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Scheme of Predictor-Corrector
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An accurate nonstandard scheme of predictor-corrector type for a SIR epidemic model

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Abstract

In this paper we construct and develop a competitive nonstandard finite difference (*NSFDCL*) numerical scheme of predictor-corrector type for the classical *SIR* epidemic model. This *NSFDCL* scheme is designed with the aim of obtaining dynamical consistency between the discrete solution and the solution of the continuous model. In order to obtain accurate numerical schemes it is necessary to transfer essential properties of the continuous model to the discrete schemes. The *NSFDCL* scheme developed here satisfies some important properties associated with the mathematical modeling of epidemics in populations, such as positivity, boundedness, monotonicity, stability and conservation of frequency of the oscillations. Furthermore, the proposed *NSFDCL* scheme satisfies the “Conservation Law” associated to the considered *SIR* epidemic model. Numerical comparisons between the *NSFDCL* numerical scheme developed here and Runge-Kutta type schemes show its effectiveness.

Keywords: Nonstandard finite difference schemes, Numerical solution, Epidemic model *SIR*, Predictor-Corrector.

1 Introduction

Ordinary differential initial value problems appear in many physical, biological and economic applications. Exact solutions are few and usually complicated, so good approximations are necessary. Numerical methods based on difference schemes are often the first method of choice. Many problems in mathematical epidemiology are modeled by autonomous systems of nonlinear ordinary differential equations, which implies the assumption that the parameters of the model are independent of time. In these models the variables represent subpopulations of susceptibles, infected, recovered, transmitted diseases vectors, and so forth. Thus, the solutions of ODE system describe the evolution of the different classes of subpopulations in the model for different times and, therefore, one important task of the mathematical modeling is to obtain accurate numerical solutions in order to predict, for instance, when the infectives will peak. Several discretizations of nonlinear equations have been developed in different areas [1, 2, 3].

The application of difference schemes raises questions such as what is the truncation error or the region of stability. It is well known that traditional schemes like forward Euler, Runge-Kutta and others, sometimes fail by generating non-physical oscillations, bifurcations, chaos and false steady states, see [4]. Moreover, some methods despite using adaptative step sizes still fail [5]. One way to prevent these types of numerical instabilities is the construction of numerical schemes based on nonstandard finite-difference methods (*NSFD*). These techniques, developed by Mickens [1, 6, 7], have produced new numerical schemes preserving the physical properties,

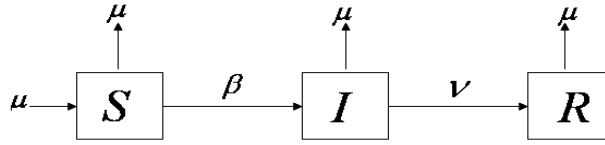


Figure 1: Flow diagram for the *SIR* model.

especially the equilibria and their stability properties [8, 9, 10, 11, 12, 13]. In [14, 15] the authors developed competitive *NSFD* schemes for epidemic diseases. Piyanwong et al. [16] and Jansen and Twizell [17] have designed positive and unconditionally stable schemes for the *SIR* and *SEIR* models, respectively. However, in their developed schemes they have not applied the conservation law explicitly, which can lead to unfeasible or unrealistic solutions.

The best scenario to solve accurately a model based is when an exact difference scheme can be constructed. In [18, 19, 20] the authors have been developed exact nonstandard difference schemes. However, several times exact difference schemes are not easy to find, therefore we rely on *NSFD* schemes. Many of these *NSFD* schemes preserve some properties of the continuous model for small step sizes, but sometimes the frequency of the oscillations of the solutions is not preserved for large step sizes. Motivated by the work presented in [16], in this paper we develop a *NSFD* scheme of predictor-corrector type to obtain numerical solutions to the *SIR* epidemic model, where we apply the "Conservation Law" in the numerical scheme in addition to the nonlocal approximation in order to preserve the frequency of the oscillation for step sizes bigger than the ones proposed in [16], and that the ones for the traditional Runge-Kutta schemes. In [8] the authors apply the central difference method to an epidemic *SIR* model and show how the local stability of the equilibria is changed after applying the numerical method. They also apply conformal mapping theory in complex analysis to verify the local stability results of two other implicitly defined central difference methods.

