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A nonstandard numerical scheme of predictor–corrector type for epidemic models

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ABSTRACT

In this paper we construct and develop a competitive nonstandard finite difference numerical scheme of predictor–corrector type for the classical SIR epidemic model. This proposed scheme is designed with the aim of obtaining dynamical consistency between the discrete solution and the solution of the continuous model. The nonstandard finite difference scheme with Conservation Law (NSFDCL) developed here satisfies some important properties associated with the considered SIR epidemic model, such as positivity, boundedness, monotonicity, stability and conservation of frequency of the oscillations. Numerical comparisons between the NSFDCL numerical scheme developed here and Runge–Kutta type schemes show its effectiveness.

1. Introduction

Ronald Mickens began developing numerical schemes using nonstandard finite difference (NSFD) schemes for solving physical problems such that the physical properties of the original systems (in particular stability properties) is preserved, [1–4]. In this way, several discretizations of nonlinear equations have been developed in different areas [5–12].

This methodology has been used for the construction of numerical schemes to solve ordinary differential initial value problems appearing in biology, especially in mathematical epidemiology models, in order to guarantee the positivity of the solutions [13–15]. However, as these models represent the flow of traffic between their subpopulations, it is necessary that the numerical schemes satisfy the Conservation Population Law, [3,16]. On the other hand, the NSFD schemes must preserve other properties of the continuous model for larger step sizes that some times the traditional schemes such as forward Euler, Runge–Kutta and others do not for extreme values in the parameters of the models, see [17]. In addition, in several cases the frequency of the oscillations of the solutions is not preserved by some numerical schemes when the time step size increases. Thus, in order to obtain accurate numerical schemes it is necessary to transfer essential properties of the continuous model to the discrete schemes.

The best scenario to solve accurately a mathematical model based on ordinary differential equations is when an exact difference scheme can be constructed, [1,9,2]. However, several times exact difference schemes are not easy to find, therefore it is necessary to create accurate NSFD schemes. Using this premise in [11], the authors have developed an NSFD scheme for a nonautonomous model combining the nonstandard finite difference techniques with the solution of an equivalent integral equation for the proposed model. Following these ideas, in this paper we develop an NSFD scheme of predictor–corrector type to obtain numerical solutions to an SIR epidemic model type autonomous, where we apply the "Conservation Law" in

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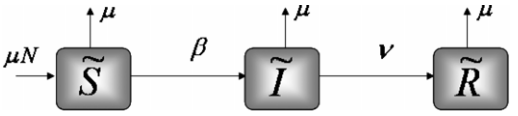

Fig. 1. Flow diagram for the SIR model.

the numerical scheme in addition to the nonlocal approximation in order to preserve the frequency of the oscillation of the solutions for time step sizes bigger than the ones proposed in [13], and the ones for the traditional Runge–Kutta schemes. In addition, the proposed NSFDCL predictor scheme preserves the local stability property of the disease free equilibrium point and allows us to compute numerically the correct endemic equilibrium point. Furthermore, this NSFDCL numerical scheme can be used with large time step sizes, saving computational costs when integrating over long time periods. This scheme has been designed with the aim of obtaining dynamical consistency between the discrete solution and the solution of the continuous model.

The organization of this paper is as follows: In Section 2 we present the continuous epidemic model SIR, with its equilibrium points and the basic reproductive number $\mathcal{R}_0$. In Section 3 an NSFDCL numerical scheme is constructed as a predictor scheme conserving the properties of the total population. Next, in Section 4 the convergence of the proposed method is studied, and in Section 5 we present a predictor–corrector type NSFD numerical scheme for larger step sizes. The numerical simulations presented in 6 show the convergence properties and performance versus other well-known schemes. Conclusions are presented in Section 7.

2. Mathematical model

In this section we present the mathematical model for the transmission of infectious diseases in populations, which is the classical SIR epidemic model as discussed in [13], where the population is divided into three classes: $\tilde{S}(t)$ susceptible at time t, $\tilde{I}(t)$ infected at time t and $\tilde{R}(t)$ recovered at time t and it is assumed that this class has acquired immunity. This SIR mathematical model was used in [18] to describe the dynamics of whooping cough epidemics in London using periodic variations in susceptibility. The flow diagram is shown in Fig. 1 and the model is given analytically by the following scaled system of ordinary differential equations:

$$\begin{aligned}
\dot{\tilde{S}}(t) &= \mu N - \mu\tilde{S}(t) - \beta\tilde{S}(t)\tilde{I}(t),\\
\dot{\tilde{I}}(t) &= \beta\tilde{S}(t)\tilde{I}(t) - (\mu+\nu)\tilde{I}(t),\\
\dot{\tilde{R}}(t) &= \nu\tilde{I}(t) - \mu\tilde{R}(t),
\end{aligned} \tag{1}$$

where

- β is the transmission coefficient,
- μ is the death rate and it is assumed equal to the birth rate,
- ν is the rate of recovery from disease and
- N is the total population.

