Non-Standard Finite Difference Modeling for Transmission Dynamics of Dengue Fever

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Abstract-Mathematical models have been widely used in various areas of infectious disease epidemiology. In this paper, the transmission dynamics of a vector borne infectious disease "Dengue Fever" has been analyzed numerically. An unconditionally convergent numerical scheme has been constructed for the model for Dengue Fever and numerical experiments are performed for different values of discretization parameter '*l*'. Results are compared with well-known numerical method i.e. Runge-Kutta method of order four (RK4). Unlike Rk4 which fails for large time steps, the developed scheme gives results that converged to true steady states for any time step used.

Keywords:Dengue Fever, Infectious Diseases, Transmission Dynamics, Runge-Kutta method of order 4,NSFD, Convergence

I. Introduction

Infectious diseases play a vital role in population dynamics and are responsible for ¼ of all human deaths [I- ii].Being the second largest cause of debilitation and premature death to large portions of the human population, infectious diseases lead to serious social-economic concerns [iii-v].

An infectious disease due to dengue virus is dengue fever. Dengue fever is estimated to have an effect on more than one hundred million people in over 100 countries of the world, so it has become a grand public health issue [vi]. This virus contains four serotypes known as DEN-1, DEN-2, DEN-3 and DEN-4. All of the four serotypes occur in many areas of Asian and European countries. Biting of an infected female Aedes mosquito to a human caused the transmission of these viruses to the human. Since the mosquito breed in water, so dengue fever mainly occurs in municipal and semi municipal areas around the world [x].

The following is the variety of illness of dengue ranges from gentle infection to brutal fatal infection.

- Dengue Fever (DF)
- Dengue Hemorrhagic Fever (DHF)
- Dengue Shock Syndrome (DSS).

If a person is infected by one serotype, it gives permanent protection to him against that serotype only. The person is still temporarily or partially secured from other three viruses. The person nowbecomes more favorable to brutal fatal infection and may catch other three viruses within few months [xi].

II. Mathematical Model

A. Assumptions

- Constant population of both human and mosquito.
- Infection by one DEN virus gives lifelong protection from that virus only but an object become more susceptible to other three viruses, this leads to omit the recovered compartment.
- First assumption leads to third assumption taking the birth rate of human and mosquito population equal to their death rate.

