Modeling the transmission of second-wave COVID-19 caused by imported cases: A case study

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As the first-wave COVID-19 has passed in 2020, people’s awareness of self-protection began to decline gradually. How to prevent and control the second-wave COVID-19 has become an important issue in many countries and regions. By analyzing the transmission of the second-wave COVID-19 caused by an imported case in Tonghua City, Jilin Province, China, in January 2021, we establish a new mathematical COVID-19 model to simulate the transmission characteristics of the second-wave COVID-19. First, we analyze the basic properties of the model, prove the existence of the equilibrium point, and obtain the expression of the basic reproduction number with important biological significance. Secondly, we use the weighted nonlinear least square estimation method to fit the cases in Tonghua City of Jilin Province in January 2021, and get the estimated value of the parameters. The basic reproduction number of the second-wave COVID-19 in Tonghua City is $R_0 = 1.0695$, which is much smaller than that of the first-wave COVID-19 in Wuhan in 2020. Finally, in the optimal control part, we consider two control methods (keeping social distance and nucleic acid detection of all people in the city) to simulate the control of the disease. The results show that the control intensity of the two control methods needs to be dynamically changed and adjusted, so that the cost can be minimized with the least infection. The results of this paper can not only provide suggestions for health management departments, but also provide a reference for the analysis of the second-wave COVID-19 in other countries or regions.

KEYWORDS
basic reproduction number, optimal control, second-wave COVID-19, stability analysis, weighted nonlinear least square estimation

MSC CLASSIFICATION
34D23; 49J15

1 | INTRODUCTION

According to WHO statistics, as of April 30, 2021, 1,499,107,744 people have been confirmed infected with the Novel Coronavirus (COVID-19), and 3,155,168 people have died. COVID-19 has spread to 223 countries or areas, seriously affecting people’s daily life and health.\textsuperscript{1} In early 2020, the first outbreak of COVID-19 occurred in Wuhan, China. Because it is highly infectious, the Chinese government immediately issued an order to block Wuhan and implemented a series
of policies to prevent the spread of the virus. In April 2020, the first-wave COVID-19 epidemic in China was basically under control, and Wuhan was able to reopen. As people's life gradually returned to normal, some sporadic imported cases caused the spread of the second-wave COVID-19.\(^2\)

For example, on April 1, 2020, in Heilongjiang Province, China, the imported cases caused the second-wave COVID-19 transmission.\(^3\) As of May 1, 2020, a total of 558 confirmed cases have been added in 1 month. On July 23, 2020, in Dalian City, China, the second-wave COVID-19 was transmitted due to the presence of COVID-19 virus on imported cold chain goods.\(^4\) It took a month for the number of new cases per day to drop to zero after the local government began implementing strict controls. As of August 28, 2020, 98 people have been diagnosed with infection.\(^5\) In addition, in January 2021, an imported case caused an outbreak in Tonghua City of Jilin Province.\(^6\) Then in the next 30 days, 300 people in Tonghua City were confirmed to be infected.\(^7\) It can be seen from the above examples that after the first-wave COVID-19 was controlled, the key prevention and control target is the second-wave COVID-19 transmission caused by imported cases and cold chain goods from abroad. If the prevention and control of the second-wave COVID-19 is not timely, it may cause another large-scale spread of COVID-19.

Since the first COVID-19 outbreak in 2020, many scholars used infectious disease dynamics models to simulate, analyze, and predict the spread of diseases around the world. According to the communication characteristics of different places and the control measures of the government, a series of specific mathematical models are established to simulate the communication of COVID-19 in a region. Their work provides people with a series of valuable research ideas and important methods.\(^8\)–\(^18\)

Sun et al\(^8\) established a SEIQR mathematical model to simulate the occurrence of COVID-19 in Wuhan in 2020. On the basis of mathematical analysis and data analysis, they systematically discussed the impact of locking down Wuhan and increasing health resources on the spread of COVID-19. Tsay et al\(^9\) constructed a SEAIR model to simulate the spread of the COVID-19 in the United States, and used the nonlinear least squares method to fit the number of infected, recovered and perished cases in the United States published on the Hopkins University website from January 22, 2020 to April 16, 2020. Finally, the optimal design scheme of maintaining social distance and government control was discussed. Considering the influence of environment as the vector of virus transmission, Asamoah et al\(^10\) established a SEAIRV mathematical model to simulate the number of confirmed cases in Ghana from March 12, 2020 to May 7, 2020. The results showed that in Ghana, the basic reproduction number of COVID-19 was \(R_0 = 2.68\). Ullah and Khan\(^11\) divided the infected population into four types (asymptomatic, symptomatic, hospitalized, severe), and established an 8-dimensional \(SEI_\alpha I_h I_c QR\) mathematical model to simulate the prevalence of COVID-19 in Pakistan. The authors considered that the only way to reduce infection in the absence of effective vaccine is non drug behavior intervention (keeping social distance, isolation, hospitalization, etc.), and then studied the optimal control scheme of these control interventions. There are also many studies on the popularity of COVID-19 around the world. Please refer to the references.

Although severe social alienation measures have been proved to be effective in slowing down the pandemic of the first-wave COVID-19 in 2020, with the cancelation of restrictive measures, the second-wave COVID-19 will appear with the imported cases or cold chain goods. After the first-wave COVID-19, people have some sense of self-protection in their daily social behaviors. Therefore, the impact of the second-wave COVID-19 and the first-wave COVID-19 are different, and the intensity of their control measures are different too. But up to now, there are few dynamical studies on the second-wave COVID-19.

Inspired by the above literatures, we model and analyze the propagation of the second-wave COVID-19 in Tonghua City of Jilin Province in January 2021. According to the official report data, the confirmed patients were divided into four categories.\(^7\) Patients with different degrees of infection will be treated with different treatments, and their recovery rates are different. So we establish a more objective nine-dimensional \(SEAIT_1 T_2 T_3 T_4 R\) dynamic model, in which the treated cases are divided into four situations.

