Punjab University Journal of Mathematics (2025), 57(09), 964-991
https://doi.org/10.52280/pujm.2025.57(09)03

Mathematical Modeling for Transmission Dynamics of Hepatitis B Virus

Received
02 June, 2025

Revised
12 December, 2025

Accepted
18 December, 2025

Published Online
20 January, 2026

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Abstract. Hepatitis B virus (HBV) remains a major global public health concern, motivating the use of mathematical models to better understand its transmission dynamics and control strategies. In this study, a compartmental mathematical model based on a system of linear differential equation is formulated to describe the spread of HBV in a population. The basic reproduction number $\mathcal{R}_0$ is derived to characterized the transmission potential of the disease. Analytical results show that the disease-free

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equilibrium (DFE) is locally asymptotically stable when $\mathcal{R}_0 < 1$ and become unstable when $\mathcal{R}_0 > 1$, while the endemic equilibrium (EE) exists and is stable for $\mathcal{R}_0 > 1$. To investigate the dynamic behavior of the model numerically, both the standard finite difference (SFD) scheme and a non-standard finite difference (NSFD) scheme are implemented. The SFD scheme exhibits conditional convergence and may produce nonphysical results for certain step sizes, whereas the proposed NSFD scheme preserves essential qualitative properties of the continuous model, including positivity and stability of solutions. A stability analysis of the NSFD scheme is also presented. Numerical simulations and comparative analysis of both schemes validate the theoretical findings and demonstrate the superior performance of the NSFD method in accurately capturing the transmission dynamics of HBV.

AMS (MOS) Subject Classification Codes: 92D30; 34K20; 92D25
Key Words: Hepatitis B virus model; compartmental epidemic model; non-standard finite difference method; standard finite difference method; stability and convergence; positivity preserving scheme.

1. INTRODUCTION

The liver is a significant organ of the human body. When the Hepatitis B virus enters the body, it irritates the liver, along with inflammation. The virus was designated Australia Antigen after an Australian aborigine blood sample that reacted with an antibody in an American syphilitic patient's serum. Continuous vulnerability to toxic compounds, drugs, and alcohol, among other things, causes inflammation. Inflammation is fervently uncomfortable, and tissues all through the body are affected. Hepatitis B is an infectious disease that can cause inflammation of the liver. When HBV infects the cells of the liver, known as hepatocytes, the immune system assaults the hepatocytes, causing liver inflammation. Acute and chronic hepatitis are the two sorts of HB [2,31,32]. In Acute hepatitis, the inflammation lasts less than six months, if the inflammation lasts more than six months, it is referred to as chronic hepatitis. Acute symptoms develop 60-150 days after a viral infection and last for several weeks to six months. Chronic Hepatitis B can produce fascinating health challenges if it is still in the body for an extended time, including liver cancer. In addition, the risk of developing liver cancer is 100 times higher for individuals infected with the HBV virus than for those who are not. Hepatitis B is a highly endemic virus that affects people all over the world [1,9].

HBV may be transmitted in a variety of isolated, including unprotected sexual contact, sperm, blood transmission, razors, and tooth brushes, etc. Viruses can also be passed from mother to child. Unsafe medical procedures can deficiency health care workers. HBV cannot be transferred by food, water, sneezing, coughing, hugging, or at work. HBV is a worldwide public health issue. According to WHO, more than 95 percent of infants have protective antibody levels. According to the WHO, nearly 400 million individuals are irritated. China's population of 93 million people is threatened [1-13,33,34]. Computational

analysis is a powerful tool for analyzing the dynamical behavior of various collapses in the real world. Mclean, A, R and Blumberg developed a mathematical model for HBV transmission in 1994. Hepatitis B transmission access described by Zou, L. et al. Many researchers used mathematical modeling to investigate the spread of HBV.

To analyze the dissemination of various illnesses in the population, the contribution of some authors is provided in references [2,3,4,18,24,27]. In [15,26], the author fabricated a mathematical model of HBV transmission. The author divides the influenced individuals into two groups: acute and chronic. The complete population is partitioned into four phases: susceptible, $S(t)$, $I_1(t)$ infected with Acute hepatitis B, $I_2(t)$ infected with Chronic hepatitis B and $R(t)$ cured individuals. In the present model, three Time-dependent parameters are used. These are vaccination, isolation and treatment. The control strategy is developed in order to mitigate the contaminated and maximize the number of recovered populations. We used two different schemes to numerically analyze the HBV model [31]. Moreover, the standard finite difference (SFD) methods are easy to implement but are only first-order accurate and conditionally stable, often requiring small step sizes to avoid non-physical solutions. In contrast, the non-standard finite difference (NSFD) method preserves positivity, boundedness, and equilibrium stability for larger step sizes, ensuring dynamical consistency with the continuous model. Despite its higher construction complexity, the NSFD scheme provides more reliable long-term simulations of Hepatitis B virus dynamics.

The present work is organized in the following manner. Section one presents the introduction of HBV. In section 2, the model of HBV is formulated, and with the help of this model, differential equations are derived. The parameters involved in the mentioned model are also discussed. Disease-free equilibrium and endemic points of the Hepatitis B virus model (2.1) are also discussed in subsection 4.1 and 4.2. In subsection 4.3, with the help of DFE points, we calculate $\mathcal{R}_0$ basic reproduction number, and sensitivity analysis is done in subsection 4.3.1. We prove this model is locally stable under certain conditions using $\mathcal{R}_0$ in section 4.4. Numerical analysis of the HBV model of system (1) is discussed in section 5. In subsections 5.1 and 5.2, and 5.3, the forward Euler and Rk-4 and proposed NSFD scheme is derived respectively [30]. After that the stability analysis of proposed scheme and positivity discussed in subsection 5.4. The numerical simulations are drawn in each sub-section of 5. Boundedness and consistency analysis discussed in section 5.6 and 5.7 furthermore, the comparison of SFD and proposed NSFD scheme is discussed numerically in subsection 5.8. The brief conclusion is given in section 6.

2. Flow Chart

The flow chart of the model (S, I_1, I_2, R) is given below [15]. The state variables and parameters of the Hepatitis B virus are given below. The parameters reflect the biological and epidemiological processes that determine population turnover, infection, and disease

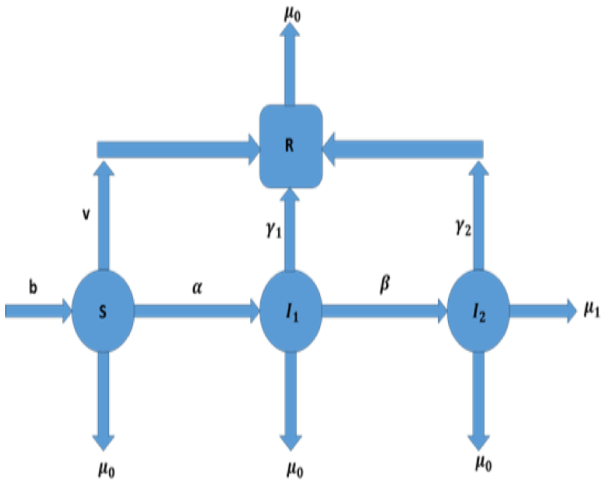


FIGURE 1. $(SLII_sR)$ Model

progression.

$$S(t) = \text{Susceptible individuals},$$
$$I_1(t) = \text{Infected},$$
$$I_2(t) = \text{Individuals},$$
$$R(t) = \text{Recovered individuals}.$$

Parameters	Values	Description	Ref.
μ_0	0.03	Natural death rate due to causes unrelated to HBV	[15]
μ_1	0.002	Disease-induced death rate associated with HBV	[15]
γ_1	0.05	Recovery rate of individuals from the acute HBV stage	[15]
γ_2	0.06	Recovery rate of individuals from the chronic stage	[15]
b	0.4	Birth rate of individuals	[15]
v	0.02	Vaccination rate of susceptible individuals against HBV	[15]
α	0.05	Effective rate from susceptible to the acutely infected class	[15]
β	0.1	Rate from acute HBV infection to the chronic infection	[15]

TABLE 1. Parametric Values

3. MODEL ANALYSIS

In this section, we qualitative analyze the dynamical behavior of the Hepatitis B virus model. The analysis focuses on fundamental mathematical properties of the model, including the positivity of solutions, the existence of equilibrium points, and the boundedness of the system trajectories.