B. Parameters used in the Model

S_H = Number of susceptible human population

I_H = Number of infected human population

S_V = Number of susceptible mosquito population

I_V = Number of infected mosquito population

$A = \mu_V N_V$ = The recruitment rate of mosquito population

m = The number of other animals that the mosquitos can feed on

N_H = Number of human population

N_V = Number of mosqito population

b = Biting rate of mosquitos

μ_V = Death rate of mosquitos

r_H = Recovery rate of human population

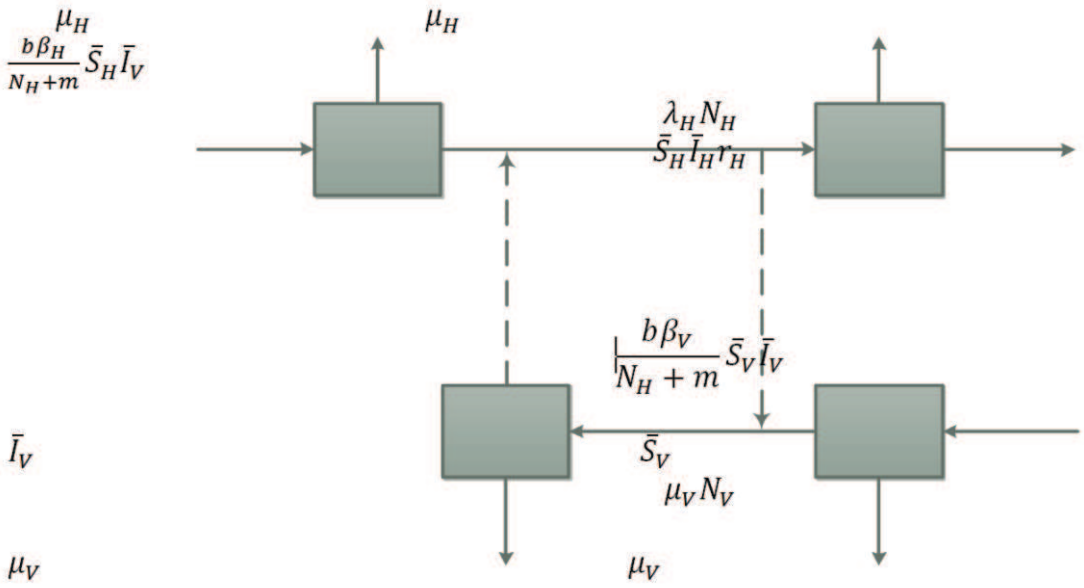

Fig. 1. shows the compartmental diagram of transmission of dengue disease [x].

There are two compartments for each human population and mosquito population described below,

- Susceptible human compartment ($\bar{S}_H$)
- Infected human compartment($\bar{I}_H$)
- Susceptible mosquito compartment ($\bar{S}_V$)
- Infected mosquito compartment ($\bar{I}_V$)

The flow chart above leads to the following differential equations with the consideration of given assumptions[x].

$$\begin{aligned}
\frac{d\bar{S}_H}{dt} &= \lambda_H N_H - \frac{b\beta_H}{N_H + m}\bar{S}_H\bar{I}_V - \mu_H\bar{S}_H \\
\frac{d\bar{I}_H}{dt} &= \frac{b\beta_H}{N_H + m}\bar{S}_H\bar{I}_V - (\mu_H + r_H)\bar{I}_H \\
\frac{d\bar{S}_V}{dt} &= A - \frac{b\beta_V}{N_H + m}\bar{S}_V\bar{I}_V - \mu_V\bar{S}_V \\
\frac{d\bar{I}_V}{dt} &= \frac{b\beta_V}{N_H + m}\bar{S}_V\bar{I}_V - \mu_V\bar{I}_V
\end{aligned} \quad (1)$$

With two conditions: $N_H = \bar{S}_H + \bar{I}_H, N_V = \bar{S}_V + \bar{I}_V$

Mosquito population is taken to be constant so the third equation can be omitted $\bar{S}_V = N_V - \bar{I}_V$. With the omission of third equation we are left with only three variables as $\bar{S}_H, \bar{I}_H, \bar{I}_V$.

Normalizing the model will lead new variables define as $S_H = \frac{\bar{S}_H}{N_H}$, $I_H = \frac{\bar{I}_H}{N_H}, S_V = \frac{\bar{S}_V}{N_V} = \frac{\bar{S}_V}{A/\mu_V}$

$$I_V = \frac{\bar{I}_V}{N_V} = \frac{\bar{I}_V}{A/\mu_V}$$

As death rate = birth rate, so $\lambda_H = \mu_H, \lambda_V = \mu_V$

As $A = \lambda_V N_V = \mu_V N_V$ or $N_V = \frac{A}{\mu_V}$

Utilizing all the information Eq. 1 will reduce to Eq. 2 as:

$$\begin{aligned}
\frac{dS_H}{dt} &= \mu_H(1 - S_H) - \frac{Ab\beta_H}{\mu_V(N_H + m)}S_H I_V \\
\frac{dI_H}{dt} &= \frac{Ab\beta_H}{\mu_V(N_H + m)}S_H I_V - (\mu_H + r_H)I_H \\
\frac{dI_V}{dt} &= \frac{b\beta_V N_H}{N_H + m}(1 - I_V)I_H - \mu_V I_V
\end{aligned} \quad (2)$$

2.3 Equilibrium Points

Equilibrium points are of two types described below.

