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The impact of vaccination on the spread of COVID-19: Studying by a mathematical model

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\textbf{A B S T R A C T}

The global spread of COVID-19 has not been effectively controlled, posing a huge threat to public health and the development of the global economy. Currently, a number of vaccines have been approved for use and vaccination campaigns have already started in several countries. This paper designs a mathematical model considering the impact of vaccination to study the spread dynamics of COVID-19. Some basic properties of the model are analyzed. The basic reproductive number $\mathcal{R}_0$ of the model is obtained, and the conditions for the existence of endemic equilibria are provided. There exist two endemic equilibria when $\mathcal{R}_0 < 1$ under certain conditions, which will lead to backward bifurcation. The stability of equilibria are analyzed, and the condition for the backward bifurcation is given. Due to the existence of backward bifurcation, even if $\mathcal{R}_0 < 1$, COVID-19 may remain prevalent. Sensitivity analysis and simulations show that improving vaccine efficacy can control the spread of COVID-19 faster, while increasing the vaccination rate can reduce and postpone the peak of infection to a greater extent. However, in reality, the improvement of vaccine efficacy cannot be realized in a short time, and relying only on increasing the vaccination rate cannot quickly achieve the control of COVID-19. Therefore, relying only on vaccination may not completely and quickly control COVID-19. Some non-pharmaceutical interventions should continue to be enforced to combat the virus. According to the sensitivity analysis, we improve the model by including some non-pharmaceutical interventions. Combining the sensitivity analysis with the simulation of the improved model, we conclude that together with vaccination, reducing the contact rate of people and increasing the isolation rate of infected individuals will greatly reduce the number of infections and shorten the time of COVID-19 spread. The analysis and simulations in this paper can provide some useful suggestions for the prevention and control of COVID-19.

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1. Introduction

“Coronavirus disease 2019” (COVID-19) \cite{1}, a pneumonia epidemic caused by a new type of coronavirus named “Severe Acute Respiratory Syndrome-related Coronavirus type 2” (SARS-CoV-2) \cite{2}, remains a serious global issue since its...
emergence at the end of 2019. For more than a year, COVID-19 has not been effectively controlled, and the numbers of new cases remain at some of the highest levels currently [3]. According to the report by World Health Organization (WHO), as of 21 June, 2021, the cumulative number of confirmed cases worldwide reached 177,108,695, and the cumulative number of deaths stood at 3,840,223 [4]. The COVID-19 pandemic poses a serious threat to public health and economic challenges across the world. Three variants of SARS-CoV-2, Alpha (VOC 202012/01), Beta (501Y.V2) and Gamma (P.1), were identified in the United Kingdom, South Africa and Brazil a few months ago, respectively. Their contagion rate has been confirmed to be higher, aggravating the spread of COVID-19 in multiple countries [5,6]. Recently, India has suffered from a rapid surge of COVID-19 infection. From April 22 to May 16, there have been more than 300,000 new confirmed cases in a single day in India for 25 consecutive days [4]. The new variant Delta (B.1.617) [5], which has a so-called double mutation, is thought to be fueling India’s deadlier new wave of cases that has made it the world’s second worst-hit country, surpassing Brazil [7].

Since there is no specific medicine, in order to curb the spread of COVID-19, countries mainly adopted non-pharmaceutical intervention measures in the early stage, including contact-tracking, social-distancing, isolating and treating infected persons, lockdown, etc. However, these measures cause a lot of inconvenience to people’s lives and seriously hinder the development of economy. Therefore, in order to develop economy, many countries relaxed these interventions when the COVID-19 epidemic slowed down. As a result, the spread of COVID-19 has not been completely controlled. In order to thoroughly control the spread of COVID-19 and reduce the impact on economic development, people are looking forward to the development and use of effective vaccines. Vaccination is an effective means to control the spread of an epidemic. Through unremitting efforts of all parties, some vaccines have been approved for use, which brings hope to the complete control of the spread of COVID-19.

Can the COVID-19 epidemic be completely eliminated by vaccination? Here we analyze it by designing a mathematical model. Mathematical models are important tools for predicting and simulating the spread of epidemics, and can provide a theoretical basis for decision-makers to formulate various epidemic prevention measures. There are many mathematical models related to the spread of COVID-19, such as those in [8–18]. There are also some studies on the impact of vaccination on the spread of COVID-19. In [19], the impact of a hypothetical imperfect vaccine on the control of COVID-19 in the United States is studied using a mathematical model. A new SIRV model is proposed to forecast and simulate the COVID-19 epidemic evolution under the effect of vaccination in [20]. In [21], a mathematical model is presented to study the impacts of drugs (vaccination with perfect efficacy) and non-drug prevention measures on the spread of COVID-19 in South Africa. A detailed agent-based model is proposed to study the impact of various prevention and control measures on the spread of COVID-19 in Luxembourg, including testing, contact tracing, lockdown, curfew and vaccination [22]. In [23], utilizing a modified SIR model and using relevant data of COVID-19 in Ontario, Canada, different vaccination strategies are simulated and compared, including without vaccination. The authors believe that non-pharmacological interventions should be continued in the early stage of vaccination and gradually relaxed. In [24], a mathematical model considering vaccination is established to analyze the spread of COVID-19. The authors point out that due to the slow COVID-19 vaccination rate, non-drug prevention and control measures still need to be enforced until a sufficient proportion of the population is vaccinated. There are also some studies discussing vaccination prioritization strategies, such as [25–28]. In this paper, we present a SVAIRS (susceptible–vaccinated–asymptomatic–symptomatic–removed–susceptible) model to analyze whether the COVID-19 epidemic can be completely eliminated by vaccination alone. By analyzing the basic reproductive number of the model and the existence of the equilibria, as well as the stability of the equilibria and backward bifurcation, we theoretically prove that relying on vaccination alone may not completely control the COVID-19 epidemic. It is still necessary to properly enforce some non-pharmaceutical intervention measures.

This paper is organized as follows. A mathematical spread model of COVID-19 considering only vaccination is presented in Section 2. The basic reproductive number is obtained and the existence conditions of the endemic equilibria are given in Section 3. In Section 4, the stability of the equilibria is analyzed and the condition for backward bifurcation of the model is given. Numerical simulation and sensitivity analysis are done in Section 5. The last Section concludes this paper.

2. Modeling

Vaccines are vital to the control of an epidemic. At present, a number of COVID-19 vaccines have been used worldwide. In order to study whether relying solely on vaccination can control the spread of COVID-19, we consider vaccination alone without other prevention and control measures. According to the classic deterministic mathematical spread model SVIR [29], and considering the spread characteristics of COVID-19, we divide the total population into five groups, as shown in Table 1. Here we do not consider the population in the incubation period. Since the incubation period of COVID-19 is short and people in the incubation period are also infectious, we merge the incubation period into the asymptomatic infection period. According to the actual situation, the following assumptions are made:

(i) Only susceptible individuals are vaccinated.
(ii) COVID-19 vaccines are imperfect; that is, some of the vaccinated individuals can become infected and infectious even though they have been vaccinated.
(iii) Asymptomatic individuals will experience symptoms or recover after a period of time.
(iv) Symptomatic individuals will either recover or die after a period of time.
Table 1
Population classification.

| Group       | Symbol | Description                                                                                           |
|-------------|--------|-------------------------------------------------------------------------------------------------------|
| susceptible | S      | People who do not have antibodies and are easily infected by COVID-19                                 |
| vaccinated  | V      | People who have been vaccinated against COVID-19                                                      |
| asymptomatic| A      | People who are infected but do not have any symptoms                                                  |
| symptomatic | I      | People who have obvious symptoms after being infected                                                 |
| removed     | R      | People who have recovered from infection or died as a result of infection                             |

Fig. 1. The state transformation process of individuals, where \( \lambda_1 = \frac{\alpha(I + \beta A)}{N} \), \( \lambda_2 = \frac{\rho \alpha(I + \beta A)}{N} \), \( \delta_1 = \theta \delta \) and \( \delta_2 = (1 - \theta) \delta \).

