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Nonstandard finite difference method for solving the multi-strain TB model

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ABSTRACT

In this paper, numerical studies for the mathematical model of tuberculosis (TB), that incorporates three strains, i.e., drug - sensitive, emerging multi - drug resistant(MDR) and extensively drug - resistant (XDR), are presented. Special class of numerical methods, known as nonstandard finite difference method (NSFDM) is introduced to solve this model. Numerical stability analysis of fixed points are studied. The obtained results by NSFDM are compared with other known numerical methods such as implicit Euler method and fourth-order Runge–Kutta method (RK4). It is concluded that NSFD scheme preserves the positivity of the solution and numerical stability in larger region than the other methods.

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1. Introduction

Tuberculosis (TB) is an important international public health issue. It is spread through the air when people who have an active TB an infection cough, sneeze, or transmit respiratory fluids through the air. Only approximately 10% of people infected with mycobacterium tuberculosis develop active TB disease, whereas approximately 90% of infected people remain latent. Latently infected TB people are asymptomatic and do not transmit TB, but may progress to active TB through either endogenous reactivation or exogenous reinfection, for more details (see [1–3]), and the references cited therein.

On other hand, mathematical models are quite important and efficient tool to describe and investigate several problems in natural sciences disciplines such as biology, physics, weather science and many other fields [4,5]. Numerical simulations are sometimes the only way to solve these mathematical models or to derive the desired information out of it. The accuracy of these numerical solutions is a major factor to consider while deciding on which numerical method is to be used in solving a mathematical model. Several papers considered modeling TB, see [6–11], but the model considered here includes several factors of spreading TB such as the fast infection, the exogenous reinfection and secondary infection along with the resistance factor. In the case when the secondary infection generated by an infected individual is below the unity, very strong and important mathematical results on the global stability of the disease-free equilibrium and the existence of the backward bifurcation phenomena are proven for the model, see [12]. In this case, we use these results to validate NSFD numerical scheme. Moreover, we developed and compared the obtained results with other well known numerical methods such as implicit Euler and RK4 methods. When the secondary infection generated by an infected individual exceeds one, there are no analytical results proved for the model, such as the existence and stability of the endemic equilibrium (*EE*). In this case, we use the developed NSFD numerical scheme to approximate the endemic solution numerically and investigate its stability. Furthermore, with the help of the NSFD method, we answer the following question: Given the data provided by the World Health Organization (2012) on the current parameters corresponding to the propagation of the TB in Egypt. What would be the required rate of treatment to achieve in order to control the disease?. The proposed method showed its superiority in preserving the positivity (compared to the other numerical methods considered in this work) of the state

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Table 1
All variables in the system (1)–(8) and their definition.

Variable	Definition
$S(t)$	The susceptible population ,individuals who have never encountered TB.
$L_s(t)$	The individuals infected with the drug-sensitive TB strain but who are in a latent stage, *i.e.*, who are neither showing symptoms nor infecting others.
$L_m(t)$	Individuals latently infected with MDR - TB.
$L_x(t)$	Individuals latently infected with XDR - TB.
$I_s(t)$	Individuals infected with the drug-sensitive TB strain who are infectious to others (and most likely, showing symptoms as well).
$I_m(t)$	Those individuals who are infectious with the MDR - TB strain.
$I_x(t)$	Individuals who infectious with the XDR - TB strain.
$R(t)$	Those individuals for whom treatment was successful.
$N(t)$	The total population . $N = S + L_s + L_m + L_x + I_s + I_m + I_x + R$.

variables of the systems under study. This is an essential requirement when simulating systems especially those arising in biology. Apart from the works mentioned in, some more research in this field can be found in [13–16]. We will present different numerical simulations to test whether our solutions are dynamically consistent with the solution of the continuous mathematical model. In addition, these simulations allow us to compare the constructed NSFD scheme with implicit Euler, and RK4 methods to show that the NSFD scheme preserves numerical stability in larger regions for the same time step size.

This paper is organized as follows: In Section 2, the mathematical model and the stability analysis of the model are presented. In Section 3, the construction of NSFD scheme is introduced. In Section 4, the stability and convergence properties of the proposed method is presented. In Section 5, numerical results and numerical simulations are presented to test the numerical stability of NSFD scheme. Finally, in Section 6, conclusions.

2. Mathematical model

In this section, we introduce a multi-strain TB model which is given in [12], this model incorporates three strains: drug sensitive, MDR, XDR. The population of interest is divided into eight compartments, see Table 1. The adopted model is described by a system of nonlinear ODEs as follows:

$$\dot{S} = b - dS - \beta_s \frac{SI_s}{N} - \beta_m \frac{SI_m}{N} - \beta_x \frac{SI_x}{N}, \tag{1}$$

$$\dot{L_s} = \lambda_s \beta_s \frac{SI_s}{N} + \sigma_s \lambda_s \beta_s \frac{RI_s}{N} - \alpha_{ss} \beta_s \frac{L_s I_s}{N} - \alpha_{sm} \beta_m \frac{L_s I_m}{N} - \alpha_{sx} \beta_x \frac{L_s I_x}{N} + \gamma_s I_s - (d + \varepsilon_s + t_{1s}) L_s, \tag{2}$$

$$\dot{L_m} = \lambda_m \beta_m \frac{SI_m}{N} + \sigma_m \lambda_m \beta_m \frac{RI_m}{N} + \alpha_{sm} \beta_m \lambda_m \frac{L_s I_m}{N} - \alpha_{mm} \beta_m \frac{L_m I_m}{N} - \alpha_{mx} \beta_x \frac{L_m I_x}{N} + \gamma_m I_m - (d + \varepsilon_m) L_m + (1 - P_1) t_{1s} L_s + (1 - P_2) t_{2s} I_s, \tag{3}$$

$$\dot{L_x} = \lambda_x \beta_x \frac{SI_x}{N} + \sigma_x \lambda_x \beta_x \frac{RI_x}{N} + \alpha_{sx} \beta_x \lambda_x \frac{L_s I_x}{N} + \alpha_{mx} \beta_x \lambda_x \frac{L_m I_x}{N} - \alpha_{xx} \beta_x \frac{L_x I_x}{N} - (d + \varepsilon_x) L_x + \gamma_x I_x + (1 - P_3) t_{2m} I_m, \tag{4}$$

$$\dot{I_s} = \alpha_{ss} \beta_s \frac{L_s I_s}{N} + (1 - \lambda_s) \beta_s \left(\frac{SI_s}{N} + \sigma_s \frac{RI_s}{N} \right) + \varepsilon_s L_s - (d + \delta_s + t_{2s} + \gamma_s) I_s, \tag{5}$$

$$\dot{I_m} = \alpha_{mm} \beta_m \frac{L_m I_m}{N} + (1 - \lambda_m) \beta_m \left(\frac{SI_m}{N} + \sigma_m \frac{RI_m}{N} + \alpha_{sm} \frac{L_s I_m}{N} \right) + \varepsilon_m L_m - (d + \delta_m + t_{2m} + \gamma_m) I_m, \tag{6}$$

$$\dot{I_x} = \alpha_{xx} \beta_x \frac{L_x I_x}{N} + (1 - \lambda_x) \beta_x \left(\frac{SI_x}{N} + \sigma_x \frac{RI_x}{N} + \alpha_{sx} \frac{L_s I_x}{N} + \alpha_{mx} \frac{L_m I_x}{N} \right) + \varepsilon_x L_x - (d + \delta_x + t_{2x} + \gamma_x) I_x, \tag{7}$$

$$\dot{R} = P_1 t_{1s} L_s + P_2 t_{2s} I_s + P_3 t_{2m} I_m + t_{2x} I_x - \sigma_s \beta_s \frac{RI_s}{N} - \sigma_m \beta_m \frac{RI_m}{N} - \sigma_x \beta_x \frac{RI_x}{N} - dR. \tag{8}$$

All variables in above system and their definition in Table 1, and all parameters and their interpretation in Table 2.

2.1. The basic reproduction number R_0

Definition 2.1. The basic reproduction number [17], denoted R_0, is the expected number of secondary cases produced, in a completely susceptible population, by a typical infective individual. If $R_0 < 1$, then on average an infected individual produces less than one new infected individual over the course of his infectious period, and the infection cannot grow. Conversely, if $R_0 > 1$, then each infected individual produces, on average, more than one new infection, and the disease can invade the population.