Since the population is assumed constant, we can solve the system (1) using only the first two equations and $\tilde{R}(t)$ can be computed by means of the following equation:

$$\tilde{S}(t) + \tilde{I}(t) + \tilde{R}(t) = N. \tag{2}$$

We define Eq. (2) as the conservation law associated with the system (1). For the sake of clarity and without loss of generality we write system (1) in terms of the fraction of the population in each class by introducing the scaled population size; $S = \tilde{S}/N$, $I = \tilde{I}/N$ and $R = \tilde{R}/N$. Thus one gets:

$$\begin{aligned}
\dot{S}(t) &= \mu - \mu S(t) - N\beta S(t)I(t),\\
\dot{I}(t) &= N\beta S(t)I(t) - (\mu+\nu)I(t),\\
\dot{R}(t) &= \nu I(t) - \mu R(t).
\end{aligned} \tag{3}$$

Therefore, we define a new conservation law associated with the scaled system (3) and this equation must be satisfied by any reliable numerical scheme,

$$S(t) + I(t) + R(t) = 1. \tag{4}$$

It is important to mention that the steady states of (3) are the following points: the disease free point $(S_0^*, I_0^*, R_0^*) = (1, 0, 0)$ and the endemic point

$$(S_e^*, I_e^*, R_e^*) = \left(\frac{1}{\mathcal{R}_0}, \frac{\mu}{\mu+\nu}\left(1 - \frac{1}{\mathcal{R}_0}\right), \frac{\nu}{\mu+\nu}\left(1 - \frac{1}{\mathcal{R}_0}\right)\right),$$

where $\mathcal{R}_0 = \frac{N\beta}{\mu+\nu} > 1$ is the basic reproductive number associated with the SIR model [13].

3. Nonstandard scheme with conservation law (NSFDCL)

In this section we construct a numerical scheme to compute numerical solutions for the systems (3). The main idea behind the construction of most of the NSFDCL schemes is to obtain unconditional stability and positivity in the variables representing the subpopulations. The first motivation, unconditional stability, is important since large time step sizes can be used, saving computational costs when integrating over long time periods. The second motivation is important due to the fact that variables representing subpopulations must never take negative values. Following the ideas of Micken's, a scheme is called nonstandard if at least one of the following conditions is satisfied [5,6,19],

(1) A nonlocal approximation is used.
(2) The discretization of the derivative is not traditional and uses a nonnegative function $\psi(h) = h + \mathcal{O}(h^2)$.

For the construction of numerical schemes, the discretization of the system (3) is made based on the approximation of the temporal derivatives by the traditional forward scheme of first order and nonlocal approximation. Thus, if $f(t)$ is derivable, then $\dot{f}(t)$ it can be approximated by

$$\frac{\mathrm{d}f(t)}{\mathrm{d}t} = \frac{f(t+h) - f(t)}{h} + \mathcal{O}(h) \quad \text{as } h \longrightarrow 0. \tag{5}$$

Let us denote by S^n, I^n and R^n the approximations of $S(nh)$, $I(nh)$ and $R(nh)$, respectively, for $n = 0, 1, 2, \ldots$, and by h the time-step of the scheme. The sequences S^n, I^n and R^n should be nonnegative in order to be consistent with the biological nature of the model.

The NSFDCL numerical scheme to solve system (3) is constructed so that it satisfies the conservation law property proposed by Mickens's techniques in [3,4]. Thus, the NSFDCL scheme for system (3) takes the following form:

$$\begin{aligned}
\frac{S^{n+1} - S^n}{h} &= \mu - \mu S^{n+1} - N\beta S^{n+1} I^n, \\
\frac{I^{n+1} - I^n}{h} &= N\beta S^{n+1} I^n - (\mu + \nu) I^{n+1}, \\
\frac{R^{n+1} - R^n}{h} &= \nu I^{n+1} - \mu R^{n+1}.
\end{aligned} \tag{6}$$

Notice that this scheme uses nonlocal approximation and satisfies $\dot{S}(t) + \dot{I}(t) + \dot{R}(t) = 0$, (the total population is constant) as $n \longrightarrow \infty$ (i.e., as $h \longrightarrow 0$). Moreover, from (6) we can see that

$$S^{n+1} + I^{n+1} + R^{n+1} = \frac{h\mu + S^n + I^n + R^n}{1 + h\mu}. \tag{7}$$

Thus, if $S^n + I^n + R^n = 1$ for all $n \geq 0$, then $S^{n+1} + I^{n+1} + R^{n+1} = 1$ for all $n \geq 0$. Therefore, the conservation law property holds. Next, after rearranging the explicit formulations, we obtain the following discrete system,

$$S^{n+1} = \frac{S^n + h\mu}{1 + h\mu + hN\beta I^n}, \tag{8a}$$

$$I^{n+1} = \frac{I^n(1 + hN\beta S^{n+1})}{1 + h(\mu + \nu)}, \tag{8b}$$

$$R^{n+1} = 1 - S^{n+1} - I^{n+1}. \tag{8c}$$

Now, the positivity of the different subpopulations S^{n+1}, I^{n+1} and R^{n+1} is guaranteed if $0 < S^n < 1, 0 < I^n < 1, 0 < R^n < 1$ for all $n \geq 0$. Based on the difference system (8) we perform the respective convergence analysis of this NSFDCL scheme. In summary, it can be seen from (6) and (8) that we have constructed an NSFDCL scheme for the system (3) having the following properties:

- It satisfies the conservation law, i.e. the population is constant.
- It has positivity and boundedness: For the system (8) we have that if $0 < S^n < 1$, $0 < I^n < 1$ and $0 < R^n < 1$, then $0 < S^{n+1} < 1, 0 < I^{n+1} < 1$ and $0 < R^{n+1} < 1$, for all $n \geq 0$.

