Dynamic Behaviour of Multi-Stage Epidemic Model with Imperfect Vaccine

Yuan Wang, Shidong Zhai, Ming Du and Penglei Zhao

***Abstract*—This paper introduces a general multi-stage epidemiological model with imperfect vaccine, which allows for possible deterioration and improvement between any two stages of infection. The proposed model can describe disease progression through multiple latent or infectious stages. We conduct a detailed theoretical analysis of the proposed model and find that the basic reproduction number $\Re_0$ is very important for the demise of the disease. When $\Re_0$ is less than or equal to one, the disease will eventually die out. When $\Re_0$ is greater than one, the disease will eventually become pandemic, and we propose a new Lyapunov function to prove this fact. Moreover, we obtain a relationship between $\Re_0$ and vaccination ratio, which indicates that $\Re_0$ decreases as the vaccination ratio increases. This property can be used to control the disease epidemic by adjusting the vaccination ratio. Finally, we use two numerical examples to illustrate the effectiveness of the obtained results.**

***Index Terms*—Multi-stage, vaccination ratio, pandemic, basic reproduction number.**

I. Introduction

In nature, there are a wide variety of infectious diseases, many of which the hosts go through multiple distinct stages, such as HIV, viral hepatitis, bacterial tuberculosis and cholera which are transmitted virally, Plague, Typhoid Bacillus, Diphtheria Bacillus, etc. which are all transmitted by bacteria. Although there were many infectious diseases have been effectively controlled, such as Smallpox which has been eliminated worldwide, plague and cholera which have been effectively controlled. The pandemic of COVID-19 has made people pay more attention to the spread of the virus [1]–[6]. COVID-19 is a highly contagious multi-host infectious disease. Its pathogen can not only survive in wild animals for a long time and cause transmission among animals, but also can be transmitted to humans through wild animals. It is of great significance to predict the epidemic trend of diseases by using mathematical models for evaluating public health status and formulating prevention and control strategies [7]–[13].

In order to describe the multiple stages of virus development, various models have been proposed, such as the Markovchain model or the staged progression (SP) model which can describe the temporal variability of infection [14]–[18], and multistage transmission models which have been established in the literature for long-delayed disease development [19]. In [20], a system of differential and integral equations was used to build a multi-stage model with a general distribution function for the infection stages. If the distributions are of Gamma type, the resulting models are described as larger systems of ODEs using the "linear chain trick" [21]. In [15], the SP model was derived directly from ordinary differential equations (ODEs). In [18], disease amelioration was added to the SP model of HIV for the first time. In [22], an infectious disease model was proposed in which susceptible individuals can be transferred to any stage of infection. When individuals in a susceptible population come into contact with infected individuals, these newly infected patients may skip the initial stages of the disease and go directly to any stage of infection. In [23], the authors analyzed the global dynamics of a general n-stage phase progression model with bilinear incidence. The reference [24] used graph theory to study the global dynamics of the staged development model for the first time.

While vaccination is the most effective way to completely control the spread of various viruses, many people have reduced immunity over time after vaccination [25]–[28]. Therefore, although vaccines can reduce the rate of infection, they do not completely prevent infection. For multistage virus models, there is no literature on partial immunity, which is common in real life. To this end, this paper proposes a multi-stage virus transmission model with partial immunity. This model allows for possible deterioration and improvement between any two stages of infection. The total population is divided into a susceptible compartment, a vaccinated compartment, a recovered compartment, and some infective compartments.

For the proposed model, we conduct a detailed theoretical analysis, and find that the basic reproduction number $\Re_0$ is very important for the demise of the disease. If $\Re_0$ is less than or equal to one, the disease will eventually die out. We propose a new Lyapunov function to prove that if $\Re_0$ is greater than one, the disease will eventually become pandemic. The relationship between $\Re_0$ and vaccination ratio shows that $\Re_0$ decreases as the vaccination ratio increases. This property can be used to control the disease epidemic by adjusting the vaccination ratio.

The structure of this paper is as follows. We present the multi-stage epidemiological model in Section 2. In Section 3, we give a mathematical definition of $\Re_0$ and explain what it represents in biology. In Sections 4 and 5, we carry out mathematical analysis of the global dynamics of the model for the case $y(N) \equiv 1$. In Section 6, we give two numerical examples to illustrate the effectiveness of the obtained results.

Manuscript received June 25, 2022; revised October 15, 2022.

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II. Formulation of the Model

We divide the host of the infection stage into n states according to the severity of the disease, where n is a finite number. Let $I_i(t)$ represents the number of infected individuals in stage i at time t, where $1 \leq i \leq n$. $S(t)$ represents the number of susceptible people at time t, $V(t)$ represents the number of individuals vaccinated at time t, and $R(t)$ represents the number of patients who recovered to health at time t. If an individual in a compartment dies, the individual will be removed from the entire transport network. $N(t) = S(t)+V(t)+I_1(t)+I_2(t)+\cdots+I_n(t)$ represents the number of people transmitted throughout the network. When all $I_i(t) = 0$, it means that there is no virus transmission, and the population dynamics in the entire network can be described by the differential equation: $\dot{S} = \omega(S)$, where $\omega(S) = \Lambda - dS - pS$. Using the function $\phi_{ij}(I_j)$ denotes the rate at which individuals transition from the jth stage to the ith stage, where $1 \leq i, j \leq n$. $\phi_{ij}(I_j)$ expresses the rate at which the disease progresses towards worsening, where $i > j$. When $i < j$, it indicates the rate of improvement. We assume that $\phi_{ii} \equiv 0$. $\phi_{n+1,i}$ represents the probability of recovery from the ith state of infection, where $1 \leq i, j \leq n$. Alternatively, the infected individuals were moved to the recovered compartment R.

Viral infection can occur when a susceptible individual comes into contact with any infected individual in stage i. The incidence term usually uses the form: $\Sigma_{i=1}^{n} y(N)h_i(S, I_i)$. We take $y(N)$ as the density dependence. Infection can also happen when a vaccinated individual comes into contact with any infected individual in stage i when the vaccine is ineffective. The incidence term usually uses the following general form: $\Sigma_{i=1}^{n} y(N)g_i(V, I_i)$. The function y takes the classical form: $y(N) = N^{-t}, 0 \leq t \leq 1$. h_i represents the incidence of infection between S and I_i in the stage i. If a person is vaccinated, the infection rate will be drastically reduced compared to an unvaccinated susceptible population. g_i represents the incidence of infection from contact between V and I_i in the stage i. p denotes the vaccination rate. Let $\zeta_i(I_i)$ represents the removal rate from I_i, including those who died naturally, those who died after being infected by the virus, and those who left the virus transmission network for other reasons. It's common form is exponential removal: $\zeta_i(I_i) = d_i I_i$. According to the above assumptions and changes in the number of R are not taken into account. Our model can be described by the following system of ordinary differential equations(ODEs):

$$
\begin{aligned}
\dot{S} &= \omega(S) - y(N)\sum_{j=1}^{n} h_j(S, I_j), \\
\dot{V} &= pS - d_0 V - y(N)\sum_{j=1}^{n} g_j(V, I_j), \\
\dot{I}_1 &= y(N)\sum_{j=1}^{n} h_j(S, I_j) + y(N)\sum_{j=1}^{n} g_j(V, I_j) \\
&\quad + \sum_{j=1}^{n} \phi_{1j}(I_j) - \sum_{j=1}^{n+1} \phi_{j1}(I_1) - \zeta_1(I_1), \\
\dot{I}_i &= \sum_{j=1}^{n} \phi_{ij}(I_j) - \sum_{j=1}^{n+1} \phi_{ji}(I_i) - \zeta_i(I_i),
\end{aligned}
\tag{1}
$$

where $i = 2, 3, \ldots, n$.

