



Bergische Universität Wuppertal

Fakultät für Mathematik und Naturwissenschaften

Institute of Mathematical Modelling, Analysis and Computational
Mathematics (IMACM)

Preprint BUW-IMACM 26/21

Matthias Ehrhardt, Burhanuddin Safi, A. H. Hasmani,
and Purnachandra Rao Koya

**A Dynamically Consistent Nonstandard Finite Difference
Scheme for an HCV–HIV Co-infection
and Super-infection Model**

October 2, 2026

<http://www.imacm.uni-wuppertal.de>

RESEARCH ARTICLE

A Dynamically Consistent Nonstandard Finite Difference Scheme for an HCV–HIV Co-infection and Super-infection Model

Matthias Ehrhardt¹ | Burhanuddin Safi^{2,3} | A. H. Hasmani³ | Purnachandra Rao Koya⁴

¹Applied and Computational Mathematics,
University of Wuppertal, Wuppertal, Germany

²Department of Mathematics, Kabul University,
Kart-e-Char, Kabul, Afghanistan

³Department of Mathematics, Sardar Patel
University, Vallabh Vidyanagar, Gujarat, India

⁴Department of Computer Applications, Siddhardha
Academy of Higher Education, Deemed to be
University, Vijayawada, Andhra Pradesh, India

Correspondence

Corresponding author Burhanuddin Safi,

Email: burhansafi2@gmail.com;

naderi2024@ku.edu.af

Abstract

This paper presents a dynamically consistent nonstandard finite difference (NSFD) scheme for a mathematical model describing the transmission dynamics of HCV–HIV co-infection and superinfection. The proposed discretization employs a nonstandard denominator function and suitable nonlocal representations of nonlinear transmission terms. The denominator function is derived from the dominant dynamics of the total population to ensure consistency with the continuous model's long-term behavior. We rigorously establish several key structural properties of the resulting discrete system. Notably, the scheme preserves the non-negativity of all epidemiological compartments for arbitrary positive time step sizes; maintains a positively invariant feasible region; and has the same equilibrium points and existence conditions as the continuous model. The scheme also incorporates the relevant conservation property in the absence of demographic and disease-related losses. These results demonstrate that the proposed NSFD method is a reliable, structure-preserving alternative to conventional time discretizations, which can produce unphysical solutions when the time step is large. Numerical simulations illustrate the dynamical behavior of the discrete model and demonstrate its ability to reproduce the qualitative characteristics of the continuous HCV–HIV system.

KEYWORDS

Nonstandard finite difference, structure preserving discretization, HCV–HIV model, optimal control

1 | INTRODUCTION

Mathematical models based on systems of ordinary differential equations (ODEs) are an important framework for describing the transmission and progression of infectious diseases, as well as for evaluating potential intervention strategies. Compartmental models, in particular, have been extensively used to describe the evolution of subpopulations that are susceptible, infected, or recovered, among others that are epidemiologically relevant. These models can be extended to include multiple infection pathways, disease stages, co-infections, super-infections, demographic effects, and control measures. An important example is the transmission of the hepatitis C virus (HCV) and the human immunodeficiency virus (HIV), where the interaction between the two infections can lead to substantially more complex dynamics than either disease considered separately. The continuous HCV–HIV coinfection and superinfection model considered in this work was introduced and analyzed by Safi et al. [14], who established its principal epidemiological and dynamical properties, including positivity, boundedness, disease-free and endemic equilibria, the basic reproduction number, and stability properties. This study focuses on a complementary yet essential question: How can the continuous model be discretized without destroying the qualitative properties on which its epidemiological interpretation relies?

Achieving a small local truncation error is not the only consideration when solving epidemiological ODE systems numerically. The state variables represent population compartments and have an intrinsic physical meaning. Negative populations are inadmissible, the total population should remain within a biologically meaningful region, and the equilibrium structure of the continuous model should not be modified by discretization. Conventional numerical integrators, including the explicit Euler method and the classical Runge–Kutta method, generally do not preserve positivity or the invariant region unconditionally, see e.g. [8]. Their qualitative behavior can depend strongly on the time step size, particularly for nonlinear or stiff epidemiological systems. Consequently, a numerical solution may exhibit negative compartment populations or exhibit spurious long-time

behavior, even when the underlying continuous model is well-posed and its solutions remain non-negative. This issue is particularly relevant when simulations are performed over long time intervals or when relatively large time steps are desirable for parameter studies, uncertainty quantification, or optimal control computations.

Nonstandard finite difference (NSFD) methods provide a systematic framework for addressing this issue. Mickens [10, 11] introduced and extensively developed this methodology, which is based on the principle that a discretization should reproduce the essential qualitative and dynamical properties of the differential equation rather than merely approximate its derivatives in a conventional local sense. In a standard first-order discretization, the derivative is approximated using the step size $k = \Delta t$. However, an NSFD method replaces k with a suitable denominator function, $\varphi(k)$, satisfying $\varphi(k) = k + \mathcal{O}(k^2)$ as $k \rightarrow 0$. Additionally, nonlinear terms are discretized nonlocally whenever necessary to reproduce the relevant dynamical properties of the continuous system. Thus, the numerical method is designed based on the structure of the differential equations themselves rather than by merely increasing the order of a standard discretization.

The central concept of *dynamic consistency* has also been investigated from the perspective of discrete dynamical systems. Mickens emphasized that a discrete model should reproduce the essential dynamics of the underlying differential system, including positivity, conservation laws, invariant sets, equilibrium points, and stability properties when relevant to the model [12]. Cresson and Pierret [2] established conditions under which NSFD discretizations preserve the fixed points of the continuous system and their stability properties independently of the discretization parameter. Their analysis provides a rigorous dynamical systems foundation for constructing qualitative behavior-preserving NSFD schemes, which is particularly relevant to epidemiological models. In these models, preserving equilibria and their stability is essential for maintaining the interpretation of disease-free and endemic states.

The choice of the denominator function is an important part of the NSFD methodology. Instead of setting $\varphi(k) = k$, the denominator can be derived from the dominant linear dynamics of the continuous system. Mickens [13] developed a systematic methodology for determining denominator functions that guarantee positivity and reproduce the appropriate asymptotic behavior. For a scalar decay equation $u'(t) = -au(t)$, for example, matching the exact exponential decay over one time step leads to

$$\frac{1}{1 + a\varphi(k)} = e^{-ak}, \quad \text{i.e.} \quad \varphi(k) = \frac{e^{ak} - 1}{a},$$

which satisfies $\varphi(k) = k + \mathcal{O}(k^2)$. This choice can provide substantially better dynamic behavior than the standard denominator h , especially for long-time integration. Thus, the denominator-function approach therefore provides a direct connection between the discrete dynamics and the exact evolution of a suitably selected dominant subsystem.

NSFD methods have found particularly broad application in mathematical epidemiology, where positivity and invariant population regions are fundamental modeling requirements. A substantial body of work has developed NSFD schemes for compartmental epidemic models, including SIR, SEI, and SICA, and related systems. For instance, Mehdizadeh Khalsaraei et al. [7] constructed positivity-preserving NSFD schemes for an SIR model, while Vaz and Torres [16] developed a dynamically consistent NSFD discretization for an SICA epidemic model. These studies demonstrate that appropriately designed nonlocal discretizations can preserve the epidemiologically meaningful region of the continuous system while allowing for less restrictive time-step choices than standard schemes. More recently, Hoang and Ehrhardt [5] developed a dynamically consistent NSFD method for a generalized SEIR model with nonlinear incidence and proved the preservation of important qualitative properties of the epidemic dynamics. NSFD methodology has also been extended to more complicated settings. Maamar, Ehrhardt, and Tabharit [8], for example, developed NSFD schemes for Zika transmission models involving human, mosquito, and non-human primate populations, and considered a time-fractional extension. Their numerical results illustrate the practical importance of positivity preservation and correct asymptotic behavior when standard numerical solvers may generate nonphysical solutions.

The importance of structure preservation extends beyond classical integer-order compartmental models. Recent work has considered NSFD approaches for systems with nonlinear incidence, multiple interacting populations, fractional derivatives, and spatially distributed epidemic models. Notably, extending the methodology to reaction-diffusion epidemiological systems shows that preserving positivity, boundedness, and stability is still valuable when spatial heterogeneity and diffusion are included. These developments reinforce the idea that NSFD methods are a general structure-preserving discretization philosophy rather than a specific finite-difference formula related to one class of epidemic models.

Despite this progress, the numerical treatment of multi-compartment co-infection models remains challenging. These systems incorporate various infection mechanisms and nonlinear interactions. Even a seemingly minor change in the discretization of a product term can eliminate positivity or alter the equilibrium structure. The HCV-HIV model considered here contains eight epidemiological compartments that describe susceptible individuals, acute and chronic HCV infection, HIV infection, AIDS,

co-infection, superinfection, and recovery. Its nonlinear transmission terms couple several compartments and therefore require careful design of the nonlocal discretization. Directly applying a standard explicit scheme does not automatically preserve the positive invariant region. Furthermore, the previous analysis of the continuous model does not imply the properties of a numerical approximation by itself.

In this work, we construct a dynamically consistent NSFD scheme for the HCV-HIV co-infection and superinfection model of Safi et al. [14]. This scheme combines a common denominator function with nonlocal approximations of nonlinear transmission terms. Specifically, one factor associated with the advancing variable is evaluated at the new time level, while the other factors are evaluated at the current or previously computed time level. This ordering enables the resulting scheme to be evaluated sequentially, eliminating the need to solve a coupled nonlinear algebraic system. At the same time, the nonlocal structure is retained to enforce the epidemiological model's qualitative properties.

A primary goal is to prove these properties analytically instead of relying solely on numerical experiments. We prove that the proposed scheme preserves the non-negativity of all epidemiological compartments for every positive time step. Furthermore, we demonstrate that the corresponding feasible region is positively invariant and that the discrete system has the same equilibrium points and existence conditions as the continuous model. The denominator function is derived from the dominant dynamics of the total population to ensure consistency with the long-time behavior of the continuous system. Thus, the proposed method is not merely a numerical approximation of the HCV-HIV model, but rather, a dynamically consistent discrete model that retains its essential epidemiological structure.

The remainder of this paper is organized as follows. Section 2 reviews the continuous HCV-HIV co-infection and super-infection model. Section 3 introduces the NSFD methodology and constructs the proposed discretization, including the denominator function. Section 4 establishes the positivity, boundedness, equilibrium preservation, and consistency properties of the model. Section 5 extends the proposed NSFD scheme by incorporating time-dependent control strategies. Section 6 presents numerical simulations illustrating the behavior of the proposed scheme. Finally, we summarize the main findings and discuss possible extensions.

2 | THE CONTINUOUS HCV-HIV MODEL

This work builds upon the HCV-HIV co-infection and superinfection model proposed and analyzed in Safi, Hasmani, and Koya [14]. The objective is to construct and analyze a structure-preserving numerical discretization. In this section we briefly recall the continuous model and refer readers to [14] for its epidemiological formulation and complete qualitative analysis.