The basic reproduction number R_0 for the system (1)–(8) is given by [12]:

$$R_0 = max(R_{0s}, R_{0m}, R_{0x}), \quad where \tag{9}$$

$$R_{0s} = \frac{\beta_s(\varepsilon_s + (1 - \lambda_s)(d + t_{1s}))}{(\varepsilon_s + d + t_{1s})(t_{2s} + \delta_s + d) + \gamma_s(t_{1s} + d)},$$

$$R_{0m} = \frac{\beta_m(\varepsilon_m + (1 - \lambda_m)d)}{(\varepsilon_m + d)(t_{2m} + \delta_m + d) + d\gamma_m},$$

$$R_{0x} = \frac{\beta_x(\varepsilon_x + (1 - \lambda_x)d)}{(\varepsilon_x + d)(t_{2x} + \delta_x + d) + d\gamma_x}.$$

2.2. Some mathematical tools

Proposition 2.1. *[12] Given non negative initial conditions, solutions to (1)–(8) are bounded for all $t \geq 0$. Furthermore, the closed set*

$$C = \left\{ (S, L_s, L_m, L_x, I_s, I_m, I_x, R) \in \mathbf{R}^8_+ : S + L_s + L_m + L_x + I_s + I_m + I_x + R \leq \frac{b}{d} \right\},$$

is attracts of (1)–(8) for any initial condition belongs to R^8_+.

Theorem 2.1. *[12] Assume that:*

$$0 \leq \alpha_{ss} \leq (1 - \lambda_s), \quad 0 \leq \alpha_{mm} \leq (1 - \lambda_m), \quad 0 \leq \alpha_{xx} \leq (1 - \lambda_x).$$

Table 2
All parameters in the system (1)–(8) and their interpretation.

Parameter	Interpretation
b	Birth/recruitment rate
d	Per capita natural death rate
	Disease dynamics
β_r	Transmission coefficient for strain r
λ_r	Proportion of newly infected individuals developing *LTBI* with strain r
$1-\lambda_r$	Proportion of newly infected individuals progressing to active TB with strain r due to fast infection
ε_r	Per capita rate of endogenous reactivation of L_r
α_{r1}, α_{r2}	Proportion of exogenous reinfection of L_{r1} due to contact with I_{r2}
γ_r	Per capita rate of natural recovery to the latent stage L_r
δ_r	Per capita rate of death due to*TB* of strain r
	Treatment related
t_{1s}	Per capita rate of treatment for L_s
t_{2r}	Per capita rate of treatment for I_r. Note that t_{2x} is the rate of successful treatment of I_x, $r \in \{x, m, s\}$
$1-\sigma_r$	Efficiency of treatment in preventing infection with strain r
P_1	Probability of treatment success for L_s
P_2	Probability of treatment success for I_s
P_3	Probability of treatment success for I_m

Then the disease-free equilibrium is globally asymptotically stable when $R_0 < 1$ and endemic equilibria is locally asymptotically stable when $R_0 > 1$.

Theorem 2.2. *[18] Let us consider the nonlinear system $\varphi(X_{t+1}) = X_t$, where, $\varphi : \mathbb{R}^n \longrightarrow \mathbb{R}^n$, is a C^1 diffeomorphism with a fixed point X^*. Then a steady-state equilibria X^*, is locally (asymptotically) stable if and only if the module of all eigenvalues of the Jacobian matrix, $J(X^*)$, are smaller than one.*

Definition 2.2. [19] The finite-difference method is called unconditionally positive, if for any value of the step-size h and $Z(0) \in \mathbb{R}^n_+$ its solution remains positive, i.e., $Z_n \in \mathbb{R}^n_+$, for $n = 1, 2, 3, \cdots$.

3. Construction of NSFD scheme

In this section, we construct the proposed scheme for the systems (1)–(8). The main idea of this scheme is to obtain unconditionally stability and positivity in the variables representing the subpopulations $S(t)$, $L_s(t)$, $L_m(t)$, $L_x(t)$, $I_s(t)$, $I_m(t)$, $I_x(t)$ and $R(t)$. The first motivation is important since large time step sizes can be used, saving computational cost when integrating over long time periods. The second motivation is important due to the fact that variables representing subpopulation must never take negative values [20].

Definition 3.1. A numerical scheme is called NSFD discretization if at least one of the following conditions are satisfied :

1. The nonlocal approximation is used.
2. The discretization of the derivative is not traditional and uses a nonnegative function [21,24].

For the construction of the numerical scheme, discretization of system (1)–(8) are made based on the approximations of temporal derivatives by a generalized forward scheme of first order. Hence, if $f(t) \in C^1(\mathbf{R})$, let us define its derivative as follows:

$$\frac{df(t)}{dt} = \frac{f(t+h) - f(t)}{\varphi(h)} + O(\varphi(h)), \ as \quad h \to 0, \tag{10}$$

where $\varphi(h)$ is a real-valued function on $\mathbb{R}$. In our work, we will also make use of denominator functions which are little complex functions of the time step-size than the classical one [22].

Remark 1. If the denominator function is different than h,with the use of nonlocal approximation the scheme is called NSFD-II.

Remark 2. If the denominator function is h, and only uses nonlocal approximation the scheme is called nonstandard finite difference method NSFD-I.

In addition to this replacement, if there are nonlinear terms such as $\frac{y(t)x(t)}{N(t)}$ in the differential equation, these are replaced by $\frac{y(t+h)x(t)}{N(t)}$ or $\frac{x(t+h)y(t)}{N(t)}$, for more details see [23,24].

Let us denote by S^n, L^n_s, L^n_m, L^n_x, I^n_s, I^n_m, I^n_x and R^n the values of the approximations of $S(nh)$, $L_s(nh)$, $L_m(nh)$, $L_x(nh)$, $I_s(nh)$, $I_m(nh)$, $I_x(nh)$ and $R(nh)$ respectively, for $n = 0, 1, 2, \cdots$ and h is the timestep of the scheme. The sequences S^n, L^n_s, L^n_m , L^n_x , I^n_s, I^n_m, I^n_x and R^n should be nonnegative in order to be consistent with the biological nature of the model [25].

3.1. NSFD-II discretization

We apply Micken's scheme by replacing the step-size h by functions $\varphi_i(h)$, $i = 1, 2, 3, \ldots .8$ and use nonlocal representations for the function terms. Let us discretize the system (1)–(8) as following :

$$\frac{S^{n+1} - S^n}{\varphi_1(h)} = b - dS^{n+1} - \beta_s \frac{S^{n+1} I^n_s}{N^n} - \beta_m \frac{S^{n+1} I^n_m}{N^n} - \beta_x \frac{S^{n+1} I^n_x}{N^n}, \tag{11}$$

$$\begin{aligned}\frac{L^{n+1}_s - L^n_s}{\varphi_2(h)} &= \lambda_s \beta_s \frac{S^{n+1} I^n_s}{N^n} + \sigma_s \lambda_s \beta_s \frac{R^{n+1} I^n_s}{N^n} + \gamma_s I^n_s - \alpha_{ss} \beta_s \frac{L^{n+1}_s I^n_s}{N^n} \\ &\quad - \alpha_{sm} \beta_m \frac{L^{n+1}_s I^n_m}{N^n} - \alpha_{sx} \beta_x \frac{L^{n+1}_s I^n_x}{N^n} - (d + \varepsilon_s + t_{1s}) L^{n+1}_s, \end{aligned} \tag{12}$$

$$\begin{aligned}\frac{L^{n+1}_m - L^n_m}{\varphi_3(h)} &= \lambda_m \beta_m \frac{S^{n+1} I^n_m}{N^n} + \sigma_m \lambda_m \beta_m \frac{R^{n+1} I^n_m}{N^n} + \lambda_m \alpha_{sm} \beta_m \frac{L^{n+1}_s I^n_m}{N^n} + \gamma_m I^n_m \\ &\quad - \alpha_{mm} \beta_m \frac{L^{n+1}_m I^n_m}{N^n} + (1 - P_1) t_{1s} L^{n+1}_s + (1 - P_2) t_{2s} I^n_s \\ &\quad - \alpha_{mx} \beta_x \frac{L^{n+1}_m I^n_x}{N^n} - (d + \varepsilon_m) L^{n+1}_m, \end{aligned} \tag{13}$$

$$\begin{aligned}\frac{L^{n+1}_x - L^n_x}{\varphi_4(h)} &= \lambda_x \beta_x \frac{S^{n+1} I^n_x}{N^n} + \sigma_x \lambda_x \beta_x \frac{R^{n+1} I^n_x}{N^n} \\ &\quad + \lambda_x \alpha_{sx} \beta_x \frac{L^{n+1}_s I^n_x}{N^n} + \lambda_x \alpha_{mx} \beta_x \frac{L^{n+1}_m I^n_x}{N^n} \\ &\quad + (1 - P_3) t_{2m} I^n_m + \gamma_x I^n_x - \alpha_{xx} \beta_x \frac{L^{n+1}_x I^n_x}{N^n} - (d + \varepsilon_x) L^{n+1}_x, \end{aligned} \tag{14}$$

Table 3
All parameters in the system (1)–(8) and the reference of the parameters.

