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Research article

A SEIARQ model combine with Logistic to predict COVID-19 within small-world networks

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Abstract: Since the COVID-19 epidemic, mathematical and simulation models have been extensively utilized to forecast the virus's progress. In order to more accurately describe the actual circumstance surrounding the asymptomatic transmission of COVID-19 in urban areas, this research proposes a model called Susceptible-Exposure-Infected-Asymptomatic-Recovered-Quarantine in a small-world network. In addition, we coupled the epidemic model with the Logistic growth model to simplify the process of setting model parameters. The model was assessed through experiments and comparisons. Simulation results were analyzed to explore the main factors affecting the spread of the epidemic, and statistical analysis that was applied to assess the model's accuracy. The results are consistent well with epidemic data from Shanghai, China in 2022. The model can not only replicate the real virus transmission data, but also anticipate the development trend of the epidemic based on available data, so that health policy-makers can better understand the spread of the epidemic.

Keywords: SEAIRQ epidemic model; small-world networks; Logistic growth model; COVID-19; prediction

1. Introduction

The COVID-19 epidemic is still significantly affecting our lives today. Worldwide, there are still sporadic, and as viruses evolve, more novel coronavirus strains are emerging, and their infectiousness is growing. Even if the majority of people are currently vaccinated, the infection cannot be completely prevented. We need to be prepared to coexist with viruses for a long period.

In actuality, this is not the first time in human history that an epidemic has spread widely. Disastrous epidemics such as SARS and H1N1 had also seriously harmed humanity. To predict how infectious diseases spread in human society, many models have been proposed to model epidemic transmission patterns, such as Susceptible-Infective (SI) [1], Susceptible-Infective-Recovered (SIR) [2], Susceptible-Infective-Susceptible (SIS) [3], and Susceptible-Exposed-Infective-Recovered (SEIR) [4]. Researchers have also suggested other derivative models in addition to these fundamental simple models, which are distinguished by an incubation period. Robert A Brown proposed the SIARQ model, a simple model for controlling COVID-19 infection in urban campuses and studied the spread of campus epidemics with asymptomatic patients as the main source of infection [5]. Liu et al presented an adaptive SEIARD model with internal source and isolation intervention to simulate the effects of changing behavior of the SARS-COV-2 in the US [6]. These studies were mainly based on modeling the different states of patients in the course of the disease, the majority of them used an epidemiological model and did not consider the social network in real life.

In 1998, Watts and Strogatz proposed a small-world network (SW) [7], a network between random and regular networks. This kind of network randomizes the node connections with probability p, and the resulting system can not only have a high degree of aggregation like a regular network, but also have a small characteristic path length like a random network. SW has been shown to exist in many interactive networks, including social networks [8]. And, there have been many cases of modeling infectious diseases using a small-world network. For example, Liu and Xiao used differential equations and Routh-Hurwiz theory to prove two different models based on SW networks, SEIRS and SEIQRS [9]. A SEIR-SW model based on graph theory was proposed by Younsi et al. [10]. Saramäki and Kaski proposed a dynamic small-world network-based SIR model to analyze the spread of random infectious diseases [11]. Compared with traditional compartment models, these models take into account the influence of social networks, making the spread of infectious diseases more in line with the actual situation. But, the models have too many parameters, which makes parameter adjustment extremely complicated. And, many key parameters mainly refer to previous research results or manual adjustments.

In this study, we simulate and evaluate the large-scale Omicron virus outbreak in Shanghai using an infectious disease model (SEIARQ) based on small-world networks. Additionally, we combined the Logistic growth model with the SEIARQ model to simulate and optimize it. This increased the model's accuracy while minimizing the need for labor-intensive parameter adjustments, making the model simpler to use.

The remainder of the paper is organized as follows. Section 2 presents the SEIARQ model considering the small-world network effect. Section 3 introduces the Logistic growth model and explains how to combine SEIARQ with the Logistic growth model. Section 4 shows the simulations and discussions. Finally, Section 5 presents the conclusions.