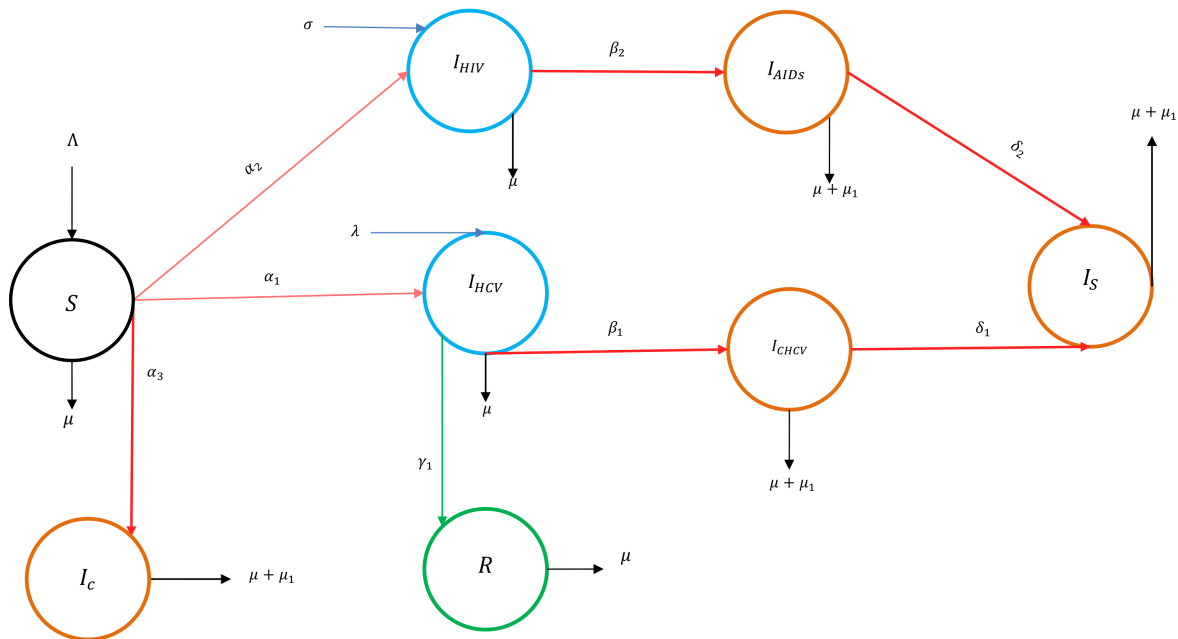
In the proposed model the considered population is divided into the following compartments: susceptible individuals (S), infected individuals with acute HCV (I_{HCV}), infected individuals with chronic HCV (I_{CHCV}), HIV infected individuals (I_{HIV}), AIDS infected individuals (I_{AIDS}), co-infected individuals (I_C), super-infected individuals (I_S) and recovered individuals (R). The governing system of equation is given by a system of eight ODEs

$$\begin{aligned}
 \frac{dS}{dt} &= \Lambda - (\alpha_1 I_{\text{HCV}} + \alpha_2 I_{\text{HIV}} + \alpha_3 I_C)S - \mu S, \\
 \frac{dI_{\text{HCV}}}{dt} &= \lambda + \alpha_1 I_{\text{HCV}}S - (\beta_1 + \gamma_1 + \mu)I_{\text{HCV}}, \\
 \frac{dI_{\text{CHCV}}}{dt} &= \beta_1 I_{\text{HCV}} - \delta_1 I_{\text{CHCV}}I_S - (\mu + \mu_1)I_{\text{CHCV}}, \\
 \frac{dI_{\text{HIV}}}{dt} &= \sigma + \alpha_2 I_{\text{HIV}}S - (\beta_2 + \mu)I_{\text{HIV}}, \\
 \frac{dI_{\text{AIDS}}}{dt} &= \beta_2 I_{\text{HIV}} - \delta_2 I_{\text{AIDS}}I_S - (\mu + \mu_1)I_{\text{AIDS}}, \\
 \frac{dI_C}{dt} &= \alpha_3 I_C S - (\mu + \mu_1)I_C, \\
 \frac{dI_S}{dt} &= (\delta_1 I_{\text{CHCV}} + \delta_2 I_{\text{AIDS}})I_S - (\mu + \mu_1)I_S, \\
 \frac{dR}{dt} &= \gamma_1 I_{\text{HCV}} - \mu R.
 \end{aligned} \tag{1}$$

for $t > 0$ and subject to the non-negative initial conditions $S(0) > 0$, $I_{\text{HCV}}(0)$, $I_{\text{CHCV}}(0)$, $I_{\text{HIV}}(0)$, $I_{\text{AIDS}}(0)$, $I_C(0)$, $I_S(0)$ and $R(0) \geq 0$, and list of the non-negative parameters in Table 1.

TABLE 1 List of model parameters along with their descriptions and assumed numerical values.

Parameters	Description	Value
Λ	Recruitment rate	0.949071
λ	Vertical transmission rate of HCV	0.00321
σ	Vertical transmission rate of HIV	0.00533
μ	Natural death rate	0.005001
μ_1	Disease death rate	0.02816667
α_1	Transmission rate of HCV infection	0.01108333
α_2	Transmission rate of HIV infection	0.0231
α_3	Rate of HCV-HIV co-infection	0.0264
β_1	Rate at which acute HCV develops to chronic HCV	0.16666667
β_2	Rate at which HIV infection develop to AIDS stage	0.05833333
δ_1	Infection rate at which chronic HCV infectives acquire HIV	0.075864
δ_2	Infection rate at which AIDS infected patients get HCV	0.097753
γ_1	Self-limiting recovery rate for acute HCV	0.02083333

**FIGURE 1** Schematic diagram of the HCV-HIV dynamics, cf. [14]

The positivity, boundedness, disease-free and endemic equilibria, basic reproduction number, and stability properties of system (1) were established in [14]. These basic properties, such as positivity, should be respected by any reasonable numerical method, which yields the stability of the scheme as a byproduct. However, the numerical simulations in [14] were obtained using the classical fourth-order Runge-Kutta method. This method's solutions do not necessarily preserve the qualitative properties of the continuous system for arbitrary time steps. For example, [8] showed that the standard Runge-Kutta scheme can produce unphysical negative values in the solution. This limitation motivates developing a dynamically consistent NSFD scheme that preserves the essential dynamical characteristics of system (1). The construction of the proposed NSFD scheme is discussed in the following section.

3 | THE STRUCTURE-PRESERVING DISCRETIZATION

3.1 | Nonstandard Finite Difference Schemes

NSFD methods for the numerical integration of differential equations were first introduced by Mickens [10, 11, 12]. In this section, we construct an NSFD scheme that inherently preserves positivity and satisfies the underlying conservation law under

the condition $\Lambda = \lambda = \sigma = 0$ and $\mu = \mu_1 = 0$, which additionally guarantees the stability of the method. Furthermore, we verify that the equilibrium points of the original continuous ODE system are precisely preserved in the proposed discrete model. Standard numerical integrators, such as classical Runge-Kutta methods, can fail by generating unphysical negative solutions (see e.g. [8]) or introducing spurious fixed points absent from the original continuous system [13]. In Section 3.2, we determine an appropriate denominator function $\phi(k)$ to capture the correct long-time asymptotic behavior.

A numerical scheme for a system of first-order differential equations is classified as an NSFD scheme if it satisfies at least one of the criteria established by Mickens [10]. First, the orders of the discrete derivatives should equal the orders of the corresponding derivatives appearing in the continuous differential equations. Second, discrete derivatives generally incorporate non-standard denominator functions rather than the step size $k = \Delta t$ alone. Specifically, first-order derivatives are approximated using a generalized forward difference formula,

$$\left. \frac{du}{dt} \right|_{t=t_n} \approx \frac{u^{n+1} - u^n}{\phi(k)},$$

where $u^n \approx u(t_n)$ for $n = 0, 1, 2, \dots$ on the uniform grid $t_n = nk$ with step size $k = \Delta t$. Here, $\phi \equiv \phi(k) > 0$ is a denominator function satisfying the consistency condition $\phi(k) = k + \mathcal{O}(k^2)$, which is chosen so that the discrete solution exhibits the same asymptotic behavior as the analytical solution. Third, nonlinear terms are represented nonlocally across multiple mesh points, for instance by replacing $u^2(t_n)$ with $u^n u^{n+1}$ or $u^3(t_n)$ with $(u^n)^2 u^{n+1}$. Fourth, essential physical and mathematical properties of the continuous ODE system – such as positivity, convexity, conservation laws, equilibrium points, and local asymptotic stability – must be directly inherited by the discrete model. More generally, time derivatives in NSFD schemes are modeled by

$$\left. \frac{du(t)}{dt} \right|_{t=t_n} \rightarrow \frac{u^{n+1} - \psi(k) u^n}{\phi(k)}, \quad (2)$$

where $t_n = nk$, u^n is the approximation of $u(t_n)$, and $\psi(k) = 1 + \mathcal{O}(k)$. The purpose of this general time discretization (2) is to ensure that the discrete model faithfully replicates the true long-time asymptotic behavior of the continuous system.

3.2 | Construction of the Nonstandard Finite Difference Scheme for the HCV-HIV Model

In this section we present the derivation of the NSFD scheme for the continuous HCV-HIV model in (1) by replacing the standard finite difference quotient with a generalized denominator function and by employing suitable nonlocal approximations of the nonlinear terms. Applying this nonstandard discretization strategy to the system (1) yields the following NSFD scheme

$$\begin{aligned} \frac{S^{n+1} - S^n}{\phi(k)} &= \Lambda - (\alpha_1 I_{\text{HCV}}^n + \alpha_2 I_{\text{HIV}}^n + \alpha_3 I_C^n) S^{n+1} - \mu S^{n+1}, \\ \frac{I_{\text{HCV}}^{n+1} - I_{\text{HCV}}^n}{\phi(k)} &= \lambda + \alpha_1 I_{\text{HCV}}^n S^{n+1} - (\beta_1 + \gamma_1 + \mu) I_{\text{HCV}}^{n+1}, \\ \frac{I_{\text{CHCV}}^{n+1} - I_{\text{CHCV}}^n}{\phi(k)} &= \beta_1 I_{\text{HCV}}^{n+1} - \delta_1 I_{\text{CHCV}}^{n+1} I_S^n - (\mu + \mu_1) I_{\text{CHCV}}^{n+1}, \\ \frac{I_{\text{HIV}}^{n+1} - I_{\text{HIV}}^n}{\phi(k)} &= \sigma + \alpha_2 I_{\text{HIV}}^n S^{n+1} - (\beta_2 + \mu) I_{\text{HIV}}^{n+1}, \\ \frac{I_{\text{AIDS}}^{n+1} - I_{\text{AIDS}}^n}{\phi(k)} &= \beta_2 I_{\text{HIV}}^{n+1} - \delta_2 I_{\text{AIDS}}^{n+1} I_S^n - (\mu + \mu_1) I_{\text{AIDS}}^{n+1}, \\ \frac{I_C^{n+1} - I_C^n}{\phi(k)} &= \alpha_3 I_C^n S^{n+1} - (\mu + \mu_1) I_C^{n+1}, \\ \frac{I_S^{n+1} - I_S^n}{\phi(k)} &= (\delta_1 I_{\text{CHCV}}^{n+1} + \delta_2 I_{\text{AIDS}}^{n+1}) I_S^n - (\mu + \mu_1) I_S^{n+1}, \\ \frac{R^{n+1} - R^n}{\phi(k)} &= \gamma_1 I_{\text{HCV}}^{n+1} - \mu R^{n+1}. \end{aligned} \quad (3)$$

with initial conditions $S^0 > 0$, $I_{\text{HCV}}^0 \geq 0$, $I_{\text{CHCV}}^0 \geq 0$, $I_{\text{HIV}}^0 \geq 0$, $I_{\text{AIDS}}^0 \geq 0$, $I_C^0 \geq 0$, $I_S^0 \geq 0$ and $R^0 \geq 0$, and also with positive denominator function $\phi(k) = \mathcal{O}(k)$ for $k \rightarrow 0$, $k = \Delta t$, to be determined from the asymptotic behaviour, cf. [5].

