Effectiveness Analysis of Large-Scale Infectious Virus Detection Strategy Based on SEIQR Model

Xin Wang[1a], Shitong Wang[2b*]

{20241214@bjtu.edu.cn[a], 20241213@bjtu.edu.cn[b]}

Beijing Jiaotong University[1,2]

Abstract: The severe impact of the novel coronavirus outbreak in 2019 on human society warns us that large-scale infectious diseases are always the natural enemies of human health. In the process of epidemic prevention and control, virus detection plays an important role, but there are still some problems in the detection strategy, such as the formulation of nucleic acid detection frequency is mainly based on subjective judgment, and there is a lack of quantitative nucleic acid testing frequency research. Therefore, this paper introduces the parameter of detection frequency for the first time, proposes the SEIQR model, takes the epidemic data in Beijing in the normalized epidemic prevention and control stage as an example to analyze, and finds that the SEIQR model can fit the actual data well, which confirms the effectiveness of the 72-hour nucleic acid detection strategy in the normalized epidemic prevention and control stage in Beijing, and provides a new method for the analysis of virus detection effectiveness.

Keywords: large infectious virus; virus detection; SEIQR model

1 Introduction

Since 2019, the coronavirus outbreak around the world has caused millions of deaths. With the improvement of the global epidemic prevention and control situation, some countries and regions have gradually resumed normal production and living order, and orderly promoted the normalization of epidemic prevention and control work. Nucleic acid testing can quickly detect infected people and carry out epidemic control, which is a necessary part of the normalized epidemic prevention and control stage, however, if the testing is too frequent, the cost of testing will increase accordingly, which may lead to false positive or false negative results, increasing the risk of misdiagnosis. However, if the frequency of testing is low, it may lead to missed diagnosis, which will lead to further spread of the epidemic, and it will cost more to prevent the epidemic. Therefore, the scientific and reasonable frequency of nucleic acid testing can not only reduce the cost of testing, but also help improve the effectiveness and credibility of testing and better control the epidemic.

Since the outbreak of the epidemic, many scholars at home and abroad have done relevant research on the new crown virus from different angles. Li et al.[1] proposed the SISR model considering that COVID-19 is already highly infectious during the incubation period. Ding Zhongxing et al.[2] added asymptomatic infected people and those found and quarantined to construct a SEIAQR kinetic model. Shengli Cao et al.[3] established a dynamic model of COVID-19 SEIR infectious diseases that jointly considers incubation period transmission

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capacity and tracking isolation interventions. Lu Xuepeng et al.[4] set the isolation rate and other parameters, and proposed the SE4IR2 model. Yan Yue et al.[5] introduced a time-lag process in the model to describe the virus latency and treatment cycle. Huang Senzhong et al.[6] based on transmission dynamics, universal SEIR model and procedure EpiSIX, studied and judged the epidemic trend, clarified the basic epidemiological parameters of the epidemic, and evaluated the efficiency of disease control strategies.

In the process of epidemic prevention and control, nucleic acid testing can effectively slow down the spread of the epidemic, so how to formulate a scientific and reasonable nucleic acid testing plan has become an important topic. Zeng Ting et al.[7] proposed a random COVID-19 model with large-scale nucleic acid detection and isolation measures. He Xiaozhou et al.[8] optimized large-scale nucleic acid detection through dynamic detection site deployment strategy, proposed a multi-period location allocation model, and proved that the optimal total cost of the strategy is lower than the actual implementation scheme. Zhu Wenlong et al.[9] used the branch process model to evaluate different management strategies.

Based on the above literature, this paper innovates the model based on the classic SEIR, and constructs the SEIQR model based on the characteristics of normalized epidemic prevention and control and virus transmission to explore the effectiveness of virus detection strategies. Taking the normalization of the new crown pneumonia epidemic in Beijing as an example, the frequency of nucleic acid testing was studied in depth, including establishing a scientific testing frequency evaluation system, analyzing the impact of testing frequency on epidemic transmission, and optimizing the effect of testing frequency on epidemic control, etc., to provide a more scientific reference for epidemic prevention and control and nucleic acid testing.