4. Convergence analysis

In this section stability and convergence properties of the proposed NSFDCL numerical scheme are studied. In order to study the convergence of the scheme (8), it is enough to only consider Eqs. (8a) and (8b). Thus, we define the following functions:

$$F_1(S, I) = \frac{h\mu + S}{1 + h\mu + hN\beta I}, \qquad F_2(S, I) = \frac{I + hN\beta I F_1(S, I)}{1 + h(\mu + \nu)}, \tag{9}$$

and we analyze the behavior of the eigenvalues of the Jacobian of the linearized scheme at the free equilibrium point and at the endemic point, i.e.,

$$J(S,I)=\begin{bmatrix}\dfrac{\partial F_1}{\partial S} & \dfrac{\partial F_1}{\partial I}\\ \dfrac{\partial F_2}{\partial S} & \dfrac{\partial F_2}{\partial I}\end{bmatrix}.$$

In this way, the scheme (8) converges to a fixed point if and only if the spectral radius at the fixed point $\rho(J)$ of the Jacobian $J(S,I)$ satisfies $\rho(J)<1$.

We denote by (S^*,I^*) an equilibrium point of system (3). Calculating $J(S,I)$ at (S^*,I^*), one gets the following matrix

$$J(S^*,I^*)=\begin{pmatrix}\dfrac{1}{1+h\mu+hN\beta I^*} & -\dfrac{(h\mu+S^*)hN\beta}{(1+h\mu+hN\beta I^*)^2}\\ \dfrac{hN\beta I^*}{1+h(\mu+\nu)}\dfrac{1}{1+h\mu+hN\beta I^*} & \dfrac{1+hN\beta F_1(S^*,I^*)-I^*\frac{(hN\beta)^2(h\mu+S^*)}{(1+h\mu+hN\beta I^*)^2}}{1+h(\mu+\nu)}\end{pmatrix}.$$

Next, we evaluate the above Jacobian at the equilibrium points.

4.1. Disease free equilibrium

At the point $(S_0^*,I_0^*)=(1,0)$, the Jacobian is given by:

$$J(1,0)=\begin{pmatrix}\dfrac{1}{1+h\mu} & -\dfrac{hN\beta}{1+h\mu}\\ 0 & \dfrac{1+hN\beta}{1+h(\mu+\nu)}\end{pmatrix}. \tag{10}$$

Therefore, if the basic reproductive number $\mathcal{R}_0<1$, i.e., $N\beta<\mu+\nu$, then the spectral radius of $J(1,0)$ is strictly less than unity for all h. Thus, if $\mathcal{R}_0<1$, from any starting values $S^0>0$, $I^0\geq 0$, $R^0\geq 0$ such that $S^0+I^0+R^0=1$ the numerical schemes (8) will converge unconditionally to the disease free equilibrium point (1, 0, 0). □

4.2. Endemic equilibrium

If $\mathcal{R}_0>1$ the model (3) has an endemic equilibrium point. Therefore, evaluating the Jacobian at the point $(S_e^*,I_e^*)=\left(\frac{1}{\mathcal{R}_0},\frac{\mu}{\mu+\nu}\left(1-\frac{1}{\mathcal{R}_0}\right)\right)$, one gets

$$J(S_e^*,I_e^*)=\begin{pmatrix}\dfrac{1}{a} & -\dfrac{d}{a^2}\\ \dfrac{c}{ab} & \dfrac{1}{b}\left(1+\dfrac{d}{a}-\dfrac{cd}{a^2}\right)\end{pmatrix},$$

where

$$\begin{aligned}a&=1+h\mu+hN\beta I^*=1+h\mu\mathcal{R}_0>1,\\ b&=1+h(\mu+\nu)=1+\frac{hN\beta}{\mathcal{R}_0}>1,\\ c&=hN\beta I^*=h\mu(\mathcal{R}_0-1)>0,\\ d&=(h\mu+S^*)hN\beta=\left(h\mu+\frac{1}{\mathcal{R}_0}\right)hN\beta>0.\end{aligned}$$

The magnitude of the two eigenvalues of $J(S_e^*,I_e^*)$, will be determined using the following lemma:

