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A mathematical model reveals the influence of NPIs and vaccination on SARS-CoV-2 Omicron Variant

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A mathematical model reveals the influence of NPIs and vaccination on SARS-CoV-2 Omicron Variant

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Abstract

A SVEIR SARS-CoV-2 Omicron variant model is proposed to provide some insight to coordinate non-pharmaceutical interventions(NPIs) and vaccination. Mathematically, we define the basic reproduction number $\mathscr{R}_0$ and the effective reproduction number $\mathscr{R}_e$ to measure the infection potential of Omicron variant and formulate a optimal disease control strategy. Our inversion results imply that the sick period of Omicron variant in the United States is longer than that of Delta variant in Indian; The decreasing of the infectious period of the infection with infectiousness implies that the risk of hospitalization is reduced; but the increasing period of the infection with non-infectiousness signifies that Omicron variant lengthens the period of nucleic acid test being negative; Optimistically, Omicron's death rate is only a quarter of Delta's. Moreover, we forecast that the cumulative cases will exceed 100 million in the United States on 28 February, 2022 and the daily confirmed cases will reach a peak on 2 February, 2022. The results of parameters sensitivity analysis imply that NPIs is helpful to reduce the number of confirmed cases. Especially, NPIs are indispensable even if all the people were vaccinated when the efficiency of vaccine is relatively low. By simulating the relation ships of the effective reproduction number $\mathscr{R}_e$, the vaccination rate and the efficacy of vaccine, we find that it is impossible to achieve the herd immunity without NPIs while the efficiency of vaccine is lower than 88.7%. Therefore, the herd immunity area is defined by the evolution of relationships between the vaccination rate and the efficacy of vaccine. Finally, we present that the disease-induced mortality rate demonstrates the periodic oscillation and an almost periodic function is deduced to match the curve. A discussion completes the paper.

Keywords: SVEIR Omicron model; Reproduction numbers; NPIs; Vaccines; Sensitivity analysis; Herd immunity

AMS Subject Classification (2020): 34A34; 34D20; 92D30

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1 Introduction

Coronavirus disease 2019 (COVID-19), caused by a novel virus of the coronavirus genus (SARS-CoV-2), has lasted for more than two years and caused a Once-in-a-Century global crisis [47]. Despite scientists worldwide racing to develop antiviral drugs, curative treatments are unavailable at the time of writing, and vaccinations against the COVID-19 has been recently distributed around the world, the global economy is experiencing the worst plunge in recent history amid fears of further deterioration of the COVID-19 situation [13]. Since the outbreak of COVID-19 was first detected in December 2019 in Wuhan, China [22], many authors have studied the transmission dynamics of COVID-19 by various means and methods [3, 7, 12, 17, 21, 31, 36, 44–46].

As same as all viruses, SARS-CoV-2 which causes COVID-19 pandemic changes over time. For those changes, most of them do not impact on the virus's properties. However, there may be some changes that have an important impact on the characteristics of the virus, such as how easily it is to spread, the severity of the associated diseases, the performance of vaccines and therapeutic medicines, the applications of the diagnostic tools, and/or the other public health and control measures [48]. For example, the B.1.1.529 (Omicron) variant, which was first identified in South Africa in early November 2021 [5], has rapidly become the dominant variant in many countries. The published research on live-virus neutralization assays revealed that Omicron could be escape antibody neutralization by the BNT162b2 messenger RNA vaccine (PfizerioNTech) [29].

Generally, population-wide rapid nucleic acid testing, isolation, sterilizing, and social distancing, which are called NPIs(non-pharmaceutical interventions), have played an important role to prevent and control the transmission of SARS-CoV-2 [6]. For example, many countries have been enforcing NPIs, such as social distancing (also called contact restrictions) and travel restrictions, to control the development of the SARS-CoV-2 [18, 19]. Tian et al. [37] showed that the confirmed COVID-19 cases outside Wuhan would have decreased to 744,000 ($\pm$ 156,000) due to the Wuhan travel ban or the national emergency response. Pavelka et al. [26] have investigated the influence of population-wide rapid antigen testing on SARS-CoV-2 prevalence in Slovakia. Their results showed that the prevalence decrease was not solely contributed by infection control measures, while the addition measures, such as the isolation and quarantine of household members of those testing positivity, were also required. Since SARS-CoV-2 is transmitted by droplets and aerosols, Cheng et al. [8] showed that the surgical masks were effective on preventing virus spread under conditions of low virus abundance (virus-limited). However, more advanced masks and other protective equipments were required in potentially virus-rich indoor environments, including medical centers and hospitals. Senapati et al. [34] revealed that it is necessary to take a higher intervention effort to control the disease outbreak within a shorter period of time in India. Further researches which has been proposed for considering the impact of NPIs on the spread of SARS-CoV-2 could be found in [20, 27, 28, 33, 38, 41, 43].

In fact, an excessive NPIs has restricted the development of the global economies and impacted on the general quality of life (in particular, mental health) [24]. That's a general public perception that vaccines are the most effective defense to control the disease completely. Saad-Roy et al. [35] explored three scenarios of selection and found that a one-dose policy may increase the potential for antigenic evolution under certain conditions of partial population immunity. Moreover, they

highlighted the critical need to test viral loads and quantify immune responses after one vaccine dose, and to ramp up vaccination efforts throughout the world. In consideration of limited initial supply of SARS-CoV-2 vaccine, Bubar et al. [3] used a mathematical model to compare five age-stratified prioritization strategies. Following some of the WHO-SAGE recommendations, Acuña-Zegarraa et al. [2] formulated an optimal control problem with mixed constraints to describe vaccination schedules.

Since someone was diagnosed with the Omicron variant of COVID-19 despite having received two shots of the vaccine, NPIs remain very indispensable to terminate the pandemic of SARS-CoV-2. Hence, it is necessary to identify strategies for safely relaxing nonpharmaceutical measures [16,25]. Drawing support from optimization-based control on an age-differentiated compartmental model, Grundel et al. [14] studied the relations of vaccination and social distancing. However, the published which coordinated NPIs and vaccination comprehensively to prevent the outbreak of Omicron variant is less common. In this paper, we propose a SVEIR SARS-CoV-2 Omicron variant model to reveal the influence of NPIs and vaccination on SARS-CoV-2 Omicron variant in four key aspects: (1)Mathematically, we define the basic reproduction number $\mathscr{R}_0$ and the effective reproduction number $\mathscr{R}_e$ to measure the infection potential of Omicron variant and develop disease control strategies. (2)Parameter inversion is conduted to explore the mechanism of Omicron variant and give some suggestions to stay home and isolate from other people. (3)Sensitivity analysis find the main factors affecting the spread of Omicron variant, and formulate prevention and control strategies. (4)Facing a low vaccination willingness and efficacy of vaccines, we explore the herd immunity area.

The remainder of this paper is structured as follows. We present the compartmental model in section 2 and describe the extinction and uniform persistence in section 3. Section 4 is dedicated to the case study, and the paper is concluded in section 5.