We briefly comment on the discretization of the nonlinear (in this case, quadratic) terms. For instance, in the first line of (3), the nonlinear term $\alpha_1 I_{\text{HCV}}(t)S(t)$ from (1) is discretized as $\alpha_1 I_{\text{HCV}}^n S^{n+1}$ rather than $\alpha_1 I_{\text{HCV}}^n S^n$ or $\alpha_1 I_{\text{HCV}}^{n+1} S^{n+1}$. The guiding rule is that exactly one factor of the state variable corresponding to the time derivative (here, S) must be evaluated at the advanced time level $n + 1$. This non-local treatment is essential for ensuring that the scheme preserves positivity, as shown in (4). To maintain an explicit sequential solution procedure, all remaining variables are evaluated at the current time level n , unless their updated values at level $n + 1$ have already been computed in a preceding step of the sequence, as with I_{HCV}^{n+1} in the third line. Furthermore, discrete conservation properties – such as the preservation of total human and vector populations – are incorporated wherever applicable. Consequently, although the original formulation (3) appears formally implicit, the variables at the $(n + 1)$ -th time level can be evaluated explicitly and sequentially using the previously computed values, yielding a fully uncoupled explicit scheme. To see this, the scheme (3) is rewritten as

$$\begin{aligned}
 S^{n+1} &= \frac{S^n + \phi(k)\Lambda}{1 + \phi(k)(\alpha_1 I_{\text{HCV}}^n + \alpha_2 I_{\text{HIV}}^n + \alpha_3 I_C^n + \mu)}, \\
 I_{\text{HCV}}^{n+1} &= \frac{I_{\text{HCV}}^n + \phi(k)(\lambda + \alpha_1 I_{\text{HCV}}^n S^{n+1})}{1 + \phi(k)(\beta_1 + \gamma_1 + \mu)}, \\
 I_{\text{CHCV}}^{n+1} &= \frac{I_{\text{CHCV}}^n + \phi(k)(\beta_1 I_{\text{HCV}}^{n+1})}{1 + \phi(k)(\delta_1 I_S^n + \mu + \mu_1)}, \\
 I_{\text{HIV}}^{n+1} &= \frac{I_{\text{HIV}}^n + \phi(k)(\sigma + \alpha_2 I_{\text{HIV}}^n S^{n+1})}{1 + \phi(k)(\beta_2 + \mu)}, \\
 I_{\text{AIDS}}^{n+1} &= \frac{I_{\text{AIDS}}^n + \phi(k)\beta_2 I_{\text{HIV}}^{n+1}}{1 + \phi(k)(\delta_2 I_S^n + \mu + \mu_1)}, \\
 I_C^{n+1} &= \frac{I_C^n + \phi(k)\alpha_3 I_C^n S^{n+1}}{1 + \phi(k)(\mu + \mu_1)}, \\
 I_S^{n+1} &= \frac{I_S^n + \phi(k)(\delta_1 I_{\text{CHCV}}^{n+1} + \delta_2 I_{\text{AIDS}}^{n+1})I_S^n}{1 + \phi(k)(\mu + \mu_1)}, \\
 R^{n+1} &= \frac{R^n + \phi(k)\gamma_1 I_{\text{HCV}}^{n+1}}{1 + \phi(k)\mu}.
 \end{aligned} \tag{4}$$

Remark 1. Although system (3) is formally implicit, the unknown variables can be computed from (4) sequentially in the order

$$S^{n+1} \rightarrow I_{\text{HCV}}^{n+1} \rightarrow I_{\text{CHCV}}^{n+1} \rightarrow I_{\text{HIV}}^{n+1} \rightarrow I_{\text{AIDS}}^{n+1} \rightarrow I_C^{n+1} \rightarrow I_S^{n+1} \rightarrow R^{n+1}, \tag{5}$$

without solving any nonlinear algebraic system. E.g. in the second line of (3) we have S^{n+1} on the r.h.s., but this quantity is already known from the first line. Consequently, the recursive form (4) can be implemented as a sequential explicit algorithm without solving a nonlinear algebraic system, while preserving the nonlocal structure of the NSFD methodology.

3.3 | The Denominator Function

Following the denominator function methodology of Mickens [13], the denominator function is constructed from the dominant linear dynamics of the continuous HCV-HIV model in (1).

To do so, summing up all compartments in (1) yields an ODE for the total compartment sum N :

$$\frac{dN}{dt} = \Lambda + \lambda + \sigma - \mu N - \mu_1(I_{\text{CHCV}} + I_{\text{AIDS}} + I_C + I_S), \quad t > 0. \tag{6}$$

$N(t)$ can be regarded as a conserved quantity of the above ODE system (1), if we set $\Lambda = \lambda = \sigma = 0$ and $\mu = \mu_1 = 0$. We will consider the subsolution $\underline{N}$ of N that exhibits the dominant dynamics and satisfies

$$\frac{d\underline{N}}{dt} = \Lambda + \lambda + \sigma - (\mu + \mu_1)\underline{N}, \quad t > 0. \tag{7}$$

It is solved by

$$\underline{N}(t) = \frac{\Lambda + \lambda + \sigma}{\mu + \mu_1} + \left(\underline{N}(0) - \frac{\Lambda + \lambda + \sigma}{\mu + \mu_1} \right) e^{-(\mu + \mu_1)t} = \underline{N}(0) + \left(\underline{N}(0) - \frac{\Lambda + \lambda + \sigma}{\mu + \mu_1} \right) (e^{-(\mu + \mu_1)t} - 1), \tag{8}$$

From the representation (8) we immediately deduce that we have in the long term $\lim_{t \rightarrow \infty} \underline{N}(t) = (\Lambda + \lambda + \sigma)/(\mu + \mu_1)$.

Next, we add the equations in the discrete NSFD model (3) which yields

$$\frac{N^{n+1} - N^n}{\phi(k)} = \Lambda + \lambda + \sigma - \mu N^{n+1} - \mu_1 (I_{\text{CHCV}}^{n+1} + I_{\text{AIDS}}^{n+1} + I_C^{n+1} + I_S^{n+1}), \quad n \geq 0. \quad (9)$$

i.e. for the discrete subsolution

$$\frac{\underline{N}^{n+1} - \underline{N}^n}{\phi(k)} = \Lambda + \lambda + \sigma - (\mu + \mu_1) \underline{N}^{n+1}, \quad n \geq 0. \quad (10)$$

that can be rewritten as

$$\begin{aligned} \underline{N}^{n+1} &= \frac{\underline{N}^n + \phi(k)(\Lambda + \lambda + \sigma)}{1 + \phi(k)(\mu + \mu_1)} = \underline{N}^n - \left(\underline{N}^n - \frac{\Lambda + \lambda + \sigma}{\mu + \mu_1} \right) \frac{\phi(k)(\mu + \mu_1)}{1 + \phi(k)(\mu + \mu_1)} \\ &= \underline{N}^n + \left(\underline{N}^n - \frac{\Lambda + \lambda + \sigma}{\mu + \mu_1} \right) \left(\frac{1}{1 + \phi(k)(\mu + \mu_1)} - 1 \right). \end{aligned} \quad (11)$$

The denominator function $\phi(k)$ is found by comparing (10) with the discrete version of (8), that is

$$\underline{N}^{n+1} = \underline{N}^n + \left(\underline{N}^n - \frac{\Lambda + \lambda + \sigma}{\mu + \mu_1} \right) (e^{-(\mu + \mu_1)k} - 1), \quad k = \Delta t, \quad (12)$$

such that the (positive) denominator function is defined by the relation

$$\frac{1}{1 + \phi(k)(\mu + \mu_1)} = e^{-(\mu + \mu_1)k}, \quad (13)$$

i.e.

$$\phi(k) = \frac{e^{(\mu + \mu_1)k} - 1}{\mu + \mu_1} = \frac{1 + (\mu + \mu_1)k + \frac{1}{2}(\mu + \mu_1)^2 k^2 + \dots - 1}{\mu + \mu_1} = k + \frac{(\mu + \mu_1)k^2}{2} + \dots = k + \mathcal{O}(k^2). \quad (14)$$

Note that the conservation property requires all the denominator functions $\phi(k)$ for the compartments to be the same, at least for all compartments in a subsystem, cf. [8], which is needed for stability reasons.

The qualitative properties of the proposed scheme are established in the following section.

4 | PROPERTIES OF THE PROPOSED NSFD SCHEME

In this section, we establish the qualitative properties of the proposed NSFD scheme, including positivity, boundedness, equilibrium preservation, stability, and consistency. Throughout the analysis, we use the recursive form (4) together with the denominator function (14), and we write $X^n = (S^n, I_{\text{HCV}}^n, I_{\text{CHCV}}^n, I_{\text{HIV}}^n, I_{\text{AIDS}}^n, I_C^n, I_S^n, R^n)$ for the state vector at time level n .

4.1 | Well-posedness

We first show that the proposed NSFD scheme is well-defined for arbitrary admissible initial conditions. The following theorem shows that the scheme preserves the non-negativity of all state variables for arbitrary time step sizes.

Theorem 1 (Positivity). *For every admissible initial condition, the numerical solution generated by the recursive system (4) remains non-negative for all $n \geq 0$ and every time step $k > 0$.*

Proof. The proof follows by induction. The result is true for $n = 0$ by the prescribed initial conditions. Assume that $X^n \geq 0$. Since all parameters are non-negative, every denominator in (4) is strictly positive, while each numerator is a non-negative combination of non-negative quantities. Therefore, $X^{n+1} \geq 0$. Hence, the numerical solution remains non-negative for all $n \geq 0$ $\square$

Theorem 2 (Boundedness). *The feasible region*

$$\Omega_h = \left\{ X^n \in \mathbb{R}_+^8 : 0 \leq N^n \leq \frac{\Lambda + \lambda + \sigma}{\mu} \right\}, \quad (15)$$

is positively invariant under the proposed NSFD scheme.

Proof. Let us consider

$$N^n = S^n + I_{\text{HCV}}^n + I_{\text{CHCV}}^n + I_{\text{HIV}}^n + I_{\text{AIDS}}^n + I_C^n + I_S^n + R^n.$$

Adding all equations of the proposed NSFD scheme in (3) yields

$$\frac{N^{n+1} - N^n}{\phi(k)} = \Lambda + \lambda + \sigma - \mu N^{n+1} - \mu_1 (I_{\text{CHCV}}^{n+1} + I_{\text{AIDS}}^{n+1} + I_C^{n+1} + I_S^{n+1}). \quad (16)$$

By the positivity property stated in Theorem 1, $I_{\text{CHCV}}^{n+1}, I_{\text{AIDS}}^{n+1}, I_C^{n+1}, I_S^{n+1} \geq 0$, therefore (16) can be simplified to

$$\frac{N^{n+1} - N^n}{\phi(k)} \leq \Lambda + \lambda + \sigma - \mu N^{n+1}, \quad (17)$$

i.e.

$$N^{n+1} \leq \frac{1}{1 + \mu\phi(k)} N^n + \frac{\phi(k)(\Lambda + \lambda + \sigma)}{1 + \mu\phi(k)}. \quad (18)$$

Iterating the recursion (18), we get

$$N^n \leq \frac{\Lambda + \lambda + \sigma}{\mu} + \left(N^0 - \frac{\Lambda + \lambda + \sigma}{\mu} \right) a^n, \quad a = \frac{1}{1 + \mu\phi(k)}. \quad (19)$$

By Theorem 1, the total population size $N^n \geq 0$, and $a^n \rightarrow 0$ as $n \rightarrow \infty$, hence

$$0 \leq N^n \leq \frac{\Lambda + \lambda + \sigma}{\mu}, \quad n \geq 0.$$

Therefore, the feasible region Ω_h in (15) is positively invariant under the proposed NSFD scheme, cf. [16]. $\square$

4.2 | Qualitative Analysis

Theorem 3 (Equilibrium points). *The proposed NSFD scheme in (4) possesses exactly the same equilibrium points and existence conditions as the continuous HCV-HIV model (1).*

Proof. An equilibrium point of the NSFD scheme in (4) is a fixed point of the associated discrete map. Let

$$X^* = (S^*, I_{\text{HCV}}^*, I_{\text{CHCV}}^*, I_{\text{HIV}}^*, I_{\text{AIDS}}^*, I_C^*, I_S^*, R^*)^\top, \quad (20)$$

be an equilibrium of the scheme (4). At the equilibrium, the state variables remain unchanged from one iteration to the next,

$$S^{n+1} = S^n = S^*, \quad I_{\text{HCV}}^{n+1} = I_{\text{HCV}}^n = I_{\text{HCV}}^*, \quad \dots, \quad R^{n+1} = R^n = R^*. \quad (21)$$