Lemma 4.1 ([20, p. 82]). *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 $A=\operatorname{Trace}J(S_e^*,I_e^*)$, $B=\operatorname{Det}J(S_e^*,I_e^*)$. Thus, $A=\frac{ab+a^2+(a-c)d}{a^2b}>0$, since $a>c$. Also, $B=\frac{a^2+ad-cd}{a^3b}+\frac{cd}{a^3b}=\frac{a+d}{a^2b}>0$. Define the function $f(\lambda)=\lambda^2-\lambda A+B$ and since $\frac{1}{a}<1$ one gets that

$$f(0) = B = \frac{1}{ab} + \frac{d}{a^2b} < \frac{1+d}{ab} = \frac{1 + h^2\mu N\beta + \frac{hN\beta}{\mathcal{R}_0}}{h\mu\mathcal{R}_0 + 1 + h^2\mu N\beta + \frac{hN\beta}{\mathcal{R}_0}} < 1, \tag{11}$$

$$f(-1) = 1 + A + B > 0. \tag{12}$$

Moreover,

$$\begin{aligned} a^2b + a + d &= 2 + \frac{2hN\beta}{\mathcal{R}_0} + 3h\mu\mathcal{R}_0 + 3h^2\mu N\beta + h^2\mu^2\mathcal{R}_0^2 + h^3\mu^2 N\beta\mathcal{R}_0 \\ &= a^2 + ab + ad. \end{aligned}$$

Thus, it follows that

$$\begin{aligned} &1 + \frac{1}{ab} + \frac{d}{a^2b} = \frac{1}{a} + \frac{1}{b} + \frac{d}{ab} > \frac{1}{a} + \frac{1}{b} + \frac{d}{ab} - \frac{cd}{a^2b}, \\ &1 + \frac{a+d}{a^2b} > \frac{ab + a^2 + (a-c)d}{a^2b}, \\ &1 + B > A. \end{aligned}$$

Therefore

$$f(1) = 1 - A + B > 0. \tag{13}$$

From (11), (12) and (13) we see that the conditions of Lemma 4.1 hold. Then, the eigenvalues of $J(S_e^*, I_e^*)$ are less than unity in modulus, irrespective of the size of h, when $\mathcal{R}_0 > 1$. It can be concluded that the NSFDCL numerical scheme (8) will converge unconditionally from any starting values $S^0 > 0$, $I^0 > 0$, $R^0 > 0$, such that $S^0 + I^0 + R^0 = 1$ to the endemic fixed point whenever $\mathcal{R}_0 > 1$, for any $h > 0$. □

5. NSFDCL scheme of predictor–corrector type (*P–C*)

In this section, we improve the NSFDCL scheme (8) using a predictor–corrector type approach. The NSFD schemes usually preserve some properties such as conservation law (total population), convergence to the equilibrium points and positivity of the population. However, if the time step size h increases to a relatively large size, some of the previous properties are lost. A special case of it occurs when the frequency of oscillation is lost from some critical step size h_c. Thus, it is necessary to construct robust numerical algorithms that reproduce approximately the solution for large step sizes h. Explicit schemes, by their use of values at the previous time step, produce larger errors in the frequency of oscillations than implicit schemes. But implicit schemes require the solution of nonlinear equations, which can be expensive. A common way to obtain the benefits of both methods is to use predictor–corrector schemes. In this section, we present a combination of two NSFDCL schemes to develop a predictor–corrector type scheme, which improves the accuracy of the numerical solutions for larger step sizes h and preserves the properties listed in the previous section. To develop this scheme, first we use the system (8) as a predictor scheme, i.e.,

$$S_p^{n+1} = \frac{S^n + h\mu}{1 + h\mu + hN\beta I^n}, \tag{14a}$$

$$I_p^{n+1} = \frac{I^n(1 + hN\beta S_p^{n+1})}{1 + h(\mu + \nu)}. \tag{14b}$$

Now, we evaluate system (3) at time $t + h$ and introduce the term $\frac{\epsilon^{-1}S^{n+1}}{h}$ (where $0 < \epsilon < 1$) as a way to accelerate the convergence of the NSFDCL scheme of predictor–corrector type. Thus, one gets the following expression:

$$\begin{aligned} &\frac{S^{n+1} - S^n}{h} = \mu - \mu S^{n+1} - N\beta S^{n+1} I^{n+1} - \frac{\epsilon^{-1}S^{n+1}}{h} + \frac{\epsilon^{-1}S^{n+1}}{h}, \\ &\frac{I^{n+1} - I^n}{h} = N\beta S^{n+1} I^{n+1} - (\mu + \nu) I^{n+1}, \\ &\frac{R^{n+1} - R^n}{h} = \nu I^{n+1} - \mu R^{n+1}, \end{aligned}$$

which is an NSFDCL scheme that satisfies the conservation law, i.e. preserves the constant population. Thus, we obtain the following corrector scheme,

$$S_c^{n+1} = \frac{S^n + h\mu + \epsilon^{-1}S_p^{n+1}}{1 + \epsilon^{-1} + h\mu + hN\beta I_p^{n+1}}, \tag{15a}$$

Table 1
Values μ and ν are expressed as rates per *year*.