The structure of the paper is as follows: the model formulation is given in Section 2; the existence of equilibria and the basic reproduction number are obtained in Section 3; the globally asymptotically stability of the Disease-Free Equilibrium is proved in Section 4; optimal control analysis is shown in Section 5; parameter estimation is given in Section 6; numerical simulations are shown in Section 7; some key findings are given in last section.
2 | THE MODEL FORMULATION

2.1 | System description

According to official reports of COVID-19 infection, the total population $N(t)$ is divided into nine different warehouses: Susceptible class $S(t)$, Exposed class $E(t)$, Asymptomatic infectious class $A(t)$, Symptomatic infectious class $I(t)$, Mild treated class $T_1(t)$, Common treated class $T_2(t)$, Severe treated class $T_3(t)$, Critical treated class $T_4(t)$, Recovered class $R(t)$. Thus, the total population $N(t)$ is given by

$$N(t) = S(t) + E(t) + A(t) + I(t) + T_1(t) + T_2(t) + T_3(t) + T_4(t) + R(t).$$  \[(1)\]

There is a limit to the number of people a patient can touch per unit of time. In general, the standard incidence $\beta SI/N$ is more realistic than the bilinear incidence $\beta SI$ in humans and some social animals.\textsuperscript{19–21} COVID-19 is contagious during the incubation period, and asymptomatic COVID-19 patients are also contagious. Considering these reasons, we use the following nonlinear terms as incidence rates:

$$S(\beta_1 E + \beta_2 A + \beta_3 I).$$

The population flow among all compartments is shown in Figure 1. The meanings of all parameters are shown in Table 1.

The transmission dynamic properties of COVID-19 studied by us are given by the following nonlinear differential equations.

\[
\begin{align*}
S' &= \Lambda - \mu S - S\beta \frac{E + A + I}{N}, \\
E' &= S\frac{\beta E + \beta A + \beta I}{N} - (\alpha_1 + \alpha_2 + \mu)E, \\
A' &= \alpha_1 E - (v_1 + v_2 + \mu)A, \\
I' &= \alpha_2 E - (v_3 + v_4 + v_5 + v_6 + \mu)I, \\
T_1' &= v_1 A + v_3 I - (w_1 + \mu)T_1, \\
T_2' &= v_2 A + v_4 I - (w_2 + \mu)T_2, \\
T_3' &= v_5 I - (w_3 + \mu)T_3, \\
T_4' &= v_6 I - (w_4 + \mu + \eta)T_4, \\
R' &= w_1 T_1 + w_2 T_2 + w_3 T_3 + w_4 T_4 - \mu R.
\end{align*}
\]

\[(2)\]

![FIGURE 1 Transfer diagram of model](Color figure can be viewed at wileyonlinelibrary.com)
Progression from symptomatic compartment

The death rate due to infection with COVID-19

Progression from symptomatic compartment

The recovery rate in

The effective contact rate of

Proportion of disease progression from exposed compartment

And the non-negative initial conditions are given by

\[ S(0) \geq 0, \quad E(0) \geq 0, \quad A(0) \geq 0, \quad I(0) \geq 0, \]
\[ T_1(0) \geq 0, \quad T_2(0) \geq 0, \quad T_3(0) \geq 0, \quad T_4(0) \geq 0, \quad R(0) \geq 0. \]  

### 2.2 | Positivity and boundedness

From the biological point of view, the initial value of the total population is positive, and the population in each warehouse is non-negative for any \( t > 0 \). Therefore, it is necessary to prove that the solution of system (2) is non-negative under the initial condition (3).

From the first equation of system (2):

\[
\frac{dS}{dt} = \Lambda - \lambda S,
\]

where \( \lambda = \mu + \frac{\beta_1 E + \beta_2 A + \beta_3 I}{N} \). The solution of (4) can be found as follows.

\[
S(t) = S(0) \exp \left( - \int_0^t \lambda d\zeta \right) + \exp \left( - \int_0^t \lambda d\zeta \right) \int_0^t \Lambda \exp \left( \int_0^\zeta \lambda d\zeta \right) \, dp.
\]

Thus, we can get \( S(t) > 0 \). Through a similar process, we can get that the other variables are positive. System (2) can be rewritten in the following matrix form.

\[
X' = G(X),
\]

where \( X = (S, E, A, I, T_1, T_2, T_3, T_4, R)^T \in \mathbb{R}_0^+ \) and \( G(X) \) is given by

\[
G(X) = \begin{pmatrix}
G_1(X) \\
G_2(X) \\
G_3(X) \\
G_4(X) \\
G_5(X) \\
G_6(X) \\
G_7(X) \\
G_8(X) \\
G_9(X)
\end{pmatrix} = \begin{pmatrix}
\Lambda - \mu S - S \frac{\beta_1 E + \beta_2 A + \beta_3 I}{N} \\
S \frac{\beta_1 E + \beta_2 A + \beta_3 I}{N} - \left( \alpha_1 + \alpha_2 + \mu \right) E \\
\alpha_1 E - \left( v_1 + v_2 + \mu \right) A \\
\alpha_2 E - \left( v_3 + v_4 + v_5 + v_6 + \mu \right) I \\
v_1 A + v_3 I - \left( w_1 + \mu \right) T_1 \\
v_2 A + v_4 I - \left( w_2 + \mu \right) T_2 \\
v_5 I - \left( w_3 + \mu \right) T_3 \\
v_6 I - \left( w_4 + \mu + \eta \right) T_4 \\
w_1 T_1 + w_2 T_2 + w_3 T_3 + w_4 T_4 - \mu R
\end{pmatrix}
\]
Because of
\[
\frac{dN}{dt} = \sum_{i=1}^{9} G_i(x) = \Lambda - \mu N - \eta T_4 \leq \Lambda - \mu N,
\]
which yields that
\[
\limsup_{t \to \infty} N(t) \leq \frac{\Lambda}{\mu}.
\]
Therefore, we obtain the biologically feasible region
\[
\Omega = \left\{ (S, E, A, I, T_1, T_2, T_3, T_4, R) \in \mathbb{R}^9_+ : S + E + A + I + T_1 + T_2 + T_3 + T_4 + R \leq \frac{\Lambda}{\mu} \right\},
\]
and it is a positive invariant set of system (2).

3 THE BASIC REPRODUCTION NUMBER AND EXISTENCE OF ENDEMIC EQUILIBRIUM

3.1 The basic reproduction number

If we let \( E = A = I = 0 \) in system (2), it means that there is no disease at this time. It is easy to know that the Disease-Free Equilibrium \( D_0 \) of system (2) is given by
\[
D_0 = \left( \frac{\Lambda}{\mu}, 0, 0, 0, 0, 0, 0 \right).
\]

With the help of the next generation matrix method, the basic reproduction number with biological significance can be obtained. The value of basic reproduction number will reflect whether the disease will be endemic in a certain area.

