



Numerical Modeling for Transmission Dynamics of Hepatitis B Virus

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Abstract

Numerical modeling of communicable disease is a device to appreciate the instrument in what way syndrome pushovers and in what way stately. we have studied numerically the dynamics of HBV. We frame an entirely constant Non-Standard Finite Difference (NSFD) structure for a mathematical model of HBV. The introduce numerical array is bounded, dynamically designate and contain the positivity of the solution, which is one of the important requirements when modeling a prevalent contagious. The comparison between the innovative Non-Standard Finite Alteration structure, Euler method and Runge-Kutta scheme of order four (RK-4) displays the usefulness of the suggested Non-Standard Finite Alteration scheme. NSFD scheme shows convergence to the exact equilibrium facts of the model for any time steps used but Euler and RK-4 fail for large time steps.

Keywords: Hepatitis B Disease; Dynamical System; Numerical Modeling; Convergence

Introduction

HBV affects millions of people worldwide each year, where over 40 million cases are reported and kills approximately 600,000 annually. For instance, in Africa it is estimated that annually 400,000 cases happen and an incidence of 50 per 100,000 [5].

The mathematical modeling for transmission dynamics of hepatitis B disease is a capable attitude to grow the conduct of syndrome the population and the foundation, some capable trials of the modeled to the preclude septicity. Dynamical models for the transmission of disease items in a social population, established the Kermack and McKendrick SIR classical epidemic model [1-4], of recommended. These models deliver evaluations for the sequential advancement of infested nodes in a population [5-10].

Now we construct an unreservedly convergent to the numerical model for the transmission dynamics for HBV which conserves all the critical assets of the incessant model [6].

Mathematical model

A: Variables and Parameters

$x(t)$: Susceptible entities class at time t .

$y(t)$: Infected individuals class at time t .

$v(t)$: Recover individuals class at time t .

λ : Uninfected target cell.

$d_1(x)$: Natural death rate.

βvx : Infected target rate.

ay : Death rate.

ky : Rate of treatment.

uv : Disease induced mortality rate.

The Scheme of Nonlinear Differential Equations(DE) on behalf of the Typical remains specified by:

$$\begin{aligned}x' &= \lambda - d_1 - \beta vx \\y' &= \beta vx - ay \\v' &= ky - uv\end{aligned}\quad (1)$$

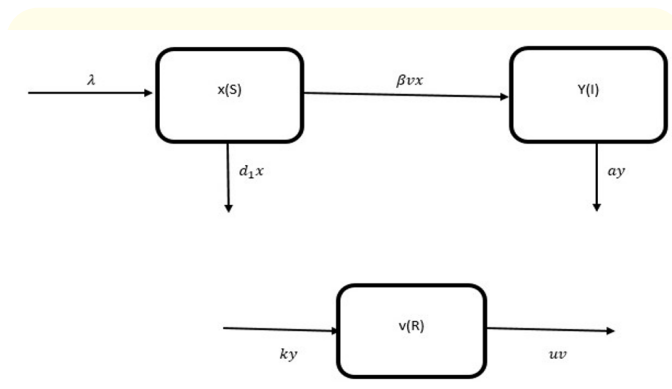


Figure 1: PSIT Hepatitis B Virus Disease Model.

Analysis of the model

We describe two equilibrium points of system i.e Disease free equilibrium (DFE) and Endemic equilibrium (EE).

$E_1 = (\frac{\lambda}{d_1 + \beta v}, 0, 0)$ and $E_2 = (x^*, y^*, v^*)$ are stability facts of scheme (1), where

$$x^* = \frac{\lambda}{d_1 + \beta v}$$

$$y^* = \frac{\beta v \lambda}{a(d_1 + \beta \lambda)}$$

$$v^* = \frac{k \beta v \lambda}{a u (d_1 + \beta \lambda)}$$

$$\text{Where } R_0 = \frac{\theta(\gamma + \mu - \alpha\mu)}{(\gamma + \mu)(\delta + \beta + \mu)}$$

R_0 recognized as Procreative integer who describes the usual number of inferior impurities introduced of the main impurity. R_0 is a beginning influence who describe the disease of the exit or persist? If $R_0 < 1$ then we say that the scheme will observed disease Free Equilibrium (DFE) and iff $R_0 > 1$ the scheme to involvement Endemic Equilibrium (EE).

