

Research Article

Threshold Dynamics for a Time-Periodic Viral Infection Model with Cell-to-Cell Transmission and Drug Treatments

Jinhu Xu  and Guokun Huang

School of Sciences, Xi'an University of Technology, Xi'an 710048, China

Correspondence should be addressed to Jinhu Xu; xujinhu09@163.com

Received 10 January 2022; Accepted 21 February 2022; Published 21 March 2022

Academic Editor: Zahir Shah

Copyright © 2022 Jinhu Xu and Guokun Huang. This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

In this study, a time-periodic viral infection model incorporating cell-to-cell infection and antiretroviral therapy has been investigated. The basic reproduction number \mathcal{R}_0 has been defined as a threshold parameter which governs whether or not the disease dies out. Theoretical results indicate that the disease goes to extinction if $\mathcal{R}_0 < 1$ and otherwise the disease will uniformly persist. The global stabilities of the equilibria for the corresponding autonomous model have been investigated by constructing suitable Lyapunov functions. Moreover, numerical simulations have been carried out to validate the obtained results. The results show that cell-to-cell infection mode may be a barrier to curing the viral infection and increasing the efficacy of protease inhibitors for blocking cell-to-cell infection which will benefit to weaken the severity of the viral infection.

1. Introduction

Recently, much attention and great effort have been paid on modelling of HIV, and many models have been proposed and studied on HIV spreading. Many earlier models of HIV infection models describe the interaction between virus and target cells by assuming that the infected cells produce virions instantaneously [1, 2]. However, research studies have been carried out to show that a latent period exists before the infected cells are activated to produce virus [3–5]. Therefore, it is reasonable to introduce the latent period into a model. As we know, antiretroviral drugs can effectively suppress viral replication to a low level, but cannot eradicate the virus permanently. An important reason is that HIV provirus can reside in latently infected CD4 + T-cells, which can live longer and cannot be affected by antiretroviral drugs or immune responses, but can be activated to produce virus by relevant antigens [5]. Thereafter, motivated by this factor, many viral infection models with latent cells have been proposed and studied to describe this phenomena [6–13] and references therein. For example, Pankavich [6] proposed and studied the following viral infection model:

$$\begin{cases} T'(t) = \lambda - d_T T - k(1 - \eta_{rt})TV, \\ L'(t) = p(1 - \eta_{rt})kTV - (\alpha + d_L)L, \\ I'(t) = (1 - p)(1 - \eta_{rt})kTV + \alpha L - d_I I, \\ V_I'(t) = (1 - \eta_p)Nd_I I - d_V V_I(t), \\ V_{NI}'(t) = \eta_p Nd_I I - d_V V_{NI}(t), \end{cases} \quad (1)$$

where T, L, I, V_I , and V_{NI} represent the concentration of uninfected target T-cells, latent cells, productively infected T-cells, infectious virions, and noninfectious virions at time t , respectively. λ, k, α , and p are the production rate of T-cells, virus-to-cell infection rate, the activation rate of latent cells, and the fraction of infections leading to latency. d_T, d_L, d_I, d_V are the death rate of susceptible T-cells, latent cells, actively infected T-cells, and virions, respectively. N denotes the burst rate of actively infected cells. η_{rt} and η_p are the efficacies of RTIs (reverse transcriptase inhibitors) and PIs (protease inhibitors), respectively. The global dynamics of model (1) have been investigated in [6].

Notice that the drug efficacy in model (1) is assumed to be a constant coefficient. In fact, drugs are often administered for patients periodically. As we known, drug

concentration will reach a peak value within a very short time when a dose is administrated, and the concentration down to a lower value as time goes and then reaches a peak value again when another dose is administrated [14–16]. Therefore, drug concentration may vary periodically during the dose interval. Moreover, only cell-free infection has been considered in earlier work; the cell-to-cell transmission was not considered in model (1). However, a recent research work has shown that cell-to-cell transmission may be one of the main infection mode which leads to a failed therapy and potentially contribute to viral persistence [17]. Because a better understanding of the viral dynamics is very significant in terms of applications, thus motivated by these arguments many viral infection models with cell-to-cell transmission

have been proposed and studied [18–29] and references therein. Besides, drugs' efficacy about cell-to-cell infection was not taken into consideration in model (1). However, the results obtained in [30] show that PIs can effectively block cell-to-cell spread of HIV by preventing cleavage of viral polyproteins into functional subunits leading to the formation of immature noninfectious virus particles, while RTIs are less effective inhibitors of HIV cell-to-cell spread compared to virus-to-cell infection. To the best of our knowledge, the time-periodic viral infection model with cell-to-cell infection and latency have not been studied. Hence, motivated by the abovementioned work and arguments, we consider the following time-periodic model with two infection modes:

$$\left\{ \begin{array}{l} T'(t) = \lambda - d_T T(t) - (1 - \eta_{rt}(t)) \frac{k_1 TV_I}{1 + m_1 V_I} - (1 - \eta_p^{(1)}(t)) \frac{k_2 TI}{1 + m_2 I}, \\ L'(t) = p(1 - \eta_{rt}(t)) \frac{k_1 TV_I}{1 + m_1 V_I} + p(1 - \eta_p^{(1)}(t)) \frac{k_2 TI}{1 + m_2 I} - (\alpha + d_L)L, \\ I'(t) = (1 - p)(1 - \eta_{rt}(t)) \frac{k_1 TV_I}{1 + m_1 V_I} + (1 - p)(1 - \eta_p^{(1)}(t)) \frac{k_2 TI}{1 + m_2 I} + \alpha L - d_I I, \\ V_I'(t) = (1 - \eta_p^{(2)}(t)) N d_I I - d_V V_I(t), \\ V_{NI}'(t) = \eta_p^{(2)}(t) N d_I I - d_V V_{NI}(t), \end{array} \right. \quad (2)$$

where k_2 is the infection rate of productively infected T-cells. Assume $\eta_{rt}(t), \eta_p^{(1)}(t), \eta_p^{(2)}(t): \mathbb{R} \rightarrow [0, 1]$ are the efficiencies of RTIs and PIs, and we assume they are continuous and periodic in time t with a same period ω . Here, we considered two saturated incidence rates, where m_1 and m_2 are the saturation parameters and are positive constants.

Other parameters have the same meaning of model (1). For convenience, we denote $\beta_1(t) = k_1(1 - \eta_{rt}(t))$, $\beta_2(t) = k_2(1 - \eta_p^{(1)}(t))$, and $a(t) = (1 - \eta_p^{(2)}(t))$. Since the last equation of model (2) is independent with the others. Thus, we will focus on the following reduced model:

$$\left\{ \begin{array}{l} T'(t) = \lambda - d_T T(t) - \beta_1(t) \frac{TV_I}{1 + m_1 V_I} - \beta_2(t) \frac{TI}{1 + m_2 I}, \\ L'(t) = p\beta_1(t) \frac{TV_I}{1 + m_1 V_I} + p\beta_2(t) \frac{TI}{1 + m_2 I} - (\alpha + d_L)L, \\ I'(t) = (1 - p)\beta_1(t) \frac{TV_I}{1 + m_1 V_I} + (1 - p)\beta_2(t) \frac{TI}{1 + m_2 I} + \alpha L - d_I I, \\ V_I'(t) = N d_I a(t) I - d_V V_I(t). \end{array} \right. \quad (3)$$

This study is organized as follows. In Section 2, preliminary results and the definition of the basic reproduction number are studied. In Section 3, global extinction of the

disease and the uniform persistence are investigated in terms of the basic reproduction number. The global asymptotic stability of the infection equilibrium to the corresponding

autonomous model are discussed by applying the method of Lyapunov functions. In Section 4, some numerical simulations are carried out. A brief conclusion and discussion ends the paper.

2. The Basic Reproduction Number

In this section, we investigate the definition of the basic reproduction number \mathcal{R}_0 for model (3) according to the work [31, 32]. The following result shows that solutions of model (3) are bounded.

Theorem 1. *The solutions $(T(t), L(t), I(t), V_I(t))$ of model (3) are uniformly and ultimately bounded, i.e., there exist an $M_1 > 0$ and $t^* > 0$ such that $(T(t), L(t), I(t), V_I(t)) \leq (M, M, M, M)$, for $t \geq t^*$.*

Proof. From model (3), we can obtain that

$$\frac{d(T + L + I)}{dt} = \lambda - d_T T - d_L L - d_I I \leq \lambda - \sigma(T + L + I), \quad (4)$$

where $\sigma = \min\{d_T, d_L, d_I\}$. Thus, there exists $t_1 > 0$ such that $T + L + I \leq \lambda/\sigma$, for $t \geq t_1$. It follows from the last equation of model (3); we have, for $t \geq t_1$, $dV_I/dt \leq Nd_I \cdot \max_{t \in [0, \omega]} \{a(t)\} \cdot \lambda/\sigma - d_V V_I$, which implies that there exist $t^* \geq t_1$ such that $V_I(t) \leq Nd_I \cdot \max_{t \in [0, \omega]} \{a(t)\} \cdot \lambda/\sigma 1/d_V$, for $t \geq t^*$. Let

$M = \max\left\{\lambda/\sigma, Nd_I \cdot \max_{t \in [0, \omega]} \{a(t)\} \cdot \lambda/\sigma 1/d_V\right\}$. It then follows that $((T(t), L(t), I(t), V_I(t))) \leq (M, M, M, M)$, for $t \geq t^*$. Hence, the solutions of model (3) are uniformly and ultimately bounded. This finishes the proof.

