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A Retrospective Study of COVID-19 Based on A Dual-Stage Model

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ABSTRACT

This study proposed initial stage SE$I_1I_2I_3$RD and final stage SEQ $I_1I_2I_3$RD models to deeply analyze the transmission dynamics of COVID-19 at different stages and propose scientific prevention and control strategies. The initial stage SE $I_1I_2I_3$RD model divides infected individuals into mild, moderate, and severe cases during the early stage of the epidemic, effectively predicting the number of new infections and cumulative recoveries. The final stage SEQ $I_1I_2I_3$RD model builds on the initial stage SE $I_1I_2I_3$RD model by adding a quarantine compartment, which reflects the impact of nucleic acid testing and quarantine measures on epidemic control. By introducing dynamic parameters and nonlinear processing, the final stage SEQ $I_1I_2I_3$RD model significantly improves prediction accuracy. The study demonstrates that increasing the isolation rate, reducing the daily contact rate of infected persons, and improving the recovery rate of mildly infected persons are effective control strategies. Based on the model's predictions, policy recommendations such as enhancing public health education, strictly implementing isolation measures, restricting population movement, and optimizing medical resource allocation are proposed to effectively control the spread of the epidemic, reduce the burden on the healthcare system, and create favorable conditions for economic recovery.

KEYWORDS

SEIR model; Infectious disease dynamics; Quarantine measures; Public health policy

1. INTRODUCTION

At the end of 2019, the rapid outbreak of the novel coronavirus quickly became a global pandemic, posing unprecedented challenges to public health systems worldwide. Over time, with the improvement of control measures and the widespread administration of vaccines, the pandemic transitioned from regular control to a stage of full reopening. In this context, systematically reviewing and deeply analyzing the transmission dynamics of COVID-19, control measures, and their social impacts is crucial. Currently, there are four main research methods for studying infectious diseases: descriptive research, analytical research, experimental research, and theoretical research. Among these, the use of mathematical models in infectious disease dynamics is particularly widespread. These models analyze dynamics both qualitatively and quantitatively to seek optimal prevention and control strategies, providing a theoretical basis and quantitative support for decision-making.

In 1927, Kemack and McKendrick developed the foundational Susceptible-Infectious-Recovered (SIR) model based on the epidemics of necrotic disease in London and the 1906 plague in Bombay [1]. They later proposed the SIS compartment model and the "threshold theory" for infectious diseases in 1932, laying important groundwork for understanding the transmission and control strategies of infectious diseases [2]. Building on the classical SIR model, Cooper et al. found that appropriate control measures can effectively control community transmission of COVID-19 [3]. Alenezi et al. applied the SIR model to analyze and predict the COVID-19 epidemic in Kuwait, successfully predicting the country's infection peak [4].

In 1984, Aron and Schwartz introduced the SEIR model by adding an exposed compartment (E) to account for the incubation period [5]. Xu et al. further studied an SEIR epidemiological model with saturated incidence rate and time delay in the latent period, obtaining characteristics of local and global stability of equilibrium states [6]. Tang et al. used the SEIR model to evaluate the impact of public health interventions on infection, predicting 7,723 confirmed cases by January 29, 2020, closely matching the actual number of 7,711 cases [7]. The team led by Nanshan Zhong used the SEIR model to analyze COVID-19 infection data, deriving the epidemic development curve and predicting the peak and scale of the epidemic. [8] Denis Efimov et al. used a discrete-time SEIR model to predict the impact of quarantine on COVID-19 spread in France, Italy, Spain, Germany, Brazil, Russia, New York State, and China, showing good reliability within a 30-120 day range [9].

With the rapid development of computer technology and statistical analysis methods, researchers have made numerous improvements to the SEIR model. To address the inability of traditional SEIR models to account for the infectiousness of patients during the incubation period of the novel coronavirus, Chen et al. proposed a segmented SEIUR model [10]. Wan et al. incorporated asymptomatic infections, pending confirmed isolated infections, and hospitalized compartments into the original SEIR model to establish an infectious disease model under intervention policies, analyzing the domestic epidemic trend [11]. Maher Ala’raj et al. accurately predicted the number of infections, recoveries, and deaths using a modified SEIRD dynamic model and ARIMA model [12]. Raslan used the SEQIHR model to analyze and predict COVID-19 in Egypt, with predictions closely matching actual data and examining the impact of quarantine duration on the epidemic [13]. Singh proposed an improved SEIR model, SEIHRP, incorporating viral shedding effects to analyze COVID-19 transmission dynamics among different individual categories [14]. Ahmed H. Msmali et al. studied the rationality, positivity, and convergence of NSFD numerical schemes generated to discuss disease transmission heterogeneity, using fuzzy theory to consider uncertainties in data, and finding a negative correlation between natural immunity variation and disease infection [15]. Xian-Xian Liu et al. used neural networks to learn from actual epidemic data, combining epidemic development and control for simulation, establishing a nonlinear, adaptive dynamic coefficient epidemic prediction SEAIRD model [16]. Phitchayapak Wintachai et al. incorporated the impact of COVID-19 vaccine efficacy on virus transmission into the SEIR model, analyzing the effect of vaccination rates and efficacy on virus transmission, showing that vaccination significantly reduces transmission rates [17]. However, this study is limited to mathematical modeling and actual vaccination effects may be influenced by more factors. Brody H. Foy et al. evaluated age-specific vaccine allocation strategies for COVID-19 in India using an age-structured extended SEIR model combined with social contact matrices, concluding that prioritizing elderly populations results in the largest relative reduction in mortality [18]. However, this model lacks consideration of seasonal impacts and vaccine delivery schedules on COVID-19. Constantino Caetano et al. used an age-structured deterministic SEIR model to study the impact of different vaccination strategies on the spread of COVID-19 in Portugal, but the study did not consider the waning effectiveness of vaccines over time or the introduction of more transmissible and drug-resistant variants [19].