In order to make the expression more concise and convenient, we substitute the coefficients of system (2) as follows.
\[
k_1 = \mu + \alpha_1 + \alpha_2, \quad k_2 = \mu + v_1 + v_2, \quad k_3 = \mu + v_3 + v_4 + v_5 + v_6, \quad k_4 = \mu + w_1, \quad k_5 = \mu + w_2, \quad k_6 = \mu + w_3, \quad k_7 = \mu + \eta + w_4.
\]

Letting \( x = (E, A, I, T_1, T_2, T_3, T_4, R, S)^T \), then system (2) can be written as
\[
\frac{dx}{dt} = \mathcal{F}(x) - \mathcal{V}(x),
\]
where
\[
\mathcal{F}(x) = \begin{pmatrix}
S^{\beta_1E+\beta_2A+\beta_3I} \\
\begin{pmatrix}
\alpha_1E \\
\alpha_2E \\
0 \\
0 \\
0 \\
0 \\
0 \\
0
\end{pmatrix} \\
\begin{pmatrix}
k_1E \\
k_2A \\
k_3I \\
-(v_1A + v_3I) + k_4T_1 \\
-(v_2A + v_4I) + k_5T_2 \\
-v_5I + k_6T_3 \\
-v_6I + k_7T_4 \\
-w_1T_1 - w_2T_2 - w_3T_3 - w_4T_4 + \mu R \\
-\Lambda + \mu S + S^{\beta_1E+\beta_2A+\beta_3I}
\end{pmatrix}
\end{pmatrix},
\]
\[
\mathcal{V}(x) = \begin{pmatrix}
k_1E \\
k_2A \\
k_3I \\
-(v_1A + v_3I) + k_4T_1 \\
-(v_2A + v_4I) + k_5T_2 \\
-v_5I + k_6T_3 \\
-v_6I + k_7T_4 \\
-w_1T_1 - w_2T_2 - w_3T_3 - w_4T_4 + \mu R \\
-\Lambda + \mu S + S^{\beta_1E+\beta_2A+\beta_3I}
\end{pmatrix}.
\]

The Jacobian matrices of \( \mathcal{F}(x) \) and \( \mathcal{V}(x) \) at the Disease-Free Equilibrium \( D_0 \) are
\[
D\mathcal{F}(D_0) = \begin{pmatrix}
F_{3 \times 3} & 0 \\
0 & 0
\end{pmatrix},
D\mathcal{V}(D_0) = \begin{pmatrix}
V_{3 \times 3} & 0 \\
J_1 & J_2
\end{pmatrix},
\]
where

\[
F_{3\times3} = \begin{pmatrix} \beta_1 & \beta_2 & \beta_3 \\ \alpha_1 & 0 & 0 \\ \alpha_2 & 0 & 0 \end{pmatrix}, \quad V_{3\times3} = \begin{pmatrix} k_1 & 0 & 0 \\ 0 & k_2 & 0 \\ 0 & 0 & k_3 \end{pmatrix}, \\
J_1 = \begin{pmatrix} 0 & -v_1 & -v_3 \\ 0 & -v_2 & -v_4 \\ 0 & 0 & -v_5 \end{pmatrix}, \quad J_2 = \begin{pmatrix} k_4 & 0 & 0 & 0 & 0 \\ 0 & k_5 & 0 & 0 & 0 \\ 0 & 0 & k_6 & 0 & 0 \\ 0 & 0 & 0 & k_7 & 0 \end{pmatrix}.
\]

The basic reproduction number, denoted by \( R_0 \), is given by

\[
R_0 = \rho(FV^{-1}) = \frac{\beta_1 + \sqrt{\beta_1^2 + 4\alpha_1\beta_2k_1k_2 + 4\alpha_2\beta_3k_3k_4}}{2k_1},
\]

where \( \rho(A) \) denotes the spectral radius of the matrix \( A \).

### 3.2 Existence of endemic equilibrium

If we make \( E \neq 0, A \neq 0, I \neq 0 \) in system (2), it means that the infectious disease is endemic at this time. The Endemic Equilibrium \( D^* = (S^*, E^*, A^*, I^*, T_1^*, T_2^*, T_3^*, T_4^*, R^*) \) of system (2) is determined by equations:

\[
\begin{align*}
\Lambda - \mu S - S\frac{\beta_1 E + \beta_2 A + \beta_3 I}{N} &= 0, \\
S\frac{\beta_1 E + \beta_2 A + \beta_3 I}{N} - k_1 E &= 0, \\
\alpha_1 E - k_2 A &= 0, \\
\alpha_2 E - k_3 I &= 0, \\
v_1 A + v_3 I - k_4 T_1 &= 0, \\
v_2 A + v_4 I - k_5 T_2 &= 0, \\
v_5 I - k_6 T_3 &= 0, \\
v_6 I - k_7 T_4 &= 0, \\
w_1 T_1 + w_2 T_2 + w_3 T_3 + w_4 T_4 - \mu R &= 0,
\end{align*}
\]

where \( k_1 = \mu + \alpha_1, k_2 = \mu + v_1 + v_2, k_3 = \mu + v_3 + v_4 + v_5 + v_6, k_4 = \mu + w_1, k_5 = \mu + w_2, k_6 = \mu + w_3, k_7 = \mu + \eta + w_4 \).

Adding the first two equations of (10), we have

\[
S = \frac{\Lambda}{\mu} - \frac{k_1}{\mu} E.
\]

Combining the first, third, and fourth equations of system (10), we get

\[
A = \frac{\alpha_1}{k_2} E, \quad I = \frac{\alpha_2}{k_3} E, \quad E = \frac{\Lambda}{k_1} - \frac{\mu N}{\beta_1 + \beta_2 \frac{\alpha_1}{k_2} + \beta_3 \frac{\alpha_2}{k_3}}.
\]

From the last five equations of (10), we can obtain

\[
\begin{align*}
T_1 &= \left( \frac{v_1 \alpha_1}{k_2 k_4} + \frac{v_3 \alpha_2}{k_3 k_4} \right) E, \\
T_2 &= \left( \frac{v_2 \alpha_1}{k_2 k_5} + \frac{v_4 \alpha_2}{k_3 k_5} \right) E, \\
T_3 &= \frac{v_5 \alpha_2}{k_3 k_6} E, \\
T_4 &= \frac{v_6 \alpha_2}{k_3 k_7} E, \\
R &= \frac{1}{\mu} (w_1 T_1 + w_2 T_2 + w_3 T_3 + w_4 T_4).
\end{align*}
\]
By adding all equations of (10), we have \( \Lambda - \mu N - \eta T_4 = 0 \). Hence,

\[
\Lambda - \mu N - \eta \frac{v_6 \alpha_2}{k_3 k_7} \left( \Lambda \frac{k_1}{k_1} - \frac{\mu N}{\beta_1 + \beta_2 + \beta_3} \right) = 0.
\]