Table 2
Description of parameters.

| Parameter | Description                                           | Value          | Source          |
|-----------|-------------------------------------------------------|----------------|-----------------|
| \( \alpha \) | Transmission rate of symptomatic individuals          | 0.8883         | [13]            |
| \( \beta \) | Correction factor for transmission rate of asymptomatic individuals | 0.45           | [13]            |
| \( \tau \) | Vaccination rate                                       | 0.01/day       | Assume          |
| \( 1 - \rho \) | Vaccine efficacy                                       | 0.8            | Assume          |
| \( 1/\delta \) | Average time of asymptomatic duration                 | 7 days         | [14]            |
| \( \theta \) | Proportion of asymptomatic individuals who develop to symptomatic cases | 0.2            | [14]            |
| \( 1 - \theta \) | Proportion of asymptomatic individuals who recover    | 0.8            | [14]            |
| \( 1/\sigma \) | Average removal time for symptomatic individuals      | 10 days        | Assume          |
| \( \gamma \) | Immunization loss rate                                 | 0.005/day      | Assume          |
| \( \mu \) | Natural death rate                                     | 0.000003349/day | [13]            |
| \( M \) | Birth/recruitment rate into the population             | 1500/day       | Assume          |

(v) Individuals who have recovered from COVID-19 infection will produce antibodies; however, after a period of time, the antibodies will weaken or disappear and the recovered people will become susceptible again.

(vi) New individuals, including birth and recruitment, are susceptible.

Based on the above assumptions, the transmission relationship of various groups of people is shown in Fig. 1, and the descriptions of parameters are shown in Table 2. The mathematical spread model of COVID-19 is as follows:

\[
\begin{align*}
\frac{dS}{dt} &= -\mu S - \frac{\alpha(I + \beta A)S}{N} - \gamma R \\
\frac{dV}{dt} &= \tau S - \frac{\rho \alpha(I + \beta A)V}{N} - \mu V \\
\frac{dA}{dt} &= \frac{\alpha(I + \beta A)S}{N} + \frac{\rho \alpha(I + \beta A)V}{N} - \delta A - \mu A \\
\frac{dI}{dt} &= \theta \delta A - \sigma I - \mu I \\
\frac{dR}{dt} &= (1 - \theta) \delta A + \sigma I - \gamma R - \mu R
\end{align*}
\]

with the initial condition \((S(0), V(0), A(0), I(0), R(0)) \geq 0\), where \( S, V, A, I \) and \( R \) are the abbreviations of the state variables \( S(t), V(t), A(t), I(t) \) and \( R(t) \), respectively, representing the number of various groups of people at time \( t \). \( N = S + V + A + I + R \) is the total population.
Model (1) has the following properties:

**Proposition 2.1.** For the given initial condition \((S(0), V(0), A(0), I(0), R(0)) > 0\), the solution of system (1) satisfies \((S(t), V(t), A(t), I(t), R(t)) > 0\) for all \(t > 0\).

**Proof.** We prove the proposition by contradiction. If not, there exists \(t_1 > 0\) such that at least one of \(S(t), V(t), A(t), I(t)\) and \(R(t)\) is non-positive. The continuity of the solution implies that there exists \(t_0\) such that at least one of \(S(t_0), E(t_0), Q(t_0), A(t_0), I(t_0), J(t_0)\) and \(R(t_0)\) is equal to 0. Without loss of generality, we assume that \(t_0\) is the minimal time with such property.

(a) If \(S(t_0) = 0\), then the rest of the state variables are non-negative at \(t_0\), and \(\frac{dS}{dt}|_{t=t_0} = M + \gamma R(t_0) > 0\), which implies that there exists \(\epsilon > 0\) such that \(S(t)\) is strictly monotone increasing in interval \((t_0 - \epsilon, t_0 + \epsilon)\). Let \(t_2 \in (t_0 - \epsilon, t_0)\). Then \(S(t_2) < S(t_0) = 0\), and since \(S(0) > 0\), there exists \(t_3 \in (0, t_2)\) such that \(S(t_3) = 0\) by Bolzano’s theorem, which contradicts the assumption of \(t_0\).

(b) If \(S(t_0) > 0\) and \(V(t_0) = 0\), then \(\frac{dV}{dt}|_{t=t_0} = \tau S(t_0) > 0\). Similar to (a), we can obtain a contradiction.

(c) If \(S(t_0) > 0, V(t_0) > 0\) and \(A(t_0) = 0\), then
\[
\frac{dA}{dt}|_{t=t_0} = \underbrace{\alpha(S(t_0) + \rho V(t_0))}_{N(t_0)} I(t_0) > 0.
\]

There are two cases:

(1) \(I(t_0) > 0\). Then \(\frac{dI}{dt}|_{t=t_0} > 0\), which is a contradiction similar to (a).

(2) \(I(t_0) = 0\). Then \(\frac{dI}{dt}|_{t=t_0} = 0\). It is easy to know that \(A(t) = 0\) for all \(t \geq 0\) is the solution with \(A(0) = 0\). This is a contradiction to the uniqueness of the solution since \(A(0) > 0\) and \(A(t_0) = 0\).

(d) If \(S(t_0) > 0, V(t_0) > 0, A(t_0) > 0\) and \(I(t_0) = 0\), then \(\frac{dR}{dt}|_{t=t_0} = \theta \delta A(t_0) > 0\). Also similar to (a), a contradiction can be obtained. Similarly, \(R(t_0) = 0\) will lead to a contradiction. Thus, we have \(S(t), V(t), A(t), I(t)\) and \(R(t)\) are all positive for all \(t > 0\). □

**Proposition 2.2.** System (1) is bounded.

**Proof.** Adding up all equations of system (1) yields
\[
\frac{dN}{dt} = M - \mu N.
\]
Its solution is \(N(t) = \frac{M}{\mu} + \left(N(0) - \frac{M}{\mu}\right)e^{-\mu t}\). Note that \(t \in [0, +\infty)\), we have \(0 < N(t) \leq \max\left\{\frac{M}{\mu}, N(0)\right\} = \hat{M}. □

**Remark 1.** By Propositions 2.1 and 2.2, the set
\[
\Omega = \left\{(S, V, A, I, R) : (S, V, A, I, R) \geq 0, S + V + A + I + R \leq \hat{M}\right\}
\]
is a positively invariant set of system (1).

3. Equilibria and basic reproductive number

In this section, we analyze the equilibria (including disease-free equilibrium and endemic equilibria) and the basic regenerative number of system (1). In order to find equilibriums, let
\[
\begin{align*}
M - \tau S - \frac{\alpha(I + \beta A)S}{N} - \mu S + \gamma R &= 0, \\
\tau S - \frac{\rho \alpha(I + \beta A)V}{N} - \mu V &= 0, \\
\frac{\alpha(I + \beta A)S}{N} + \frac{\rho \alpha(I + \beta A)V}{N} - \delta A - \mu A &= 0, \\
\delta_1 A - \sigma I - \mu I &= 0, \\
\delta_2 A + \sigma I - \gamma R - \mu R &= 0,
\end{align*}
\]
where \(\delta_1 = \theta \delta, \delta_2 = (1 - \theta)\delta\).