In this study, an initial stage model was constructed by dividing infected individuals into mild, moderate, and severe cases, and the differential equations were also established to describe the transmission dynamics during the early stages of the epidemic. In addition, the impact of key parameters was analyzed, which included the infection rate of mild cases, the recovery rate of moderate cases, and the rate of transition from exposed to mild cases. Subsequently, based on the initial stage model, a final stage model was proposed by introducing a quarantine compartment to reflect the impact of nucleic acid testing and quarantine measures on epidemic control. Additionally, by nonlinearly processing the daily contact rate of exposed individuals and the recovery rate of mild cases, the accuracy of the model to predict the complexity of epidemic transmission was significantly improved. The comparison between the proposed model with traditional SEIR was carried out based on relative errors. Based on model predictions, policy recommendations were proposed. These measures aim to effectively control epidemic spread, reduce the burden on healthcare systems, and create favorable conditions for economic recovery.

2. MODELS AND METHODS

In predicting the transmission and development of the COVID-19 pandemic, initial-stage $\mathrm{SEI_1I_2I_3RD}$ and final-stage $\mathrm{SEQI_1I_2I_3RD}$ models suitable for the Beijing area were constructed to simulate the initial stage of the pandemic and the situation after the implementation of quarantine measures, respectively. By combining these two models and utilizing data on daily new infections and cumulative recoveries in Beijing from January 23, 2020, to March 18, 2020, released by the National Health Commission of China and the Chinese Center for Disease Control and Prevention, a comprehensive prediction of infection and recovery numbers was achieved.

2.1. Initial Stage $SEI_1I_2I_3RD$ Model

In the initial stage (January 23, 2020 - February 2, 2020), the total population of Beijing during the pandemic was divided into seven distinct compartments: S (Susceptible), E (Exposed), I_1 (Mild Infected), I_2 (Moderate Infected), I_3 (Severe Infected), R (Recovered), and D (Deceased).

Before establishing the model, the following assumptions were made:

a. The total population kept stable, with birth and death rates negligible in the short term, and large-scale migration in and out of the population not considered.

b. The population is generally susceptible, and only human-to-human transmission is considered.

c. Mildly infected individuals do not require hospitalization, are infectious, and their mortality rate is not considered.

d. Moderately infected individuals receive hospital treatment, are considered isolated, and are not infectious; their mortality rate is not considered.

e. Severely infected individuals receive hospital treatment, are considered isolated, and are not infectious; their mortality rate is considered.

f. Recovered individuals are immune in the short term and do not become susceptible again.

Based on these assumptions, the initial stage $\mathrm{SEI_1I_2I_3RD}$ model was constructed, as illustrated in Figure 1. During the initial stage of the pandemic, mildly infected persons were infectious. When susceptible individuals came into contact with them, they could be infected and become exposed. Exposed individuals, typically showing no significant symptoms, would not take preventive measures and would turn into mildly infected persons after an incubation period. Due to individual differences and environmental influences, some mildly infected persons would recover through self-treatment and become recovered persons, while others would progress to moderately infected persons. Moderately infected persons required hospitalization; some recovered, while others progressed to severely infected persons. Severely infected persons received intensive treatment; some recovered, but due to the lack of targeted medication in hospitals during the initial stage of the pandemic, some severely infected persons ultimately succumbed to the disease.

The model in Supplementary Mateirals Figure 1 can be expressed by the differential equation:

$$\frac{dS}{dt} = -\beta_1 I_1 S - \beta_2 I_2 S - \beta_3 I_3 S$$

$$\frac{dE}{dt} = \beta_1 I_1 S + \beta_2 I_2 S + \beta_3 I_3 S - w_1 E$$

$$\frac{dI_1}{dt} = w_1 E - \gamma_1 I_1 - w_2 I_1$$

$$\frac{dI_2}{dt} = w_2 I_1 - \gamma_2 I_2 - w_3 I_2 \tag{1}$$

$$\frac{dI_3}{dt} = w_3 I_2 - \gamma_3 I_3 - \mu I_3$$

$$\frac{dR}{dt} = \gamma_1 I_1 + \gamma_2 I_2 + \gamma_3 I_3$$

$$\frac{dD}{dt} = \mu I_3$$

In Equation (1), $\beta_1$was the probability of infection in mildly infected persons, β_2 was the probability of infection in moderately infected persons, $\beta_3$was the probability of infection in severely infected persons, $w_1$was the transfer rate of exposed persons to mildly infected persons,

w_2 was the transfer rate of mild infected persons to moderate infected persons, $w_3$was the transfer rate of moderate infected persons to severe infected persons, $\gamma_1$was the recovery rate of mildly infected persons, γ_2 was the recovery rate of moderate infected persons, γ_3 was the recovery rate of severely infected persons,μ was the mortality rate of severely infected persons.