Let $(\mathbb{R}^n, \mathbb{R}_+^n)$ be the standard ordered n -dimensional Euclidean space with a norm $\|\cdot\|$. For $u, v \in \mathbb{R}^n$, we write $u \geq v$ if $u - v \in \mathbb{R}_+^n$, $u > v$ if $u - v \in \mathbb{R}_+^n \setminus \{0\}$, and $u \gg v$ if $u - v \in \text{Int}(\mathbb{R}_+^n)$. Let $A(t)$ be a continuous, cooperative, irreducible, and ω -periodic $n \times n$ matrix function and $\Phi_A(t)$ be the fundamental solution matrix of the following linear system:

$$\frac{dx}{dt} = A(t)x. \quad (5)$$

Let $r(\Phi_A(\omega))$ be the spectral radius of $\Phi_A(\omega)$. It follows from the Perron–Frobenius theorem that $r(\Phi_A(\omega))$ is the principal eigenvalue of $\Phi_A(\omega)$ in the sense that it is simple and admits an eigenvector $v^* \gg 0$. The following lemma comes from [33] which will be used for the discussion in the next section. \square

Lemma 1 (see [33]). *Let $\mu = 1/\omega \ln r(\Phi_A(\omega))$. Then, there exists a positive ω -periodic function $v(t)$ such that $e^{\mu t} v(t)$ is a solution of (5).*

Obviously, model (3) has a unique infection-free equilibrium $E_0 = (T_0, 0, 0, 0)$, where $T_0 = \lambda/d_T$. Linearizing (3) at E_0 yields that

$$\begin{cases} L'(t) = p\beta_2(t)T_0I + p\beta_1(t)T_0V_I - (\alpha + d_L)L, \\ I'(t) = (1-p)\beta_2(t)T_0I + (1-p)\beta_1(t)T_0V_I + \alpha L - d_I I, \\ V_I'(t) = Nd_I a(t)I - d_V V_I(t). \end{cases} \quad (6)$$

Define

$$\mathbf{F} = \begin{pmatrix} 0 & p\beta_2(t)T_0 & p\beta_1(t)T_0 \\ 0 & (1-p)\beta_2(t)T_0 & (1-p)\beta_1(t)T_0 \\ 0 & 0 & 0 \end{pmatrix}, \quad (7)$$

$$\mathbf{V} = \begin{pmatrix} \alpha + d_L & 0 & 0 \\ -\alpha & d_I & 0 \\ 0 & -Nd_I a(t) & d_V \end{pmatrix}.$$

Then, system (6) can be written as

$$\frac{dx}{dt} = (\mathbf{F}(t) - \mathbf{V}(t))x(t). \quad (8)$$

Assume that $Y(t, s)$, $t \geq s$, is the evolution operator of the following system:

$$\frac{dy}{dt} = -\mathbf{V}(t)y. \quad (9)$$

Then, the 3×3 matrix $Y(t, s)$ satisfies

$$\begin{aligned} \frac{dY(t, s)}{dt} &= -\mathbf{V}(t)Y(t, s), \quad \forall t \geq s, Y(s, s) \\ &= I \text{ is a } 3 \times 3 \text{ identity matrix.} \end{aligned} \quad (10)$$

Let C_ω be the ordered Banach space of all ω -periodic functions from \mathbb{R} to \mathbb{R}^3 , which is equipped with the maximum norm $\|\cdot\|$ and the positive cone $C_\omega^+ := \{\phi \in C_\omega : \phi(t) \geq 0, \forall t \in \mathbb{R}\}$. Suppose $\phi(s) \in C_\omega^+$ is the initial distribution of infectious cells and virus in this periodic environment; then, $\mathbf{F}(s)\phi(s)$ is the rate of new infections produced by the infected cells and virus who were introduced at time s , and $Y(t, s)\mathbf{F}(s)\phi(s)$ represents the distribution of those infected cells and virus who were newly infected at time s and remain in the infected compartments at time t , for $t \geq s$. Hence,

$$\begin{aligned} \psi(t) &:= \int_{-\infty}^t Y(t, s)\mathbf{F}(s)\phi(s)ds \\ &= \int_0^\infty Y(t, t-a)\mathbf{F}(t-a)\phi(t-a)da \end{aligned} \quad (11)$$

is the distribution of accumulative new infections at time t produced by all those infected cells and virus introduced before t .

Define the linear operator $\mathcal{L}: C_\omega \rightarrow C_\omega$ as follows:

$$\begin{aligned} [\mathcal{L}\phi](t) &= \int_0^\infty Y(t, t-a)\mathbf{F}(t-a)\phi(t-a)da, \\ &\quad \forall t \in \mathbb{R}, \phi \in C_\omega. \end{aligned} \quad (12)$$

It follows from the idea in [32] that the basic reproduction number \mathcal{R}_0 of system (3) is defined as the spectral radius of \mathcal{L} , i.e.,

$$\mathcal{R}_0 = r(\mathcal{L}). \tag{13}$$

Moreover, the local asymptotic stability of the infection-free equilibrium E_0 follows from [32].

Theorem 2 (see [32]). *The following statements are valid:*

- (i) $\mathcal{R}_0 < 1$ if and only if $r(\Phi_{(F-V)}(\omega)) < 1$
- (ii) $\mathcal{R}_0 = 1$ if and only if $r(\Phi_{(F-V)}(\omega)) = 1$
- (iii) $\mathcal{R}_0 > 1$ if and only if $r(\Phi_{(F-V)}(\omega)) > 1$

Thus, infection-free equilibrium E_0 of (3) is asymptotically stable if $\mathcal{R}_0 < 1$ and unstable if $\mathcal{R}_0 > 1$.

3. The Threshold Dynamics

3.1. Stability and Persistence of the Disease. In this section, we will investigate the global asymptotic stability of infection-

free equilibrium and the disease persistence by regarding \mathcal{R}_0 as a threshold parameter.

Theorem 3. *If $\mathcal{R}_0 < 1$, then the infection-free equilibrium E_0 is globally asymptotically stable, and it is unstable for $\mathcal{R}_0 > 1$.*

Proof. It follows from Theorem 2 that if $\mathcal{R}_0 < 1$, then E_0 is locally asymptotically stable and E_0 is unstable when $\mathcal{R}_0 > 1$. Hence, it is sufficient to show that E_0 is global attractive for $\mathcal{R}_0 < 1$.

From the first equation of (3) and nonnegativity of the solutions, we then have $dT/dt \leq \lambda - d_T T$, which implies that $\forall \varepsilon > 0$; there exists $\tilde{t} > 0$ such that $T(t) \leq T_0 + \varepsilon, t > \tilde{t}$.

Consider the following auxiliary system:

$$\begin{cases} \tilde{L}'(t) = p\beta_2(t)(T_0 + \varepsilon)\tilde{I} + p\beta_1(t)(T_0 + \varepsilon)\tilde{V}_I - (\alpha + d_L)\tilde{L}, \\ \tilde{I}'(t) = (1-p)\beta_2(t)(T_0 + \varepsilon)\tilde{I} + (1-p)\beta_1(t)(T_0 + \varepsilon)\tilde{V}_I + \alpha\tilde{L} - d_I\tilde{I}, \\ \tilde{V}'_I(t) = Nd_I a(t)\tilde{I} - d_V\tilde{V}_I(t), \end{cases} \tag{14}$$

which is equivalent to

$$\begin{pmatrix} \tilde{L}' \\ \tilde{I}' \\ \tilde{V}'_I \end{pmatrix} = (F - V) \begin{pmatrix} \tilde{L} \\ \tilde{I} \\ \tilde{V}_I \end{pmatrix} + \varepsilon M(t) \begin{pmatrix} \tilde{L} \\ \tilde{I} \\ \tilde{V}_I \end{pmatrix}, \tag{15}$$

where

$$M(t) = \begin{pmatrix} 0 & p\beta_2(t) & p\beta_1(t) \\ 0 & (1-p)\beta_2(t) & (1-p)\beta_1(t) \\ 0 & 0 & 0 \end{pmatrix}. \tag{16}$$

It then follows from Lemma 1 that there exists a positive ω -periodic function $v(t) = (v_1(t), v_2(t), v_3(t))$ such that $e^{\mu t} v(t)$ is a solution of (14), where $\mu = 1/\omega \ln r(\Phi_{F-V+\varepsilon M}(\omega))$. Choose $\tilde{t} > \tilde{t}$ and a real number $\alpha_1 > 0$ such that $(\tilde{L}(\tilde{t}), \tilde{I}(\tilde{t}), \tilde{V}_I(\tilde{t}))^T \leq \alpha_1 v(0)$, which implies that

$$(\tilde{L}(\tilde{t}), \tilde{I}(\tilde{t}), \tilde{V}_I(\tilde{t}))^T \leq \alpha_1 e^{\mu(t-\tilde{t})} v(t-\tilde{t}), \quad t \geq \tilde{t}. \tag{17}$$

The comparison principle yields that

$$(L(t), I(t), V_I(t))^T \leq \alpha_1 e^{\mu(t-\tilde{t})} v(t-\tilde{t}), \quad t \geq \tilde{t}. \tag{18}$$

Recall Theorem 2 that $\mathcal{R}_0 < 1$ if and only if $r(\Phi_{F-V}(\omega)) < 1$. Since the continuity of the spectrum for matrices [34], then choose $\varepsilon > 0$ small enough such that $r(\Phi_{F-V+\varepsilon M}(\omega)) < 1$, which implies that $\mu < 0$. Then, we have $(L(t), I(t), V_I(t))^T \rightarrow 0$ as $t \rightarrow \infty$. Furthermore, it follows from the first equation of model (3) and the theory of asymptotically periodic semiflows [35] that $\lim_{t \rightarrow \infty} T(t) = T_0$.