The proposed 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 arbitrarily large time step sizes, saving computational cost when integrating over long time periods. 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 a *NSFDCL* numerical scheme is constructed as a predictor scheme conserving the properties of the total population. Next, in Section 4 the convergence of proposed method is studied, and in Section 5 we present another scheme *NSFDCL* as a corrector 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 [16], where the population is divided into three classes: $S(t)$ susceptible at time t , $I(t)$ infected at time t and $R(t)$ recovered at time t and it is assumed that this class has acquired immunity. This *SIR* mathematical model was used in [21] 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:

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

where

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

Since the population is assumed constant it can be normalized to one:

$$S(t) + I(t) + R(t) = 1. \tag{2}$$

We define equation (2) as the conservation law associated with the system (1) and this equation must be satisfied by any reliable numerical scheme. It is important to mention that the steady states of (1) are the following points: the disease free point $(1, 0, 0)$ and the endemic point $\left(\frac{1}{R_0}, \frac{\mu}{\mu + \nu}\left(1 - \frac{1}{R_0}\right), \frac{\nu}{\mu + \nu}\left(1 - \frac{1}{R_0}\right)\right)$, where $R_0 = \frac{N\beta}{\mu + \nu} > 1$ is the basic reproductive number associated with the *SIR* model [16].

3 Nonstandard scheme with conservation law (NSFDCL)

In this section we construct a numerical scheme to compute numerical solutions for the systems (1). 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 cost 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 Mickens's, a scheme is called nonstandard if at least one of the following conditions is satisfied [10, 11, 22],

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 (1) is made based on the approximation of the temporal derivatives by a generalized forward scheme of first order. Thus, if $f(t)$ is derivable, then $f'(t)$ it can be approximated by

$$\frac{df(t)}{dt} = \frac{f(t+h) - f(t)}{h} + \mathcal{O}(h) \text{ as } h \rightarrow 0. \tag{3}$$

Let us denote by S^n , I^n and R^n the approximations of $S(nh)$, $I(nh)$ and $R(nh)$, respectively, for $n = 0, 1, 2, \dots$, 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 (1) is constructed so that it satisfies the conservation law property proposed by Mickens's techniques in [23, 7]. Thus, the *NSFDCL* scheme for system (1) takes the following form:

$$\begin{aligned}\frac{S^{n+1} - S^n}{h} &= \mu - \mu S^{n+1} - N\beta S^{n+1} I^n, \\ \frac{I^{n+1} - I^n}{h} &= N\beta S^{n+1} I^n - (\mu + \nu) I^{n+1}, \\ \frac{R^{n+1} - R^n}{h} &= \nu I^{n+1} - \mu R^{n+1}.\end{aligned}\tag{4}$$

Notice that this scheme satisfies $\dot{S}(t) + \dot{I}(t) + \dot{R}(t) = 0$, (the total population is constant) as $n \rightarrow \infty$ (i.e., as $h \rightarrow 0$). Moreover, from (4) we can see that

$$S^{n+1} + I^{n+1} + R^{n+1} = \frac{h\mu + S^n + I^n + R^n}{1 + h\mu}.\tag{5}$$

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,

$$S^{n+1} = \frac{S^n + h\mu}{1 + h\mu + hN\beta I^n},\tag{6i}$$

$$I^{n+1} = \frac{I^n(1 + hN\beta S^{n+1})}{1 + h(\mu + \nu)},\tag{6ii}$$

$$R^{n+1} = 1 - S^{n+1} - I^{n+1}.\tag{6iii}$$

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 difference system (6) we perform the respective convergence analysis of this *NSFDCL* scheme. In summary, it can be seen from (4) and (6) that we have constructed a *NSFDCL* scheme for the system (1) having the following properties:

- It satisfies the Conservation law, i.e. the population is constant.
- It has positivity and boundedness: For the system (6) 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 (6), it is enough to only consider equations (6i) and (6ii). Thus, we define the following functions:

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

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

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

In this way, the scheme (6) 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 (1). Calculating $J(S, I)$ at (S^*, I^*) , one gets the following matrix

$$J(S^*, I^*) = \begin{pmatrix} \frac{1}{1 + h\mu + h\beta NI^*} & -\frac{(\mu + S^*)h\beta N}{(1 + h\mu + h\beta NI^*)^2} \\ \frac{h\beta NI^*}{1 + h(\mu + \nu)} & \frac{1}{1 + h\mu + h\beta NI^*} \frac{1 + h\beta NF_1(S^*, I^*) + I^* \frac{(h\beta N)^2(h\mu + S^*)}{(1 + h\mu + h\beta NI^*)^2}}{1 + h(\mu + \nu)} \end{pmatrix}.$$

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

4.1 Disease free equilibrium

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

$$J(1, 0) = \begin{pmatrix} \frac{1}{1 + h\mu} & -\frac{h\beta N}{1 + h\mu} \\ 0 & \frac{1 + h\mu + h\beta N}{(1 + h\mu)(1 + h(\mu + \nu))} \end{pmatrix}.$$

Therefore, if the basic reproductive number $\mathcal{R}_0 < 1$, i.e., $\beta < \mu + \nu$, then the spectral radius of $J(1, 0)$ is strictly less than unity for all h . Thus, the numerical schemes (6) 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 equilibrium point $(1, 0, 0)$ if $\mathcal{R}_0 < 1$.

4.2 Endemic equilibrium

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

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

where

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

To calculate the two eigenvalues of $J(S_e^*, I_e^*)$, we will use the following Lemma:

Lemma 4.1 [24, 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 to define $A = \text{Trace}J(S_e^*, I_e^*)$, $B = \text{Det}J(S_e^*, I_e^*)$. Therefore, $A = \frac{ab + a^2 + (a - c)d}{a^2b} > 0$, 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

$$f(0) = B = \frac{1}{ab} + \frac{d}{a^2b} < \frac{1+d}{ab} = \frac{1 + h^2\mu\beta N + \frac{h\beta N}{\mathcal{R}_0}}{h\mu\mathcal{R}_0 + 1 + h^2\mu\beta N + \frac{h\beta N}{\mathcal{R}_0}} < 1, \quad (7i)$$

$$f(-1) = 1 + A + B > 0. \quad (7ii)$$

Moreover,

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

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

$$f(-1) = 1 - A + B > 0. \quad (8)$$

From (7i), (7ii) and (8) 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 (6) will converge unconditionally from any starting values S^0, I^0, R^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 (6) using a predictor corrector type approach. The *NSDF* schemes usually preserve some properties such as conservation law (total population), convergence to the equilibrium points, positivity of the population. However, if the 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 on. 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 (6) as a predictor scheme, i.e.,

$$S_p^{n+1} = \frac{S^n + h\mu}{1 + h\mu + hN\beta I^n}, \quad (9i)$$

$$I_p^{n+1} = \frac{I^n(1 + hN\beta S_p^{n+1})}{1 + h(\mu + \nu)}, \quad (9ii)$$

Now, we evaluate system (1) at time $t + h$ to obtain the following expression:

$$\begin{aligned} \frac{S^{n+1} - S^n}{h} &= \mu - \mu S^{n+1} - N\beta S^{n+1} I^{n+1} - \frac{2000S^{n+1}}{h} + \frac{2000S^n}{h}, \\ \frac{I^{n+1} - I^n}{h} &= N\beta S^{n+1} I^{n+1} - (\mu + \nu) I^{n+1}, \\ \frac{R^{n+1} - R^n}{h} &= \nu I^{n+1} - \mu R^{n+1}, \end{aligned}$$