Numerical modeling

Now we have conferred two standard finite difference structures to unravel the endless dynamical scheme (1) i.e. Euler's Method and Runge-Kutta Method of Order 4.

Euler method

The Forward Euler's Structure for the unceasing model (1) certain through:

$$x^{n+1} = x^n + h\{\lambda - d_1 - \beta v x^n\}$$

$$y^{n+1} = y^n + h\{\beta v x^n - a y^n\}$$

$$v^{n+1} = v^n + h\{k y^n - u v^n\}$$

Numerical experiments

Now solve numerical tryouts by expending the values of given parameters table 1 [6].

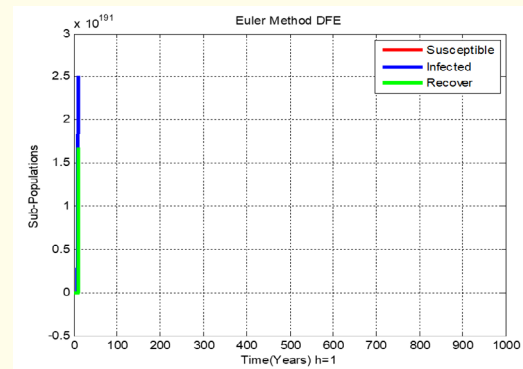


Figure 2: Euler Method (DFE), h=1.

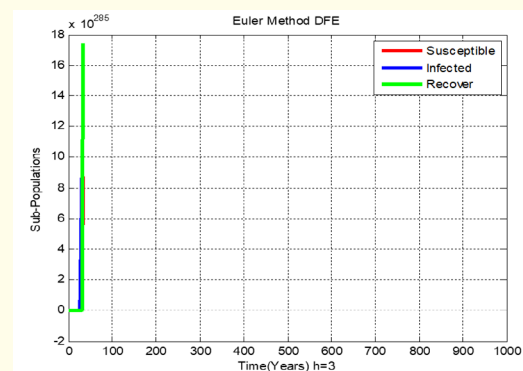


Figure 3: Euler Method (DFE), h=3.

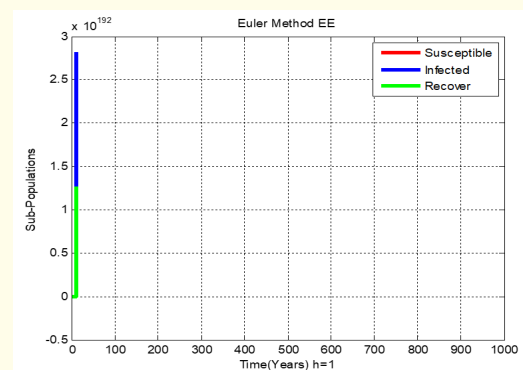


Figure 4: Euler Method (EE), h=1.

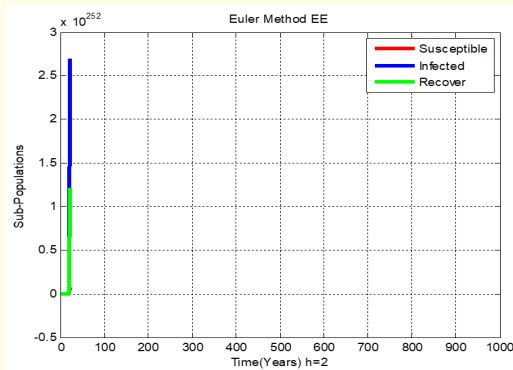


Figure 5: Euler Method (EE), h=2.