2 A compartmental model with NPIs and vaccination.

A SEIR model has been used to study the transmission of COVID-19 [30, 42]. Furthermore, in this paper, each of the exposed and infectious class is further divided into two groups, one contagious and other non-contagious [17]. Consider the transmission of Omicron variant with NPIs and vaccines, the population is divided into the following categories: Let S be the number of susceptible individuals, V be the number of the vaccinated individuals, E_1 be the number of the exposed individuals who are not contagious in the early stages, E_2 be the number of the exposed individuals who can infect the susceptible, and I_1 be the number of the infectious individuals who are contagious, I_2 be the number of the infectious individuals who are not contagious, R be the number of recovery individuals, N be the total population, that is, $N = S+V+E_1+E_2+I_1+I_2+R$. Furthermore, we suppose that N is constant. Refer to [17], the population growth process can be described as in Figure 1.

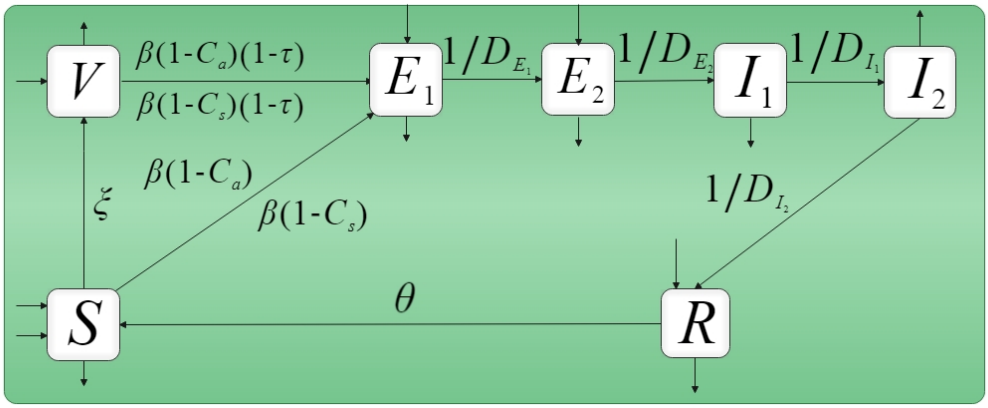


Figure 1: Compartmental diagram of COVID-19 transmission dynamics

The model is given by an autonomous system of ordinary differential equations

$$\begin{aligned}
&\tfrac{dS}{dt} = \Lambda - \beta(1-C_a)\tfrac{SE_2}{N} - \beta(1-C_s)\tfrac{SI_1}{N} - \xi S - \mu S + \theta R,\\
&\tfrac{dV}{dt} = \xi S - \beta(1-C_a)(1-\tau)\tfrac{VE_2}{N} - \beta(1-C_s)(1-\tau)\tfrac{VI_1}{N} - \mu V,\\
&\tfrac{dE_1}{dt} = \beta(1-C_a)\tfrac{SE_2}{N} + \beta(1-C_s)\tfrac{SI_1}{N} + \beta(1-C_a)(1-\tau)\tfrac{VE_2}{N} + \beta(1-C_s)(1-\tau)\tfrac{VI_1}{N}\\
&\qquad - \tfrac{E_1}{D_{E_1}} - \mu E_1,\\
&\tfrac{dE_2}{dt} = \tfrac{E_1}{D_{E_1}} - \tfrac{E_2}{D_{E_2}} - \mu E_2 - dE_2,\\
&\tfrac{dI_1}{dt} = \tfrac{E_2}{D_{E_2}} - \tfrac{I_1}{D_{I_1}} - \mu I_1 - dI_1,\\
&\tfrac{dI_2}{dt} = \tfrac{I_1}{D_{I_1}} - \tfrac{I_2}{D_{I_2}} - \mu I_2,\\
&\tfrac{dR}{dt} = \tfrac{I_2}{D_{I_2}} - \mu R - \theta R,
\end{aligned} \tag{2.1}$$

where Λ is the recruitment rate of susceptible class, C_a and C_s denote the intensity of NPIs for the individuals of the exposed individuals and the infectious individuals who can infect the susceptible, respectively. β denotes the effective contact rate, ξ denotes the vaccination coverage rate, θ is the antibody disappear rate of recovery class, μ is the natural death rate of the population, D_{E_1} and D_{E_2} are lengths of the incubation with non-infectiousness and incubation with infectiousness, respectively. $0 \le \tau \le 1$ denotes the vaccine efficacy($\tau = 1$ represents a vaccine that offers 100% protection against infection, $\tau = 0$ models a vaccine that offers no protection at all). D_{I_1} and D_{I_2} are lengths of the infection with infectiousness and infection with non-infectiousness, respectively. d denotes the disease-induced mortality rate. Biologically, we could suppose that the number of total human population stabilizes at $N > 0$.

For simplicity, set $\psi_t(x^0)$ be the solution of (2.1) with initial value $\psi_0(x^0) = x^0 \in \mathbb{R}^7_+$. By [11, Theorem 2.1], we have the following.

Theorem 2.1 *For any $x^0 \in \mathbb{R}^7_+$, system (2.1) has a unique nonnegative solution $\psi_t(x^0)$ with initial value $\psi_0(x^0) = x^0$, and all solutions are ultimately bounded and uniformly bounded.*

Remark 2.2 If we take $\tau = 0$ or $\xi = 0$ in (2.1), then the model consider that NPIs for the exposed and the infectious individuals who can infect the susceptible is the only measure. Similarly, let $C_a = C_s = 0$ in the above discussion, system (2.1) implies that the vaccination is only gotten involved. If $\tau = \xi = C_a = C_s = 0$, it means that there are no external factors involved (no vaccines, masks or other epidemic prevention measures). In this situation, the transmission dynamics of Omicron variant are studied based on the natural characteristics of Omicron variant itself.

3 Reproduction number

Reproduction numbers (ratio) are a crucial threshold parameter in the study of disease transmission. In epidemiology, it is defined as the expected number of secondary cases produced by a single (typical) infection in a completely susceptible population and is used to measure the infection potential of an infectious disease [9, 23]. At the beginning of the transmission of coronavirus, based on likelihood and model analysis, Tang et al. [3,7,31,36] revealed that the basic reproduction number may be as high as 6.47, which showed that COVID-19 is highly infectious. By means of the basic reproduction number, Bubar et al. [3] found a highly mitigated spread during vaccine rollout. Riley et al. [31] used a model of constant exponential growth and decay, and quantified this fall and rise in prevalence in terms of halving and doubling times and the basic reproduction number. Noting that an important quantity in epidemiological models, the basic reproduction number, Cuevas-Maraver et al. [7] discussed in the realm of the model what consequences different additional intervention measures would have had at the level of deaths and of cumulative infections. In this section, the definition and computation formulae of the basic reproduction number and the effective reproduction number for system (2.1) are established.

