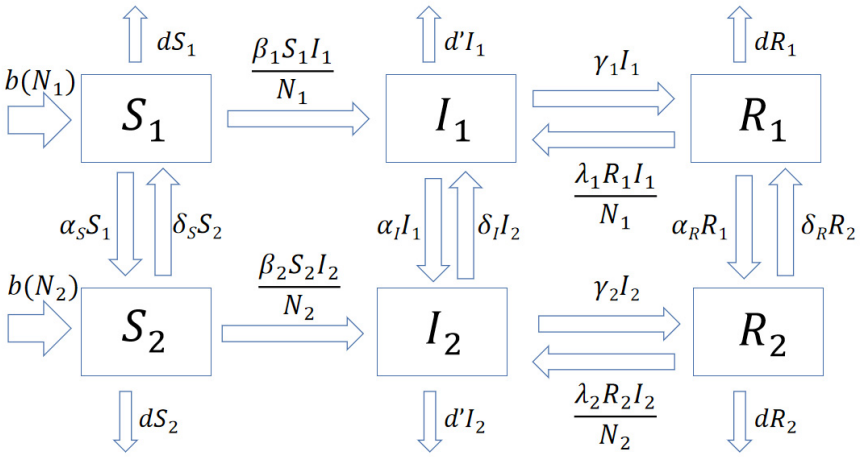

Figure 2. The Corrected SIR Model with Population Movements [Owner-draw]

Table 1. Model Parameters [Owner-draw]

Symbol	Description
$\beta_i\ (i = 1,2)$	Rate of infection of susceptible people in the region i (i=1,2)
$\alpha_S, \alpha_I, \alpha_R$	Rate of movement of susceptible, infected, or recovered populations from region 1 to region 2
$\gamma_i\ (i = 1,2)$	Rate of recovery in the region i (i=1,2)
$\delta_S, \delta_I, \delta_R$	Rate of movement of susceptible, infected, or recovered populations from region 2 to region 1
$\lambda_i\ (i = 1,2)$	Rate of infection of recovered people in the region i (i=1,2)
d	Death rate of susceptible or recovered people
d'	Death rate of infected people
$b(N_i)\ (i = 1,2)$	Birth rate in the region i (i=1,2)

The assumptions about parameters are as follows:

(A1). Given the death due to disease, suppose $d < d'$.

(A2). Without loss of generality, it is assumed that the epidemic prevention policy in region 2 is stricter than that in region 1, that is, the contact rate with infected persons is lower in region 2. So $\beta_1 > \beta_2$ and $\lambda_1 > \lambda_2$.

(A3). The death rate between uninfected and infected persons is the same across regions.

Under such assumptions, the corresponding equations of the dynamical system are as follows.

$$\frac{dI_1}{dt} = \frac{\beta_1 S_1 I_1}{N_1} + \frac{\lambda_1 R_1 I_1}{N_1} - \alpha_I I_1 - \gamma_1 I_1 - d' I_1 + \delta_I I_2 \quad (1)$$

$$\frac{dI_2}{dt} = \frac{\beta_2 S_2 I_2}{N_2} + \frac{\lambda_2 R_2 I_2}{N_2} + \alpha_I I_1 - \gamma_2 I_2 - d' I_2 - \delta_I I_2 \quad (2)$$

$$\frac{dS_1}{dt} = b(N_1) - \alpha_S S_1 - \frac{\beta_1 S_1 I_1}{N_1} + \delta_S S_2 - dS_1 \quad (3)$$

$$\frac{dS_2}{dt} = b(N_2) + \alpha_S S_1 - \frac{\beta_2 S_2 I_2}{N_2} - \delta_S S_2 - dS_2 \quad (4)$$

$$\frac{dR_1}{dt} = \gamma_1 I_1 - \alpha_R R_1 + \delta_R R_2 - dR_1 - \frac{\lambda_1 R_1 I_1}{N_1} \quad (5)$$

$$\frac{dR_2}{dt} = \gamma_2 I_2 + \alpha_R R_1 - \delta_R R_2 - dR_2 - \frac{\lambda_2 R_2 I_2}{N_2} \quad (6)$$

2.2 Basic Reproduction Number

The disease-free equilibrium with $I_1 = I_2 = 0$ has the form $x_0 = (0, 0, S_1, S_2, 0, 0)$. Without loss of generality, assume $S_0 = 1$.