A. Disease Free equilibrium (DFE)

When the disease will no longer persist within a population; there will be no infected vector and human, so the total population is considered as susceptible. Thus we have

$I_H = 0, I_V = 0$ *and* $S_H = 1$. Thus point when the disease will die out is $E_0(1, 0, 0)$.

$$(S_H^*, I_H^*, I_V^*) = \left(\frac{\beta + M}{\beta + MR_0}, \frac{R_0 - 1}{\beta + MR_0}, \frac{\beta[R_0 - 1]}{R_0[M + \beta]}\right)$$

Where

$$M = \frac{\mu_H + r_H}{\mu_H}, \beta = \frac{b\beta_V N_H}{\mu_V(N_H + m)}, R_0 = \frac{Ab^2\beta_H\beta_V N_H}{\mu_V^2(\mu_H + r_H)(N_H + m)^2}$$

III. Numerical Model

In order to construct numerical model, time $(t \geq 0)$ will be taken at the points $t_n = nl$ for $n = 0, 1, 2, 3, \ldots\ldots$ where l is taken as step size of time and is constant. Solution of Eq. 2 at the point t_n are $S_H(t_n), I_H(t_n), I_V(t_n)$.

In numerical method, the solution at the same point t_n will be denoted by S_H^n, I_H^n, I_V^n respectively

First we make approximation to $\frac{dS_H}{dt}$, $\frac{dI_H}{dt}$ and $\frac{dI_V}{dt}$ using first order forward differences [vii]:

$$\frac{dS_H(t)}{dt} = \frac{1}{l}[S_H(t+l) - S_H(t)] + O(l) \text{ as } l \to 0 \text{ and } t = t_n$$

$$\frac{dI_H(t)}{dt} = \frac{1}{l}[I_H(t+l) - I_H(t)] + O(l) \text{ as } l \to 0 \text{ and } t = t_n$$

$$\frac{dI_V(t)}{dt} = \frac{1}{l}[I_V(t+l) - S_V(t)] + O(l) \text{ as } l \to 0 \text{ and } t = t_n$$

Using these approximations to the derivatives and non-local approximations [viii, ix]for non-linear terms, system (2) can be written as:

$$\frac{1}{l}(S_H^{n+1} - S_H^n) = \mu_H(1 - S_H^{n+1}) - \frac{Ab\beta_H}{\mu_V(N_H+m)} S_H^{n+1} I_V^n$$

$$\frac{1}{l}(I_H^{n+1} - I_H^n) = \frac{Ab\beta_H}{\mu_V(N_H+m)} S_H^{n+1} I_V^n - (\mu_H + r_H) I_H^{n+1}$$

$$\frac{1}{l}(I_V^{n+1} - I_V^n) = \frac{b\beta_V N_H}{N_H+m}(1 - I_V^{n+1}) I_H^{n+1} - \mu_V I_V^{n+1}$$

Solving the above equations for $\frac{dS_H}{dt}$, $\frac{dI_H}{dt}$ and $\frac{dI_V}{dt}$ we have:

$$S_H^{n+1} = \frac{(\mu_H\, l + S_H^n)}{\left(1 + \mu_H\, l + \frac{Abl\beta_H}{\mu_V(N_H+m)} I_V^n\right)} \quad (3)$$

$$I_H^{n+1} = \frac{\left[\frac{Abl\beta_H}{\mu_V(N_H+m)} S_H^{n+1} I_V^n + I_H^n\right]}{(1 + l\mu_H + lr_H)} \quad (4)$$

$$I_V^{n+1} = \frac{\left(\frac{bl\beta_V N_H}{N_H+m} I_H^{n+1} + I_V^n\right)}{\left(1 + \frac{bl\beta_V N_H}{N_H+m} I_H^{n+1} + l\mu_V\right)} \quad (5)$$

The discrete system given by Eq. (3) and (5) is the proposed Non-Standard Finite Difference (NSFD) scheme for the continuous model (2).