Parameter	Value	Reference
b	3190	Assumed
d	0.38	[26]
$\beta_s = \beta_m = \beta_x$	14	[26]
$\lambda_s = \lambda_m = \lambda_x$	0.5	Assumed
$\varepsilon_s = \varepsilon_m = \varepsilon_x$	0.5	Assumed
$\alpha_{r1,\,r2}$	0.05	Assumed
$\gamma_s = \gamma_m = \gamma_x$	0.3	Assumed
t_{1s}	0.88	[26]
t_{2r}: $r \in (s,\, m,\, x)$	$t_{2s} = 0.88$; $t_{2m} = t_{2x} = 0.034$	[26]
σ_r	0.25	[26]
P_r	0.88	[26]
δ_r	0.045	[26]

$$\frac{I_s^{n+1}-I_s^n}{\varphi_5(h)} = \alpha_{ss}\beta_s\frac{L_s^{n+1}I_s^n}{N^n} + (1-\lambda_s)\beta_s\left(\frac{S^{n+1}I_s^n}{N^n} + \sigma_s\frac{R^{n+1}I_s^n}{N^n}\right) + \varepsilon_s L_s^{n+1} - (d+\delta_s)I_s^{n+1} - (\gamma_s + t_{2s})I_s^n, \tag{15}$$

$$\frac{I_m^{n+1}-I_m^n}{\varphi_6(h)} = \alpha_{mm}\beta_m\frac{L_m^{n+1}I_m^n}{N^n} + (1-\lambda_m)\beta_m\left(\frac{S^{n+1}I_m^n}{N^n} + \sigma_m\frac{R^{n+1}I_m^n}{N^n} + \alpha_{sm}\frac{L_s^{n+1}I_m^n}{N^n}\right) + \varepsilon_m L_m^{n+1} - (d+\delta_m)I_m^{n+1} - (\gamma_m + t_{2m})I_m^n, \tag{16}$$

$$\frac{I_x^{n+1}-I_x^n}{\varphi_7(h)} = \alpha_{xx}\beta_x\frac{L_x^{n+1}I_x^n}{N^n} + (1-\lambda_x)\beta_m\left(\frac{S^{n+1}I_x^n}{N^n} + \sigma_x\frac{R^{n+1}I_x^n}{N^n} + \alpha_{mx}\frac{L_x^{n+1}I_m^n}{N^n}\right) + \varepsilon_x L_x^{n+1} - (d+\delta_x)I_x^{n+1} - (\gamma_x + t_{2x})I_x^n, \tag{17}$$

$$\frac{R^{n+1}-R^n}{\varphi_8(h)} = P_1 t_{1s}L_s^{n+1} + P_2 t_{2s}I_s^n + P_3 t_{2m}I_m^n + t_{2x}I_x^n - dR^{n+1} - \sigma_s\beta_s\frac{R^{n+1}I_s^n}{N^n} - \sigma_m\beta_m\frac{R^{n+1}I_m^n}{N^n} - \sigma_x\beta_x\frac{R^{n+1}I_x^n}{N^n}. \tag{18}$$

The discretizations for $N(t)$ is given as:

$$N^n = S^n + L_s^n + L_m^n + L_x^n + I_s^n + I_m^n + I_x^n + R^n.$$

Where, the nonlocal approximations are used for the nonlinear terms and the following denominator functions are used:

$$\varphi_1(h) = \frac{e^{dh}-1}{d}, \quad \varphi_2(h) = \frac{e^{(d+\varepsilon_s+t_{1s})h}-1}{(d+\varepsilon_s+t_{1s})}, \quad \varphi_3(h) = \frac{e^{(d+\varepsilon_m)h}-1}{(d+\varepsilon_m)},$$
$$\varphi_4(h) = \frac{e^{(d+\varepsilon_x)h}-1}{(d+\varepsilon_x)}, \quad \varphi_5(h) = \frac{1-e^{-(d+\delta_s)h}}{(\gamma_s+t_{2s})}, \quad \varphi_6(h) = \frac{1-e^{-(d+\delta_m)h}}{(\gamma_m+t_{2m})},$$
$$\varphi_7(h) = \frac{1-e^{-(d+\delta_x)h}}{(\gamma_x+t_{2x})}, \quad \varphi_8(h) = \frac{e^{dh}-1}{d}.$$

Then we obtain:

$$S^{n+1} = \frac{S^n + \varphi_1(h)b}{1 + \varphi_1(h)d + \varphi_1(h)\frac{\beta_s I_s^n + \beta_m I_m^n + \beta_x I_x^n}{N^n}}, \tag{19}$$

$$L_s^{n+1} = \frac{L_s^n + \varphi_2(h)\frac{\beta_s I_s^n}{N^n}\lambda_s(S^{n+1} + \sigma_s R^{n+1}) + \varphi_2(h)\gamma_s I_s^n}{1 + \varphi_2(h)(d + t_{1s} + \varepsilon_s) + \frac{\varphi_2(h)}{N^n}(\alpha_{ss}\beta_s I_s^n + \alpha_{sm}\beta_m I_m^n + \alpha_{sx}\beta_x I_x)}, \tag{20}$$

$$L_m^{n+1} = \frac{L_m^n + \varphi_3(h)\frac{\beta_m\lambda_m I_m^n}{N^n}(S^{n+1} + \sigma_m R^{n+1} + \alpha_{sm}L_s^{n+1}) + \varphi_3(h)t_{1s}L_s^{n+1}(1-P_1)}{1 + \varphi_3(h)(d+\varepsilon_m) + \frac{\varphi_3(h)}{N^n}(\alpha_{mm}\beta_m I_m^n + \alpha_{mx}\beta_x I_x^n)} + \frac{\varphi_3(h)\gamma_m I_m^n + \varphi_3(h)t_{2s}I_s^n(1-P_2)}{1 + \varphi_3(h)(d+\varepsilon_m) + \frac{\varphi_3(h)}{N^n}(\alpha_{mm}\beta_m I_m^n + \alpha_{mx}\beta_x I_x^n)}, \tag{21}$$

Table 4
The spectral radii of the Jacobian matrix corresponding to the free disease point of NSFD-II when $B_s = B_m = B_x = 0.1$ and $R_0 < 1$.

h	ρ(NSFD-II)
0.05	0.9812 (Convergent)
0.1	0.9627 (Convergent)
1	0.7108 (Convergent)
100	0.5459 (Convergent)

Table 5
The spectral radii of the Jacobian matrix corresponding to the endemic equilibria of NSFD-II when $B_s = B_m = B_x = 14$ and $R_0 > 1$.

h	ρ(NSFD-II)
0.05	0.9939 (Convergent)
0.1	0.9823 (Convergent)
1	0.8947 (Convergent)
100	0.8190 (Convergent)

$$L_x^{n+1} = \frac{L_x^n + \varphi_4(h)\frac{\beta_x\lambda_x I_x^n}{N^n}(S^{n+1} + \sigma_x R^{n+1} + \alpha_{sx}L_s^{n+1} + \alpha_{mx}L_m^{n+1}) + \varphi_4(h)\gamma_x I_x^n}{1 + \varphi_4(h)(d+\varepsilon_x) + \frac{\varphi_4(h)}{N^n}(\alpha_{xx}\beta_x I_x^n)} + \frac{\varphi_4(h)t_{2m}I_m^n(1-P_3)}{1 + \varphi_4(h)(d+\varepsilon_x) + \frac{\varphi_4(h)}{N^n}(\alpha_{xx}\beta_x I_x^n)}, \tag{22}$$

$$I_s^{n+1} = \frac{\varphi_5(h)\beta_s\frac{I_s^n}{N^n}(\alpha_{ss}L_s^{n+1} + (1-\lambda_s)(S^{n+1} + \sigma_s R^{n+1})) + (1-\varphi_5(h)(t_{2s}+\gamma_s))I_s^n}{1 + \varphi_5(h)(d+\delta_s)} + \frac{\varphi_5(h)\varepsilon_s L_s^{n+1}}{1 + \varphi_5(h)(d+\delta_s)}, \tag{23}$$

$$I_m^{n+1} = \frac{\varphi_6(h)\beta_m\frac{I_m^n}{N^n}(\alpha_{mm}L_m^{n+1} + (1-\lambda_m)(S^{n+1} + \sigma_m R^{n+1} + \alpha_{sm}L_s^{n+1}))}{1 + \varphi_6(h)(d+\delta_m)} + \frac{(1-\varphi_6(h)(t_{2m}+\gamma_m))I_m^n + \varphi_6(h)\varepsilon_m L_m^{n+1}}{1 + \varphi_6(h)(d+\delta_m)}, \tag{24}$$

$$I_x^{n+1} = \frac{\varphi_7(h)\beta_x\frac{I_x^n}{N^n}(\alpha_{xx}L_x^{n+1} + (1-\lambda_x)(S^{n+1} + \sigma_x R^{n+1} + \alpha_{sx}L_s^{n+1} + \alpha_{mx}L_m^{n+1}))}{1 + \varphi_7(h)(d+\delta_x)} + \frac{(1-\varphi_7(h)(t_{2x}+\gamma_x))I_x^n + \varphi_7(h)\varepsilon_x L_x^{n+1}}{1 + \varphi_7(h)(d+\delta_x)}, \tag{25}$$

$$R^{n+1} = \frac{R^n + \varphi_8(h)t_{1s}P_1L_s^{n+1} + \varphi_8(h)P_2t_{2s}I_s^n + \varphi_8(h)t_{2m}P_3I_m^n + \varphi_8(h)t_{2x}I_x^n}{1 + \varphi_8(h)d + \frac{\varphi_8(h)}{N^n}(\sigma_s\beta_s I_s^n + \sigma_m\beta_m I_m^n + \sigma_x\beta_x I_x^n)}. \tag{26}$$