We first consider the disease-free solution of system (2.1). Let $E_1 = E_2 = I_1 = I_2 = 0$, then we have

$$\begin{aligned} &\tfrac{dS}{dt} = \Lambda - \xi S - \mu S, \\ &\tfrac{dV}{dt} = \xi S - \mu V. \end{aligned} \tag{3.1}$$

By the similar arguments to those in [40], system (3.1) has a positive equilibrium $(S^*, V^*) = (\frac{\Lambda}{\xi+\mu}, \frac{\xi\Lambda}{\mu(\xi+\mu)})$, which is globally attractive. Linearizing system (2.1) at the disease-free equilibrium $(S^*, V^*, 0, 0, 0, 0, 0)$, we get

$$\begin{aligned} \tfrac{dE_1}{dt} &= \beta(1-C_a)\tfrac{S^*E_2}{N} + \beta(1-C_s)\tfrac{S^*I_1}{N} + \beta(1-C_a)(1-\tau)\tfrac{V^*E_2}{N} + \beta(1-C_s)(1-\tau)\tfrac{V^*I_1}{N} \\ &\quad - \tfrac{E_1}{D_{E_1}} - \mu E_1, \\ \tfrac{dE_2}{dt} &= \tfrac{E_1}{D_{E_1}} - \tfrac{E_2}{D_{E_2}} - \mu E_2 - dE_2, \\ \tfrac{dI_1}{dt} &= \tfrac{E_2}{D_{E_2}} - \tfrac{I_1}{D_{I_1}} - \mu I_1 - dI_1. \end{aligned} \tag{3.2}$$

Let

$$Y = \begin{pmatrix} 0 & F_1 & F_2 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}, Z = \begin{pmatrix} V_1 & 0 & 0 \\ -V_4 & V_2 & 0 \\ 0 & -V_5 & V_3 \end{pmatrix},$$

where $F_1 = \beta(1-C_a)\frac{S^*+(1-\tau)V^*}{N}$, $F_2 = \beta(1-C_s)\frac{S^*+(1-\tau)V^*}{N}$, $V_1 = \frac{1}{D_{E_1}} + \mu$, $V_2 = \frac{1}{D_{E_2}} + \mu + d$,

$V_3 = \frac{1}{D_{I_1}} + \mu + d$, $V_4 = \frac{1}{D_{E_1}}$ and $V_5 = \frac{1}{D_{E_2}}$. Then we can rewritten (3.2) as

$$\frac{du}{dt} = (Y - Z)u. \tag{3.3}$$

Motivated by the concept of next generation matrices introduced in [9, 23], we define the effective reproduction number of system (2.1) as

$$\mathscr{R}_e := \rho(YZ^{-1}), \tag{3.4}$$

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

The following two theorems give a threshold-type result on the extinction and uniform persistence of the disease in terms of $\mathscr{R}_e$ in the natural state. The proof of the following two theorems can be seen in Appendix A.

Theorem 3.1 *Assume* $(A1)$-$(A2)$ *holds and* $\mathscr{R}_e < 1$*, then the disease-free equilibrium* $\mathcal{E}^* = (S^*, V^*, 0, 0, 0, 0, 0)$ *of system* (2.1) *is globally attractive.*

Theorem 3.2 *If* $\mathscr{R}_e > 1$*, then there exists* $\tilde{\varepsilon} > 0$ *such that the solution* $(S(t), V(t), E_1(t), E_2(t), I_1(t), I_2(t), R(t))$ *of system* (2.1) *with initial data* x^0 *in* $\mathbb{R}^7_+$ *and* $(E_1(0), E_2(0), I_1(0)) > \hat{0}$ *satisfies*

$$\liminf_{t\to\infty} E_1(t) > \tilde{\varepsilon}, \liminf_{t\to\infty} E_2(t) > \tilde{\varepsilon}, \liminf_{t\to\infty} I_1(t) > \tilde{\varepsilon}.$$

Remark 3.3 If $\tau = 0$ or $\xi = 0$ hold in the above discussion, then we call (3.4) as the NPIs reproduction number, denoted by $\mathscr{R}_e^N$. Similarly, in the case of $C_a = C_s = 0$, (3.4) denotes the vaccines reproduction number $\mathscr{R}_e^V$. If $\tau = \xi = C_a = C_s = 0$, then (3.4) is just the basic reproduction number $\mathscr{R}_0$. Furthermore, the conclusions of Theorem 3.1 and Theorem 3.2 remain available under different situations if we replace $\mathscr{R}_e$ by $\mathscr{R}_e^N$, $\mathscr{R}_e^V$ and $\mathscr{R}_0$.

4 Numerical simulations

Omicron variant is a new type of SARS-CoV-2. In this section, we take the data in the United States to explore the transmission mechanism and predict the development trend of Omicron.

4.1 Parameters inversions

We select the data in the United States showed in [49] from December 1, 2021 to January 30, 2022, and use the fminsearch function in MATLAB to perform parametric inversion. The value of the vaccination coverage rate ξ can be seen in [50]. In order to search the difference between Delta and Omicron variant, we compare the data in India [39] with that in the United States. The specific values are shown in Table 1.

According to Table 1, we find that the Omicron variant highly infectious in the sense that $\beta = 0.8993$ and the sick period of Omicron variant in the United States is 0.91 days longer than that of Delta variant in Indian; The decreasing of D_{I_1} implies that the risk of hospitalization is reduced; but the increasing period of D_{I_2} signifies that Omicron variant lengthens the period of

nucleic acid test being negative; Optimistically, Omicron's death rate is only a quarter of Delta's. According to the value of θ, we call for the four months interval of booster shot. Furthermore, if one who is an asymptomatic person has confirmed or suspected Omicron variant, regardless of the result of parameters inversion, should stay home and isolate from other people for at least 6 full days; the isolation time of symptomatic patients should be 3 days. Testing may be used to help determine when to end your isolation period.

Table 1: The parameters of disease in different regions

Parameters	Definitions	India	the United States	Unit
β	effective contact rate	0.70	0.8993	/
D_{E_1}	length of incubation with non-infectiousness	2.9	3.07	$Days$
D_{E_2}	length of incubation with infectiousness	2.3	1.51	$Days$
D_{I_1}	length of infection with infectiousness	2.9	1.43	$Days$
D_{I_2}	length of infection with non-infectiousness	12	15.00	$Days$
d	disease-induced mortality rate	1.3×10^{-4}	2.97×10^{-5}	Day^{-1}
C_a	NPIs for incubation with infectiousness	0.20	0.1716	/
C_s	NPIs for infection with infectiousness	0.20	0.2991	/
μ	natural death rate of the population	4×10^{-5}	2.44×10^{-5}	Day^{-1}
N	total human population	1380004000	120552473	$People$
Λ	recruitment rate of susceptible class	65786	9877	$People/Day$
θ	antibody disappear ratio of recover class	0	0.0085	/
τ	vaccine efficacy	0.85	0.3300	/
ξ	vaccination coverage rate	0.05	0.60	/

4.2 Infection potential estimation

By a simple calculation, the effective reproduction number of system (2.1) can be denoted that

$$\mathscr{R}_e = \frac{\beta\Lambda(\mu+\xi(1-\tau))(D_{E_2}(d+\mu+\frac{1}{D_{I_1}})(1-C_a)+1-C_s)}{\mu N D_{E_1} D_{E_2}(\xi+\mu)(\mu+\frac{1}{D_{E_1}})(d+\mu+\frac{1}{D_{I_1}})(d+\mu+\frac{1}{D_{E_2}})}. \tag{4.1}$$

It then follows from the inversion results in above subsection that $\mathscr{R}_0 = 8.883$, $\mathscr{R}_e^N = 6.811$, $\mathscr{R}_e^V = 5.952$ and $\mathscr{R}_e = 4.564$. Therefore, it is shown that the infection potential of Omicron variant is very high without NPIS and vaccination in the United States. Even if one of NPIS and vaccination is implemented, Omicron variant might infect a large number of individuals. Obviously, the vaccination is better than that of NPIs for reducing the infectious potential of Omicron variant. Two countermeasures being implemented simultaneously remain the best way to protect oneself from COVID-19 and reduce its impact on our communities. Furthermore, we analysis the correlation between parameters and the effective reproduction number $\mathscr{R}_e$ by random sample method with N=8000, the result is shown in Figure 2. We can find however the parameters change, $\mathscr{R}_e$ mainly ranges $[3, 5]$. This result reflects that the United States is facing a strong pressure for the prevention and control of Omicron.