IV. Convergence Analysis

In this section we shall discuss the convergence of proposed numerical model. Let us consider

$$F_1(S_H, I_H, I_V) = \frac{(\mu_H\, l + S_H)}{\left(1 + \mu_H\, l + \frac{Abl\beta_H}{\mu_V(N_H+m)} I_V\right)}, F_2(S_H, I_H, I_V) = \frac{\left[\frac{Abl\beta_H}{\mu_V(N_H+m)} S_H I_V + I_H\right]}{(1 + l\mu_H + lr_H)}$$

$$F_3(S_H, I_H, I_V) = \frac{\left(\frac{bl\beta_V N_H}{N_H+m} I_H + I_V\right)}{\left(1 + \frac{bl\beta_V N_H}{N_H+m} I_H + l\mu_V\right)}$$

The Jacobian for this system is:

$$J(S_H, I_H, I_V) = \begin{bmatrix} \frac{\partial F_1}{\partial S_H} & \frac{\partial F_1}{\partial I_H} & \frac{\partial F_1}{\partial I_V} \\ \frac{\partial F_2}{\partial S_H} & \frac{\partial F_2}{\partial I_H} & \frac{\partial F_2}{\partial I_V} \\ \frac{\partial F_3}{\partial S_H} & \frac{\partial F_3}{\partial I_H} & \frac{\partial F_3}{\partial I_V} \end{bmatrix}$$

The numerical scheme (3)-(5) will converge to a fixed point of the system if and only if absolute value of each eigenvalue of the jacobian matrix is less than unity at that point i.e $|\lambda_i| < 1, i = 1,2,3.$

The Jacobian matrixat disease free equilibrium point $(S_H, I_H, I_V) = (1,0,0)$ is given by:

$$J(1,0,0) = \begin{bmatrix} \frac{1}{1+l\mu_H} & 0 & -\frac{Abl\beta_H}{\mu_V(1+l\mu_H)(N_H+m)} \\ 0 & \frac{1}{1+l\mu_H+lr_H} & \frac{Abl\beta_H}{\mu_V(1+l\mu_H+lr_H)(N_H+m)} \\ 0 & \frac{bl\beta_V N_H}{(1+l\mu_V)(N_H+m)} & \frac{1}{1+l\mu_V} \end{bmatrix}$$

$\lambda_1 = \frac{1}{1+l\mu_H} < 1.$ The remaining two eigenvalues are given by the matrix:

$$J^* = \begin{bmatrix} \frac{1}{1+l\mu_H+lr_H} & \frac{Abl\beta_H}{\mu_V(1+l\mu_H+lr_H)(N_H+m)} \\ \frac{bl\beta_V N_H}{(1+l\mu_V)(N_H+m)} & \frac{1}{1+l\mu_V} \end{bmatrix}$$

To calculate the eigenvalues of J^* we will use the following lemma:

A. Lemma:[2] *For the quadratic equation* $\lambda^2 - \lambda A + B = 0$ *both roots satisfy* $|\lambda_i| < 1, i = 1,2$ *if and only if the following conditions are satisfied:*

1. $1 - A + B > 0$
2. $1 + A + B > 0$
3. $B < 1$

Let us define $A = TraceJ^*, B = DetJ^*$.Therefore

$$A = \frac{2 + l(\mu_H + r_H + \mu_V)}{(1+l\mu_V)(1+l\mu_H+lr_H)} > 0$$

$$B = \frac{1}{(1+l\mu_V)(1+l\mu_H+lr_H)} - \frac{Ab^2 l^2 \beta_H \beta_V N_H}{\mu_V(1+l\mu_V)(1+l\mu_H+lr_H)(N_H+m)^2}$$

$$B = \frac{1 - R_0 l^2 \mu_V(\mu_H + r_H)}{(1+l\mu_V)(1+l\mu_H+lr_H)} < 1 \text{ if } R_0 < 1$$

$$\Rightarrow B < 1 \quad (6i)$$

$$1 + A + B = 1 + \frac{2 + l(\mu_H + r_H + \mu_V)}{(1+l\mu_V)(1+l\mu_H+lr_H)}$$

$$+\frac{1-R_0 l^2 \mu_V(\mu_H+r_H)}{(1+l\mu_V)(1+l\mu_H+lr_H)}$$

$$=\frac{4+2l(\mu_H+r_H+\mu_V)+l^2\mu_V(\mu_H+r_H)[1-R_0]}{(1+l\mu_V)(1+l\mu_H+lr_H)}>0 \text{if } R_0<1$$