2. SEIARQ model in a small-world network

2.1. Basic introduction

At present, the Omicron virus shows high infectivity and low toxicity. Most of the infected people have no symptoms, but they are still contagious [12]. It can also be seen from Figure 1 that number of asymptomatic patients is significantly larger than confirmed patients. At the same time, with the

intervention of the government, patients detected by nucleic acid testing will be sent to treatment or isolation, and close contacts will also be required to self-isolate, cutting off the transmission route of the virus to a certain extent. In addition, owing to the higher-frequency nucleic acid testing and immediate isolation measure in China, the number of people being quarantined also need to be considered. Therefore, we divide the population in the small-world network into six parts, assuming that the impact of the number of deaths on the network is negligible, and that the infected persons become immune and will not be reinfected after recovering. In order to model social contacts among human populations, we can construct a small-world network by representing individuals as nodes and social relationships as edges [10]. In this paper, we used the average degree distribution k to represent the connection of the network, which means that each node in the network has an average of k neighbors. If the node is infected, it will infect k neighbors with a certain probability. The schematic of the model is shown in Figure 2.

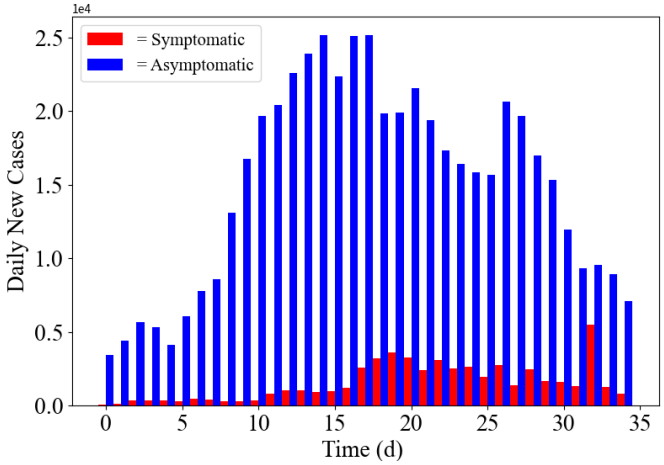

Figure 1. Daily new cases in Shanghai, China from March 27 to April 30.

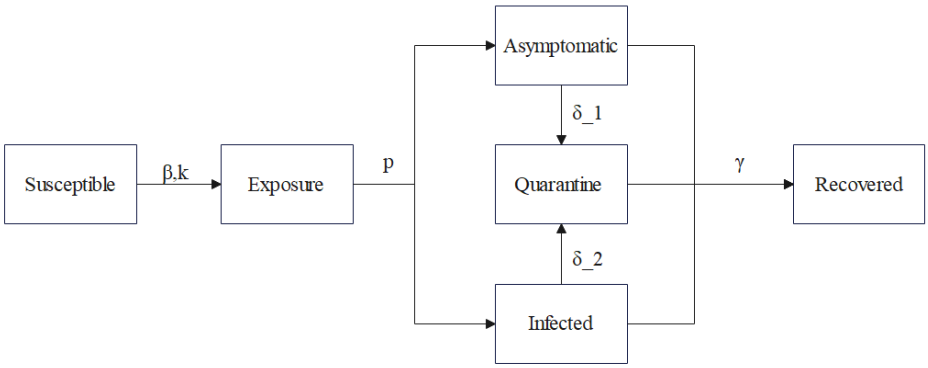

Figure 2. Schematic of the SEIARQ model.

According to the mean-field theory, the mean field equations of the epidemic spread in the small-

world network are:

$$\frac{dS(t)}{dt} = -\frac{\beta_1 <k_1> S(t)I(t)}{N} - \frac{\beta_2 <k_2> S(t)A(t)}{N} \tag{1}$$

$$\frac{dE(t)}{dt} = \frac{\beta_1 <k_1> S(t)I(t)}{N} + \frac{\beta_2 <k_2> S(t)A(t)}{N} - (p_1 + p_2)E(t) \tag{2}$$

$$\frac{dI(t)}{dt} = p_1 E(t) - \delta_1 I(t) - (1 - \delta_1)\gamma_1 I(t) \tag{3}$$

$$\frac{dA(t)}{dt} = p_2 E(t) - \delta_2 A(t) - (1 - \delta_2)\gamma_2 A(t) \tag{4}$$

$$\frac{dQ(t)}{dt} = \delta_1 I(t) + \delta_2 A(t) - \gamma Q(t) \tag{5}$$

$$\frac{dR(t)}{dt} = (1 - \delta_1)\gamma_1 I(t) + (1 - \delta_2)\gamma_2 A(t) + \gamma Q(t) \tag{6}$$

The meaning of each parameter of the model is as Table 1:

Table 1. The meaning of Parameters.