Parameter	μ	ν	$N\beta$
Value	0.04	24	123

$$I_c^{n+1} = \frac{I^n + hN\beta S_c^{n+1} I_p^{n+1}}{1 + h(\mu + \nu)}, \tag{15b}$$

$$R^{n+1} = 1 - S_c^{n+1} - I_c^{n+1}. \tag{15c}$$

To compute the numerical solutions, we use the following algorithm:

Step 0. Select values: $0 < \epsilon < 1$ and, S^0, I^0, R^0 such that $S^0 + I^0 + R^0 = 1$.
Step 1. For $n = 0, 1, 2, \ldots,$ do.
Step 2. Calculate S_p^{n+1} from (14a).
Step 3. Using this value of S_p^{n+1} and I^n, calculate I_p^{n+1} from (14b).
Step 4. Correct the value S_c^{n+1}, using S^n, S_p^{n+1}, I_p^{n+1} and Eq. (15a).
Step 5. Correct the value I_c^{n+1}, using I^n, S_c^{n+1}, I_p^{n+1} and Eq. (15b).
Step 6. Calculate the value R^{n+1}, using Eq. (15c).

Note that the sequential form of calculation is a generic feature of NSFDCL schemes [3]. In addition, it can be seen that the main part of the local truncation error associated with each equation of system (8) is of order $\mathcal{O}(h^2)$, confirming that the constructed NSFDCL schemes are first order accurate. The proof of convergence to this scheme can be see in the Appendix.

6. Numerical simulations

In this section we show numerical results that illustrate the advantages of the proposed NSFDCL schemes. In order to support our theoretical results and test convergence and stability properties of the scheme, we do several numerical simulations varying the time step size. Since an exact analytic solution for the SIR epidemic mathematical model (3) is unknown, we take in the numerical comparisons as the correct solution the computational expensive 4th order Runge–Kutta scheme with a very small time step size $h = 0.005$ after checking its numerical consistency with other numerical schemes. For the parameter values of the SIR model, we used the values presented in [13], which are summarized in Table 1.

The epidemic model (3) has an asymptotically stable disease free point if $R_0 < 1$ and an endemic equilibrium point if $R_0 > 1$. In Fig. 2 for $R_0 > 1$ it can be observed that the predictor–corrector NSFDCL scheme converges to the correct endemic point and only producing positive values for all time t. However, the routines of Matlab software program with their default error tolerance did not converge or in some cases took unreal negative values for the infective population. It is important to remark that the routines with smaller error tolerances take a long computation time in comparison to the explicit NSFD schemes. Notice that the 4th order Runge–Kutta scheme with a time step size $h = 0.005$ converges to the correct endemic point, but our predictor–corrector NSFDCL scheme can use a larger time step $h = 0.01$. As can be seen in Fig. 3 the predictor–corrector NSFDCL scheme improves the accuracy of the predictor NSFDCL.

In Figs. 4 and 5, it can be seen that the numerical solutions corresponding to different schemes do not have the same oscillation frequency. However, taking the 4th order Runge–Kutta (RK4) with a small time step $h = 0.005$ as the correct solution, we can see that with a time step size $h = 0.01$ the best result is with the proposed predictor–corrector P–C scheme. On the other hand in Fig. 6, it is shown that the unconditional stable NSFD scheme proposed in [13] gives unreal positive solutions since the proportion of infectives goes beyond the total population while our predictor–corrector (P–C) scheme gives physically realistic solutions. In addition, in Fig. 7 it can be observed that the 4th order Runge–Kutta (RK4) diverge, meanwhile the predictor–corrector NSFDCL scheme converges correctly to the endemic equilibrium point using both methods with the same time step size. In this way the predictor–corrector NSFDCL scheme is competitive in terms of numerical stability.

7. Conclusion

In this paper we construct and develop a competitive nonstandard finite difference (NSFD) numerical scheme of predictor–corrector type for the classical SIR epidemic model. This model has two biological equilibrium points: one is the disease free equilibrium point F^* which is an asymptotically stable node if and only if $R_0 < 1$ and the other is the endemic equilibrium point E^*. The proposed NSFDCL scheme is designed in order to satisfy several properties as positivity, boundedness and stability. It also produces solutions with the correct frequency of oscillation. The aim was to obtain dynamical consistency between the discrete solution and the continuous model. Dynamic consistency plays an essential role in the construction of the developed nonstandard schemes as is illustrated in this study.

One important property used to construct the NSFD numerical scheme of predictor–corrector type is the "Conservation Law" proposed by Mickens [3]. Numerical comparisons between the NSFD numerical scheme developed here and