2.2. Final Stage $\mathbf{SEQI_1I_2I_3RD}$ Model

In the second phase (February 3, 2020 - March 18, 2020), against the backdrop of significantly increased transmissibility of the COVID-19 virus, the sharp rise in the number of infections prompted government authorities to adopt stricter control measures. To effectively curb the further spread of the epidemic, the government implemented nucleic acid testing and necessary quarantine measures for the exposed population starting from the 11th day of the epidemic's progression.

Therefore, when constructing the epidemic transmission model, we added the isolation compartment (Q) based on the initial stage $SEI_1I_2I_3RD$ model to reflect the new prevention and control strategy and constructed the final stage$SEQI_1I_2I_3RD$ model. Figure 2 shows the transmission link.

It was assumed that exposed individuals were at risk of infection after contact with mildly infected individuals who were not isolated. Exposed individuals with abnormal nucleic acid test results were immediately quarantined and subjected to medical observation and intervention. While some quarantined individuals, upon receiving prophylactic medication and treatment, managed to avoid illness or recover, differences in the degree of contact, immunity, and viral load caused some quarantined individuals to experience worsening conditions and progress to moderately infected individuals.

The model in Supplementary Mateirals Figure 2 can be expressed by the differential equation as:

$$\frac{dS}{dt} = -c\beta\frac{S}{N}(I_1 + \sigma E)$$

$$\frac{dE}{dt} = c\beta\frac{S}{N}(I_1 + \sigma E)(1 - q) - \omega_1 E$$

$$\frac{dQ}{dt} = qc\beta\frac{S}{N}(I_1 + \sigma E) - \gamma Q - \omega_4 Q$$

$$\frac{dI_1}{dt} = \omega_1 E - \omega_2 I_1 - \gamma_1 I_1 \tag{2}$$

$$\frac{dI_2}{dt} = \omega_2 I_1 + \omega_4 Q - \gamma_2 I_2 - \omega_3 I_2$$

$$\frac{dI_3}{dt} = \omega_3 I_2 - \gamma_3 I_3$$

$$\frac{dR}{dt} = \gamma Q + \gamma_1 I_1 + \gamma_2 I_2 + k_1\gamma_3 I_3$$

$$\frac{dD}{dt} = (1 - k_1)\gamma_3 I_3$$

Where β was the disease infection rate, q is the isolation rate of the exposed persons, w_1 is the transfer rate of exposed persons to mildly infected persons, w_2 was the transfer rate of mildly infected persons to moderate infected persons, w_3 was the transfer rate of moderate infected persons to severely infected persons, w_4 was the transfer rate of isolated persons to moderate infected persons, γ was the recovery rate of isolated persons, γ_1 was the recovery rate of mildly infected persons, γ_2 was the recovery rate of moderate infected persons, γ_3 was the recovery rate of severe infected persons, $k_1$was proportion of recovery in severe cases. At the same time, considering that both exposed and mildly infected groups could infect susceptible individuals, but the transmissibility of the exposed group was relatively lower, an exposure infection attenuation factor σ was introduced. This factor described the lower transmissibility of exposed individuals compared to mildly infected individuals, reflecting their actual impact on virus transmission.

2.3. Nonlinear Treatment of the Parameters In the Final Stage $SEQI_1I_2I_3RD$ Model

According to Ref. [23], the daily contact rate of infected persons without intervention measures was 14, while the lowest daily contact rate of infected persons with intervention measures was 2. Therefore, considering the improvement of isolation measures over time and the gradual strengthening of control over the infected population as the epidemic progressed, a nonlinear function was established in the final stage $SEQI_1I_2I_3RD$ model to represent the daily reduction of exposed persons over time:

$$\mathrm{c(t)} = \mathrm{e}^{(\ln(12) - \frac{t}{2})} + 2 \tag{3}$$

Furthermore, considering the gradual increase in population resistance and the production of immune antibodies, γ_1 in the final stage $SEQI_1I_2I_3RD$ model was set as a variable coefficient, which gradually increased to $\mathrm{m_1}$ during this period:

$$\gamma_1(\mathrm{t}) = \mathrm{m_1} \times \mathrm{e}^{(\mathrm{t}-45)\times \mathrm{m_2}} \tag{4}$$

2.4. Mean Relative Error Formula

To quantitatively evaluate the prediction performance, average relative error formulas were established for both the initial stage $SEI_1I_2I_3RD$ and final stage $SEQI_1I_2I_3RD$ models. The average errors for I and R were calculated as follows.

$$E_I = \frac{\sum_{t=t_0}^{T} \frac{|PI_t - AI_t|}{AI_t}}{T - t_0} \quad , \ E_R = \frac{\sum_{t=t_0}^{T} \frac{|PR_t - AR_t|}{AR_t}}{T - t_0} \tag{5}$$