Parameters	Meaning
N	size of small world network
$S(t)$	number of susceptible people
$E(t)$	number of exposed people
$I(t)$	number of infected people
$A(t)$	number of asymptomatic people
$R(t)$	number of recovered people
$Q(t)$	number of quarantine people
β_1	propagation coefficient of the infected people
β_2	propagation coefficient of the asymptomatic people
k_1,k_2	average degree distribution of small world network
p_1	proportion of exposed people converted to infected people
p_2	proportion of exposed people converted to asymptomatic people
δ_1	isolation rate of infected people
δ_2	isolation rate of asymptomatic people
$\gamma_1, \gamma_2, \gamma$	recovered rate

2.2. Analysis of the SEIARQ model

In the infectious disease dynamics model, the basic reproduction number R_0 is a very important parameter, which represents the number of people infected by a patient in an average disease cycle in a disease-free equilibrium (DFE) state. R_0 is a marker that determines whether a virus is prevalent. The calculation of R_0 has guiding significance for disease prevention and control strategies. R_0 is also a threshold number of the model, if $R_0 < 1$, the DFE is local asymptotically stable, and the disease cannot

invade the population, but if R_0 >1, then the DFE is unstable and invasion is always possible [13].

According to the next-generation matrix method, R_0 is obtained by calculating the spectral radius of the reproduction matrix [14,15].

First, the variables are divided into two categories: infection class-$\{E(t),I(t),A(t),Q(t)\}$, non-infection class $\{S(t), R(t)\}$. Then, let F_i be the rate of newly infected individuals in group i, $V_i=V_i^- - V_i^+$ be the transfer rate, V_i^- be the rate of individuals removed from group i, and V_i^+ be moved into group i by any means other than infection ratio of individuals. It can be obtained from formula Eqs (1)–(6) that

$$F_{EIAQ} = \begin{bmatrix} \frac{\beta_1 <k_1> S(t) I(t)}{N} + \frac{\beta_2 <k_2> S(t) A(t)}{N} \\ 0 \\ 0 \\ 0 \end{bmatrix} \tag{7}$$

$$V_{EIAQ} = \begin{bmatrix} (p_1 + p_2)E(t) \\ \delta_1 I(t) + (1-\delta_1)\gamma I(t) - p_1 E(t) \\ \delta_2 A(t) + (1-\delta_2)\gamma A(t) - p_2 E(t) \\ \gamma Q(t) - \delta_1 I(t) - \delta_2 A(t) \end{bmatrix} \tag{8}$$

Let $F=\left[\frac{\partial F_i}{\partial x_i}(x_0)\right], V=\left[\frac{\partial V_i}{\partial x_i}(x_0)\right]$, x_0 is the disease-free equilibrium point. Thus, we get

$$F=(E,I,A,Q) = Jacobian\left(F_{EIAQ}\right) = \begin{bmatrix} 0 & 0 & 0 & 0 \\ \frac{\beta_1 <k_1> S(t)}{N} & 0 & 0 & 0 \\ \frac{\beta_2 <k_2> S(t)}{N} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}^T \tag{9}$$

$$V(E,I,A,Q) = Jacobian\left(V_{EIAQ}\right) = \begin{bmatrix} p_1 + p_2 & 0 & 0 & 0 \\ -p_1 & \delta_1 + (1-\delta_1)\gamma & 0 & 0 \\ -p_2 & 0 & \delta_2 + (1-\delta_2)\gamma & 0 \\ 0 & -\delta_1 & -\delta_2 & \gamma \end{bmatrix} \tag{10}$$

$$FV^{-1} = \begin{bmatrix} \frac{p_1\beta_1 <k_1> S(t)}{N(p_1+p_2)(\delta_1+(1-\delta_1)\gamma)} + \frac{p_2\beta_2 <k_2> S(t)}{N(p_1+p_2)(\delta_2+(1-\delta_2)\gamma)} & 0 & 0 & 0 \\ \frac{\beta_1 <k_1> S(t)}{N(\delta_1+(1-\delta_1)\gamma)} & 0 & 0 & 0 \\ \frac{\beta_2 <k_2> S(t)}{N(\delta_2+(1-\delta_2)\gamma)} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}^T \tag{11}$$