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

$$S_c^{n+1} = \frac{S^n + h\mu + 2000S_p^{n+1}}{2001 + h\mu + hN\beta I_p^{n+1}}, \quad (10i)$$

$$I_c^{n+1} = \frac{I^n + hN\beta S_p^{n+1} I_p^{n+1}}{1 + h(\mu + \nu)}, \quad (10ii)$$

$$R^{n+1} = 1 - S_c^{n+1} - I_c^{n+1}. \quad (10iii)$$

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

Step 0 Select values: $0 < \epsilon \ll 1$ and S^0, I^0, R^0 , such that $S^0 + I^0 + R^0 = 1$.

Step 1 For $n = 0, 1, 2, \dots$, do

Step 2 Calculate S_p^{n+1} from (9i).

Step 3 Using this value of S_p^{n+1} and I^n , calculate I_p^{n+1} from (9ii).

Step 4 Correct the value S_c^{n+1} , using $S^n, S_p^{n+1}, I_p^{n+1}$ and the equation (10i).

Step 5 Correct the value I_c^{n+1} , using $I^n, S_p^{n+1}, I_p^{n+1}$ and the equation (10ii).

Step 6 If $\|S_c^{n+1} - S^n\| < \epsilon$ and $\|I_c^{n+1} - I^n\| < \epsilon$ then

Step 7 Calculate R^{n+1} from (10iii), else $S^n = S_c^{n+1}, I^n = I_c^{n+1}$ and go to step 4.

Note that the sequential form of calculation is a generic feature of *NSFDCL* schemes [23]. In addition, it can be seen that the main part of the local truncation error associated with each equation of system (6) is of order $\mathcal{O}(h^2)$, confirming that the constructed *NSFDCL* schemes are first order accurate.

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 step size. For the parameter

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

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

values of the *SIR* model, we used the values presented in [16], which it are summarized in Table 1.

The epidemic model (1) 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 *NSFDCL* scheme converges to the correct endemic point and only producing positive values for all time t . However, the routines from the Matlab software program did not converge or in some cases took unreal negative values for the infective population. Notice, that the Runge-Kutta fourth order scheme with a time step size $h = 0.005$ converges to the correct endemic point, but our $P - C$ scheme of predictor-corrector type can use a larger time step $h = 0.01$.

In Fig. 3, it can be seen that the numerical solutions corresponding to different schemes do not have the same oscillation frequency. However, taking the fourth order Runge-Kutta (RK4) with a small time step $h = 0.005$ as the true 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. 4, it is shown that the unconditional stable *NSFD* scheme proposed in [16] gives unreal positive solutions since the proportion of infectives go beyond the total population while our predictor-corrector ($P - C$) scheme gives physically realistic solutions. In addition, it can be observed that fourth order Runge-Kutta (RK4) oscillates around the correct endemic equilibrium point meanwhile the *NSFD* scheme proposed in [16] and the predictor-corrector $P - C$ scheme converge asymptotically.

7 Conclusion

In this paper we construct and develop a competitive nonstandard finite difference (*NSFDCL*) numerical scheme of predictor-corrector type for the classical *SIR* epidemic model. This model have 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 *NSFDCL* numerical scheme of predictor-corrector type is the ‘‘Conservation Law’’ proposed by Mickens [23]. Numerical comparisons between the *NSFDCL* numerical scheme developed here and Runge-Kutta type schemes show its effectiveness. We showed that the *NSFDCL* numerical scheme satisfying the conservation law is unconditionally stable for $R_0 < 1$ and converges to the disease free equilibrium point irrespective of the time step size. In addition, the same behavior is obtained for the $R_0 > 1$. Furthermore, well known methods implemented in the Matlab software package did not converge to the endemic equilibrium point. Also, the fourth order Runge-Kutta (RK4) oscillates around the correct endemic equilibrium point while the *NSFD* scheme proposed in [16] and predictor-corrector *NSFDCL* scheme converge asymptotically.

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 can reproduce the dynamics of original 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.