The positivity of the solution reflects from the above method because if the initial conditions $S(0)$, $L_s(0)$, $L_m(0)$, $L_x(0)$, $I_s(0)$, $I_m(0)$, $I_x(0)$ and $R(0)$ are non-negative, then the right hand side of equations (19)–(26) admit no negative terms for any of n = 0, 1, 2, 3, ..., because $0 < \varphi_5(h)(\gamma_s + t_{2s}) < 1$, $0 < \varphi_6(h)(\gamma_m + t_{2m}) < 1$, $0 < \varphi_7(h)(\gamma_x + t_{2x}) < 1$, $0 < P_i < 1$, $i = 1, 2, 3$, $0 < \lambda_i < 1$, $i \in \{s, m, x\}$.

4. Fixed points and stability analysis

In this section, we study the stability and convergence properties of fixed points of the proposed NSFD-II. Let us consider X^*, to be the fixed point of the system (11)–(18), then it will take the form:

$$X^* = (\hat{S}, \hat{L_s}, \hat{L_m}, \hat{L_x}, \hat{I_s}, \hat{I_m}, \hat{I_x}, \hat{R}).$$

By noting that the fixed point X^*, of the (11)–(18) can be found by solving:

Table 6
Result obtained by different numerical methods for $B_s = B_m = B_x = 0.1$, $R_0 < 1$, and initial condition as (5000, 50, 50, 50, 30, 30, 30, 60) with different time step size.

h	Implicit Euler	RK4	NSFD-I	NSFD-II
0.01	Convergent	Convergent	Convergent	Convergent
0.1	Convergent	Convergent	Convergent	Convergent
0.5	Divergent	Convergent	Convergent	Convergent
3	Divergent	Divergent	Convergent	Convergent
10	Divergent	Divergent	Divergent	Convergent
100	Divergent	Divergent	Divergent	Convergent

Table 7
Results obtained by different numerical methods for $B_s = B_m = B_x = 14$, $R_0 > 1$ and initial condition as (5000, 50, 50, 50, 30, 30, 30, 60) with different time step size.

h	Implicit Euler	RK4	NSFD-I	NSFD-II
0.01	Convergent	Convergent	Convergent	Convergent
0.1	Convergent	Convergent	Convergent	Convergent
1	Divergent	Divergent	Convergent	Convergent
20	Divergent	Divergent	Divergent	Convergent
100	Divergent	Divergent	Divergent	Convergent

$$
\begin{aligned}
f_1(\hat{S},\hat{L_s},\hat{L_m},\hat{L_x},\hat{I_s},\hat{I_m},\hat{I_x},\hat{R}) &= \hat{S}, \quad & f_2(\hat{S},\hat{L_s},\hat{L_m},\hat{L_x},\hat{I_s},\hat{I_m},\hat{I_x},\hat{R}) &= \hat{L_s},\\
f_3(\hat{S},\hat{L_s},\hat{L_m},\hat{L_x},\hat{I_s},\hat{I_m},\hat{I_x},\hat{R}) &= \hat{L_m}, \quad & f_4(\hat{S},\hat{L_s},\hat{L_m},\hat{L_x},\hat{I_s},\hat{I_m},\hat{I_x},\hat{R}) &= \hat{L_x},\\
f_5(\hat{S},\hat{L_s},\hat{L_m},\hat{L_x},\hat{I_s},\hat{I_m},\hat{I_x},\hat{R}) &= \hat{I_s}, \quad & f_6(\hat{S},\hat{L_s},\hat{L_m},\hat{L_x},\hat{I_s},\hat{I_m},\hat{I_x},\hat{R}) &= \hat{I_m},\\
f_7(\hat{S},\hat{L_s},\hat{L_m},\hat{L_x},\hat{I_s},\hat{I_m},\hat{I_x},\hat{R}) &= \hat{I_x}, \quad & f_8(\hat{S},\hat{L_s},\hat{L_m},\hat{L_x},\hat{I_s},\hat{I_m},\hat{I_x},\hat{R}) &= \hat{R}.
\end{aligned}
$$

Where $f_i(\hat{S},\hat{L_s},\hat{L_m},\hat{L_x},\hat{I_s},\hat{I_m},\hat{I_x},\hat{R}),\ \ i = 1,2,3,\cdots,8$, can be obtained by considering the right hand sides of equations (19)–(26), i.e.,

$$
\begin{aligned}
&f_1(\hat{S},\hat{L_s},\hat{L_m},\hat{L_x},\hat{I_s},\hat{I_m},\hat{I_x},\hat{R})\\
&= \frac{\hat{S}+\varphi_1(h)b}{1+\varphi_1(h)d+\varphi_1(h)\frac{\beta_s\hat{I_s}+\beta_m\hat{I_m}+\beta_x\hat{I_x}}{\hat{N}}},
\end{aligned}
\tag{27}
$$

$$
\begin{aligned}
&f_2(\hat{S},\hat{L_s},\hat{L_m},\hat{L_x},\hat{I_s},\hat{I_m},\hat{I_x},\hat{R})\\
&= \frac{\hat{L_s}+\varphi_2(h)\frac{\beta_s\hat{I_s}}{\hat{N}}\lambda_s(\hat{S}+\sigma_s\hat{R})+\varphi_2(h)\gamma_s\hat{I_s}}{1+\varphi_2(h)(d+t_{1s}+\varepsilon_s)+\frac{\varphi_2(h)}{\hat{N}}(\alpha_{ss}\beta_s\hat{I_s}+\alpha_{sm}\beta_m\hat{I_m}+\alpha_{sx}\beta_x\hat{I_x})},
\end{aligned}
\tag{28}
$$

$$
\begin{aligned}
&f_3(\hat{S},\hat{L_s},\hat{L_m},\hat{L_x},\hat{I_s},\hat{I_m},\hat{I_x},\hat{R})\\
&= \frac{\hat{L_m}+\varphi_3(h)\frac{\beta_m\lambda_m\hat{I_m}}{\hat{N}^n}(\hat{S}+\sigma_m\hat{R}+\alpha_{sm}\hat{L_s})+\varphi_3(h)\gamma_m\hat{I_m}}{1+\varphi_3(h)(d+\varepsilon_m)+\frac{\varphi_3(h)}{\hat{N}}(\alpha_{mm}\beta_m\hat{I_m}+\alpha_{mx}\beta_x\hat{I_x})}\\
&\quad+\frac{\varphi_3(h)t_{1s}\hat{L_s}(1-P_1)+\varphi_3(h)t_{2s}\hat{I_s}(1-P_2)}{1+\varphi_3(h)(d+\varepsilon_m)+\frac{\varphi_3(h)}{\hat{N}}(\alpha_{mm}\beta_m\hat{I_m}+\alpha_{mx}\beta_x\hat{I_x})},
\end{aligned}
\tag{29}
$$

$$
\begin{aligned}
&f_4(\hat{S},\hat{L_s},\hat{L_m},\hat{L_x},\hat{I_s},\hat{I_m},\hat{I_x},\hat{R})\\
&= \frac{\hat{L_x}+\varphi_4(h)\frac{\beta_x\lambda_x\hat{I_x}}{\hat{N}^n}(\hat{S}+\sigma_x\hat{R}+\alpha_{sx}\hat{L_s}+\alpha_{mx}\hat{L_m})}{1+\varphi_4(h)(d+\varepsilon_x)+\frac{\varphi_4(h)}{\hat{N}}(\alpha_{xx}\beta_x\hat{I_x})}\\
&\quad+\frac{\varphi_4(h)\gamma_x\hat{I_x}+\varphi_4(h)t_{2m}\hat{I_m}(1-P_3)}{1+\varphi_4(h)(d+\varepsilon_x)+\frac{\varphi_4(h)}{\hat{N}}(\alpha_{xx}\beta_x\hat{I_x})},
\end{aligned}
\tag{30}
$$