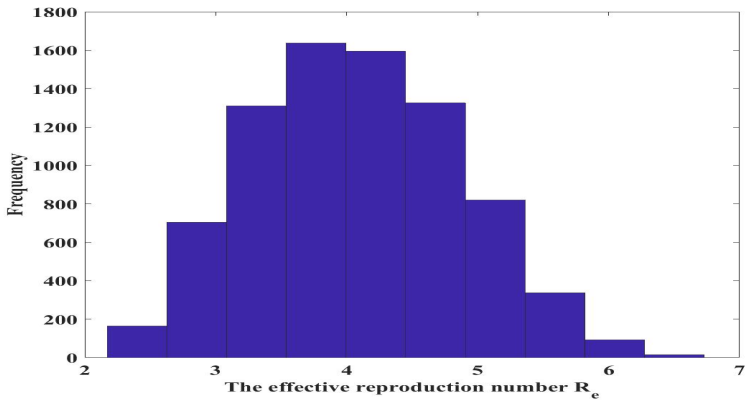
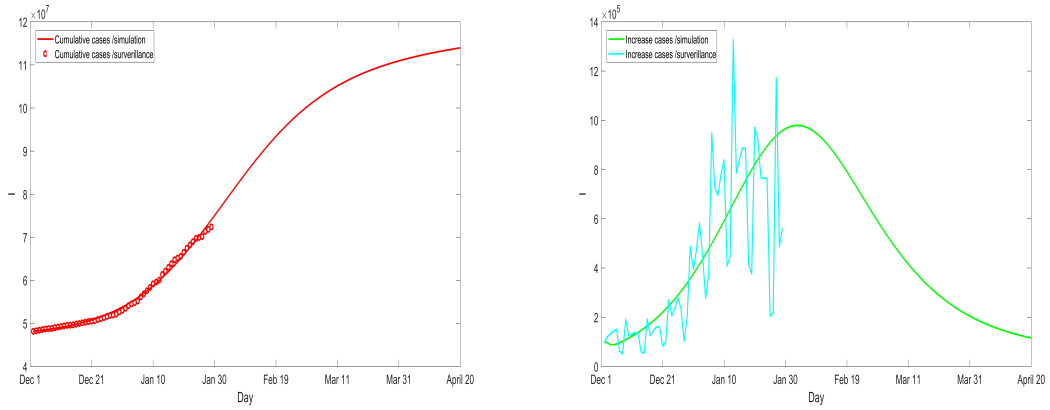


Figure 2: The peculiarity of $\mathscr{R}_e$

4.3 Model fitting and tend predicting

In the following, we forecast the spreading trend of Omicron pandemic in the United States. By a calculation, the numerical simulation results are shown in Figure 3.



(a) (b)

Figure 3: Numerical simulation of cumulative cases and increase cases

The discrete points and the blue line represent the real data of cumulative cases and increase cases from December 1, 2021 to January 30, 2022 in the United States, respectively. The red line and green line represent the simulation of cumulative cases and increase cases, respectively. We found that the dynamical results fit well with the statistical data [49](see Figure 3). During December 1, 2021 to April 20, 2022, Figure 3 forecasts that daily comfirmed cases will maintain an upward trend and reach the maximum value 979360 on February 2, 2022. And the cumulative cases will more than 100 million on February 28, 2022. Since the period of the infection with infectiousness decreases, we think many people are treated at home. It leads to the fact that the

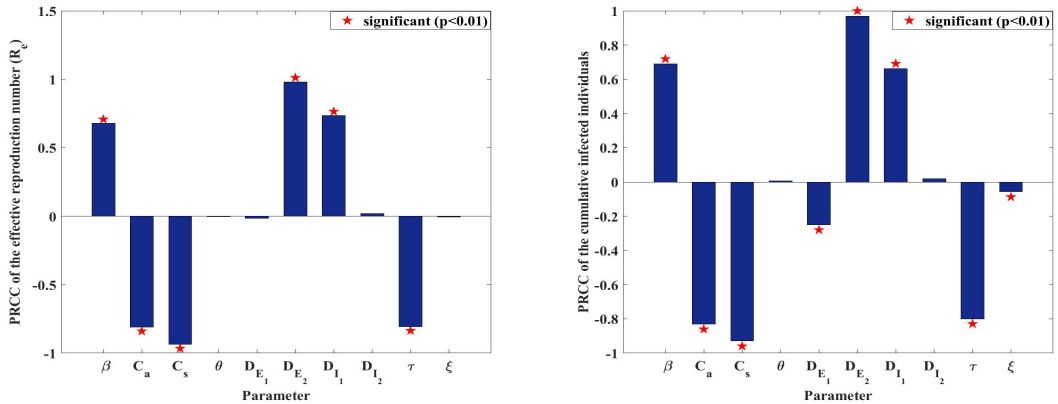
number of reports is lower than the predicted. There is a huge problem that some of American without any face coverings and unwilling to take the vaccine. Furthermore, if the existing protection intensity and vaccine injection schedule are maintained, the numerical simulation forecasts the COVID-19 in the United States will uniformly exist and form an endemic disease. Thus, it is imminent to tighten NPIs and accelerate vaccine programmes.

4.4 Sensitivity analysis

In this part, we compute Partial Rank Correlation Coefficients (PRCC) to identify the key factors which affect the change of $\mathscr{R}_e$ and the total infectious cases. In our experiment, we set that the parameters have a significant effect when p-value< 0.01. The results can be seen in Figure 4.

From Figure 4(a), we can easily see that the parameters β, C_a, C_s,D_{E_2} and D_{I_1} have significant effect on $\mathscr{R}_e$. Furthermore, the effective contact rate β and $\mathscr{R}_e$ are positively correlated, which means that the increasing of effective contact rate can augment $\mathscr{R}_e$. The parameters C_a and C_s are negatively correlated with $\mathscr{R}_e$, which shows that NPIs are strengthened for incubation and infection with infectiousness can help to reduce the infection potential of Omicron variant. The parameters D_{E_2}, D_{I_1} and $\mathscr{R}_e$ are positively correlated, which reflect the peculiarity of Omicron.

Figure 4(b) reveals that β, C_a, C_s, θ, D_{E_2}, D_{I_1}, D_{I_2}, ξ and τ effect mainly on the the cumulative infected cases. Logically, the decreasing effective contact rate β can decrease the cumulative infected cases, which tell us that an environmental decontamination is an important measures to control the pandemic. For C_a and C_s, we can strengthen NPIs, such as keeping social distance, wearing a well-fitting mask, staying home and isolating from other people for incubation and infection with infectiousness to control Omicron pandemic. Considering ξ, τ and θ, we suggest that everyone should get vaccinated and boosted as soon as they are eligible, including people who have already had COVID-19. Since D_{E_2}, D_{I_1} and D_{I_2} reflect the peculiarity of Omicron, a drug intervention may be the most effective means.