The so-called disease-free equilibrium is the equilibrium where the infected person is 0. Let \(A = 0\), and it can be obtained \(I = R = 0\) by the last two equations of Eqs. (2). Substituting them into the first two equations of (2), we have
\[
S^0 = \frac{M}{\tau + \mu}, \quad V^0 = \frac{\tau}{\mu} S^0.
\]
Thus, the disease-free equilibrium is \(P_0 = (S^0, V^0, 0, 0, 0)\), and \(N^0 = S^0 + V^0 = \frac{M}{\mu}\).
We use the next-generation approach [30,31] to calculate the basic reproductive number. The equations related to infection are the 3rd and the 4th in system (1). Thus, let

\[
F = \begin{pmatrix} \frac{\alpha \beta S}{N} + \frac{\beta S}{N} & \alpha k_1 \\ 0 & 0 \end{pmatrix}, \quad V = \begin{pmatrix} (\delta + \mu)A \\ -\delta A + (\sigma + \mu) \end{pmatrix}.
\]

The Jacobian matrices of \( F \) and \( V \) at \( P_0 \) are

\[
\tilde{F} = \begin{pmatrix} \alpha \beta k_1 & \alpha k_1 \\ 0 & 0 \end{pmatrix}, \quad \tilde{V} = \begin{pmatrix} \delta + \mu & 0 \\ -\delta_1 & \sigma + \mu \end{pmatrix},
\]

where

\[
k_1 = \frac{S^0 + \rho V^0}{N^0} = \frac{\mu + \rho \tau}{\tau + \mu} < 1.
\]

Then we have

\[
\tilde{V}^{-1} = \frac{1}{(\delta + \mu)(\sigma + \mu)} \begin{pmatrix} \alpha \mu \delta_1 & \delta_1 \\ \delta + \mu & \delta + \mu \end{pmatrix},
\]

and the basic reproductive number of vaccination is

\[
\mathcal{R}_1 = \rho(\tilde{F} \tilde{V}^{-1}) = \alpha k_1 \left[ \frac{\beta}{\delta + \mu} + \frac{\delta_1}{\delta + \mu} \right],
\]

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

The basic reproductive number of vaccination refers to the number of people infected by an infected individual during the average infection period. Expand \( \mathcal{R}_1 \) as follows

\[
\mathcal{R}_1 = \frac{\alpha \beta \mu}{(\delta + \mu)(\tau + \mu)} + \frac{\alpha \beta \rho \tau}{(\delta + \mu)(\tau + \mu)} + \frac{\alpha \mu \delta_1}{(\delta + \mu)(\sigma + \mu)(\tau + \mu)} + \frac{\alpha \rho \tau \delta_1}{(\delta + \mu)(\sigma + \mu)(\tau + \mu)},
\]

and each part has its specific meaning. \( \frac{\alpha \beta S}{N} \) represents the infected number of susceptible individuals per unit time for asymptomatic individuals. Thus the infected number of susceptible individuals per unit time for one asymptomatic individual is \( \frac{\alpha S^0}{N^0} \). Note that the proportion of susceptible individuals in the disease-free population is \( \frac{S}{N} = \frac{\mu}{\tau + \mu} \) and the average time of asymptomatic duration is \( \frac{1}{\tau + \mu} \). The first term in \( \mathcal{R}_1 \), \( \frac{\alpha \beta \mu}{(\tau + \mu)} \), gives the average infected number of susceptible individuals for one asymptomatic individual. Similarly, the second term \( \frac{\alpha \beta \rho \tau}{(\tau + \mu)} \) gives the average infected number of vaccinated individuals for one asymptomatic individual, \( \frac{\alpha S^0}{N^0} \) gives the average infected number of susceptible individuals per unit time for symptomatic individuals. Therefore, the infected number of susceptible individuals per unit time for one asymptomatic individual is \( \frac{\alpha S^0}{N^0} \). Since the average duration of symptoms is \( \frac{1}{\tau + \mu} \) and asymptomatic individuals develop into symptomatic with proportion \( \frac{\delta_1}{\tau + \mu} \) per unit time, the third item \( \frac{\alpha \mu \delta_1}{(\tau + \mu)(\sigma + \mu)(\tau + \mu)} \) gives the average infected number of susceptible individuals for one symptomatic individual. Similarly, the last term in \( \mathcal{R}_1 \) gives the average infected number of vaccinated individuals for one symptomatic individual.

If not vaccinated, i.e., \( \tau = 0 \), the basic reproductive number is

\[
\mathcal{R}_0 = \alpha \left[ \frac{\beta}{\delta + \mu} + \frac{\delta_1}{(\delta + \mu)(\sigma + \mu)} \right],
\]

which is called the basic reproductive number in the absence of vaccination. It is not difficult to see that \( \mathcal{R}_1 \) is a decreasing function of \( \tau \), which means the larger the vaccination rate \( \tau \), the smaller the basic reproductive number of vaccination \( \mathcal{R}_1 \). This also indicates that vaccination plays an important role in controlling the spread of COVID-19. On the other hand, we have

\[
\lim_{\tau \to \infty} \mathcal{R}_1 = \rho \mathcal{R}_0.
\]

It can be seen that if the efficacy of the COVID-19 vaccine is not high (\( \rho \) is large), even if everyone is vaccinated, it may not be possible to make the basic reproductive number of vaccination \( \mathcal{R}_1 \) to be less than 1, which means that COVID-19 cannot be eliminated. Therefore, the efficacy of the vaccines is also critical.

**Remark 2.** When \( \rho \mathcal{R}_0 < 1 \) or the efficacy of the vaccine \( 1 - \rho > 1 - \frac{1}{\mathcal{R}_0} \), the COVID-19 epidemic might be controlled by vaccination. In order to make \( \mathcal{R}_1 < 1 \), the vaccination rate \( \tau \) must satisfy

\[
\tau > \frac{\mu(\mathcal{R}_0 - 1)}{1 - \rho \mathcal{R}_0}.
\]

The remainder of this section discusses the existence of endemic equilibria. Adding up all equations of (2) yields

\[
M - \mu N = 0,
\]
which implies that $N = N^0 = \frac{M}{\mu}$ when the system is in equilibrium. Assume $A > 0$. Divide all equations in (2) by $N$, and let
\[
\frac{s}{N} = \frac{V}{N}, \quad \frac{a}{N} = \frac{A}{N}, \quad \frac{i}{N} = \frac{l}{N}, \quad \frac{r}{N} = \frac{R}{N}.
\]
Then in equilibrium, (2) becomes
\[
\begin{align*}
\mu - \tau s - a(i + \beta a)s - \mu s + \gamma r &= 0 \\
\tau s - \rho a(i + \beta a)v - \mu v &= 0 \\
\alpha(i + \beta a)s + \rho a(i + \beta a)v - \delta a - \mu a &= 0 \\
\delta_1 a - \sigma i - \mu i &= 0 \\
\delta_2 a + \sigma i - \gamma r - \mu r &= 0
\end{align*}
\] (4)

From the last two equations of (4), we obtain
\[
\begin{align*}
i &= \frac{\delta_1}{\sigma + \mu}, \\
r &= \frac{\delta_2 + a + \sigma i}{\gamma + \mu} = \frac{\delta_2(\sigma + \mu) + \sigma \delta_1}{(\gamma + \mu)(\sigma + \mu)} a = \frac{\sigma \delta + \delta_2 \mu}{(\gamma + \mu)(\sigma + \mu)} a = \eta r a,
\end{align*}
\] (5)

and
\[
\alpha(i + \beta a) = \alpha \left( \frac{\delta_1}{\sigma + \mu} + \beta \right) a = \eta a,
\]
where
\[
\eta = \alpha \left( \frac{\delta_1}{\sigma + \mu} + \beta \right) = \frac{\delta + \mu}{k_1} \eta_1.
\]

By the first two equations of (4), we have
\[
\begin{align*}
s &= \frac{\mu + \gamma r}{\eta a + \tau + \mu} = \frac{\mu + \gamma \eta a}{\eta a + \tau + \mu}, \\
v &= \frac{\tau s}{\rho \eta a + \mu}.
\end{align*}
\] (6)

Substituting (5) and (6) into the third equation of (4), and eliminating $a(a \neq 0)$, we obtain
\[
\eta \frac{\mu + \gamma \eta a}{\eta a + \tau + \mu} + \rho \eta \frac{\tau (\mu + \gamma \eta a)}{(\rho \eta a + \mu)(\eta a + \tau + \mu)} = \delta + \mu.
\]