Thus, E_0 is globally attractive. \square

Theorem 4. *If $\mathcal{R}_0 > 1$, then there exists an $\varepsilon > 0$ such that any solution $(T(t), L(t), I(t), V_I(t))$ of model (3) with initial values $(T(0), L(0), I(0), V_I(0)) = (T^0, L^0, I^0, V_I^0) \in \mathbb{R}_+ \times \text{Int}(\mathbb{R}_+^3)$; the solution of (3) satisfies $\liminf (T(t), L(t), I(t), V_I(t)) \geq (\varepsilon, \varepsilon, \varepsilon, \varepsilon)$ and admits at least one positive periodic solution.*

Proof. Let

$$\begin{aligned} X &= \mathbb{R}_+^4, \\ X_0 &= \mathbb{R}_+ \times \text{Int}(\mathbb{R}_+^3), \end{aligned} \tag{19}$$

$$\partial X_0 = \frac{X}{X_0}.$$

Define Poincaré map $P: \mathbb{R}_+^4 \rightarrow \mathbb{R}_+^4$, satisfying $P(x^0) = u(\omega, x^0), \forall x^0 \in \mathbb{R}_+^4$, with $u(t, x^0)$ as the unique solution of (3) satisfying $u(0, x^0) = x^0$.

We first show that P is uniformly persistent with respect to $(X_0, \partial X_0)$. It is easy to see that X and X_0 are positively invariant. Moreover, ∂X is a relatively closed set in X . Recall Theorem 1 that the solutions of model (3) are uniformly and ultimately bounded; thus, the semiflow P is point dissipative on \mathbb{R}_+^4 , and $P: \mathbb{R}_+^4 \rightarrow \mathbb{R}_+^4$ is compact. Consequently, it follows from [36] that the semiflow P admits a global attractor, which attracts every bounded set in \mathbb{R}_+^4 .

Define

$$M_\partial = \{(T^0, L^0, I^0, V_I^0) \in \partial X_0: P^m(T^0, L^0, I^0, V_I^0) \in \partial X_0, \forall m \geq 0\}. \tag{20}$$

Then, we claim that $M_{\partial} = \{(T, 0, 0, 0) : T \geq 0\}$. In fact, it is obvious that $\{(T, 0, 0, 0) : T \geq 0\} \subseteq M_{\partial}$. For any $(T^0, L^0, I^0, V_I^0) \in \partial X_0 / \{(T, 0, 0, 0) : T \geq 0\}$, considering the following cases: (1) $L^0 = 0, I^0 > 0, V_I^0 > 0$, (2) $L^0 > 0, I^0 = 0, V_I^0 > 0$, (3) $L^0 > 0, I^0 > 0, V_I^0 = 0$, (4) $L^0 = I^0 = 0, V^0 > 0$, (5) $L^0 = V_I^0 = 0, I^0 > 0$, and (6) $L^0 > 0, I^0 = V_I^0 = 0$. For case (1), we have $dL/dt|_{t=0} = p\beta_1(0)T(0)V_I(0) + p\beta_2(0)T(0)I(0) > 0$, which implies that $(T(t), L(t), I(t), V_I(t)) \notin \partial X_0$, for $0 < t \ll 1$; then, $(T(t), L(t), I(t), V_I(t)) \notin M_{\partial}$. Similarly, for the other cases, it also has the same result; here, we omit the proof. Thus, for any $(T^0, L^0, I^0, V_I^0) \notin \{(T, 0, 0, 0) : T \geq 0\}$, $(T^0, L^0, I^0, V_I^0) \notin M_{\partial}$, it indicates that $M_{\partial} \subseteq \{(T, 0, 0, 0) : T \geq 0\}$.

Clearly, E_0 is one fixed point of P in M_{∂} . If $(T(t), L(t), I(t), V_I(t))$ is a solution of model (3) from M_{∂} , it then follows from that model (3) that $T(t) \rightarrow T_0, L(t) \rightarrow 0, I(t) \rightarrow 0, V_I(t) \rightarrow 0$ as $t \rightarrow \infty$.

Next, we will show that if the invariant set E_0 is isolated, then $\{E_0\}$ is an acyclic covering. To do this, it needs to prove any solution of model (3) initiating from M_{∂} will remain into M_{∂} , which can be obtained easily. The isolated invariance of E_0 will follow proof.

Now, we need to prove that $W^s(E_0) \cap X_0 = \emptyset$. Denote $x^0 = (T^0, L^0, I^0, V_I^0) \in X_0$. Since the continuity of solutions with respect to the initial values, thus for $\forall \varepsilon > 0$, there exists $\delta_0 > 0$ such that, for all $x^0 \in X_0$ with $\|x^0 - E_0\| \leq \delta_0$, yields

$$\|u(t, x^0) - u(t, E_0)\| \leq \varepsilon, \quad \forall t \in [0, \omega]. \quad (21)$$

Then, we claim that

$$\limsup_{m \rightarrow \infty} d(P^m(x^0), E_0) \geq \delta_0. \quad (22)$$

If it is not true, then we have

$$\limsup_{m \rightarrow \infty} d(P^m(x^0), E_0) < \delta_0. \quad (23)$$

For some $x^0 \in X_0$, without loss of generality, we suppose that $\limsup / \liminf_t \rightarrow \infty d(P^m(x^0), E_0) < \delta_0, \quad \forall m > 0$. Then, we can obtain that

$$\|u(t, P^m(x^0)) - u(t, E_0)\| \leq \varepsilon, \quad \forall t \in [0, \omega]. \quad (24)$$

For any $t \geq 0$, let $t = m\omega + t_1$, where $t_1 \in [0, \omega]$ and $m = [t/\omega]$, which is the greatest integer less than or equal to t/ω . Then, we have

$$\|u(t, P^m(x^0)) - u(t, E_0)\| = \|u(t_1, P^m(x^0)) - u(t_1, E_0)\| \leq \varepsilon, \quad \forall t \in [0, \omega]. \quad (25)$$

Set $(T(t), L(t), I(t), V_I(t)) = u(t, x^0)$; then, we have $T_0 - \varepsilon \leq T \leq T_0 + \varepsilon, 0 \leq L \leq \varepsilon, 0 \leq I \leq \varepsilon$, and $0 \leq V_I \leq \varepsilon$, for $t \geq 0$. Then, $T/1 + m_1V_I \geq T_0 - \varepsilon/1 + m_1\varepsilon = T_0 - \varepsilon(1 + m_1T_0)/1 + m_1\varepsilon \geq T_0 - \varepsilon(1 + m_1T_0)$ and $T/1 + m_2I \geq T_0 - \varepsilon/1 + m_2\varepsilon = T_0 - \varepsilon(1 + m_2T_0)/1 + m_2\varepsilon \geq T_0 - \varepsilon(1 + m_2T_0)$. It follows from model (3) that

$$\begin{cases} L'(t) \geq p\beta_1(t)(T_0 - \varepsilon(1 + m_1T_0))V_I + p\beta_2(t)(T_0 - \varepsilon(1 + m_2T_0))I - (\alpha + d_L)L, \\ I'(t) \geq (1 - p)[\beta_1(t)(T_0 - \varepsilon(1 + m_1T_0))V_I + \beta_2(t)(T_0 - \varepsilon(1 + m_2T_0))I] + \alpha L - d_I I, \\ V_I'(t) = Nd_I a(t)I - d_V V_I(t). \end{cases} \quad (26)$$

Set

$$M_{\varepsilon} = \begin{pmatrix} 0 & \varepsilon(1 + m_2T_0)p\beta_2(t) & \varepsilon(1 + m_1T_0)p\beta_1(t) \\ 0 & \varepsilon(1 + m_2T_0)(1 - p)\beta_2(t) & \varepsilon(1 + m_1T_0)(1 - p)\beta_1(t) \\ 0 & 0 & 0 \end{pmatrix}. \quad (27)$$

It follows from Theorem 2 that $r(\Phi_{F-V}(\omega)) > 1$; then, we can select $\varepsilon > 0$ small enough such that $r(\Phi_{F-V-M_{\varepsilon}}(\omega)) > 1$. It follows from Lemma 1 and the standard comparison principle that there exists a positive ω -periodic function $\bar{v}(t) = (\bar{v}_1(t), \bar{v}_2(t), \bar{v}_3(t))^T$ such that $\mathcal{Q}(t) \geq \bar{v}(t)e^{\mu_1 t}$, where $\mathcal{Q}(t) = (L(t), I(t), V_I(t))^T$ and $\mu_1 = 1/\omega \ln r(\Phi_{F-V-M_{\varepsilon}}(\omega)) > 0$, which implies that $\lim / \liminf_t \rightarrow \infty (L(t), I(t), V_I(t)) = \infty$; this is a contradiction in M_{∂} which converges to E_0 , and hence, E_0 is acyclic in M_{∂} . By Theorem 1.3.1 and Remark 1.3.1 in [35], we obtain that P is uniformly persistent

with respect to $(X_0, \partial X_0)$. It then follows from Theorem 3.1.1 in [35] that the solution of (3) is uniformly persistent.