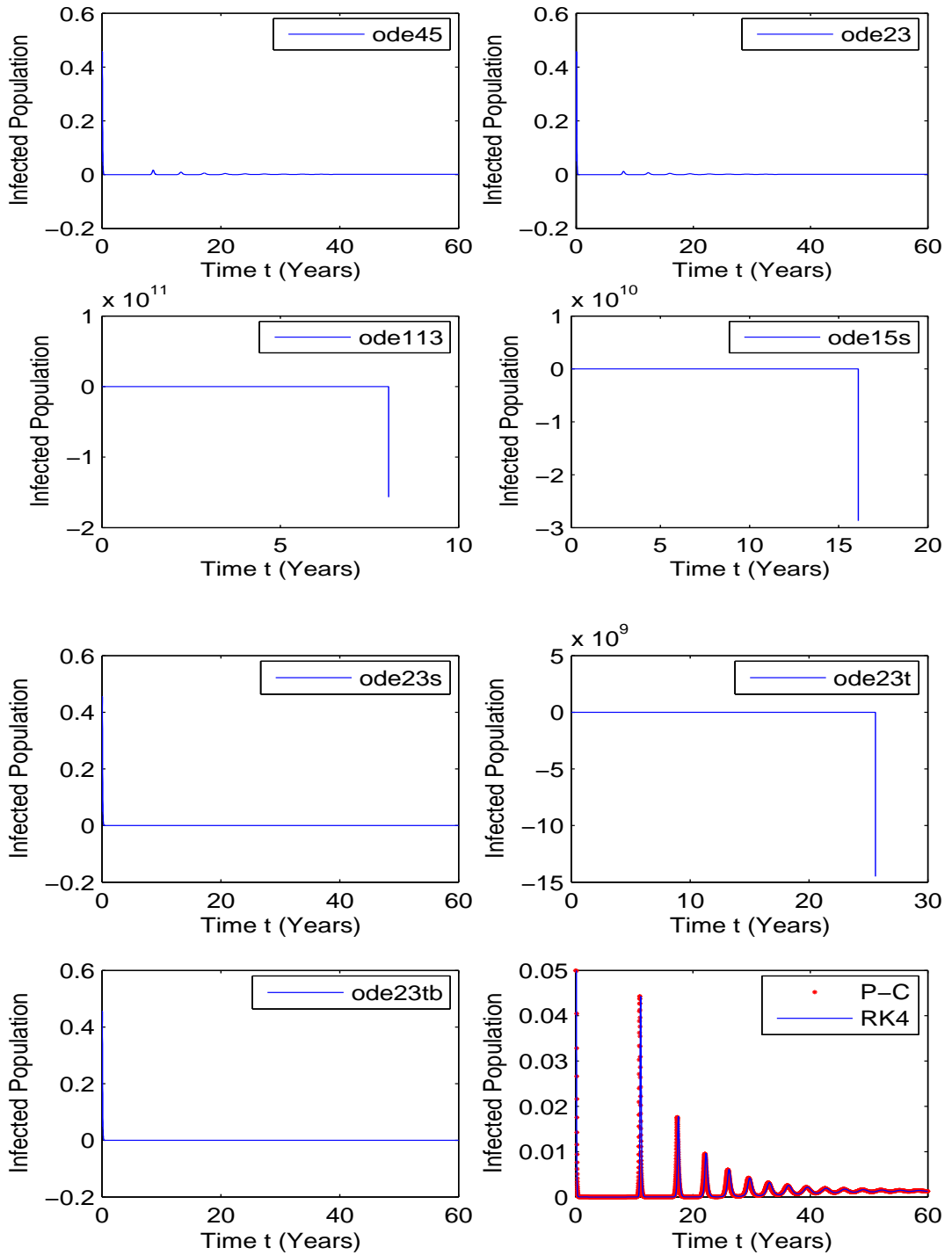


Figure 2: Profile of infected subpopulation $I(t)$ using Matlab mathematical package and the proposed predictor-corrector $P - C$ scheme with the following parameter values ($R_0 > 1$) and initial conditions; $x_0 = 0.9$, $y_0 = 0.05$, $z_0 = 0.05$, $N\beta = 123$, $\mu = 0.04$, $\nu = 24$, $h_{RK4} = 0.005$, $h_{P-C} = 0.01$.