Expanding the above formula and dividing both sides by $\eta$, we get a quadratic equation about $a$.
\[
b_2 a^2 + b_1 a + b_0 = 0,
\] (7)

where
\[
\begin{align*}
b_2 &= \eta \rho (\delta + \mu - \gamma \eta a) = \frac{(\delta + \mu)^2 \rho}{k_1} \left( 1 - \frac{\gamma \eta_1}{\delta + \mu} \right) \eta_1, \\
b_1 &= (\delta + \mu)[\rho(\tau + \mu) + \mu] - \gamma \eta_1(\mu + \rho \tau) - \rho \eta \mu = \frac{(\delta + \mu) \rho \mu}{k_1} (\eta_1^* - \eta_1), \\
b_0 &= \frac{\mu(\delta + \mu)(\tau + \mu)}{\eta} - \mu(\mu + \rho \tau) = \mu(\mu + \rho \tau) \left( \frac{1}{\eta_1} - 1 \right)
\end{align*}
\] (8)

and
\[
\eta_1^* = \frac{k_1}{\rho \mu} \left[ \rho \mu + (\rho \tau + \mu) \left( 1 - \frac{\gamma \eta_1}{\delta + \mu} \right) \right].
\]

Noticing that $\delta = \delta_1 + \delta_2 > \delta_2$, we have
\[
1 - \frac{\gamma \eta_1}{\delta + \mu} = 1 - \frac{\gamma \delta_2(\sigma + \mu) + \sigma \delta_1}{\delta + \mu (\gamma + \mu)(\sigma + \mu)} = 1 - \frac{\gamma \delta_2 \mu + \sigma \delta}{\gamma + \mu (\delta + \mu)(\sigma + \mu)} > 1 - \frac{\gamma \delta}{\gamma + \mu \delta + \mu} > 0,
\] (11)

which implies that
\[
\eta_1^* - k_1 = \frac{k_1(\mu + \rho \tau)}{\rho \mu} \left( 1 - \frac{\gamma \eta_1}{\delta + \mu} \right) > 0.
\] (12)
The discriminant of quadratic Eq. (7) is
\[ \Delta = b_1^2 - 4b_0b_2 \]
\[ = \left[ \frac{(\delta + \mu)\rho \mu}{k_1} (\mathcal{R}_1^* - \mathcal{R}_1) \right]^2 - \frac{4(\delta + \mu)^3 \rho \mu (\mu + \rho \tau)}{k_1} \left( 1 - \frac{\gamma \eta r}{\delta + \mu} \right) (1 - \mathcal{R}_1) \]
\[ = \left[ \frac{(\delta + \mu)\rho \mu}{k_1} \right]^2 \left[ (\mathcal{R}_1^* - \mathcal{R}_1)^2 - \frac{4k_1 (\mu + \rho \tau)}{\rho \mu} \left( 1 - \frac{\gamma \eta r}{\delta + \mu} \right) (1 - \mathcal{R}_1) \right] \]
\[ = \left[ \frac{(\delta + \mu)\rho \mu}{k_1} \right]^2 \left[ (\mathcal{R}_1^* - \mathcal{R}_1)^2 - 4 (\mathcal{R}_1^* - k_1) (1 - \mathcal{R}_1) \right] \]
\[ = \frac{(\delta + \mu)\rho \mu}{k_1} (\mathcal{R}_1^* - \mathcal{R}_1 + 2(\mathcal{R}_1^* - k_1) \mathcal{R}_1 + 4 (\mathcal{R}_1^* - k_1) ). \]

By \( \Delta = 0 \) and Eq. (12), we obtain
\[ \mathcal{R}_1 = 2k_1 - \mathcal{R}_1^* + 2\sqrt{(\mathcal{R}_1^* - k_1)(1 - k_1)} \triangleq r_1 \quad \text{(13)} \]
or
\[ \mathcal{R}_1 = 2k_1 - \mathcal{R}_1^* - 2\sqrt{(\mathcal{R}_1^* - k_1)(1 - k_1)} \triangleq r_2. \]

**Remark 3.** It is clear that \( r_2 < r_1 \) by Eq. (3) and (12). According to the discriminant \( \Delta \), Eq. (7) has two different real roots if \( \mathcal{R}_1 < r_2 \) or \( \mathcal{R}_1 > r_1 \), has two same real roots if \( \mathcal{R}_1 = r_2 \) or \( \mathcal{R}_1 = r_1 \), and has no real root if \( r_2 < \mathcal{R}_1 < r_1 \).

**Lemma 3.1.** \( r_1 \) and \( r_2 \) have the following properties:

1. \( r_1 \leq 1 \), and the equal holds if and only if \( \mathcal{R}_1^* = 1 \).
2. \( r_2 < \mathcal{R}_1^* < r_1 \) if \( \mathcal{R}_1^* < 1 \).

**Proof.** (1) Since \( 1 + \mathcal{R}_1^* - 2k_1 = (1 - k_1) + (\mathcal{R}_1^* - k_1) > 0 \) and
\[ (1 + \mathcal{R}_1^* - 2k_1)^2 - 4(\mathcal{R}_1^* - k_1)(1 - k_1) = (1 - \mathcal{R}_1^*)^2 \geq 0, \]
we have
\[ 1 + \mathcal{R}_1^* - 2k_1 \geq 2\sqrt{(\mathcal{R}_1^* - k_1)(1 - k_1)}. \]
which is equivalent to
\[ 1 \geq 2k_1 - \mathcal{R}_1^* + 2\sqrt{(\mathcal{R}_1^* - k_1)(1 - k_1)} = r_1. \]
(2) If \( \mathcal{R}_1^* < 1 \), then
\[ r_1 - \mathcal{R}_1^* = 2\sqrt{\mathcal{R}_1^* - k_1} \left( \sqrt{1 - k_1} - \sqrt{\mathcal{R}_1^* - k_1} \right) > 0, \]
that is, \( \mathcal{R}_1^* < r_1 \). Similarly, \( r_2 < \mathcal{R}_1^* \). \( \square \)

Regarding the existence of the positive roots of Eq. (7), we have the following result:

**Proposition 3.2.** (1) Eq. (7) has only one positive real root if \( \mathcal{R}_1 > 1 \), or \( \mathcal{R}_1^* < \mathcal{R}_1 = 1 \), or \( \mathcal{R}_1^* < \mathcal{R}_1 = r_1 \).
(2) Eq. (7) has two positive real roots if \( \mathcal{R}_1^* < r_1 < \mathcal{R}_1 < 1 \).
(3) Eq. (7) has no positive real root on the other cases.

**Proof.** It is easy to see that \( b_2 > 0 \) by Eqs. (8) and (11). Combining with Eqs. (9), (10) and Lemma 3.1, according to Veda’s theorem and Remark 3, it is easy to verify the conclusions. \( \square \)

Correspondingly, we have the following result about the existence of the equilibria of system (1).

**Theorem 3.3.** (1) System (1) has a disease-free equilibrium and an endemic equilibrium if \( \mathcal{R}_1 > 1 \), or \( \mathcal{R}_1^* < \mathcal{R}_1 = 1 \), or \( \mathcal{R}_1^* < \mathcal{R}_1 = r_1 \).
(2) System (1) has only a disease-free equilibrium and no endemic equilibrium if \( \mathcal{R}_1 < \min\{1, \mathcal{R}_1^*\} \) or \( \mathcal{R}_1^* \leq \mathcal{R}_1 < r_1 \).
(3) System (1) has a disease-free equilibrium and two different endemic equilibria if \( \mathcal{R}_1^* < r_1 < \mathcal{R}_1 < 1 \).