The transfer network in Fig. 1 depicts the way in which the population is transferred across the compartments in this network.

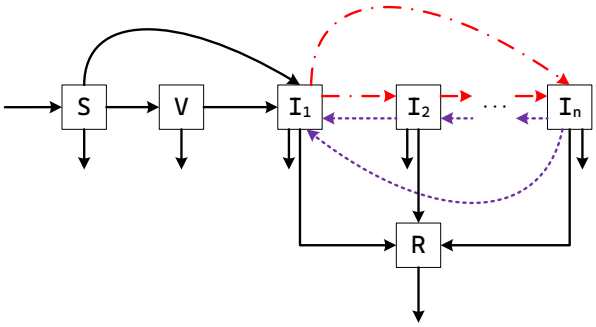

Fig. 1. The transfer diagram for model (1). Forward arrows between I_j compartments indicate disease progression and backward arrows indicate disease amelioration.

The general form of the functions in model (1): $y(N)$, h_j, g_j, $\phi_{ij}(I_j)$, and $\zeta_i(I_i)$ are assumed to be smooth enough to satisfy the existence and uniqueness of the solution. Based on biological principles, we make the following assumptions:

(A_1) There exists $\bar{S} > 0$ such that $\omega(\bar{S}) = 0$ and $\omega(S)(S - \bar{S}) < 0$ for all $S \geq 0$ and $S \neq \bar{S}$.

(A_2) For all $N > 0$, $y(N) > 0$ and $y(N)$ is nonincrementing.

(A_3) For $1 \leq i \leq n$, $h_i(S, I_i) \geq 0$ for all $S(t) \geq 0$, $I_i(t) \geq 0$; $g_i(V, I_i) \geq 0$, for all $V(t) \geq 0$, $I_i(t) \geq 0$ and $g_i(0, I_i) = h_i(S, 0) = h_i(0, I_i) = g_i(V, 0) = 0$.

(A_4) For $1 \leq i, j \leq n$, $\phi_{ij} \geq 0$ for all $I_j \geq 0$; $\sum_{j=1}^{n} \phi_{ji}(I_i) = 0$ only when $I_i = 0$.

(A_5) For $1 \leq j \leq n$, $\zeta_j(0) = 0$, the constant $d_j > 0$ makes $\zeta_j(I_j) \geq d_j I_j$ hold, where all $I_j \geq 0$ and $j = 1, 2, 3, \ldots, n$.

The Assumption (A_1) ensures $\bar{S} > 0$ when the disease is absent. A common form of ω is $\omega(S) = \Lambda - dS - pS = 0$, and $\bar{S}$ is a positive root of the equation. Consider the practical implications, we only consider solutions in the non-negative and bounded range. This can be verified that for all $t \geq 0$, if the initial conditions of system (1) are non-negative, then the solutions of system (1) are all non-negative. Moreover, from the first differential equation of system (1) we get that $\dot{S}(t) \leq \omega(S)$. Hence, according to (A_1), $\limsup_{t\to\infty} S(t) \leq \bar{S}$.

The Assumption (A_5) guarantees that the total population in the network remains bounded. If we add all the differential equations of system (1), then we can get the derivative with respect to the total number of people $\dot{N} = \Lambda - dS - d_0 V - \zeta_1(I_1) - \cdots - \zeta_n(I_n) \leq \Lambda - d^* N$, where $d^* = \min\{d, d_0, d_1, \ldots, d_n\}$. This leads to $\limsup_{t\to\infty} N(t) \leq \frac{\Lambda}{d^*}$. Similarly, from the second differential equation of (1), we know that $\dot{V} \leq pS - d_0 V$, and thus, $\limsup_{t\to\infty} V(t) \leq \frac{p}{d_0}\bar{S}$. R^n stands for n-dimensional real vector space. Therefore, all solutions of model (1) are bounded and its feasible region can be written as: $\Gamma = \{(S, V, I_1, I_2, \ldots, I_n) \in R^{n+2} : 0 \leq S \leq \bar{S}, 0 \leq V \leq \frac{p\bar{S}}{d_0} = \bar{V}, 0 \leq S + V + I_1 + I_2 + \cdots + I_n \leq \frac{\Lambda}{d^*}\}$. This set is positive and invariant to system (1), and this conclusion can be proved.

The Assumption (A_2) is satisfied by the class of functions $y(N) = N^{-t}$, $0 \leq t \leq 1$. The Assumption (A_3) allows

the possibility of $g_i \equiv 0$ and $h_i \equiv 0$ for some stages while requiring that overall transmission is nonzero. In this way, we can consider certain stages of infection as latent or quarantined. The Assumption $(A4)$ implies that transfers out of a stage i is nonzero while transfers into the stage may be zero. This ensures the disease progresses through all the I_j stages and the only terminal stage is R.

For notational convenience, we set:

$$K_i(I_i) = \sum_{j=1}^{n+1} \phi_{ji}(I_i) + \zeta_i(I_i), \quad 1 \le i \le n. \tag{2}$$

Then, the Assumption $(A4)$ implies that $K_i(I_i) = 0$ if and only if $I_i = 0$, for $i = 1, \ldots, n$. We can rewrite model (1) in the following form:

$$\begin{aligned}
\dot{S} &= \omega(S) - y(N)\sum_{j=1}^{n} h_j(S, I_j),\\
\dot{V} &= pS - d_0 V - y(N)\sum_{j=1}^{n} g_j(V, I_j),\\
\dot{I}_1 &= y(N)\sum_{j=1}^{n} h_j(S, I_j) + y(N)\sum_{j=1}^{n} g_j(V, I_j)\\
&\quad + \sum_{j=1}^{n} \phi_{1j}(I_j) - K_1(I_1),\\
\dot{I}_i &= \sum_{j=1}^{n} \phi_{ij}(I_j) - K_i(I_i), \quad i = 2, 3, \ldots, n.
\end{aligned} \tag{3}$$

III. Equilibria and the basic reproduction number $\Re_0$

The basic reproduction number $\Re_0$ can be represented by the spectral radius of the next generation matrix [29]. The unique positive solution $\bar{S}$ can be obtained from the equation $\omega(S) = 0$. Different values of $\Re_0$ have different biological meanings. When $\Re_0 \le 1$, the disease-free equilibrium is globally asymptotically stable. Regardless of the scale of the outbreak, the disease will eventually become extinct. When $I_j = 0$, $h_j(S, I_j) = 0$, $g_j(V, I_j) = 0$, $\phi_{ij}(I_j) = 0$, $K_i(I_i) = \sum_{j=1}^{n+1} \phi_{ji}(I_i) + \zeta_i(I_i) = 0$. The system (3) has a unique disease-free equilibrium $P_0 = (\bar{S}, \bar{V}, 0, \ldots, 0)$. When $\Re_0 > 1$, the disease-free equilibrium is unstable, and if the state transition graph of the system is strongly connected, then the system has a unique epidemic equilibrium at this time. Then the disease will always exist and will not go extinct. A positive equilibrium of (3) is called an endemic equilibrium, and denoted by $P^* = (S^*, V^*, I_1^*, \ldots, I_n^*)$, where $S^*, V^*, I_1^*, \ldots, I_n^* > 0$ satisfies the following equilibrium equations:

$$\begin{aligned}
\omega(S^*) &= y(N^*)\sum_{j=1}^{n} h_j(S^*, I_j^*),\\
d_0 V^* &= pS^* - y(N^*)\sum_{j=1}^{n} g_j(V^*, I_j^*),\\
K_1(I_1^*) &= y(N^*)\sum_{j=1}^{n} h_j(S^*, I_j^*)\\
&\quad + y(N^*)\sum_{j=1}^{n} g_j(V^*, I_j^*) + \sum_{j=1}^{n} \phi_{1j}(I_j^*),\\
K_i(I_i^*) &= \sum_{j=1}^{n} \phi_{ij}(I_j^*), \quad i = 2, 3, \ldots, n,\\
N^* &= S^* + V^* + \sum_{j=1}^{n} I_i^*.
\end{aligned} \tag{4}$$

In order to derive the basic reproduction number $\Re_0$, we make the following assumptions:

(A_6) There exist constants $0 \le \mu_j \le \infty$, $1 \le j \le n$, and $\max_j\{\mu_j\} > 0$ such that $\lim_{I_j \to 0^+} \frac{h_j(\bar{S}, I_j) + g_j(\bar{V}, I_j)}{K_j(I_j)} = \mu_j$.