$$
\begin{aligned}
&f_5(\hat{S},\hat{L_s},\hat{L_m},\hat{L_x},\hat{I_s},\hat{I_m},\hat{I_x},\hat{R})\\
&= \frac{\varphi_5(h)\beta_s\frac{\hat{I_s}}{\hat{N}}(\alpha_{ss}\hat{L_s}+(1-\lambda_s)(\hat{S}+\sigma_s\hat{R}))}{1+\varphi_5(h)(d+\delta_s)}\\
&\quad+\frac{(1-\varphi_5(h)(t_{2s}+\gamma_s))\hat{I_s}+\varphi_5(h)\varepsilon_s\hat{L_s}}{1+\varphi_5(h)(d+\delta_s)},
\end{aligned}
\tag{31}
$$

$$
\begin{aligned}
&f_6(\hat{S},\hat{L_s},\hat{L_m},\hat{L_x},\hat{I_s},\hat{I_m},\hat{I_x},\hat{R})\\
&= \frac{\varphi_6(h)\beta_m\frac{\hat{I_m}}{\hat{N}}(\alpha_{mm}\hat{L_m}+(1-\lambda_m)(\hat{S}+\sigma_m\hat{R}+\alpha_{sm}\hat{L_s}))}{1+\varphi_6(h)(d+\delta_m)}\\
&\quad+\frac{(1-\varphi_6(h)(t_{2m}+\gamma_m))\hat{I_m}+\varphi_6(h)\varepsilon_m\hat{L_m}}{1+\varphi_6(h)(d+\delta_m)},
\end{aligned}
\tag{32}
$$

$$
\begin{aligned}
&f_7(\hat{S},\hat{L_s},\hat{L_m},\hat{L_x},\hat{I_s},\hat{I_m},\hat{I_x},\hat{R})\\
&= \frac{\varphi_7(h)\beta_x\frac{\hat{I_x}}{\hat{N}}(\alpha_{xx}\hat{L_x}+(1-\lambda_x)(\hat{S}+\sigma_x\hat{R}+\alpha_{sx}\hat{L_s}+\alpha_{mx}\hat{L_m}))}{1+\varphi_7(h)(d+\delta_x)}\\
&\quad+\frac{(1-\varphi_7(h)(t_{2x}+\gamma_x))\hat{I_x}+\varphi_7(h)\varepsilon_x\hat{L_x}}{1+\varphi_7(h)(d+\delta_x)},
\end{aligned}
\tag{33}
$$

$$
\begin{aligned}
&f_8(\hat{S},\hat{L_s},\hat{L_m},\hat{L_x},\hat{I_s},\hat{I_m},\hat{I_x},\hat{R})\\
&= \frac{\hat{R}+\varphi_8(h)t_{1s}P_1\hat{L_s}+\varphi_8(h)P_2t_{2s}\hat{I_s}+\varphi_8(h)t_{2m}P_3\hat{I_m}}{1+\varphi_8(h)d+\frac{\varphi_8(h)}{\hat{N}}(\sigma_s\beta_s\hat{I_s}+\sigma_m\beta_m\hat{I_m}+\sigma_x\beta_x\hat{I_x})}\\
&\quad+\frac{\varphi_8(h)t_{2x}\hat{I_x}}{1+\varphi_8(h)d+\frac{\varphi_8(h)}{\hat{N}}(\sigma_s\beta_s\hat{I_s}+\sigma_m\beta_m\hat{I_m}+\sigma_x\beta_x\hat{I_x})}.
\end{aligned}
\tag{34}
$$

where,

$$\hat{N} = \hat{S}+\hat{L_s}+\hat{L_m}+\hat{L_x}+\hat{I_s}+\hat{I_m}+\hat{I_x}+\hat{R}.$$

In the above system, if $\hat{I_s}=0,\ \hat{I_m}=0,\ \hat{I_x}=0$, and given that the fixed point of different equation satisfied $f_i(X^*)=X^*, i=1,2,3,\cdots,8$, then :

$$\hat{S} = \frac{\hat{S}+\varphi_1(h)b}{1+d\varphi_1(h)} \Rightarrow \hat{S} = \frac{b}{d}, \tag{35}$$

$$\hat{L_s} = \frac{\hat{L_s}}{1+\varphi_2(h)(d+\varepsilon_s+t_{1s})} \Rightarrow \hat{L_s} = 0, \tag{36}$$

$$\hat{L_m} = \frac{\hat{L_m}}{1+\varphi_3(h)(d+\varepsilon_m)} \Rightarrow \hat{L_m} = 0, \tag{37}$$

$$\hat{L_x} = \frac{\hat{L_x}}{1+\varphi_4(h)(d+\varepsilon_s)} \Rightarrow \hat{L_x} = 0, \tag{38}$$

$$\hat{R} = \frac{\hat{R}}{1+d\varphi_8(h)} \quad \Rightarrow \hat{R} = 0. \tag{39}$$

Then the disease free equilibrium is unique and is given by $(\frac{b}{d},0,0,0,0,0,0,0)$.

If at least one of the infected variables is non-zero, then this solution correspond to the Endemic equilibrium of NSFD-II for the full model (11)–(18). Equations of system (27)–(34) are highly nonlinear in $\hat{I_s}$, $\hat{I_m}$ and $\hat{I_x}$, and hence explicit solutions are not obtainable so, we solve the system (19)–(26) numerically to obtain endemic fixed point.

4.1. Numerical stability analysis of the fixed points

In this section, let us consider the following initial condition for the multi-strain model (1)–(8):

$$
\begin{aligned}
&(S(0),L_s(0),L_m(0),L_x(0),I_s(0),I_m(0),I_x(0),R)\\
&= (5000,50,50,50,30,30,30,60).
\end{aligned}
$$

Concerning the system parameters, all the parameters are given in [26] or we assume their values as it shown in Table 3.

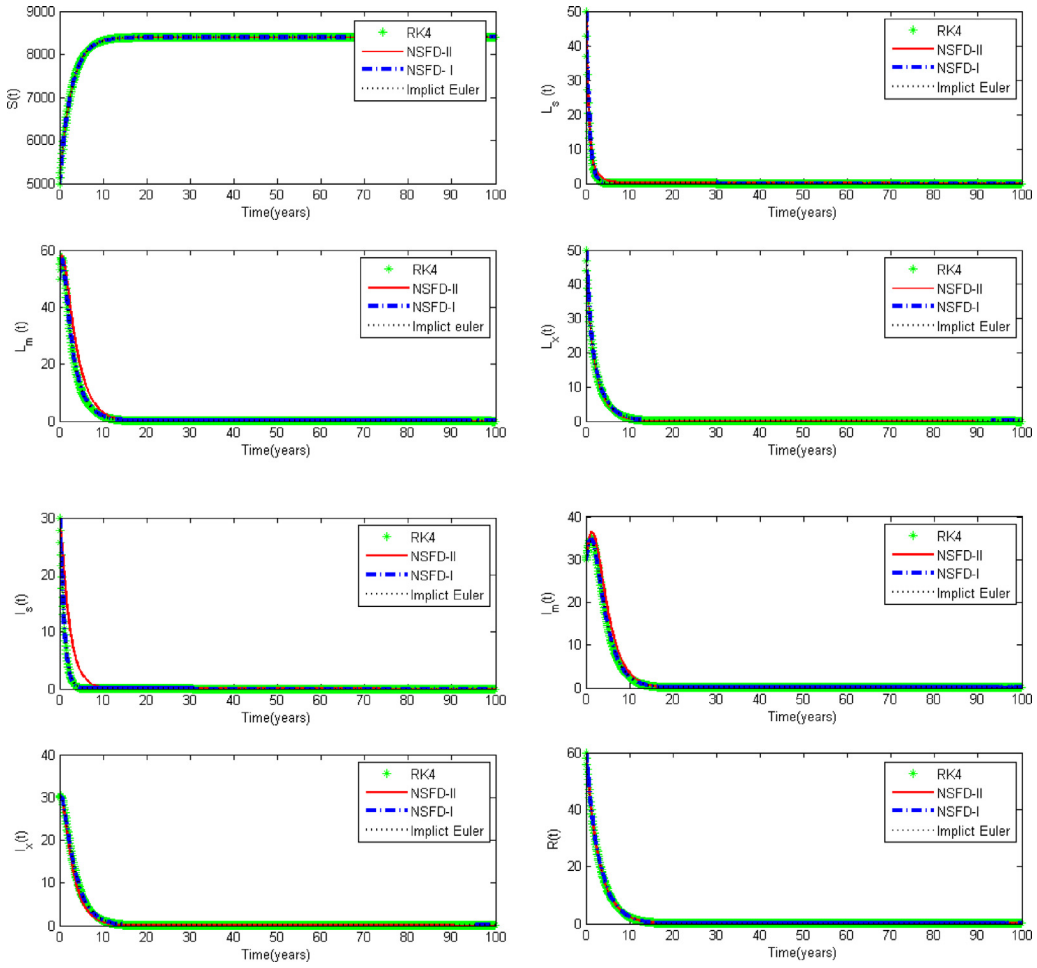

Fig. 1. Profiles obtained by different numerical methods for $h = 0.1$, when $\beta_s = \beta_m = \beta_x = 0.1$, and $R_0 < 1$.