4. Analysis of stability and backward bifurcation

4.1. Stability of the disease-free equilibrium

**Theorem 4.1.** Disease-free equilibrium \( P_0 \) is locally asymptotically stable if \( \mathcal{R}_1 < 1 \) and unstable if \( \mathcal{R}_1 > 1 \).
**Proof.** The Jacobian matrix of system (1) at the disease-free equilibrium $P_0$ is

$$J_0 = \begin{pmatrix} -(\tau + \mu) & 0 & -\alpha \beta s_0 & -\alpha s_0 & \gamma \\ \tau & -\mu & -\rho \alpha \beta v_0 & -\rho \alpha v_0 & 0 \\ 0 & 0 & \alpha \beta k_1 - (\delta + \mu) & \alpha k_1 & 0 \\ 0 & 0 & \delta_1 & -(\sigma + \mu) & 0 \\ 0 & 0 & \delta_2 & \sigma & -(\gamma + \mu) \end{pmatrix},$$  \hspace{1cm} (14)

where

$$s_0 = \frac{S^0}{N^0} = \frac{\mu}{\tau + \mu}, \quad v_0 = \frac{V^0}{N^0} = \frac{\tau}{\tau + \mu}.$$  

Its characteristic equation is

$$0 = \det(\lambda E_2 - J_0)$$

$$= (\lambda + \tau + \mu)(\lambda + \mu)(\lambda + \gamma + \mu) \left| \begin{array}{ccc} \lambda + (\delta + \mu) - \alpha \beta k_1 & -\alpha k_1 \\ -\delta_1 & \lambda + (\sigma + \mu) \end{array} \right|$$

It can be seen that $J_0$ has at least three negative real eigenvalues $\lambda_1 = -\tau - \mu, \lambda_2 = -\mu$ and $\lambda_3 = -\gamma - \mu$. Thus, we only need to consider the following equation.

$$0 = \left| \begin{array}{ccc} \lambda + (\delta + \mu) - \alpha \beta k_1 & -\alpha k_1 \\ -\delta_1 & \lambda + (\sigma + \mu) \end{array} \right|$$

$$= \lambda^2 + [(\sigma + \mu)(\delta + \mu) - \alpha \beta k_1]\lambda + (\sigma + \mu)(\delta + \mu)(1 - \Re_1).$$

If $\Re_1 < 1$, or

$$\alpha k_1 \left[ \frac{\beta}{\delta + \mu} + \frac{\delta_1}{(\delta + \mu)(\sigma + \mu)} \right] < 1,$$

which implies $\alpha k_1 \beta < \delta + \mu$, we have

$$(\sigma + \mu)(\delta + \mu) - \alpha \beta k_1 > \delta + \mu > 0.$$  

In this case, we also have $(\sigma + \mu)(\delta + \mu)(1 - \Re_1) > 0$. By the Veda theorem, the real parts of the two roots of Eq. (15) are all negative. Thus, all eigenvalues of $J_0$ have negative real parts if $\Re_1 < 1$, which implies that $P_0$ is locally asymptotically stable.

If $\Re_1 > 1$, we have $(\sigma + \mu)(\delta + \mu)(1 - \Re_1) < 0$, which implies that Eq. (15) has a positive real root, or $J_0$ has a positive eigenvalue. Thus $P_0$ is unstable if $\Re_1 > 1$.  \hspace{1cm} □

4.2 Bifurcation analysis

By Theorem 3.3, when $\Re^*_1 < \Re_1 < 1$, in addition to a disease-free equilibrium, there may exist two endemic equilibria in system (1), and backward bifurcation may occur. That is, there may exist a locally stable endemic equilibrium. In this case, the disease-free equilibrium $P_0$ is not globally stable when $\Re_1 < 1$, which means that the spread of COVID-19 may not be completely controlled even if $\Re_1 < 1$. Therefore, it is necessary to analyze the backward bifurcation phenomenon of system (1). Here we apply Castillo-Chavez and Song Bifurcation Theorem [32] to analyze the bifurcation phenomenon of system (1).

**Theorem 4.2.** (1) System (1) undergoes backward bifurcation at $\Re_1 = 1$ if $\Re^*_1 < 1$.

(2) System (1) undergoes forward bifurcation at $\Re_1 = 1$ if $\Re^*_1 > 1$.

**Proof.** Let $x_1 = S, x_2 = V, x_3 = A, x_4 = I$ and $x_5 = R$. System (1) is rewritten as

$$\begin{align*}
  x'_1 &= M - \frac{\alpha (x_4 + \beta x_3) x_1}{x_1 + x_2 + x_3 + x_4 + x_5} - (\tau + \mu)x_1 + \gamma x_5 = f_1 \\
  x'_2 &= \tau x_1 - \frac{\rho \alpha (x_4 + \beta x_3) x_2}{x_1 + x_2 + x_3 + x_4 + x_5} - \mu x_2 = f_2 \\
  x'_3 &= \frac{\alpha (x_4 + \beta x_3) x_3}{x_1 + x_2 + x_3 + x_4 + x_5} + \frac{\rho \alpha (x_4 + \beta x_3) x_2}{x_1 + x_2 + x_3 + x_4 + x_5} - (\delta + \mu)x_3 = f_3 \\
  x'_4 &= \delta_1 x_3 - (\sigma + \mu)x_4 = f_4 \\
  x'_5 &= \delta_2 x_3 + \sigma x_4 - (\gamma + \mu)x_5 = f_5
\end{align*}$$

Choose $\alpha$ as a bifurcation parameter. According to $\Re_1 = 1$, the critical value of $\alpha$ is

$$\alpha^* = \frac{(\sigma + \mu)(\delta + \mu)}{k_1[\beta(\sigma + \mu) + \delta_1]}.$$
Substituting it into the Jacobian matrix $J_{0,a^*}$, we have

$$J_{0,a^*} = \begin{pmatrix}
-(\tau + \mu) & 0 & -\alpha^*\beta s_0 & -\alpha^* s_0 & \gamma \\
\tau & -\mu & -\rho\alpha^*\beta v_0 & -\rho\alpha^* v_0 & 0 \\
0 & 0 & \alpha^*\beta k_1 - (\delta + \mu) & \alpha^* k_1 & 0 \\
0 & 0 & \delta_1 & -\sigma & 0 \\
0 & 0 & \delta_2 & \sigma & -(\gamma + \mu)
\end{pmatrix}$$

By (15), it is not difficult to know that only one eigenvalue of $J_{0,a^*}$ is 0, and the other four eigenvalues are all negative. After a simple calculation, a right eigenvector $p = (p_1, p_2, p_3, p_4, p_5)^T$ and a left eigenvector $q^T = (q_1, q_2, q_3, q_4, q_5)$ corresponding to eigenvalue 0 of $J_{0,a^*}$ are obtained respectively, where

$$p_1 = \frac{1}{\tau + \mu} \left[ \frac{\gamma(\delta_2 \mu + \sigma)}{\gamma + \mu} - \frac{\mu(\delta + \mu)(\sigma + \mu)}{\mu + \rho \tau} \right],$$

$$p_2 = \frac{1}{\mu(\tau + \mu)} \left[ \frac{\gamma \tau (\delta_2 \mu + \sigma)}{\gamma + \mu} - \frac{\tau(\delta + \mu)(\sigma + \mu)(\mu + \rho \tau + \rho \mu)}{\mu + \rho \tau} \right],$$

$$p_3 = \sigma + \mu, \quad p_4 = \delta_1, \quad p_5 = \frac{\sigma \delta + \delta_2 \mu}{\gamma + \mu},$$

and

$$q_1 = q_2 = q_3 = 0, \quad q_3 = \beta(\sigma + \mu) + \delta_1, \quad q_4 = \delta + \mu.$$

After tedious calculations, we obtain

$$b = \sum_{i,k=1}^{5} q_i p_i \frac{\partial^2 f_k}{\partial x_i \partial x_j}igg|_{x=x_0, a=a^*} = q_3 p_3 \frac{\partial^2 f_3}{\partial x_3 \partial a}igg|_{x=x_0, a=a^*} + q_3 p_4 \frac{\partial^2 f_3}{\partial x_4 \partial a}igg|_{x=x_0, a=a^*} = \beta k_3 q_3 p_3 + k_1 q_3 p_4 = k_1 q_3 (\beta p_3 + p_4) > 0,$$

and

$$a = \sum_{i,j,k=1}^{5} q_i p_i p_j \frac{\partial^2 f_k}{\partial x_i \partial x_j}igg|_{x=x_0, a=a^*} = \frac{2a^*}{\gamma q_1} (\beta p_3 + p_4) (1 - k_1 p_1 + (\rho - k_1) p_2 - k_1 (p_3 + p_4 + p_5)).$$