(a) (b)

Figure 4: Sensitivity analysis among parameters, $\mathscr{R}_e$ and the total infections cases

The specific impact of parameters on the effective reproduction number $\mathscr{R}_e$ and the cumulative infected individuals is shown in Table 2.

Table 2: PRCC of the cumulative infected individuals (C) and the effective reproduction number (R_e)

Parameter	R_e		C	
	PRCC	p-value	PRCC	p-value
β	0.6773	0.0000	0.6888	0.0000
C_a	-0.8100	0.0000	-0.8306	0.0000
C_s	-0.9360	0.0000	-0.9294	0.0000
θ	-0.0031	0.7829	0.0055	0.6243
D_{E_1}	-0.0161	0.1489	-0.2503	0.0000
D_{E_2}	0.9815	0.0000	0.9695	0.0000
D_{I_1}	0.7344	0.0000	0.6613	0.0000
D_{I_2}	0.0188	0.0931	0.0186	0.0960
τ	-0.8061	0.0000	-0.7994	0.0000
ξ	-0.0073	0.5124	-0.0577	0.0000

4.5 The influence of NPIs and vaccines

In order to visually reflect the effect of parameters, we increase the negative correlation parameters C_a, C_s, ξ, τ to see the change of the cumulative infected (see Figure 5).

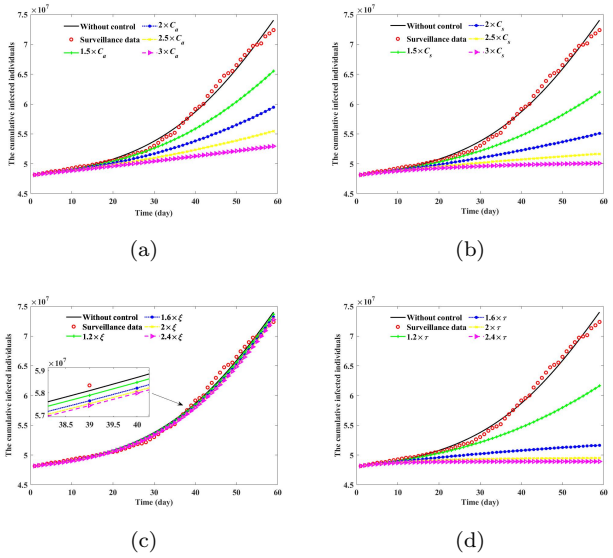


Figure 5: The influence of C_a, C_s, ξ, τ on the cumulative infected individuals

Figure 5 reflects the trend of the impact of key and changeable parameters on cumulative infected individuals. It then follows from Figure 5(a) and (b) that the cumulative infected individuals

decrease with the increase of C_a and C_s, and the decreasing range is relatively large. Figure 5(c) and (d) reveal that vaccination remains the best way to protect yourself from COVID-19 and reduce its impact on our communities. Obviously, the efficacy of vaccines has a significant effect on reducing the cumulative infected individuals. Due to the B.1.1.529 (Omicron) variant reducing the efficacy of vaccines and the low vaccination rate it will take months/years until herd immunity is achieved, NPIs play an important role in the prevention and control of COVID-19 pandemic. In the following, we accurately analyze the impact of of Non-pharmaceutical interventions(NPIs) in the controlling of Omicron.

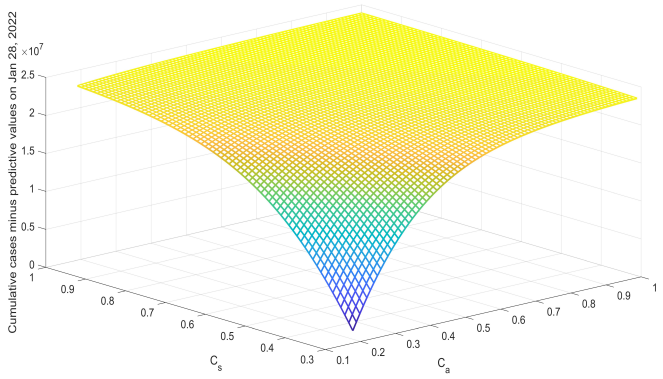


Figure 6: The decrement of numbers of infectious with the increase of C_s and C_a.

Figure 6 shows that C_s and C_a can effectively reduce the cumulative cases. Let P be the decrement of numbers of infectious with the increase of C_s and C_a and other parameters remain unchanged. More intuitively, we have listed the specific numbers under the different intensity of NPIs(see Table 3).

Table 3: The relationship between P and C_s and C_a

P \ C_a / C_s	0.25	0.30	0.35	0.40	0.45	0.50	0.55
0.25	2193012	6829268	10628490	13655266	16015034	17826122	19202489
0.30	6278878	10204768	13339429	15785173	17662236	19087127	20162639
0.35	9763993	13009947	15545466	17491289	18967047	20079078	20915447
0.40	12666658	15295503	17313090	18841975	19992234	20855512	21504429
0.45	15034670	17127191	18711686	19901940	20793364	21461773	21965320
0.50	16933247	18575890	19808021	20728878	21417641	21935110	22326802
0.55	18434315	19710283	20661943	21371969	21903948	22305474	22611549

It then follows from the data in Table 3 if C_s is raised from 0.30 to 0.50 and C_a is raised from 0.17 to 0.35, then there will be 19,808,021 fewer infected individual. Supposing that C_a

changes from 0.17 to 0.50 and C_s is raised from 0.30 to 0.35, then there will be 20,079,078 fewer infected individual. If both C_a and C_s are increased to 0.50, then there will be 21,935,110 fewer infected individual. According to the disease-induced mortality rate in the United States, if we take $C_s = 0.35$, $C_a = 0.50$, then 35,185 people are saved; If $C_s = 0.50$, $C_a = 0.35$, then 34,710 people are saved; If $C_s = 0.50$ and $C_a = 0.50$, then 38,437 people are saved.

4.6 The relationship among $\mathscr{R}_e$, NPIs and vaccine

At present, the efficacy of vaccine is not relatively low, and someone was diagnosed with the Omicron variant of COVID-19 despite having received two shots of the vaccine. In the following, we assume that all people are vaccined Janssen COVID-19 Vaccine and consider the relationship between $\mathscr{R}_e$ and C_s, C_a(see Figure 7).

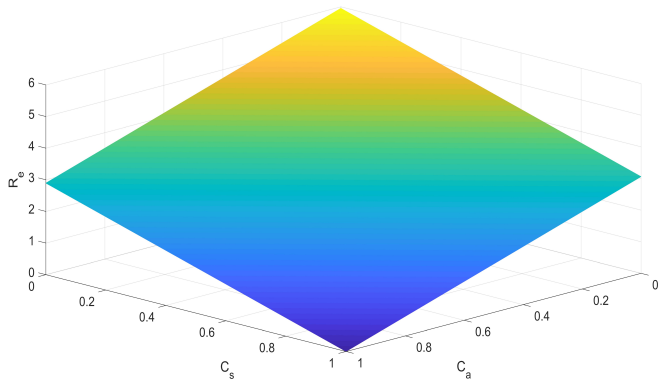


Figure 7: When $\tau = 0.33$ and $\xi = 1$, the image in three dimensions of relationship among $\mathscr{R}_e$, C_s and C_a.