Let the right-hand side of the differential equation system be 0, and $I = 0$, $A = 0$, it is easy to get the disease-free equilibrium point $E_0 = (N(0),0,0,0,0,0)$, and find it at the disease-free equilibrium point

$$R_0 = \rho(FV^{-1}) = \frac{p_1\beta_1 <k_1>}{(p_1+p_2)(\delta_1+(1-\delta_1)\gamma)} + \frac{p_2\beta_2 <k_2>}{(p_1+p_2)(\delta_2+(1-\delta_2)\gamma)} \tag{12}$$

From Eq (12), it can be found that the spread threshold of the epidemic depends on some key parameters. R_0 is positively correlated with the average degree distribution of the small-world network

and the infection rate, and negatively correlated with the isolation rate, which is the same as our perception.

3. Combine with Logistic growth model

3.1. Logistic growth model

The logistic equation is a well-known population growth model proposed by mathematical biologist Pierre Francois Verhulst, which is widely used in population growth and forecasting [16]. The model is represented by the following differential equation:

$$\frac{dN}{dt} = rN(1 - \frac{N}{K}) \tag{13}$$

The solution to the equation is

$$N(t) = \frac{K}{1+(\frac{K}{N_0}-1)e^{-rt}} \tag{14}$$

Among them, K is the environmental capacity, representing the maximum cumulative number of infected people in the infectious disease model; N_0 is the initial value of the population, representing the initial number of infected people in the infectious disease model; r is the infection rate in the infectious disease model; t is time, $N(t)$ is the population number that changes over time, representing the cumulative number of infected people changing over time in the infectious disease model.

3.2. The application of Logistic growth model

In the case of known parameters K, N_0, r, the logistic growth model can be used to predict infectious diseases, for example, Morsi and Alzahrani [17] used logistic growth model for the complex spread of COVID-19 and forecasted future values in Australia and Brazil within a time interval of six days, but since the model is monotonically increasing, it can only predict the cumulative number of infected people, but not the existing confirmed number of people. The SEIARQ model can predict the number of confirmed daily diagnoses, and can also obtain the turning point of infectious diseases, but due to plenty of model parameters, the task of adjustment will be particularly difficult. Although the forms of the two models are quite different, when describing the same type of infectious disease, because the characteristics of the infectious disease and the environment are the same, the parameters of the two models can be interchanged, which is also verified in subsequent simulation tests. Therefore, consider combining the Logistic with SEIARQ.

The specific idea is as follows:

1) Using actual data of infected and asymptomatic to fit Logistic equation, and getting parameters of Logistic equation.

2) Assume N_0 in the Logistic growth model to be the initial number of infections (A_0 or I_0) in the SEIARQ model and r as the infection rate β in the SEIARQ model. Multiply the environmental capacity K by ε (ε>1) to estimate the size of the small world network and the initial number of susceptible populations in the SEIARQ model S_0. p is determined by the environmental capacity obtained from the infected and asymptomatic fits. Assume that there is no person exposed, recovered or isolated at the beginning of transmission, so E_0, R_0 and Q_0 are 0.

3) Initialize the remaining parameters of the model and use the model to make predictions and

compare to the true value.

4. Simulation and results

4.1. Numerical simulation and error estimation

We conducted experiments to examine the proposed SEIARQ model. The statistics used in this paper is the daily epidemic data from Shanghai, China since February 2022 [18]. To fit the Logistic growth model, it is necessary to divide the entire dataset into training set and test set. In this paper, the training set represents the known epidemic data used for logistic model parameter fitting, and the test set represents the known epidemic data used to compare with the SEIARQ model. Here we limited the training set from February 27th, 2022 to April 21st, 2022 and used the following 7 days to predict. In the experiments, we employed the grid search approach and the nonlinear least squares method to fit the Logistic growth model's parameters. The parameter values obtained by fitting the logistic growth model and the estimated values of the remaining parameters are shown in the following Table 2:

Table 2. Parameters value for SEIARQ model.