In order to determine the stability properties of the equilibria of system (11)–(18). We calculate the Jacobian matrix of the system (11)–(18), at the disease-free equilibrium point:

$$E_0 = \left(\frac{b}{d}, 0, 0, 0, 0, 0, 0, 0\right).$$

It will take the following form:

$$J(E_0) = \begin{pmatrix} a_{11} & 0 & 0 & 0 & a_{15} & a_{16} & a_{17} & 0 \\ 0 & a_{22} & 0 & 0 & a_{25} & 0 & 0 & 0 \\ 0 & a_{32} & a_{33} & 0 & a_{35} & a_{36} & 0 & 0 \\ 0 & 0 & 0 & a_{44} & 0 & a_{46} & a_{47} & 0 \\ 0 & a_{52} & 0 & 0 & a_{55} & 0 & 0 & 0 \\ 0 & 0 & a_{63} & 0 & 0 & a_{66} & 0 & 0 \\ 0 & 0 & 0 & a_{74} & 0 & 0 & a_{77} & 0 \\ 0 & a_{82} & 0 & 0 & a_{85} & a_{86} & a_{87} & a_{88} \end{pmatrix},$$

where:

$$a_{11} = \frac{1}{1+\varphi_1(h)}, \quad a_{15} = \frac{-d\beta_s\varphi_1(h)}{b(1+\varphi_1(h))}, \quad a_{16} = \frac{-d\beta_m\varphi_1(h)}{b(1+\varphi_1(h))},$$

$$a_{17} = \frac{-d\beta_x\varphi_1(h)}{b(1+\varphi_1(h))}, \quad a_{22} = \frac{1}{(d+t_{1s}+\varepsilon_s)\varphi_2(h)},$$

$$a_{25} = \frac{(\lambda_s\beta_s+\gamma_s)\varphi_2(h)}{1+(d+\varepsilon_s)\varphi_2(h)}, \quad a_{32} = \frac{(t_{1s}-P_1t_{1s})\varphi_3(h)}{(d+\varepsilon_m)\varphi_3(h)},$$

$$a_{33} = \frac{1}{(d+\varepsilon_m)\varphi_3(h)}, \quad a_{35} = \frac{(t_{2s}-P_1t_{2s})\varphi_3(h)}{(d+\varepsilon_m)\varphi_3(h)},$$

$$a_{36} = \frac{(\lambda_m\beta_m+\gamma_m)\varphi_3(h)}{1+(d+\varepsilon_m)\varphi_3(h)}, \quad a_{44} = \frac{1}{(d+\varepsilon_x)\varphi_4(h)},$$

$$a_{46} = \frac{(t_{2m}-P_2t_{2m})\varphi_4(h)}{(d+\varepsilon_x)\varphi_4(h)}, \quad a_{47} = \frac{(\lambda_x\beta_x+\gamma_x)\varphi_4(h)}{1+(d+\varepsilon_x)\varphi_4(h)},$$

$$a_{52} = \frac{\varepsilon_s\varphi_5(h)}{(1+(d+\delta_s)\varphi_5(h)},$$

$$a_{55} = \frac{1-\varphi_5(h)(t_{2s}+\gamma_s-(1-\lambda_s)\beta_s)}{(1+(d+\delta_s)\varphi_5(h)},$$

$$a_{63} = \frac{\varepsilon_m\varphi_6(h)}{(1+(d+\delta_m)\varphi_6(h)},$$

$$a_{66} = \frac{1-\varphi_6(h)(t_{2m}+\gamma_m-(1-\lambda_m)\beta_m)}{(1+(d+\delta_m)\varphi_6(h)},$$

$$a_{74} = \frac{\varepsilon_x\varphi_7(h)}{(1+(d+\delta_x)\varphi_7(h)},$$

$$a_{77} = \frac{1-\varphi_7(h)(t_{2x}+\gamma_x-(1-\lambda_x)\beta_x)}{(1+(d+\delta_x)\varphi_7(h)}, \quad a_{82} = \frac{\varphi_8(h)P_1t_{1s}}{1+d\varphi_8(h)},$$

$$a_{85} = \frac{\varphi_8(h)P_2t_{2s}}{1+d\varphi_8(h)}, \quad a_{86} = \frac{\varphi_8(h)P_3t_{2m}}{1+d\varphi_8(h)}, \quad a_{87} = \frac{\varphi_8(h)t_{2x}}{1+d\varphi_8(h)},$$

$$a_{88} = \frac{1}{1+d\varphi_8(h)}.$$

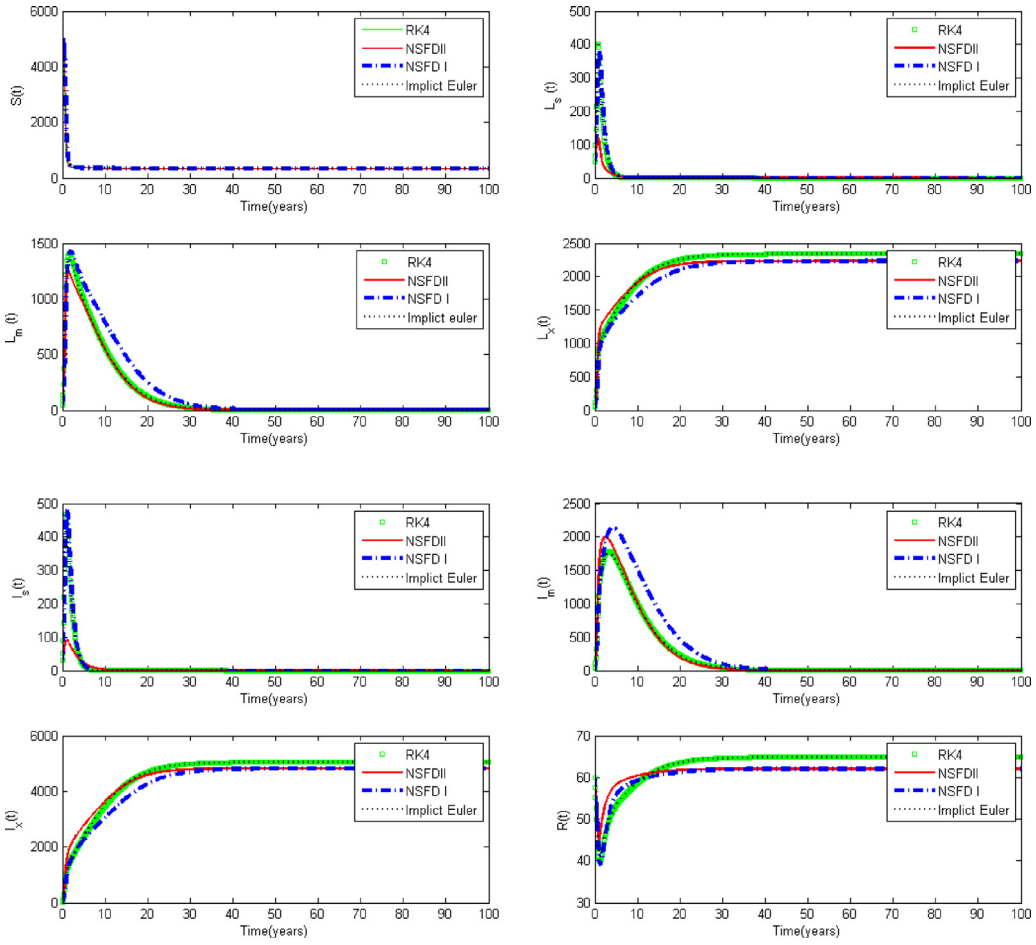

Fig. 2. Profiles obtained by different numerical methods for $h = 0.1$, when $\beta_s = \beta_m = \beta_x = 14$ and $R_0 > 1$.