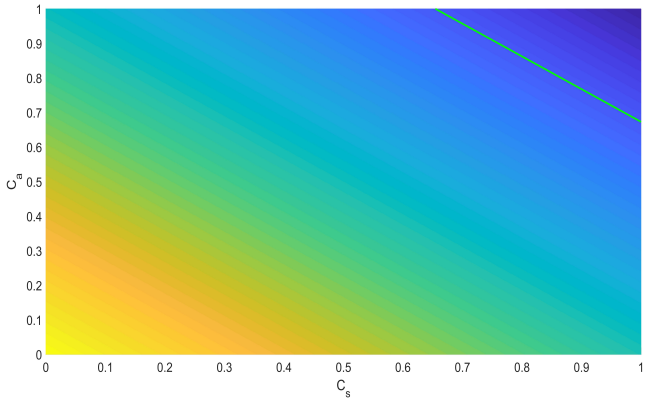


Figure 8: When $\tau = 0.33$ and $\xi = 1$, the relationship between C_s and C_a.

It can be seen from the above discussion that NPIs play a very significant role for the disease control. Figure 8 is the projection of Figure 7 on the $C_s \times C_a$ plane. The green line in Figure 8 represents $\mathscr{R}_e = 1$. Figure 7 shows if (C_a, C_s) belongs the area above the green line, then $\mathscr{R}_e < 1$, while $\mathscr{R}_e > 1$ in the area below the green line. Our numerical results shows that NPIs are indispensable even if all the people were vaccinated when the efficiency of vaccine is relatively low. In other words, in order to control the spread of Omicron, NPIs must be strengthened to make C_s and C_a in the area above the green line even if each people is vaccinated. Particularly, we suggest that NPIs should be strengthened, not weakened in the United States.

In the following, we study the role of the vaccine in the absence of NPIs.

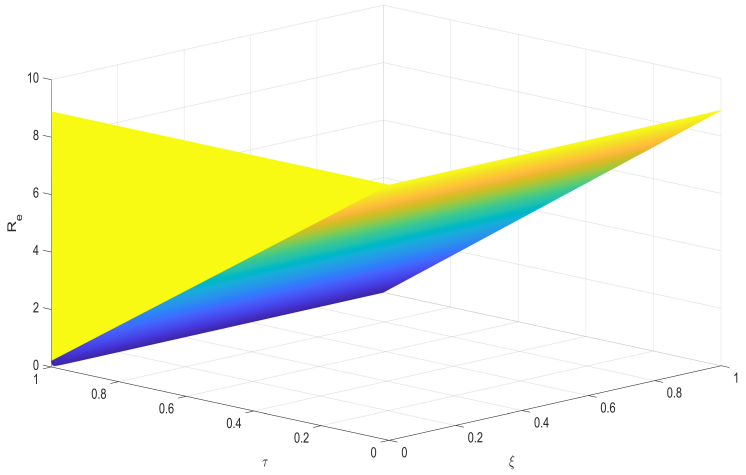


Figure 9: When $C_s = 0$ and $C_a = 0$, the relationship between ξ and τ and $\mathscr{R}_e$.

We observe that $\mathscr{R}_e$ decreases with the improvement of ξ, and finally $\mathscr{R}_e$ is less than 1 when $\tau = 0.9$(see Figure 9). $\mathscr{R}_e > 1$ holds even if $\xi = 1$ when $\tau = 0.33$. Let $\mathscr{R}_e = 1$, $C_a = C_s = 0$ and $\xi = 1$, it then follows from (4.1) that $\tau = 0.887$. In other words, $\mathscr{R}_e > 1$ always holds when $\tau < 0.887$. Hence, we have gotten a minimum standard of the efficacy rate of vaccine.

4.7 Herd immunity

In the following, we look for the possibility of herd immunity in the United States. It is easy see that $\tau\xi$ indicates the proportion of antibody produced after vaccination. Let $C_a = C_s = \xi = \tau = 0$ and $\mathscr{R}_0 = 8.883$. Theoretically, we conclude if $1 - \frac{1}{\mathscr{R}_0} < \tau\xi$ is satisfied [10], then the herd immunity is formed.

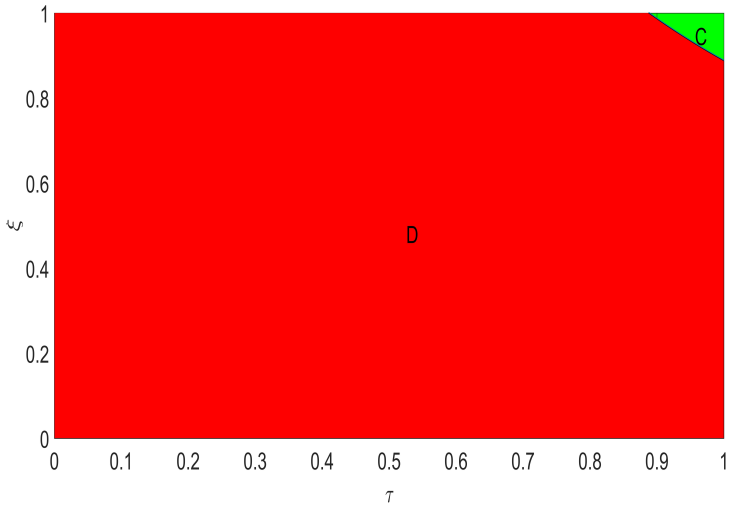


Figure 10: When $C_a = 0$ and $C_s = 0$, the relationship between herd immunity and τ and ξ

From Figure 10, it reveals that $\xi = 0.887$ when $\tau = 1$, and $\tau = 0.887$ if $\xi = 1$. The intersection of the area C and D is called the herd immunity line which satisfies $\tau\xi = 0.887$ and C is the herd immunity area where the condition $\tau\xi > 0.887$ is satisfied. Since there is a huge problem that some of American without any face coverings and unwilling to take the vaccine, and the efficacy of vaccines is low against Omicron, everyone should get vaccinated and boosted as soon as they are eligible, including people who have already had COVID-19.

4.8 Almost periodicity of disease-induced mortality rate

In the process of parameters analysis, we find that the disease-induced mortality rate demonstrates the periodic oscillation. To further confirm this, we use an almost periodic function

$$d(t) = 2.687608\times10^{-5}+1.419898\times10^{-5}\times\cos((407/400)*\sqrt{5}\pi t)+1.317339\times10^{-6}\times\sin((103/100)*\sqrt{6}\pi t)$$

to simulate the curve by MATLAB, and the simulation result can be shown in Figure 11. It's obviously that the surveillance and simulation fit very well. Since seasonal variations in temperature, rainfall, resource availability, contact rates, the birth and death rates of populations and immune defences are ubiquitous and can exert strong pressures on population dynamics [1], we think that this result is reasonable.