Parameters	Value	Source
$S_0, I_0, A_0, E_0, R_0, Q_0$	716800,0,33,0,0,0	Fit
β_1, β_2	0.23,0.22	Fit
k_1, k_2	10,10	Estimate
p_1, p_2	0.0145,0.1283	Fit
δ_1, δ_2	0.7,0.62	Estimate
$\gamma_1, \gamma_2, \gamma$	0.1,0.1,0.1	Ref [19]

All experiments are run on Microsoft Windows 10, the computer hardware environment is Intel(R) Core (TM) i5-9300H CPU 2.40 GHz with 12GB RAM, the Interpreter is Python 3.10.

The numerical simulation results of the model are shown in Figure 3. The 7-day forecast results are compared with the actual results as shown in Table 3. Please note that the data compared in Table 3 are the total number of cases, including confirmed and asymptomatic.

Table 3. Comparison of 7-day prediction results with actual results.

Date	Real value	Predict value	Relative error
4-22	23370	19475	16.67%
4-23	21058	17908	14.96%
4-24	19455	16390	15.75%
4-25	16980	14939	12.02%
4-26	13562	13569	0.05%
4-27	10622	12289	15.69%
4-28	15032	11100	26.16%

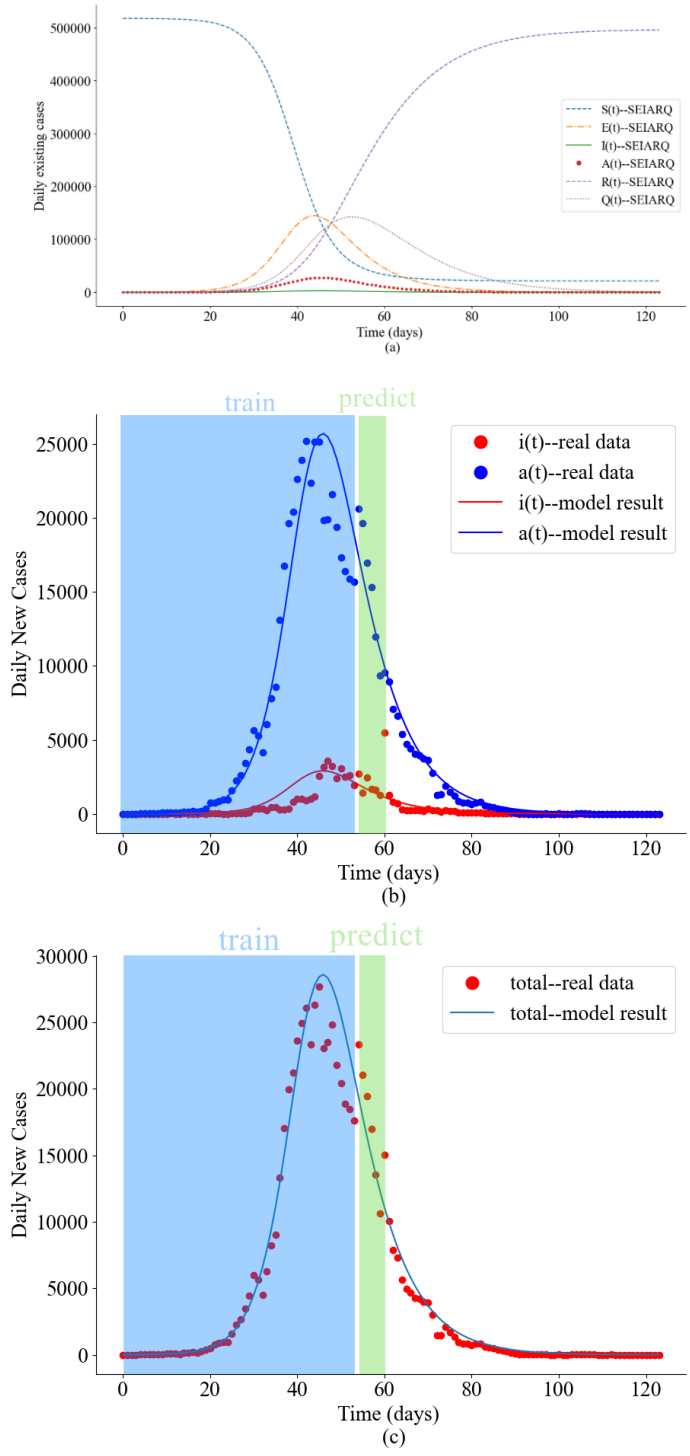

Figure 3. Numerical simulation results of the model. (a) The meaning of each segment of the curves is shown in Table 1. (b) i(t) shows the number of the new diagnoses every day, and a(t) indicates the number of new asymptomatic people every day. (c) total shows the sum of number of new diagnoses and the number of asymptomatic people every day.

It can be seen that due to changes in local epidemic prevention policies and other external factors, the model parameters are not fully applicable to all stages of the epidemic development, resulting in a

gap between the predicted value and the actual value, but the predicted curve of the model and the actual epidemic situation curves are still highly similar.