By sorting out the above formula,

\[
(1 - \eta \frac{v_6 \alpha_2}{k_1 k_3 k_7}) \Lambda = \left(1 - \eta \frac{v_6 \alpha_2}{k_1 k_7} \frac{1}{\beta_1 + \beta_2 + \beta_3} \right) \mu N.
\]

From the formulas of \( k_1, k_3 \) and \( k_7 \), \( 1 - \eta \frac{v_6 \alpha_2}{k_1 k_3 k_7} > 0 \) is true. When \( R_0 > 1 \), we have \( \beta_1 + \beta_2 + \beta_3 > k_1 \). Thus, we can get that the value of \( N \) is unique and positive. So there is a unique positive Endemic Equilibrium \( D^* \) as \( R_0 > 1 \).

**Theorem 1.** *In the system (2), there is a Disease-Free Equilibrium \( D_0 = (\Lambda, 0, 0, 0, 0, 0, 0, 0, 0) \). When \( R_0 > 1 \), the system (2) has a unique Endemic Equilibrium \( D^* = (S^*, E^*, A^*, I^*, T_1^*, T_2^*, T_3^*, T_4^*, R^*) \).*

### 4 | STABILITY ANALYSIS OF DISEASE-FREE EQUILIBRIUM

**Theorem 2.** *For the system (2), the Disease-Free Equilibrium \( D_0 \) is locally asymptotically stable if \( R_0 < 1 \).*

**Proof.** The Jacobian matrix of model (2) at \( D_0 \) is given by

\[
J(D_0) = \begin{pmatrix}
\beta_1 - k_1 & \beta_2 & \beta_3 & 0 & 0 & 0 & 0 & 0 & 0 \\
-\kappa_1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
-\kappa_2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & \kappa_3 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & \kappa_4 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & \mu & 0 & 0 & 0 \\
-\kappa_5 & -\kappa_6 & -\beta_3 & 0 & 0 & 0 & 0 & 0 & 0
\end{pmatrix}.
\]

We can get its characteristic roots: \( \lambda_1 = -\kappa_4, \lambda_2 = -\kappa_5, \lambda_3 = -\kappa_6, \lambda_4 = -\kappa_7, \lambda_5 = \lambda_6 = -\mu \), and the rest of the characteristic roots can be obtained from this following equations:

\[
\lambda^3 + a_1 \lambda^2 + a_2 \lambda + a_3 = 0,
\]

where

\[
a_1 = k_1 + k_2 + k_3 - \beta_1,
\]

\[
a_2 = k_2(k_1 - \beta_1) - \alpha_1 \beta_2 + k_3(k_1 + k_2 - \beta_1) - \alpha_2 \beta_3,
\]

\[
a_3 = k_3 k_2(k_1 - \beta_1) - k_5 \alpha_1 \beta_2 - k_3 \beta_3 k_2.
\]

Then

\[
a_1 a_2 - a_3 = (k_1 + k_2 - \beta_1)(k_1 k_2 + k_2 k_3 - k_2 \beta_1 - \alpha_1 \beta_2)
\]

\[
+ (k_1 + k_3 - \beta_1)(k_1 k_3 + k_2 k_3 - k_3 \beta_1 - \alpha_2 \beta_3).
\]

When \( R_0 < 1 \), we can derive the following result from equation (9):

\[
k_1 k_2 k_3 > \beta_1 k_2 k_3 + \alpha_1 \beta_3 k_2 + \alpha_2 \beta_2 k_3 > 0.
\]
This also means that the following inequalities are true.

\[ k_1 > \beta_1, \quad k_1k_2 > \beta_1\beta_2, \quad k_1k_3 > \beta_1k_3 + \alpha_2\beta_3. \]

Thus, we know that \( a_1 > 0, \ a_2 > 0 \) and \( a_1a_2 - a_3 > 0 \). Using the Routh–Hurwitz criterion, we obtain that all determinants of the Hurwitz matrices are positive. Thus, when \( R_0 < 1 \), the Disease-Free Equilibrium \( D_0 \) is locally asymptotically stable.

Before introducing the global asymptotic stability of DFE, we introduce a related and important lemma: the LaSalle's invariant set principle[18].

**Lemma 1.** If a positive definite function \( V(x) \) exists in the neighborhood \( U \) of the origin, such that \( \dot{V}(x) \) is semi-negative definite, and if the set

\[ M = \{ x | \dot{V}(x) = 0 \} \]

contains no orbits of the system except the origin, then the zero solution of the system is globally asymptotically stable.

**Theorem 3.** For the model (2), the Disease-Free Equilibrium \( D_0 \) is globally asymptotically stable if \( R_0 < 1 \).

**Proof.** A continuous differentiable and positive definite Lyapunov function for model (2) is as follows.

\[ L(t) = x_1E + x_2A + x_3I + x_4T_1 + x_5T_2 + x_6T_3 + x_7T_4 + x_8R, \]

where \( x_i, \ (i = 1, 2, \ldots, 8) \) are nonnegative constants to be determined. The derivative of \( L(t) \) along the solution path of system (2) is

\[
\frac{dL(t)}{dt} = x_1 \left( S\frac{\beta_1E + \beta_2A + \beta_3I}{N} - k_1E \right) + x_2(\alpha_1E - k_2A) + x_3(\alpha_2E - k_3I)
+ x_4(v_1A + v_2I - k_4T_1) + x_5(v_2A + v_4I - k_5T_2) + x_6(v_3I - k_6T_3)
+ x_7(v_6I - k_7T_4) + x_8(w_1T_1 + w_2T_2 + w_3T_3 + w_4T_4 - \mu R)
\leq x_1(\beta_1E + \beta_2A + \beta_3I - k_1E) + x_2(\alpha_1E - k_2A) + x_3(\alpha_2E - k_3I)
+ x_4(v_1A + v_2I - k_4T_1) + x_5(v_2A + v_4I - k_5T_2) + x_6(v_3I - k_6T_3)
+ x_7(v_6I - k_7T_4) + x_8(w_1T_1 + w_2T_2 + w_3T_3 + w_4T_4 - \mu R)
= E(x_1\beta_1 - k_1x_1 + x_2a_1 + x_3a_2) + A(x_1\beta_2 - k_2x_2 + x_4v_1 + x_5v_2)
+ I(x_1\beta_3 - k_3x_1 + x_4v_3 + x_5v_4 + x_6v_5 + x_7v_6)
+ T_1(-x_2k_4 + x_3w_1) + T_2(-x_3k_5 + x_8w_2) + T_3(-x_6k_6 + x_8w_3)
+ T_4(-x_7k_7 + x_9w_4) + R(-\mu x_8).
\]

