



An effective numerical technique to solve a stochastic delayed HIV infection model

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Abstract— In this paper, we employ a step-collocation method based on Jacobi polynomials (JPs) to solve a stochastic delayed HIV (SD-HIV) infection model. For this reason, first, we convert the SD-HIV system with a finite delay into a non-delay system by using a stepwise approach. Then, by applying a Jacobi-collocation scheme in each step, a non-delay nonlinear system is obtained. Finally, the numerical simulation is implemented to validate the robustness of the proposed scheme.

Keywords— Stochastic delay system, HIV infection model, Step-collocation scheme, Jacobi polynomials.

I. Introduction

Human immunodeficiency virus is a lentivirus that causes acquired immunodeficiency syndrome [1]. The disease of HIV infection has become one of the major public health problems in the world. Recently, dynamics models of HIV infection with time delay have received much attention and many results have been reported [2, 3, 4].

In this paper, we focus on the following SD-HIV infection model [5]

$$(1) \quad \begin{cases} \dot{T}(t) = s - dT(t) - \beta T(t)G(V(t)) + \sigma_1 T(t)\dot{B}_1(t), \\ \dot{I}(t) = \beta e^{-\gamma\tau} T(t-\tau)G(V(t-\tau)) - pI(t) + \sigma_2 I(t)\dot{B}_2(t), \\ \dot{V}(t) = \alpha I(t) - \mu V(t) + \sigma_3 V(t)\dot{B}_3(t), \end{cases}$$

where $T(t)$, $I(t)$ and $V(t)$ represent the concentration of uninfected target cells, infected cells that produce virus, and HIV virus particles at time t , respectively. Also, τ is delay parameter and G is the incidence function that includes some special incidence rates. Moreover, $\dot{B}_i(t)$, $i = 1, 2, 3$, are time white noises on probability space $(\Omega, \mathcal{F}, \mathbb{P})$ and $\sigma_i^2 > 0$, $i = 1, 2, 3$, denote the intensities of the white noises. The initial

conditions of system (1) are

$$(2) \quad \begin{cases} T(t) = \eta_1(t), & I(t) = \eta_2(t), & V(t) = \eta_3(t), \\ \eta_i(t) \geq 0, & t \in [-\tau, 0], & i = 1, 2, 3, \\ (\eta_1, \eta_2, \eta_3) \in \mathbf{C}([-\tau, 0]; \mathbb{R}_+^3). \end{cases}$$

Other parameters have the biological meanings and described in Table I.

Table I. Description of the parameters in SD-HIV infection model.

<i>Parameter</i>	<i>Description</i>
Λ	Birth rate
s	New target cell production rate
d	The death rate of uninfected target cells
p	The death rate of infected cells
α	Free virus production rate from the infected cells
μ	The rate of removal of HIV virus particles from the immune system
β	The incidence rate of HIV infection
γ	The death rate for infected but not yet virus-producing cells

II. Description of the Step-Collocation Approach

Definition 1. The shifted JPs $\theta_i^{(\alpha, \gamma)}(t; \mathbf{e}_1, \mathbf{e}_2)$ over $[\mathbf{e}_1, \mathbf{e}_2]$ are defined by [6]

$$(3) \quad \theta_i^{(\alpha, \gamma)}(t; \mathbf{e}_1, \mathbf{e}_2) = \sum_{k=0}^i \Pi_{k,i}^{(\alpha, \gamma)} \left(\frac{t - \mathbf{e}_1}{\mathbf{e}_2 - \mathbf{e}_1} \right)^k,$$

where

$$\Pi_{k,i}^{(\alpha, \gamma)} := \frac{(-1)^{i-k} \Gamma(i + \gamma + 1) \Gamma(i + \alpha + \gamma + k + 1)}{(i - k)! k! \Gamma(k + \gamma + 1) \Gamma(i + \alpha + \gamma + 1)}.$$