To compute the equilibria, we set the left hand side of (3) to zero and obtain the nonlinear algebraic system

$$\begin{aligned} 0 &= \Lambda - (\alpha_1 I_{\text{HCV}}^* + \alpha_2 I_{\text{HIV}}^* + \alpha_3 I_C^* + \mu) S^*, \\ 0 &= \lambda + \alpha_1 I_{\text{HCV}}^* S^* - (\beta_1 + \gamma_1 + \mu) I_{\text{HCV}}^*, \\ 0 &= \beta_1 I_{\text{HCV}}^* - (\delta_1 I_S^* + \mu + \mu_1) I_{\text{CHCV}}^*, \\ 0 &= \sigma + (\alpha_2 S^* + \beta_2 + \mu) I_{\text{HIV}}^*, \\ 0 &= \beta_2 I_{\text{HIV}}^* - (\delta_2 I_S^* + \mu + \mu_1) I_{\text{AIDS}}^*, \\ 0 &= \alpha_3 I_C^* S^* - (\mu + \mu_1) I_C^*, \\ 0 &= (\delta_1 I_{\text{CHCV}}^* + \delta_2 I_{\text{AIDS}}^*) I_S^* - (\mu + \mu_1) I_S^*, \\ 0 &= \gamma_1 I_{\text{HCV}}^* - \mu R^*. \end{aligned} \quad (22)$$

This system (22) coincides exactly with the equilibrium system derived from the continuous HCV-HIV model (1). Therefore, the NSFD scheme (4) possesses exactly the same equilibrium points and the same existence conditions as the continuous HCV-HIV model. Consequently, the proposed NSFD scheme is equilibria-preserving, cf. [9, 16]. $\square$

5 | OPTIMAL CONTROL OF THE PROPOSED NSFD SCHEME

This section extends the proposed NSFD scheme by incorporating time-dependent control strategies. Following the optimal control formulation developed in [14, Section 5], two control functions $u_1(t)$ and $u_2(t)$ are introduced to represent treatment interventions against HCV and HIV, respectively, together with the reinfection (ζ) associated with loss of immunity after *antiretroviral therapy* (ART). Hereby, the objective is to minimize the infected populations together with the implementation cost of the control measures over a finite time horizon. The continuous HCV-HIV optimal control model is discretized using the NSFD methodology outlined in Section 3.1, while preserving the qualitative properties established there. Then, the discrete optimality system is derived using the discrete Pontryagin maximum principle [1, 4, 6, 15].

5.1 | Controlled NSFD model

To investigate the optimal treatment strategies for HCV-HIV co-infection and super-infection, we introduce two discrete control variables $u_1^n, u_2^n \in [0, 1]$, $n = 0, 1, 3, \dots$, to represent treatment efforts against HCV, HIV. The admissible control set is defined by

$$U_h = \{(u_1^n, u_2^n) : 0 \leq u_i^n \leq 1, i = 1, 2, n = 0, 1, 2, \dots\}. \quad (23)$$

Applying the proposed NSFD methodology to the controlled continuous HCV-HIV model in [14, Section 5] yields the following recursively controlled NSFD system

$$\begin{aligned} S^{n+1} &= \frac{S^n + \phi(k)\Lambda}{1 + \phi(k)(\alpha_1 I_{\text{HCV}}^n + \alpha_2 I_{\text{HIV}}^n + \alpha_3 I_C^n + \mu)}, \\ I_{\text{HCV}}^{n+1} &= \frac{I_{\text{HCV}}^n + \phi(k)(\lambda + \alpha_1 I_{\text{HCV}}^n S^{n+1})}{1 + \phi(k)(\beta_1 + \gamma_1 + u_1^n + \mu)}, \\ I_{\text{CHCV}}^{n+1} &= \frac{I_{\text{CHCV}}^n + \phi(k)\beta_1 I_{\text{HCV}}^{n+1}}{1 + \phi(k)(\delta_1 I_S^n + u_1^n + \mu + \mu_1)}, \\ I_{\text{HIV}}^{n+1} &= \frac{I_{\text{HIV}}^n + \phi(k)(\sigma + \alpha_2 I_{\text{HIV}}^n S^{n+1} + \zeta R^n)}{1 + \phi(k)(\beta_2 + u_2^n + \mu)}, \\ I_{\text{AIDS}}^{n+1} &= \frac{I_{\text{AIDS}}^n + \phi(k)\beta_2 I_{\text{HIV}}^{n+1}}{1 + \phi(k)(\delta_2 I_S^n + u_2^n + \mu + \mu_1)}, \\ I_C^{n+1} &= \frac{I_C^n + \phi(k)\alpha_3 I_C^n S^{n+1}}{1 + \phi(k)(u_1^n + u_2^n + \mu + \mu_1)}, \\ I_S^{n+1} &= \frac{I_S^n + \phi(k)(\delta_1 I_{\text{CHCV}}^{n+1} + \delta_2 I_{\text{AIDS}}^{n+1}) I_S^n}{1 + \phi(k)(u_1^n + u_2^n + \mu + \mu_1)}, \\ R^{n+1} &= \frac{R^n + \phi(k) \left[\gamma_1 I_{\text{HCV}}^{n+1} + u_1^n (I_{\text{HCV}}^{n+1} + I_{\text{CHCV}}^{n+1} + I_C^{n+1} + I_S^{n+1}) + u_2^n (I_{\text{HIV}}^{n+1} + I_{\text{AIDS}}^{n+1} + I_C^{n+1} + I_S^{n+1}) \right]}{1 + \phi(k)(\zeta + \mu)} \end{aligned} \quad (24)$$

The scheme (24) exhibits positivity and its unknown variables can be evaluated successively in the order stated in (5). The corresponding discrete optimal control problem is formulated in the next subsection.

5.2 | Discrete Optimal Control Formulation

Our objective is to determine an optimal control pair $(u_1^*, u_2^*) \in U_h$, that minimizes the infected population and the implementation costs of the treatment strategies over the finite time horizon $[0, T]$, on the uniform mesh $t_n = nk$, $n = 0, \dots, N$, $T = Nk$. The *discrete optimal control problem* reads

$$(u_1^*, u_2^*) = \arg \min_{(u_1, u_2) \in U_h} J_h(u_1, u_2), \quad (25)$$

subject to the controlled NSFD system (24), with the *discrete objective functional*

$$J_h(u_1, u_2) = \phi(k) \sum_{n=0}^{N-1} \left[A_1 I_{\text{HCV}}^n + A_2 I_{\text{CHCV}}^n + A_3 I_{\text{HIV}}^n + A_4 I_{\text{AIDS}}^n + A_5 I_C^n + A_6 I_S^n + \frac{B_1}{2} (u_1^n)^2 + \frac{B_2}{2} (u_2^n)^2 \right], \quad (26)$$

where $A_i, i = 1, \dots, 6$, are the weights of the infected classes and B_1, B_2 are the treatment-cost weights, as in [14, Section 5].

5.3 | Existence of Optimal Controls

Since Ω_h denotes the positively invariant feasible region for the uncontrolled scheme established in Theorem 2, the controlled scheme (24) is likewise positively invariant on the extended region

$$\bar{\Omega}_h = \left\{ (X^n, u_1^n, u_2^n) \in \mathbb{R}_+^8 \times U_h : 0 \leq N^n \leq \frac{\Lambda + \lambda + \sigma}{\mu} \right\}. \quad (27)$$

That is, $\bar{\Omega}_h$ is precisely Ω_h augmented with the control constraint $u_1^n, u_2^n \in U_h$. The state bound itself is unaffected by the inclusion of controls, since u_1^n and u_2^n appear only as additional non-negative removal terms in the controlled NSFD (24). Thus, the total-population argument of Theorem 2 carries over unchanged with $u_1^n, u_2^n \geq 0$.

Theorem 4 (Existence). *There exist optimal controls $u_1^*, u_2^* \in U_h$ and optimal trajectories of the controlled NSFD system (24) that minimize $J_h(u_1, u_2)$ over U_h .*

Proof. The admissible control set U_h in (23) is closed, bounded, and convex; thus, it is compact. Therefore, the state trajectories generated by (24) remain in the compact, positively invariant set $\bar{\Omega}_h$ for every $(u_1, u_2) \in U_h$, so the map $(u_1, u_2) \mapsto (X^0, \dots, X^N)$ is well-defined and continuous on U_h . Consequently, J_h is continuous on the compact set U_h . Since the summand of J_h is strictly convex in (u_1^n, u_2^n) for $B_1, B_2 > 0$, J_h attains its minimum at some $(u_1^*, u_2^*) \in U_h$. This completes the proof. $\square$

5.4 | Discrete Optimality System

We use the discrete *Pontryagin maximum principle* (PMP) to derive the necessary optimality conditions. Let

$$X^n = (S^n, I_{\text{HCV}}^n, I_{\text{CHCV}}^n, I_{\text{HIV}}^n, I_{\text{AIDS}}^n, I_C^n, I_S^n, R^n)^\top$$

the state vector at time level n , and write (24) compactly as $X^{n+1} = F_h(X^n, u_1^n, u_2^n)$, where $F_h = (F_1, \dots, F_8)^\top$. Let $\lambda^n = (\lambda_1^n, \dots, \lambda_8^n)^\top$ denote the discrete adjoint (costate) vector associated with the state variables, and define the running cost as

$$L_h(X^n, u_1^n, u_2^n) = A_1 I_{\text{HCV}}^n + A_2 I_{\text{CHCV}}^n + A_3 I_{\text{HIV}}^n + A_4 I_{\text{AIDS}}^n + A_5 I_C^n + A_6 I_S^n + \frac{B_1}{2} (u_1^n)^2 + \frac{B_2}{2} (u_2^n)^2.$$

The discrete Hamiltonian is then defined by

$$H^n = \phi(k) L_h(X^n, u_1^n, u_2^n) + (\lambda_i^{n+1})^\top F_h(X^n, u_1^n, u_2^n) = \phi(k) L_h + \sum_{i=1}^8 \lambda_i^{n+1} F_h, \quad i = 1, 2, \dots, 8, \quad (28)$$

which becomes

$$\begin{aligned} H^n = \phi(k) & \left[A_1 I_{\text{HCV}}^n + A_2 I_{\text{CHCV}}^n + A_3 I_{\text{HIV}}^n + A_4 I_{\text{AIDS}}^n + A_5 I_C^n + A_6 I_S^n + \frac{B_1}{2} (u_1^n)^2 + \frac{B_2}{2} (u_2^n)^2 \right] \\ & + \lambda_1^{n+1} \left[\frac{S^n + \phi(k)\Lambda}{1 + \phi(k)(\alpha_1 I_{\text{HCV}}^n + \alpha_2 I_{\text{HIV}}^n + \alpha_3 I_C^n + \mu)} \right] + \lambda_2^{n+1} \left[\frac{I_{\text{HCV}}^n + \phi(k)(\lambda + \alpha_1 I_{\text{HCV}}^n S^{n+1})}{1 + \phi(k)(\beta_1 + \gamma_1 + u_1^n + \mu)} \right] \\ & + \lambda_3^{n+1} \left[\frac{I_{\text{CHCV}}^n + \phi(k)\beta_1 I_{\text{HCV}}^{n+1}}{1 + \phi(k)(\delta_1 I_S^n + u_1^n + \mu + \mu_1)} \right] + \lambda_4^{n+1} \left[\frac{I_{\text{HIV}}^n + \phi(k)(\sigma + \alpha_2 I_{\text{HIV}}^n S^{n+1} + \zeta R^n)}{1 + \phi(k)(\beta_2 + u_2^n + \mu)} \right] \\ & + \lambda_5^{n+1} \left[\frac{I_{\text{AIDS}}^n + \phi(k)\beta_2 I_{\text{HIV}}^{n+1}}{1 + \phi(k)(\delta_2 I_S^n + u_2^n + \mu + \mu_1)} \right] + \lambda_6^{n+1} \left[\frac{I_C^n + \phi(k)\alpha_3 I_C^n S^{n+1}}{1 + \phi(k)(u_1^n + u_2^n + \mu + \mu_1)} \right] \end{aligned}$$

$$\begin{aligned}
& + \lambda_7^{n+1} \left[\frac{I_S^n + \phi(k)(\delta_1 I_{\text{HCV}}^{n+1} + \delta_2 I_{\text{AIDS}}^{n+1}) I_S^n}{1 + \phi(k)(u_1^n + u_2^n + \mu + \mu_1)} \right] \\
& + \lambda_8^{n+1} \left[\frac{R^n + \phi(k) \left[\gamma_1 I_{\text{HCV}}^{n+1} + u_1^n (I_{\text{HCV}}^{n+1} + I_{\text{HCV}}^{n+1} + I_C^{n+1} + I_S^{n+1}) + u_2^n (I_{\text{HIV}}^{n+1} + I_{\text{AIDS}}^{n+1} + I_C^{n+1} + I_S^{n+1}) \right]}{1 + \phi(k)(\zeta + \mu)} \right]. \quad (29)
\end{aligned}$$

As recalled from (5), the controlled NSFD (24) updates the state variables sequentially rather than simultaneously. Each newly computed state variable is immediately used in the subsequent NSFD equations. Therefore, exactly evaluating the costate equations $\lambda_i^n = \partial H^n / \partial X_i^n$, together with the control stationarity conditions $\partial H^n / \partial u_1^n = 0$ and $\partial H^n / \partial u_2^n = 0$, would require computing the total derivatives of the F_h , accounting for every indirect dependence propagated through the successive updates, in addition to the direct dependence of each component F_i , $i = 1, \dots, 8$, on the variable being differentiated. As the recursion proceeds according to (5), these nested dependencies become analytically unwieldy.