Theorem 1. *The proposed model of disease possesses a non-negative solution, provided non-negative initial conditions for all*

$$t \geq 0.$$

Proof. it is clear from the system of equation,

$$\left.\frac{dS}{dt}\right|_{S=0} = b \geq 0$$

$$\left.\frac{dI_1}{dt}\right|_{S=0} = \alpha S I_2 \geq 0$$

$$\left.\frac{dI_2}{dt}\right|_{S=0} = \beta I_1 \geq 0$$

$$\left.\frac{dR}{dt}\right|_{S=0} = \gamma_1 I_1 + \gamma_2 I_2 + vS \geq 0$$

So, this shows the positivity in the system with the initial conditions. □

Theorem 2. *Solution of the equations are all bounded in probable region ω.*

Proof. The total population is N(t) and the sum of all the differential equations,

We start with the total population equation:

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dI_1}{dt} + \frac{dI_2}{dt} + \frac{dR}{dt}.$$

Substituting the right-hand side of the population equation:

$$\frac{dN}{dt} = b - \mu N,$$

we can rewrite it as

$$\frac{dN}{b - \mu N} = dt.$$

Integrating both sides gives:

$$\int \frac{dN}{b - \mu N} = \int dt.$$

The integral yields:

$$-\frac{1}{\mu} \ln |b - \mu N| = t + C,$$

where C is the constant of integration.

Taking the exponential of both sides, we obtain:

$$b - \mu N = Be^{-\mu t},$$

where $B = e^{-\mu C}$ is a new constant.

Solving for $N(t)$:

$$N(t) = \frac{b}{\mu} + \left(N(0) - \frac{b}{\mu}\right) e^{-\mu t}.$$

As $t \to \infty$, the exponential term tends to zero:

$$e^{-\mu t} \to 0,$$

so that

$$N(t) \to \frac{b}{\mu}.$$

Thus, we have

$$0 < N(t) \leq \frac{b}{\mu} \quad \text{for all } t \geq 0.$$

This ensures that the whole population $N(t)$ is bounded and remains within the feasible region ω. □

4. Disease-free and endemic equilibrium points

4.1. **Disease-free equilibrium points.** When the disease fully disappears from a community, it has reached the DFE point. The disease-free equilibrium points of system (2.1) are given below, The disease-free equilibrium of the system is

$$E_0 = (S_0, 0, 0, R_0) = \left(\frac{b}{\mu_0 + v}, 0, 0, \frac{vb}{\mu_0(\mu_0 + v)} \right).$$

4.2. **Endemic equilibrium points.** EE point at which disease persists in a population. The endemic equilibrium points of system (2.1) are denoted by

$$E^* = (S^*, I_1^*, I_2^*, R^*),$$

$$S^* = \frac{(\mu_0 + \mu_1 + \gamma_2)(\mu_0 + \beta + \gamma_1)}{\alpha\beta},$$

$$I_1^* = \frac{(\mu_0 + v)(\mu_0 + \mu_1 + \gamma_2)(R_0 - 1)}{\alpha\beta},$$

$$I_2^* = \frac{(\mu_0 + v)(R_0 - 1)}{\alpha},$$

$$R^* = \frac{1}{\mu_0} \left[\frac{\gamma_1(\mu_0 + v)(\mu_0 + \mu_1 + \gamma_2)}{\alpha\beta} + \frac{\gamma_2(\mu_0 + v)(R_0 - 1)}{\alpha} + \frac{v(\mu_0 + \mu_1 + \gamma_2)(\mu_0 + \beta + \gamma_1)}{\alpha\beta} \right].$$

4.3. **Basic Reproductive Number ($\mathcal{R}_0$).** The primary factor determining the spread of any infectious disease is the basic reproduction number. It plays a crucial role in assessing whether an infectious disease will propagate within a population. Considering our emphasis on the infected population, the Next Generation Matrix aids in deriving the basic reproduction number [17]. Consider the next-generation matrices:

$$F = \begin{pmatrix} 0 & \alpha S \\ 0 & 0 \end{pmatrix}, \quad V = \begin{pmatrix} \mu_0 + \beta + \gamma_1 & 0 \\ \beta & \mu_0 + \mu_1 + \gamma_2 \end{pmatrix}.$$

The matrix FV^{-1} is given by

$$FV^{-1} = \begin{pmatrix} \dfrac{\alpha\beta S}{(\mu_0+\beta+\gamma_1)(\mu_0+\mu_1+\gamma_2)} & -\dfrac{\alpha S}{\mu_0+\mu_1+\gamma_2} \\ 0 & 0 \end{pmatrix}.$$

At the disease-free equilibrium (DFE) point, the basic reproduction number $\mathcal{R}_0$ is

$$\mathcal{R}_0 = \frac{\alpha\beta b}{(\mu_0+v)^2(\mu_0+\beta+\gamma_1)(\mu_0+\mu_1+\gamma_2)}.$$

4.3.1. *Sensitivity Analysis of* $\mathcal{R}_0$. In this section, we present a sensitivity analysis of the basic reproduction number $\mathcal{R}_0$. The partial derivatives of the basic reproduction number $\mathcal{R}_0$ with respect to the parameters are:

$$\frac{\partial\mathcal{R}_0}{\partial\alpha} = \frac{\beta b}{(\mu_0+\nu)^2(\mu_0+\beta+\gamma_1)(\mu_0+\mu_1+\gamma_2)} \cdot \frac{\alpha}{\mathcal{R}_0} > 0,$$

$$\frac{\partial\mathcal{R}_0}{\partial b} = \frac{\alpha\beta}{(\mu_0+\nu)^2(\mu_0+\beta+\gamma_1)(\mu_0+\nu)(\mu_0+\mu_1+\gamma_2)} \cdot \frac{b}{\mathcal{R}_0} > 0,$$

$$\frac{\partial\mathcal{R}_0}{\partial\mu_1} = -\frac{\alpha\beta b(\mu_0+\nu)^2(\mu_0+\beta+\gamma_1)}{[(\mu_0+\nu)^2(\mu_0+\beta+\gamma_1)(\mu_0+\mu_1+\gamma_2)]^2} \cdot \frac{\mu_1}{\mathcal{R}_0} > 0,$$

$$\frac{\partial\mathcal{R}_0}{\partial\mu_0} = k \cdot \frac{\mu_0}{\mathcal{R}_0} < 0,$$

here k is

$$\frac{g+(\mu_0+\nu)^2(\mu_0+\mu_1+\gamma_2)+(\mu_0+\nu)^2(\mu_0+\beta+\gamma_1)}{[(\mu_0+\nu)^2(\mu_0+\beta+\gamma_1)(\mu_0+\mu_1+\gamma_2)]^2},$$

here

$$g = -\alpha\beta b(\mu_0+\nu)^2(\mu_0+\beta+\gamma_1)(\mu_0+\mu_1+\gamma_2),$$

$$\frac{\partial\mathcal{R}_0}{\partial\beta} = \frac{\alpha b(\mu_0+\nu)^2(\mu_0+\mu_1+\gamma_2)\big[(\mu_0+\beta+\gamma_1)-\beta\big]}{\big[(\mu_0+\nu)^2(\mu_0+\beta+\gamma_1)(\mu_0+\mu_1+\gamma_2)\big]^2} \cdot \frac{\beta}{\mathcal{R}_0} > 0.$$

$$\frac{\partial\mathcal{R}_0}{\partial\gamma_1} = \frac{-\alpha\beta b(\mu_0+\nu)^2(\mu_0+\mu_1+\gamma_2)}{[(\mu_0+\nu)^2(\mu_0+\beta+\gamma_1)(\mu_0+\mu_1+\gamma_2)]^2} \cdot \frac{\gamma_1}{\mathcal{R}_0} < 0,$$

$$\frac{\partial\mathcal{R}_0}{\partial\gamma_2} = \frac{-\alpha\beta b(\mu_0+\nu)^2(\mu_0+\beta+\gamma_1)}{[(\mu_0+\nu)^2(\mu_0+\beta+\gamma_1)(\mu_0+\mu_1+\gamma_2)]^2} \cdot \frac{\gamma_2}{\mathcal{R}_0} < 0,$$

$$\frac{\partial\mathcal{R}_0}{\partial\nu} = \frac{-\alpha\beta b(\mu_0+\nu)(\mu_0+\beta+\gamma_1)(\mu_0+\mu_1+\gamma_2)}{[(\mu_0+\nu)^2(\mu_0+\beta+\gamma_1)(\mu_0+\mu_1+\gamma_2)]^2} \cdot \frac{\nu}{\mathcal{R}_0} < 0.$$

The numerical values of the above partial derivatives can be used to determine how much $\mathcal{R}_0$ is sensitive to a particular parameter.