Parameters	Values	
	DFE	EE
	0.00379	0.8
	0.00379	0.0044
	0.67	10
	9	0.1
	0	0.005
	0.982	0.9

Table 1

Fourth order runge-kutta scheme

For Stage-1

$$K_1 = h[\lambda - d_1 - \beta v x^n]$$

$$l_1 = h[\beta v x^n - a y^n]$$

$$m_1 = h[k y^n - u v^n]$$

For Stage-2

$$k_2 = h[\lambda - d_1 - \beta v(x^n + \frac{k_1}{2})]$$

$$l_2 = h[\beta v(x^n + \frac{k_1}{2}) - a(y^n + \frac{l_1}{2})]$$

$$m_2 = h[k(y^n + \frac{l_1}{2}) - u(v^n + \frac{m_1}{2})]$$

For Stage-3

$$k_3 = h[\lambda - d_1 - \beta v(x^n + \frac{k_2}{2})]$$

$$l_3 = h[\beta v(x^n + \frac{k_2}{2}) - a(y^n + \frac{l_2}{2})]$$

$$m_3 = h[k(y^n + \frac{l_2}{2}) - u(v^n + \frac{m_2}{2})]$$

For Stage-4

$$k_4 = h[\lambda - d_1 - \beta v(x^n + \frac{k_3}{2})]$$

$$l_4 = h[\beta v(x^n + \frac{k_3}{2}) - a(y^n + \frac{l_3}{2})]$$

$$m_4 = h[k(y^n + \frac{l_3}{2}) - u(v^n + \frac{m_3}{2})]$$

Finally

$$x^{n+1} = x^n + \frac{1}{6}[K_1 + 2K_2 + 2K_3 + K_4]$$

$$y^{n+1} = y^n + \frac{1}{6}[l_1 + 2l_2 + 2l_3 + l_4]$$

$$v^{n+1} = v^n + \frac{1}{6}[m_1 + 2m_2 + 2m_3 + m_4] \quad (4)$$

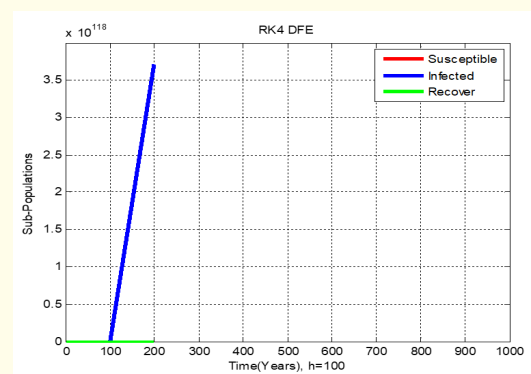


Figure 6: RK-4 Method (DFE), h=100.

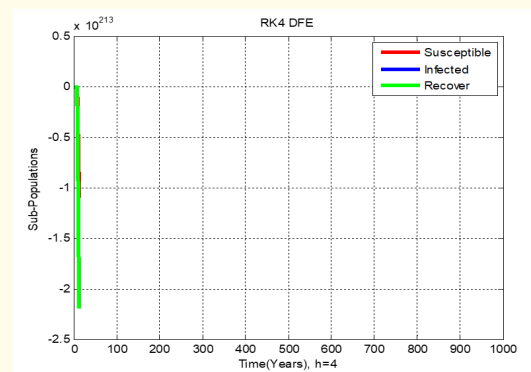


Figure 7: RK-4 Method (DFE), h=4.

Non-standard finite difference model

Now we show an unreservedly convergent non-standard finite difference(NSFD) numerical model which be there describe on non-standard finite difference modeling concept introduced by

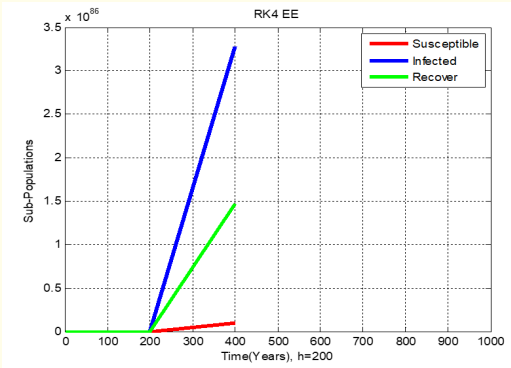


Figure 8: RK-4 Method (EE), h=200.

