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RESEARCH ARTICLE

NUMERICAL MODELING FOR TRANSMISSION DYNAMICS OF HEPATITIS B VIRUS DISEASE

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ARTICLEINFO

ABSTRACT

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We frame an entirelyconstant Non-Standard Finite Difference (NSFD) structurefor 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.

Numerical modeling of communicable disease is a device to appreciate the instrumentin what

waysyndrome pushovers and in what waystately. we have studied numerically the dynamics of HBV.

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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 (Murray, 2006). The mathematical modeling for transmission dynamics of hepatitis B diseaseisa capable attitude to grow the conduct of syndrome the population and the foundation, somecapabletrials of the modeled to the precludesepticity. Dynamical models for the transmission of disease itemsin a social population, established the Kermack and McKendrick SIR classical epidemic model (Allen, 1994; Nowak, 1996; Guidotti, 1996; Zhang, 2003), of recommended. These models deliver evaluations for the sequential advancement of infested nodes in a population (Murray, 2006; Gourley, 2008; Min, 2008; Muroya, 2011; World Health Organization, 2015). 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 (Gourley, 2008).

MATHEMATICAL MODEL

Variables and Parameters

- x(t):Susceptible entitiesclass at time t. y(t):Infected individuals classat time t. v(t):Recover individuals classat 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.



Fig.1. PSIT Hepatitis B Virus Disease Model

The Scheme of Nonlinear Differential Equations(DE)on behalf of the Typicalremainsspecifiedby:

$$\begin{aligned} x' &= \lambda - d_1 - \beta v x \\ y' &= \beta v x - a y \\ v' &= k y - u v \end{aligned} \tag{1}$$

Analysis of the Model: We describe two equilibrium points of system i.eDisease free equilibrium(DFE) and Endemic equilibrium(EE).

 $\mathcal{E}_{1} = \left(\frac{\lambda}{d_{1}+\beta\nu}, 0, 0\right) \text{ and } \mathcal{E}_{2} = (x^{*}, y^{*}, v^{*}) \text{ are stability facts of scheme (1), where}$ $x^{*} = \frac{\lambda}{d_{1}+\beta\nu}$ $y^{*} = \frac{\beta\nu\lambda}{a(d_{1}+\beta\lambda)}$ $v^{*} = \frac{k\beta\nu\lambda}{au(d_{1}+\beta\lambda)}$ 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. \mathcal{R}_0 is a beginning influence who describe the disease of the exit or persist? If $\mathcal{R}_0 < 1$ then we say that the scheme will observed disease Free Equilibrium (DFE) and iff \mathcal{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:

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

Now solve numerical tryouts by expending the values of given parameters Table 1 (6).

Parameters	Values	
	DFE	EE
<i>d</i> ₁	0.00379	0.8
a	0.00379	0.0044
u	0.67	10
R ₀	9	0.1
m	0	0.005
n	0.982	0.9

Ta	ble	1



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



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

Fourth Order Runge-Kutta Scheme

For Stage-1

$$K_1 = h(\lambda - d_1 - \beta v x^n)$$

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

$$m_1 = h[ky^n - uv^n]$$

For Stage-2

$$k_{2} = h(\lambda - d_{1} - \beta v(x^{n} + \frac{k_{1}}{2}))$$

$$l_{2} = h(\beta v(x^{n} + \frac{k_{1}}{2}) - a(y^{n} + \frac{l_{1}}{2}))$$

$$m_{2} = h\left[k(y^{n} + \frac{l_{1}}{2}) - u(v^{n} + \frac{m_{1}}{2})\right]$$

For Stage-3

$$k_{3} = h(\lambda - d_{1} - \beta v(x^{n} + \frac{k_{2}}{2}))$$

$$l_{3} = h(\beta v(x^{n} + \frac{k_{2}}{2}) - a(y^{n} + \frac{l_{2}}{2}))$$

$$m_{3} = h\left[k(y^{n} + \frac{l_{2}}{2}) - u(v^{n} + \frac{m_{2}}{2})\right]$$

For Stage-4

$$k_{4} = h(\lambda - d_{1} - \beta v(x^{n} + \frac{k_{2}}{2}))$$

$$l_{4} = h(\beta v(x^{n} + \frac{k_{2}}{2}) - a(y^{n} + \frac{l_{2}}{2}))$$

$$m_{4} = h\left[k(y^{n} + \frac{l_{2}}{2}) - u(v^{n} + \frac{m_{2}}{2})\right]$$

Finally

$$\begin{aligned} x^{n+1} &= x^n + \frac{1}{6} [K_1 + 2K_2 + 2K_3 + K_4] \\ y^{n+1} &= y^n + \frac{1}{6} (l_1 + 2l_2 + 2l_3 + l_4) \\ v^{n+1} &= v^n + \frac{1}{6} [m_1 + 2m_2 + 2m_3 + m_4] \end{aligned}$$
(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 Micken's(Guidotti, 1999).Now show the covergenence scrutiny of the suggestedstructure.The NSFD model for the incessant dynamical system is given by:

$$x^{n+1} = \frac{x^{n} + h\lambda}{1 + hd_1 + h\beta v^n}$$
$$y^{n+1} = \frac{y^n + h\beta v^n x^n}{1 + ha}$$
$$v^{n+1} = \frac{v^n + hky^n}{1 + hu}$$

Convergence Analysis of NSFD Scheme

Let us define

$$E = \frac{x + h\lambda}{1 + hd_1 + h\beta v}$$
$$F = \frac{y + h\beta vx}{1 + ha}$$
$$G = \frac{v + hky}{1 + hu}$$

Now the Jacobian Matrix is given by

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

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

$$J^{*}(\mathcal{E}_{1}) = \begin{bmatrix} \frac{1}{1+hd_{1}+h\beta v} & 0 & 0\\ \frac{h\beta v}{1+ha} & \frac{1}{1+ha} & \frac{h\beta x}{1+ha}\\ 0 & \frac{hk}{1+hu} & \frac{1}{1+hu} \end{bmatrix}$$

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

$$\lambda_{1} = \frac{1}{1 + hd_{1} + h\beta v} < 1$$
$$\lambda_{2} = \frac{1}{1 + ha} < 1$$
$$\lambda_{3} = \frac{1}{1 + hu} < 1$$
Lemma3.1[12]

For the quadratic equation $\lambda^2 - A\lambda + B = 0$, $|\lambda_i| < 1, i = 1, 2$; iff the following conditions are satisfied: (1) 1 - A + B > 0(2) 1 + A + B > 0(3) B < 1

Numerical Experiments



Fig.10. NSFD Method (DFE), h = 10



Fig.12. NSFD Method (EE), h = 10





RESULTS AND DISCUSSION

The model of transmission dynamics of Hepatitis B virus disease consumes introduced expending PSITModel. (i.e Threatened, 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 unqualifiedlyconstant Non-Standard Finite Difference (NSFD) structure aimed at the incessant dynamical system. The suggestedstructure existsdynamical consistant, numerically steady and holds all the authentic assets of the incessant model. The outcomesequaled 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 constructedNSFD scheme for every assessment usedto residues convergent.

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