3. PREDICTION RESULTS AND PARAMETER ANALYSIS

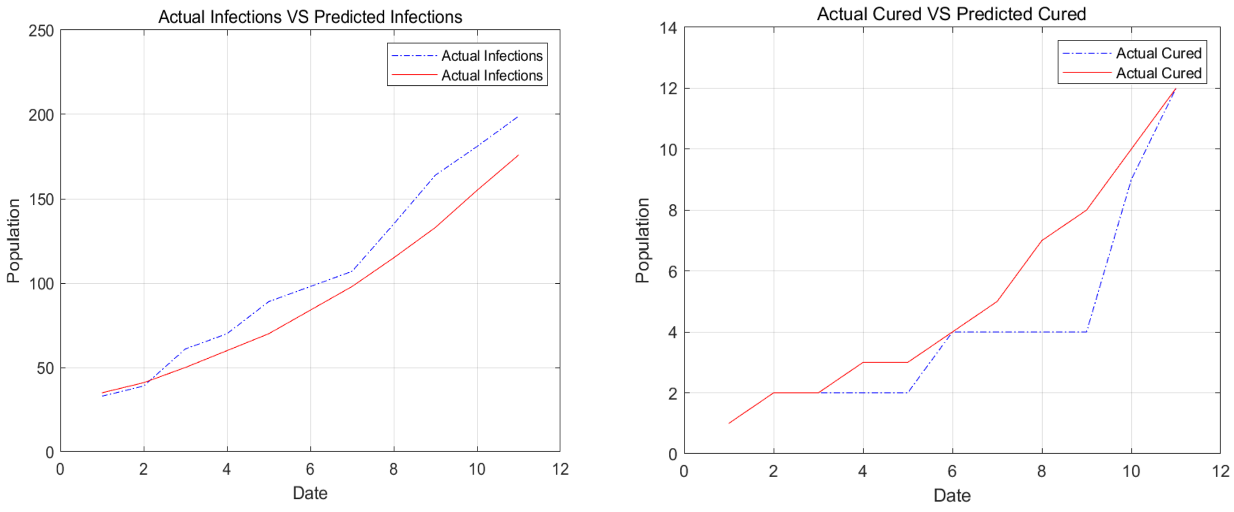
3.1. Prediction Results and Parameter Analysis of the Initial Stage $SEI_1I_2I_3RD$ Model

We conducted an in-depth analysis of the initial stage $SEI_1I_2I_3RD$ model, wrote the model code using Python, and focused on the prediction results of the model and the key parameters therein.

3.1.1. Forecast results of the initial stage $\boldsymbol{SEI_1I_2I_3RD}$ model

In the study on the initial phase of the epidemic from January 23 to February 2, 2020, the model was applied to predict the dynamics of the number of new infections and the cumulative recovered number, and the parameters are shown in Supplementary Mateirals Table 1.

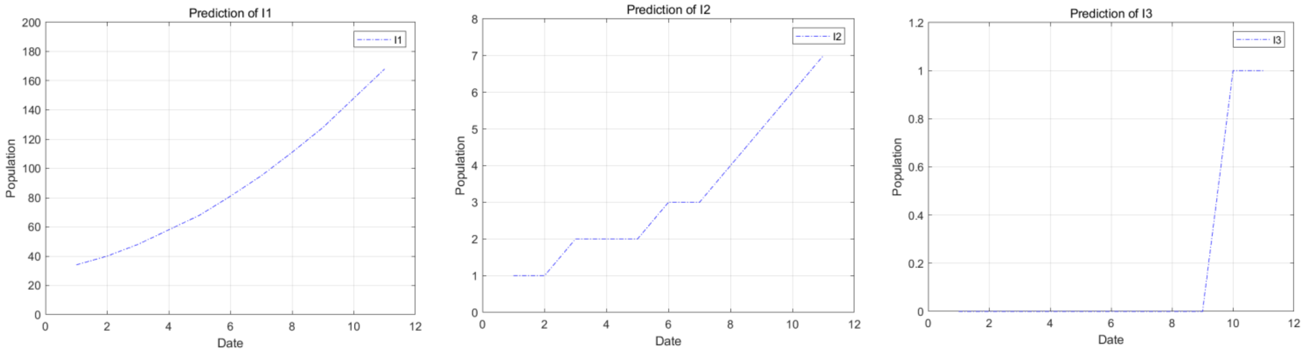
In Figure 1, Figure 1(a) represents the comparison between the predicted daily new infection numbers from January 23, 2020, to February 2, 2020, obtained by the initial stage $SEI_1I_2I_3RD$ model and the actual values, while (b) shows the comparison between the predicted cumulative recovery numbers and the actual values for the same period. The results in Figure 1 indicate that the predicted values and the actual observed values exhibited a consistent upward trend overall, especially matching well during the initial stage. However, as time progressed, the predicted number of new infections gradually fell below the actual values, whereas from January 29 to February 1, the predicted cumulative recovery numbers slightly exceeded the actual values, reflecting the complexity and dynamic changes of the epidemic transmission. Using the average relative error function, the average relative error for new infections was found to be 13.3%, and for cumulative recoveries, it was 28.2%. Although the prediction period was relatively short and a few data points with large discrepancies contributed significantly to the error, the overall error remained within an acceptable range. Both the predicted and actual values for new infections and cumulative recoveries reached their maximum on February 2. The predicted number of new infections on February 2 was 176, compared to an actual value of 199, while the predicted and actual cumulative recoveries on the same day were both 12. This validated the short-term predictive accuracy of the model.