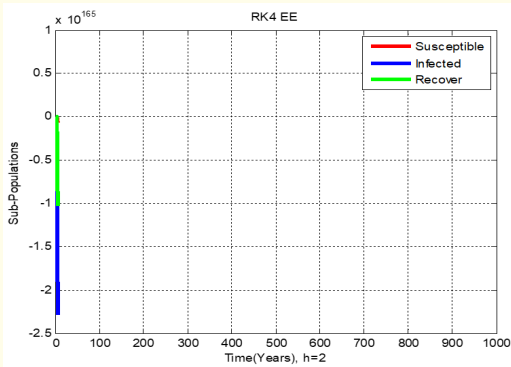


Figure 9: RK-4 Method (EE), h=2.

Micken's [3]. Now show the convergence scrutiny of the suggested structure. The NSFD model for the incessant dynamical system is given by:

$$\begin{aligned} x^{n+1} &= \frac{x^n + h\lambda}{1 + h d_1 + h \beta v^n} \\ y^{n+1} &= \frac{y^n + h \beta v^n x^n}{1 + h a} \\ v^{n+1} &= \frac{v^n + h k y^n}{1 + h u} \end{aligned}$$

Convergence Analysis of NSFD Scheme

Let us define

$$\begin{aligned} E &= \frac{x + h\lambda}{1 + h d_1 + h \beta v} \\ F &= \frac{y + h \beta v x}{1 + h a} \\ G &= \frac{v + h k y}{1 + h u} \end{aligned}$$

Now the Jacobian Matrix is given by

$$J = \begin{bmatrix} \frac{\partial E}{\partial x} & \frac{\partial E}{\partial y} & \frac{\partial E}{\partial v} \\ \frac{\partial F}{\partial x} & \frac{\partial F}{\partial y} & \frac{\partial F}{\partial v} \\ \frac{\partial G}{\partial x} & \frac{\partial G}{\partial y} & \frac{\partial G}{\partial v} \end{bmatrix}$$

At DiseaseFree Equilibrium $\mathcal{E}_1 = (\frac{\lambda}{d_1 + \beta v}, 0, 0)$

At Endemic Equilibrium $\mathcal{E}_1 = (\frac{\lambda}{d_1 + \beta v}, \frac{\beta v \lambda}{a(d_1 + \beta \lambda)}, \frac{k \beta v \lambda}{au(d_1 + \beta \lambda)})$

$$J^*(\mathcal{E}_1) = \begin{bmatrix} \frac{1}{1 + h d_1 + h \beta v} & 0 & 0 \\ \frac{h \beta v}{1 + h a} & \frac{1}{1 + h a} & \frac{h \beta x}{1 + h a} \\ 0 & \frac{h k}{1 + h u} & \frac{1}{1 + h u} \end{bmatrix}$$

There are the following eigen values of above jacobian matrix is:

$$\begin{aligned} \lambda_1 &= \frac{1}{1 + h d_1 + h \beta v} < 1 \\ \lambda_2 &= \frac{1}{1 + h a} < 1 \\ \lambda_3 &= \frac{1}{1 + h u} < 1 \end{aligned}$$

Lemma 3.1 [12]

For the quadratic equation $\lambda^2 - A\lambda + B = 0$, $|\lambda_i| < 1, i = 1, 2$; if the following conditions are satisfied:

- (1) $1 - A + B > 0$
- (2) $1 + A + B > 0$
- (3) $B < 1$

Numerical experiments

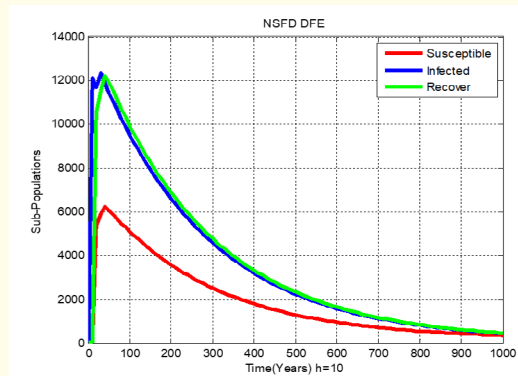


Figure 10: NSFD Method (DFE), h=10.