Let

$$\mathcal{F} = \begin{pmatrix} \frac{\beta_1 S_1 I_1}{N_1} + \frac{\lambda_1 R_1 I_1}{N_1} \\ \frac{\beta_2 S_2 I_2}{N_2} + \frac{\lambda_2 R_2 I_2}{N_2} \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix} \qquad F = \begin{pmatrix} \beta_1 + \lambda_1 & 0 \\ 0 & \beta_2 + \lambda_2 \end{pmatrix} \quad (7)$$

$$\mathcal{V} = \begin{pmatrix} \alpha_I I_1 + \gamma_1 I_1 + d' I_1 - \delta_I I_2 \\ -\alpha_I I_1 + \gamma_2 I_2 + d' I_2 + \delta_I I_2 \\ -b(N_1) + \alpha_S S_1 + \frac{\beta_1 S_1 I_1}{N_1} - \delta_S S_2 + dS_1 \\ -b(N_2) - \alpha_S S_1 + \frac{\beta_2 S_2 I_2}{N_2} + \delta_S S_2 + dS_2 \\ -\gamma_1 I_1 + \alpha_R R_1 - \delta_R R_2 + dR_1 + \frac{\lambda_1 R_1 I_1}{N_1} \\ -\gamma_2 I_2 - \alpha_R R_1 + \delta_R R_2 + dR_2 + \frac{\lambda_2 R_2 I_2}{N_2} \end{pmatrix} \quad V = \begin{pmatrix} \alpha_I + \gamma_1 + d' & -\delta_I \\ -\alpha_I & \gamma_2 + d' + \delta_I \end{pmatrix} \quad (8)$$

then

$$FV^{-1} = \frac{1}{(\alpha_I + \gamma_1 + d')(\gamma_2 + d' + \delta_I) - \alpha_I \delta_I} \begin{pmatrix} \gamma_2 + d' + \delta_I & \delta_I \\ \alpha_I & \alpha_I + \gamma_1 + d' \end{pmatrix} \quad (9)$$

Following Diekmann et al., we call FV^{-1} the next generation matrix for the model and set basic reproduction number $R_0 = \rho(FV^{-1})$, where $\rho(A)$ denotes the spectral radius of a matrix A. If $R_0 < 1$, then the disease-free equilibrium is locally asymptotically stable. If $R_0 < 1$, it is unstable [15].

$$R_0 = \frac{(\beta_1 + \lambda_1)(m + \sqrt{m^2 - 4n})}{2n} \quad (10)$$

where $m = \gamma_2 + \delta_I + \alpha_I + \gamma_1 + 2d' \quad n = (\alpha_I + \gamma_1 + d')(\gamma_2 + d' + \delta_I) - \alpha_I\delta_I$ (11)

The value of R_0 has nothing to do with the population mobility ratio of susceptible and recovered people. Controlling the movement of uninfected people has no effect on the stability of the epidemic equilibrium point. The value of R_0 is proportional to $(\beta_1 + \lambda_1)$, which indicates that for region 1 with relatively loose epidemic prevention policies, if the further liberalization of the policy leads to increased infection rate and recovery rate, R_0 will increase, and the epidemic will tend to be uncontrollable. However, the value of R_0 is independent of $(\beta_2 + \lambda_2)$, which indicates that for region 2 with relatively strict epidemic prevention policies, slightly increase or decrease of infection rate and recovery rate has no influence on the stability of epidemic equilibrium point. In general, the course of the epidemic depends more on whether it can be contained in the areas with the highest infection rates.

Next, we will focus on the influence of the infected population movement rate on R_0, and explore under what circumstances the increase or decrease of the infected population movement rate will lead to the increase or decrease of R_0. We calculate the monotonicity of R_0 with respect to α_I, δ_I.

Then

$$\frac{\partial m}{\partial \alpha_I} = 1, \qquad \frac{\partial n}{\partial \alpha_I} = \gamma_2 + d', \qquad \frac{\partial m}{\partial \delta_I} = 1, \qquad \frac{\partial n}{\partial \delta_I} = \gamma_1 + d' \quad (12)$$

$$\frac{\partial R_0}{\partial \alpha_I} = \frac{(\beta_1 + \lambda_1)}{2n\sqrt{m^2 - 4n}}\left[m + \sqrt{m^2 - 4n} - \frac{\gamma_2 + d'}{n}\left(m^2 + m\sqrt{m^2 - 4n} - 2n\right)\right] \quad (13)$$

when

$$\frac{mn + n\sqrt{m^2 - 4n}}{m^2 + m\sqrt{m^2 - 4n} - 2n} < \gamma_2 + d' \quad (14)$$

then

$$\frac{\partial R_0}{\partial \alpha_I} < 0 \qquad (15)$$

$$\frac{\partial R_0}{\partial \delta_I} = \frac{(\beta_1 + \lambda_1)}{2n\sqrt{m^2 - 4n}}\left[m + \sqrt{m^2 - 4n} - \frac{\gamma_1 + d'}{n}\left(m^2 + m\sqrt{m^2 - 4n} - 2n\right)\right] \quad (16)$$

when

$$\frac{mn + n\sqrt{m^2 - 4n}}{m^2 + m\sqrt{m^2 - 4n} - 2n} < \gamma_1 + d' \quad (17)$$

then

$$\frac{\partial R_0}{\partial \delta_I} < 0 \quad (18)$$

At last, we give a simpler way to derive the conclusion that R_0 increases with α_I. In this case, the movement of infected people does increase the risk that the epidemic will not be contained.