(a) (b)

Figure 1. (a) the blue dashed line represents the actual daily new infection numbers in Beijing, while the red solid line represents the daily new infection numbers predicted by the initial stage model. (b) the blue dashed line represents the actual cumulative number of recoveries in Beijing, while the red solid line represents the cumulative number of recoveries predicted by the initial stage model.

By subdividing the compartments of infected individuals as shown in Figure 2, the different characteristics of mildly infected, moderately infected, and severely infected individuals were fully considered. This allowed the model to more accurately reflect the actual changes in the epidemic during the prediction process.



(a) (b) (c)

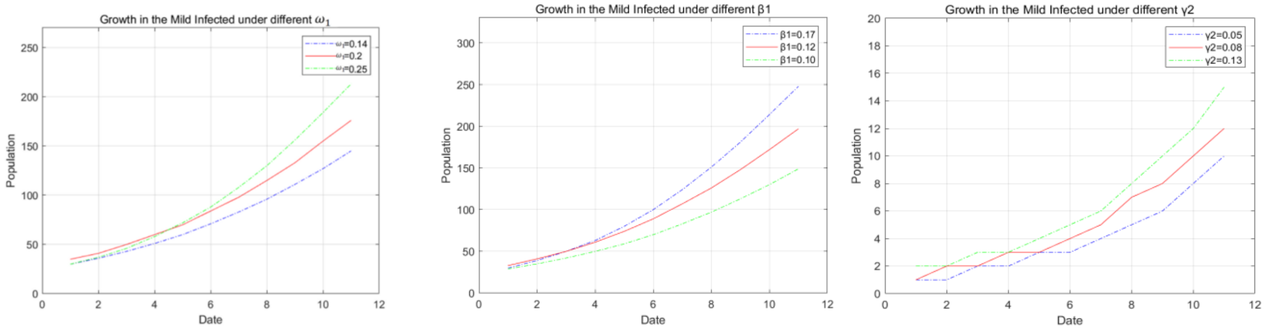
Figure 2. (a) shows the predicted number of daily new mildly infected individuals in Beijing as per the initial stage $SEI_1I_2I_3RD$ model; (b) shows the predicted number of daily new moderately infected individuals; (c) shows the predicted number of daily new severely infected individuals.

3.1.2. Important parameter effects

For the initial stage $SEI_1I_2I_3RD$ model, the specific analysis of each parameter's impact on the predicted values revealed that the transfer rate of exposed persons to mildly infected persons, the probability of infection in mildly infected persons, and the recovery rate of moderate infected persons had significant effects on the prediction results.

As shown in Figure 3 (a) the growth in daily new infection numbers in the initial stage $SEI_1I_2I_3RD$ model when the transfer rate of exposed persons to mild infected persons was set at 0.25, 0.2, and 0.14, respectively. It was found that as the value of this proportion decreased, the daily new infection numbers gradually declined. Consequently, the conclusion was drawn that reducing the transfer rate of exposed persons to mildly infected persons can decrease the daily new infection numbers, thereby reducing the peak number of infections during the epidemic peak and effectively slowing the spread of the epidemic.

As shown in Figure 3 (b), the growth in daily new infection numbers in the initial stage $SEI_1I_2I_3RD$ model was analyzed when the probability of infection in mildly infected persons was set at 0.17, 0.12, and 0.1, respectively. It was found that as the value of this infection rate decreased, the daily new infection numbers gradually declined. Consequently, the conclusion was drawn that reducing the probability of infection in mildly infected persons can significantly slow down the spread and extent of the epidemic, effectively controlling its propagation.



(a) (b) (c)

Figure 3. (a) represents daily increase in the number of new infections at the transfer rate of exposed persons to mildly infected persons of 0.14,0.2,0.25 in the initial stage $SEI_1I_2I_3RD$ model. (b) represents daily increase of new infections at the probability of infection in mildly infected persons of 0.17,0.12,0.12 in the initial stage $SEI_1I_2I_3RD$ model. (c) represents the cumulative recovery growth at the recovery rate of moderate infected persons of 0.05,0.08,0.13 in the initial stage $SEI_1I_2I_3RD$ model.

As shown in Figure 3 (c), the growth in the cumulative number of recoveries in the initial stage $SEI_1I_2I_3RD$ model was analyzed when the recovery rate of moderate infected persons was set at 0.05, 0.08, and 0.13, respectively. It was found that as the value of this recovery rate increased, the predicted cumulative number of recoveries showed a substantial increase. Consequently, the conclusion was drawn that improving the recovery rate of moderately infected persons allows more patients to recover faster, reduces the burden on the healthcare system, and effectively prevents further transmission of the virus.