Here we use mean absolute percentage error (MAPE) and root mean squared percentage error (RMSPE) to evaluate the performance of the model, and compare it with the result of the Shanghai epidemic prediction model in Ref [19]. When error $\geq$ 50%, the model is poor, 20% $\leq$ error $<$ 50% is reasonable, 10% $\leq$ error $<$ 20% is good, and error $<$ 10% is accurate. MAPE and RMSPE is define as follows:

$$MAPE = \frac{1}{n}\sum_{i=1}^{n} \left| \frac{y_i - \widehat{y_i}}{y_i} \right| \times 100\% \tag{15}$$

$$RMSPE = \sqrt{\frac{\sum_{i=1}^{n} (\frac{y_i - \widehat{y_i}}{y_i})^2}{n}} \times 100\% \tag{16}$$

where $\widehat{y_i}$ represents the predicted value of the model on the i-th day, y_i represents the true value on the i-th day, and $\overline{y_i}$ represents the average value on the ith day. The results are shown in Table 4 as follow:

Table 4. Model performance metrics.

Variable	MAPE of our model	RMSPE of our model	MAPE of Ref [19]	RMSPE of Ref [19]	Performance
Newly confirmed cases	27.98%	36.50%	33.86%	37.01%	Reasonable
Newly asymptomatic infectious	14.47%	16.14%	12.34%	16.45%	good
Newly total cases	11.97%	13.37%	/	/	good

4.2. Role of isolation rate

We further investigate the impact of the parameters that need to be tuned on the prediction performance of the model. Among them, the average degree distribution and recovery rate can be found in the literature and are relatively easy to debug. The isolation rate needs to be adjusted manually. Therefore, the impact of the isolation rate on the prediction effect of the model is mainly analyzed. It can be seen from the Figure 4 that increasing the isolation and reducing the average degree distribution can significantly inhibit the spread of the epidemic. When the isolation rate is 0, the model degenerates into the SEIAR model, and the entire prediction curve is very different from the actual value, so the introduction of isolation is necessary for epidemic prediction.