Proposition. When $(\gamma_1-\gamma_2)\delta_I > (\gamma_2+d')^2$, R_0 increases as α_I increases.

When $(\gamma_2-\gamma_1)\alpha_I > (\gamma_1+d')^2$, R_0 increases as δ_I increases.

Proof

$$R_0 = \frac{(\beta_1+\lambda_1)(m+\sqrt{m^2-4n})}{2n} = \frac{1}{2}(\beta_1+\lambda_1)\left(X+\sqrt{X^2-4Y}\right) \quad (19)$$

Where

$$X = \frac{m}{n} = \frac{\gamma_2+\delta_I+\alpha_I+\gamma_1+2d'}{(\alpha_I+\gamma_1+d')(\gamma_2+d'+\delta_I)-\alpha_I\delta_I} \quad (20)$$

$$Y = \frac{1}{n} = \frac{1}{(\alpha_I+\gamma_1+d')(\gamma_2+d'+\delta_I)-\alpha_I\delta_I} \quad (21)$$

When $(\gamma_1-\gamma_2)\delta_I > (\gamma_2+d')^2$

$$\frac{\partial X}{\partial \alpha_I} = \frac{(\gamma_1-\gamma_2)\delta_I-(\gamma_2+d')^2}{((\alpha_I+\gamma_1+d')(\gamma_2+d'+\delta_I)-\alpha_I\delta_I)^2} > 0 \quad (22)$$

As α_I increases, X increases and Y decreases, so R_0 increases.

When $(\gamma_2-\gamma_1)\alpha_I > (\gamma_1+d')^2$

$$\frac{\partial X}{\partial \delta_I} = \frac{(\gamma_2-\gamma_1)\alpha_I-(\gamma_1+d')^2}{((\alpha_I+\gamma_1+d')(\gamma_2+d'+\delta_I)-\alpha_I\delta_I)^2} > 0 \quad (23)$$

As δ_I increases, X increases and Y decreases, so R_0 increases.

When the medical level in region 1 is obviously higher than that in region 2, the recovery rate of infected people in region 1 will be obviously higher than that in region 2, that is, γ_1 is much higher than γ_2. Therefore, the condition of the above proposition is valid, which tells us that infected population transferred from regions with high medical level to regions with relatively low medical level will increase R_0, thus increasing the risk of uncontrollable epidemic.

3. Numerical Simulation

We wrote a Matlab program for numerical simulation of the proposed dynamic system, and the values of parameters are shown in Table 2. Assume the initial value $(I_1, I_2, S_1, S_2, R_1, R_2) = (1000, 1000, 10000, 12000, 0, 0)$. We figure out $R_0 = 2.92$.

Table 2. Model Parameter Assumption [Owner-draw]

Symbol	Value
(β_1, β_2)	(0.2,0.1)
$(\alpha_S, \alpha_I, \alpha_R)$	(0.5,0.3,0.3)
(γ_1, γ_2)	(0.1,0.1)
$(\delta_S, \delta_I, \delta_R)$	(0.4,0.3,0.2)
(λ_1, λ_2)	(0.15,0.05)
d	0.012

d'	0.02
$b(N_1), b(N_2)$	0.012

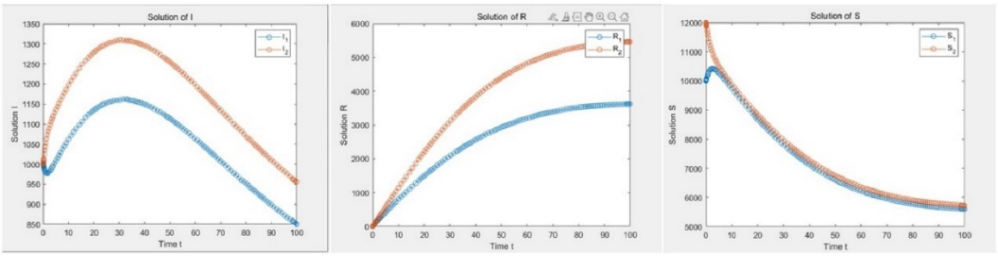

Figure 3. Simulations of the dynamic system with the assumed value of parameters [Owner-draw]

Figure 3 shows the number of infected, recovered and susceptible people in regions 1 and region 2 over time under the parameter assumption. The blue lines represent those in region 1 and the red lines represent those in region 2. From the output of the program, in the beginning of the epidemic, the number of infected people gradually rises, and it increases faster in region 2. Region 2 has a larger population, and there is a net migration from region 1 to region 2. Therefore, although the infection rate and reinfection rate in region 2 are lower than those in region 1, the epidemic in region 2 is still more serious than that in region 1. The number of infected people peaked in both regions between day 30 and day 40, and then gradually declined.