$$\Rightarrow 1-A+B>0 \quad (6ii)$$

Now for

$$1-A+B=1-\frac{2+l(\mu_H+r_H+\mu_V)}{(1+l\mu_V)(1+l\mu_H+lr_H)}$$

$$+\frac{1-R_0 l^2 \mu_V(\mu_H+r_H)}{(1+l\mu_V)(1+l\mu_H+lr_H)}$$

$$=\frac{l^2\mu_V(\mu_H+r_H)[1-R_0]}{(1+l\mu_V)(1+l\mu_H+lr_H)}>0 \text{if } R_0<1$$

$$\Rightarrow 1-A+B>0 \quad (6iii)$$

From (*6i*), (*6ii*) *and* (*6iii*) we see that the conditions for the above Lemma hold. Then the absolute value of both eigenvalues of J^* is less than 1, for every value of the step size *'l'*, when $R_0 < 1$. Therefore the proposed NSFD scheme (3)-(5) will converge unconditionally from any starting values S_H^0, I_H^0 *and* I_V^0 to the disease free equilibrium point whenever $R_0 < 1$, for any $l > 0$.

V. Numerical Experiments

Numerical experiments are performed using values of parameters given in Table I[x]:

TABLE I

Parameters	Values
A	400(DFE)
A	5000(EE)
μ_V	$0.2500\ day^{-1}$
μ_H	$\frac{1}{60\times 365}\ day^{-1}$
r_H	$0.1428\ day^{-1}$
β_H	0.7500
β_V	1.0000
N_H	10,000
m	0
b	$0.5000\ day^{-1}$