TABLE 2. Sensitivity of $\mathcal{R}_0$ with respect to model parameters

Parameter	$\frac{\partial \mathcal{R}_0}{\partial \alpha}$	$\frac{\partial \mathcal{R}_0}{\partial b}$	$\frac{\partial \mathcal{R}_0}{\partial \mu_1}$	$\frac{\partial \mathcal{R}_0}{\partial \mu_0}$	$\frac{\partial \mathcal{R}_0}{\partial \beta}$	$\frac{\partial \mathcal{R}_0}{\partial \gamma_1}$	$\frac{\partial \mathcal{R}_0}{\partial \gamma_2}$	$\frac{\partial \mathcal{R}_0}{\partial \nu}$
Value	1	20	-0.0217	3.297×10^4	0.8889	-0.5556	-0.6522	-0.4000

4.4. **Stability Analysis of Equilibria.** We assume that, Consider the system of differential equations defined by:

$$f_1 = b - \alpha S I_2 - (\mu_0 + v)S,$$

$$f_2 = \alpha S I_2 - (\mu_0 + \beta + \gamma_1) I_1,$$

$$f_3 = \beta I_1 - (\mu_0 + \mu_1 + \gamma_2) I_2,$$

$$f_4 = \gamma_1 I_1 + \gamma_2 I_2 + vS - \mu_0 R.$$

Theorem 3. *When $\mathcal{R}_0 < 1$, so the DFE points are LAS (Locally Asymptotically Stable) for system (2.1).*

Proof. The Jacobian matrix of the system is

$$J = \begin{pmatrix} \frac{\partial f_1}{\partial S} & \frac{\partial f_1}{\partial I_1} & \frac{\partial f_1}{\partial I_2} & \frac{\partial f_1}{\partial R} \\ \frac{\partial f_2}{\partial S} & \frac{\partial f_2}{\partial I_1} & \frac{\partial f_2}{\partial I_2} & \frac{\partial f_2}{\partial R} \\ \frac{\partial f_3}{\partial S} & \frac{\partial f_3}{\partial I_1} & \frac{\partial f_3}{\partial I_2} & \frac{\partial f_3}{\partial R} \\ \frac{\partial f_4}{\partial S} & \frac{\partial f_4}{\partial I_1} & \frac{\partial f_4}{\partial I_2} & \frac{\partial f_4}{\partial R} \end{pmatrix}, \tag{4. 1}$$

At the disease-free equilibrium (DFE) point

$$E_0 = \left(\frac{b}{\mu_0 + v}, 0, 0, \frac{v}{\mu_0(\mu_0 + v)} \right),$$

the Jacobian evaluates to

$$J_{E_0} = \begin{pmatrix} -(\mu_0 + v) & 0 & -\frac{\alpha b}{\mu_0 + v} & 0 \\ 0 & -(\mu_0 + \beta + \gamma_1) & \frac{\alpha b}{\mu_0 + v} & 0 \\ 0 & \beta & -(\mu_0 + \mu_1 + \gamma_2) & 0 \\ v & \gamma_1 & \gamma_2 & -\mu_0 \end{pmatrix}, \tag{4. 2}$$

The characteristic equation is

$$|J_{E_0} - \lambda I| = 0$$

$$\begin{vmatrix} -(\mu_0+v)-\lambda & 0 & -\frac{\alpha b}{\mu_0+v} & 0 \\ 0 & -(\mu_0+\beta+\gamma_1)-\lambda & \frac{\alpha b}{\mu_0+v} & 0 \\ 0 & \beta & -(\mu_0+\mu_1+\gamma_2)-\lambda & 0 \\ v & \gamma_1 & \gamma_2 & -\mu_0-\lambda \end{vmatrix} = 0,$$

Two eigenvalues are

$$\lambda_1 = -(\mu_0+v), \quad \lambda_2 = -\mu_0,$$

Consider the 2×2 submatrix

$$A = \begin{pmatrix} -(\mu_0+\beta+\gamma_1) & \frac{\alpha b}{\mu_0+v} \\ \beta & -(\mu_0+\mu_1+\gamma_2) \end{pmatrix},$$

The trace of A is

$$\mathrm{Tr}(A) = -(\mu_0+\beta+\gamma_1)-(\mu_0+\mu_1+\gamma_2) = -[2\mu_0+\beta+\gamma_1+\gamma_2] < 0,$$

The determinant of A is

$$\det(A) = (\mu_0+\beta+\gamma_1)(\mu_0+\mu_1+\gamma_2) - \frac{\alpha b\beta}{\mu_0+v},$$

$$\det(A) = (\mu_0+\beta+\gamma_1)(\mu_0+\mu_1+\gamma_2)[1-\mathcal{R}_0] > 0.$$

Since both conditions $\mathrm{Tr}(A) < 0$ and $\det(A) > 0$ are satisfied, the disease-free equilibrium E_0 is **locally asymptotically stable**. □

Theorem 4. *If $\mathcal{R}_0 > 1$, then DEE point E^* of model (2.1) is LAS.*

Proof. To prove the DEE point is LAS, we put the endemic point in equation (4.2), we get, The Jacobian matrix of the system is

$$J = \begin{pmatrix} -\alpha I_2-(\mu_0+v) & 0 & -\alpha S & 0 \\ \alpha I_2 & -(\mu_0+\beta+\gamma_1) & \alpha S & 0 \\ 0 & \beta & -(\mu_0+\mu_1+\gamma_2) & 0 \\ v & \gamma_1 & \gamma_2 & -\mu_0 \end{pmatrix},$$

At the endemic equilibrium E_0^*, it evaluates to

$$J_{E_0^*} = \begin{pmatrix} -\alpha I_2^* - (\mu_0 + v) & 0 & -\alpha S^* & 0 \\ \alpha I_2^* & -(\mu_0 + \beta + \gamma_1) & \alpha S^* & 0 \\ 0 & \beta & -(\mu_0 + \mu_1 + \gamma_2) & 0 \\ v & \gamma_1 & \gamma_2 & -\mu_0 \end{pmatrix},$$

The characteristic equation is

$$\left| J_{E_0^*} - \lambda I \right| = 0$$

$$\begin{vmatrix} -\alpha I_2^* - (\mu_0 + v) - \lambda & 0 & -\alpha S^* & 0 \\ \alpha I_2^* & -(\mu_0 + \beta + \gamma_1) - \lambda & \alpha S^* & 0 \\ 0 & \beta & -(\mu_0 + \mu_1 + \gamma_2) - \lambda & 0 \\ v & \gamma_1 & \gamma_2 & -\mu_0 - \lambda \end{vmatrix} = 0,$$

Two eigenvalues are

$$\lambda_1 = -\mu_0, \quad \lambda_2 = -\alpha I_2^* - (\mu_0 + v).$$

The remaining 2×2 submatrix is

$$\begin{pmatrix} -(\mu_0 + \beta + \gamma_1) - \lambda & \alpha S^* \\ \beta & -(\mu_0 + \mu_1 + \gamma_2) - \lambda \end{pmatrix},$$

Let

$$d_1 = -(\mu_0 + \beta + \gamma_1), \quad d_2 = \alpha S^*, \quad d_3 = \beta, \quad d_4 = -(\mu_0 + \mu_1 + \gamma_2),$$

Then the characteristic equation for this submatrix is

$$|JE_0^* - \lambda I| = \begin{vmatrix} d_1 - \lambda & d_2 \\ d_3 & d_4 - \lambda \end{vmatrix} = 0,$$

which expands to

$$(d_1 - \lambda)(d_4 - \lambda) - d_2 d_3 = 0,$$

$$\lambda^2 - \lambda(d_1 + d_4) + (d_1 d_4 - d_2 d_3) = 0,$$

$$\lambda^2 - \lambda(d_1 + d_4) + (d_1 d_4 - d_2 d_3)(\mathcal{R}_0 - 1) > 0. \tag{A}$$

Thus, the roots of (A) are positive. Therefore, if $\mathcal{R}_0 > 1$, the system is **locally asymptotically stable** at the endemic equilibrium. □

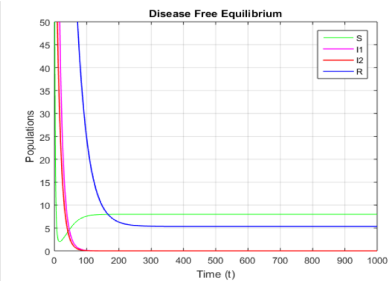


FIGURE 2. (Numerical trajectories of the HBV model at DFE, confirming stability and biological feasibility) Model

Numerical outcome in Fig. 2 for Hepatitis B virus is obtained from the ODE-45 scheme for DFE points, which shows the conditionally convergent result at limited parameter h, as shown in the graph. The values of parameters involved in simulations are given in Table 1.

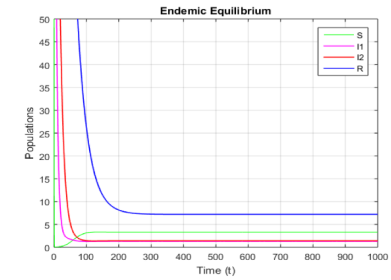


FIGURE 3. Numerical trajectories of the HBV model at EE, confirming stability and biological feasibility

Numerical outcome in Fig. 3 for Hepatitis B virus is obtained from the ODE-45 scheme for EE points, which shows the conditionally convergent result at limited parameter h, as shown in the graph. The values of parameters involved in simulations are given in Table 1.