To obtain a tractable discrete optimality system, we exploit the recursive structure of the proposed NSFD scheme. Since each recursive update already contributes a factor of order $\mathcal{O}(\phi(k))$, any dependence propagated through two or more successive updates contributes only higher-order terms $\mathcal{O}(\phi(k)^2)$ or smaller. These terms are already within the local truncation error of the proposed NSFD discretization. Therefore, retaining only the leading-order (explicit) contributions preserves the first-order consistency of the scheme without affecting its qualitative dynamics.

For the state equations, the resulting discrete adjoint system is equivalent to discretizing the continuous costate equations using the same nonstandard denominator functions as in (24). This preserves the recursive structure of the controlled NSFD model. Similarly, applying the same leading-order approximation to the stationarity conditions preserves the explicit dependence of the Hamiltonian on the control variables, including the nonstandard denominator functions, while consistently neglecting higher-order chain-rule contributions. This construction follows the practical strategy adopted in NSFD-based optimal control formulations (see, [15, 17]). Consequently, the resulting optimality system is first-order consistent with the continuous model while preserving its qualitative optimality structure.

Under the first-order consistent approximation described above, the discrete optimality system is characterized by the following theorem.

Theorem 5 (Discrete Optimality System). *Let $(u_1^*, u_2^*) \in U_h$ be an optimal control pair that minimizes (26), and let $X^* = (S^*, I_{\text{HCV}}^*, I_{\text{HCV}}^*, I_{\text{HIV}}^*, I_{\text{AIDS}}^*, I_C^*, I_S^*, R^*)$ be the corresponding optimal trajectory of (24). Then there exists an adjoint vector $\lambda^n = (\lambda_1^n, \dots, \lambda_8^n)^\top$, that satisfies the backward discrete adjoint system*

$$\lambda_1^n = \frac{\lambda_1^{n+1} + \phi(k)(\alpha_1 \lambda_2^{n+1} I_{\text{HCV}}^{n+1} + \alpha_2 \lambda_4^{n+1} I_{\text{HIV}}^{n+1} + \alpha_3 \lambda_6^{n+1} I_C^{n+1})}{1 + \phi(k)(\alpha_1 I_{\text{HCV}}^{n+1} + \alpha_2 I_{\text{HIV}}^{n+1} + \alpha_3 I_C^{n+1} + \mu)}, \quad (30a)$$

$$\lambda_2^n = \frac{\lambda_2^{n+1} + \phi(k)(\alpha_1 S^{n+1} \lambda_1^{n+1} + \beta_1 \lambda_3^{n+1} + (\gamma_1 + u_1^n) \lambda_8^{n+1} + A_1)}{1 + \phi(k)(\beta_1 + \gamma_1 + \mu + u_1^n - \alpha_1 S^{n+1})}, \quad (30b)$$

$$\lambda_3^n = \frac{\lambda_3^{n+1} + \phi(k)(\delta_1 I_S^{n+1} \lambda_7^{n+1} + u_1^n \lambda_8^{n+1} + A_2)}{1 + \phi(k)(\delta_1 I_S^{n+1} + \mu + \mu_1 + u_1^n)}, \quad (30c)$$

$$\lambda_4^n = \frac{\lambda_4^{n+1} + \phi(k)(\alpha_2 S^{n+1} \lambda_1^{n+1} + \beta_2 \lambda_5^{n+1} + u_2^n \lambda_8^{n+1} + A_3)}{1 + \phi(k)(\beta_2 + \mu + u_2^n - \alpha_2 S^{n+1})}, \quad (30d)$$

$$\lambda_5^n = \frac{\lambda_5^{n+1} + \phi(k)(\delta_2 I_S^{n+1} \lambda_7^{n+1} + u_2^n \lambda_8^{n+1} + A_4)}{1 + \phi(k)(\delta_2 I_S^{n+1} + \mu + \mu_1 + u_2^n)}, \quad (30e)$$

$$\lambda_6^n = \frac{\lambda_6^{n+1} - \phi(k) \alpha_3 S^{n+1} \lambda_1^{n+1} + \phi(k)(u_1^n + u_2^n) \lambda_8^{n+1} + \phi(k) A_5}{1 + \phi(k)(\mu + \mu_1 + u_1^n + u_2^n - \alpha_3 S^{n+1})}, \quad (30f)$$

$$\lambda_7^n = \frac{\lambda_7^{n+1} - \phi(k)(\delta_1 I_{\text{HCV}}^{n+1} \lambda_3^{n+1} + \delta_2 I_{\text{AIDS}}^{n+1} \lambda_5^{n+1}) + \phi(k)(u_1^n + u_2^n) \lambda_8^{n+1} + \phi(k) A_6}{1 + \phi(k)(\mu + \mu_1 + u_1^n + u_2^n - \delta_1 I_{\text{HCV}}^{n+1} - \delta_2 I_{\text{AIDS}}^{n+1})}, \quad (30g)$$

$$\lambda_8^n = \frac{\lambda_8^{n+1} + \phi(k) \zeta \lambda_4^{n+1}}{1 + \phi(k)(\zeta + \mu)}, \quad (30h)$$

together with the transversality (terminal) conditions

$$\lambda_i^N = 0, \quad i = 1, \dots, 8, \quad (31)$$

where S^{n+1} , I_{HCV}^{n+1} , I_{AIDS}^{n+1} are the optimal-trajectory values generated by (24) at $(u_1^n, u_2^n) = (u_1^{*n}, u_2^{*n})$.

Furthermore, writing $\ell_1^{n+1} = I_{\text{HCV}}^{n+1} + I_{\text{CHCV}}^{n+1} + I_C^{n+1} + I_S^{n+1}$ and $\ell_2^{n+1} = I_{\text{HIV}}^{n+1} + I_{\text{AIDS}}^{n+1} + I_C^{n+1} + I_S^{n+1}$, the optimal controls satisfy the projected stationarity conditions $u_1^{*n} = \min\{1, \max(0, \hat{u}_1^n)\}$, $u_2^{*n} = \min\{1, \max(0, \hat{u}_2^n)\}$, where

$$\hat{u}_1^n = \frac{1}{B_1} \left[\frac{\lambda_2^{n+1} I_{\text{HCV}}^{n+1}}{1 + \phi(k)(\beta_1 + \gamma_1 + u_1^n + \mu)} + \frac{\lambda_3^{n+1} I_{\text{CHCV}}^{n+1}}{1 + \phi(k)(\delta_1 I_S^n + u_1^n + \mu + \mu_1)} + \frac{\lambda_6^{n+1} I_C^{n+1} + \lambda_7^{n+1} I_S^{n+1}}{1 + \phi(k)(u_1^n + u_2^n + \mu + \mu_1)} - \frac{\lambda_8^{n+1} \ell_1^{n+1}}{1 + \phi(k)(\zeta + \mu)} \right], \quad (32)$$

$$\hat{u}_2^n = \frac{1}{B_2} \left[\frac{\lambda_4^{n+1} I_{\text{HIV}}^{n+1}}{1 + \phi(k)(\beta_2 + u_2^n + \mu)} + \frac{\lambda_5^{n+1} I_{\text{AIDS}}^{n+1}}{1 + \phi(k)(\delta_2 I_S^n + u_2^n + \mu + \mu_1)} + \frac{\lambda_6^{n+1} I_C^{n+1} + \lambda_7^{n+1} I_S^{n+1}}{1 + \phi(k)(u_1^n + u_2^n + \mu + \mu_1)} - \frac{\lambda_8^{n+1} \ell_2^{n+1}}{1 + \phi(k)(\zeta + \mu)} \right]. \quad (33)$$

Proof. According to the discrete Pontryagin maximum principle for the constrained system $X^{n+1} = F_h(X^n, u^n)$, the adjoint variables satisfy $\lambda_i^n = \partial H^n / \partial X_i^n$ and the unconstrained controls satisfy $\partial H^n / \partial u_i^n = 0$, with H^n as in (28) [4, 6]. Since F_h is built through the sequential substitutions (5), the exact evaluation of these derivatives requires chain-rule contributions along the induced dependency graph. Each successive update contributes an additional factor $\mathcal{O}(\phi(k))$. Contributions transmitted through two or more updates are thus $\mathcal{O}(\phi(k)^2)$, which already lies within the local truncation error of the forward NSFD discretization. Therefore, retaining only the leading-order (direct) contributions preserves first-order consistency.

Applying this rule to $\lambda_i^n = \partial H^n / \partial X_i^n$ discretizes the continuous costate equations with the same denominator functions as (24), giving the adjoint recursion (30). Applying it to $\partial H^n / \partial u_1^n = 0$ and $\partial H^n / \partial u_2^n = 0$, retaining the direct dependence of F_2, F_3, F_6, F_7, F_8 on u_1^n and of F_4, F_5, F_6, F_7, F_8 on u_2^n , gives the control characterizations (32) and (33). These are both first-order consistent, discrete necessary conditions for (24).

The transversality conditions (31) follow since (26) carries no terminal cost. Thus, projection onto U_h gives the admissible optimal controls, as in the continuous case [14, Theorem 6]. $\square$

Remark 2. The conditions (32)–(33) are implicit rather than in closed form, since the state values on their right-hand side come from (24) evaluated at (u_1^n, u_2^n) , and their denominators depend on those same controls. The coupled system consists of (24), the adjoint equations (30) with the terminal conditions (31), and the control characterizations (32)–(33). It is therefore solved using the standard forward-backward sweep, the state system (24) is integrated forward from an initial control guess, the adjoint system (30) is integrated backward from (31), the controls are updated through (32)–(33), and the process is repeated until convergence. Since $\phi(k) = k + \mathcal{O}(k^2)$, every denominator in (32)–(33) tends to unity as $k \rightarrow 0$. Thus, the discrete characterizations reduce to the continuous optimality conditions in [14, Equation (70)]. In this sense, the discrete optimality system preserves the qualitative structure of the continuous model while remaining fully consistent with the controlled NSFD discretization.