3.2. Prediction Results and Parameter Analysis of the Final Stage $SEQI_1I_2I_3RD$ Model

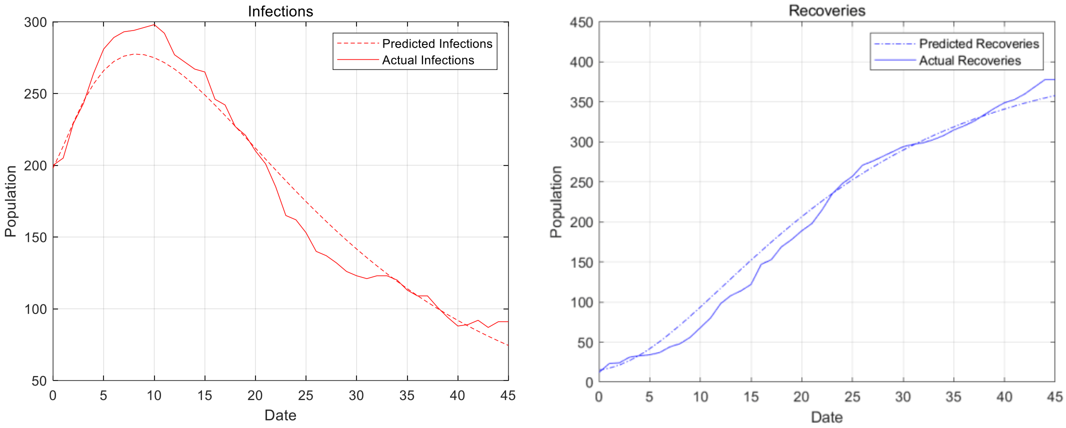
Building on the initial stage $SEI_1I_2I_3RD$ model, the final stage $SEQI_1I_2I_3RD$ model introduced a quarantine variable (Q) and applied nonlinear processing to certain parameters. The model code was developed using MATLAB. The focus was placed on the parameter fitting results, the comparison of predicted data, and the impact of key parameters within the model.

3.2.1. Forecast results

The parameter definitions in the final stage $SEQI_1I_2I_3RD$ model is shown in Supplementary Mateirals Table 2. By fitting the data and using the model's average relative error function, EI was found to be 6.38% and ER was found to be 9.15%.

In Figure 4, (a) represents the comparison between the predicted daily new infection numbers from February 3, 2020, to March 18, 2020, obtained by the final stage $SEQI_1I_2I_3RD$ model and the actual values, while (b) shows the comparison between the predicted cumulative recovery numbers and the actual values for the same period. The prediction results indicate that the daily new infection numbers followed a trend of initial increase followed by a decrease, reaching a peak of 277 on the 10th day after the start of the second phase. The actual peak of daily new infections occurred on the 11th day after the start of the second phase, with a total of 298 cases. Thus, the fitting results were good in terms of both the peak number and the time to reach the peak.

Through in-depth analysis and validation of the final stage $SEQI_1I_2I_3RD$ model, it was found that this model achieved an average relative error of 6.38% for EI and 9.15% for ER, which is significantly lower than the common error rate of over 30% in traditional SEIR models. This indicated the effectiveness of introducing dynamic daily contact rates and varying recovery rates for different degrees of illness.



(a) (b)

Figure 4. (a): The solid line represents the actual daily new infection numbers in Beijing, while the dashed line represents the predicted daily new infection numbers in Beijing from the final stage $SEQI_1I_2I_3RD$ model; (b): The solid line represents the actual cumulative number of recoveries in Beijing, while the dashed line represents the predicted cumulative number of recoveries in Beijing from the final stage $\mathrm{SEQI_1I_2I_3RD}$ model.

Figure 5 shows the dynamic changes in the number of different groups of infected persons during the second phase of the epidemic transmission. The number of mildly infected persons decreased significantly, reflecting the effectiveness of the control measures; the number of moderately infected persons reached a peak of 195 on the 14th day after the start of the second phase and then gradually declined; the number of severely infected persons continued to rise, indicating the severity of the conditions of critically ill persons and their low recovery rate, emphasizing the importance of timely treatment and the rational allocation of medical resources.

The number of isolated persons reached a peak of 45 on the 6th day after the start of the second phase and then continued to decline, reflecting the characteristics of the virus's incubation period and the effects of preventive and treatment measures. The decrease in the number of isolated persons was closely related to the overall control of the epidemic and the effective allocation of medical resources. Some isolated persons experienced worsening conditions and were transferred to the moderately infected person compartment, while others recovered and left the isolation compartment.