5. NUMERICAL ANALYSIS OF HEPATITIS B VIRUS MODEL

In this section, we analyze the numerical results of the developed Hepatitis B virus model. For this, we construct the SFD and NSFD schemes for the fundamental model [29,35]. In subsections 5.1 and 5.2, standard finite schemes (Forward Euler scheme, RK-4 scheme) show convergence on a small parameter h, and these schemes show divergence when we put a large increment in the parameter h. In subsection 5.3, we developed a Non-standard finite difference scheme (NSFD) which gives us the convergent result on small

and large parameter h. It means that the Non-standard finite difference scheme (NSFD) unconditionally convergent scheme and does not depend upon the values of a parameter h [21]. At the end, the numerical simulations of both standard finite schemes (forward Euler scheme, RK-4 scheme) and the Non-standard finite difference scheme (NSFD) for system (2.1) are shown.

5.1. **Forward Euler's Scheme.** We established the Forward Euler's scheme of the Hepatitis B virus in a mathematical system (2.1). The discrete-time version of the system using the forward Euler method is

$$s^{n+1} = s^n + h\Big[b - \alpha s^n i_2^n - (\mu_0 + v)s^n\Big],$$

$$i_1^{n+1} = i_1^n + h\Big[\alpha s^n i_2^n - (\mu_0 + \beta + \gamma_1)i_1^n\Big],$$

$$i_2^{n+1} = i_2^n + h\Big[\beta i_1^n - (\mu_0 + \mu_1 + \gamma_2)i_2^n\Big],$$

$$r^{n+1} = r^n + h\Big[\gamma_1 i_1^n + \gamma_2 i_2^n + vs^n - \mu_0 r^n\Big].$$

The numerical simulations of the Forward Euler's scheme show that it does not preserve positivity. When we put a large increment in the parameter h then, Froward Euler's scheme does not remain stable. From this behavior, we determine that the solution of the Forward Euler's scheme is conditionally convergent for a limited parameter h.

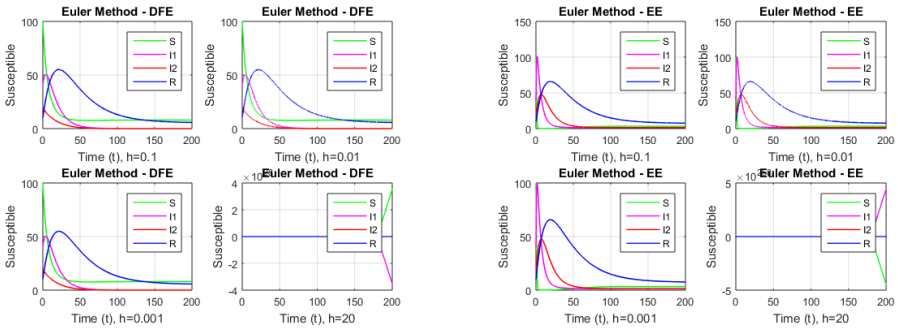


FIGURE 4. Combined behavior of the system: (A) Numerical persistence of Hepatitis B infection at disease free equilibrium using Forward Euler; (B) Numerical persistence of Hepatitis B infection at endemic equilibrium using Forward Euler.

Numerical outcomes in Fig.4 (A) for Hepatitis B virus are obtained from the Forward

Euler's scheme for EE points, which shows the conditionally convergent result at a limited parameter h, as shown in the graph. The values of parameters involved in simulations are given in Table 1. The numerical results for the Euler scheme of system (2.1) for the disease-free point are given below. The numerical simulations of Forward Euler's scheme for DFE points of Hepatitis B virus for system (2.1) are obtained in Fig.4 (B). The graph shows that Euler scheme shows convergence at lower step size, and as we increase step size the graph shows divergence. The values of parameters involved in simulations are given in Table 1.

5.2. **Fourth Order Runge-Kutta Scheme(RK4).** We construct RK-4 scheme for the mathematical modeling of the Hepatitis B virus for system (2.1), Let

$$k = s, \quad m = i_1, \quad n = i_2, \quad p = r_1$$

STAGE 1

$$k_1 = h\Big[b - \alpha s^n i_2^n - (\mu_0 + v)s^n\Big]$$

$$m_1 = h\Big[\alpha s^n i_2^n - (\mu + \beta + \gamma_1)i_1^n\Big]$$

$$n_1 = h\Big[\beta i_1^n - (\mu_0 + \mu_1 + \gamma_2)i_2^n\Big]$$

$$p_1 = h\Big[\gamma_1 i_1^n + \gamma_2 i_2^n - vs^n - \mu_0\gamma^n\Big]$$

STAGE 2

$$k_2 = h\Big[b - \alpha(s^n + k_1/2)(i_2^n + n_1/2) - (\mu_0 + v)(s^n + k_1/2)\Big]$$

$$m_2 = h\Big[\alpha(s^n + k_1/2)(i_2^n + n_1/2) - (\mu + \beta + \gamma_1)(i_1^n + m_1/2)\Big]$$

$$n_2 = h\Big[\beta(i_1^n + m_1/2) - (\mu_0 + \mu_1 + \gamma_2)(i_2^n + n_1/2)\Big]$$

$$p_2 = h\Big[\gamma_1(i_1^n + m_1/2) + \gamma_2(i_2^n + n_1/2) - v(s^n + k_1/2) - \mu_0(\gamma^n + p_1/2)\Big]$$

STAGE 3

$$k_3 = h\Big[b - \alpha(s^n + k_2/2)(i_2^n + n_2/2) - (\mu_0 + v)(s^n + k_2/2)\Big]$$

$$m_3 = h\Big[\alpha(s^n + k_2/2)(i_2^n + n_2/2) - (\mu + \beta + \gamma_1)(i_1^n + m_2/2)\Big]$$

$$n_3 = h\Big[\beta(i_1^n + m_2/2) - (\mu_0 + \mu_1 + \gamma_2)(i_2^n + n_2/2)\Big]$$

$$p_3 = h\Big[\gamma_1(i_1^n + m_2/2) + \gamma_2(i_2^n + n_2/2) - v(s^n + k_2/2) - \mu_0(\gamma^n + p_2/2)\Big]$$

STAGE 4

$$k_4 = h\Big[b - \alpha(s^n + k_3/2)(i_2^n + n_3/2) - (\mu_0 + v)(s^n + k_3/2)\Big]$$

$$m_4 = h\Big[\alpha(s^n + k_3/2)(i_2^n + n_3/2) - (\mu + \beta + \gamma_1)(i_1^n + m_3/2)\Big]$$

$$n_4 = h\Big[\beta(i_1^n + m_3/2) - (\mu_0 + \mu_1 + \gamma_2)(i_2^n + n_3/2)\Big]$$

$$p_4 = h\Big[\gamma_1(i_1^n + m_3/2) + \gamma_2(i_2^n + n_3/2) - v(s^n + k_3/2) - \mu_0(\gamma^n + p_3/2)\Big]$$

FINAL STAGE

$$s^{n+1} = s^n + \frac{1}{6}(k_1 + 2k_2 + 2k_3 + k_4)$$

$$i_1^{n+1} = i_1^n + \frac{1}{6}(m_1 + 2m_2 + 2m_3 + m_4)$$

$$i_2^{n+1} = i_2^n + \frac{1}{6}(n_1 + 2n_2 + 2n_3 + n_4)$$

$$r^{n+1} = r^n + \frac{1}{6}(p_1 + 2p_2 + 2p_3 + p_4)$$

As a result of the numerical solution through RK4. The scheme is shown below which shows that it does not preserve positivity for all step size. When we put large increment in the parameter h and RK4 the scheme does not remain stable. From this behavior, we determine that the solutions of RK4 scheme is conditionally convergent for a limited parameter h. The numerical simulations for both disease-endemic and disease-free points for system (2.1) are given below;

The simulations show the result for RK-4 scheme for EE points of Hepatitis B virus for system (2.1) in Fig.5(A). For EE points, which show the conditionally convergent result

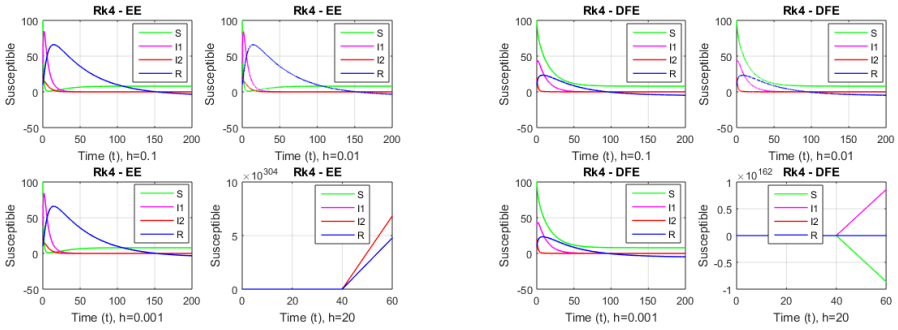


FIGURE 5. Combined behavior of the system: (A) RK-4 Numerical Trajectories Illustrating the Disease-Free Equilibrium Dynamics of Hepatitis B Virus Compartments; (B) RK-4 Numerical Trajectories Illustrating the Endemic Equilibrium Dynamics of Hepatitis B Virus Compartments.

at a limited parameter h. In Fig.5(B), the numerical simulations of RK4 scheme for the DFE point of Hepatitis B virus for system (2.1) are shown. Fig.5 (A)shows that the RK4 scheme shows a positive result at small step size and becomes divergent at large step size. The parametric values involved in the above simulations are shown in Table 1.