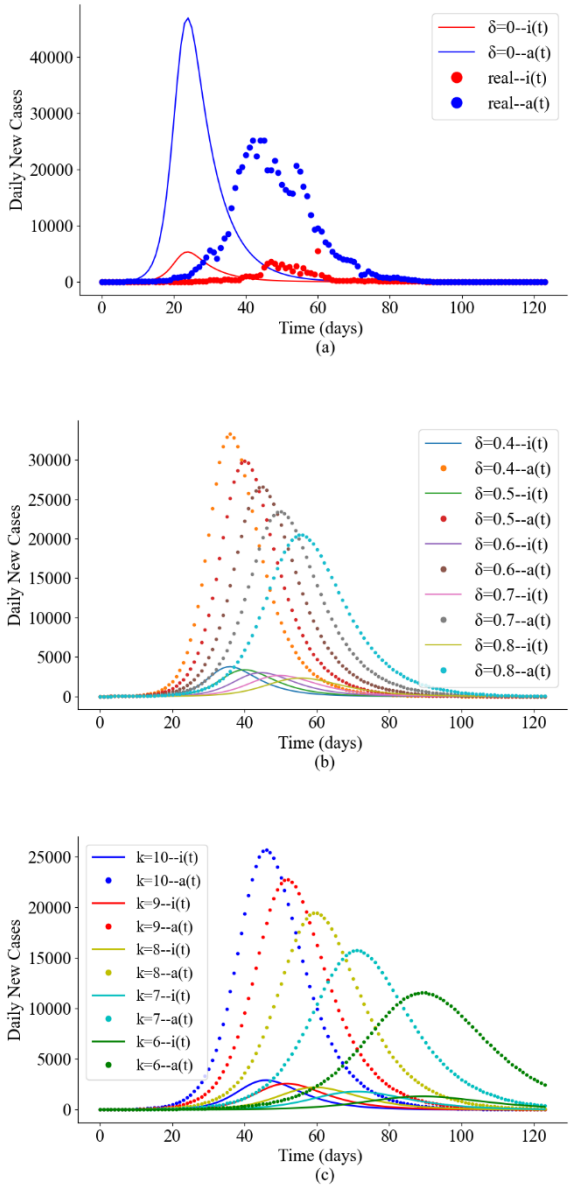

Figure 4. The isolation rate on the prediction effect of the model. (a) Comparison between the simulation results of the model and the actual data when isolation rate equal to zero. (b) number of newly diagnosed and asymptomatic people per day with different δ. (c) number of newly diagnosed and asymptomatic people per day with different k.

5. Conclusions

The COVID-19 is the largest worldwide epidemic that people have encountered in the last 100 years. The coronavirus causes daily infections or fatalities in humans. On September 1, there were more than 600 million confirmed cases worldwide, and there had been more than 6 million fatalities [20]. Modeling and analysis of the epidemic can help policymakers understand the development trend of the epidemic to formulate effective policies to control the epidemic.

This paper mainly proposes the SEIARQ model under the small world network for the new virus-

mystery clone, and combines the Logistic growth model in the numerical simulation process to improve the simulation efficiency and reduce the number of parameters to be adjusted to 3 categories (average degree distribution, isolation rate, recovered rate), which significantly reduces the complexity of parameter adjustment. Additionally, we performed a thorough examination of the model and calculated the fundamental reproduction number. The results of the calculations demonstrate that just a few important factors are relevant to the model's propagation threshold. The model's outcomes in the numerical simulation analysis are favorable. When the actual adjustment parameters are only 3, the error of the asymptomatic patients is close to 10%, the error of the confirm infectious is about 30%, and the error of the total number of patients is close to 10%, which is almost the same as the result of Ref [19]. In the contrast, Ref [19] has 10 estimated parameters. Experimental results also show that control the average degree distribution in the small world can be effectively to curb the development of the epidemic in SEIAQR model, which means weaker contact between people will slow down the spread of the epidemic.

Also, the model has several restrictions. We did not take mortality and secondary illnesses into account. Additionally, the isolation rate may alter as a result of modifications to local laws and nucleic acid testing, causing inconsistencies between the model and the real curve at specific phases. Long-term forecasts are not guaranteed to be accurate throughout our simulation, which is a drawback that most models cannot avoid.

Conflict of interest

The authors declare there is no conflict of interest.