Now, we explain a stepwise Jacobi-collocation method to solve the problem (1)-(2) on the interval $[0, T]$. Let $\mathbf{p} = [\frac{T}{\tau}]$ and $\Phi_1^0(t) = \eta_1(t)$, $\Phi_2^0(t) = \eta_2(t)$ and $\Phi_3^0(t) = \eta_3(t)$. We want to find an approximate solution of problem (1) in each subinterval $[(k - 1)\tau, k\tau]$, $k = 1, \dots, \mathbf{p}$, by employing the Jacobi-collocation technique. To this aim, we need to solve the following problem

$$(4) \quad \begin{cases} \dot{T}_k(t) = s - dT_k(t) - \beta T_k(t)V_k(t) + \sigma_1 T_k(t)\dot{B}_1(t), \\ \dot{I}_k(t) = \beta e^{-\gamma\tau} T_{k-1}(t - \tau)V_{k-1}(t - \tau) - pI_k(t) + \sigma_2 I(t)\dot{B}_2(t), \\ \dot{V}_k(t) = \alpha I_k(t) - \mu V_k(t) + \sigma_3 V_k(t)\dot{B}_3(t), \end{cases}$$

where $T_k(t) := T(t)$, $I_k(t) := I(t)$ and $V_k(t) := V(t)$ on $t \in [(k - 1)\tau, k\tau]$ and

$$(5) \quad \begin{cases} T_k((k - 1)\tau) = T_{k-1}((k - 1)\tau), \\ I_k((k - 1)\tau) = I_{k-1}((k - 1)\tau), \\ V_k((k - 1)\tau) = V_{k-1}((k - 1)\tau). \end{cases}$$

To find a numerical solution of (4)-(5), assume

$$(6) \quad \Phi_i^k(t) = \sum_{r=0}^n {}_i c_r^k \theta_r^{(\alpha, \gamma)}(t; (k-1)\tau, k\tau) \triangleq {}_i \mathbf{C}_k^T \Theta_k^{(\alpha, \gamma)}(t), \quad i = 1, 2, 3,$$

where $T(t) \simeq \Phi_1^k(t)$, $I(t) \simeq \Phi_2^k(t)$ and $V(t) \simeq \Phi_3^k(t)$ for $t \in [(k-1)\tau, k\tau]$ and

$${}_i \mathbf{C}_k := \left[{}_i c_0^k, {}_i c_1^k, \dots, {}_i c_n^k \right]^T, \quad \Theta_k^{(\alpha, \gamma)}(t) := \left[\theta_0^{(\alpha, \gamma)}(t; (k-1)\tau, k\tau), \dots, \theta_n^{(\alpha, \gamma)}(t; (k-1)\tau, k\tau) \right]^T.$$

According to (4) and (6), we have

$$(7) \quad \begin{cases} \mathbf{R}_1^k(t) = {}_1 \mathbf{C}_k^T \Psi_k^{(\alpha, \gamma)} - \left(s - d\Phi_1^k(t) - \beta\Phi_1^k(t)\Phi_3^k(t) + \sigma_1\Phi_1^k(t)\dot{\mathbf{B}}_1(t) \right) \simeq 0, \\ \mathbf{R}_2^k(t) = {}_2 \mathbf{C}_k^T \Psi_k^{(\alpha, \gamma)} - \left(\beta e^{-\gamma\tau}\Phi_1^{k-1}(t-\tau)\Phi_3^{k-1}(t-\tau) - p\Phi_2^k(t) + \sigma_2\Phi_2^k(t)\dot{\mathbf{B}}_2(t) \right) \simeq 0, \\ \mathbf{R}_3^k(t) = {}_3 \mathbf{C}_k^T \Psi_k^{(\alpha, \gamma)} - \left(\alpha\Phi_2^k(t) - \mu\Phi_3^k(t) + \sigma_3\Phi_3^k(t)\dot{\mathbf{B}}_3(t) \right) \simeq 0, \end{cases}$$

in which

$$\Psi_k^{(\alpha, \gamma)}(t) := \left[\partial_t \left(\theta_0^{(\alpha, \gamma)}(t; (k-1)\tau, k\tau) \right), \dots, \partial_t \left(\theta_n^{(\alpha, \gamma)}(t; (k-1)\tau, k\tau) \right) \right]^T.$$