(A_7) For $1 \le i, j \le n$, these constants b_{ij} make $\lim_{I_j \to 0^+} \frac{\phi_{ij}(I_j)}{K_j(I_j)} = b_{ij}$ hold, where $0 \le b_{ij} < \infty$.

(A_8) For $1 \le j \le n$, $\liminf_{I_j \to 0^+} \frac{I_j}{K_j(I_j)} > 0$. Let

$$E = \begin{bmatrix} y(\bar{S}+\bar{V})\mu_1 & y(\bar{S}+\bar{V})\mu_2 & \ldots & y(\bar{S}+\bar{V})\mu_n \\ 0 & 0 & \ldots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \ldots & 0 \end{bmatrix}$$

and

$$F = \begin{bmatrix} 1 & -b_{12} & \ldots & -b_{1n} \\ -b_{21} & 1 & \ldots & -b_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ -b_{n1} & -b_{n2} & \ldots & 1 \end{bmatrix}$$

Since $K_i(I_i) \ge \sum_{j=1}^{n+1} \phi_{ji}(I_i) + d_i I_i$, for each i, by assumption (A_8) we have $\sum_{i=1}^{n} b_{ij} < 1$, thereupon, F is diagonally dominant in rows. Consequently, F is a nonsingular M-matrix whose inverse F^{-1} is nonnegative [30]. According to [31], [32], $\Re_0$ of our given model (3) is as follows:

$$\Re_0 = \rho(EF^{-1}). \tag{5}$$

We proceed to formulate the following assumptions:

(A_9) For $1 \le j \le n$, $h_j(S, I_j) + g_j(V, I_j) \le h_j(\bar{S}, I_j) + g_j(\bar{V}, I_j)$ holds for all $0 \le S \le \bar{S}$, $0 \le V \le \bar{V}$, $I_j \ge 0$; If $h_j(S, I_j) = h_j(\bar{S}, I_j) \not\equiv 0$, then $S = \bar{S}$; If $g_i(V, I_i) = g_i(\bar{V}, I_i) \not\equiv 0$, then $V = \bar{V}$, for $I_i > 0$, $\frac{h_i(\bar{S}, I_i) + g_i(\bar{V}, I_i)}{K_i(I_i)} \le \mu_i$. If $h_i(S, I_i) + g_i(V, I_i) = h_i(\bar{S}, I_i) + g_i(\bar{V}, I_i) \not\equiv 0$, then $S = \bar{S}, V = \bar{V}$.

(A_{10}) For all $I_j > 0$, $1 \le i, j \le n$, $\sup_{I_j > 0} \frac{\phi_{ij}(I_j)}{K_j(I_j)} = b_{ij}$.

(A_{11}) We consider that $h_i(S, I_i) = \alpha_i S I_i$, $g_i(V, I_i) = \beta_i V I_i$, $\phi_{n+1,i} = \gamma_i I_i$ and $\phi_{ij} = \delta_{ij} I_j$. $\alpha_i \ge \beta_i$, then $0 \le \frac{\beta_i}{\alpha_i} \le 1$.

Theorem 1: Assume that assumptions $(A_1) - (A_9)$ hold. Let

$$(\nu_1, \nu_2, \ldots, \nu_n) = y(\bar{S} + \bar{V})(\mu_1, \mu_2, \ldots, \mu_n)F^{-1}. \tag{6}$$

Then $\nu_j \geq 0$, $1 \leq j \leq n$, and $\max_{1\leq j\leq n}\{\nu_j\} > 0$. Additionally, we can draw the following conclusions

(1) Nonnegative matrix EF^{-1} has a unique positive eigenvalue $\rho(EF^{-1})$.

(2) $\Re_0 = \rho(EF^{-1}) = \nu_1$.

Proof: Using (6) to rewrite the expression of matrix E can get

$$E = (1, 0, \ldots, 0)^T (y(\bar{S} + \bar{V})\mu_1, \ldots, y(\bar{S} + \bar{V})\mu_n). \quad (7)$$

By (6) and (7), we have $EF^{-1} = (1, 0, \ldots, 0)^T(\nu_1, \nu_2, \ldots, \nu_n)$. Then the rank of the matrix EF^{-1} is one. Therefore, ν_1 is the only positive eigenvalue of matrix EF^{-1}, leading to $\Re_0 = \rho(EF^{-1}) = \nu_1$. ■

Theorem 2: Suppose that assumptions (A_1)-(A_{11}) hold. According to Theorem 3.1, $\Re_0$ decreases with the increase of the vaccination rate p, and $\Re_0$ is a monotonically decreasing function with respect to the vaccination rate p.

Proof: ϵ is an n-dimensional column vector, which is the first column of the inverse matrix of matrix F. Furthermore, equation $\bar{S} = \frac{d_0}{p}\bar{V}$ holds.

$$\begin{aligned}
\Re_0 &= \nu_1 \\
&= y(\bar{S} + \bar{V})(\nu_1, \nu_2, \ldots, \nu_n)\epsilon \\
&= y(\frac{d_0 + p}{p}\bar{V})\frac{\sum_{i=1}^n (\frac{\alpha_i d_0}{p})\bar{V}}{\sum_{i=1}^n \sum_{j=1}^n (\delta_{ji} + \gamma_i + d_i)} \\
&= \bar{V}^{1-t}\frac{\sum_{i=1}^n (\frac{d_0}{p}\alpha_i + \beta_i)}{(\frac{d_0}{p} + 1)^t}\frac{\epsilon_i}{\sum_{i=1}^n \sum_{j=1}^n (\delta_{ji} + \gamma_i + d_i)}.
\end{aligned} \quad (8)$$

Let $l(p)$ be a function of p: $l(p) = \frac{\sum_{i=1}^n (\frac{d_0}{p}\alpha_i + \beta_i)}{(\frac{d_0}{p}+1)^t}$.

$$\dot{l} = \frac{d_0}{p^2}\left(-\sum_{i=1}^n \alpha_i + t\sum_{i=1}^n (\frac{d_0}{p}\alpha_i + \beta_i)(\frac{d_0}{p} + 1)^{-1}\right). \quad (9)$$

Because of $\frac{d_0}{p^2} > 0$, let $c(p) = -\alpha_i + t(\frac{d_0}{p}\alpha_i + \beta_i)(\frac{d_0}{p} + 1)^{-1}$, $0 \leq t \leq 1$, $0 \leq \frac{\beta_i}{\alpha_i} \leq 1$. When $c(p) < 0$, function $\Re_0$ decreases monotonically with respect to p. Solving the inequality $c(p)$, $p > 0$. Therefore, the size of $\Re_0$ can be controlled by the vaccination rate p. ■

IV. Global dynamics when $\Re_0 \leq 1$

This section will show that the disease-free equilibrium P_0 is globally asymptotically stable (unstable) when $\Re_0 \leq 1$ ($\Re_0 > 1$).