Then choosing

\[ x_1 = 1, \ x_2 = \frac{\beta_2}{k_2}, \ x_3 = \frac{\beta_1}{k_3}, \ x_4 = x_5 = x_6 = x_7 = x_8 = 0, \]

after simplification we can get

\[
\frac{dL(t)}{dt} \leq E \left( \beta_1 - k_1 + \frac{\beta_2}{k_2}a_1 + \frac{\beta_1}{k_3}a_2 \right),
= \frac{E}{k_2k_3} (\beta_1k_2k_3 + a_2\beta_3k_2 + a_1\beta_2k_3 - k_1k_2k_3). \]
If $R_0 < 1$, i.e. $k_1k_2k_3 > \beta_1k_2k_3 + \alpha_2\beta_2k_2 + \alpha_1\beta_2k_3 > 0$, we get $dL(t)/dt \leq 0$. In addition, $dV/dt = 0$ holds if and only if $S(t) = \frac{2}{\mu}$, $E(t) = 0$, $A(t) = 0$, $I(t) = 0$, $T_1(t) = 0$, $T_2(t) = 0$, $T_3(t) = 0$, $T_4(t) = 0$. So $D_0$ is the largest invariant set in the region

$$\Omega_0 = \left\{ (S, E, A, I, T_1, T_2, T_3, T_4, R) \in \mathbb{R}_+^9 \mid \frac{dL(t)}{dt} = 0 \right\}$$

for $t \geq 0$. By the LaSalle’s invariant set principle, the Disease-Free Equilibrium $D_0$ is globally asymptotically stable.

5 | OPTIMAL CONTROL ANALYSIS

From previous literature, we found that, in the first wave of COVID-19 transmission, there are generally three control measures: isolation, detection, and treatment. Isolation measure is used to stop the spread of infectious diseases among people by isolating infected patients. Since some infected people with COVID-19 do not have symptoms, it may not be very reliable to tell whether they have the disease by their symptoms. Detection is designed to detect symptomatic and asymptomatic infected people in a timely manner, so that the infected person can be detected as early as possible. Treatment is an important control measure because of the lack of disease awareness and stock of medical resources (doctors, beds, ventilators, and drugs) during the first wave of COVID-19 transmission. However, after experiencing the first wave of COVID-19, certain medical resources will be stored in all parts of mainland China. When the second wave of COVID-19 strikes, there will be enough resources and no additional treatment measures will be needed. Therefore, we have chosen only isolation and detection measures.

In order to study how to take control measures in time after finding the epidemic situation, we add two control measures (isolation and detection) in reality on the basis of system (2). Details of the two control measures are described below.

(i) Isolation: $u_1(t)$ represents a control measure to reduce contact between infected and healthy people. This can inhibit the spread of the virus to a certain extent. This is mainly achieved through media publicity and government regulations, which require people to keep social distance and wear masks outside.

(ii) Detection: $(u_2(t), u_3(t), u_4(t), u_5(t), u_6(t), u_7(t))$ represents the control of the spread of disease by means of total nucleic acid detection. Through two or three times of nucleic acid testing for all person in the city, all symptomatic and asymptomatic infected people are detected, and then be isolated for treatment. This can also reduce the spread of the disease to a certain extent.

Therefore, the optimal control model with two control measures is given by the following differential equations.

$$
\begin{align*}
S' &= \lambda - \mu S - (1 - u_1)S \frac{\beta I}{N}, \\
E' &= (1 - u_1)S \frac{\beta E}{N} - (a_1 + a_2 + \mu)E, \\
A' &= a_1E - (v_1 + v_2 + \mu + u_2\varphi_1 + u_3\varphi_2)A, \\
I' &= a_2E - (v_3 + v_4 + v_5 + v_6 + \mu + u_4\varphi_3 + u_5\varphi_4 + u_6\varphi_5 + u_7\varphi_6)I, \\
T_1' &= (u_2\varphi_1 + v_1)A + (u_4\varphi_3 + v_3)I - (w_1 + \mu)T_1, \\
T_2' &= (u_3\varphi_2 + v_2)A + (u_5\varphi_4 + v_4)I - (w_2 + \mu)T_2, \\
T_3' &= (u_6\varphi_5 + v_5)I - (w_3 + \mu)T_3, \\
T_4' &= (u_7\varphi_6 + v_6)I - (w_4 + \mu + \eta)T_4, \\
R' &= w_1T_1 + w_2T_2 + w_3T_3 + w_4T_4 - \mu R.
\end{align*}
$$

where $\varphi_i, i = 1, \ldots , 6$ indicates the proportion of patients treated after detection by $u_i$, $i = 2, \ldots , 7$, respectively. The control variables $U(t) = (u_1, u_2, u_3, u_4, u_5, u_6, u_7) \in \Theta$ are bounded and measured with

$$\Theta = \{(u_1, u_2, u_3, u_4, u_5, u_6, u_7) \mid u_i(t) \text{ is Lebesgue measurable on } [0, 1], i = 1, 2, 3, 4, 5, 6, 7\}.$$

The purpose of introducing these two control variables is to find the optimal control solution when the number of infected individuals and control cost are minimized. Therefore, the objective function of the control problem is
where \( B_1, B_2, B_3 \) are the weight coefficients relate to infected people. The constants \( C_1, C_2, C_3, C_4, C_5, C_6, C_7 \) are the weight cost coefficients of the control variables \( u_1, u_2, u_3, u_4, u_5, u_6 \) and \( u_7 \). Then we want to obtain the optimal control such that

\[
J(u^*_1, u^*_2, u^*_3, u^*_4, u^*_5, u^*_6, u^*_7) = \min_{(u_1, u_2, u_3, u_4, u_5, u_6, u_7) \in \Theta} J(u_1, u_2, u_3, u_4, u_5, u_6, u_7),
\]

