Research Article

An Accurate Predictor-Corrector-Type Nonstandard Finite Difference Scheme for an SEIR Epidemic Model

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Abstract

The present work deals with the construction, development, and analysis of a viable normalized predictor-corrector-type nonstandard finite difference scheme for the SEIR model concerning the transmission dynamics of measles. The proposed numerical scheme double refines the solution and gives realistic results even for large step sizes, thus making it economical when integrating over long time periods. Moreover, it is dynamically consistent with a continuous system and unconditionally convergent and preserves the positive behavior of the state variables involved in the system. Simulations are performed to guarantee the results, and its effectiveness is compared with well-known numerical methods such as Runge–Kutta (RK) and Euler method of a predictor-corrector type.

1. Introduction

Mathematicians and biologists have been working for a long time on the biological process of life science. They succeeded in evaluating some remarkable results from their work. An important mark in mathematical biology is the mathematical modeling of infectious diseases [1]. Measles is one of such a highly infectious childhood disease, caused by respiratory infection by a Morbilli virus, measles virus. Arthur Ransom first observed the irregular cyclic behavior of measles that is considered as a mainly conspicuous facet of measles. The age structure of the population, contact, immigration rate, and the school seasons were known as a crucial phase for the swell of measles [2–4]. William Hammer in 1906 published a discrete numerical model for the transmission of measles epidemic. Later assumption of “Mass Action” is applied to that model which is the basic rule to the current theory of deterministic modeling of infectious diseases [5].

Society has a keen concern in knowing the major evolution for the spread of diseases. Analytical results give a solution to these problems but for limited cases and causes many problems. The homotopy perturbation method and variational iteration method can be used for the solution of the epidemic models [6]. However, the first choice to solve these laws of nature is the numerical method based on a difference scheme for good approximations [7–9]. In general, already developed numerical schemes such as Euler, Runge–Kutta, and others at times stop working by generating nonphysical results. These unnecessary oscillations...
contrived chaos and false fixed points [10]. Moreover, some methods are unsuccessful if we check them on larger step sizes [11]. To avoid such discrepancies, the numerical schemes based on the “nonstandard finite difference method (NSFD)” are established. These techniques were first developed by R. E. Mickens [7, 12, 13]. The created numerical schemes preserve the essential properties such as dynamical consistency, stability, and equilibrium points [14–21]. Researchers have developed competitive NSFD schemes for epidemic diseases. Many of these NSFD schemes are consistent for small step sizes with the continuous model, but for large step sizes, the unwanted oscillations have been observed. Piyanwong, Jansen, and Twizel have constructed a positive and unconditionally stable scheme for SIR and SEIR models, respectively [22, 23]. Nevertheless, the lack of application of conservation law in their developed schemes explicitly caused impracticable and unrealistic solutions, while Abraham and Gilberto have developed NSFD schemes of the SIR epidemic model to obtain the physically realistic solutions for all step sizes, where they apply the conservation law in addition to nonlocal approximation [24].

In this paper, we have developed a normalized NSFD of predictor-corrector- (PC-) type inspired by the previous work discussed to double refine the numerical solution of a nonlinear dynamics regarding the transmission of measles. To keep the method explicit, we will use the forward difference approximations for the first derivative terms. The nonlocal approximations are used to tackle the nonlinear terms with \( \phi(h) \) as a nonclassical denominator function. By using this idea, the measles model will converge to equilibrium points, even for the larger step sizes.

### 2. The Mathematical Frame of Work

In this work, the dynamics of the measles epidemic described by the SEIR mathematical model suggested by Jansen and E. H. Twizel is considered [23]. In the SEIR model, the total human population is categorized as susceptible, exposed, infectious, and recovered subpopulations denoted by \( S, E, I, \) and \( R \), respectively. Consider the flow of the SEIR model for the measles epidemic, as shown in Figure 1.Here

- \( S = \text{susceptible individuals} \)
- \( E = \text{exposed individuals} \)
- \( I = \text{infected individual} \)
- \( R = \text{recovered individual} \)
- \( \mu = \text{birth rate and death rate} \)
- \( \beta = \text{the rate at which susceptible individuals are infected by those who are infectious} \)
- \( \sigma = \text{the rate at which exposed individuals become infected} \)
- \( \gamma = \text{the rate at which infected individuals recover} \)

Here \( \mu, \beta, \sigma, \) and \( \gamma \) are considered as positive parameters. Furthermore, we assume that \( (E^0, I^0 \neq 0) \). Consider \( N \) is the constant size of the population so that the number of recovered individuals \( R = R(t) \) at time \( t \) is defined by \( R = N - S - E - I \). A susceptible is a move to the exposed model, where the individual is infected but yet not infectious. After sometimes the individual becomes infectious and enters into the infected compartment, and in this way, the disease spreads into the population.