Theorem 3: Assume that Assumptions $(A_1) - (A_{10})$ hold. If $\Re_0 \leq 1$, then the disease-free equilibrium P_0 is globally asymptotically stable in Γ; If $\Re_0 > 1$, then the disease-free equilibrium P_0 is unstable. Moreover, if the network graph of model (3) is strongly connected, then the system is uniformly persistent in the interior $\mathring{\Gamma}$ of the scope of the feasible region Γ.

Proof: Let $y(N) \equiv 1$ and $(\nu_1, \nu_2, \ldots, \nu_n) = (\mu_1, \mu_2, \ldots, \mu_n)F^{-1} \geq 0$, then by Theorem 3.1, $\Re_0 = \nu_1 \leq 1$. Define a Lyapunov function:

$$H(I_1, I_2, \ldots, I_n) = (\nu_1, \nu_2, \ldots, \nu_n)(I_1, I_2, \ldots, I_n)^T. \quad (10)$$

Taking the derivative of H, and using the ordinary differential equations for S, I, V in model (3) to simplify the derivative of H, we get

$$\begin{aligned}
\dot{H} &= (\nu_1, \nu_2, \ldots, \nu_n)(I_1', I_2', \ldots, I_n')^T \\
&= \nu_1 \sum_{j=1}^n (h_j(S, I_j) + g_j(V, I_j)) \\
&\quad + \sum_{i=1}^n \nu_1 \left(\sum_{j=1}^n \phi_{ij}(I_j) - K_i(I_i)\right) \\
&= \nu_1 \mathcal{N}\mathcal{P} - (\nu_1, \nu_2, \ldots, \nu_n)\mathcal{M}\mathcal{P}.
\end{aligned} \quad (11)$$

where

$$\mathcal{M} = \begin{bmatrix} 1 & -\frac{\phi_{12}(I_2)}{K_2(I_2)} & \cdots & -\frac{\phi_{1n}(I_n)}{K_n(I_n)} \\ -\frac{\phi_{21}(I_1)}{K_1(I_1)} & 1 & \cdots & -\frac{\phi_{2n}(I_n)}{K_n(I_n)} \\ \vdots & \vdots & \ddots & \vdots \\ -\frac{\phi_{n1}(I_1)}{K_1(I_1)} & -\frac{\phi_{n2}(I_2)}{K_2(I_2)} & \cdots & 1 \end{bmatrix},$$

$\mathcal{N} = \left[\frac{h_1(S,I_1)+g_1(V,I_1)}{K_1(I_1)}, \ldots, \frac{h_n(S,I_n)+g_n(V,I_n)}{K_n(I_n)}\right]$, $\mathcal{P} = [K_1(I_1), K_2(I_2), \cdots, K_n(I_n)]^T$.

In the following, for two vectors $l = (l_1, l_2, \ldots, l_n)$, $s = (s_1, s_2, \ldots, s_n) \in R^n$, relation $l \leq s$ holds if and only if $l_i \leq s_i$ for $i = 1, 2, \ldots, n$. Using the Assumptions (A_9) and (A_{10}), we obtain that

$$\begin{aligned}
\dot{H} &\leq \nu_1(\mu_1, \mu_2, \ldots, \mu_n)\mathcal{P} - (\nu_1, \nu_2, \ldots, \nu_n)F\mathcal{P} \\
&= (\nu_1 - 1)(\mu_1, \mu_2, \ldots, \mu_n)\mathcal{P} \\
&= (\Re_0 - 1)(\mu_1, \mu_2, \ldots, \mu_n)\mathcal{P} \\
&\leq 0.
\end{aligned} \quad (12)$$

$\dot{H} \leq (\Re_0 - 1)\sum_{i=1}^n \mu_i K_i(I_i)$, for all $(S, V, I_1, \ldots, I_n) \in \Gamma$. $\mathcal{K}$ is the largest invariant subset of $G = \{(S, V, I_1, \ldots, I_n) \in \Gamma \mid \dot{L} = 0\}$. Then, $P_0 \in \mathcal{K}$. Let $(S, V, I_1, \ldots, I_n)$ be a solution in $\mathcal{K}$.

If $\Re_0 < 1$, $\dot{H} = 0$ implies that $\sum_{i=1}^n \mu_i K_i(I_i) = 0$. Using assumption (A_9), this implies that $\sum_{j=1}^n h_j(S, I_j) = 0$ and $\sum_{j=1}^n g_j(V, I_j) = 0$ hold along solutions in $\mathcal{K}$. By the first differential equation in system (3), we get that $S = \bar{S}$ in $\mathcal{K}$, and using the second differential equation in system (3), we get $V = \bar{V}$ in $\mathcal{K}$. From the differential equation of system (3) about the infected compartment, we can get:

$$\sum_{i=1}^n \dot{I}_i = -\sum_{i=1}^n \zeta_i(I_i) - \sum_{j=1}^n \phi_{n+1,j} I_j \leq -d^* \sum_{j=1}^n I_i. \quad (13)$$

Therefore, along any solution in $\mathcal{K}$, we have $S = \bar{S}$, $V = \bar{V}$ and $I_1 = \cdots = I_n = 0$. As a consequence, $\mathcal{K} = \{P_0\}$, if $\Re_0 < 1$.

If $\Re_0 = 1$, then $\dot{H} = 0$ indicates $h_i(S, I_i) + g_i(V, I_i) = h_i(\bar{S}, I_i) + g_i(\bar{V}, I_i) \not\equiv 0$, for all $I_i > 0$ and we can obtain $S = \bar{S}$, $V = \bar{V}$ by assumption (A_9). From the first and second differential equations in system (3), we can know that $\sum_{j=1}^n h_j(S, I_j) = 0$ and $\sum_{j=1}^n g_j(V, I_j) = 0$ hold along any solution in $\mathcal{K}$. This means that $\mathcal{K} = \{P_0\}$. If $\Re_0 \leq 1$, by LaSalle's invariance principle [33], P_0 is globally asymptotically stable in Γ.

If $\Re_0 > 1$, then, by continuity, $\dot{H} > 0$ in a neighborhood of P_0 in $\mathring{\Gamma}$. Solutions in R^{n+2} enough close to P_0 move away from P_0, except those on the invariant S-axis [34]. So P_0

is an unstable state. We use the uniform persistence result from [35] and an argument similar to that in the proof of Proposition 3.3 in [36], we can certify that the instability of P_0 indicates consistent persistence of (3). Theorem 3 is proved. The uniform persistence of system (3) and the positive invariance of compact set Γ show that there is an equilibrium state of system (3) in $\mathring{\Gamma}$ [37], [38]. ■

V. Global dynamics when $\Re_0 > 1$

In this section, assume that $y(N) \equiv 1$. We prove that if the state transition graph of the system is strongly connected, then the system has a unique epidemic equilibrium state at this time.