5.3. **Non-Standard Finite Difference (NSFD) Scheme.** In this subsection, we built the furthermost significant unconditionally stable scheme for system (2.1), which is called the Non-standard finite difference (NSFD) scheme [29,19]. The Non-standard finite difference scheme (NSFD) was first discovered by Mickens [25], which is a much better scheme than standard finite difference schemes (Forward Euler's scheme and RK4 scheme). Thus, the Non-standard finite difference scheme (NSFD) is independent and gives a convergent result for a finite value of a parameter h. Thus, we can say that the Non-standard finite difference scheme (NSFD) is most suitable scheme for the stability analysis of epidemic model of Hepatitis B virus [6,20]. The discrete-time update equations are given by

$$s^{n+1} = \frac{hb + s^n}{1 + h\alpha i_2^n + h(\mu_0 + v)}, \tag{5. 3}$$

$$i_1^{n+1} = \frac{h\alpha s^n i_2^n + i_1^n}{1 + h(\mu + \beta + \gamma_1)}, \tag{5. 4}$$

$$i_2^{n+1} = \frac{h\beta i_1^n + i_2^n}{1 + h(\mu_0 + \mu_1 + \gamma_2)}, \tag{5. 5}$$

$$r^{n+1} = \frac{h(\gamma_1 i_1^n + \gamma_2 i_2^n + v s^n) + r^n}{1 + h\mu_0}. \tag{5. 6}$$

5.4. **Stability analysis of NSFD scheme.** In this subsection, we discuss the stability of the Non-standard finite difference scheme (NSFD) for system (2.1). Suppose,

$$F = \frac{hb + s}{1 + h\alpha i_2 + h(\mu_0 + v)}, \tag{5. 7}$$

$$G = \frac{h\alpha s i_2 + i_1}{1 + h(\mu_0 + \beta + \gamma_1)}, \tag{5. 8}$$

$$H = \frac{h\beta i_1 + i_2}{1 + h(\mu_0 + \mu_1 + \gamma_2)}, \tag{5. 9}$$

$$I = \frac{h(\gamma_1 i_1 + \gamma_2 i_2 + vs) + r}{1 + h\mu_0}. \tag{5. 10}$$

Theorem 5. *If $\mathcal{R}_0 < 1$ then the DFE points of system (2.1) for the NSFD scheme are LAS.*

Proof. Let's take a Jacobean matrix of order 4×4, The Jacobian matrix of the system is defined as

$$J = \begin{bmatrix} \frac{\partial F}{\partial s} & \frac{\partial F}{\partial i_1} & \frac{\partial F}{\partial i_2} & \frac{\partial F}{\partial r} \\ \frac{\partial G}{\partial s} & \frac{\partial G}{\partial i_1} & \frac{\partial G}{\partial i_2} & \frac{\partial G}{\partial r} \\ \frac{\partial H}{\partial s} & \frac{\partial H}{\partial i_1} & \frac{\partial H}{\partial i_2} & \frac{\partial H}{\partial r} \\ \frac{\partial I}{\partial s} & \frac{\partial I}{\partial i_1} & \frac{\partial I}{\partial i_2} & \frac{\partial I}{\partial r} \end{bmatrix}$$

$$J = \begin{bmatrix} \frac{1}{1 + h\alpha i_2 + h(\mu_0 + v)} & 0 & 0 & 0 \\ \frac{h\alpha i_2}{1 + h(\mu_0 + \beta + \gamma_1)} & \frac{1}{1 + h(\mu_0 + \beta + \gamma_1)} & \frac{h\alpha s}{1 + h(\mu_0 + \beta + \gamma_1)} & 0 \\ 0 & \frac{h\beta}{1 + h(\mu_0 + \mu_1 + \gamma_2)} & \frac{1}{1 + h(\mu_0 + \mu_1 + \gamma_2)} & 0 \\ \frac{hv}{1 + h\mu_0} & \frac{h\gamma_1}{1 + h\mu_0} & \frac{h\gamma_2}{1 + h\mu_0} & \frac{1}{1 + h\mu_0} \end{bmatrix}.$$

Evaluating the Jacobian at the disease-free equilibrium E_0

$$J(E_0) = \begin{bmatrix} \frac{1}{1 + h(\mu_0 + v)} & 0 & 0 & 0 \\ 0 & \frac{1}{1 + h(\mu_0 + \beta + \gamma_1)} & \frac{h\alpha}{1 + h(\mu_0 + \beta + \gamma_1)} & 0 \\ 0 & \frac{h\beta}{1 + h(\mu_0 + \mu_1 + \gamma_2)} & \frac{1}{1 + h(\mu_0 + \mu_1 + \gamma_2)} & 0 \\ \frac{hv}{1 + h\mu_0} & \frac{h\gamma_1}{1 + h\mu_0} & \frac{h\gamma_2}{1 + h\mu_0} & \frac{1}{1 + h\mu_0} \end{bmatrix}.$$

The characteristic equation for the eigenvalues is

$$|J(E_0) - \lambda I| = 0$$

$$\begin{vmatrix} \frac{1}{1+h(\mu_0+v)}-\lambda & 0 & 0 & 0 \\ 0 & \frac{1}{1+h(\mu_0+\beta+\gamma_1)}-\lambda & \frac{h\alpha}{1+h(\mu_0+\beta+\gamma_1)} & 0 \\ 0 & \frac{h\beta}{1+h(\mu_0+\mu_1+\gamma_2)} & \frac{1}{1+h(\mu_0+\mu_1+\gamma_2)}-\lambda & 0 \\ \frac{hv}{1+h\mu_0} & \frac{h\gamma_1}{1+h\mu_0} & \frac{h\gamma_2}{1+h\mu_0} & \frac{1}{1+h\mu_0}-\lambda \end{vmatrix} = 0.$$

Some eigenvalues are easily obtained

$$\lambda_1 = \frac{1}{1+h\mu_0}, \quad \lambda_2 = \frac{1}{1+h(\mu_0+v)}.$$

The remaining eigenvalues can be obtained from the 2×2 submatrix

$$A = \begin{bmatrix} \frac{1}{1+h(\mu_0+\beta+\gamma_1)} & \frac{h\alpha}{1+h(\mu_0+\beta+\gamma_1)} \\ \frac{h\beta}{1+h(\mu_0+\mu_1+\gamma_2)} & \frac{1}{1+h(\mu_0+\mu_1+\gamma_2)} \end{bmatrix}.$$

Using the Lemma conditions

(1) $1+T+D>0$,
(2) $1-T+D>0$,
(3) $D<1$,

where $T = \mathrm{Tr}(A)$ and $D = \det(A)$

$$\mathrm{Tr}(A) = \frac{1}{1+h(\mu_0+\beta+\gamma_1)} + \frac{1}{1+h(\mu_0+\mu_1+\gamma_2)},$$

$$\begin{aligned} \det(A) = & \frac{1}{1+h(\mu_0+\beta+\gamma_1)} \cdot \frac{1}{1+h(\mu_0+\mu_1+\gamma_2)} \\ & - \frac{h\alpha}{1+h(\mu_0+\beta+\gamma_1)} \cdot \frac{h\beta}{1+h(\mu_0+\mu_1+\gamma_2)} < 1. \end{aligned}$$

These conditions are satisfied, ensuring that all remaining eigenvalues are less than one. □

In Fig.6, the numerical simulations of the NSFD scheme for the DFE point of Hepatitis B virus for system (2.1) are shown. The simulations show that the proposed NSFD scheme shows positivity at all finite step sizes without disturbing the values of variables. The parametric values involved in the above simulations are shown in Table 1.