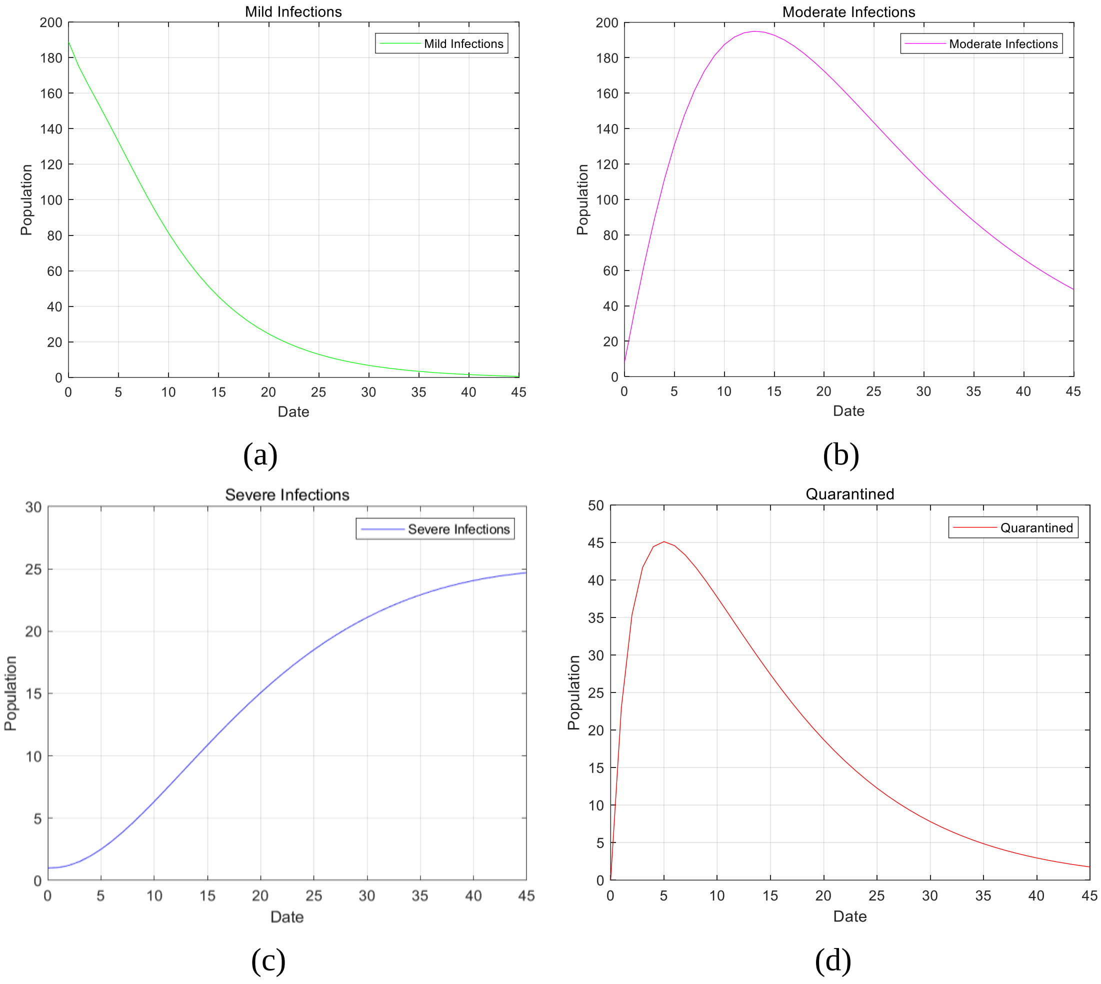
3.2.2. Important parameter effects

For the final stage $SEQI_1I_2I_3RD$ model, a specific analysis of each parameter's impact on the predicted values revealed that the isolation rate, the daily contact rate of infected persons, and the recovery rate of mildly infected persons had significant effects on the prediction results.

Figure 6 (a) shows the changes in daily new infection numbers predicted by the final stage $SEQI_1I_2I_3RD$ model when the isolation rate is set at 0.2, 0.4, 0.6, and 0.8, respectively. It was found that as the isolation rate decreased, the peak significantly decreased and the peak time was advanced with increasing isolation rate.

Figure 6 (b) shows the changes in daily new infection numbers predicted by the final stage $SEQI_1I_2I_3RD$ model when the daily contact rate of infected persons is set at 0.2, 0.4, 0.6, and 0.8, respectively. It was found that as the daily contact rate of infected persons decreased, the peak of daily new infection numbers dropped sharply.

Figure 6 (c) shows the changes in cumulative recovery numbers predicted by the final stage $SEQI_1I_2I_3RD$ model when the recovery rate of mildly infected persons is set at 0.01, 0.03, 0.05, and 0.07, respectively. It was found that when the recovery rate was 0.01, the cumulative number of recovered individuals on the 5th day was 43, and when the recovery rate was 0.07, the cumulative number of recovered individuals on the 5th day was 85, representing a growth rate of nearly 100%. Consequently, the conclusion was drawn that increasing the recovery rate of mildly infected persons can effectively alleviate the pressure on the healthcare system and improve the overall effectiveness of epidemic control.



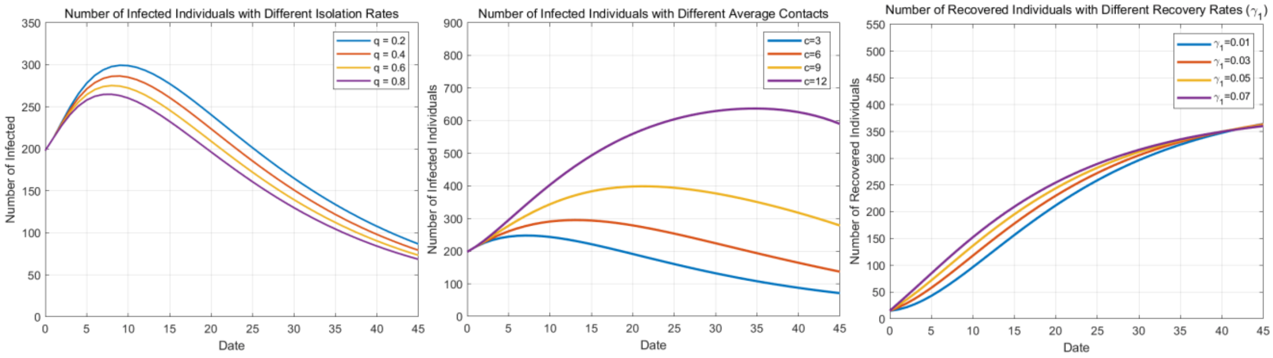
(a)

(b)

(c)

(d)

Figure 5. (a)represents the predicted daily number of new mildly infected persons by the final stage model, (b) represents the predicted daily number of new moderately infected persons, (c) represents the predicted daily number of new severely infected persons, and (d) represents the predicted current number of isolated persons by the final stage model.