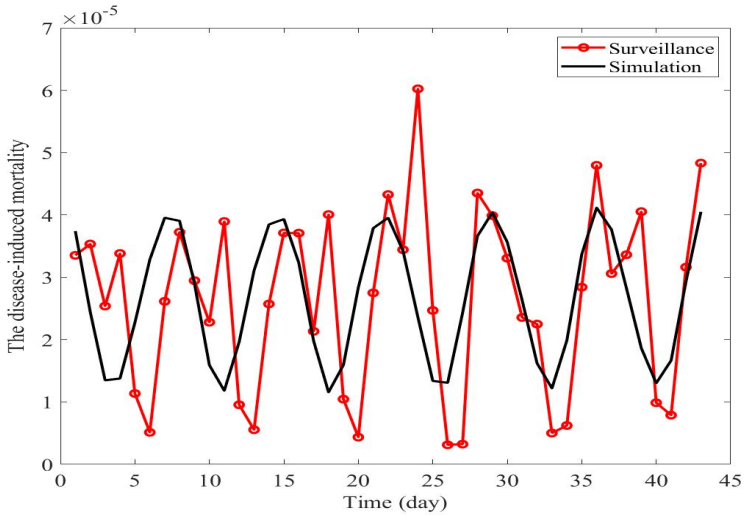


Figure 11: The simulation of the disease-induced mortality

5 Discussion

Emphasizing non-pharmaceutical interventions(NPIs) and vaccines, the transmission dynamics of an Omicron variant of COVID-19 model is considered by means of the reproduction number. In section 4, we considered the situations in the United States. Our numerical result predicts that the the United States epidemic will uniformly exist and form an endemic disease if the existing intensity of NPIs and the vaccine efficacy are maintained. If the outbreak occurs repeatedly, we suggest that NPIs should be strengthened. Furthermore, it is shown that NPIs are indispensable even if all the people were vaccinated when the efficiency of vaccine is relatively low. In order to obtain the herd immunity, we speculate in numerical simulation that the minimum efficacy of vaccine is 88.7%. In the face of the crisis of confidence of vaccine and logistical challenges, the herd immunity area is given. Certainly, we expect that COVID-19 will die out as soon as possible by the efforts of people of all over the world.

Author contributions BW contributed to conceptualization, project administration, writing-original draft, writing-review and editing; ZW and YW contributed to writing-review and editing, supervision; YX and JZ contributed to formal analysis, software, writing-original draft, writing-review and editing; ZW and ZM contributed to data curation, software.

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Availability of data and material The dataset used and/or analyzed during the current study is available from the published works.

Declarations

Conflict of interest The authors declare no conflict of interest.

Ethics approval and consent to participate The study protocol was approved by School of Mathematics and Statistics of Lanzhou University.

Appendix A. Proof of Theorem 3.1 and 3.2

Proof of Theorem 3.1: It is easy to see that $S(t)$ and $V(t)$ satisfy

$$\frac{dS}{dt} \leq \Lambda - \xi S - \mu S + \theta R$$

and

$$\frac{dV}{dt} \leq \xi S - \mu V,$$

respectively. Since system (3.1) has a unique positive constant solution (S^*, V^*), which is global asymptotically stable, by the comparsion theorem, for any $x^0 \in \mathbb{R}^7_+$ and $\varepsilon > 0$, there exists $t_0 > 0$ such that

$$S(t) \leq S^* + \varepsilon, V(t) \leq V^* + \varepsilon, \quad \forall t \geq t_0.$$

It then follows that

$$\begin{aligned}
\tfrac{dE_1}{dt} &\leq \beta(1-C_a)\tfrac{(S^*+\epsilon)E_2}{N} + \beta(1-C_s)\tfrac{(S^*+\epsilon)I_1}{N} + \beta(1-C_a)(1-\tau)\tfrac{(V^*+\epsilon)E_2}{N} \\
&\quad + \beta(1-C_s)(1-\tau)\tfrac{(V^*+\epsilon)I_1}{N} - \tfrac{E_1}{D_{E_1}} - \mu E_1, \\
\tfrac{dE_2}{dt} &\leq \tfrac{E_1}{D_{E_1}} - \tfrac{E_2}{D_{E_2}} - \mu E_2, \\
\tfrac{dI_1}{dt} &\leq \tfrac{E_2}{D_{E_2}} - \tfrac{I_1}{D_{I_1}} - \mu I_1.
\end{aligned}$$

we consider the following system

$$\begin{aligned}
\tfrac{dE_1}{dt} &= \beta(1-C_a)\tfrac{(S^*+\epsilon)E_2}{N} + \beta(1-C_s)\tfrac{(S^*+\epsilon)I_1}{N} + \beta(1-C_a)(1-\tau)\tfrac{(V^*+\epsilon)E_2}{N} \\
&\quad + \beta(1-C_s)(1-\tau)\tfrac{(V^*+\epsilon)I_1}{N} - \tfrac{E_1}{D_{E_1}} - \mu E_1, \\
\tfrac{dE_2}{dt} &= \tfrac{E_1}{D_{E_1}} - \tfrac{E_2}{D_{E_2}} - \mu E_2, \\
\tfrac{dI_1}{dt} &= \tfrac{E_2}{D_{E_2}} - \tfrac{I_1}{D_{I_1}} - \mu I_1.
\end{aligned} \tag{1}$$

Denote $F_1^\epsilon = \beta(1-C_a)\frac{(N^*+2\epsilon)-\tau(V^*+\epsilon)}{N}$ and $F_2^\epsilon = \beta(1-C_s)\frac{(N^*+2\epsilon)-\tau(V^*+\epsilon)}{N}$.

Let

$$Y^\epsilon = \begin{pmatrix} 0 & F_1^\epsilon & F_2^\epsilon \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}.$$

Since $\mathscr{R}_e < 1$, then $\omega(-Z+Y) < 0$, where $\omega(-Z+Y)$ is the exponential growth bound [40]. By the continuity of spectral bound, there exists a sufficiently small $\epsilon_1 > 0$ such that $\omega(-Z+Y^\epsilon) < 0$

for $0 < \epsilon < \epsilon_1$, which implies that the trivial solution of the system (1) is globally asymptotically stable. By the comparison theorem of ordinary differential equation, we deduce that $E_1 \to 0, E_2 \to 0, I_1 \to 0$ as $t \to \infty$. It then follows that system (3.1) is the limiting system of S, V equation in system (2.1). We also could get that I_2, R equation admit the limiting system

$$\begin{aligned} \frac{dI_2}{dt} &= -\frac{I_2}{D_{I_2}} - \mu I_2, \\ \frac{dR}{dt} &= \frac{I_2}{D_{I_2}} - \mu R - \theta R. \end{aligned} \tag{2}$$

It is easy to see that the solutions in (2) convergence to $(0, 0)$. Finally, by the theory of asymptotically autonomous systems (see, e.g. [4]), we conclude that the solution of system (2.1) converges to $(S^*, V^*, 0, 0, 0, 0, 0)$. This confirms the global attractivity of $\mathcal{E}^*$ for system (2.1) under the condition $\mathscr{R}_e < 1$, and hence completes the proof.

Proof of Theorem 3.2: Define

$$X = \mathbb{R}^7_+,$$

$$X_0 := \{(S, V, E_1, E_2, I_1, I_2, R) \in X : E_1 > 0, E_2 > 0, I_1 > 0\}$$

$$\partial X_0 := X \backslash X_0$$

Then X_0 and ∂X_0 are relatively open and closed in $\mathbb{R}^7$, respectively. For any $x^0 \in X_0$, let $\psi_t(x^0)$ be the unique solution of system (2.1) with initial data x^0. It is easy to see that X_0 is a positively invariant set. According to the arguments in Section 2, the solution of (2.1) is ultimately bounded in X, which implies that $\psi_t : X \to X$ is point dissipative on X. It follows from [15, Theorem 3.4.8] that ψ_t has a global compact attractor $\mathcal{A}$.