Moreover, it follows from Theorem 1.3.6 in [35] that the Poincaree map P has a fixed point $(\hat{T}(0), \hat{L}(0), \hat{I}(0), \hat{V}_I(0)) \in X_0$. Then, we see that $\hat{T}(0) > 0$. If not, suppose $\hat{T}(0) = 0$, from the first equation of model (3), where $\hat{T}(t)$ satisfies

$$\frac{d\hat{T}}{dt} \geq \lambda - d_T \hat{T} - (\beta_1(t)V_I + \beta_2(t)I)\hat{T}. \quad (28)$$

It follows from the comparison theorem that

$$\widehat{T}(t) \geq e^{-\int_0^t a(s)ds} \left(\widehat{T}(0) + \lambda \int_0^t e^{-\int_0^s a(\tau)d\tau} ds \right) = \lambda e^{-\int_0^t a(s)ds} \int_0^t e^{-\int_0^s a(\tau)d\tau} ds, \quad \forall t > 0, \tag{29}$$

where $a(t) = d_T + \beta_1(t)V_I(t) + \beta_2(t)I(t)$. Then, we have

$$\widehat{T}(n\omega) \geq \lambda e^{-\int_0^{n\omega} a(s)ds} \int_0^\omega e^{-\int_0^s a(\tau)d\tau} ds > 0, \tag{30}$$

$n = 1, 2, 3, \dots$

The periodicity of $\widehat{T}(t)$ implies $\widehat{T}(0) = \widehat{T}(n\omega) = 0$, which is a contradiction. Thus, $\widehat{T}(0) > 0$. Hence, $(\widehat{T}(0), \widehat{L}(0), \widehat{I}(0), \widehat{V}_I(0))$ is a positive ω -periodic solution of model (3). \square

3.2. Analysis of the Autonomous Model. If there no drug therapies, i.e., $\eta_{rt}(t) = \eta_p^{(1)}(t) = \eta_p^{(2)}(t) = 0$ or drug therapies are constants, then model (3) becomes an autonomous model. Without loss of generality, we assume drug therapy is constant. Then, model (3) leads to the following autonomous model:

$$\begin{cases} T'(t) = \lambda - d_T T(t) - \frac{\beta_1 T V_I}{1 + m_1 V_I} - \frac{\beta_2 T I}{1 + m_2 I} \\ L'(t) = p \frac{\beta_1 T V_I}{1 + m_1 V_I} + p \frac{\beta_2 T I}{1 + m_2 I} - (\alpha + d_L)L, \\ I'(t) = (1 - p) \frac{\beta_1 T V_I}{1 + m_1 V_I} + (1 - p) \frac{\beta_2 T I}{1 + m_2 I} + \alpha L - d_I I, \\ V_I'(t) = N d_I (1 - \eta_p^{(2)}) I - d_V V_I(t), \end{cases} \tag{31}$$

where $\beta_1 = k_1(1 - \eta_{rt})$ and $\beta_2 = k_2(1 - \eta_p^{(1)})$. Clearly, model (31) has an infection-free equilibrium $E_0 = (T_0, 0, 0, 0)$ with

$T_0 = \lambda/d_T$. Furthermore, we can obtain the basic reproduction number of model (31):

$$\begin{aligned} \mathcal{R}_0 &= \left((1 - p) + \frac{\alpha p}{\alpha + d_L} \right) \frac{N(1 - \eta_p^{(2)})\beta_1 T_0}{d_V} + \left((1 - p) + \frac{\alpha p}{\alpha + d_L} \right) \frac{\beta_2 T_0}{d_I} \\ &= \mathcal{R}_{01} + \mathcal{R}_{02}. \end{aligned} \tag{32}$$

Next, we will show that there exists a unique infection equilibrium $E^* = (T^*, L^*, I^*, V_I^*)$. For convenience, let $f(T, V_I) = TV_I/(1 + m_1 V_I)$ and $g(T, I) = TI/(1 + m_2 I)$. It is

easy to see that (T^*, L^*, I^*, V_I^*) satisfies the following equations:

$$\begin{aligned} \lambda - d_T T^* &= \beta_1 T^* f(T^*, V_I^*) + \beta_2 g(T^*, I^*), \\ p\beta_1 T^* f(T^*, V_I^*) + p\beta_2 g(T^*, I^*) &= (\alpha + d_L)L^*, \\ (1 - p)\beta_1 T^* f(T^*, V_I^*) + (1 - p)\beta_2 g(T^*, I^*) + \alpha L^* &= d_I I^*, \\ N(1 - \eta_p^{(2)})d_I I^* &= d_V V_I^*, \end{aligned} \tag{33}$$

Then, we can obtain

And L^* satisfies the following equation:

$$\begin{aligned} T^* &= \frac{1}{d_T} \left(\lambda - \frac{\alpha + d_L}{p} L^* \right), \\ I^* &= \frac{\alpha + d_L - p d_L}{d_I p} L^*, \\ V_I^* &= \frac{N(1 - \eta_p^{(2)}) (\alpha + d_L - p d_L)}{p d_V} L^*. \end{aligned} \tag{34}$$

$$\begin{aligned} &\beta_1 f \left(\frac{1}{d_T} \left(\lambda - \frac{\alpha + d_L}{p} L^* \right), \frac{N(1 - \eta_p^{(2)}) (\alpha + d_L - p d_L)}{p d_V} L^* \right) + \\ &\beta_2 g \left(\frac{1}{d_T} \left(\lambda - \frac{\alpha + d_L}{p} L^* \right), \frac{N(1 - \eta_p^{(2)}) (\alpha + d_L - p d_L)}{p d_V} L^* \right) = \frac{\alpha + d_L}{p} L^*. \end{aligned} \tag{35}$$

Since $T^* > 0$, which implies $0 < L^* < \lambda p / \alpha + d_L$, for $L \in (0, \lambda p / \alpha + d_L)$, let

$$\begin{aligned} H(L) &= \beta_1 f \left(\frac{1}{d_T} \left(\lambda - \frac{\alpha + d_L}{p} L \right), \frac{N(1 - \eta_p^{(2)}) (\alpha + d_L - p d_L)}{p d_V} L \right) \\ &+ \beta_2 g \left(\frac{1}{d_T} \left(\lambda - \frac{\alpha + d_L}{p} L \right), \frac{N(1 - \eta_p^{(2)}) (\alpha + d_L - p d_L)}{p d_V} L \right) - \frac{\alpha + d_L}{p} L, \end{aligned} \tag{36}$$

Then, we have

Thus, there exists a $L^* \in (0, \lambda p / \alpha + d_L)$. Consequently, model (31) admits an infection equilibrium $E^* = (T^*, L^*, I^*, V_I^*)$. Furthermore, by calculation, we have

$$\begin{aligned} H(0) &= 0, \\ H \left(\frac{\lambda p}{\alpha + d_L} \right) &= -\lambda < 0, \\ H'(0) &= \frac{\alpha + d_L}{p} (\mathcal{R}_0 - 1) > 0 \quad \text{for } \mathcal{R}_0 > 1. \end{aligned} \tag{37}$$

$$\begin{aligned} H'(L^*) &= -\frac{\alpha + d_L}{p d_T} \beta_1 \frac{\partial f(T^*, V_I^*)}{\partial T} + \frac{N(1 - \eta_p^{(2)}) (\alpha + d_L - p d_L)}{p d_V} \beta_1 \frac{\partial f(T^*, V_I^*)}{\partial V_I} \\ &- \frac{\alpha + d_L}{p d_T} \beta_2 \frac{\partial g(T^*, I^*)}{\partial T} + \frac{\alpha + d_L - p d_L}{p d_I} \beta_2 \frac{\partial g(T^*, I^*)}{\partial I} - \frac{\alpha + d_L}{p} \\ &= -\frac{\alpha + d_L}{p d_T} \beta_1 \frac{\partial f(T^*, V_I^*)}{\partial T} + \frac{V_I^*}{L^* \beta_1} \frac{\partial f(T^*, V_I^*)}{\partial V_I} - \frac{\alpha + d_L}{p d_T} \beta_2 \frac{\partial g(T^*, I^*)}{\partial T} \\ &+ \frac{I^*}{L^* \beta_2} \frac{\partial g(T^*, I^*)}{\partial I} - \frac{1}{L^*} (\beta_1 f(T^*, V_I^*) + \beta_2 g(T^*, V_I^*)) \\ &= -\frac{\alpha + d_L}{p d_T} \left(\frac{\beta_1 V_I^*}{1 + m_1 V_I^*} + \frac{\beta_2 I^*}{1 + m_2 I^*} \right) - \frac{m_1 \beta_1 T^* (V_I^*)^2}{L^* (1 + m_1 V_I^*)^2} - \frac{m_2 \beta_2 T^* (I^*)^2}{L^* (1 + m_2 I^*)^2} < 0, \end{aligned} \tag{38}$$

which implies that $H(L)$ is decreasing at each of its root. If there exists more than one root of $H(L) = 0$, then it must exist a root \widehat{L} such that $H'(\widehat{L}) \geq 0$, which leads to a contradiction. Hence, we claim that there exists a unique infection equilibrium $E^* = (T^*, L^*, I^*, V_I^*)$ for $\mathcal{R}_0 > 1$.