The mathematical model is written as

\[
\begin{align*}
\frac{dS}{dt} &= \mu N - \mu S - \beta IS, \quad t > 0, S(0) = S^0, \\
\frac{dE}{dt} &= \beta IS - \mu E - \sigma E, \quad t > 0, E(0) = E^0, \\
\frac{dI}{dt} &= \sigma E - \mu I - \gamma I, \quad t > 0, I(0) = I^0, \\
\frac{dR}{dt} &= \gamma I - \mu R, \quad t > 0, R(0) = R^0,
\end{align*}
\]

(1)

where

\[
S + E + I + R = N.
\]

Equation (2) shows that the total size of the population remains constant, which is connected with the continuous system (1). The following two points give the equilibrium points of (1):

The disease-free equilibrium (DFE) point \((N, 0, 0)\)

The endemic equilibrium (EE) point \((N/R_0, \mu N/\mu + \sigma(1 - 1/R_0), \mu / \beta (R_0 - 1))\)

Here, \( R_0 = \sigma \beta N / (\mu + \sigma) (\mu + \gamma) \) is the basic reproductive number associated with the measles model.

For the sake of brevity, we are not mentioning RK-4 and Euler-PC scheme.

### 3. Numerical Modeling

To the construction of NSFD scheme, the continuous system (1) is discretized using the forward difference approximation for the first-order time derivatives. Thus, if \( f(t) \) is differentiable, the \( f''(t) \) can be approximated by

\[
\frac{df(t)}{dt} = \frac{f(t + h) - f(t)}{\varphi(h)} + O(h) \quad \text{as} \quad h \rightarrow 0,
\]

(3)

where \( \varphi(h) \) is a real-valued function satisfying the condition \( \varphi(h) \rightarrow 0 \) as \( h \rightarrow 0 \). We have

\[
\varphi(h) = 1 - e^{-h}.
\]

(4)
Thus, the NSFD scheme for system (1) takes the form
\[
\begin{align*}
\frac{S^{n+1} - S^n}{\varphi(h)} &= \mu N - \mu S^{n+1} - \beta S^{n+1} I^n, \\
\frac{E^{n+1} - E^n}{\varphi(h)} &= \beta S^{n+1} I^n - \mu E^{n+1} - \sigma E^{n+1}, \\
\frac{I^{n+1} - I^n}{\varphi(h)} &= \sigma E^{n+1} - \mu I^{n+1} - \gamma I^{n+1}, \\
\frac{R^{n+1} - R^n}{\varphi(h)} &= \gamma I^{n+1} - \mu R^{n+1}.
\end{align*}
\]  

(5)

From equation (5), we have
\[
(1 + \varphi(h)\mu)[S^{n+1} + E^{n+1} + I^{n+1} + R^{n+1}] = \varphi(h)\mu N - \varphi(h)\mu(S^n + E^n + I^n + R^n).
\]  

(6)

Thus, if \( S^n + E^n + I^n + R^n = N \) for all \( n \geq 0 \), then \( S^{n+1} + E^{n+1} + I^{n+1} + R^{n+1} = N \) for all \( n \geq 0 \). Thus, the conservation law property is satisfied. System (5) is written as
\[
\begin{align*}
S^{n+1} &= S^n + \mu \varphi(h) N \\
E^{n+1} &= E^n + \varphi(h) \beta S^n I^n \\
I^{n+1} &= I^n + \varphi(h) \sigma E^n \\
R^{n+1} &= R^n + \varphi(h) \gamma I^n.
\end{align*}
\]  

(7)

Now, the positivity of \( S^{n+1}, E^{n+1}, I^{n+1} \), and \( R^{n+1} \) is guaranteed if \( 0 < S^n < 1, 0 < E^n < 1, 0 < I^n < 1, \) and \( 0 < R^n < 1 \) for all \( n \geq 0 \). Thus, the constructed scheme has the following properties:

- The conservation law is satisfied
- The positivity and boundedness of the solution is satisfied: for system (7), we have that if \( 0 < S^n < 1, 0 < E^n < 1, 0 < I^n < 1, \) and \( 0 < R^n < 1 \), then \( 0 < S^{n+1} < 1, 0 < E^{n+1} < 1, 0 < I^{n+1} < 1, \) and \( 0 < R^{n+1} < 1 \) for all \( n \geq 0 \).