Assume that there exists two functions Φ_1 and Φ_2: $R_+ \to R_+$ such that the following assumptions hold. The function $\Phi_0 > 0$. Let $\chi = S + V - P\int_0^t S(\omega)d\omega + d_o\int_0^t V(\omega)d\omega + t\sum_{j=1}^n g_j(V^*, I_j^*)$, $\chi^* = S^* + V^* - P\int_0^{t_1^*} S(\omega)d\omega + d_o\int_0^{t_2^*} V(\omega)d\omega + t_2^*\sum_{j=1}^n g_j(V^*, I_j^*)$. Here t_1 and t_2 are the time when S and V reach S^* and V^* respectively.

(H_1) For $S \neq S^*, \chi \neq \chi^*$,

$$(\omega(S) - \omega(S^*))\,(\Phi_0(\chi) - \Phi_0(\chi^*)) < 0.$$

(H_2) For $S \neq S^*$,

$$(\omega(S) - \omega(S^*))\,(\Phi_1(S) - \Phi_1(S^*)) < 0.$$

(H_3) Let $S = kV$, then $e(V) = (kp - d_0)V$. For $V \neq V^*$,

$$(e(V) - e(V^*))\,(\Phi_2(V) - \Phi_2(V^*)) < 0.$$

(H_4) For $0 \le S \le \bar{S}$, $0 \le V \le \bar{V}$, $I_i > 0$, $1 \le i \le n$,

$$\left(\frac{h_i(S,I_i) + g_i(V,I_i)}{\Phi_0(\chi)} - \frac{h_i(S^*,I_i^*) + g_i(V^*,I_i^*)}{\Phi_0(\chi^*)}\right) \times \left(\frac{h_i(S,I_i) + g_i(V,I_i)}{\Phi_0(\chi)K_i(I_i)} - \frac{h_i(S^*,I_i^*) + g_i(V^*,I_i^*)}{\Phi_0(\chi^*)K_i(I_i^*)}\right) \le 0.$$

When $I_j > 0$, $1 \le i, j \le n$,

$$\left(\phi_{ij}(I_j) - \phi_{ij}(I_j^*)\right)\left(\frac{\phi_{ij}(I_j)}{K_j(I_j)} - \frac{\phi_{ij}(I_j^*)}{K_j(I_j^*)}\right) \le 0.$$

(H_5) For $1 \le i \le n$, one of the functions $h_i(S^*, I_i)$, $g_i(V^*, I_i)$, $\sum_{j=1}^n \phi_{ij}(I_j)$, $K_i(I_i)$ is strictly monotone in I_i. Let matrix $D = (m_{ij})$, then give the definition of m_{ij},

$$m_{ij} = \begin{cases} \phi_{1j}(I_j^*) + h_j(S^*, I_j^*) + g_j(V^*, I_j^*) & \text{if } i = 1, \\ \phi_{ij}(I_j^*) & \text{if } i \ge 2. \end{cases}$$

As shown in Fig. 2, we regard matrix D as a weight matrix for the infection-transfer graph $\mathscr{G}$. In the weighted graph $\mathscr{G}$, solid arrows indicate transfers of individuals between compartments, and dashed arrows indicate infection. For our next result, we will require that D be an irreducible matrix. In graph-theoretic terms, irreducibility of D is equivalent to weighted graph ($\mathscr{G}$, D) being strongly connected [30].

Theorem 4: Assume that Assumptions $(A_1) - (A_8)$ hold and $y(N) \equiv 1$. Suppose that D is an irreducible matrix, and Assumptions $(H_1)(H_4)$ hold. Then, when $\Re_0 > 1$, there exists a unique endemic equilibrium P^* and it is globally asymptotically stable in $\mathring{\Gamma}$.

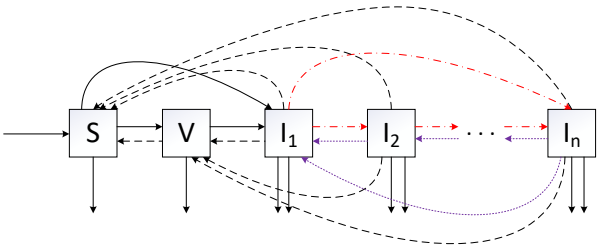

Fig. 2. The infection-transfer graph $\mathscr{G}$ at the endemic equilibrium P^* of model (1). Solid arrows indicate transfers of individuals between compartments, and dashed arrows indicate infection.

Proof: For system (3), we consider the following Lyapunov function:

$$\begin{aligned}\Psi =& T_1\int_{\chi^*}^{\chi}\left(\frac{\Phi_0(\xi) - \Phi_0(\chi^*)}{\Phi_0(\xi)}\right)d\xi \\ &+ \sum_{i=1}^n T_i\int_{I_i^*}^{I_i}\left(\frac{K_i(\xi) - K_i(I_i^*)}{K_i(\xi)}\right)d\xi \\ &+ \int_0^t (o(S) - q(V))\,d\xi. \end{aligned} \tag{14}$$

where $o(S) = (\omega(S) - \omega(S^*))\left(1 - \frac{\Phi_1(S^*)}{\Phi_1(S)}\right)$, $q(V) = (e(V) - e(V^*))\left(1 - \frac{\Phi_2(V^*)}{\Phi_2(V)}\right)$. We define specific constants $T_j > 0$, $j = 1, \ldots, n$. For convenience of expression, we define $\Phi_0^* = \frac{\Phi_0(\chi^*)}{\Phi_0(\chi)}$, $\Phi_1^* = \frac{\Phi_1(S^*)}{\Phi_1(S)}$, $\Phi_2^* = \frac{\Phi_2(V^*)}{\Phi_2(V)}$, $K_i = \frac{K_i(I_i^*)}{K_i(I_i)}, i = 1, 2, \ldots, n$, $h_j^* = h_j(S^*, I_j^*)$, $h_j = h_j(S, I_j)$, $g_j = g_j(V, I_j)$, $g_j^* = g_j(V^*, I_j^*)$, $\mathcal{G} = h_j + g_j$, $\mathcal{G}^* = h_j^* + g_j^*$. Differentiating Ψ along solutions of (3) and using equilibrium equations (4) to simplify, we obtain

$$\begin{aligned}\dot{\Psi} =& T_1\left(\omega(S) - \omega(S^*)\Phi_0^* + \sum_{j=1}^n \Phi_0^*\mathcal{G} + K_1(I_1^*)\right) \\ &+ T_1\left(\sum_{j=1}^n (1 - K_1)\phi_{1j}(I_j) + \sum_{j=1}^n (1 - \Phi_0^*)\,g_j^*\right) \\ &- T_1\left(\sum_{j=1}^n K_1\mathcal{G} + K_1(I_1)\right) + o(S) + q(V) \\ &+ \sum_{i=2}^n T_i\left(\sum_{j=1}^n (1 - K_i)\,\phi_{ij}(I_j) - K_i(I_i) + K_i(I_i^*)\right) \\ =& T_1\,(\omega(S) - \omega(S^*))\,(1 - \Phi_0^*) - T_1\sum_{j=1}^n \frac{\mathcal{G}^*}{K_1} + o(S) \\ &+ T_1\sum_{j=1}^n \mathcal{G}\left(2 + \frac{\mathcal{G}}{\mathcal{G}^*}(\Phi_0^* - K_1) - \Phi_0^*\right) + q(V) \\ &+ \sum_{i=1}^n T_i\sum_{j=1}^n \phi_{ij}(I_j^*)\left(1 + \frac{\phi_{ij}(I_j)}{\phi_{ij}(I_j^*)} - \frac{1}{K_i}\right. \\ &\left. - \frac{\phi_{ij}(I_j)}{\phi_{ij}(I_j^*)K_i}\right). \end{aligned} \tag{15}$$