By constructing suitable Lyapunov functions, we can show that the corresponding infection-free equilibrium E_0 and infection equilibrium E^* of model (31) are globally asymptotically stable.

Theorem 5. *If $\mathcal{R}_0 \leq 1$, then the infection-free equilibrium E_0 of model (31) is globally asymptotically stable.*

Proof. Define

$$U(t) = Y \left(T - T_0 - T_0 \ln \frac{T}{T_0} \right) + \frac{\alpha}{\alpha + d_L} L + I + \frac{1 - \mathcal{R}_{02}}{N(1 - \eta_p^{(2)})} V_I, \tag{39}$$

where $Y = (\alpha p / \alpha + d_L + (1 - p))$.

By a tedious computation, we have

$$\begin{aligned} U'(t) &= Y dT_0 \left(1 - \frac{T}{T_0} \right) \left(1 - \frac{T_0}{T} \right) + \frac{Y\beta_1 T_0 V_I}{1 + m_1 V_I} + \frac{Y\beta_2 T_0 I}{1 + m_2 I} - \mathcal{R}_{02} d_I I - \frac{1 - \mathcal{R}_{02}}{N(1 - \eta_p^{(2)})} d_V V_I \\ &\leq Y dT_0 \left(1 - \frac{T}{T_0} \right) \left(1 - \frac{T_0}{T} \right) + Y\beta_1 T_0 V_I + Y\beta_2 T_0 I - \mathcal{R}_{02} d_I I - \frac{1 - \mathcal{R}_{02}}{N(1 - \eta_p^{(2)})} d_V V_I \\ &= Y dT_0 \left(1 - \frac{T}{T_0} \right) \left(1 - \frac{T_0}{T} \right) + \frac{d_V V_I}{N(1 - \eta_p^{(2)})} (\mathcal{R}_0 - 1). \end{aligned} \tag{40}$$

Clearly, if $\mathcal{R}_0 \leq 1$, then $U'(t) \leq 0$. Moreover, by LaSalle's invariance principle, one can easily show that the infection-free equilibrium E_0 is globally asymptotically stable. \square

Theorem 6. *If $\mathcal{R}_0 > 1$, then the infection equilibrium E^* of model (31) is globally asymptotically stable.*

Proof. Define

$$\begin{aligned} G(t) &= Y \left(T - T^* - T^* \ln \frac{T}{T^*} \right) + \frac{\alpha}{\alpha + d_L} \left(L - L^* - L^* \ln \frac{L}{L^*} \right) \\ &\quad + I - I^* - I^* \ln \frac{I}{I^*} + Y \frac{\beta_1 f(T^*, V_I^*)}{N(1 - \eta_p^{(2)}) d_I I^*} \left(V_I - V_I^* - V_I^* \ln \frac{V_I}{V_I^*} \right), \end{aligned} \tag{41}$$

where $Y = (\alpha p / \alpha + d_L + (1 - p))$. Then, combining (33) and by a tedious computation yields

$$\begin{aligned} G'(t) &= d_I T^* Y \left(1 - \frac{T}{T^*} \right) \left(1 - \frac{T^*}{T} \right) + \frac{\alpha p}{\alpha + d_L} \beta_1 f(T^*, V_I^*) \\ &\quad \times \left[4 - \frac{T^*}{T} - \frac{L I^*}{L^* I} - \frac{I V_I^*}{I^* V_I} - \frac{f(T, V_I) L^*}{f(T^*, V_I^*) L} - \frac{V_I}{V_I^*} + \frac{T^* f(T, V_I)}{T f(T^*, V_I^*)} \right] \\ &\quad + (1 - p) \beta_1 f(T^*, V_I^*) \left[3 - \frac{T^*}{T} - \frac{V_I^* I}{V_I I^*} - \frac{I^* f(T, V_I)}{I f(T^*, V_I^*)} + \frac{T^* f(T, V_I)}{T f(T^*, V_I^*)} - \frac{V_I}{V_I^*} \right] \\ &\quad + \frac{\alpha p}{\alpha + d_L} \beta_2 g(T^*, I^*) \left[3 - \frac{T^*}{T} - \frac{L I^*}{L^* I} - \frac{L^* g(T, I)}{L g(T^*, I^*)} + \frac{T^* g(T, I)}{T g(T^*, I^*)} - \frac{I}{I^*} \right] \\ &\quad + (1 - p) \beta_2 g(T^*, I^*) \left[2 - \frac{T^*}{T} - \frac{g(T, I) I^*}{g(T^*, I^*) I} + \frac{T^* g(T, I)}{T g(T^*, I^*)} - \frac{I}{I^*} \right], \end{aligned}$$

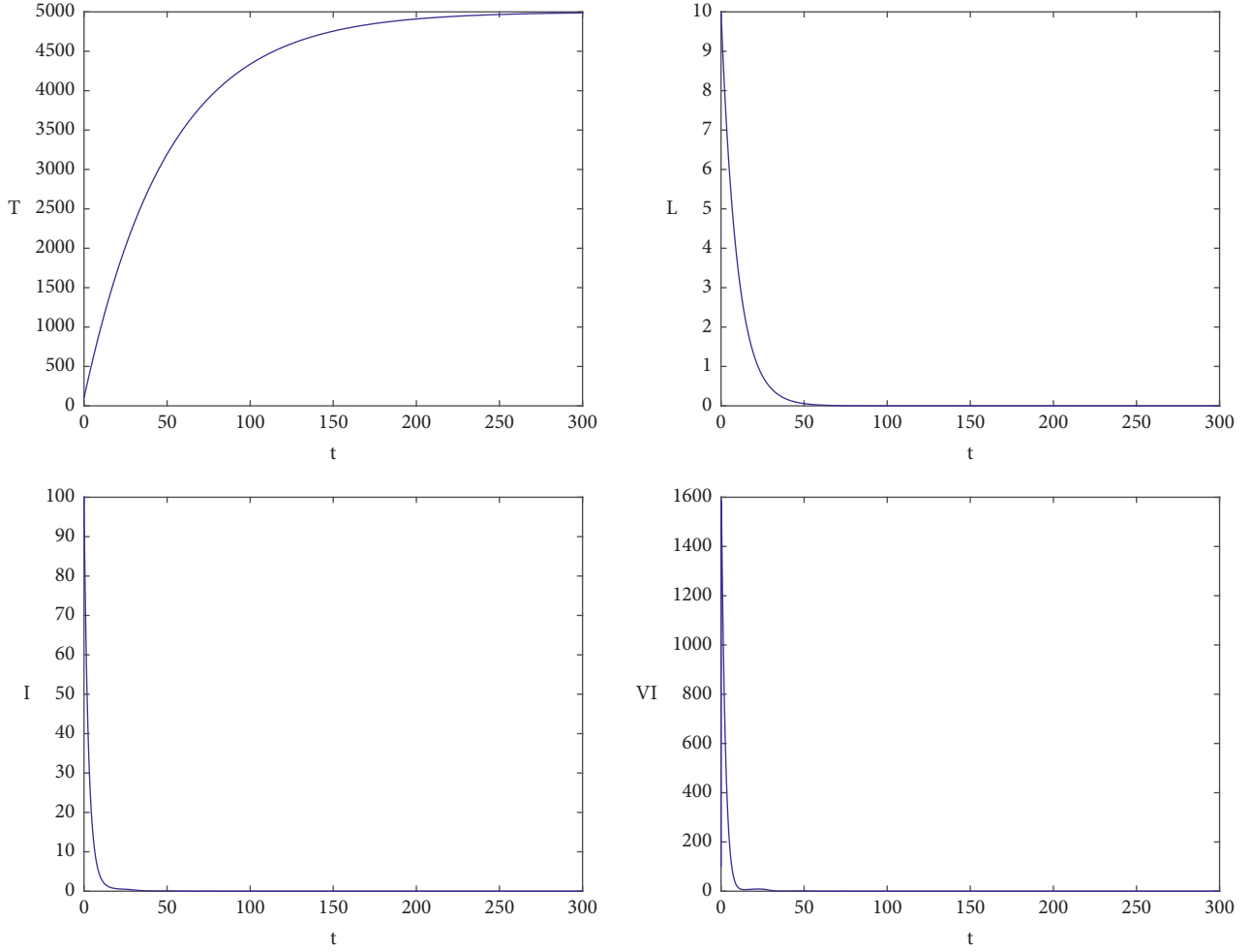


FIGURE 1: The results show that the infection-free equilibrium E_0 is globally asymptotically stable when $\mathcal{R}_0 < 1$.