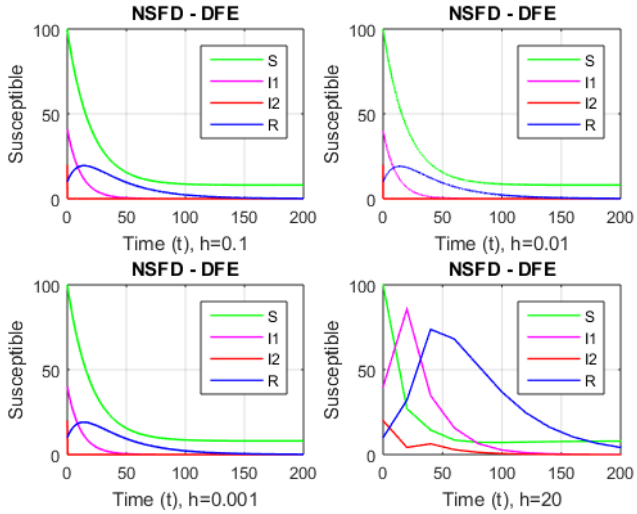


FIGURE 6. Numerical Simulations of NSFD Scheme for DFE (Disease Free Equilibrium) point of Hepatitis B Virus Model

Theorem 6. *If $\mathcal{R}_0 > 1$, then DEE points E^* of the discrete NSFD model (2.1) is LAS for all $h > 0$.*

Proof. In a similar way to theorem 5, the Jacobian matrix can be obtained as
The Jacobian matrix at any point is:

$$J = \begin{bmatrix} \frac{1}{1+h\alpha i_2 - h(\mu_0+v)} & 0 & 0 & 0 \\ \frac{h\alpha i_2}{1+h(\mu_0+\beta+\gamma_1)} & \frac{1}{1+h(\mu_0+\beta+\gamma_1)} & \frac{h\alpha s}{1+h(\mu_0+\beta+\gamma_1)} & 0 \\ 0 & \frac{h\beta}{1+h(\mu_0+\mu_1+\gamma_2)} & \frac{1}{1+h(\mu_0+\mu_1+\gamma_2)} & 0 \\ \frac{hv}{1+h\mu_0} & \frac{h\gamma_1}{1+h\mu_0} & \frac{h\gamma_2}{1+h\mu_0} & \frac{1}{1+h\mu_0} \end{bmatrix}.$$

By evaluating at the endemic equilibrium $E^* = (s^*, i_1^*, i_2^*, r^*)$, we get:

$$J(E^*) = \begin{bmatrix} \frac{1}{1+h\alpha i_2^* - h(\mu_0+v)} & 0 & 0 & 0 \\ \frac{h\alpha i_2^*}{1+h(\mu_0+\beta+\gamma_1)} & \frac{1}{1+h(\mu_0+\beta+\gamma_1)} & \frac{h\alpha s^*}{1+h(\mu_0+\beta+\gamma_1)} & 0 \\ 0 & \frac{h\beta}{1+h(\mu_0+\mu_1+\gamma_2)} & \frac{1}{1+h(\mu_0+\mu_1+\gamma_2)} & 0 \\ \frac{hv}{1+h\mu_0} & \frac{h\gamma_1}{1+h\mu_0} & \frac{h\gamma_2}{1+h\mu_0} & \frac{1}{1+h\mu_0} \end{bmatrix}.$$

The characteristic equation is:

$$|J(E^*) - \lambda I| = 0,$$

or explicitly:

$$\begin{vmatrix} \frac{1}{1+h\alpha i_2^* - h(\mu_0+v)} - \lambda & 0 & 0 & 0 \\ \frac{h\alpha i_2^*}{1+h(\mu_0+\beta+\gamma_1)} & \frac{1}{1+h(\mu_0+\beta+\gamma_1)} - \lambda & \frac{h\alpha s^*}{1+h(\mu_0+\beta+\gamma_1)} & 0 \\ 0 & \frac{h\beta}{1+h(\mu_0+\mu_1+\gamma_2)} & \frac{1}{1+h(\mu_0+\mu_1+\gamma_2)} - \lambda & 0 \\ \frac{hv}{1+h\mu_0} & \frac{h\gamma_1}{1+h\mu_0} & \frac{h\gamma_2}{1+h\mu_0} & \frac{1}{1+h\mu_0} - \lambda \end{vmatrix} = 0.$$

Some eigenvalues are directly obtained:

$$\lambda_1 = \frac{1}{1+h\mu_0}, \quad \lambda_2 = \frac{1}{1-h(\mu_0+v)}.$$

The remaining eigenvalues come from the 2×2 sub-matrix

$$A = \begin{bmatrix} \frac{1}{1+h\alpha i_2^* - h(\mu_0+v)} - \lambda & \frac{h\alpha s^*}{1+h(\mu_0+\beta+\gamma_1)} \\ \frac{h\beta}{1+h(\mu_0+\mu_1+\gamma_2)} & \frac{1}{1+h(\mu_0+\mu_1+\gamma_2)} - \lambda \end{bmatrix}.$$

Using the following Lemma conditions

(1) $1 + T + D > 0$,
(2) $1 - T + D > 0$,
(3) $D < 1$,

where $T = \mathrm{Tr}(A)$ and $D = \det(A)$

$$\mathrm{Tr}(A) = \frac{1}{1+h\alpha i_2^* - h(\mu_0+v)} + \frac{1}{1+h(\mu_0+\mu_1+\gamma_2)},$$

$$\det(A) = \frac{1}{1+h\alpha i_2^* - h(\mu_0+v)} \cdot \frac{1}{1+h(\mu_0+\mu_1+\gamma_2)} - \frac{h\alpha s^*}{1+h(\mu_0+\beta+\gamma_1)} \cdot \frac{h\beta}{1+h(\mu_0+\mu_1+\gamma_2)}.$$

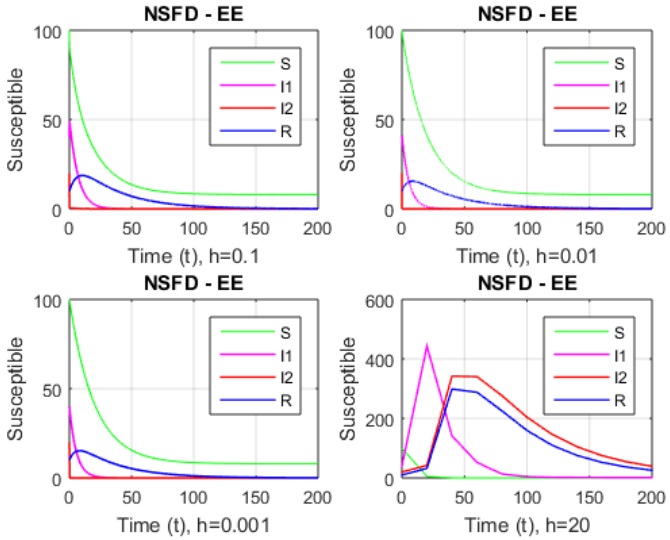


FIGURE 7. Numerical Simulations of NSFD Scheme for EE (Disease Free Equilibrium) point of Hepatitis B Virus Model

These conditions are satisfied, ensuring all remaining eigenvalues are less than one. □

In Fig.7, the numerical simulations of the NSFD scheme for the DEE point of Hepatitis B virus for system (2.1) are shown. The parametric values involved in the above simulations are shown in Table 1. The graphs of Non-standard finite difference scheme (NSFD) at both DFE and EE show unconditionally convergent, and it does not depend on the size of the parameter h.

5.5. **Positivity.**

Theorem 7. *Let the state variables $S(t)$, $I_1(t)$, $I_2(t)$, and $R(t)$ involved in the scheme be positive at $t = 0$. Furthermore, if all the parameters of the model are positive, then for all $n \geq 0$,*

$$S^{n+1} \geq 0, \quad I_1^{n+1} \geq 0, \quad I_2^{n+1} \geq 0, \quad R^{n+1} \geq 0.$$

Proof. Consider equations (5.4)-(5.7) and apply the principle of mathematical induction. We proceed as follows: The discretized system of equations is given by:

$$\begin{cases} S^{n+1} = \dfrac{hb + S^n}{1 + h\alpha I_2^n + h(\mu_0 + v)}, \\ I_1^{n+1} = \dfrac{h\alpha S^n I_2^n + I_1^n}{1 + h(\mu_0 + \beta + \gamma_1)}, \\ I_2^{n+1} = \dfrac{h\beta I_1^n + I_2^n}{1 + h\mu_0 + \mu_1 + \gamma_2}, \\ R^{n+1} = \dfrac{h(\gamma_1 I_1^n + \gamma_2 I_2^n + vS^n) + R^n}{1 + h\mu_0} \end{cases} \tag{5. 11}$$

At first, we put $n = 0$ in the above system and obtain,

$$S^1 = \frac{hb + S^0}{1 + h\alpha I_2^0 + h(\mu_0 + v)} \geq 0 \tag{5. 12}$$

Similarly,

$$\begin{cases} I_1^1 = \dfrac{h\alpha S^0 I_2^0 + I_1^0}{1 + h(\mu_0 + \beta + \gamma_1)} \geq 0, \\ I_2^1 = \dfrac{h\beta I_1^0 + I_2^0}{1 + h\mu_0 + \mu_1 + \gamma_2} \geq 0, \\ R^1 = \dfrac{h(\gamma_1 I_1^0 + \gamma_2 I_2^0 + vS^0) + R^0}{1 + h\mu_0} \geq 0 \end{cases} \tag{5. 13}$$