Also, according to (5) and (6), we have

$$(8) \quad \begin{cases} \Delta_1^k = \Phi_1^k((k-1)\tau) - \Phi_1^{k-1}((k-1)\tau) \simeq 0, \\ \Delta_2^k = \Phi_2^k((k-1)\tau) - \Phi_2^{k-1}((k-1)\tau) \simeq 0, \\ \Delta_3^k = \Phi_3^k((k-1)\tau) - \Phi_3^{k-1}((k-1)\tau) \simeq 0. \end{cases}$$

Let ${}_k \mathbf{t}_n^{(\alpha, \gamma)} := k\tau$ and $\{{}_k \mathbf{t}_j^{(\alpha, \gamma)} : j = 1, \dots, n-1\}$ are the roots of $\theta_{n-1}^{(\alpha, \gamma)}(t; (k-1)\tau, k\tau)$. Then, from Eqs. (7)-(8), we have

$$(9) \quad \begin{cases} ({}_k \mathbf{t}_j^{(\alpha, \gamma)} - {}_k \mathbf{t}_{j-1}^{(\alpha, \gamma)}) \mathbf{R}_i^k({}_k \mathbf{t}_j^{(\alpha, \gamma)}) = 0, & j = 1, \dots, n, \quad i = 1, 2, 3, \\ \Delta_i^k = 0, & i = 1, 2, 3. \end{cases}$$

In each step $k = 1, \dots, \mathbf{p}$, the system (9) can be solved by using the Newton's iterative scheme [7], for the unknown coefficients ${}_i c_r^k$, $r = 0, 1, \dots, n$, $i = 1, 2, 3$. After applying this described numerical approach, we obtain a numerical estimation on $[0, T]$ as follows:

$$(10) \quad \Phi_i(t) = \begin{cases} \Phi_i^1(t), & t \in [0, \tau], \\ \Phi_i^2(t), & t \in [\tau, 2\tau], \\ \vdots & \vdots \\ \Phi_i^{\mathbf{p}}(t), & t \in [(\mathbf{p}-1)\tau, T], \end{cases}$$

in which $T(t) \simeq \Phi_1(t)$, $I(t) \simeq \Phi_2(t)$ and $V(t) \simeq \Phi_3(t)$.

III. Numerical Simulations

In this section, we investigate our proposed approach to illustrate the obtained results of the SD-HIV infection model. The codes are written in Matlab software and the computations are performed on a machine using a 1.70 GHz processor. The parameter values used in the simulations are as given in Table II. Suppose the following initial conditions

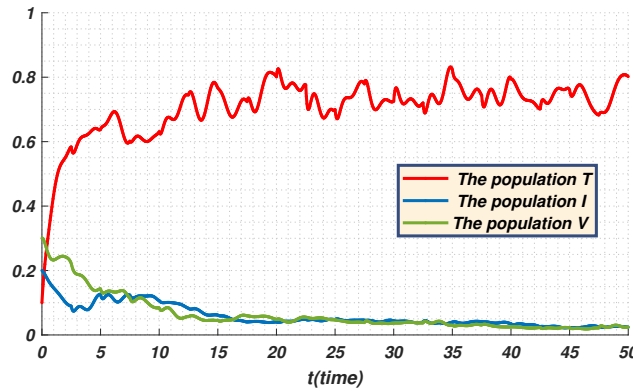
$$T(t) = 0.1, \quad I(t) = 0.2, \quad V(t) = 0.3, \quad t \in [-\tau, 0].$$

Table II. The parameter values in the SD-HIV infection model.