6 | NUMERICAL RESULTS

In this section we evaluate the numerical performance and dynamical consistency of the proposed NSFD scheme. The numerical results are conducted using the parameter values listed in Table 1, adopted from the continuous study [14], together with the initial conditions

$$S(0) = 100, I_{\text{HCV}}(0) = 5, I_{\text{CHCV}}(0) = 0, I_{\text{HIV}}(0) = 5, I_{\text{AIDS}}(0) = 0, I_C(0) = 1, I_S(0) = 1, \text{ and } R(0) = 0.$$

The continuous model (1) is solved numerically in MATLAB, using the standard `ode45` solver, i.e. an explicit Runge-Kutta (4,5) formula, the Dormand-Prince pair [3], while the NSFD approximation is obtained through the explicit recursive scheme (24). The NSFD scheme is implemented on the uniform grid $t_n = nk$, and the continuous solutions from `ode45` are evaluated at the same grid. This ensures a direct comparison of both methods at identical time points, without requiring any interpolation of the NSFD solutions.

Firstly, the solutions of the continuous model and the NSFD scheme are compared over the time interval $0 \in [0, 15]$, using the step size $k = 0.01$. The controls are taken as $u_1 = 0.20$ and $u_2 = 0.77$, where u_1 represents the treatment against HCV infection, and u_2 the treatment against individuals infected with HIV and AIDS. These control values, together with the reinfection parameter $\zeta = 0.44735$, which accounts for the loss of immunity and subsequent reinfection, are adopted from the corresponding continuous study. The following numerical results are presented to investigate the accuracy of the NSFD scheme and its ability to capture the dynamics of the continuous HCV-HIV model under various control scenarios.

The Figure 2 compares the dynamics of both acute and chronic HCV infection obtained for the NSFD scheme and `ode45`. The numerical solutions in case of NSFD scheme and `ode45` are practically indistinguishable throughout the simulation interval,

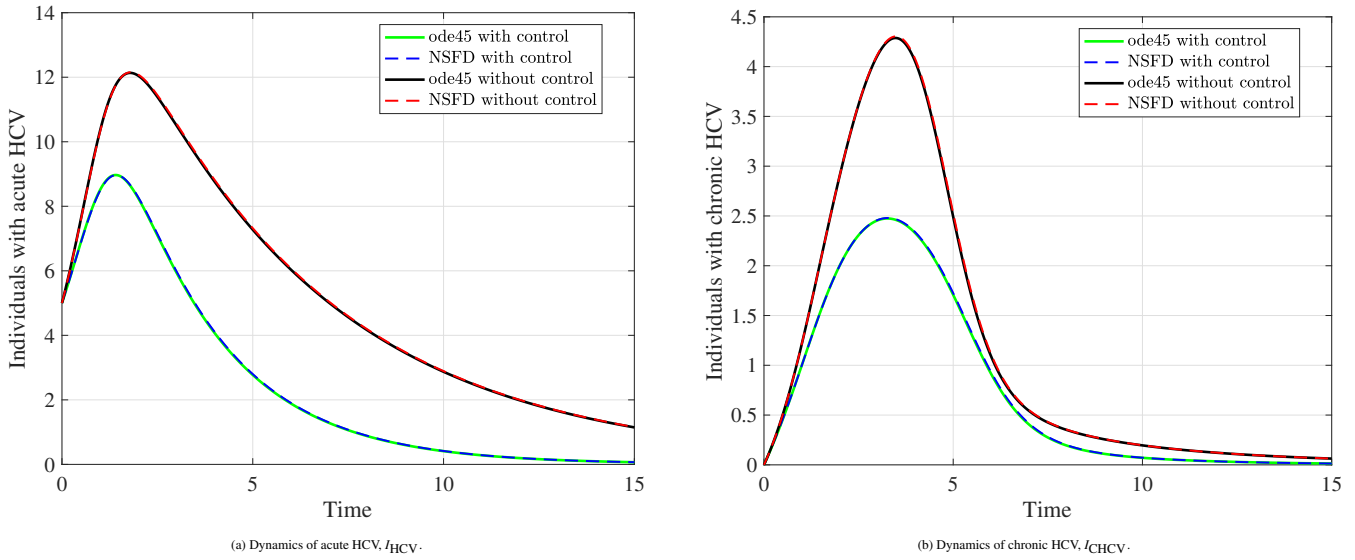


FIGURE 2 NSFD and ode45 solutions for the I_{HCV} and I_{CHCV} , with and without control.

both in the controlled and uncontrolled scenarios. In the absence of treatment, the acute HCV population increases rapidly and reaches to a maximum before gradually declining. However, when the HCV treatment control u_1 is applied, the corresponding peak is reduced, thus the control produces a substantial reduction in the maximum acute HCV burden and accelerates the subsequent decline (see Figure 2a). Similarly, the chronic HCV class exhibits a corresponding reduction in its peak when control u_1 is administered. However, it hits its peak in the absence of the control scenario (see Figure 2b).

The close agreement between the NSFD and ode45 solutions of I_{HCV} and I_{CHCV} in presence and absence of the control u_1 , confirms that the nonlocal discretization of the infection and progression terms does not introduce a visible distortion of the HCV dynamics at step size $k = 0.01$. In particular, the NSFD scheme preserves both the timing and magnitude of the principal transient features while maintaining the non-negativity properties established analytically in Section 4.

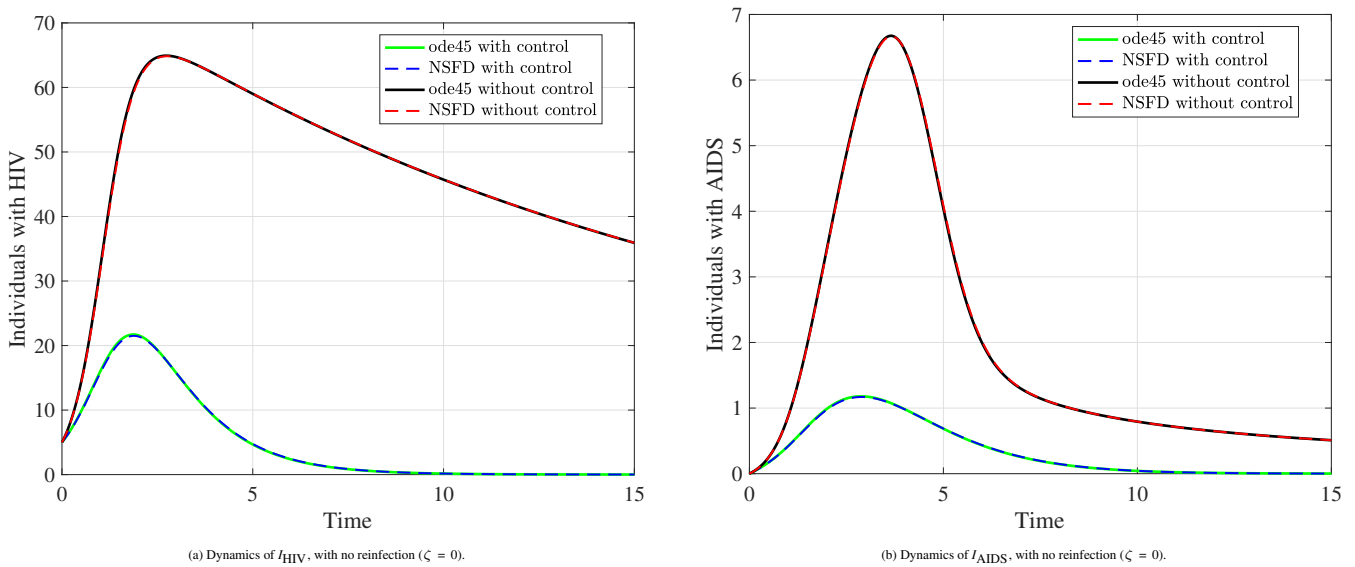


FIGURE 3 NSFD and ode45 solutions for HIV and AIDS dynamics in the absence of reinfection.

The corresponding HIV and AIDS dynamics are presented in Figure 3. When reinfection is absent i.e. $\zeta = 0$, the uncontrolled HIV population increases to nearly 65 individuals before declining (see Figure 3a), whereas the AIDS population exhibits

a delayed response and reaches a maximum of approximately 7 (see Figure 3b). The delayed AIDS peak is consistent with the progression mechanism represented by the term $\beta_2 I_{\text{HIV}}$, since individuals must first pass through the HIV class before contributing to the AIDS population. The application of the HIV treatment control u_2 considerably reduces both infection levels, which demonstrate the epidemiological effect of the control strategy over HIV and AIDS infections. Moreover, both infected populations subsequently approach zero over the simulated interval.

The NSFD and ode45 trajectories correspond to I_{HIV} and I_{AIDS} remain visually coincident at both controlled and uncontrolled scenarios, indicating that the proposed discretization accurately reproduces the transient and asymptotic behaviour of the continuous system for the step size $k = 0.01$.

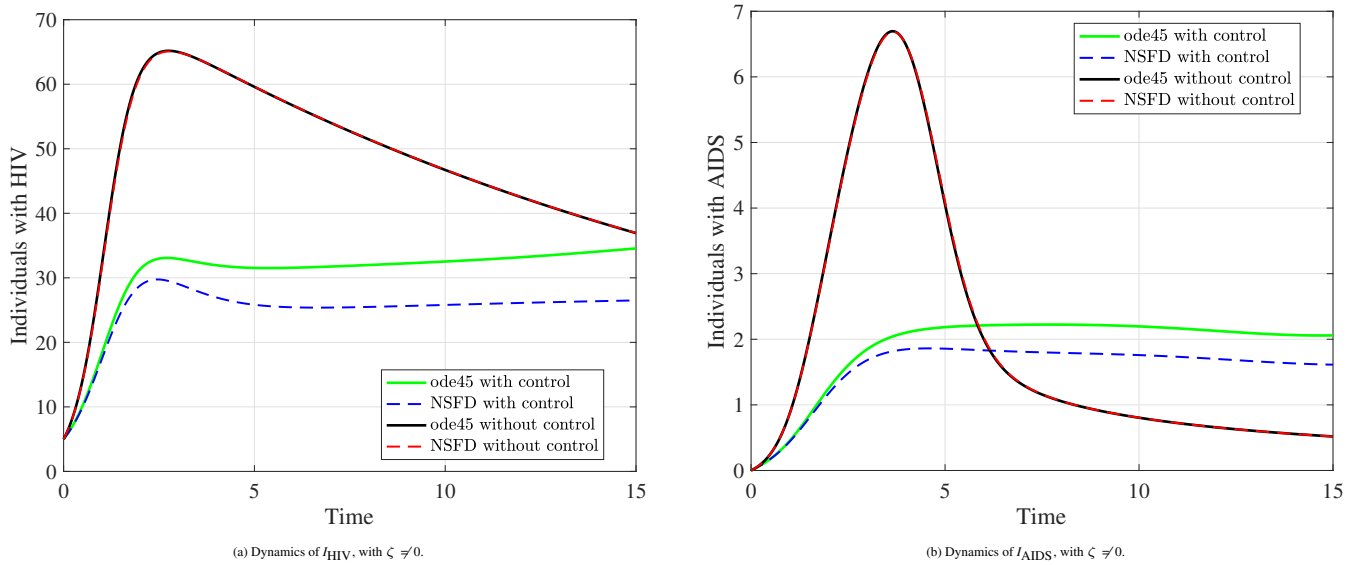


FIGURE 4 NSFD and ode45 solutions for HIV and AIDS dynamics in the presence of reinfection, $\zeta = 0.44735$.

The effect of loss of immunity among the HIV and AIDS infected populations is illustrated in Figure 4. For $\zeta > 0$, the uncontrolled HIV population continues to increase throughout the simulation (see Figure 4a), while the AIDS population also increases, although at a substantially lower level (see Figure 4b). Under the control u_2 , both populations initially decline, but the reinfection pathway subsequently leads to a renewed increase, with the HIV population remaining at a relatively high nonzero level and the AIDS population settling at a lower nonzero level. Thus, the reinfection scenario produces a more noticeable quantitative difference between the two numerical solutions, particularly for the HIV population, while retaining the same overall temporal pattern.