Now, for $n = 1$, we have,

$$S^2 = \frac{hb + S^1}{1 + h\alpha I_2^1 + h(\mu_0 + v)} \geq 0 \tag{5. 14}$$

Similarly,

$$\begin{cases} I_1^2 = \dfrac{h\alpha S^1 I_2^1 + I_1^1}{1 + h(\mu_0 + \beta + \gamma_1)} \geq 0, \\ I_2^2 = \dfrac{h\beta I_1^1 + I_2^1}{1 + h\mu_0 + \mu_1 + \gamma_2} \geq 0, \\ R^2 = \dfrac{h(\gamma_1 I_1^1 + \gamma_2 I_2^1 + vS^1) + R^1}{1 + h\mu_0} \geq 0 \end{cases} \tag{5. 15}$$

Next, suppose that the given set of equations guarantees the positivity property for $n = 2, 3, 4, \ldots, n-1$, i.e,

$$S^n \geq 0, \quad I_1^n \geq 0, \quad I_2^n \geq 0, \quad R^n \geq 0$$

for $n = 2, 3, 4, \ldots, n-1$ and the state variables. Now, the positivity will be investigated for an arbitrary positive integer n. For $n \in \mathbb{Z}$.

$$\begin{cases} S^{n+1} = \dfrac{hb + S^n}{1 + h\alpha I_2^n + h(\mu_0 + v)} \geq 0, \\ I_1^{n+1} = \dfrac{h\alpha S^n I_2^n + I_1^n}{1 + h(\mu_0 + \beta + \gamma_1)} \geq 0, \\ I_2^{n+1} = \dfrac{h\beta I_1^n + I_2^n}{1 + h\mu_0 + \mu_1 + \gamma_2} \geq 0, \\ R^{n+1} = \dfrac{h(\gamma_1 I_1^n + \gamma_2 I_2^n + vS^n) + R^n}{1 + h\mu_0} \geq 0 \end{cases} \tag{5. 16}$$

Hence, the projected scheme ensures the positivity of the state variables $S(t)$, $I_1(t)$, $I_2(t)$, and $R(t)$ for all positive integer values of n. □

5.6. **Boundedness.** Let S^0, I_1^0, I_2^0, and R^0 be finite such that

$$S^0 + I_1^0 + I_2^0 + R^0 \leq 1.$$

Then the discretized state variables S^{n+1}, I_1^{n+1}, I_2^{n+1}, and R^{n+1} are bounded by a recursively defined real constant a_{n+1} such that

$$S^{n+1} < a_{n+1}, \quad I_1^{n+1} < a_{n+1}, \quad I_2^{n+1} < a_{n+1}, \quad R^{n+1} < a_{n+1},$$

for all $n \in \mathbb{Z}^+$, where

$$a_{n+1} = 4a_n + hb + (h\alpha I_2^n + hv)S^n + I_1^n(h\beta + h\gamma_1) + h\gamma_2 I_2^n.$$

Proof. Considering the equation of an implicit numerical integration scheme for the state variables S,I_1,I_2 and R as,

$$\begin{cases} S^{n+1}(1 + h\alpha I_2^n + h(\mu_0 + v)) = hb + S^n \\ I_1^{n+1}(1 + h(\mu_0 + \beta + \gamma_1)) = h\alpha S^n I_2^n + I_1^n \\ I_2^{n+1}(1 + h\mu_0 + \mu_1 + \gamma_2) = h\beta I_1^n + I_2^n \\ R^{n+1}(1 + h\mu_0) = h(\gamma_1 I_1^n + \gamma_2 I_2^n + vS^n) + R^n \end{cases} \tag{5. 17}$$

By adding all the above-mentioned equations.

$$\begin{aligned} &(S^{n+1} + I_1^{n+1} + I_2^{n+1} + R^{n+1})(1 + h\mu_0) + h\alpha S^{n+1} I_2^n + hvS^{n+1} \\ &\quad + I_1^{n+1}(h\beta + h\gamma_1) + I_2^{n+1}(h\mu_0 + h\gamma_2) \\ &\quad = (S^n + I_1^n + I_2^n + R^n) + hb + (h\alpha I_2^n + hv)S^n + I_1^n(h\beta + h\gamma_1) + h\gamma_2 I_2^n. \end{aligned}$$

We prove the boundedness of the nonstandard numerical scheme by using the theory of mathematical induction and the constraints imposed on the parameters and state variables.

By putting $n = 0$

$$(S^1+I_1^1+I_2^1+R^1)(1+h\mu_0)+S^1h\alpha I_2^0+S^1hv+I_1^1(h\beta+h\gamma_1)+I_2^1(h\mu_0+h\gamma_2)$$
$$=(S^0+I_1^0+I_2^0+R^0)+hb+(h\alpha I_2^0+hv)S^0+I_1^0(h\beta+h\gamma_1)+h\gamma_2 I_2^0$$
$$(S^1+I_1^1+I_2^1+R^1)(1+h\mu_0)+h\alpha S^1I_2^0+hvS^1$$
$$+I_1^1(h\beta+h\gamma_1)+I_2^1(h\mu_0+h\gamma_2)$$
$$<4+hb+(h\alpha I_2^0+hv)S^0+I_1^0(h\beta+h\gamma_1)+h\gamma_2 I_2^0=a_1.$$

$$(S^1+I_1^1+I_2^1+R^1)(1+h\mu_0)+S^1h\alpha I_2^0+S^1hv+I_1^1(h\beta+h\gamma_1)+I_2^1(h\mu_0+h\gamma_2)\leq a_1$$

$$S^1(1+h\mu_0+h\alpha I_2^0+hv)+I_1^1(1+h\mu_0+h\beta+h\gamma_1)$$
$$+I_2^1((1+h\mu_0)+h\mu_0+h\gamma_2)+R^1(1+h\mu_0)\leq a_1$$

Hence,

$$S^1<a_1,\quad I_1^1<a_1,\quad I_2^1<a_1,\quad R^1<a_1$$

Now by putting $n=1$

$$S^2(1+h\mu_0+h\alpha I_2^1+hv)+I_1^2(1+h\mu_0+h\beta+h\gamma_1)$$
$$+I_2^2((1+h\mu_0)+h\mu_0+h\gamma_2)+R^2(1+h\mu_0)$$
$$=(S^1+I_1^1+I_2^1+R^1)+hb+(h\alpha I_2^1+hv)S^1+I_1^1(h\beta+h\gamma_1)+h\gamma_2 I_2^1$$

$$S^2(1+h\mu_0+h\alpha I_2^1+hv)+I_1^2(1+h\mu_0+h\beta+h\gamma_1)$$
$$+I_2^2((1+h\mu_0)+h\mu_0+h\gamma_2)+R^2(1+h\mu_0)<4a_1+hb+(h\alpha I_2^1+hv)S^1$$
$$+I_1^1(h\beta+h\gamma_1)+h\gamma_2 I_2^1=a_2$$

Thus,

$$S^2<a_2,\quad I_1^2<a_2,\quad I_2^2<a_2,\quad R^2<a_2$$

Next, consider that the following expressions are bounded for positive integers $n=2,3,4,\ldots,n-1$, i.e.,

$$S^n<a_n,\quad I_1^n<a_n,\quad I_2^n<a_n,\quad \text{and}\quad R^n<a_n$$

for all

$$n\in\{2,3,4,\ldots,n-1\}.$$

Now, we investigate the boundedness and positivity for the integer n.

$$S^{n+1}(1+h\mu_0+h\alpha I_2^n+hv)+I_1^{n+1}(1+h\mu_0+h\beta+h\gamma_1)$$

$$+I_2^{n+1}((1+h\mu_0)+h\mu_0+h\gamma_2)+R^{n+1}(1+h\mu_0)$$
$$=(S^n+I_1^n+I_2^n+R^n)+hb+(h\alpha I_2^n+hv)S^n+I_1^n(h\beta+h\gamma_1)+h\gamma_2 I_2^n$$

$$S^{n+1}(1+h\mu_0+h\alpha I_2^n+hv)+I_1^{n+1}(1+h\mu_0+h\beta+h\gamma_1)$$
$$+I_2^{n+1}((1+h\mu_0)+h\mu_0+h\gamma_2)+R^{n+1}(1+h\mu_0)<4a_n+hb+(h\alpha I_2^n+hv)S^n$$
$$+I_1^n(h\beta+h\gamma_1)+h\gamma_2 I_2^n=a_{n+1}$$

Hence,

$$S^{n+1}<a_{n+1},\quad I_1^{n+1}<a_{n+1},\quad I_2^{n+1}<a_{n+1},\quad R^{n+1}<a_{n+1}$$

Therefore, S^{n+1}, I_1^{n+1}, I_2^{n+1}, and R^{n+1} are bounded by a real number a_{n+1} for all positive integers n. □

5.7. **Consistency Analysis.** In this section, consistency analysis of an implicit numerical integration scheme is performed by using Taylor's series expansion. First, we take equation (5.4) of the implicit numerical integration scheme and apply Taylor's series expansion of S^{n+1}.