Using assumption (H_1), (H_2) and (H_3), we have

$$(\omega(S) - \omega(S^*))\,(1 - \Phi_0^*) \le 0, \tag{16}$$

$$o(S) \leq 0,\ q(V) \leq 0. \tag{17}$$

We consider a function $\varphi(x) = 1 - x + lnx$. We analyze the maximum value of this function, monotonicity, and find that when $x > 0$, all values of this function are non-positive numbers. And $\varphi(x) = 0$ if and only if $x = 1$. And by Assumption (H_4), we obtain

$$\begin{aligned}
\Delta &= 2 + \frac{\mathcal{G}}{\mathcal{G}^*}\left(\Phi_0^* - K_1\right) - \Phi_0^* - \frac{1}{K_1} \\
&= \left(\frac{\mathcal{G}\Phi_0^*}{\mathcal{G}^*} - 1\right)\left(1 - \frac{\mathcal{G}^*}{\mathcal{G}}\right) + \left(1 - \Phi_0^* + \ln \Phi_0^*\right) \\
&\quad + \left(1 - \frac{\mathcal{G}K_1}{\mathcal{G}^*} + \ln \frac{\mathcal{G}K_1}{\mathcal{G}^*}\right) \\
&\quad + \left(1 - \frac{\mathcal{G}K_1}{\mathcal{G}^*\Phi_0^*} + \ln \frac{\mathcal{G}K_1}{\mathcal{G}^*\Phi_0^*}\right) \\
&\quad + \frac{1}{K_j} - \ln \frac{1}{K_j} - \frac{1}{K_1} + \ln \frac{1}{K_1} \\
&\leq \left(1 - \Phi_0^* + \ln \Phi_0^*\right)) \\
&\quad + \left(1 - \frac{\mathcal{G}K_1}{\mathcal{G}^*} + \ln \frac{\mathcal{G}K_1}{\mathcal{G}^*}\right) \\
&\quad + \left(1 - \frac{\mathcal{G}K_1}{\mathcal{G}^*\Phi_0^*} + \ln \frac{\mathcal{G}K_1}{\mathcal{G}^*\Phi_0^*}\right) \\
&\quad + \frac{1}{K_j} - \ln \frac{1}{K_j} - \frac{1}{K_1} + \ln \frac{1}{K_1}.
\end{aligned} \tag{18}$$

Combining the function $\varphi(x) = 1 - x + lnx$, we obtain

$$\Delta \leq \frac{1}{K_j} - \ln \frac{1}{K_j} - \frac{1}{K_1} + \ln \frac{1}{K_1}. \tag{19}$$

Similarly, using inequality (H_4), we obtain

$$\begin{aligned}
\Xi &= 1 + \frac{\phi_{ij}(I_j)}{\phi_{ij}(I_j^*)} - \frac{1}{K_i} - \frac{\phi_{ij}(I_j)K_i}{\phi_{ij}(I_j^*)} \\
&= \left(\frac{\phi_{ij}(I_j)}{\phi_{ij}(I_j^*)} - 1\right)\left(1 - \frac{\phi_{ij}(I_j^*)}{\phi_{ij}(I_j)K_j}\right) \\
&\quad + \left(1 - \frac{\phi_{ij}(I_j)K_i}{\phi_{ij}(I_j^*)} + \ln \frac{\phi_{ij}(I_j)K_i}{\phi_{ij}(I_j^*)}\right) \\
&\quad + \left(1 - \frac{\phi_{ij}(I_j^*)}{\phi_{ij}(I_j)K_j} + \ln \frac{\phi_{ij}(I_j^*)}{\phi_{ij}(I_j)K_j}\right) \\
&\quad + \left(\frac{1}{K_j} - \ln \frac{1}{K_j} - \frac{1}{K_1} + \ln \frac{1}{K_1}\right) \\
&\leq \left(1 - \frac{\phi_{ij}(I_j)K_i}{\phi_{ij}(I_j^*)} + \ln \frac{\phi_{ij}(I_j)K_i}{\phi_{ij}(I_j^*)}\right) \\
&\quad + \left(1 - \frac{\phi_{ij}(I_j)}{\phi_{ij}(I_j)K_j} + \ln \frac{\phi_{ij}(I_j^*)}{\phi_{ij}(I_j)K_j}\right) \\
&\quad + \frac{1}{K_j} - \ln \frac{1}{K_j} - \frac{1}{K_i} + \ln \frac{1}{K_i} \\
&\leq \frac{1}{K_j} - \ln \frac{1}{K_j} - \frac{1}{K_i} + \ln \frac{1}{K_i}.
\end{aligned} \tag{20}$$

Then, following (15)-(20) and using the definition of m_{ij} , we obtain

$$\begin{aligned}
\dot{\Psi} \leq & T_1 \sum_{j=1}^{n} \mathcal{G}^* \left(\frac{1}{K_j} - \ln \frac{1}{K_j} - \frac{1}{K_1} + \ln \frac{1}{K_1}\right) \\
& + \sum_{i=1}^{n} T_i \sum_{j=1}^{n} \phi_{ij}(I_j^*) \left(\frac{1}{K_j} - \ln \frac{1}{K_j} - \frac{1}{K_i} + \ln \frac{1}{K_i}\right) \\
\leq & \sum_{i=1}^{n} T_i \sum_{j=1}^{n} \phi_{ij}(I_j^*) \left(1 - \frac{\phi_{ij}(I_j)K_i}{\phi_{ij}(I_j^*)} + \ln \frac{\phi_{ij}(I_j)K_i}{\phi_{ij}(I_j^*)}\right) \\
& + \sum_{i=1}^{n} T_i \sum_{j=1}^{n} \phi_{ij}(I_j^*) \left(1 - \frac{\phi_{ij}(I_j^*)}{\phi_{ij}(I_j)K_i} + \ln \frac{\phi_{ij}(I_j^*)}{\phi_{ij}(I_j)K_i}\right) \\
& + T_1 \sum_{j=1}^{n} \mathcal{G}^* \left(1 - \Phi_0^* + \ln \Phi_0^*\right) \\
& + T_1 \sum_{j=1}^{n} \mathcal{G}^* \left(1 - \frac{\mathcal{G}K_1}{\mathcal{G}^*} + \ln \frac{\mathcal{G}K_1}{\mathcal{G}^*}\right) \\
& + T_1 \sum_{j=1}^{n} \mathcal{G}^* \left(1 - \frac{\mathcal{G}^*}{\mathcal{G}K_j\Phi_0^*} + \ln \frac{\mathcal{G}^*}{\mathcal{G}K_j\Phi_0^*}\right) \\
& + \sum_{i=1}^{n} T_i \sum_{j=1}^{n} m_{ij} \left(\frac{1}{K_j} - \ln \frac{1}{K_j} - \frac{1}{K_i} + \ln \frac{1}{K_i}\right)
\end{aligned} \tag{21}$$

In order to prove that $\dot{\Psi}$ is negative definite, we choose constants $T_i > 0$ such that the last expression in (21) is equal to 0.

$$L(D) = \operatorname{diag}\left(\sum_{j=1}^{n} m_{1j}, \sum_{j=1}^{n} m_{2j}, \ldots, \sum_{j=1}^{n} m_{nj}\right) - D. \tag{22}$$

$L(D)$ is the algebraic Laplacian matrix. We choose T_i as the co-factor of the ith diagonal entry of $L(D)$. Since D is an irreducible matrix, using Kirchhoffs matrix tree theorem (see the appendix in [38]), we get that $T_i > 0$. Furthermore, using the tree cycle identity, we obtain the following identity:

$$\sum_{i=1}^{n} T_i \sum_{j=1}^{n} m_{ij} \left(\frac{1}{K_j} - \ln \frac{1}{K_j} - \frac{1}{K_i} + \ln \frac{1}{K_i}\right) \equiv 0. \tag{23}$$