4. NSFD Predictor-Corrector Scheme

This section is improved by the approach of a predictor-corrector-type NSFD scheme (7) to obtain the benefits of both methods. For the development of this scheme, firstly, system (7) is taken as a predictor scheme, i.e.,
\[
\begin{align*}
S^{n+1}_p &= S^n + \mu \varphi(h) N \\
E^{n+1}_p &= E^n + \varphi(h) \beta S^n I^n \\
I^{n+1}_p &= I^n + \varphi(h) \sigma E^n \\
R^{n+1}_p &= R^n + \varphi(h) \gamma I^n.
\end{align*}
\]  

(8)

Now, we evaluate system (1) at time \( t + \varphi(h) \) and introduce the term \( \epsilon^{-1}S^{n+1}/\varphi(h) \) (where \( \epsilon \) is just like the accelerating factor and its range is \( 0 < \epsilon < 1 \)). Thus, the expression will be NSFDCL scheme that preserves conservation law represented as
\[
\begin{align*}
S^{n+1} &= S^n + \mu \varphi(h) N + \epsilon^{-1} S^{n+1}_p \\
E^{n+1} &= E^n + \varphi(h) \beta S^{n+1}_p I^n \\
I^{n+1} &= I^n + \varphi(h) \sigma E^{n+1}_p \\
R^{n+1} &= R^n + \varphi(h) \gamma I^{n+1}_p.
\end{align*}
\]  

(9)

Thus, the corrector scheme is obtained as
\[
\begin{align*}
S^{n+1}_c &= S^n + \mu \varphi(h) N + \epsilon^{-1} S^{n+1}_p \\
E^{n+1}_c &= E^n + \varphi(h) \beta S^{n+1}_p I^n \\
I^{n+1}_c &= I^n + \varphi(h) \sigma E^{n+1}_p \\
R^{n+1}_c &= R^n + \varphi(h) \gamma I^{n+1}_p.
\end{align*}
\]  

(10)

where \( R^{n+1} = N - S^{n+1} - E^{n+1} - I^{n+1} \).

5. Convergence Analysis

In this section, the unconditional convergence of the numerical solution is presented by the proposed method. Taking the values as
\[
\begin{align*}
F_1(S, E, I) &= \frac{S + \mu N \varphi(h)}{1 + \varphi(h) [\mu + \beta \varphi(h)]}, \\
F_2(S, E, I) &= \frac{E + \beta \varphi(h) IF_1}{1 + \varphi(h) [\mu + \sigma]}, \\
F_3(S, E, I) &= \frac{I + \alpha \varphi(h) F_2}{1 + \varphi(h) [\mu + \gamma]}, \\
G_1(S, E, I) &= \frac{S + \mu N \varphi(h) + \epsilon^{-1} F_1}{1 + \epsilon^{-1} + \mu \varphi(h) + \beta \varphi(h) F_3}, \\
G_2(S, E, I) &= \frac{E + \beta \varphi(h) G_1 F_3}{1 + \varphi(h) [\mu + \sigma]}, \\
G_3(S, E, I) &= \frac{I + \alpha \varphi(h) G_2}{1 + \varphi(h) [\mu + \gamma]},
\end{align*}
\]  

(11)

where \( F_1, F_2, \) and \( F_3 \) are given as in equation (8).
The convergence and stability analysis of scheme (10) is carried out by calculating the eigenvalues of the Jacobian of the linearized scheme and studying its behavior and evaluated at the fixed points. If \((S^*, E^*, I^*)\) is the fixed point of system (1), then the Jacobian matrix \(JG\) is given by

\[
JG(S^*, E^*, I^*) = \begin{bmatrix}
\frac{\partial G_1(S^*, E^*, I^*)}{\partial S} & \frac{\partial G_1(S^*, E^*, I^*)}{\partial E} & \frac{\partial G_1(S^*, E^*, I^*)}{\partial I} \\
\frac{\partial G_2(S^*, E^*, I^*)}{\partial S} & \frac{\partial G_2(S^*, E^*, I^*)}{\partial E} & \frac{\partial G_2(S^*, E^*, I^*)}{\partial I} \\
\frac{\partial G_3(S^*, E^*, I^*)}{\partial S} & \frac{\partial G_3(S^*, E^*, I^*)}{\partial E} & \frac{\partial G_3(S^*, E^*, I^*)}{\partial I}
\end{bmatrix},
\]