$$\begin{aligned}
 &= d_T T^* \Upsilon \left(1 - \frac{T^*}{T}\right) \left(1 - \frac{T}{T^*}\right) + \Upsilon \beta_1 f(T^*, V_I^*) \left[\varphi\left(\frac{T^*}{T}\right) + \varphi\left(\frac{T f(T^*, V_I^*) V_I}{T^* f(T, V_I) V_I^*}\right) + \varphi\left(\frac{V_I^* I}{V_I I^*}\right) - \frac{m_1 (V_I - V_I^*)^2}{V_I^* (1 + m_1 V_I^*) (1 + m_1 V_I)} \right] \\
 &+ \frac{\alpha p}{\alpha + d_L} \beta_1 f(T^*, V_I^*) \left[\varphi\left(\frac{I^* L}{I L^*}\right) + \varphi\left(\frac{f(T, V_I) L^*}{f(T^*, V_I^*) L}\right) \right] + (1 - p) \beta_1 f(T^*, V_I^*) \\
 &\times \varphi\left(\frac{I^* f(T, V_I)}{I f(T^*, V_I^*)}\right) + \Upsilon \beta_2 g(T^*, I^*) \varphi\left(\frac{T^*}{T}\right) + \left[\varphi\left(\frac{T g(T^*, I^*) I}{T^* g(T, I) I^*}\right) - \frac{m_2 (I - I^*)^2}{I^* (1 + m_2 I) (1 + m_2 I^*)} \right] \\
 &+ \frac{\alpha p}{\alpha + d_L} \beta_2 g(T^*, I^*) \left[\varphi\left(\frac{g(T, I) L^*}{g(T^*, I^*) L}\right) + \varphi\left(\frac{L I^*}{L^* I}\right) \right] \\
 &+ (1 - p) \beta_2 g(T^*, I^*) \varphi\left(\frac{g(T, I) I^*}{g(T^*, I^*) I}\right) \leq 0,
 \end{aligned}$$

(42)

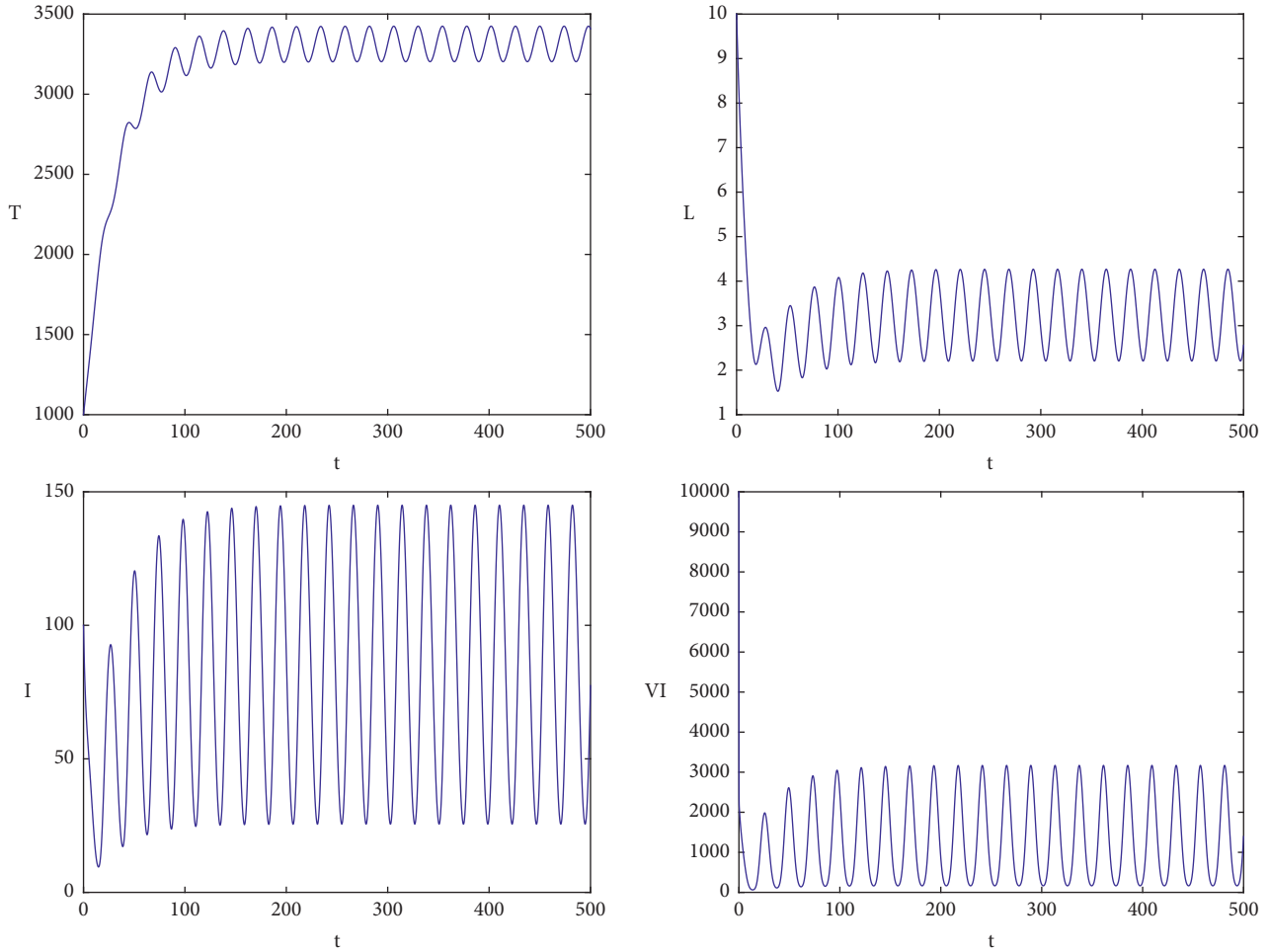


FIGURE 2: The results shows that model (3) exists as a periodic solution when $\mathcal{R}_0 > 1$.

where $\varphi(x) = 1 + \ln x - x$ with maximum value $\varphi(1) = 0$ for $x > 0$. Then, it follows from the LaSalle's invariance principle that one can show E^* is globally asymptotically stable. This completes the proof. \square

Remark 1. It follows from the above analysis of the model that the saturated incidence rates $V_I/1 + m_1 V_I$ and $I/1 + m_2 I$ can be extended to a more general form $f(V)$ and $g(I)$ with some conditions as in [27]. Thus, the saturated incidence rates of model (3) can be regarded as a special case.

4. Numerical Simulations

In this section, some numerical simulations are carried out to explain the obtained theoretical results. Most of these parameter values are taken from [6, 13].

Case 1. Let $\lambda = 100$, $d_T = 0.02$, $k_1 = 2.4 \times 10^{-6}$, $k_2 = 1.5 \times 10^{-4}$, $\alpha = 0.1$, $N = 1500$, $p = 0.01$, $d_V = 23$, $d_I = 0.4$, $d_L = 4 \times 10^{-3}$, $m_1 = 0.01$, $m_2 = 0.01$, $\eta_{rt} = 0.6 - 0.3\cos(\pi t/12)$, $\eta_p^{(1)} = 0.7 - 0.2\cos(\pi t/12)$, and $\eta_p^{(2)} = 0.6 - 0.25\cos(\pi t/12)$; then, we can obtain $\mathcal{R}_0 = 0.7875 < 1$. The simulation shows that the infection-free equilibrium $E_0 = (5000, 0, 0, 0)$ is globally asymptotically stable, which implies disease dies out. Figure 1 validates the above analysis.

Case 2. Let $\lambda = 100$, $d_T = 0.02$, $k_1 = 2.4 \times 10^{-4}$, $k_2 = 1 \times 10^{-4}$, $\alpha = 0.1$, $N = 2000$, $p = 0.01$, $d_V = 23$, $d_I = 0.4$, $d_L = 4 \times 10^{-3}$, $m_1 = 0.01$, $m_2 = 0.01$, $\eta_{rt} = 0.6 - 0.3\cos(\pi t/12)$, $\eta_p^{(1)} = 0.7 - 0.2\cos(\pi t/12)$, and $\eta_p^{(2)} = 0.6 - 0.25\cos(\pi t/12)$; then, we have $\mathcal{R}_0 = 17.0641 > 1$. The theoretical results show that the model admits a positive