Therefore, we conclude that $\dot{\Psi} \leq 0$ for all $(S, V, I_1, \ldots, I_n) \in \mathring{\Gamma}$. And $\dot{\Psi} = 0$ indicates that

$$\left(\omega(S) - \omega(S^*)\right)\left(1 - \frac{\Phi_1(S^*)}{\Phi_1(S)}\right) = 0. \tag{24}$$

$$\left(e(V) - e(V^*)\right)\left(1 - \frac{\Phi_2(V^*)}{\Phi_2(V)}\right) = 0. \tag{25}$$

By (17), we obtain $S = S^*$ and $V = V^*$. Furthermore, since the weight graph has strong connectivity and the function $\varphi(t) = 1 - t + lnt$ takes the global maximum value one if and only when $t = 1$, we obtain that

$$\frac{\mathcal{G}}{\mathcal{G}^*} = \frac{K_j(I_j)}{K_j(I_j^*)} = \frac{\phi_{ij}(I_j)}{\phi_{ij}(I_j^*)} = \tau. \tag{26}$$

for all $I_j > 0$, $1 \leq j \leq n$. Along any solution that stays in the set where $\dot{\Psi} = 0$, we must have $S = S^*$ and $V = V^*$,

$$\mathcal{G} = \tau\mathcal{G}^*, \quad i = 1, \ldots, n. \tag{27}$$

Substituting these results into the first and second differential equation of model (3), we get

$$\omega(S^*) + e(V^*) = \tau \mathcal{G}^*. \tag{28}$$

Since the right-hand side of equation (28) is linear in τ, the equation holds only at $\tau = 1$, namely at P^*. Letting $\tau = 1$ in (28) we obtain that $h_j(S, I_j) = h_j(S^*, I_j^*)$, $g_j(V, I_j) = g_j(V^*, I_j^*)$, $\phi_{ij}(I_j) = \phi_{ij}(I_j^*)$, $K_j(I_j) = K_j(I_j^*)$. And it follows from monotonicity assumption (H_5) that $I_i = I_i^*$, $i = 1, \ldots, n$. Therefore, the only invariant set in the set $\{\dot{\Psi} = 0\}$ is the singleton $\{P^*\}$. By LaSalle's invariance principle [33], P^* is globally asymptotically stable in $\mathring{\Gamma}$. As a consequence, P^* is also unique. ■

VI. Numerical Examples

This section provides two numerical examples to demonstrate the effectiveness of the obtained theoretical results. To focus our research on the state structure, we will simplify the model (3) using the simple form functions f, g, h, ϕ and K. We only consider a limited number of infection stages. Let $n = 4$, $y(N) \equiv 1$, $h_i(S, I_i) = \alpha_i S I_i$, $g_i(V, I_i) = \beta_i V I_i$, $\phi_{n+1,j} = \gamma_j I_j$ and $\phi_{ij} = \delta_{ij} I_j$. We simplify model (3) into the following differential equations:

$$\begin{aligned}
\dot{S} &= \Lambda - dS - pS - \sum_{j=1}^{4} \alpha_j S I_j, \\
\dot{V} &= pS - d_0 V - \sum_{j=1}^{4} \beta_j V I_j, \\
\dot{I}_1 &= \sum_{j=1}^{4} \alpha_j S I_j + \sum_{j=1}^{4} \beta_j V I_j + \delta_{12} I_2 + \delta_{13} I_3 + \delta_{14} I_4 \\
&\quad - (\delta_{21} + \delta_{31} + \delta_{41} + \gamma_1 + d_1) I_1, \\
\dot{I}_2 &= \delta_{21} I_1 + \delta_{23} I_3 - (\delta_{12} + \delta_{32} + \delta_{42} + \gamma_2 + d_2) I_2 \\
&\quad + \delta_{24} I_4, \\
\dot{I}_3 &= \delta_{31} I_1 + \delta_{32} I_2 - (\delta_{13} + \delta_{23} + \delta_{43} + \gamma_3 + d_3) I_3 \\
&\quad + \delta_{34} I_4, \\
\dot{I}_4 &= \delta_{41} I_1 + \delta_{42} I_2 - (\delta_{14} + \delta_{24} + \delta_{34} + \gamma_4 + d_4) I_4 \\
&\quad + \delta_{43} I_3,
\end{aligned} \tag{29}$$

Example 1: Let $\Lambda = 1000$, $p = 0.1$, $d = d_0 = 0.015$, $d_1 = d_2 = d_3 = d_4 = 0.03$, $\gamma_1 = 0.31$, $\gamma_2 = 0.29$, $\gamma_3 = 0.29$, $\gamma_4 = 0.33$. $\delta_{12} = 0.31$, $\delta_{13} = 0.34$, $\delta_{14} = 0.32$, $\delta_{21} = 0.27$, $\delta_{23} = 0.21$, $\delta_{24} = 0.29$, $\delta_{31} = 033$, $\delta_{32} = 0.31$, $\delta_{34} = 0.29$, $\delta_{41} = 0.31$, $\delta_{42} = 0.29$, $\delta_{43} = 0.26$. If one chooses the set of transfer coefficients as

$$\begin{aligned}
&\alpha_1 = 0.1274 \times 10^{-5}, \ \alpha_2 = 0.1253 \times 10^{-5}, \\
&\alpha_3 = 0.1579 \times 10^{-5}, \ \alpha_4 = 0.2175 \times 10^{-5}, \\
&\beta_1 = 0.1329 \times 10^{-6}, \ \beta_2 = 0.1577 \times 10^{-6}, \\
&\beta_3 = 0.1867 \times 10^{-6}, \ \beta_4 = 0.2119 \times 10^{-6},
\end{aligned}$$

then the basic reproduction number $\Re_0 = 0.0673 < 1$. Based on Theorem 3, the disease-free equilibrium P_0 is globally asymptotically stable. Fig. 3 depicts time-dependent trajectories of susceptible S and vaccinated V populations when $\Re_0 = 0.0673$. Fig. 4 depicts time-dependent trajectories of the population in different infection stages I_i when $\Re_0 = 0.0673$. If one chooses the set of transfer coefficients as

$$\begin{aligned}
&\alpha_1 = 0.2178 \times 10^{-4}, \ \alpha_2 = 0.3589 \times 10^{-4}, \\
&\alpha_3 = 0.4516 \times 10^{-4}, \ \alpha_4 = 0.5125 \times 10^{-4}, \\
&\beta_1 = 0.1217 \times 10^{-5}, \ \beta_2 = 0.2867 \times 10^{-5}, \\
&\beta_3 = 0.3633 \times 10^{-5}, \ \beta_4 = 0.4566 \times 10^{-5},
\end{aligned}$$

then one can get the basic reproduction number $\Re_0 = 1.3625 > 1$. According to Theorem 4, there exists a unique P^* which is globally stable. Fig. 5 depicts time-dependent trajectories of susceptible S and vaccinated V populations when $\Re_0 = 1.3625$. Fig. 6 depicts time-dependent trajectories of the population in different infection stages I_i when $\Re_0 = 1.3625$.