With the help of Pontryagin's maximum principle, we establish the following Hamiltonian function.

\[
H = B_1 E + B_2 A + B_3 I + \frac{C_1}{2} u^2_1 + \frac{C_2}{2} u^2_2 + \frac{C_3}{2} u^2_3 + \frac{C_4}{2} u^2_4 + \frac{C_5}{2} u^2_5 + \frac{C_6}{2} u^2_6 + \frac{C_7}{2} u^2_7
\]

\[
\quad + \lambda_1 \left[ \lambda - \mu S - (1 - u_1) S \frac{\beta_1 E + \beta_2 A + \beta_3 I}{N} \right]
\]

\[
\quad + \lambda_2 \left[ (1 - u_1) S \frac{\beta_1 E + \beta_2 A + \beta_3 I}{N} - (\alpha_1 + \alpha_2 + \mu) E \right]
\]

\[
\quad + \lambda_3 [\alpha_1 E - (v_1 + v_2 + \mu + u_2 \varphi_1 + u_5 \varphi_2) A]
\]

\[
\quad + \lambda_4 [\alpha_2 E - (v_3 + v_4 + v_5 + v_6 + \mu + u_4 \varphi_3 + u_5 \varphi_4 + u_6 \varphi_5 + u_7 \varphi_6) I]
\]

\[
\quad + \lambda_5 [(u_2 \varphi_1 + v_1) A + (u_4 \varphi_3 + v_2) I - (w_1 + \mu) T_1]
\]

\[
\quad + \lambda_6 [(u_3 \varphi_2 + v_2) A + (u_5 \varphi_4 + v_4) I - (w_2 + \mu) T_2]
\]

\[
\quad + \lambda_7 [(u_6 \varphi_5 + v_5) I - (w_3 + \mu) T_3]
\]

\[
\quad + \lambda_8 [(u_7 \varphi_6 + v_6) I - (w_4 + \mu + \eta) T_4]
\]

\[
\quad + \lambda_9 [w_1 T_1 + w_2 T_2 + w_3 T_3 + w_4 T_4 - \mu R],
\]

where \( \lambda_i (i = 1, 2, 3, 4, 5, 6, 7, 8, 9) \) are the adjoint variables. Accordingly, we can get the following adjoint system.
\[ \lambda_6'(t) = -\frac{\partial H}{\partial T_2}(t) \]
\[ = \lambda_6 \mu + (\lambda_6 - \lambda_9)w_2. \]
\[ \lambda_7'(t) = -\frac{\partial H}{\partial T_3}(t) \]
\[ = \lambda_7 \mu + (\lambda_7 - \lambda_9)w_3. \]
\[ \lambda_8'(t) = -\frac{\partial H}{\partial T_4}(t) \]
\[ = \lambda_8 \mu + \eta + (\lambda_8 - \lambda_9)w_4. \]
\[ \lambda_9'(t) = -\frac{\partial H}{\partial R}(t) \]
\[ = \lambda_9 \mu. \]

The terminal condition of the adjoint system is
\[ \lambda_i(t_f) = 0, \quad i = 1, 2, 3, 4, 5, 6, 7, 8, 9. \]  \hspace{1cm} (14)

The optimal controls \( u_1^*, \, u_2^*, \, u_3^*, \, u_4^*, \, u_5^*, \, u_6^*, \, u_7^* \) are given by
\[ u_i^* = \max\{0, \min\{1, \frac{\phi_i^*}{u_i^*}\}\}, \quad i = 1, 2, 3, 4, 5, 6, 7, \]
where
\[ u_1^* = \frac{(\lambda_2 - \lambda_1)S(\beta_1E + \beta_2A + \beta_3I)}{C_1N}, \quad u_2^* = \frac{(\lambda_3 - \lambda_2)\varphi_1A}{C_2}, \quad u_3^* = \frac{(\lambda_3 - \lambda_6)\varphi_2A}{C_3}, \]
\[ u_4^* = \frac{(\lambda_4 - \lambda_3)\varphi_3I}{C_4}, \quad u_5^* = \frac{(\lambda_4 - \lambda_6)\varphi_4I}{C_5}, \quad u_6^* = \frac{(\lambda_4 - \lambda_7)\varphi_5I}{C_6}, \quad u_7^* = \frac{(\lambda_4 - \lambda_8)\varphi_6I}{C_7}. \]

6 | PARAMETER ESTIMATION

6.1 | Data collection

The data in this paper is selected from the official website of Tonghua Health Committee of Jilin Province, China, which publishes the daily case data since January 16, 2021. Because the incubation period of COVID-19 is generally within 14 days, we take the number of cases from January 16, 2021 to January 30, 2021 as our research object. These data can reflect the characteristics of second-wave COVID-19 transmission in Tonghua City when there is some routine epidemic prevention measures without strong government intervention policy.

Figure 2 shows the change of the cumulative confirmed people in the second-wave COVID-19 under the routine epidemic prevention in Tonghua city. From the Figure 2 we can see that their growth trend is obviously different from that of the first-wave COVID-19 outbreak in Wuhan in January 2020. This may be due to the fact that people already have some experience in fighting against the spread of COVID-19. Therefore, the daily health protection can play a very important role in the outbreak of infectious diseases.

6.2 | Parameter estimation method

The daily infection data published on the official website of Tonghua Health Committee is shown in Appendix A. The confirmed cases were divided into four types: mild, common, severe and critical. This is based on different states to determine different treatment options, their recovery probabilities are not the same. Therefore, we use the weighted nonlinear least square method to fit the number of cases treated each day in these four warehouses.
Before parameter estimation, the values of some parameters can be obtained from the existing literature. According to the population statistics report of China in 2020, the average life expectancy of Chinese is 77 years old. So we chose the natural mortality rate $\mu = 1/(77 \times 365)$ per day. The total population of Tonghua City at the end of 2019 is 2.1474 million, so we estimate that the number of births per day is about 76.4. $\eta$ represents the daily mortality due to COVID-19 infection in the critical warehouse. We used the cumulative number of deaths in the sample divided by the cumulative number of confirmed critical cases as the estimation of the death rate. So we suppose $\eta = 7.4515 \times 10^{-3}$.

In this estimation method, the data is fitted by minimizing the weighted error square sum between the estimated values and the reported data. The FMINSEARCH function in MATLAB is used to find the estimated parameters. We set the objective function as follows.