(a) (b) (c)

Figure 6. (a) represents the predicted daily new infection numbers at the isolation rate of 0.2, 0.4, 0.6, and 0.8 in the final stage $SEQI_1I_2I_3RD$ model. (b) represents the predicted daily new infection numbers at the daily contact rate of infected persons of 0.2, 0.4, 0.6, and 0.8 in the final stage $SEQI_1I_2I_3RD$ model. (c) represents the predicted cumulative recovery numbers at recovery rates of mildly infected persons of 0.01, 0.03, 0.05, and 0.07 in the final stage $SEQI_1I_2I_3RD$ model.

3.3. Impact of Key Parameters and Policy Recommendations

An analysis of the significant influencing parameters in both the initial stage $SEI_1I_2I_3RD$ model and the final stage $SEQI_1I_2I_3RD$ model was conducted, and reasonable policy recommendations were provided.

3.3.1. Parameter study of the initial stage $\boldsymbol{SEI_1I_2I_3RD}$ model

In the predictions of the initial stage $SEI_1I_2I_3RD$ model, it was found that the rate at which exposed persons transition to mildly infected persons is a crucial control parameter. By reducing this rate, the spread of the epidemic can be effectively slowed, decreasing the daily number of new infections and thus gaining more time for control measures. To achieve this, public awareness campaigns should be intensified to educate the population on preventive measures, encouraging habits such as wearing masks, frequent handwashing, and maintaining social distancing.

According to the prediction results, lowering the infection rate of mildly infected persons will significantly slow down the spread of the epidemic, reduce the number of infections during the peak period, shorten the duration of the epidemic, and alleviate the burden on the healthcare system. Therefore, accurate and efficient nucleic acid testing and subsequent isolation measures should be implemented by the relevant authorities to control the spread of the epidemic.

Additionally, increasing the recovery rate of moderately infected persons will help reduce the number of new infections, lower the mortality rate, and promote social stability and economic recovery. Healthcare departments can optimize treatment plans, develop personalized treatment strategies, and introduce advanced medical equipment and technologies to provide better medical services for moderately infected persons.

3.3.2. Parameter study of the final stage $\boldsymbol{SEQI_1I_2I_3RD}$ model

In the predictions of the final stage $SEQI_1I_2I_3RD$ model, it was found that increasing the isolation rate of exposed persons significantly reduced the epidemic peak and advanced its occurrence. Increasing the isolation rate reduced virus transmission, lowered the epidemic peak, and alleviated the burden on the healthcare system. Therefore, isolation, as a key measure to control the spread of infectious diseases, can effectively cut off the transmission routes of the virus and prevent the spread of the epidemic. The government should recognize the importance of isolation measures and take steps to improve the isolation rate and efficiency, clearly define isolation requirements and procedures through media campaigns, and build sufficient isolation facilities.

Finally, increasing the recovery rate of mildly infected persons is crucial for controlling the epidemic and reducing the pressure on the healthcare system. The government should allocate more resources to the treatment and care of mild cases, strengthen isolation measures to prevent mildly infected persons from spreading the virus and establish a comprehensive case monitoring and tracking system to promptly identify and isolate infected persons.

4. CONCLUSIONS

(1) This study constructs and analyzes initial stage $SEI_1I_2I_3RD$ and final stage $SEQI_1I_2I_3RD$ models to detail the transmission dynamics of the epidemic at different stages and propose scientific prevention and control strategies. The initial stage $SEI_1I_2I_3RD$ model subdivides infected individuals into mildly, moderately, and severely infected categories, accurately reflecting the transmission dynamics during the initial stage of the epidemic and effectively predicting the number of new infections and cumulative recoveries. The final stage $SEQI_1I_2I_3RD$ model builds on the initial stage $SEI_1I_2I_3RD$ model by adding an isolation compartment to reflect the impact of nucleic acid testing and quarantine measures on epidemic control. By nonlinearly processing the parameters, the initial stage $SEI_1I_2I_3RD$ model more accurately simulates the complexity of the epidemic transmission and the effectiveness of control measures.

(2) Based on the model predictions, the following policy recommendations are proposed: enhance public health education to raise awareness and understanding of the epidemic, disseminate scientific prevention knowledge; strictly implement isolation measures to ensure timely and safe isolation and plan for adequate isolation facilities; dynamically adjust prevention strategies by timely modifying key parameters based on the development of the epidemic and model predictions to ensure the effectiveness and flexibility of control measures.

(3) These measures can effectively control the spread of the epidemic, alleviate the burden on the healthcare system, protect public health, and create favorable conditions for social and economic recovery.

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