<i>Parameter</i>	<i>Value</i>	<i>Parameter</i>	<i>Value</i>
s	0.6	d	0.8
β	0.8	γ	0.2
p	0.4	α	0.4
μ	0.5	τ	2.5

Figure 1 shows the trajectories of solution for the stochastic model (1) with $\sigma_1^2 = 0.1$, $\sigma_2^2 = 0.2$, $\sigma_3^2 = 0.2$ and $n = 8$ in one sample path. Let $\sigma = \sigma_1 = \sigma_2 = \sigma_3$. Figures 2, 3, 4 display the trajectories of $T(t)$, $I(t)$ and $V(t)$ for the deterministic model $\sigma = 0$ and the stochastic model with $\sigma^2 = 0.3$ and $n = 7$.

Figures 5 and 6 display the behaviors of $I(t)$ and $V(t)$ for the stochastic model by $\sigma^2 = 0.1$ and $n = 6$, with different values of μ and β . Figure 5 shows that by increasing μ , infected cells producing virus, $I(t)$, and HIV particles at time t , $V(t)$, are decreased. Also, Figure 6 indicates that, increasing β will lead to increasing in the values of $I(t)$ and $V(t)$. This confirms the direct relationship between decreasing of the parameter β with the reduction of infected cells producing virus and HIV concentration.


Fig. 1. The trajectories of $T(t)$, $I(t)$ and $V(t)$ with $\sigma_1^2 = 0.1$, $\sigma_2^2 = 0.2$, $\sigma_3^2 = 0.2$ and $n = 8$.

IV. Conclusion

In this paper, a stochastic delayed HIV (SD-HIV) infection model with nonlinear incidence was considered. In order to simulate the behavior of the model, a step-by-step collocation method based on the Jacobi polynomials was presented. Some numerical simulations are provided to better understanding the dynamical behaviors of deterministic and stochastic SD-HIV models.

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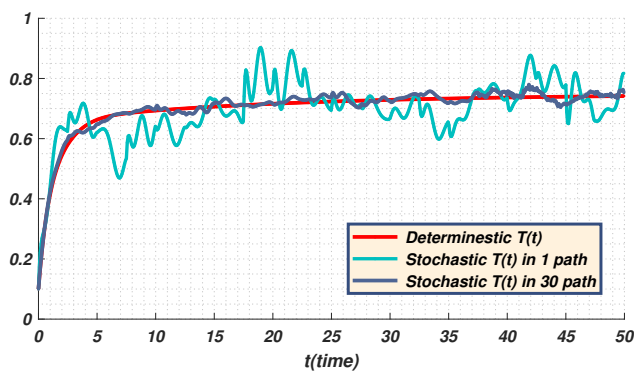


Fig. 2. The trajectories of $T(t)$ for the deterministic model ($\sigma = 0$) and the stochastic model with $\sigma^2 = 0.3$ and $n = 7$.

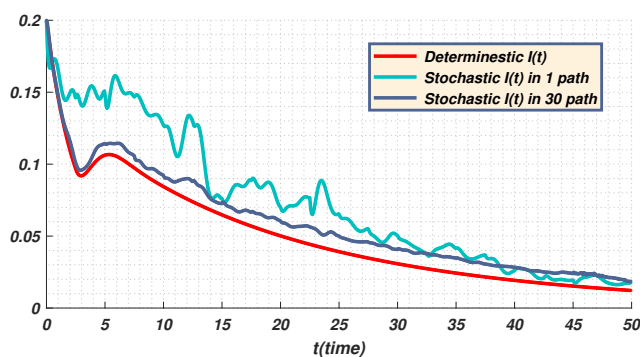


Fig. 3. The trajectories of $I(t)$ for the deterministic model ($\sigma = 0$) and the stochastic model with $\sigma^2 = 0.3$ and $n = 7$.