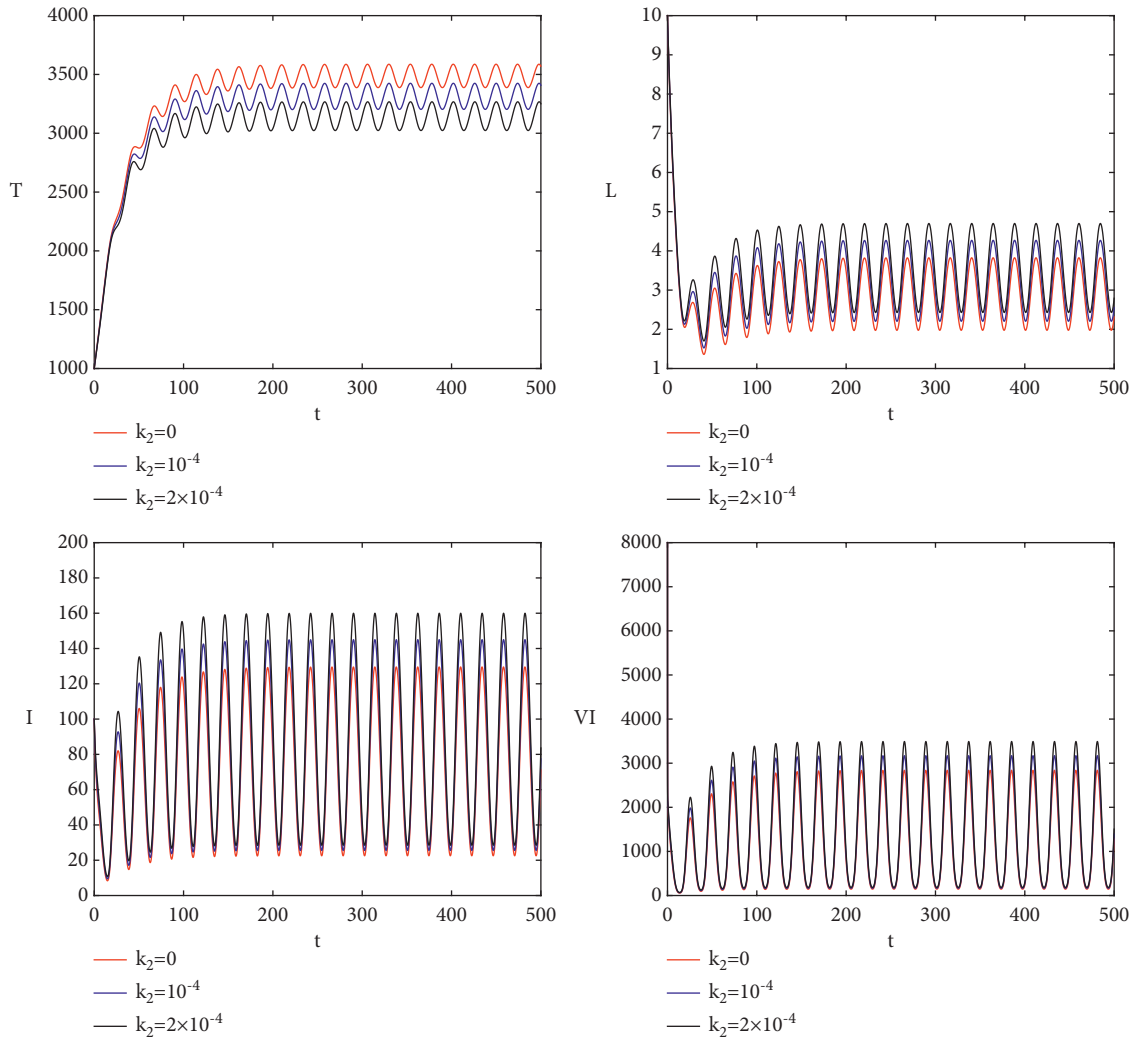


FIGURE 3: The effect of cell-to-cell transmission (k_2) on the dynamics of model (3). This shows that the existence of cell-to-cell transmission is benefit for viral infection.

periodic solution and disease keeps persistent in the host. Figure 2 confirms this conclusion.

Figure 3 shows the impact of cell-to-cell transmission (k_2) on the dynamics of the model, and the other parameters are the same with Figure 2. The results imply that the peak level of the density of latent cells, infected cells, and viral load increase as k_2 increases. Hence, cell-to-cell transmission existing may contribute to viral persistence and under-evaluate the risk of disease spreading for without considering cell-to-cell transmission. Thus, cell-to-cell transmission will be a barrier to curing the viral infection.

Figure 4 shows that the effects of PIs on the dynamics of the model by blocking cell-to-cell transmission, and the other parameters are the same with Figure 2. By varying the drug efficacy $\eta_p^{(1)}$ of PIs for blocking cell-to-cell transmission from the baseline value ($\eta_p^{(1)} = 0.7 - 0.2\cos(\pi t/12)$) to 50% and 0%, the numerical results imply that the peak level of the density of latent cell, infected cells, and viral load decrease under PIs' blocking cell-to-cell transmission. This implies that increase of the efficacy of PIs for blocking cell-to-cell transmission may contribute to weakening the severity of the viral infection.

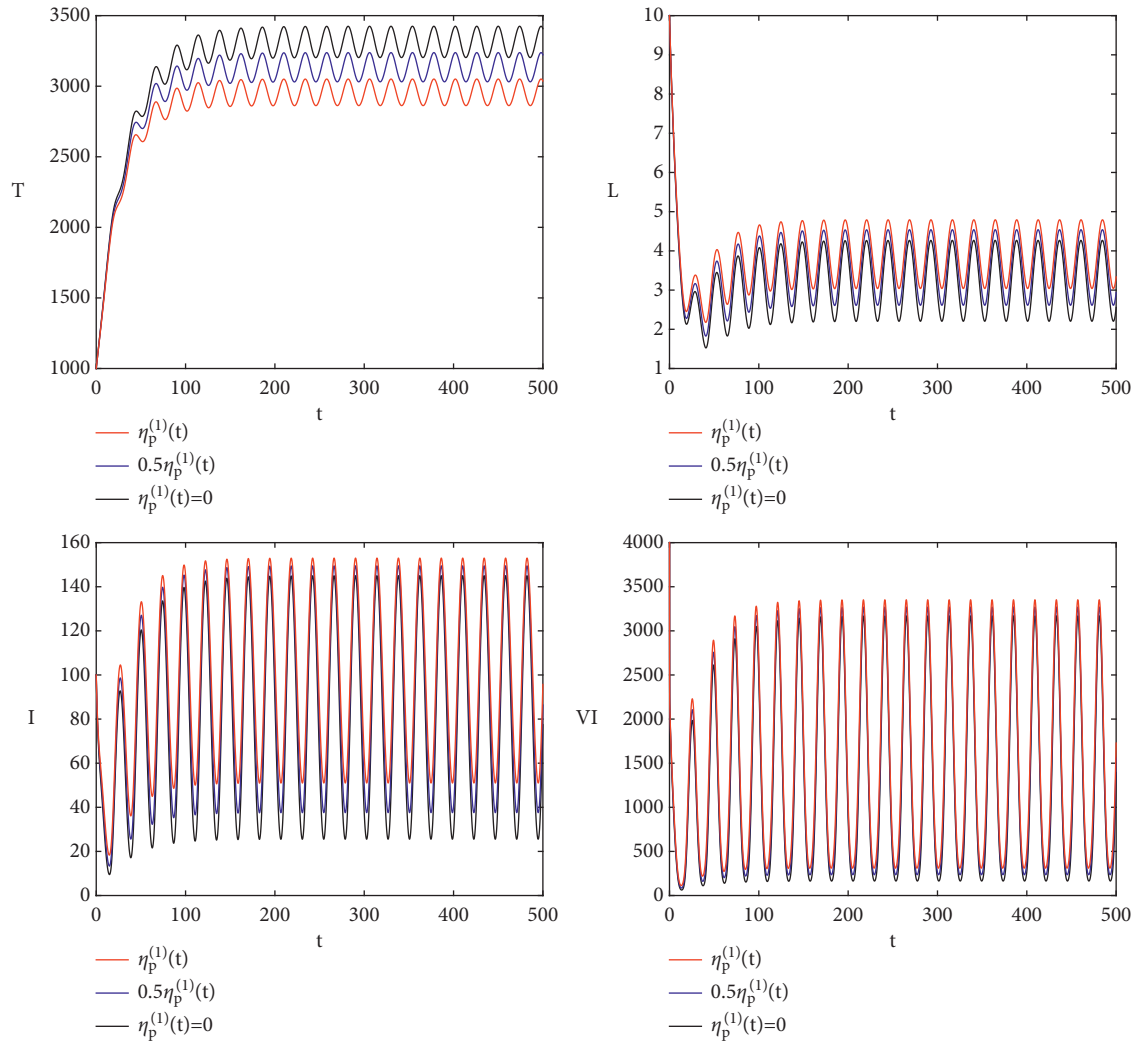


FIGURE 4: The effect of PIs for blocking cell-to-cell transmission ($\eta_p^{(1)}$) on the dynamics of model (3). The results show that PIs' blocks the cell-to-cell transmission (i.e., $\eta_p^{(1)} \neq 0$) may contribute to decreasing the peak level of the density of latent cells, infected cells, and viral load on some recent.

5. Summary and Discussion

In this study, a time-periodic viral infection model with cell-cell transmission was investigated. We have shown that the infection-free equilibrium E_0 is globally asymptotically stable if $\mathcal{R}_0 < 1$ which implies that infection will be eradicated, and the infection will persistent when $\mathcal{R}_0 > 1$. Furthermore, for the corresponding autonomous model, we have shown that the corresponding equilibria are globally asymptotically stable by applying the method of Lyapunov function. The results imply that cell-to-cell transmission existing may contribute to viral persistence and be a barrier to curing the viral infection. At the same time, increasing the efficacy of PIs for blocking cell-to-cell transmission is beneficial to weakening the severity of the viral infection.