The characteristic equation associated with above matrix is $|J(E_0) - \lambda I| = 0 \Rightarrow (a_{11} - \lambda)(a_{88} - \lambda)(\lambda^2 - (a_{44} + a_{77})\lambda - a_{47}a_{74} + a_{77}a_{44})(-\lambda^2 + (a_{44} + a_{66})\lambda - a_{66}a_{33} + a_{36}a_{63})(-\lambda^2 + (a_{22} + a_{55})\lambda + a_{52}a_{25} - a_{55}a_{22}) = 0$. Then the eigenvalues of Jacobian matrix are $\lambda_1 = a_{11}$, $\lambda_2 = a_{88}$, $\lambda_{3,4} = \frac{a_{44}+a_{77} \pm \sqrt{(a_{44}^2 - 2a_{44}a_{77} + a_{77}^2 + 4a_{74}a_{47})}}{2}$, $\lambda_{5,6} = \frac{a_{66}+a_{33} \pm \sqrt{(a_{66}^2 - 2a_{66}a_{33} + a_{33}^2 + 4a_{63}a_{36})}}{2}$, $\lambda_{7,8} = \frac{a_{55}+a_{22} \pm \sqrt{(a_{55}^2 - 2a_{55}a_{22} + a_{22}^2 + 4a_{52}a_{25})}}{2}$, which are all less than one if $R_0 < 1$. Thus, by Theorem 2.2, the scheme (19)–(26) is unconditionally stable if $R_0 < 1$.

However, we will determine the stability of the fixed points of the system (11)–(18) numerically. In Table 4 we report the spectral radii of the Jacobian matrix corresponding to the free disease point of NSFD-II when $B_s = B_m = B_x = 0.1$ and $R_0 < 1$.

In Table 5, we report the spectral radii of the Jacobian matrix corresponding to the endemic equilibria of NSFD-II when $B_s = B_m = B_x = 14$ and $R_0 > 1$.

It can be seen from Tables 4 and 5 that, all the spectral radii are less than one in magnitude irrespective of the time step size used in the simulations. Hence, by Theorem 2.2, we have the following result.

- The disease-free equilibrium $E_0 = (\frac{b}{d}, 0, 0, 0, 0, 0, 0, 0)$ for the system (11)–(18) when $B_s = B_m = B_x = 0.1$ and $R_0 < 1$, is unconditionally locally asymptotically stable.
- The endemic equilibrium of the system (11)–(18) when $B_s = B_m = B_x$=14, and $R_0 > 1$, is locally asymptotically stable from Theorem 2.2. Moreover, the system (11)–(18) is unconditionally locally asymptotically stable.

5. Numerical results

In this section numerical comparisons between NSFD-II method, implicit Euler, RK4 and NSFD-I methods are presented. Numerical simulations for both the disease-free equilibrium and for the endemic equilibria are presented.

5.1. Numerical simulation for the disease free equilibrium

In this section, we report the convergence behavior of numerical methods to the disease-free equilibrium. We provide the results for $B_s = B_m = B_x = 0.1$ and $R_0 < 1$. It can be seen from Fig. 1 that all numerical methods converge almost to the disease-free equilibrium. However, in Table 6, numerical comparisons between NSFD-II, implicit Euler, fourth-order Runge-Kutta and NSFD-I methods are presented. It can be concluded that NSFD-II converges to the correct disease free equilibrium for large h, and preserves the positivity of the model state variables, so NSFD-II is unconditionally positive, as we drive in the previous mathematical analysis. The other numerical methods converge to the correct disease free equilibrium for small step-size and diverge for larger h. In addition, it can be observed from Table 4 that although the spectral radii of Jacobian matrix associated with NSFD-II scheme are less than one, it seems to be unconditionally convergent to the correct disease-free steady state of the model. Moreover, the system (11)–(18) is unconditionally locally asymptotically stable.

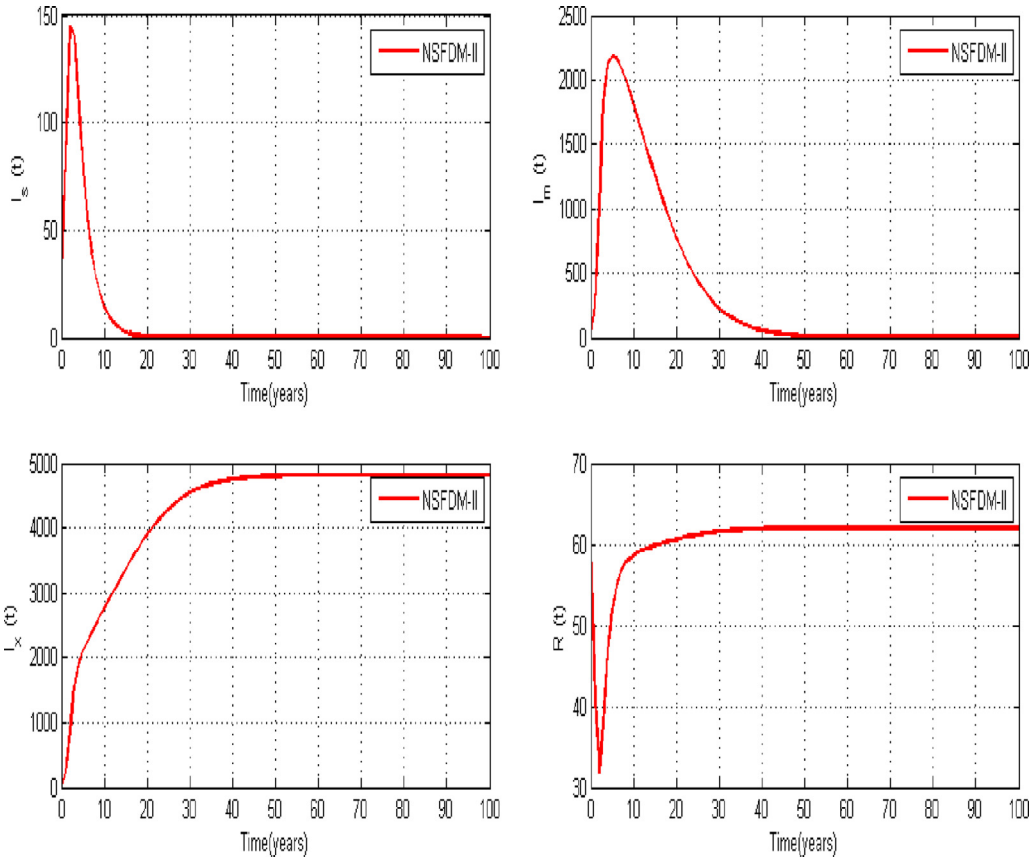

Fig. 3. Profiles obtained by NSFDM-II for h=1 when $\beta_s = \beta_m = \beta_x = 14$ and $R_0 > 1$.