The co-infected and super-infected compartments provide a useful assessment of the proposed NSFD construction because their dynamics involve nonlinear interactions among several epidemiological variables, including the terms $\alpha_3 I_C S$ and $(\delta_1 I_{\text{CHCV}} + \delta_2 I_{\text{AIDS}}) I_S$, which are discretized nonlocally in (24). As shown in Figure 5, the NSFD trajectories closely aligns with the corresponding continuous model behaviour. In absence of intervention, the co-infected population rises to approximately 21 before declining, whereas the super-infected population continues to increase and reaches approximately 42 by the time horizon. Under the combined controls u_1 and u_2 , both populations decline rapidly towards zero and remain non-negative throughout the simulation. The NSFD and continuous solutions correspond to I_C and I_S with and without controls u_1 and u_2 are closely consistent and remain non-negative, confirming the preservation of the relevant qualitative dynamics.

The recovered population under the two reinfection scenarios is visualized in Figure 6. In the absence of reinfection ($\zeta = 0$), the uncontrolled recovered population remains relatively small, whereas employing controls produce a noticeable increase in R , reaching approximately to 105 (see Figure 6a). When reinfection is introduced with $\zeta = 0.44735$, the controlled recovered population declines to approximately 72 (see Figure 6b), where these individuals move from the recovered class to the HIV-infected class through the term ζR . Thus, comparison of the two panels shows that loss of immunity reduces the accumulation of recovered individuals under treatment by allowing a proportion of them to re-enter the infected population. In this case as well

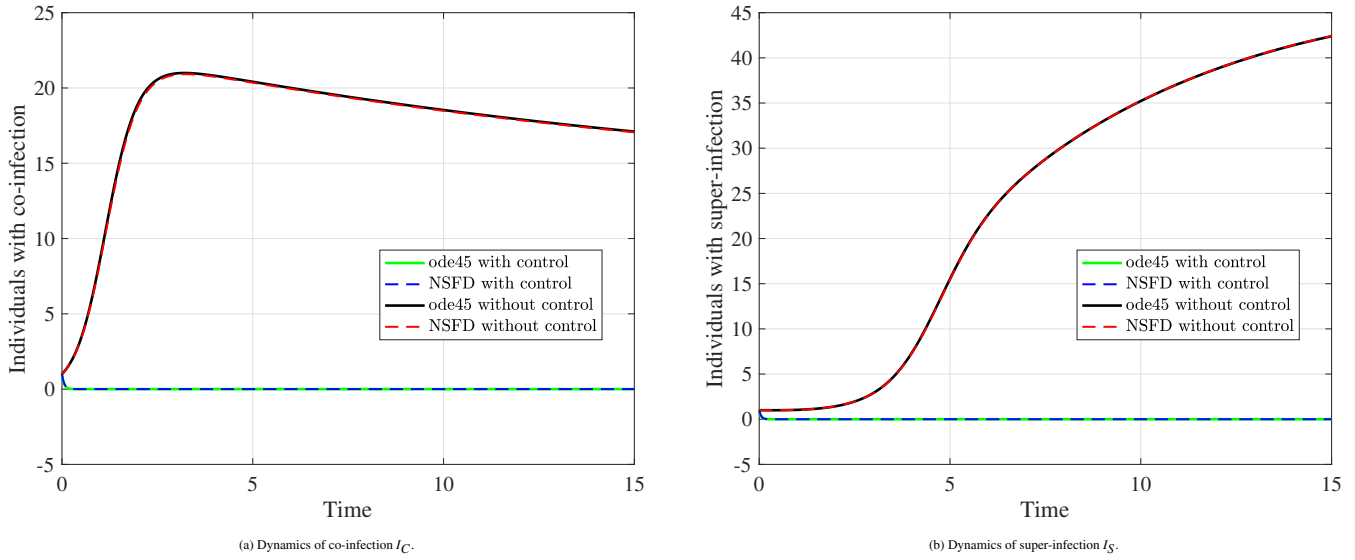


FIGURE 5 NSFD and ode45 solutions for the co-infected and super-infected populations.

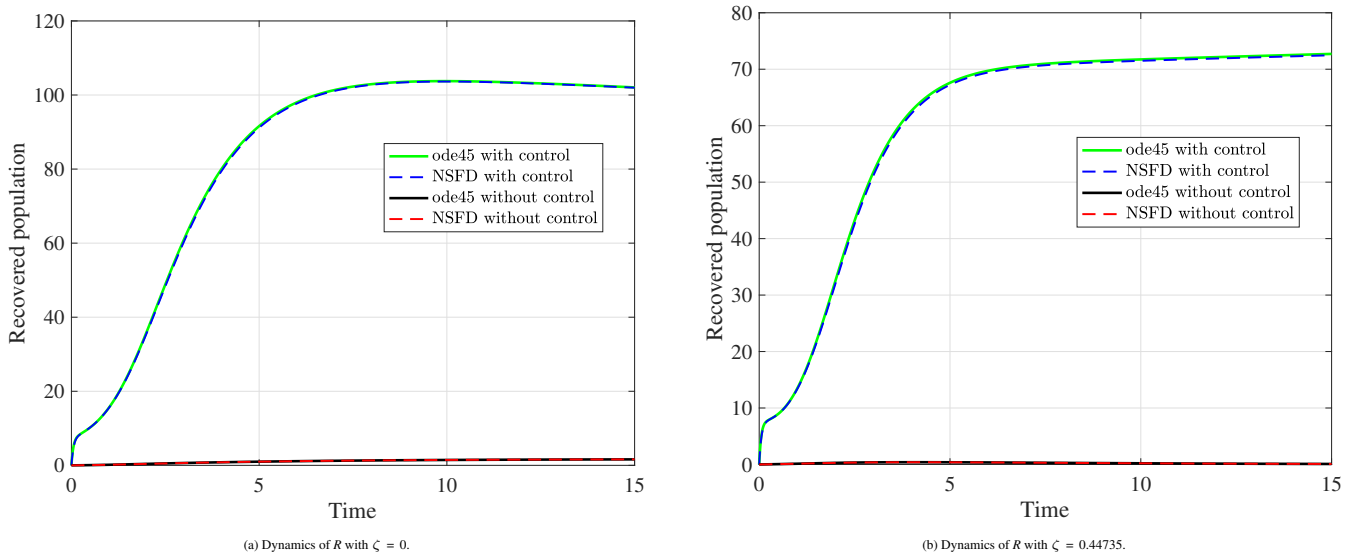


FIGURE 6 Recovered population R under the controls in the absence and presence of reinfection.

as, the NSFD and ode45 solutions of R are indistinguishable, demonstrating that the numerical method preserves the transfer of population between epidemiological compartments rather than merely reproducing isolated trajectories.

The Figures 2–6 demonstrate that the proposed NSFD scheme is highly consistent with the continuous HCV–HIV model, it captures the major epidemiological mechanisms of the continuous model, including infection generation, progression between disease stages, co-infection and super-infection, the effects of the introduced controls, and reinfection following loss of immunity. Throughout these results, the numerical solutions remain within the epidemiologically meaningful region.

In the preceding figures, the results are simulated with the step size $k = 0.01$. To examine whether the qualitative behaviour is preserved under larger discretization steps, the proposed NSFD scheme with reinfection is simulated over the extended interval $t \in [0, 35]$, while using the step sizes as $k = 1, 0.5, 0.1$, and 0.01 . The corresponding results are presented in Figures 7–14, providing a direct assessment of the robustness of the NSFD scheme with respect to the time-step size.

Several important properties of the NSFD discretization are evident from these simulations. First, positivity is preserved for all considered step sizes, and none of the numerical trajectories becomes negative, even for the relatively large step size

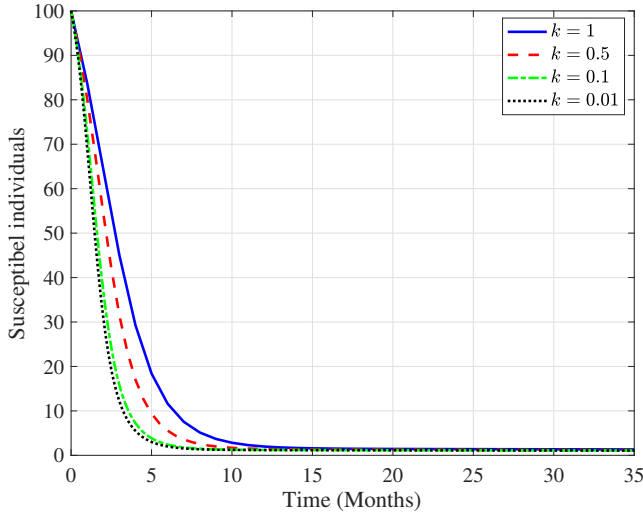


FIGURE 7 NSFD solution of S with different step sizes.

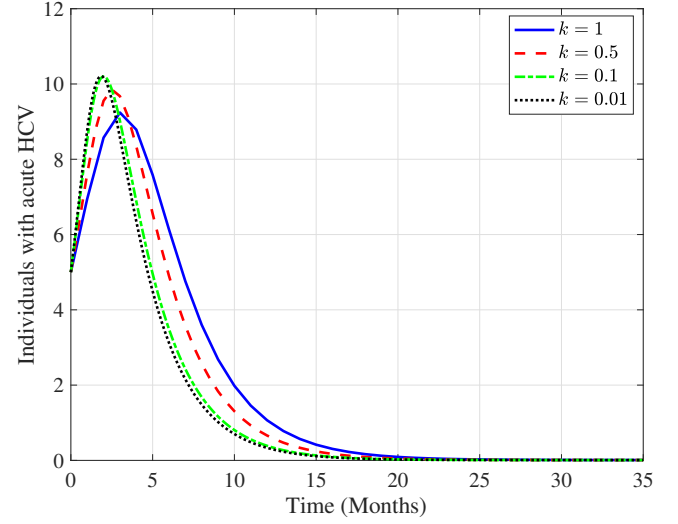


FIGURE 8 NSFD solution of I_{HCV} with different step sizes.

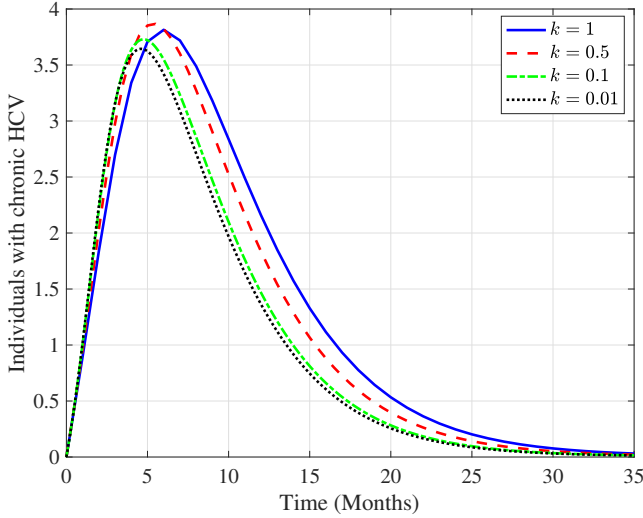


FIGURE 9 NSFD solution of I_{CHCV} with different step sizes.

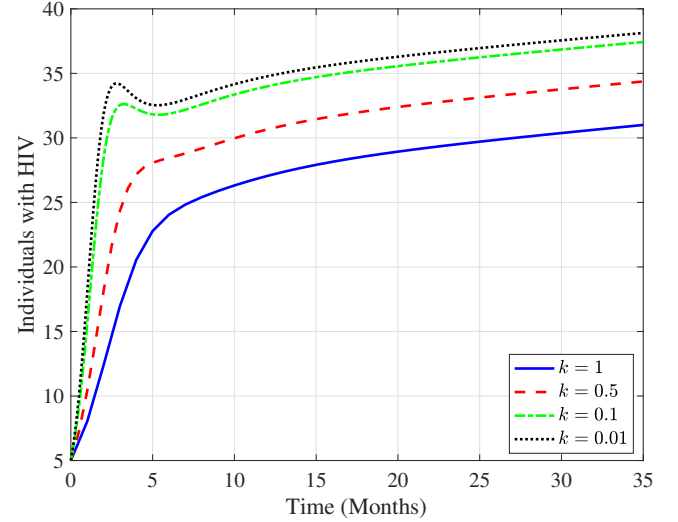


FIGURE 10 NSFD solution of I_{HIV} with different step sizes.