where

\[
\begin{align*}
\frac{\partial F_1}{\partial S} &= \frac{1}{[1 + \mu \phi(h) + \beta \phi(h) I]} \frac{\partial F_1}{\partial E} \\
\frac{\partial F_1}{\partial I} &= -(S + \mu N \phi(h)) \phi(h) \\
\frac{\partial F_2}{\partial S} &= \frac{\beta \phi(h) I \partial F_1 / \partial S}{1 + \phi(h)[\mu + \sigma]} \\
\frac{\partial F_2}{\partial E} &= \frac{1 + \beta \phi(h) I \partial F_1 / \partial E}{1 + \phi(h)[\mu + \sigma]} \\
\frac{\partial F_2}{\partial I} &= \frac{\beta \phi(h)[F_1 + I \partial F_1 / \partial I]}{1 + \phi(h)[\mu + \sigma]} \\
\frac{\partial F_3}{\partial S} &= \frac{\beta \phi(h)[1 + \mu \phi(h) + \beta \phi(h) F_3]}{1 + \phi(h)[\mu + \gamma]} \\
\frac{\partial F_3}{\partial E} &= \frac{\beta \phi(h)[1 + \mu \phi(h) + \beta \phi(h) F_3]}{1 + \phi(h)[\mu + \gamma]} \\
\frac{\partial F_3}{\partial I} &= \frac{\beta \phi(h)[1 + \mu \phi(h) + \beta \phi(h) F_3]}{1 + \phi(h)[\mu + \gamma]}
\end{align*}
\]
5.1 Disease-Free Equilibrium \((S_o, E_o, I_o) = (N, 0, 0)\). The values of functions and its derivatives at DFE point \((N, 0, 0)\) are as

\[
F_1 (N, 0, 0) = N, \quad F_2 (N, 0, 0) = 0, \quad F_3 (N, 0, 0) = 0,
\]

\[
G_1 (N, 0, 0) = N, \quad G_2 (N, 0, 0) = 0, \quad G_3 (N, 0, 0) = 0,
\]

\[
\frac{\partial F_1 (N, 0, 0)}{\partial S} = \frac{1}{1 + \mu \phi (h)},
\]

\[
\frac{\partial F_1 (N, 0, 0)}{\partial E} = 0,
\]

\[
\frac{\partial F_1 (N, 0, 0)}{\partial I} = \frac{-N \beta \phi (h)}{[1 + \mu \phi (h)]},
\]

\[
\frac{\partial F_2 (N, 0, 0)}{\partial S} = 0,
\]

\[
\frac{\partial F_2 (N, 0, 0)}{\partial E} = \frac{1}{1 + \phi (h) \mu + \sigma}],
\]

\[
\frac{\partial F_2 (N, 0, 0)}{\partial I} = \frac{\beta \phi (h)}{1 + \phi (h) \mu + \sigma}.
\]

\[
\frac{\partial F_3 (N, 0, 0)}{\partial S} = 0,
\]

\[
\frac{\partial F_3 (N, 0, 0)}{\partial E} = \frac{\sigma \phi (h)}{[1 + \phi (h) \mu + \sigma], [1 + \phi (h) \mu + \gamma]}],
\]

\[
\frac{\partial F_3 (N, 0, 0)}{\partial I} = \frac{1 + [\sigma \phi (h) \beta \phi (h)] / 1 + \phi (h) \mu + \gamma]}{1 + \phi (h) \mu + \gamma},
\]

\[
\frac{\partial G_1 (N, 0, 0)}{\partial S} = \frac{1}{1 + \mu \phi (h)},
\]