Define

$$M_\partial := \{x^0 \in \partial X_0 : \psi_t(x^0) \in \partial X_0, \forall t \geq 0\}$$

and

$$\mathcal{M} := \{x^0 \in X : x^0_1 = S^*, x^0_2 = V^*, x^0_3 = x^0_4 = x^0_5 = 0\}.$$

We now show that

$$M_\partial = \mathcal{M}.$$

For any $x^0 \in \mathcal{M}$, the solution $\psi_t(x^0)$ satisfies $E_1(t, x^0) = 0, E_2(t, x^0) = 0, I_1(t, x^0) = 0$ for all $t \geq 0$. Hence, $x^0 \in M_\partial$ and $\mathcal{M} \subset M_\partial$.

For any $x^0 \in \partial X_0 \backslash \mathcal{M}$, there is (x^0_3, x^0_4, x^0_5) such that $(x^0_3, x^0_4, x^0_5) = (E_1(0), E_2(0), I_1(0)) > (0, 0, 0)$.

Case 1 Let $E_1(0) > 0$. Then the third equation of system (2.1) satisfies

$$\frac{dE_1}{dt} \geq -\frac{E_1}{D_{E_1}} - \mu E_1.$$

Furthermore, there exists a $t_0 > 0$ such that $E_1(t) > 0$ for all $t \geq t_0$.

From the third equation of system (2.1), we can get $E_2(t) > 0\ \forall t \geq t_0 + 1$. Then, from the fourth equation of system (2.1), we deduct that $I_1(t) > 0$ for all $t \geq t_0 + 2$.

Case 2 Let $E_2(0) > 0$. By the fourth equation of system (2.1), we have

$$\frac{dE_2}{dt} \geq -\frac{E_2}{D_{E_2}} - \mu E_2.$$

Thus, we can get $E_2(t) > 0, \forall t > 0$. Now, the third equation satisfies

$$\frac{dE_1}{dt} \geq \beta(1 - C_a)\frac{SE_2}{N} - \frac{E_1}{D_{E_1}} - \mu E_1.$$

It is easy to see that $E_1(t) > 0$ for $t > 1$. By the arguments in **Case 1**, we can obtain that $(E_1(t), E_2(t), I_1(t)) \gg (0, \cdots, 0, 0 \cdots, 0, 0, \cdots, 0)$ for all $t > t_0 + 3$.

Case 3 Let $I_1(0) > 0$. By the fifth equation of system (2.1), we have

$$\frac{dI_1}{dt} \geq -\frac{I_1}{D_{I_1}} - \mu I_1.$$

Hence, we can get $I_1(t) > 0, \forall t > 0$. Now, the second equation of system (2.1) satisfies

$$\frac{dE_1}{dt} \geq \beta(1 - C_s)\frac{SI_1}{N} - \frac{E_1}{D_{E_1}} - \mu E_1.$$

It is easy to see that $E_1(t) > 0$ for $t > 1$. By the arguments in **Case 1**, we can obtain that $(E_1(t), E_2(t), I_1(t)) \gg (0, \cdots, 0, 0 \cdots, 0, 0, \cdots, 0)$ for all $t > t_0 + 3$.

Then $M_\partial \subset \mathcal{M}$. Hence, $M_\partial = \mathcal{M}$.

We claim that $W^s(\mathcal{M}) \cap X_0 = \emptyset$, where $W^s(\mathcal{M})$ is the stable manifold of $\mathcal{M}$. Let $\bar{\lambda} = \beta(1 - C_a)\frac{(N^* - 2\epsilon) - \tau(V^* - \epsilon)}{N}$ and $\bar{\eta} = \beta(1 - C_s)\frac{(N^* - 2\epsilon) - \tau(V^* - \epsilon)}{N}$. Denote

$$\bar{F}_1^\epsilon = \bar{\lambda},\ \bar{F}_2^\epsilon = \bar{\eta}$$

Let

$$\bar{Y}^\epsilon = \begin{pmatrix} 0 & F_1^\epsilon & F_2^\epsilon \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}.$$

Since $\mathscr{R}_e > 1$, then $\omega(Y - Z) > 0$. By the continuity of spectral bound, there exists a sufficiently small $\epsilon_1 > 0$ such that $\omega(\bar{Y}_\epsilon - Z) > 0$ for $0 < \epsilon \leq \epsilon_1$.

Claim. If $x^0 \in X_0$, then

$$\limsup_{t \to \infty} d(\psi_t(x^0), \mathcal{M}) \geq \epsilon_1$$

On the contrary, we assume that there exists $\bar{x}^0 \in X_0$ such that $\limsup_{t \to \infty} d(\psi_t(\bar{x}^0), \mathcal{M}) < \varepsilon_1$. It then follows that there exists $t_0 > 0$ such that

$$S^* - \varepsilon_1 < S(t) < S^* + \varepsilon_1, V^* - \varepsilon_1 < V(t) < V^* + \varepsilon_1$$

for all $t \geq t_0$. Hence, we have

$$\begin{array}{ll} \frac{dE_1}{dt} & \geq \beta(1 - C_a)\frac{(S^* - \varepsilon_1)E_2}{N} + \beta(1 - C_s)\frac{(S^* - \varepsilon_1)I_1}{N} + \beta(1 - C_a)(1 - \tau)\frac{(V^* - \varepsilon_1)E_2}{N} \\ & \quad + \beta(1 - C_s)(1 - \tau)\frac{(V^* - \varepsilon_1)I_1}{N} - \frac{E_1}{D_{E_1}} - \mu E_1, \\ \frac{dE_2}{dt} & \geq \frac{E_1}{D_{E_1}} - \frac{E_2}{D_{E_2}} - \mu E_2, \\ \frac{dI_1}{dt} & \geq \frac{E_2}{D_{E_2}} - \frac{I_1}{D_{I_1}} - \mu I_1. \end{array} \tag{3}$$

Since $-Z+\bar{Y}_\epsilon$ is irreducible and essentially nonnegative, it has a positive eigenvector associated with $\omega(-Z+\bar{Y}_\epsilon)>0$. By the comparison theorem of ordinary differential equations, we have $\lim_{t\to\infty} E_1(t)=\infty, \lim_{t\to\infty} E_2(t)=\infty, \lim_{t\to\infty} I_1(t)=\infty$, a contradiction. The claim is proved.

The set $M_\partial=\mathcal{M}$ is an isolated invariant set and acyclic. By [32, Theorem 4.6], we conclude that system (2.1) is uniformly persistent in X_0 whenever $\mathscr{R}_e>1$. That is, there is a $\tilde{\varepsilon}>0$ such that

$$\liminf_{t\to\infty} E_1(t)>\tilde{\varepsilon}, \liminf_{t\to\infty} E_2(t)>\tilde{\varepsilon}, \liminf_{t\to\infty} I_1(t)>\tilde{\varepsilon}.$$

This completes the proof.

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