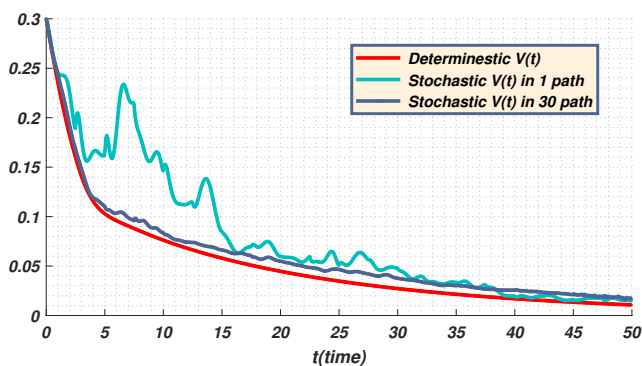


Fig. 4. The trajectories of $V(t)$ for the deterministic model ($\sigma = 0$) and the stochastic model with $\sigma^2 = 0.3$ and $n = 7$.

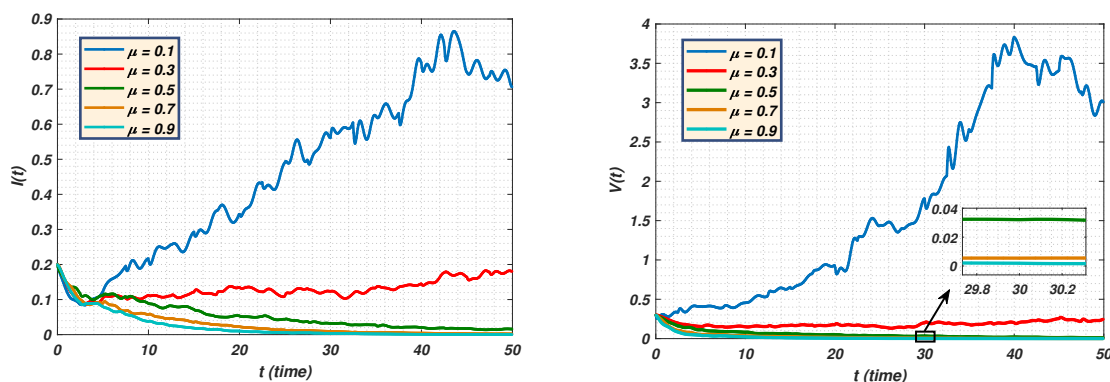


Fig. 5. The behaviors of $I(t)$ and $V(t)$ for the stochastic model by $\sigma^2 = 0.3$, with different values of μ .

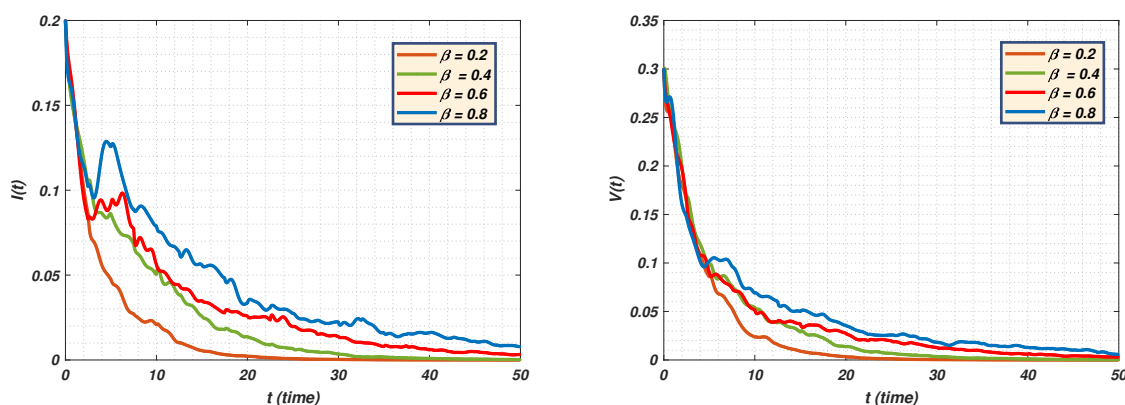


Fig. 6. The behaviors of $I(t)$ and $V(t)$ for the stochastic model by $\sigma^2 = 0.3$, with different values of β .

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