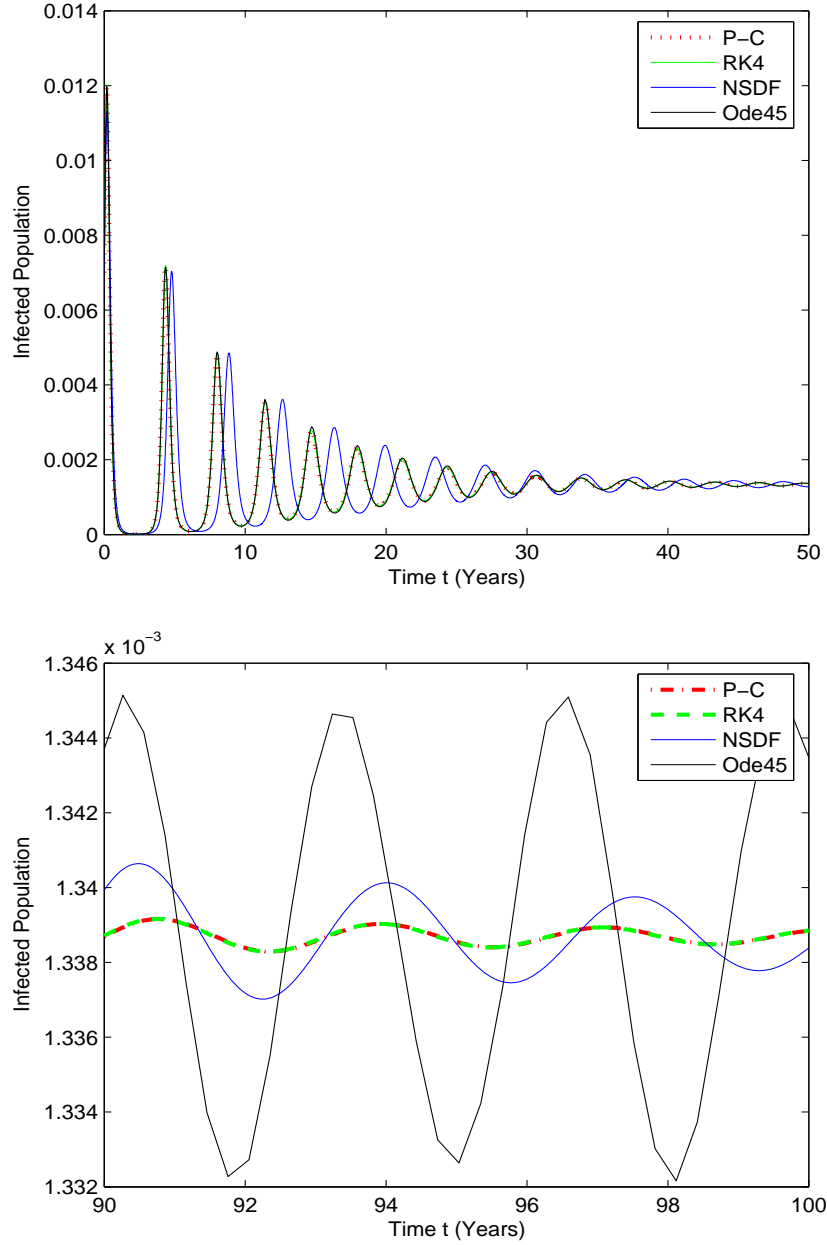


Figure 3: Profile of infected subpopulation $I(t)$ using different numerical schemes with the following parameter values ($R_0 > 1$) and initial conditions; $x_0 = 0.9$, $y_0 = 0.05$, $z_0 = 0.05$, $N\beta = 123$, $\mu = 0.04$, $\nu = 24$, $h_{RK4} = 0.005$, $h_{P-C} = 0.01$.