2 SEIQR model construction

2.1 Model assumptions

Based on the classical SEIR virus transmission kinetic model, this paper redefines the population segmentation. Considering the transmission of the virus in the population under the normalization scenario of the virus with incubation period, the five types of population divided into the model are susceptible (S), lurker (E), infected (I), isolated (Q), and recovered (R). In order to reduce the complexity of the model and make the internal logic of the model clearer, the following assumptions are made about the model without changing the essence of the problem:

(1) The virus fatality rate is extremely low, and patients who are treated for the disease recover long enough without being reinfected;

(2) The amount of virus contained in the incubation period of patients is not enough to detect and is not enough to infect susceptible people;

(3) The new coronavirus does not mutate within a certain period of time;

(4) The test is correct, and the infected person can detect positive at the first virus test;

(5) The model treats all populations as a closed system, and the number of people within the system is negligible due to migration in and out of the system during the prediction period, and

the total number of people in the study is always unchanged and is a constant N(t), that is $N(t) = S(t) + E(t) + I(t) + Q(t) + R(t)$, it always holds.

2.2 Model building

Based on the transmission mechanism of infectious diseases, different transformation

Based on the transmission mechanism of infectious diseases, there are different conversion probabilities between the above types of people. This document provides as follows:

(1) For susceptible people, the disease may become latent due to close contact with an infected person, and C is the probability of a susceptible person in a unit time due to contact with a sick patient. p is the probability of disease transmission at each exposure, and the rate of transformation from susceptible to latent population is: $\mu = pc$;

(2) For the latent population, the new coronavirus will only manifest itself after a period of incubation in the body, and the rate at which the latent becomes infected per unit time is expressed as: $g = 1/\theta$;

(3) For infected people, the period ($\Delta t \le \omega$)from the manifestation of symptoms to the diagnosis of the disease. The time of diagnosis of patients is regarded as showing an even distribution on $[0, \omega]$, the average time of illness of patients is $\omega / 2$, and the rate of conversion of infected people into quarantined people is: $\lambda = 2/\omega$;

(4) For the quarantined population, considering that the cure rate over time is non-fixed, the cure coefficient σ is regarded as a time-varying parameter.

The various parameters are further explained in this article, as shown in Table 1.

Table 1 Description of SEIQR model parameters

Parameter	Parameter explanation	Parameter determination method
ω	Average detection period	Estimated interval
θ	Average incubation period	Estimated interval
c	Proportion of close contacts infected with the virus	Estimated interval
p	Probability of disease transmission per occurrence of contact	Estimated interval
μ	Infection rate	Estimated interval
g	Probability of apparent symptoms in incubators	Estimated interval
λ	Daily diagnosis rate of infected persons	Estimated interval
σ	Recovery rate of isolated patients per unit of time	Time-varying parameters

3 Example analysis

In this study, we conducted experiments based on the data of the New Crown epidemic in Beijing from April 16 to June 15, 2022, published on the official website of the Beijing Municipal Health and Wellness Commission in China , and used MATLAB to write a program to construct the above model to simulate the New Crown virus transmission changes in various populations. In this paper, the coefficient of determination (R2), root mean square error (RMSE) and mean relative error (MAPE) of evaluation indicators were selected to verify the accuracy of the model. At the same time, the number of quarantine cases and the number of cured cases after June 15 are predicted to verify the effectiveness of the current outbreak prevention and control policies.

3.1 Time-varying parameter fitting results

The cure rate is measured by a time-varying parameter, calculated as the ratio of the number of new cures among the isolates on that day to the number of isolates on the previous day. In this paper, a polynomia function was used to fit this time-varying parameter, as shown in Figure 1. It is shown by the calculation of the coefficient of determination, as shown in Table 2, the fitted function was able to describe the trend in the cure rate relatively well.

The small deviation between the actual data points and the model predictions can be seen through the residuals Figure 2, which further confirms the better fitting of the model. Based on the fitted functional expressions and the coefficients of determination, it can be seen that there is a relatively clear trend of increase in the cure rate at different time periods, with a slowdown in the subsequent time periods. This may be due to the improvement in the medical field regarding the treatment of covid-19 over time, the emergence of new drugs and treatment regimens, and the introduction of a three-day routine nucleic acid testing policy, which improved the cure rate and reduced the severity of viral pathogenicity. Because of the improved cure rates, more quarantines were cured and released back into society. Thus, these results indicate that the new crown outbreak is being effectively controlled and treated to safeguard public health and lives.