Since $\frac{2a^*}{\gamma q_1} (\beta p_3 + p_4) > 0$, the sign of $a$ is determined by $(1 - k_1) p_1 + (\rho - k_1) p_2 - k_1 (p_3 + p_4 + p_5)$,

$$= (1 - k_1) p_1 + (\rho - k_1) p_2 - k_1 (p_3 + p_4 + p_5) + \rho(1 - \rho)(\tau(\delta_2 \mu + \sigma) + \sigma(\delta + \sigma \mu) + \mu(\delta + \mu)(\sigma + \mu) + \gamma \mu)$$

$$= (\sigma + \mu)(\delta + \mu) - (\rho + \tau)(\sigma(\delta + \sigma \mu) + \mu(\delta + \mu)(\sigma + \mu) + \gamma \mu)$$

$$= (\sigma + \mu)\delta + \mu (1 - k_1) (\rho + \tau(\delta + \mu))(1 - \frac{\gamma \eta}{\delta + \mu})$$

$$= \frac{\rho(\sigma + \mu)(\delta + \mu)}{\tau + \mu k_1} (1 - \frac{1}{\gamma \eta})$$

By Castillo-Chavez and Song Bifurcation Theorem, if $\Re_1 < 1$, equivalent to $a > 0$, system (1) undergoes backward bifurcation at $\Re_1 = 1$. If $\Re_1 > 1$, equivalent to $a < 0$, system (1) undergoes forward bifurcation at $\Re_1 = 1$. □

**Remark 4.** According to Lemma 3.1, it follows that $\Re_1 < r_1 < 1$ if $\Re_1 < 1$. Meanwhile, combining with Theorem 3.3, Theorem 4.1 and Theorem 4.2, it can be seen that system (1) has not only a locally asymptotically stable disease-free equilibrium but also a locally asymptotically stable endemic equilibrium when $r_1 < \Re_1 < 1$, and has only a locally asymptotically stable disease-free equilibrium when $\Re_1 < r_1$.

Theorem 4.2 shows that relying only on imperfect COVID-19 vaccine may lead to backward bifurcation. Even if the basic regenerative number is less than 1, there may exist a locally asymptotically stable endemic equilibrium. In this case, it cannot completely eliminate the spread of COVID-19. In order to completely eliminate COVID-19, it is necessary to reduce the basic regenerative number $\Re_1$ to no more than $r_1$, a positive number smaller than 1, which will bring greater difficulties to the prevention and control of COVID-19. The reason for the backward bifurcation is that an incompletely effective COVID-19 vaccine leads to two types of susceptible individuals, naive susceptible and the vaccinated susceptible.
In order to show the bifurcation phenomenon of system (1), the coefficients of Eq. (7) are expressed by $\mathcal{R}_1$. Divide both sides of Eq. (7) by $\rho \mu$ and substitute $a = \frac{A}{N}$. Noticing that $N = \frac{M}{\mu}$ when system (1) is in equilibrium, we rewrite Eq. (7) as

$$\tilde{b}_2 A^2 + \tilde{b}_1 A + \tilde{b}_0 = 0,$$

where

$$\tilde{b}_2 = \frac{\delta + \mu}{k_1 \mu} (\delta + \mu - \gamma \eta) \mathcal{R}_1,$$

$$\tilde{b}_1 = \frac{(\delta + \mu) M}{k_1 \mu} (\mathcal{R}_1^* - \mathcal{R}_1),$$

$$\tilde{b}_0 = \frac{(\mu + \rho \tau) M^2}{\rho \mu^2} \left( \frac{1}{\mathcal{R}_1} - 1 \right).$$

Choose appropriate parameters and consider Eq. (17) to define a curve in the $(\mathcal{R}_1, a)$ positive quadrant, see Fig. 2. In Fig. 2(a), we set the parameter values $\rho = 0.3, \tau = 0.03, \delta = 0.2, \theta = 0.2, \sigma = 0.1, \gamma = 0.01, \mu = 0.0001$ and $M = 1000$. We obtain $\mathcal{R}_1^* = 1.2738 > 1$ and system (1) undergoes forward bifurcation at $\mathcal{R}_1 = 1$. In this case, a stable endemic equilibrium exists if $\mathcal{R}_1 > 1$ and no endemic equilibrium exists if $\mathcal{R}_1 < 1$. In Fig. 2(b), the parameters are taken as $\rho = 0.3, \tau = 0.001, \theta = 0.4, \delta = 0.3, \sigma = 0.1, \gamma = 0.05, \mu = 0.0002$ and $M = 1000$. Then we have $\mathcal{R}_1^* = 0.43556 < 1$ and system (1) undergoes backward bifurcation at $\mathcal{R}_1 = 1$. Furthermore, through calculation, we obtain $r_1 = 0.6078$. In this case, there are two endemic equilibria if $0.6078 < \mathcal{R}_1 < 1$ (the upper is locally stable and the lower is unstable) and only one stable endemic equilibrium exists if $\mathcal{R}_1 > 1$.

## 5. Simulation

In this section, we simulate the effect of vaccination on the prevention and control of COVID-19 to verify the previous analysis. The values of some parameters in system (1) are derived from some literature, and the others are assumptions made based on actual conditions. According to reports from relevant departments, currently, the efficacies of the most widely used types of vaccines recognized by WHO are 95% for COVID-19 mRNA vaccine BNT162b2 (Pfizer), 94.1% for mRNA-1273 vaccine (Moderna), 70.4% for ChAdOx1 nCoV-19 vaccine/AZD1222 (AstraZeneca) vaccine and 78% for sinovac respectively [33]. Combining the efficacies of these vaccines, we take $\rho = 0.2$. People who have recovered from COVID-19 will develop antibodies, but over time, the antibodies will gradually weaken and disappear. In [34], a follow-up study was conducted on 37 asymptomatic infections, and it was found that after two or three months, their antibodies to COVID-19 were significantly weakened. A screening study of 30082 survivors infected with COVID-19 in New York showed that the antibodies of infected individuals will remain stable for several months [35]. Based on these studies, we assume that the antibodies in the recovered patient can exist for an average of 200 days, that is, $\gamma = 1/200 = 0.005$. The average time spent for removing (recovery or death) from symptomatic infections ranges from 7 days [15] to 14 days [19]. Here
we choose an intermediate value 10 days. The values of the rest parameters are derived from [13,14]. The all values of parameters are shown in Table 2. Based on these parameters, the basic reproductive number without vaccination is calculated as $R_0 = 4.573$, which indicates that a person infected with COVID-19 can infect an average of 4 to 5 susceptible persons during the infection period. In this case, the spread of COVID-19 is very fast. After vaccination, the basic reproductive number is $R_1 = 0.9268$, which is already less than 1. Although it is very close to 1, it is much smaller than $R_0$. This shows that vaccination is effective in controlling the spread of COVID-19. Taking the initial state values as shown in Table 3, we compare the trends of the number of different populations within 350 days in the two cases of with and without vaccination, as shown in Fig. 3.

Fig. 3(a) is the change trend of the number of asymptomatic individuals, $A(t)$. Without vaccination, $A(t)$ reaches its peak on the 38th day, and there are about $1.752 \times 10^7$ asymptomatic individuals. In the case of vaccination ($\rho = 0.2$), the peak of $A(t)$ appeared on the 44th day, and there are about $1.111 \times 10^7$ asymptomatic individuals. It can be seen that vaccination delays and reduces the peak of $A(t)$. Fig. 3(b) is the change curve of symptomatic individuals $I(t)$. Symptomatic individuals are the focus of the prevention and control of COVID-19. Without vaccination, $I(t)$ peaks on about the 45th
day, and there are about $3.409 \times 10^6$ symptomatic individuals. In the case of vaccination ($\rho = 0.2$), the peak of $l(t)$ appears on about the 52nd day, and there are about $2.397 \times 10^6$ asymptomatic individuals. The peak of $l(t)$ is postponed by 7 days, and also reduced by about 1 million, which will greatly reduce the burden of medical resources due to COVID-19, allowing more people to receive timely medical treatment, thereby reducing mortality. After about 130 days, the number of symptomatic individuals is always smaller in the case of vaccination ($\rho = 0.2$).