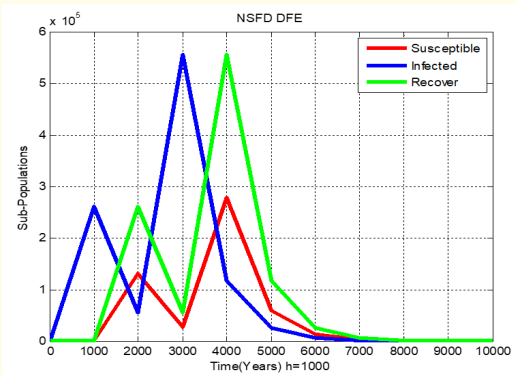


Figure 11: NSFD Method (DFE), h=1000.

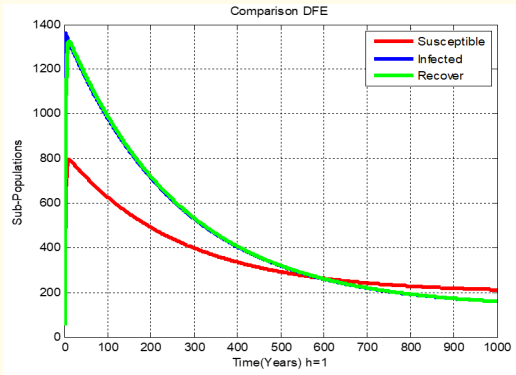


Figure 14: Comparison (DFE), h=1.

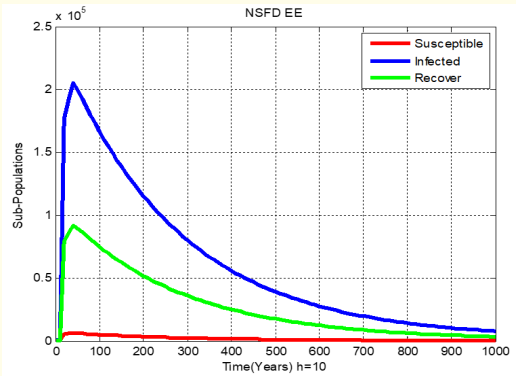


Figure 12: NSFD Method (EE), h=10.

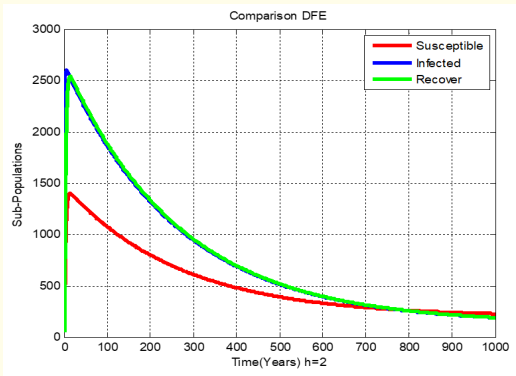


Figure 15: Comparison (DFE), h=2.

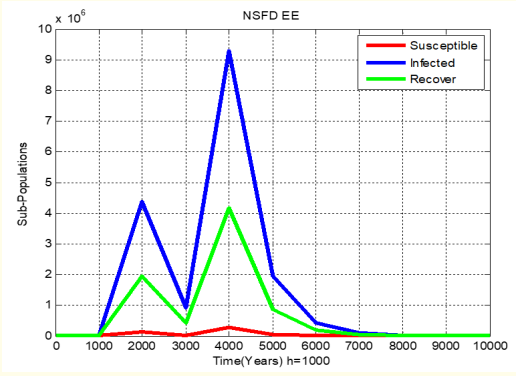


Figure 13: NSFD Method (EE), h=1000.