Table 2 Time-varying parameter fitting results

Parameter	Fit function	Coefficient of determination
Cure rate	$\mathrm{y}_t = -0.002394t^2 + 0.01593t + 0.08432$	91.27%

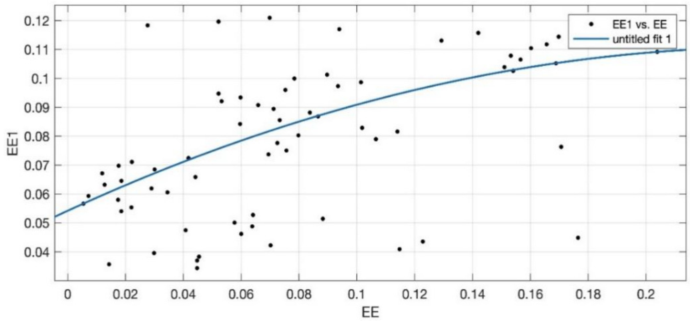

Figure 1 Fitting results of cure rate

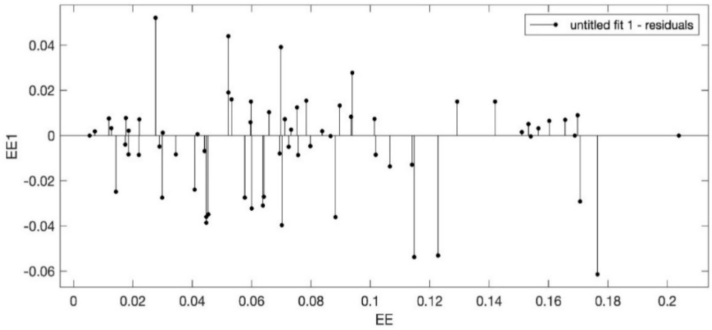

Figure 2 Residuals of time-varying parameters

3.2 Fitting results for the number of lurkers

The actual number of lurkers cannot be obtained directly from the data shown on the official website. In this paper, the number of lurkers in each period is derived using the lsqcurvefit function for the known number of groups in the model. The fitting results show that the modified SEIQR model has higher accuracy compared to the traditional SEIR model, with a 6.71% reduction in root mean square error (RMSE) and 8.98% reduction in mean relative error (MAPE). As shown in Table 3. Therefore, the improved SEIQR model is more applicable to the current virus transmission model under the regular epidemic prevention and control policy.

In this paper, we analyze the trend of lurkers by observing Figure 3, where the number of lurkers shows peaks and valleys with large fluctuations. This directly reflects the transmission effectiveness of the virus. Viral transmission intensity does not show a fixed trend over time. This suggests that strategy makers must always keep an eye on virus transmission potency and consider its critical role in developing sound and effective prevention and control policies.