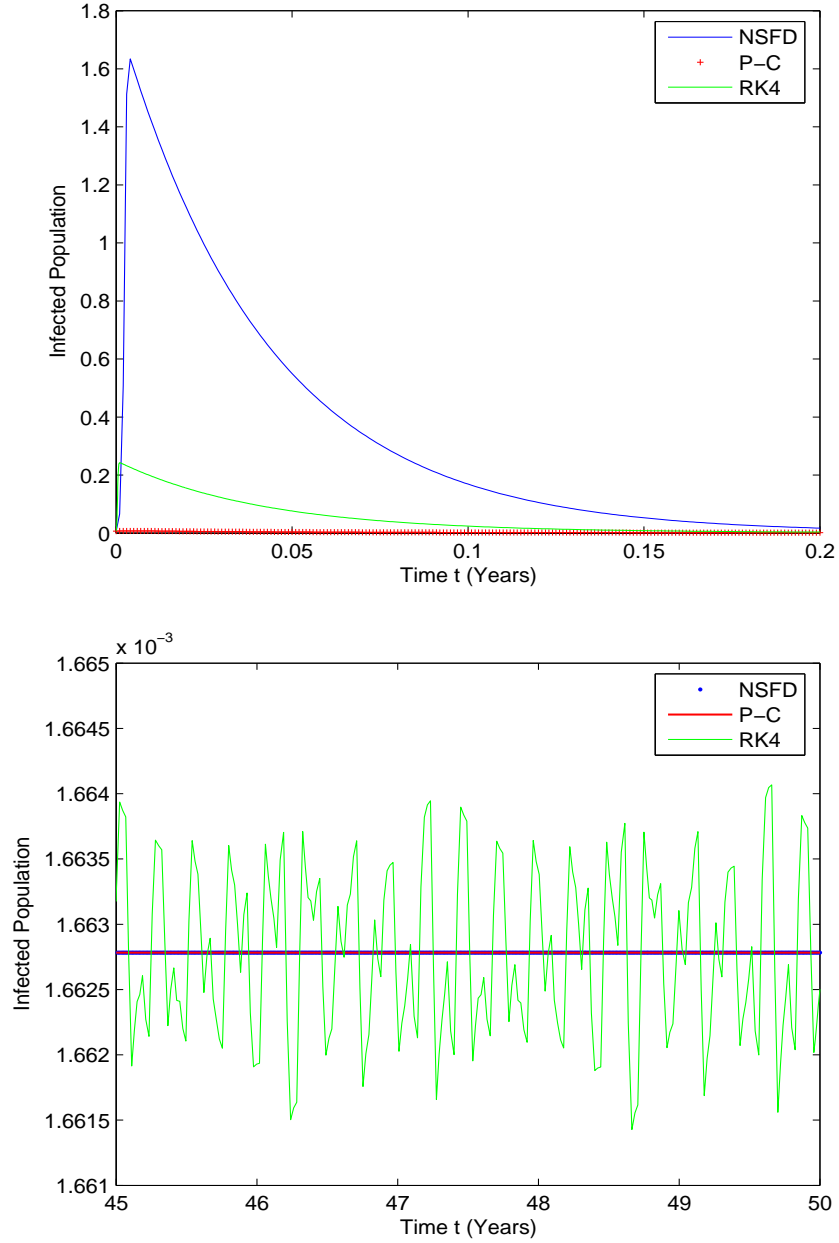


Figure 4: Profile of infected subpopulation $I(t)$ using different numerical schemes with the following parameter values ($R_0 > 1$) and initial conditions; $x_0 = 0.24$, $y_0 = 0.007$, $z_0 = 0.753$, $\beta = 36000$, $\mu = 0.04$, $\nu = 24$, $h_{RK4} = 0.01$, $h_{P-C} = 0.01$

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