*FIGURE 2* The cumulative confirmed cases per day in China from January 16, 2021 to January 30, 2021 [Color figure can be viewed at wileyonlinelibrary.com]

| Parameters | Descriptions | Values | Source |
|------------|--------------|--------|--------|
| $\Lambda$  | Recruitment rate | 76.4   | Estimated |
| $\mu$      | Natural death rate | $\frac{1}{77} \times \frac{1}{365}$ day$^{-1}$ | $^{32}$ |
| $\beta_1$  | Relative transmissibility of exposed class $E$ | 0.045527 | Fitted |
| $\beta_2$  | Relative transmissibility of asymptomatic class $A$ | 0.444761 | Fitted |
| $\beta_3$  | Relative transmissibility of symptomatic class $I$ | 0.254117 | Fitted |
| $\alpha_1$ | Proportion of disease progression from $E$ to $A$ | 0.130700 | Fitted |
| $\alpha_2$ | Proportion of disease progression from $E$ to $I$ | 0.035127 | Fitted |
| $v_1$      | Rate of moving from $A$ to $T_1$ | 0.056832 | Fitted |
| $v_2$      | Rate of moving from $A$ to $T_2$ | 0.375067 | Fitted |
| $v_3$      | Rate of moving from $I$ to $T_1$ | 0.145330 | Fitted |
| $v_4$      | Rate of moving from $I$ to $T_2$ | 0.770234 | Fitted |
| $v_5$      | Rate of moving from $I$ to $T_3$ | 0.294667 | Fitted |
| $v_6$      | Rate of moving from $I$ to $T_4$ | 0.174561 | Fitted |
| $w_1$      | The recovery rate in $T_1$ | 0.054994 | Fitted |
| $w_2$      | The recovery rate in $T_2$ | 0.382655 | Fitted |
| $w_3$      | The recovery rate in $T_3$ | 0.086252 | Fitted |
| $w_4$      | The recovery rate in $T_4$ | 0.108301 | Fitted |
| $\eta$     | The death rate due to infection with COVID-19 in $T_4$ | 0.007452 | Estimated |
\[ J = W_1 \sum_{i=1}^{n} [(T_1)_i - (\tilde{T}_1)_i]^2 + W_2 \sum_{i=1}^{n} [(T_2)_i - (\tilde{T}_2)_i]^2 + W_3 \sum_{i=1}^{n} [(T_3)_i - (\tilde{T}_3)_i]^2 + W_4 \sum_{i=1}^{n} [(T_4)_i - (\tilde{T}_4)_i]^2, \] (15)

FIGURE 3  Fitting diagram of cumulative reported cases from January 16, 2021 to January 30, 2021 [Color figure can be viewed at wileyonlinelibrary.com]

FIGURE 4  Fitting diagram of the reported number of mild treated \((T_1)\), common treated \((T_2)\), severe treated \((T_3)\) and critical treated \((T_4)\) cases from January 16, 2021 to January 30, 2021 [Color figure can be viewed at wileyonlinelibrary.com]
where $T_1, T_2, T_3, T_4$ is the estimated number of mild treated, common treated, severe treated and critical treated compartment; $\tilde{T}_1, \tilde{T}_2, \tilde{T}_3, \tilde{T}_4$ is the reported number of mild treated, common treated, severe treated and critical treated compartment; $W_i, (i = 1, 2, 3, 4)$ is the weight coefficient in each compartment, and the value of $W_i$ is the reciprocal of the sample point variance. The selection of weight can effectively reduce the fitting deviation caused by the difference in the order of magnitude of different warehouses’ data. To estimate the parameters of the model, we need to minimize the following objective function.

\[
\begin{align*}
\min J \\
\text{subject to system (2)}.
\end{align*}
\]  

6.3 | Fitting results

By using the parameter estimation method mentioned above in MATLAB, the estimated values of all parameters are shown in Table 2. The comparison between the fitting results and the reported data is shown in Figures 3 and 4.

The blue asterisks in Figure 3 represent the reported confirmed case, and the pink lines represent simulated results. Figure 4A shows the simulation results of mild confirmed cases; Figure 4B shows the simulated results of the common confirmed cases; Figure 4C shows the simulation results of the severe confirmed cases. Simulation results of the critical confirmed cases are shown in Figure 4D. From Figures 3 and 4, we can see that the simulated results are very close to the real data in each compartment, and the simulated results are relatively reliable.

We substitute the fitted parameter values in Table 2 into the basic reproduction number and get that $R_0 = 1.0695$. From a biological point of view, because the value of the basic reproduction number is slightly greater than 1, the disease will gradually spread in the population.

![FIGURE 5](https://www.wileyonlinelibrary.com) The effect of strategy A on the Exposed $E(t)$, Asymptomatic $A(t)$ and Symptomatic infectious class $I(t)$ [Color figure can be viewed at wileyonlinelibrary.com]
In view of the first large-scale COVID-19 outbreak in Wuhan, China in early 2020, many scholars considered different factors and established mathematical models of different forms of COVID-19 transmission.25–30 Through the fitting of official data, the basic reproduction number of different models is estimated, which is roughly distributed between 2.5 and 6.6.

In the second-wave of COVID-19 outbreak, the basic reproduction number has been greatly reduced compared with the first-wave of COVID-19. Therefore, some self-protection measures that people establish in their daily life are effective. At the same time, however, we can also see that the second wave of COVID-19 will still emerge in the population under current prevention and control measures. Therefore, some control measures should be implemented in time to avoid a large-scale epidemic.

7 | OPTIMAL CONTROL

Based on the above simulation of the second-wave epidemic situation in Tonghua City, Jilin Province, with the help of the knowledge of optimal control theory, we consider two most common control means in the model to explore its optimal control problem.

The solution of system (11) is solved numerically by using the forward-backward sweep method with RK4 method.33 The parameter values in system (11) are shown in Table 2. The time interval is [0, 30] days. The selection of weight coefficient and conversion coefficient is as follows. $B_1 = 5$, $B_2 = 20$, $B_3 = 40$, $C_1 = 20$, $C_2 = 40$, $C_3 = 60$, $C_4 = 15$, $C_5 = 25$, $C_6 = 6$, $C_7 = 2$, $\varphi_1 = 0.15$, $\varphi_2 = 0.38$, $\varphi_3 = 0.06$, $\varphi_4 = 0.14$, $\varphi_5 = 0.02$, $\varphi_6 = 0.01$. It is worth noting that the weight coefficient values taken in the simulation are theoretical values, because they are only used to implement the control

![Figure 6](https://wileyonlinelibrary.com)
strategy formulated in this section. Due to the influence of objective factors, the maximum value of control force is set to 0.9. In order to further explore the control effect of the control measures, we design the following three control strategies.