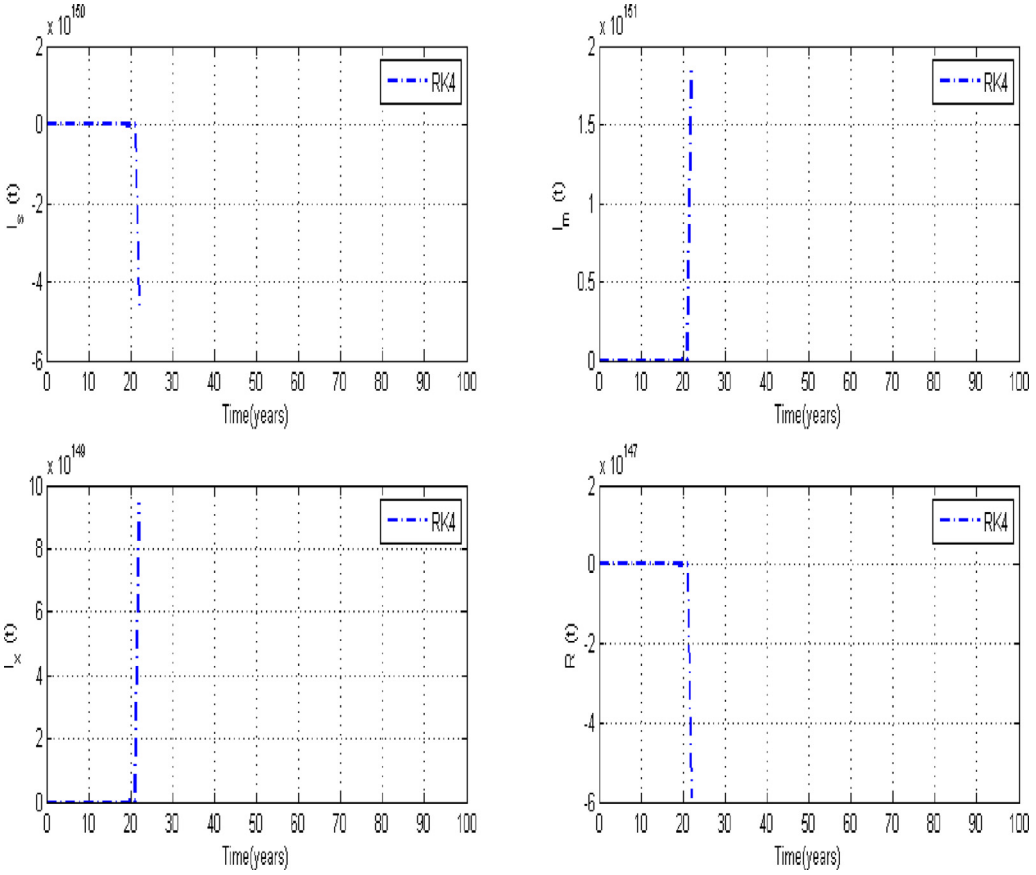

Fig. 4. Profiles obtained by RK4 method for h=1 when $\beta_s = \beta_m = \beta_x = 14$ and $R_0 > 1$.

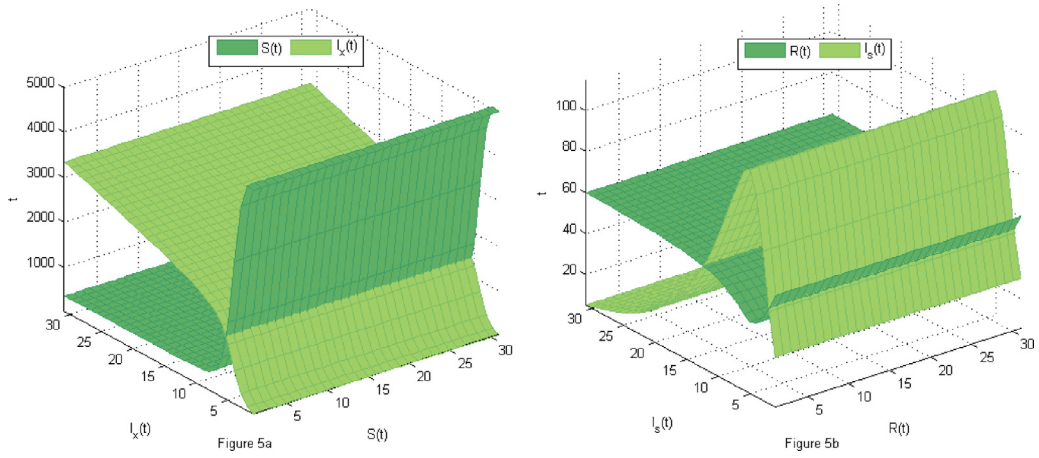

Fig. 5. The relationship between some variables of the model by using NSFD-II, when $\beta_s = \beta_m = \beta_x = 14$, $h = 0.33$ and $R_0 > 1$.

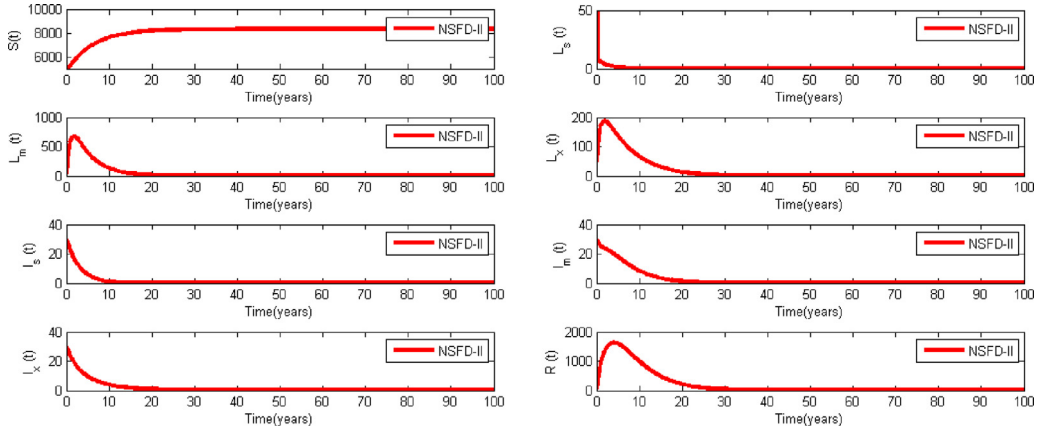

Fig. 6. Profiles obtained by NSFD-II for $h = 0.1$ when $\beta_s = \beta_m = \beta_x = 14$, $t_{2s} = t_{2m} = t_{2x} = 22$.

5.2. Numerical simulation for the endemic equilibrium

In this section, we study the convergence behavior of the numerical methods to endemic equilibria. We provide the results for $B_s = B_m = B_x = 14$ and $R_0 > 1$. It can be concluded from Fig. 2 that all numerical methods converge almost to the endemic equilibrium. However, in Table 7, numerical comparisons between NSFD-II, implicit Euler, RK4 and NSFD-I methods are presented. It can be seen that, NSFD-II converge to the correct endemic equilibrium for large h, and preserves the positivity of the model state variables see Fig. 3, so NSFD-II is unconditionally positive, supporting the previous mathematical analysis. Moreover, NSFD-II converges more accurately than other methods. The other numerical methods converge to the correct endemic equilibrium for small step-size and diverge for larger h see Fig. 4. In addition, it can be observed in Table 5, although the spectral radii of Jacobian matrix associated with NSFD-II scheme are less than one, it seems to be unconditionally convergent to the correct endemic equilibrium. Moreover, the system (11)–(18) is unconditionally locally asymptotically stable. Previous Fig. 5(a-b) illustrate propagation of TB along the time when $h = 0.33$, $B_s = B_m = B_x = 14$, $R_0 > 1$ and initial condition as (5000, 50, 50, 50, 30, 30, 30, 60), as following:

- In Fig. 5a, the relationship between $S(t)$ and $I_x(t)$, describes the spread of infection from the members of the third strain to healthy people, then the number of infectious people will be increases and the number of healthy people are decreases with time.
- In Fig. 5b, the relationship between $R(t)$ and $I_s(t)$ illustrate that, there are individuals succeeded treatment with them, may are exposed to infection again by contagious members $I_s(t)$ of the first strain. At the beginning of time period, the number of $I_s(t)$ members are increases and the number of $R(t)$ members are decreases, then after time steps the curves are intersecting again and $I_s(t)$ will be the response to treatment and their numbers will be decreased.

Moreover, from these numerical results obtained in this work we can control the disease and turn the endemic point to the disease free point as follows:

Let us consider:

$$R_{0s} < 1 \Rightarrow \frac{-t_{2s}^2 + 5.3950t_{2s} + 8.6060}{t_{2s}^2 + 1.6050t_{2s} + 1.050} < 0, \text{ where } t_{1s} = t_{2s}. \quad (40)$$

$$R_{0m} < 1 \Rightarrow \frac{9.1720 - 0.8800t_{2m}}{0.8800t_{2m} + 0.4880} < 0, \quad (41)$$

$$R_{0x} < 1 \Rightarrow \frac{9.1720 - 0.8800t_{2x}}{0.8800t_{2x} + 0.4880} < 0, \quad (42)$$

$$\text{Then } t_{1s} = t_{2s} \geq 6.6828,\ t_{2m} \geq 10.4227,\ t_{2x} \geq 10.4227. \quad (43)$$

$$T = max\{t_{2s} \geq 6.6828,\ t_{2m} \geq 10.4227,\ t_{2x} \geq 10.4227\},$$
$$\Rightarrow T = t_{2m} = t_{2x} \geq 10.4227. \quad (44)$$

So, we derive the rate of treatment required for achieving control of the disease.

For example, if we choose $t_{2s} = t_{2m} = t_{2x} = 22$, $B_s = B_m = B_x = 14$, and $h = 0.1$, by using NSFD-II we obtained the disease free point (see Fig. 6).

6. Conclusion

It can be concluded from the numerical results presented inSections 5.1 and 5.2, that NSFD-II scheme is more efficient than the well known numerical methods and preserves the positivity of the solution and numerical stability in larger regions, whereas the solutions obtained by other numerical methods experience difficulties in either preserving the positivity of the solutions or in converging to the correct equilibria for large h. All results were obtained by using MATLAB (R2013a). on a computer machine with intel(R) core $i3 - 3110M$ @ 2.40 GHz and 4 GB RAM.

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