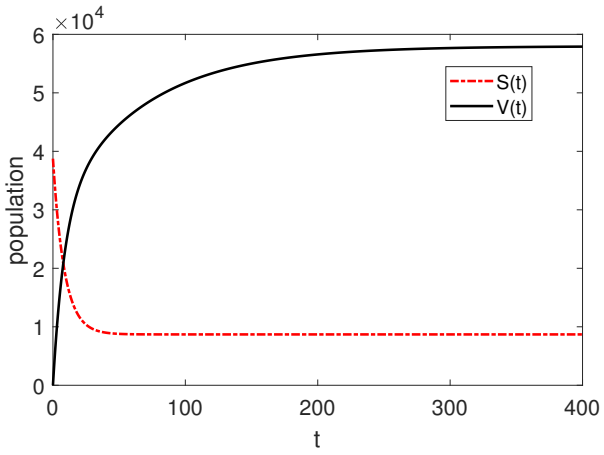

Fig. 3. When $\Re_0 < 1$, time-dependent trajectories of susceptible S and vaccinated V populations.

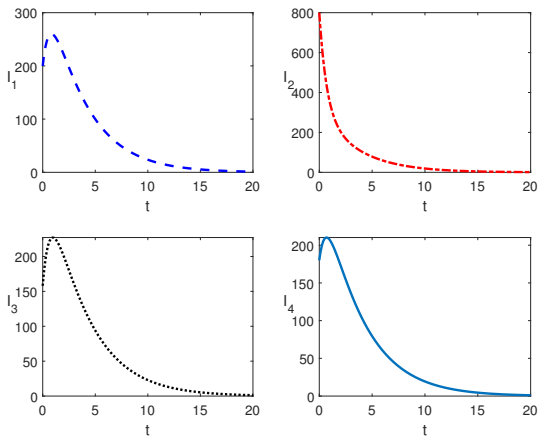

Fig. 4. When $\Re_0 < 1$, time-dependent trajectories of the population in different infection stages I_i.

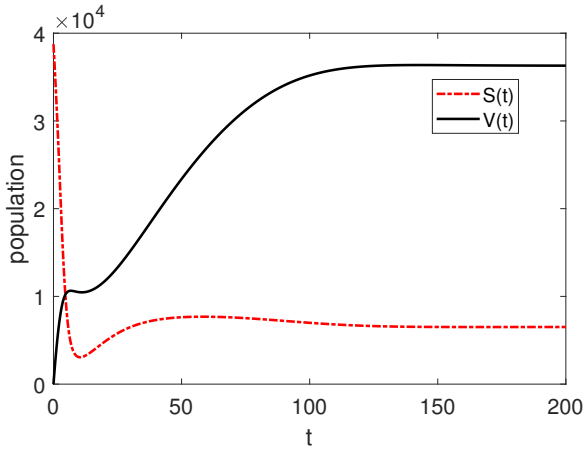

Fig. 5. When $\Re_0 > 1$, time-dependent trajectories of susceptible S and vaccinated V populations.

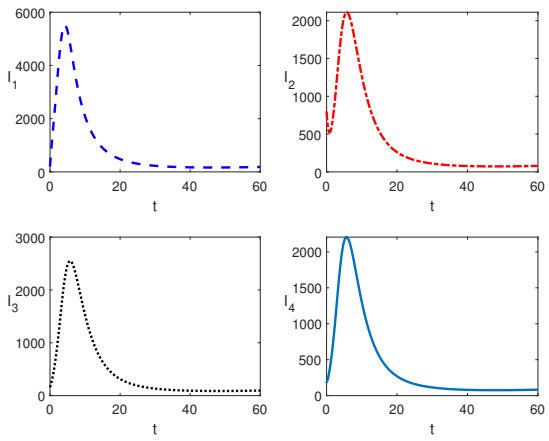

Fig. 6. When $\Re_0 > 1$, time-dependent trajectories of the population in different infection stages I_i.

Example 2: In this example, we use the real COVID-19 data of the Principality of Liechtenstein for numerical analysis. Parameter values are given in Table I. From the data in Table I, we can calculate the basic reproduction number $\Re_0 = 17.8487 > 1$. Fig. 7 shows the time-dependent trajectories of susceptible S and vaccinated V populations. Fig. 8 shows the time-dependent trajectories of the population in different infection stages I_i.

TABLE I
DETAILS OF MODEL PARAMETERS IN EXAMPLE 2.

Symbol	Value	Source
S	38747	[39]
V	0	Assumed
I_i	300, 400	Assumed
Λ	1000	Assumed
p	0.535	[39]
d,d_0	0.001	Estimated
d_1,d_2	0.2522×10^{-2}	[40]
γ_1,γ_2	0.5253, 0.3222	Estimated
δ_{ij}	0.3, 0.5	Assumed
α_1,α_2	0.2839×10^{-4}, 0.5355×10^{-4}	[41]
β_1,β_2	0.775×10^{-5}	Estimated

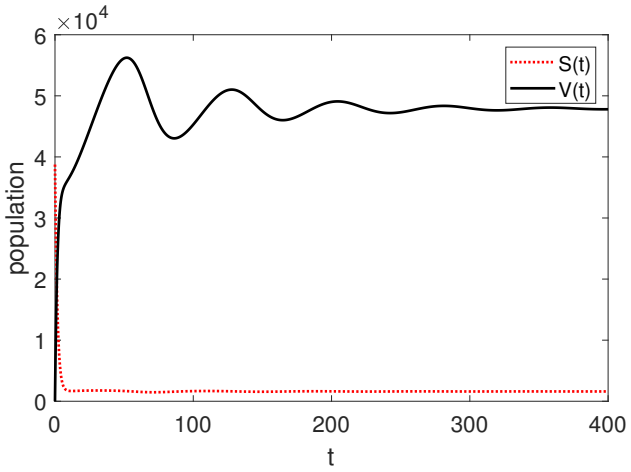

Fig. 7. Time-dependent trajectories of susceptible S and vaccinated V populations.

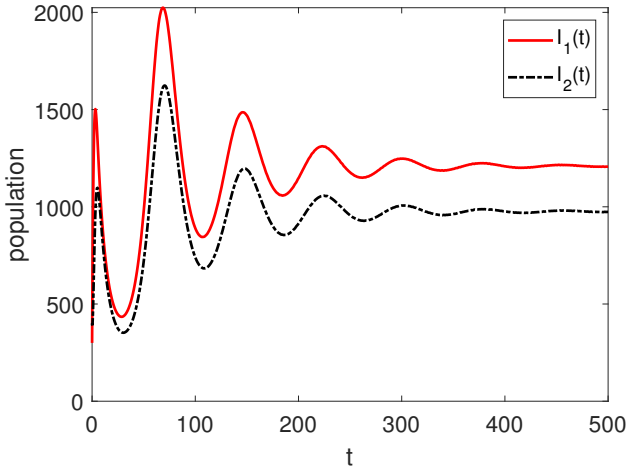

Fig. 8. Time-dependent trajectories of the population in different infection stages I_i.

VII. CONCLUDING REMARKS

We builded a multistage virus transmission model with partial immunity, which is described by ordinary differential equations. We used the Lyapunov method to analyze the stability of the disease-free equilibrium point. When $\Re_0 \leq 1$, the disease-free equilibrium is globally asymptotically stable. This means that no matter how large the virus spreads, eventually the disease will die out in nature. When the basic regeneration number is greater than one, the system is unstable. At this time, the system has an equilibrium state P^*, indicating that the disease will not disappear and will always exist. We got the relationship between $\Re_0$ and vaccination rate, which shows that $\Re_0$ decreases as vaccination rate increases. This property can be used to control epidemics by adjusting vaccination rates. Future studies will consider a multistage virus transmission model with immunity under early warning measures.

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