Strategy A: Using only isolation (i.e., \( u_1 \neq 0 \), and \( u_i = 0 \), \( i = 2, \ldots, 7 \))

Strategy B: Using only detection (i.e., \( u_1 = 0 \), and \( u_i \neq 0 \), \( i = 2, \ldots, 7 \))

Strategy C: Using isolation and detection (i.e., \( u_1 \neq 0 \), and \( u_i \neq 0 \), \( i = 2, \ldots, 7 \))

Strategy A: Using only isolation \( u_1 \neq 0 \)

In this strategy, only additional isolation measures are considered to control the spread of the disease. In Figure 5A–C, the blue line represents the change trend of the number of warehouse people without control, while the pink dotted line represents the change trend of the number of warehouse people under the control of strategy A. Figure 5D shows the control strength of isolation measures. The maximum isolation intensity should be maintained from the beginning until the 28th day, and then gradually reduced to 0.

From Figure 5A–C, we can see that in the absence of control, the number of people in all infected compartments will continue to increase. Under the control of Strategy A, the population of all infected compartments will immediately begin to decrease, and by day 30, it will be almost zero. This shows that isolation measures can effectively inhibit the spread of the disease. As shown in Figure 5D, the intensity of quarantine measures can be gradually reduced as the number of infected people drops to almost zero. This dynamic adjustment can reduce costs accordingly.

Strategy B: Using only detection \( u_i \neq 0 \), \( i = 2, \ldots, 7 \)

In this strategy, only additional detection is considered to control the spread of the disease. The control effect of the detection measure is shown in Figure 6. Similarly, in Figure 6A–C, the blue line represents the change trend of the number of infected compartments without control, while the dotted pink line represents the change trend of the number of infected compartments under the control of strategy B. Figure 6D shows the optimal control strength of the control variables. \( u_2-u_7 \) control variables maintained the maximum control intensity at the beginning, which lasted until day 28, day 29, day 12, day 17, day 8, and day 15, respectively, and then gradually decreased to 0.

FIGURE 7 The effect of strategy C on the Exposed \( E(t) \), Asymptomatic \( A(t) \) and Symptomatic infectious class \( I(t) \) [Color figure can be viewed at wileyonlinelibrary.com]
It can be seen from Figure 6A–C that the number of people infected in the warehouse will be greatly reduced compared with that without control measure. By comparing Figures 6A–C and 5A–C, it can be found that asymptomatic infected persons in Figure 6B will decline faster than Figure 5B under the implementation of detection measures. This is consistent with the actual situation, and it is through nucleic acid testing that we find asymptomatic infected people and then send them to hospital for treatment. However, in Figures 6A and 6C, we found that the detection measures of strategy B had little effect on exposed persons and symptomatic infected persons.

**Strategy C: Using isolation and detection** $u_1 \neq 0, u_i \neq 0, (i = 2, \ldots, 7)$

In this strategy, additional isolation and detection measures are considered to control the spread of the disease. The comparison between the control effect of strategy C and the effect of without control is shown in Figure 7. In Figure 7A–C, we can see that compared with Figures 5 and 6, the number of infected people not only decreases faster, but also decreases more greatly. Figure 7D shows the change of the optimal control strength of the control variable. The results show that if the control measures are implemented in strict accordance with the control strength in Figure 7D, the spread of the virus can be inhibited as much as possible.

In the optimal control strategy we seek, we should not only minimize the number of infected people, but also minimize the objective function $J$ in (12). In order to distinguish each control strategy more clearly, we show the data of each strategy in Table 3.

From the data of infection averted ratio (IAR) in Table 3, we can see that strategy C has the highest rate of avoiding infection. From the value of objective function in the last column of Table 3, we can also see that the objective function of strategy C is the smallest. Therefore, we consider strategy C as the optimal control strategy.

### 8 | CONCLUSION

Since the first imported case of COVID-19 was found in Tonghua City on January 11, 2021, 282 cases of COVID-19 were confirmed by January 30, 2021. These confirmed cases were divided into four types according to the degree of infection, and different treatment schemes were arranged according to different types.

In this paper, based on the existing SEAITR mathematical model, according to the treatment classification of the actual situation, a more realistic dynamic model of the second-wave COVID-19 was established. Then we studied the basic properties, stability of the equilibria and the basic reproduction number of the model. With the help of the optimal control theory, the isolation method of keeping social distance and the control method of nucleic acid detection in the whole city were added to the model, and the expression of the optimal control pair was obtained.

In parameter estimation, we first selected the number of cases of four confirmed types reported from January 16, 2021 to January 30, 2021 as the sample of parameter estimation. The weighted nonlinear least square estimation method was used to fit the data of four confirmed warehouses, and the estimated values of parameters were obtained. The results show that the basic reproduction number $R_0 = 1.0695$, which is much smaller than the basic reproduction number in Wuhan in early 2020. This should be attributed to the fact that people already have some understanding and awareness of the virus, as well as the protective measures people take in social activities.

Finally, in the optimal control process, we designed three control strategies to explore the effect of control measures. Through the simulation of the three control strategies, the control results and dynamic changes of control variables were obtained. Then through the data of infection averted ratio and the objective function, the optimal control strategy was strategy C. The results show that if the two control measures are implemented according to the optimal control strength in Figure 7D, more people can be prevented from being infected to the greatest extent. These results not only provided suggestions for health management departments to control the outbreak of the second-wave COVID-19 but also provided a reference for other regions or countries.
It is worth mentioning that the ordinary differential equation is established on the basis of ignoring spatial factors. Spatial effects play an important role in the spread of disease. In order to get closer to reality, the evolution of biological systems in space must be considered further. In recent years, many scholars have proposed many important theories and methods to solve space biodynamic systems, which have made important contributions to the analysis and control of the spatial spread of infectious diseases. It will be very interesting to consider the spatial factor further on the basis of the COVID-19 transmission issue in this paper. We leave it for the future.

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CONFLICT OF INTEREST
There are no conflicts of interest by the authors.

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**APPENDIX A: AVAILABILITY OF DATA AND MATERIALS**

Data of confirmed cases in Tonghua City, Jilin Province, China in January 2021.