Figs. 3(a) and (b) show that vaccination ($\rho = 0.2$) is effective in reducing the number of infected individuals and has a positive effect on the prevention and control of COVID-19. However, it can also be seen that even if the COVID-19 vaccines have an efficacy of 80%, the epidemic could not be eliminated within 350 days. There are two possible reasons: one is the occurrence of backward bifurcation; $A(t)$ and $l(t)$ both converge to non-zero constants. In this case, COVID-19 eventually develops into an endemic disease and coexists with humans for a long time. The other is that $A(t)$ and $l(t)$ both converge to 0, but the convergence speed is very slow because that the basic regenerative number $\mathbb{R}_1 = 0.9268$ is close to 1 and not small enough. In order to find out the reason, we need to calculate $\mathbb{R}_1^*$ and $r_1$. It is not difficult to obtain that $\mathbb{R}_1^* = 0.6305$ and $r_1 = 0.9429$ (the second column of Table 4). Since $\mathbb{R}_1^* = 0.6305 < 1$, backward bifurcation appears in system (1), as shown in Fig. 4(a) (the curve corresponding to $\rho = 0.2$). However, $\mathbb{R}_1 < r_1$ implies that system (1) has only one disease-free equilibrium and no endemic equilibrium in this case, which means that COVID-19 will eventually be eliminated. Since $\mathbb{R}_1$ is not small enough, the final elimination will take a long time.

In order to quickly and completely control the spread of COVID-19, in addition to avoiding backward bifurcation, reducing the basic reproductive number $\mathbb{R}_1$ to make it sufficiently small is more important. Therefore, it is necessary to study how robust $\mathbb{R}_1$ and $\mathbb{R}_1^*$ are with respect to the changes of parameters and which parameters are the key factors that affect $\mathbb{R}_1$ and $\mathbb{R}_1^*$ respectively. Sensitivity analysis can provide valuable insights.

5.1. Sensitivity analysis

We adopt the sensitivity analysis method in [36]. Suppose that function $f$ is differentiable to parameter $x$. Then, the sensitivity index of $f$ for $x$ is defined as

$$\gamma_f^x = \frac{\partial f}{\partial x} f.$$
Sensitivity index $\gamma^x$ reflects the robustness of function $f$ to variable $x$. Specifically, when the values of other variables (or parameters) remain unchanged, if $\gamma^x > 0$, $f$ increases (or decreases) by $\gamma^x \%$ when $x$ increases (or decreases) by $1\%$; if $\gamma^x < 0$, $f$ decreases (or increases) by $-\gamma^x \%$ when $x$ increases (or decreases) by $1\%$. Sensitivity indices of $\mathcal{R}_1$ and $\mathcal{R}_{1}^*$ to each parameter are shown in Table 5. It can be seen that $\alpha$ has the greatest influence on $\mathcal{R}_1$. The sensitivity index is 1; that is, when $\alpha$ decreases (increases) by 10%, $\mathcal{R}_1$ will also decrease (increase) by 10%. Since $\mathcal{R}_{1}^*$ does not contain $\alpha$, $\alpha$ has no effect on it. $\rho$ has similar impacts on $\mathcal{R}_1$ and $\mathcal{R}_{1}^*$. When $\rho$ decreases (increases) by 10%, $\mathcal{R}_1$ and $\mathcal{R}_{1}^*$ decrease (increase) by 9.8353% and 9.7236%, respectively. The effects of $\tau$ on $\mathcal{R}_1$ and $\mathcal{R}_{1}^*$ are opposite. When $\tau$ increases by 10%, $\mathcal{R}_1$ decreases by 0.13131%, while $\mathcal{R}_{1}^*$ increases by 6.5424%. Similarly, both $\delta$ and $\sigma$ have little effect on $\mathcal{R}_{1}^*$, but have relatively greater effect on $\mathcal{R}_1$.

When non-pharmaceutical interventions are not adopted, in order to control the spread of COVID-19 as soon as possible, we can only consider two aspects: improving the vaccine efficacy (reducing $\rho$) and increasing the vaccination rate (increasing $\tau$). From the sensitivity analysis results (Table 5), $\rho$ has a great effect on both $\mathcal{R}_1$ and $\mathcal{R}_{1}^*$. When $\rho$ decreases by 10%, $\mathcal{R}_1$ and $\mathcal{R}_{1}^*$ decrease by 9.8353% and 9.7236%, respectively. It can be seen that as long as $\mathcal{R}_1 < \mathcal{R}_{1}^*$ and other conditions remain unchanged, improving the vaccine efficacy (reducing $\rho$) will greatly reduce $\mathcal{R}_1$, such that COVID-19 can be controlled as soon as possible. If other parameters remain unchanged, the trends of $A(t)$ and $I(t)$ are shown as in Fig. 3 for $\rho = 0.2, 0.1$ and 0.03, respectively. The corresponding $\mathcal{R}_{1}^*$, $\mathcal{R}_1$, and $\mathcal{R}_1$ are shown in Table 4, where when $\rho = 0.1$ and $\rho = 0.03$, $\mathcal{R}_1 = 0.3240$ and 0.1099, respectively, both of which are less than 1. These two cases both mean that backward bifurcation occurs in system (1), and the bifurcation diagrams are shown in Fig. 4(a). Regardless of $\rho = 0.2, 0.1$ or 0.03, $\mathcal{R}_1$ is less than $\mathcal{R}_{1}^*$, which means system (1) has only one disease-free equilibrium and no endemic equilibrium, and COVID-19 will eventually be effectively controlled. It can also be seen from Table 4 that the smaller the $\rho$, the smaller the corresponding $\mathcal{R}_1$, and the faster the numbers of people infected with COVID-19, $A(t)$ and $I(t)$, decrease, which is also manifested in Fig. 3.

Although improving vaccine efficacy has a very positive effect on the prevention and control of COVID-19, it cannot be achieved in a short term. For this reason, another measure that is easier to implement needs to be considered — increasing the vaccination rate (increasing $\tau$). From the sensitivity index (Table 5), $\tau$ has a small impact on $\mathcal{R}_1$, but has a large impact on $\mathcal{R}_{1}^*$. If $\tau$ increases by 10%, $\mathcal{R}_1$ will only decrease by 0.13131%, while $\mathcal{R}_{1}^*$ will increase by 6.5424%. Let the remaining parameter values be unchanged (where $\rho = 0.2$). Take $\tau = 0.01, 0.015$ and 0.025 to simulate the trends of $A(t)$ and $I(t)$, and the results are shown in Fig. 5. The corresponding values of $\mathcal{R}_1$, $\mathcal{R}_{1}^*$, $\tau_1$ and $\mathcal{R}_1$ are shown in Table 4, and the bifurcation diagrams are shown in Fig. 4(b). From Table 4 and Fig. 4(b), we can see that when $\tau = 0.01$ and 0.015, the corresponding $\mathcal{R}_{1}^*$ is all less than 1, and backward bifurcation occurs in system (1). When $\tau = 0.025$, $\mathcal{R}_{1}^* = 1.2516 > 1$, and forward bifurcation (transcritical bifurcation) occurs in system (1). From Table 4, it can be seen that although $\mathcal{R}_1$ decreases as $\tau$ increases, the magnitude of the decrease is very small, which is consistent with the sensitivity analysis results. However, as shown in Fig. 5, increasing the vaccination rate (increasing $\tau$) has a significant effect on reducing and delaying the peak of the number of people infected with COVID-19, which is very helpful to avoid a serious run on medical resources.

### 5.2 Combining non-pharmaceutical interventions

Comparing Figs. 3 and 5, we can see that improving vaccine efficiency can control the spread of COVID-19 faster, while increasing the vaccination rate can reduce and postpone the peak of infection to a greater extent. However, in reality, the improvement of vaccine efficacy cannot be realized in a short time, and only relying on increasing the vaccination rate cannot quickly achieve the control of COVID-19. Therefore, in addition to vaccination, some non-pharmaceutical interventions need to be taken. In addition to $\rho$ and $\tau$, according to the sensitivity analysis, the basic regenerative number $\mathcal{R}_1$ can also be reduced by measures such as reducing $\alpha$ and increasing $\delta$ and $\sigma$. The details are as follows:

(i) Reduce $\alpha$. The essence is to reduce the contact rate between people, such as wearing a mask, maintaining social distance, imposing curfews and lockdown.