$$S^{n+1}=S^n+h\frac{dS}{dt}+\frac{h^2}{2!}\frac{d^2S}{dt^2}+\frac{h^3}{3!}\frac{d^3S}{dt^3}+\cdots$$

In the following expression,

$$\left(S^n+h\frac{dS}{dt}+\frac{h^2}{2!}\frac{d^2S}{dt^2}+\frac{h^3}{3!}\frac{d^3S}{dt^3}+\cdots\right)(1+h\alpha I_2^n+h(\mu_0+v))=hb+S^n$$

$$S^n+S^nh\alpha I_2^n+S^nh(\mu_0+v)+h\frac{dS}{dt}+h^2\alpha I_2^n\frac{dS}{dt}+h^2(\mu_0+v)\frac{dS}{dt}$$
$$+\left(\frac{h^2}{2!}\frac{d^2S}{dt^2}+\frac{h^3}{3!}\frac{d^3S}{dt^3}+\cdots\right)(1+h\alpha I_2^n+h(\mu_0+v))=hb+S^n$$

$$S^nh\alpha I_2^n+S^nh(\mu_0+v)+h\frac{dS}{dt}+h^2\alpha I_2^n\frac{dS}{dt}+h^2(\mu_0+v)\frac{dS}{dt}$$
$$+\left(\frac{h^2}{2!}\frac{d^2S}{dt^2}+\frac{h^3}{3!}\frac{d^3S}{dt^3}+\cdots\right)(1+h\alpha I_2^n+h(\mu_0+v))=hb$$

$$h\Bigg(S^n\alpha I_2^n+S^n(\mu_0+v)+\frac{dS}{dt}+h\alpha I_2^n\frac{dS}{dt}+h(\mu_0+v)\frac{dS}{dt}$$
$$+\left(\frac{h}{2!}\frac{d^2S}{dt^2}+\frac{h^2}{3!}\frac{d^3S}{dt^3}+\cdots\right)(1+h\alpha I_2^n+h(\mu_0+v))\Bigg)=hb$$

$$S^n\alpha I_2^n+S^n(\mu_0+v)+\frac{dS}{dt}+h\alpha I_2^n\frac{dS}{dt}+h(\mu_0+v)\frac{dS}{dt}$$
$$+\left(\frac{h}{2!}\frac{d^2S}{dt^2}+\frac{h^2}{3!}\frac{d^3S}{dt^3}+\cdots\right)(1+h\alpha I_2^n+h(\mu_0+v))=b$$

By applying $h\to 0$, we obtain

$$S^n\alpha I_2^n+S^n(\mu_0+v)+\frac{dS}{dt}=b$$

$$\frac{dS}{dt} = b - S\alpha I_2 - S(\mu_0 + v) \tag{5. 18}$$

Similarly, choose equation (5.5) and apply Taylor's series expansion of I_1^{n+1}.

$$I_1^{n+1} = I_1^n + h\frac{dI_1}{dt} + \frac{h^2}{2!}\frac{d^2I_1}{dt^2} + \frac{h^3}{3!}\frac{d^3I_1}{dt^3} + \cdots$$

$$\left(I_1^n + h\frac{dI_1}{dt} + \frac{h^2}{2!}\frac{d^2I_1}{dt^2} + \frac{h^3}{3!}\frac{d^3I_1}{dt^3} + \cdots\right)(1 + h(\mu_0 + \beta + \gamma_1)) = h\alpha SI_2^n + I_1^n$$

By applying $h \to 0$, we obtain

$$\frac{dI_1}{dt} = \alpha SI_2 - I_1(\mu_0 + \beta + \gamma_1) \tag{5. 19}$$

Similarly, take equation (5.6) and apply Taylor's series expansion of I_2^{n+1}.

$$I_2^{n+1} = I_2^n + h\frac{dI_2}{dt} + \frac{h^2}{2!}\frac{d^2I_2}{dt^2} + \frac{h^3}{3!}\frac{d^3I_2}{dt^3} + \cdots$$

$$\left(I_2^n + h\frac{dI_2}{dt} + \frac{h^2}{2!}\frac{d^2I_2}{dt^2} + \frac{h^3}{3!}\frac{d^3I_2}{dt^3} + \cdots\right)(1 + h\mu_0 + \mu_1 + \gamma_2) = h\beta I_1^n + I_2^n$$

By applying $h \to 0$, we obtain

$$\frac{dI_2}{dt} = \beta I_1 - I_2(\mu_0 + \mu_1 + \gamma_2) \tag{5. 20}$$

Similarly, take equation (5.7) and apply Taylor's series expansion of R^{n+1}.

$$R^{n+1} = R^n + h\frac{dR}{dt} + \frac{h^2}{2!}\frac{d^2R}{dt^2} + \frac{h^3}{3!}\frac{d^3R}{dt^3} + \cdots$$

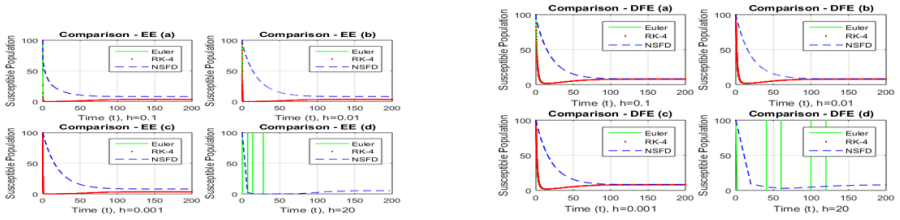
$$\left(R^n + h\frac{dR}{dt} + \frac{h^2}{2!}\frac{d^2R}{dt^2} + \frac{h^3}{3!}\frac{d^3R}{dt^3} + \cdots\right)(1 + h\mu_0) = h(\gamma_1 I_1^n + \gamma_2 I_2^n + vS^n) + R^n$$

By applying $h \to 0$, we obtain

$$\frac{dR}{dt} = \gamma_1 I_1 + \gamma_2 I_2 + vS + R\mu_0 \tag{5. 21}$$

Hence, the discretized implicit numerical integration scheme is consistent with the ODE system (2.1).

5.8. **Comparison Analysis of SFD and NSFD Schemes.** The comparison analysis of both numerical schemes is presented in this sub-section, which shows the reliability of these schemes. Numerical simulation shows the comparison of SFD and NSFD schemes in Fig.8 (A) and Fig.8 (B). These results are for the endemic equilibrium points and the Disease-Free Equilibrium points, respectively.



(A) (B)

FIGURE 8. Combined behavior of the system: (A) Numerical simulation shows the comparison of SFD and NSFD schemes; (B) Numerical simulation shows the comparison of SFD and NSFD schemes.

6. CONCLUSION

This research presents a quantitative examination of Hepatitis B and its dynamics. A mathematical model is constructed utilizing four variables, and differential equations are derived based on these variables. Through the utilization of these differential equations, we can determine equilibrium points where there is no disease present and equilibrium points where the disease is prevalent. The basic reproductive numbers are determined by utilizing the next-generation matrix. The stability of equilibrium points is analyzed using fundamental reproductive numbers. We employed two numerical techniques, namely SFD (Standard Finite Difference) and NSFD (Non-Standard Finite Difference), to investigate the transmission of HBV (Hepatitis B Virus). The SFD scheme exhibits negativity when the step size is big, indicating that it does not sustain positivity. Following the SFD scheme, we have devised an unconditionally convergent NSFD scheme for the Hepatitis B model that ensures positivity at any limited step size. Additionally, a stability study of the proposed scheme is also provided. Finally, numerical experiments are conducted to evaluate the theoretical conclusions of both schemes, and a numerical comparison of the two schemes is offered. Future directions include stochastic, fractional, and fuzzy extensions of the current work.

CREDIT AUTHORSHIP CONTRIBUTION'S STATEMENT

Shah Zeb: Supervision, Project Management, Methodology, Formal Analysis, Research, Data Curation, Original Draft Writing , funding acquisition, and supervision. **Muhammad Bilal**: Conceptualization, Methodology, Formal Analysis, Research, Data Curation, Original Draft Writing, and Visualization. **Muhammad Rafiq**: Formal analysis, method-ology, data curation, project administration. **Siti Ainor Mohd Yatim**: Supervision, Project Management, Methodology, Formal Analysis, Research, Data Curation, Original Draft Writing , funding acquisition, and supervision. **Affan Ahmad**: Formal analysis, data cu-ration, and methodology. **Muhammad Irfan**: Formal analysis, data curation, and method-ology. **Muhammad Sarwar Ehsan**: Data curation and investigation. The final version of the manuscript has been read and approved by all authors.

DECLARATION

Conflict of Interest:There are no conflicts of interest, according to the authors.

Funding: This research has received the financial support from the Universiti Sains Malaysia by Bridging Grant (Project No: R501-LR-RND003-0000002103-0000) and Malaysian International Scholarship. All the authors acknowledge this financial support.

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