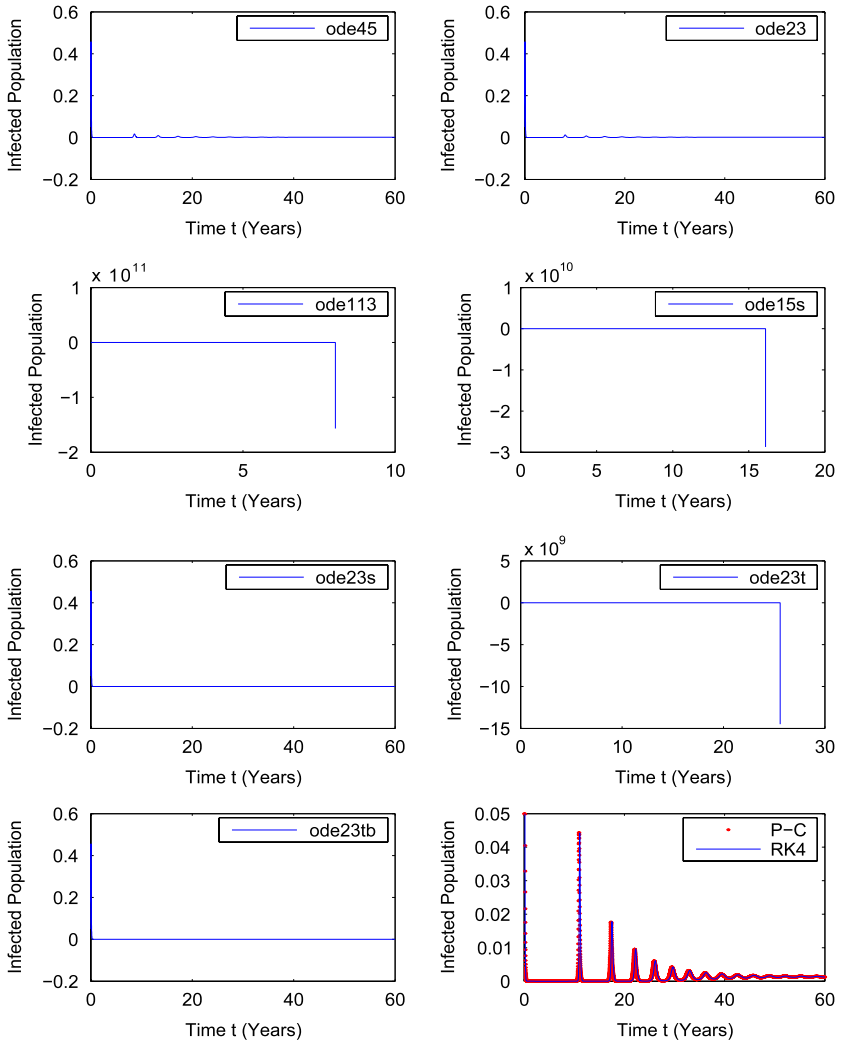

Fig. 2. Profile of infected subpopulation $I(t)$ using Matlab mathematical package and the proposed predictor–corrector P–C scheme with the following parameter values ($\mathcal{R}_0 > 1$); $N\beta = 123$, $\mu = 0.04$, $\nu = 24$, $h_{\mathrm{RK4}} = 0.005$, $\epsilon = \frac{1}{2000}$, and $h_{P-C} = 0.01$.

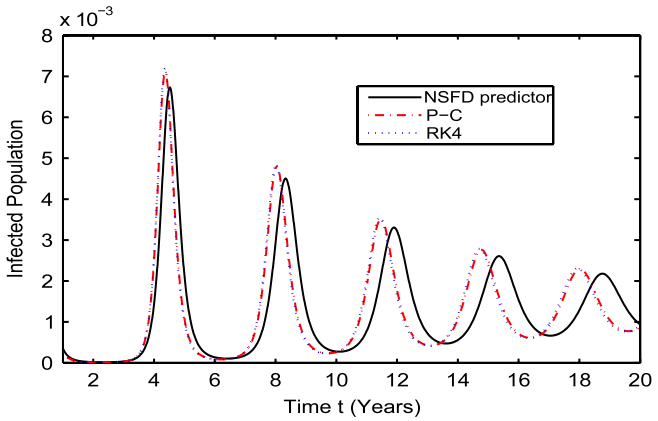

Fig. 3. Profile of infected subpopulation $I(t)$ using the predictor NSFD and predictor–corrector NSFDCL schemes with the following parameter values ($\mathcal{R}_0 > 1$); $N\beta = 123$, $\mu = 0.04$, $\nu = 24$, $\epsilon = \frac{1}{2000}$, and $h = 0.005$.

Runge–Kutta type schemes show its effectiveness. We showed that the NSFD numerical scheme satisfying the conservation law is unconditionally stable for $\mathcal{R}_0 < 1$ and converges to the disease free equilibrium point irrespective of the time

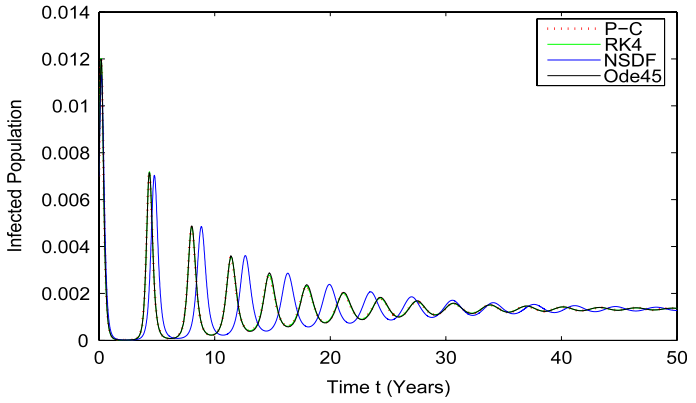

Fig. 4. Profile of infected subpopulation $I(t)$ using different numerical schemes with the following parameter values ($\mathcal{R}_0 > 1$); $N\beta = 123$, $\mu = 0.04$, $\nu = 24$, $h_{\mathrm{RK4}} = 0.005$, $h_{\mathrm{NSFD}} = 0.01$, $\epsilon = \frac{1}{2000}$, and $h_{P-C} = 0.01$.