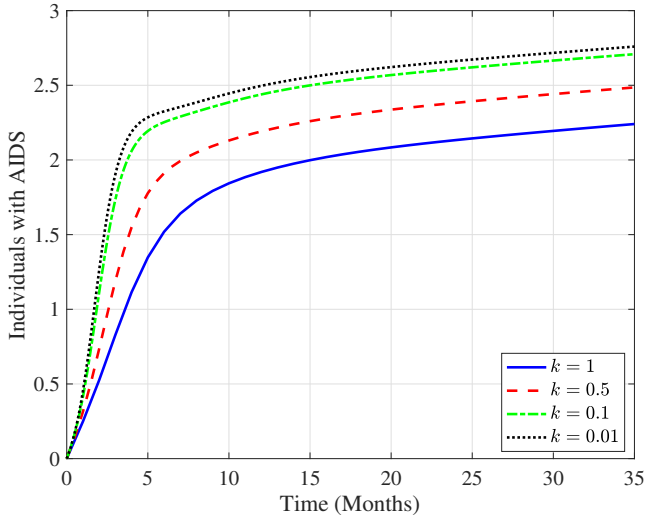
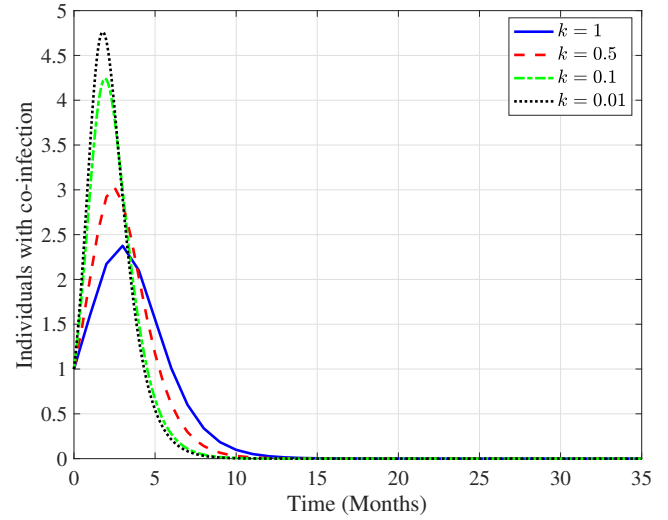
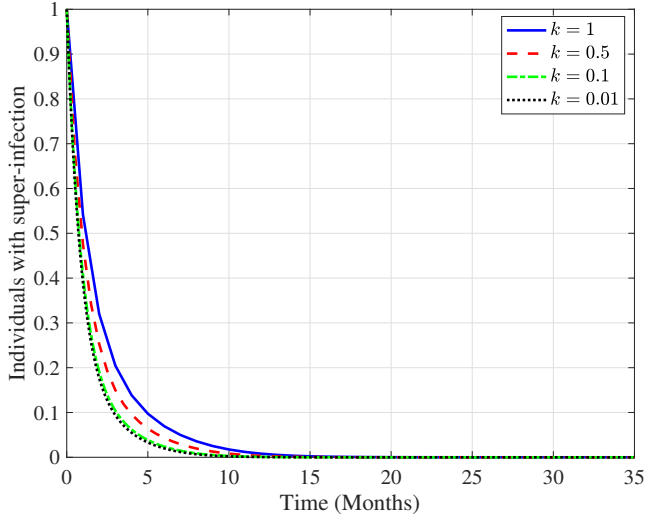
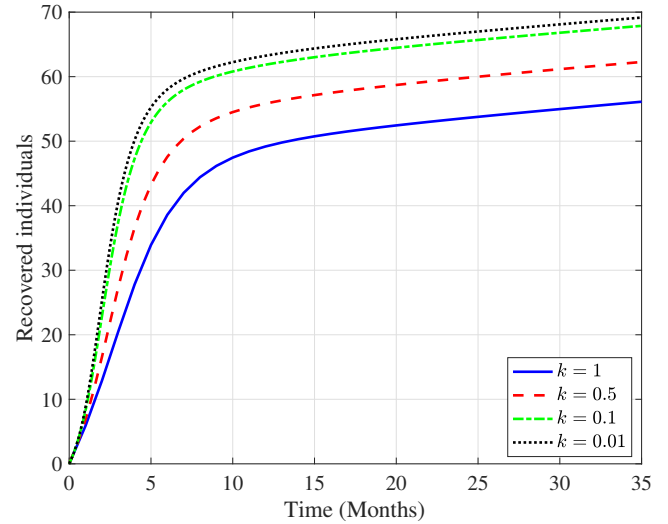
$k = 1$. These numerical results therefore provide direct evidence supporting the positivity property established analytically in Theorem 1. Second, increasing the step size does not introduce spurious oscillations or qualitatively inconsistent epidemiological behaviour. Although the trajectories may exhibit differences in transient timing and peak magnitude, their overall progression remains consistent across the considered step sizes.

For instance, the susceptible population in Figure 7 provides a particularly clear illustration. Starting from $S(0) = 100$, all four trajectories decrease rapidly and subsequently approach the same long-term level. In particular, from the endemic equilibrium, we have

$$S^* = \frac{\mu + \mu_1}{\alpha_3} = \frac{0.005001 + 0.02816667}{0.0264} \approx 1.2563.$$

The numerical trajectories of S approach this equilibrium value for all four step sizes, indicating that the choice of step size primarily affects the transient resolution rather than the long-term equilibrium behaviour. This observation is consistent with the analytical result that the proposed NSFD scheme preserves the equilibrium points and their existence conditions of the continuous model (see Theorem 3). Similar behaviour is observed across the remaining figures.

The step-size visualizations show that the proposed NSFD scheme retains the principal numerical behaviour of the model over the considered ranges of k . In particular, the trajectories remain non-negative for all considered step sizes, while reducing k leads

FIGURE 11 NSFD solution of I_{AIDS} with different step sizes.FIGURE 12 NSFD solution of I_C with different step sizes.FIGURE 13 NSFD solution of I_S with different step sizes.FIGURE 14 NSFD solution of R with different step sizes.

to closer agreement of the transient profiles, with $k = 0.1$ and $k = 0.01$ producing very similar solutions but smaller step sizes require more computational effort. The long-term behaviour is likewise maintained across all the step sizes.

Taken together, Figures 2-14 provide numerical evidence for the robustness and consistency of the proposed NSFD scheme over the considered time-step ranges. The results are consistent with the analytical properties established for the discrete system and demonstrate that the scheme maintains the essential behaviour of the continuous model while preserving non-negativity under the tested discretizations.

CONCLUSION

We have constructed a nonstandard finite difference scheme for the HCV-HIV co-infection and super-infection model that preserves key dynamical properties of the continuous system. The proposed NSFD formulation employs a denominator function derived from the dominant population dynamics together with nonlocal discretizations of the nonlinear transmission terms. The resulting scheme preserves non-negativity and the positively invariant region for arbitrary positive step sizes and has the same equilibrium points and existence conditions as the continuous model. The controlled formulation further incorporates HCV and

HIV treatment interventions, and a reinfection mechanism associated with loss of immunity, for which a discrete optimality system is derived using the discrete Pontryagin maximum principle. Numerical simulations show close agreement with the continuous solution for small step sizes and preservation of the essential numerical behaviour over a wider range of step sizes, including $k = 1$. These results support the use of the proposed NSFD scheme as a dynamically consistent discretization for numerical investigation of the continuous HCV-HIV model, particularly for simulations of its long-term dynamics.

DATA AVAILABILITY

The data supporting the conclusions of this article will be made available by the authors on request.

CONFLICT OF INTEREST

The authors declare that there is no conflict of interest regarding the publication of this article.

References

- [1] V. G. Boltyanskii. *Optimal Control of Discrete Systems*. John Wiley & Sons, New York, 1978.
- [2] J. Cresson and F. Pierret. Non standard finite difference scheme preserving dynamical properties. *J. Comput. Appl. Math.*, 303:15–30, 2016. . <https://doi.org/10.1016/j.cam.2016.02.007>.
- [3] J.R. Dormand and P.J. Prince. A family of embedded Runge-Kutta formulae. *J. Comput. Appl. Math.*, 6(1):19–26, 1980.
- [4] H. Halkin. A maximum principle of the Pontryagin type for systems described by nonlinear difference equations. *SIAM Journal on Control*, 4(1):90–111, 1966. <https://doi.org/10.1137/0304009>.
- [5] M. T. Hoang and M. Ehrhardt. A dynamically consistent nonstandard finite difference scheme for a generalized SEIR epidemic model. *J. Differ. Eqs Appl.*, 30(4):409–434, 2024. <https://doi.org/10.1080/10236198.2023.2291151>.
- [6] C. L. Hwang and L. T. Fan. A discrete version of Pontryagin’s maximum principle. *Operations Research*, 15(1):139–146, 1967. <https://doi.org/10.1287/opre.15.1.139>.
- [7] M. Mehdizadeh Khalsaraei, A. Shokri, S. Noeiaghdam, and M. Molayi. Nonstandard finite difference schemes for an SIR epidemic model. *Mathematics*, 9(23):3082, 2021. <https://doi.org/10.3390/math9233082>.
- [8] M. H. Maamar, M. Ehrhardt, and L. Tabharit. A nonstandard finite difference scheme for a time-fractional model of Zika virus transmission. *Math. Biosci. Engrg.*, 21(1):924–962, 2024. <https://doi.org/10.3934/mbe.2024039>.
- [9] R. Memarbashi, F. Alipour, and A. Ghasemabadi. A nonstandard finite difference scheme for a SEI epidemic model. *Punjab Univ. J. Math.*, 49(3):133–147, 2017. https://pu.edu.pk/images/journal/math/PDF/Paper-11_49_3_17.pdf.
- [10] R. E. Mickens. *Nonstandard Finite Difference Models of Differential Equations*. World Scientific, Singapore, 1994. <https://doi.org/10.1142/2081>.
- [11] R. E. Mickens. Nonstandard finite difference schemes for differential equations. *J. Differ. Eqs Appl.*, 8(9):823–847, 2002. <https://doi.org/10.1080/1023619021000000807>.
- [12] R. E. Mickens. Dynamic consistency: A fundamental principle for constructing nonstandard finite difference schemes for differential equations. *J. Differ. Eqs Appl.*, 11(7):645–653, 2005. <https://doi.org/10.1080/10236190412331334527>.
- [13] R. E. Mickens. Calculation of denominator functions for nonstandard finite difference schemes for differential equations satisfying a positivity condition. *Numer. Meth. Part. Diff. Eqs*, 23(3):672–691, 2007. <https://doi.org/10.1002/num.20198>.
- [14] B. Safi, A. H. Hasmani, and P. R. Koya. A mathematical framework for the transmission dynamics and optimal control of HCV-HIV coinfection and superinfection. *Int. J. Math. Math. Sci.*, 2026:3321786, 2026. <https://doi.org/10.1155/ijmm/3321786>.
- [15] S. M. Salman. A nonstandard finite difference scheme and optimal control for an HIV model with Beddington-DeAngelis incidence and cure rate. *Euro. Phys. J. Plus*, 135(10):808, 2020. <https://doi.org/10.1140/epjp/s13360-020-00839-1>.
- [16] S. Vaz and D. F. M. Torres. A dynamically-consistent nonstandard finite difference scheme for the SICA model. *Math. Biosci. Engrg.*, 18(4):4552–4571, 2021. <https://doi.org/10.3934/mbe.2021231>.
- [17] B. D. Yasin and H. M. Youssef. Exact dynamics and optimization for a discrete-time SIR model using time-dependent parameters. *Fractal and Fractional*, 10(6):371, 2026. <https://doi.org/10.3390/fractalfract10060371>.