References

1. M. EI-Doma, Analysis of an age-dependent SI epidemic model with disease-induced mortality and proportionate mixing assumption: The case of vertically transmitted diseases, *J. Appl. Math.*, **2004** (2004), 235–254. https://doi.org/10.1155/S1110757X0430118X
2. W. O. Kermack, A. G. McKendrick, A contribution to the mathematical theory of epidemics, *Proc R. Soc. Lond. B Biol. Sci.*, **115** (1927), 700–721. https://doi.org/10.1098/rspa.1927.0118
3. I. Mimmo, M. Y. Kim, E. J. Park, Asymptotic behavior for an SIS epidemic model and its approximation, *Nonlinear Anal. Theory Methods Appl.*, **35** (1999), 797–814. https://doi.org/10.1016/S0362-546X(97)00597-X
4. I. B. Schwartz, H. L. Smith, Infinite subharmonic bifurcation in an SEIR epidemic model, *J. Math. Biol.*, **18** (1983), 233–253. https://doi.org/10.1007/BF00276090
5. R. A. Brown, A simple model for control of COVID-19 infections on an urban campus, *Proc. Natl. Acad. Sci. U S A*, **118** (2021), e2105292118. https://doi.org/10.1073/pnas.2105292118
6. X. X. Liu, S. J. Fong, N. Dey, R. G. Crespo, E. H. Viedma, A new SEAIRD pandemic prediction model with clinical and epidemiological data analysis on COVID-19 outbreak, *Appl. Intell.*, **51** (2021), 4162–4198. https://doi.org/10.1007/s10489-020-01938-3
7. D. J. Watts, S. H. Strogatz, Collective dynamics of small-world9 networks, *Nature*, **393** (1998), 440–442. https://doi.org/10.1038/30918
8. L. A. Amaral, A. Scala, M. Barthelemy, H. E. Stanley, Classes of small-world networks, *Proc. Natl. Acad. Sci. U S A*, **97** (2000), 11149–11152. https://doi.org/10.1073/pnas.200327197

9. M. Liu, Y. Xiao, Modeling and analysis of epidemic diffusion within small-world network, *J. Appl. Math.*, **2012** (2012), 841531. https://doi.org/10.1155/2012/841531
10. F. Z. Younsi, A. Bounnekar, D. Hamdadou, O. Boussaid, SEIR-SW, simulation model of influenza spread based on the Small World network, *Tsinghua Sci. Technol.*, **20** (2015), 460–473. https://doi.org/10.1109/TST.2015.7297745
11. J. Saramäki, K. Kaski, Modelling development of epidemics with dynamic small-world networks, *J. Theor. Biol.*, **234** (2005), 413–421. https://doi.org/10.1016/j.jtbi.2004.12.003
12. S. Ren, W. Wang, R. Gao, A. Zhou, Omicron variant (B.1.1.529) of SARS-COV-2: Mutation, infectivity, transmission, and vaccine resistance, *World J. Clin. Cases*, **10** (2022), 1–11. https://doi.org/10.12998/wjcc.v10.i1.1
13. H. W. Hethcote, The mathematics of infectious diseases, *SIAM Rev.*, **42** (2000), 599–653, https://doi.org/10.1137/S0036144500371907.
14. P. Driessche, J. Watmough, Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission, *Math. Biosci.*, **180** (2002), 29–48. https://doi.org/10.1016/S0025-5564(02)00108-6
15. O. Diekmann, J. A. P. Heesterbeek, J. A. J. Metz, On the definition and the computation of the basic reproduction ratio R_0 in models for infectious diseases in heterogeneous populations, *J. Math. Biol.*, **28** (1990), 365–382. https://doi.org/10.1007/BF00178324
16. E. Y. Boateng, D. A. Abaye, A review of the Logistic Regression model with emphasis on medical research, *J. Data Anal. Inform. Proc.*, **7** (2019), 190–207. https://doi.org/10.4236/jdaip.2019.74012
17. S. A. Morsi, M. E. Alzahrani, Advanced computing approach for modeling and prediction COVID-19 pandemic, *Appl. Bionics and Biomech.*, **2022** (2022), 6056574. https://doi.org/10.1155/2022/6056574
18. *Shanghai Municipal Health Commission, Shanghai Municipal Bureau Statistics*: From epidemic notification. Available from: https://wsjkw.sh.gov.cn.
19. Y. Ma, S. Xu, Q. An, M. Qin, S. Li, K. Lu, et al., Coronavirus disease 2019 epidemic prediction in Shanghai under the dynamic zero-COVID policy using time-dependent SEAIQR model, *J. Biosaf. Biosecur.*, **4** (2022), 105–113. https://doi.org/10.1016/j.jobb.2022.06.002
20. *World Health Organization*: WHO Coronavirus (COVID-19) Dashboard with Vaccination Data, 2022. Available from: https://covid19.who.int.

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