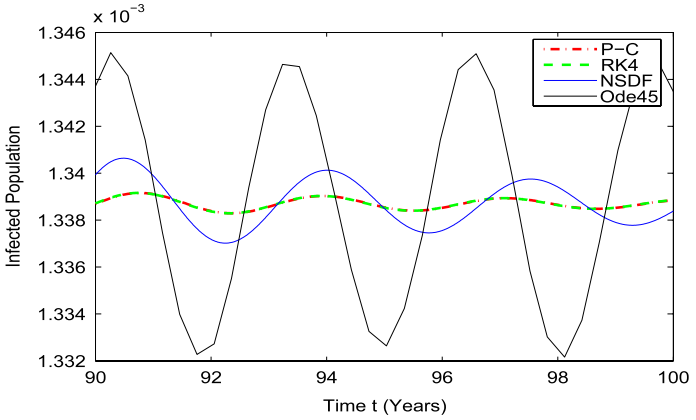

Fig. 5. Profile of infected subpopulation $I(t)$ using different numerical schemes with the following parameter values ($\mathcal{R}_0 > 1$); $N\beta = 123$, $\mu = 0.04$, $\nu = 24$, $h_{\mathrm{RK4}} = 0.005$, $h_{\mathrm{NSFD}} = 0.01$, $\epsilon = \frac{1}{2000}$, and $h_{P-C} = 0.01$.

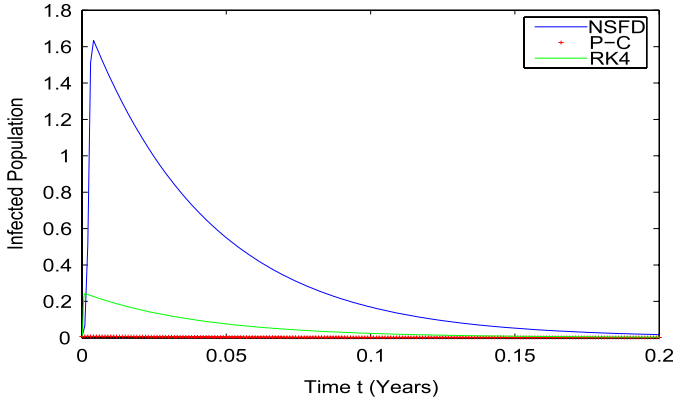

Fig. 6. Profile of infected subpopulation $I(t)$ using different numerical schemes with the following parameter values ($\mathcal{R}_0 > 1$) and initial conditions; $N\beta = 36\,000$, $\mu = 0.04$, $\nu = 24$, $h_{\mathrm{RK4}} = 0.005$, $\epsilon = \frac{1}{2000}$, and $h_{P-C} = 0.01$.

step size. In addition, the same behavior is obtained for the $\mathcal{R}_0 > 1$. Furthermore, well known methods implemented in the Matlab software package did not converge to the endemic equilibrium point for default error tolerances and for smaller error tolerances they take a long computation time. Also, the 4th order Runge–Kutta (RK4) oscillates around the correct endemic equilibrium point while the NSFD scheme proposed in [13] and predictor–corrector NSFDCL scheme converge correctly.

We conclude that the developed nonstandard schemes are competitive and preserve essential properties of the continuous SIR model. These numerical integration schemes are useful since they reproduce the dynamics of original

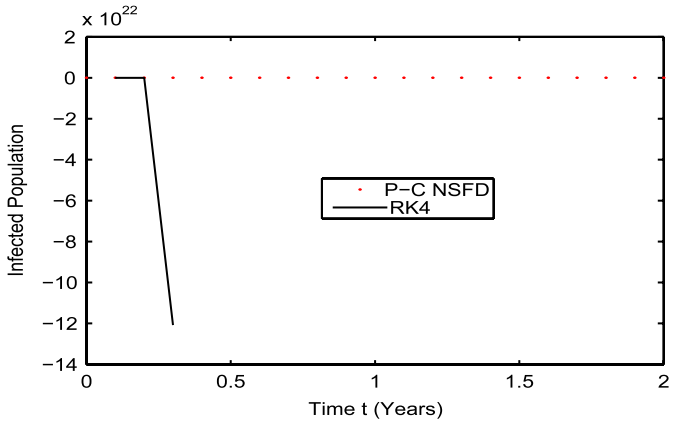

Fig. 7. Profile of infected subpopulation $I(t)$ using the predictor–corrector NSFDCL and the 4th order Runge–Kutta schemes with the following parameter values ($\mathcal{R}_0 > 1$); $N\beta = 2500$, $\mu = 0.04$, $\nu = 24$, $\epsilon = \frac{1}{2000}$, and a time step size $h = 0.01$ for both numerical schemes.

differential equations. Furthermore, large time step sizes can be used, thus making it more economical to use when integrating over long time periods to reach steady states.