(ii) Increase $\delta$ and $\sigma$. These can be achieved through quarantine of asymptomatic cases, hospital isolation and treatment of symptomatic cases.

| Table 5 Sensitivity index. | Parameter | Value | Sensitivity index of $\mathcal{R}_1$ | Sensitivity index of $\mathcal{R}_{1}^*$ |
|---------------------------|-----------|-------|--------------------------------------|---------------------------------------|
| $\alpha$                  | 0.8883    | 1     |                                      | 0                                     |
| $\rho$                    | 0.2       | 0.98353 | 0.97236                             |                                       |
| $\tau$                    | 0.01      | -0.013131 | 0.65424                            |                                       |
| $\delta$                  | 1/7       | -0.61149 | -0.022714                           |                                       |
| $\sigma$                  | 0.1       | -0.38814 | -0.0064874                          |                                       |
Based on the above two aspects of non-pharmacological intervention, model (1) is improved as follows:

\[
\begin{align*}
\frac{dS}{dt} &= M - \tau S - \frac{u(1 + \beta A)S}{N - Q} - \mu S + \gamma R \\
\frac{dV}{dt} &= \tau S - \frac{\mu u(1 + \beta A) V}{N - Q} - \mu V \\
\frac{dA}{dt} &= \frac{u(1 + \beta A)S}{N - Q} + \frac{\mu u(1 + \beta A) V}{N - Q} - (\delta_1 + \delta_2 + \delta_3) A - \mu A \\
\frac{dI}{dt} &= \delta_1 A - (\sigma + \sigma_2) I - \mu I \\
\frac{dQ}{dt} &= \delta_3 A + \sigma_2 I - \varepsilon Q - \mu Q \\
\frac{dR}{dt} &= \delta_2 A + \sigma I + \varepsilon Q - \gamma R - \mu R
\end{align*}
\]

where \( u \in (0, 1) \) measures the control over the contact rate of people. The smaller \( u \) means the stricter the prevention and control measures, and the lower the contact rate of people. \( Q \) represents infected individuals treated in isolation, including symptomatic and asymptomatic. We assume that once an infected individual is diagnosed, he/she will be isolated and treated, and the isolation measures are strict, in other words, the isolated individuals no longer have the opportunity to infect others. Using the next-generation approach, the basic reproductive number of model (18) is obtained as

\[
\mathcal{R}_2 = u\alpha k_1 \left[ \frac{\beta}{\delta + \mu} + \frac{\tilde{\delta}_1}{(\delta + \mu)(\tilde{\sigma} + \mu)} \right],
\]

where \( \tilde{\delta} = \delta_1 + \delta_2 + \delta_3, \tilde{\sigma} = \sigma + \sigma_2. \)
From the sensitivity index in Table 5, it follows that $\alpha$ has the greatest impact on the basic reproductive number $\mathcal{R}_1$, followed by $\delta$ and $\sigma$. Corresponding to $\mathcal{R}_2$ are $u$, $\delta_3$ and $\sigma_2$, respectively. We focus on the impact of measures to reduce the contact rate (reducing $u$) on the spread of COVID-19 firstly. Since the asymptomatic individuals are difficult to be diagnosed, the isolation rate is not high, so set $\delta_3 = 0.2$. The diagnosis rate of symptomatic individuals is higher as they generally seek medical treatment. Their isolation rate is taken as $\sigma_2 = 0.8$. The average days for isolated individuals to be removed are shorter than that for non-isolated infected individuals, which is taken as $1/0.15$ days, i.e., $\varepsilon = 0.15$. Other parameters and state initial values remain unchanged, see Tables 2 and 3. Let $u = 1, 0.8$ and 0.6. Then the corresponding basic reproductive numbers $\mathcal{R}_2 = 0.2529$, 0.2023 and 0.1518, respectively. The simulation results are shown in Fig. 6. It can be seen that the smaller the $u$, the smaller the basic reproductive number $\mathcal{R}_2$, and the faster the spread of COVID-19 is controlled. When $u = 0.6$, COVID-19 can be completely controlled in about 40 days, as shown in Fig. 6.

Secondly, we study the impact of the isolation rate of asymptomatic infections on the spread of COVID-19. Let the remaining parameters be unchanged, where $u = 0.8$ and $\sigma_2 = 0.8$. Let $\delta_3 = 0.15, 0.2$ and 0.25. Then the corresponding basic reproductive numbers $\mathcal{R}_2 = 0.2369, 0.2023$ and 0.1766, respectively. The spread dynamics of COVID-19 are shown in Fig. 7. It can be seen that the larger $\delta_3$, the smaller $\mathcal{R}_2$, and the faster COVID-19 is controlled. As shown in Fig. 7, when $\delta_3 = 0.25$, the spread of COVID-19 is completely controlled in about 50 days.

Finally, we focus on the impact of the isolation rate ($\sigma_2$) on the spread of COVID-19. Let the remaining parameters be unchanged, where $u = 0.8$ and $\delta_3 = 0.2$. Let $\sigma_2 = 0.8, 0.6$ and 0.4, then the corresponding basic reproductive numbers $\mathcal{R}_2 = 0.2023, 0.2062$ and 0.2130, respectively. The spread dynamics of COVID-19 are shown in Fig. 8. Compared with $u$
and $\delta_3$, we can see that $\sigma_2$ has a much smaller impact on the basic reproductive number $R_2$. As shown in Fig. 7, the larger $\sigma_2$, the more helpful it is to control the spread of COVID-19. However, the time spent to eliminate the epidemic cannot be significantly reduced in the three cases when $\sigma_2 = 0.8, 0.6$ and $0.4$, which all need about 80 days.

Based on the above simulations and analysis, it can be seen that when non-pharmaceutical intervention is not implemented, whether improving the vaccine efficiency or increasing the vaccination rate, the spread of COVID-19 cannot be effectively and quickly controlled. Therefore, some non-pharmaceutical intervention measures need to be implemented. Among non-pharmaceutical interventions, reducing the contact rate of people (reducing $u$) and increasing the isolation rate of asymptomatic individuals (increasing $\delta_3$) are very effective, which can greatly reduce the peak of infection and quickly control the spread of COVID-19.

6. Conclusion

COVID-19 has been spreading globally for more than a year, and it has not yet been effectively controlled. In addition, multiple variants of SARS-CoV-2 have been identified, which are more infectious, posing greater challenges to the global COVID-19 epidemic prevention. Especially in the recent outbreak of COVID-19 in India, the number of confirmed cases in a single day has repeatedly reached new highs. The number of confirmed cases in a single day has exceeded 300,000 for 25 consecutive days, and the number of deaths per day has also remained high. The prevention and control of COVID-19 remains a long-term and arduous task. Although a number of vaccines have been put in use, relying only on vaccines to control the spread of COVID-19 will lead to backward bifurcation. In this case, when the basic reproduction number $R_1 < 1$, there exists a locally asymptotically stable endemic equilibrium in addition to a locally asymptotically stable disease-free equilibrium, which means that even if the basic reproduction number is less than 1, COVID-19 cannot be completely eliminated. In order to achieve a complete and quick control of COVID-19, in addition to population vaccination, it is still necessary to appropriately enforce some non-pharmaceutical intervention measures, such as reducing the contact rate of people and increasing the isolation rate of asymptomatic individuals.

CRediT authorship contribution statement

Bo Yang: Investigation, Methodology, Writing – original draft, Writing – review & editing. Zhenhua Yu: Formal analysis, Investigation, Writing – review & editing. Yuanli Cai: Conceptualization, Formal analysis, Investigation, Methodology, Project administration, Supervision, Writing – review & editing.

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