4. Conclusion

The purpose of this study is to establish SIR Models with population movement and study the influence of population movement rates on the development of the epidemic. We calculated the basic reproduction number of the model and figured out the relationship between the basic reproduction number and the movement rate of the infected people. Then, we simulated the development of the epidemic between two regions under the parameter assumption. This study will help us understand what factors influence the spread of the epidemic between different regions and formulate measures to control the epidemic based on regional differences in infection rates, medical care, population movements and other factors.

A limitation of this study is that it only considers the population transmission between two regions. We can extend the similar model to multiple regions. Also, we can consider more factors affecting the spread of the epidemic, such as the population vaccinated, the population quarantined due to the virus, etc., to modify the SIR model and make it more consistent with the actual situation.

REFERENCES

[1] Kermack WO, McKendrick AG (1927). "A Contribution to the Mathematical Theory of Epidemics"(https://doi.org/10.1098% 2Frspa.1927.0118).

[2] Beckley R, Weatherspoon C, Alexander M, Chandler M, Johnson A, Bhatt GS (2013). "Modelingepidemics with differential equations" (http://www.tnstate.edu/mathematics/mathreu/filesreu/GroupProjectSIR.pdf) (PDF). Tennessee State University Internal Report. Retrieved July 19, 2020.
[3] Hye Md. Abdul, Biswas M. A. Haider Ali, Uddin Mohammed Forhad, Saifuddin Mohammad.Mathematical Modeling of Covid-19 and Dengue Co-Infection Dynamics in Bangladesh: Optimal Control and Data-Driven Analysis[J]. Computational Mathematics and Modeling,2023,33(2).
[4] Thomas Reetha, Jose Sayooj Aby, Raja R., Alzabut J., Cao Jinde, Balas Valentina E.. Modeling and analysis of SEIRS epidemic models using homotopy perturbation method: A special outlook to 2019-nCoV in India[J]. International Journal of Biomathematics,2022,15(08).
[5] Faizunnesa Khondaker, Md. Kamrujjaman, Md. Shahidul Islam. Optimal Control Analysis of COVID-19 Transmission Model with Physical Distance and Treatment[J]. Advance in Biological Research,2022,3(1).
[6] Kammegne Brice, Oshinubi Kayode, Babasola Oluwatosin, Peter Olumuyiwa James, Longe Olumide Babatope, Ogunrinde Roseline Bosede, Titiloye Emmanuel Olurotimi, Abah Roseline Toyin, Demongeot Jacques. Mathematical Modelling of the Spatial Distribution of a COVID-19 Outbreak with Vaccination Using Diffusion Equation[J]. Pathogens,2023,12(1).
[7] Lan Zou, Shigui Ruan, Weinian Zhang. On the sexual transmission dynamics of hepatitis B virus in China[J]. Journal of Theoretical Biology,2015,369.
[8] AlQadi Hadeel,BaniYaghoub Majid. Incorporating global dynamics to improve the accuracy of disease models: Example of a COVID-19 SIR model. [J]. PloS one,2022,17(4).
[9] Salimipour Ayoob,Mehraban Toktam,Ghafour Hevi Seerwan,Arshad Noreen Izza,Ebadi M.J.. SIR model for the spread of COVID-19: A case study[J]. Operations Research Perspectives,2023,10.
[10] Lu Yang,Williams Therese L.. Modeling analytics in COVID-19: prediction, prevention, control, and evaluation[J]. Journal of Management Analytics,2021,8(3).
[11] Pei Lijun,Zhang Mengyu. Long-Term Predictions of COVID-19 in Some Countries by the SIRD Model[J]. COMPLEXITY,2021,2021.
[12] Yu Yue,Zhou Yuxing,Meng Xiangzhong,Li Wenfei,Xu Yang,Hu Manfeng,Zhang Jingxiang. Evaluation and Prediction of COVID-19 Prevention and Control Strategy Based on the SEIR-AQ Infectious Disease Model[J]. WIRELESS COMMUNICATIONS & MOBILE COMPUTING,2021,2021.
[13] Qianqian Bai,Yajun Wu,Haiyang Mu. Curve Fitting of COVID-19 Epidemic Transmission Mechanism Based on SIR Model[J]. Journal of Research in Science and Engineering,2022,4(5).
[14] Maki Koichiro. An interpretation of COVID-19 in Tokyo using a combination of SIR models. [J]. Proceedings of the Japan Academy. Series B, Physical and biological sciences,2022,98(2).
[15] P. van den Driessche,James Watmough. Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission[J]. Mathematical Biosciences,2002,180(1).