Appendix

To study the convergence of scheme (15), we consider the following expressions:

$$G_1(S,I) = \frac{S + h\mu + \epsilon^{-1}F_1(S,I)}{1 + \epsilon^{-1} + h\mu + hN\beta F_2(S,I)}, \qquad G_2(S,I) = \frac{I + hN\beta G_1(S,I)F_2(S,I)}{1 + h(\mu+\nu)}, \tag{16}$$

where F_1, F_2 are given as in (9). For convenience in the notation we use the following conventions:

$$\begin{aligned} &\alpha = h\mu, \\ &\theta = 1 + \epsilon^{-1} + h\mu = 1 + \epsilon^{-1} + \alpha, \\ &\eta = hN\beta, \\ &\delta = 1 + h(\mu+\nu). \end{aligned} \tag{17}$$

It is clear that $\theta > \alpha$, and $1 + \gamma < \delta$ if $\mathcal{R}_0 = \frac{N\beta}{\mu+\nu} < 1$. Thus, from (16) and (17) we obtain

$$G_1(S,I) = \frac{S + \alpha + \epsilon^{-1}F_1(S,I)}{\theta + \eta F_2(S,I)}, \qquad G_2(S,I) = \frac{I + \eta G_1(S,I)F_2(S,I)}{\delta}. \tag{18}$$

The analysis of the convergence of scheme (15) is given by the magnitude of eigenvalues of the Jacobian of the linearized scheme, evaluated in the equilibrium points. If (S^*, I^*) is a equilibrium point of system (3), then the Jacobian matrix JG is given by

$$\mathrm{JG}(S^*,I^*) = \begin{pmatrix} \dfrac{\partial G_1(S^*,I^*)}{\partial S} & \dfrac{\partial G_1(S^*,I^*)}{\partial I} \\ \dfrac{\partial G_2(S^*,I^*)}{\partial S} & \dfrac{\partial G_2(S^*,I^*)}{\partial I} \end{pmatrix} \tag{19}$$

where

$$\begin{aligned} \frac{\partial G_1(S^*,I^*)}{\partial S} &= \frac{\left(1 + \epsilon^{-1}\frac{\partial F_1(S^*,I^*)}{\partial S}\right)(\theta + \eta F_2(S^*,I^*)) - (S^* + \alpha + \epsilon^{-1}F_1(S^*,I^*))\frac{\eta \partial F_2(S^*,I^*)}{\partial S}}{(\theta + \eta F_2(S^*,I^*))^2}, \\ \frac{\partial G_1(S^*,I^*)}{\partial I} &= \frac{\left(\epsilon^{-1}\frac{\partial F_1(S^*,I^*)}{\partial I}\right)(\theta + \eta F_2(S^*,I^*)) - (S^* + \alpha + \epsilon^{-1}F_1(S^*,I^*))\frac{\eta \partial F_2(S^*,I^*)}{\partial I}}{(\theta + \eta F_2(S^*,I^*))^2}, \\ \frac{\partial G_2(S^*,I^*)}{\partial S} &= \frac{\eta}{\delta}\frac{\partial G_1(S^*,I^*)}{\partial S}F_2(S^*,I^*) + \frac{\eta}{\delta}G_1(S^*,I^*)\frac{\partial F_2(S^*,I^*)}{\partial S}, \\ \frac{\partial G_2(S^*,I^*)}{\partial I} &= \frac{1}{\delta} + \frac{\eta}{\delta}\frac{\partial G_1(S^*,I^*)}{\partial I}F_2(S^*,I^*)\frac{\eta}{\delta}G_1(S^*,I^*)\frac{\partial F_2(S^*,I^*)}{\partial I}. \end{aligned}$$

Since $F_1(1,0) = 1, F_2(1,0) = 0, \frac{\partial}{\partial S}F_1(1,0) = \frac{1}{1+\alpha}, \frac{\partial}{\partial I}F_1(1,0) = \frac{-\eta}{1+\alpha}, \frac{\partial}{\partial S}F_2(1,0) = 0, \frac{\partial}{\partial I}F_2(1,0) = \frac{1+\eta}{\delta}$, the Jacobian evaluated at disease free point $(S_0^*, I_0^*) = (1,0)$ is given by

$$\mathrm{JG}(1,0) = \begin{pmatrix} \dfrac{1}{1+\alpha} & \dfrac{-\epsilon^{-1}\eta}{(1+\alpha)\theta} - \dfrac{1+\eta}{\delta\theta} \\ 0 & \dfrac{1}{\delta}\dfrac{\delta+\eta(1+\eta)}{\delta} \end{pmatrix}, \tag{20}$$

and the eigenvalues are: $\Lambda_1 = \frac{1}{1+\alpha} < 1$, and $\Lambda_2 = \frac{1}{\delta}\frac{\delta+\eta(1+\eta)}{\delta} < \frac{1}{\delta}\frac{\delta+\eta\delta}{\delta} = \frac{1}{\delta}(1+\eta) < 1$, since $1+\eta < \delta$ if $\mathcal{R}_0 < 1$. Therefore, we can conclude that the numerical scheme (15) will converge unconditionally from any starting values S^0, I^0, R^0 such that $S^0 + I^0 + R^0 = 1$ to the disease free fixed point whenever $\mathcal{R}_0 < 1$, for any $h > 0$. □

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