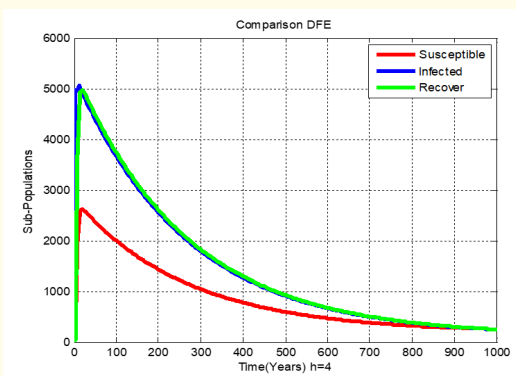


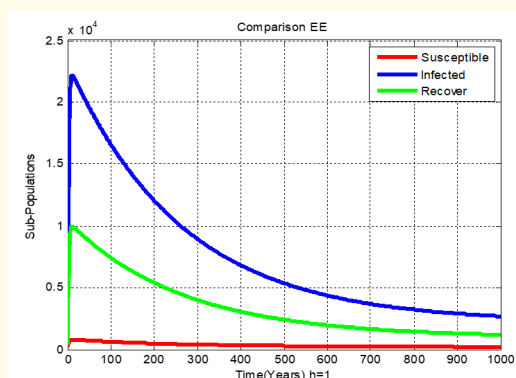
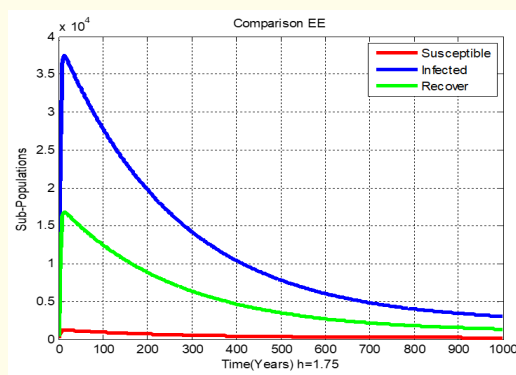
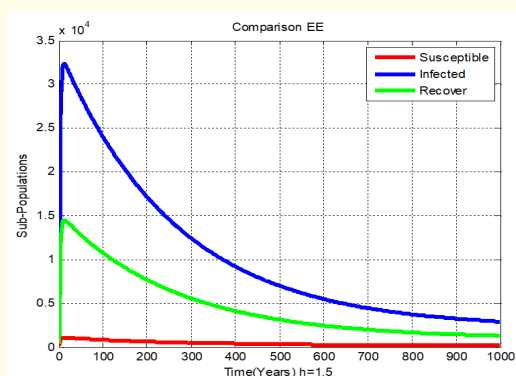
Figure 16: Comparison (DFE), h=4.

Comparison analysis

In this section, we see the comparison among of two standard difference schemes and non-standard difference scheme in epidemiology.

Results and Discussion

The model of transmission dynamics of Hepatitis B virus disease consumes introduced expending PSIT Model. (i.e Threatened,


 Figure 17: Comparison (EE), $h=1$.

 Figure 18: Comparison (EE), $h=1.75$.

 Figure 19: Comparison (EE), $h=1.5$.

Susceptible, Infected and Treated). The constancy of solid positions i.e the Disease free equilibrium (DFE) and Endemic equilibrium facts (EE) deliberated numerically. We describe an unqualifiedly constant Non-Standard Finite Difference (NSFD) structure aimed

at the incessant dynamical system. The suggested structure exists dynamical constant, numerically steady and holds all the authentic assets of the incessant model. The outcomes equaled well known standard finite difference schemes i.e Euler's and Runge-Kutta method of order 4 (RK-4). The Euler and RK-4 are provisionally convergent and diverge of the assured ethics of step size 'h' while the constructed NSFD scheme for every assessment used to residues convergent.

Conclusion

The Non-Standard Finite Difference Scheme created for the communication dynamics of HBV Euler and RK-4 are unsuccessful they depend on step size. Thus as Euler and RK-4 are conditionally convergent. Euler and RK-4 are divergent and from time to time give variation in solution. The new advanced numerical scheme like Non Standard Finite Difference Scheme is independent on step size. Uncertainty we intensify the step size in hundreds and thousands then NSFD motionless convergent. The NSFD scheme is informal implement that gives mathematically stable, positivity, bounded-ness and shows an equal behaviour of continuous model and discrete model. The graphical behaviour Euler, RK-4 and NSFD schemes are given in figure no.1 to 19. The kindness of variations is a condensed amount of than the other structures. This symbol that NSFD is more well-known as related to the other three categorizations.

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