Note that only a constant recruitment of uninfected T-cells has been considered in our model. However, T-cells can also be created by proliferation of existing T-cells with a logistic form instead of a constant recruitment [19] and the

incidence rates can be a more general form $f(V)$ and $g(I)$ [27], which formulated a further work. Furthermore, immune response and dynamics of the drug are also a good choice to extend the current work, which will be another future work.

Data Availability

All the data used to support the study are included in the article.

Conflicts of Interest

The authors declare that they have no conflicts of interest.

Acknowledgments

This work was supported by National Natural Science Foundation of China (#11701445, #11971379, and #11801439), Natural Science Basic Research Plan in Shaanxi

Province of China (2022JM-042, 2020JQ-831, and 2021JM-320), and Scientific Research Program Funded by Shaanxi Provincial Education Department (20JK0642).

References

- [1] A. S. Perelson and P. W. Nelson, "Mathematical analysis of HIV-1 dynamics in vivo," *SIAM Review*, vol. 41, no. 1, pp. 3–44, 1999.
- [2] P. De Leenheer and H. L. Smith, "Virus dynamics: a global analysis," *SIAM Journal on Applied Mathematics*, vol. 63, pp. 1313–1327, 2003.
- [3] T.-W. Chun, D. Finzi, and J. Margolick, "In vivo fate of HIV-1-infected T cells: quantitative analysis of the transition to stable latency," *Nature Medicine*, vol. 1, pp. 1284–1290, 1995.
- [4] T. W. Chun, L. Carruth, D. Finzi et al., "Quantification of latent tissue reservoirs and total body viral load in HIV-1 infection," *Nature*, vol. 387, pp. 183–188, 1997.
- [5] T. W. Chun, L. Stuyver, S. B. Mizell et al., "Presence of an inducible HIV-1 latent reservoir during highly active antiretroviral therapy," *Proceedings of the National Academy of Sciences*, vol. 94, no. 24, Article ID 13193, 1997.
- [6] S. Pankavich, "The effects of latent infection on the dynamics of HIV," *Differential Equations and Dynamical Systems*, vol. 24, no. 3, pp. 281–303, 2016.
- [7] L. Rong and A. S. Perelson, "Modeling latently infected cell activation: viral and latent reservoir persistence, and viral blips in HIV-infected patients on potent therapy," *PLoS Computational Biology*, vol. 5, no. 10, Article ID e1000533, 2009.
- [8] A. Alshorman, X. Wang, M. J. Meyer, and L. Rong, "Analysis of HIV models with two time delays," *Journal of Biological Dynamics*, vol. 11, pp. 40–64, 2017.
- [9] X. Wang, S. Tang, X. Song, and L. Rong, "Mathematical analysis of an HIV latent infection model including both virus-to-cell infection and cell-to-cell transmission," *Journal of Biological Dynamics*, vol. 11, pp. 455–483, 2017.
- [10] Y. Yang, Y. Dong, and Y. Takeuchi, "Global dynamics of a latent HIV infection model with general incidence function and multiple delays," *Discrete Continuous Dynamical Systems-B*, vol. 24, no. 2, pp. 783–800, 2019.
- [11] H. Liu and J. Zhang, "Dynamics of two time delays differential equation model to HIV latent infection," *Physica A: Statistical Mechanics and Its Applications*, vol. 514, no. 15, pp. 384–395, 2019.
- [12] Y. Wang, M. Lu, and J. Liu, "Global stability of a delayed virus model with latent infection and Beddington-DeAngelis infection function," *Applied Mathematics Letters*, vol. 107, Article ID 106463, 2020.
- [13] A. Mojaver and H. Kheiri, "Mathematical analysis of a class of HIV infection models of CD4⁺ T-cells with combined antiretroviral therapy," *Applied Mathematics and Computation*, vol. 259, pp. 258–270, 2015.
- [14] R. J. Smith and L. M. Wahl, "Distinct effects of protease and reverse transcriptase inhibitors in an immunological model of HIV-1 infection with impulsive drug effects," *Bulletin of Mathematical Biology*, vol. 66, no. 5, pp. 1259–1283, 2004.
- [15] H. Fung, E. Stone, and F. Piacenti, "Tenofovir disoproxil fumarate: a nucleotide reverse transcriptase inhibitor for the treatment of HIV infection," *Clinical Therapeutics*, vol. 24, pp. 1515–1548, 2002.
- [16] C. Pinto, A. Carvalho, and J. Tavares, "Time-varying pharmacodynamics in a simple noninteger HIV infection model," *Mathematical Biosciences*, vol. 307, pp. 1–12, 2019.
- [17] A. Sigal, J. Kim, A. Balazs et al., "Cell-to-cell spread of HIV permits ongoing replication despite antiretroviral therapy," *Nature*, vol. 477, pp. 95–98, 2011.
- [18] X. L. Lai and X. F. Zou, "Modeling HIV-1 virus dynamics with both virus-to-cell infection and cell-to-cell transmission," *SIAM Journal on Applied Mathematics*, vol. 74, pp. 898–917, 2014.
- [19] X. L. Lai and X. F. Zou, "Modeling cell-to-cell spread of HIV-1 with logistic target cell growth," *Journal of Mathematical Analysis and Applications*, vol. 426, pp. 563–584, 2015.
- [20] Y. Yang, L. Zou, and S. Ruan, "Global dynamics of a delayed within-host viral infection model with both virus-to-cell and cell-to-cell transmissions," *Mathematical Biosciences*, vol. 270, pp. 183–191, 2015.
- [21] F. Li and J. Wang, "Analysis of an HIV infection model with logistic target-cell growth and cell-to-cell transmission, Chaos," *Solitons Fractals*, vol. 81, pp. 136–145, 2015.
- [22] J. Wang, M. Guo, X. Liu, and Z. Zhao, "Threshold dynamics of HIV-1 virus model with cell-to-cell transmission, cell-mediated immune responses and distributed delay," *Applied Mathematics and Computation*, vol. 291, pp. 149–161, 2016.
- [23] J. Wang, J. Yang, and T. Kuniya, "Dynamics of a PDE viral infection model incorporating cell-to-cell transmission," *Journal of Mathematical Analysis and Applications*, vol. 444, pp. 1542–1564, 2016.
- [24] Y. Gao and J. Wang, "Threshold dynamics of a delayed nonlocal reaction-diffusion HIV infection model with both cell-free and cell-to-cell transmissions," *Journal of Mathematical Analysis and Applications*, vol. 488, Article ID 124047, 2020.
- [25] P. Wu and H. Zhao, "Dynamics of an HIV infection model with two infection routes and evolutionary competition between two viral strains," *Applied Mathematical Modelling*, vol. 84, pp. 240–264, 2020.
- [26] Y. Xu, Z. Zhu, Y. Yang, and F. Meng, "Vectored immunoprophylaxis and cell-to-cell transmission in HIV dynamics," *Inter. J. Bifur. Chaos*, vol. 30, no. 13, Article ID 2050185, 2020.
- [27] J. Xu, Y. Geng, and J. Hou, "Global dynamics of a diffusive and delayed viral infection model with cellular infection and nonlinear infection rate," *Computers & Mathematics with Applications*, vol. 73, pp. 640–652, 2017.
- [28] A. M. Elaiw and N. H. AlShamrani, "Global stability of a delayed adaptive immunity viral infection with two routes of infection and multi-stages of infected cells, Commun," *Nonlinear. Sci. Numer. Simulat.*, vol. 86, Article ID 105259, 2020.
- [29] A. M. Elaiw, N. H. AlShamrani, and A. D. Hobiny, "Stability of an adaptive immunity delayed HIV infection model with active and silent cell-to-cell spread," *Mathematical Biosciences and Engineering*, vol. 17, no. 6, pp. 6401–6458, 2021.
- [30] B. K. Titanji, M. Aasa-Chapman, D. Pillay, and C. Jolly, "Protease inhibitors effectively block cell-to-cell spread of HIV-1 between T cells," *Retrovirology*, vol. 10, 2013.
- [31] N. Bacaer and S. Guernaoui, "The epidemic threshold of vector-borne diseases with seasonality," *Journal of Mathematical Biology*, vol. 53, pp. 421–436, 2006.
- [32] W. D. Wang and X. Q. Zhao, "Threshold dynamics for compartmental epidemic models in periodic environments," *Journal of Dynamics and Differential Equations*, vol. 20, no. 3, pp. 699–717, 2008.
- [33] F. Zhang and X. Q. Zhao, "A periodic epidemic model in a patchy environment," *Journal of Mathematical Analysis and Applications*, vol. 325, pp. 496–516, 2007.
- [34] T. Kato, *Perturbation Theory for Linear Operators*, Springer-Verlag, Berlin, Germany, 1976.

- [35] X. Q. Zhao, *Dynamical Systems in Population Biology*, Springer-Verlag, New York, NY, USA, 2003.
- [36] J. K. Hale, "Asymptotic behavior of dissipative systems," *Math. Surveys Monogr*, Vol. 25, Amer. Math. Soc., Providence, RI, 1988.