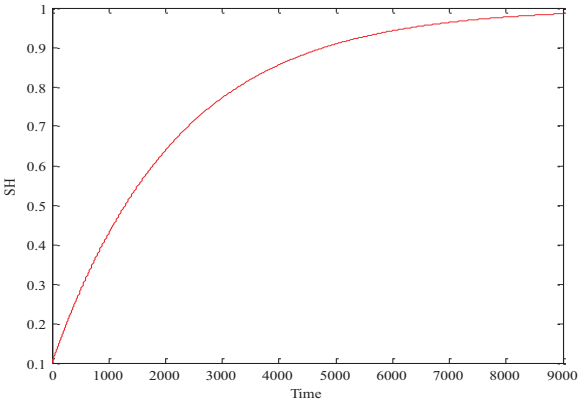

Fig. 2.1 Susceptible Human Fraction-DFE

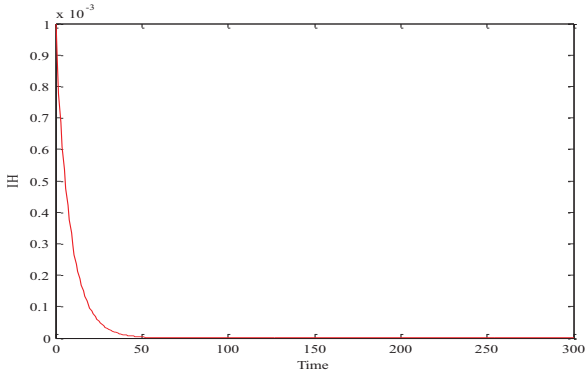

Fig. 2.2 Infected Human Fraction-DFE

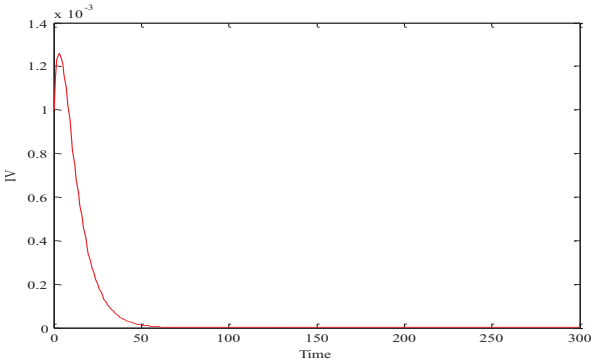

Fig. 2.3 Infected Vector Fraction-DFE

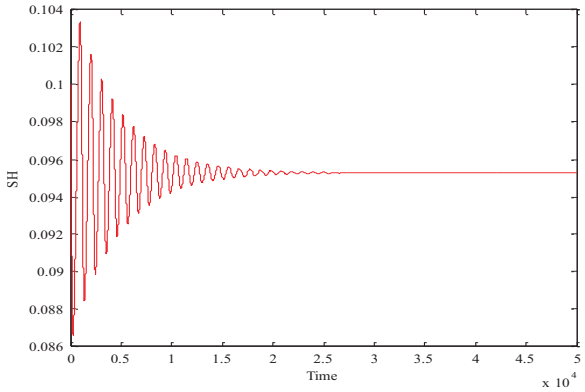

Fig. 2.4 Susceptible Human Fraction-EE

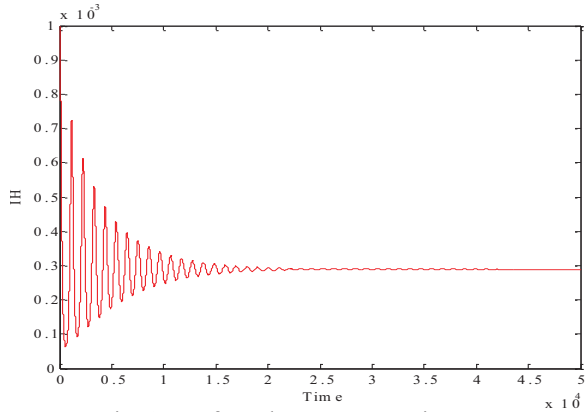

Fig. 2.5 Infected Human Fraction-EE

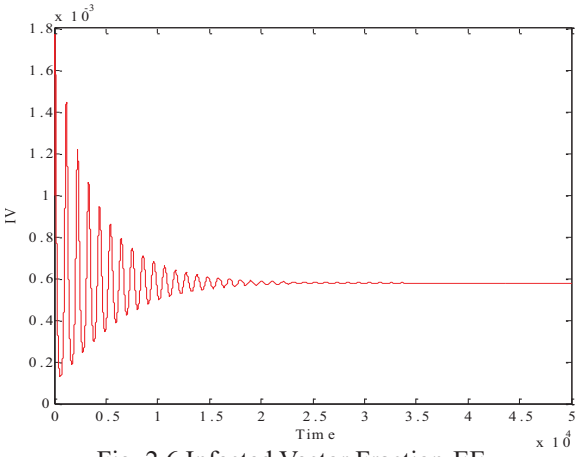

Fig. 2.6 Infected Vector Fraction-EE

I. Results and Discussion

A Non-Standard Finite Difference (NSFD) numerical model has been constructed for the continuous model and numerical experiments are performed for different values of discretizationparameter *l*. Results are compared with well known numerical method i.e. Runge-Kutta method of order four (RK4).Observations are listed in Table II.

TABLE II

	RK-4	NSFD
1	Convergence	Convergence
10	Divergence(method failed)	Convergence
100	Divergence	Convergence
1000	Divergence	Convergence

Table II shows that the Rk4 method converge for a small value of parameter *l* and it diverges for the large values but proposed NSFD scheme will remain convergent even for a very large value of discretization parameter i.e. $l = 1000$.

VII. Conclusions

An unconditionally convergent numerical scheme has been developed for the transmission dynamics of Dengue Fever. Unlike Rk4 which fails for large time steps, the developed scheme gives results that converged to true steady states for any time step used. The scheme is numerically stable, dynamically consistent and shows a good agreement with analytic results produced in [x].

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