Table 3 Fitting effect of lurkers

Model	RMSE	MAPE
SEIQR	34.5152	61.76%
SEIR	37.0007	70.74%

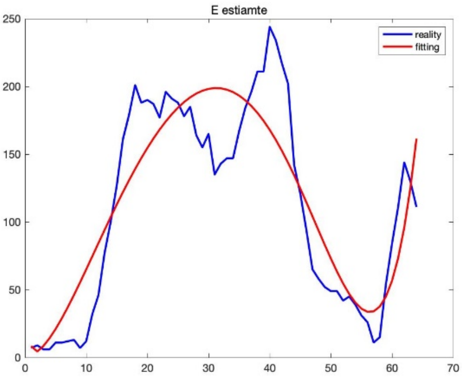

Figure 3 Fitting results of the number of lurkers

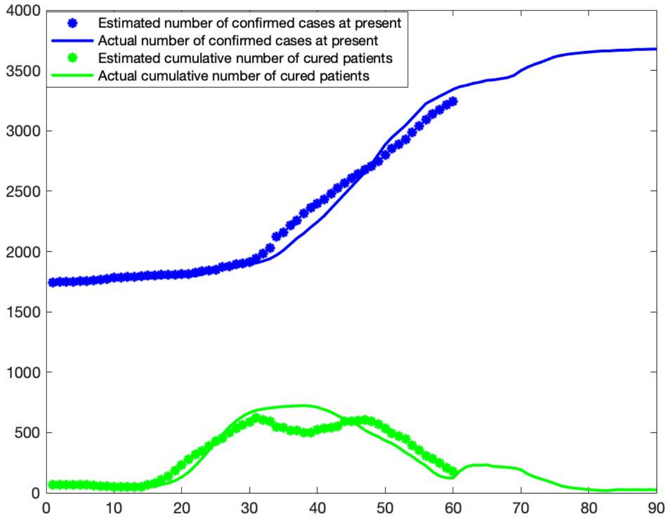

Figure 4 Fitting results for the number of isolates and cures

3.3 Fitting and prediction results of the number of isolates and cures

The simulated changes in the number of quarantines and cures are a direct measure of the effectiveness of the epidemic prevention policy, and these data are available from the official website. The fitting results show that the SEIQR model proposed in this paper has 8.40% and 12.14% lower error and 3.25% and 9.35% lower MAPE in the fitting results of quarantines and healers, which is a better fit and shows a significant error reduction effect.as shown in Table 4.

Regarding the trend of the number of isolated and cured patients, it is shown in Figure 4. The number of cured patients showed an overall increasing trend, indicating that more patients recovered over time. During the two-month time period, the increasing trend of the number of cured persons changed from flat to steep, indicating that the effect of epidemic prevention was not obvious at the beginning of the policy implementation and became significant after some time. The trend of the number of quarantines changed in a wave pattern, which indicates that in the middle of the epidemic prevention, the area of virus infection was larger, corresponding to the number of incubators in the previous section also reached a wave around May 15, when the epidemic was more serious in Beijing. A larger number of isolated patients will emerge under the control of a regular 3-day testing policy.

In order to better verify the effectiveness of the implementation of the nucleic acid testing strategy, this paper predicts the data of cured and isolated patients one month after June 15, and finds that the number of isolated patients gradually decreases to a lower level (initially), which indicates that the epidemic will gradually stabilize in the coming month and the nucleic acid testing strategy plays a great role. At the same time, the cured showed a continuous trend of growth, which slowed down due to the decreasing number of quarantines and also affected the number of cured, which is in line with the reality.

Table 4 Fitting effect of the number of isolates and cured

Population type	Model	RMSE	MAPE
Isolated people	*SEIQR*	80.3956	7.49%
	SEIR	87.1453	10.74%
Healers	*SEIQR*	94.9268	23.68%
	SEIR	106.4530	33.03%

4 Conclusions and Recommendations

4.1 Conclusion

In this paper, we propose a SEIQR virus transmission model considering isolates by combining the special transmission characteristics of viruses with latent period and using time-varying parameters, and innovatively consider the virus detection frequency in the virus model. In this paper, we fit and predict the existing lurkers, existing isolates, and cumulative cures, and the results show that 1) the SEIQR model has higher fitting accuracy. The fitting error is reduced by 8%-10%. 2) The SEIQR model can simulate the specific changes of time-varying parameters. It can uncover hidden data that are difficult to be fully accounted for in actual epidemic data statistics, and at the same time can predict future virus transmission and verify the effectiveness and feasibility of current virus detection strategies. 3) The model in this paper can simulate different virus detection measures through quantitative control parameters, and the fitting results can more intuitively assess the impact of different measures on the development of the epidemic, which is conducive to the formulation of reasonable epidemic prevention policies. In conclusion, for viruses with latent transmission characteristics, the SEIQR model has greater guidance and reference value for validating the effectiveness of virus detection strategies.

4.2 Recommendations

This paper makes the following recommendations: strengthen the control of key populations. Develop appropriate virus detection strategies for different epidemic risk levels. Combine surveillance results for precise prevention and control. Introduce rapid detection technologies. Emphasize prevention and control in parallel. In addition, provide public education to the population and strengthen preventive measures such as disinfection of public places in order to strengthen the effectiveness of the implementation of prevention and control policies.

In conclusion, the arrangement of virus detection strategies should be combined with the epidemic situation and risk level to develop corresponding detection strategies and strike a balance between economic costs and epidemic prevention benefits to finally achieve complete control of the epidemic.

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