\[
\frac{\partial G_1 (N, 0, 0)}{\partial E} = \frac{-N \sigma \phi (h) \beta \phi (h)}{[1 + \mu \phi (h) + \epsilon^{-1}]} [1 + \phi (h) \mu + \sigma]) [1 + \phi (h) \mu + \gamma]}.
\]
\[
\frac{\partial G_1(N,0,0)}{\partial I} = \frac{-N\beta \phi(h)}{1 + e^{-1} + \mu \phi(h)} \left[ \frac{e^{-1}}{1 + \mu \phi(h)} + \frac{1}{1 + \phi(h)(\mu + \gamma)} + \frac{\sigma N\beta^2 \phi^2(h)}{[1 + \phi(h)(\mu + \sigma)][1 + \phi(h)(\mu + \gamma)]} \right],
\]
\[
\frac{\partial G_2(N,0,0)}{\partial S} = 0,
\]
\[
\frac{\partial G_2(N,0,0)}{\partial E} = \frac{1}{1 + \phi(h)(\mu + \sigma)} \left[ \frac{N\beta \phi^2(h)}{1 + [1 + \phi(h)(\mu + \sigma)][1 + \phi(h)(\mu + \gamma)]} \right],
\]
\[
\frac{\partial G_3(N,0,0)}{\partial I} = \frac{\sigma \phi(h)}{[1 + \phi(h)(\mu + \sigma)][1 + \phi(h)(\mu + \gamma)]} \left[ 1 + \frac{\sigma \beta \phi^2(h)}{[1 + \phi(h)(\mu + \sigma)][1 + \phi(h)(\mu + \gamma)]} \right] \frac{\partial G_3(N,0,0)}{\partial I}
\]
\[
= \frac{1}{[1 + \phi(h)(\mu + \sigma)]} + \frac{N\sigma \beta^2 \phi^2(h)}{[1 + \phi(h)(\mu + \sigma)][1 + \phi(h)(\mu + \gamma)]} \frac{\partial G_3(N,0,0)}{\partial I}
\]
\[
\text{(14)}
\]

For ease in the calculation, we use the following conventions:

\[
\begin{align*}
\alpha &= \mu N\phi(h) > 0, \quad \eta_1 = \mu \phi(h) > 0, \quad \eta_2 \\
&= \beta \phi(h) > 0, \quad \eta_3 = \sigma \phi(h) > 0, \\
\theta &= 1 + e^{-1} + \mu \phi(h) = 1 + e^{-1} + \eta_1 > 1, \\
\delta_1 &= 1 + \phi(h)[\mu + \sigma] > 1, \quad \delta_2
\end{align*}
\]

(15)

It is clear that \(\theta > \eta_1, 1 + \eta_1 > \delta_1, 1 + \eta_1 > \delta_2\), and \(\delta_2 = \theta - e^{-1} + \gamma \phi(h)\). If \(R_0 = \sigma \beta N / (\mu + \sigma)(\mu + \gamma) < 1\), the Jacobian calculated at disease-free points \((S_0^*, E_0^*, I_0^*) = (N,0,0)\) is given as

\[
JG(N,0,0) = \begin{bmatrix}
\frac{\partial G_1(N,0,0)}{\partial S} & \frac{\partial G_1(N,0,0)}{\partial E} & \frac{\partial G_1(N,0,0)}{\partial I} \\
\frac{\partial G_2(N,0,0)}{\partial S} & \frac{\partial G_2(N,0,0)}{\partial E} & \frac{\partial G_2(N,0,0)}{\partial I} \\
\frac{\partial G_3(N,0,0)}{\partial S} & \frac{\partial G_3(N,0,0)}{\partial E} & \frac{\partial G_3(N,0,0)}{\partial I}
\end{bmatrix}
\]

(16)

Since the partial derivatives using the conventions are

\[
\begin{align*}
\frac{\partial G_1(N,0,0)}{\partial S} &= \frac{1}{1 + \eta_1}, \\
\frac{\partial G_1(N,0,0)}{\partial E} &= \frac{-N\eta_3 \eta_1}{\theta \delta_1 \delta_2}, \\
\frac{\partial G_1(N,0,0)}{\partial I} &= \frac{-N\eta_2 \left( e^{-1} + \frac{1}{\theta} + \frac{N\eta_2 \eta_3}{\delta_1 \delta_2} \right)}{\theta \delta_1 \delta_2}, \\
\frac{\partial G_2(N,0,0)}{\partial S} &= 0, \\
\frac{\partial G_2(N,0,0)}{\partial E} &= \frac{1}{\delta_1 \delta_2 + \frac{N\eta_2 \eta_3}{\delta_1 \delta_2}}, \\
\frac{\partial G_2(N,0,0)}{\partial I} &= \frac{N\eta_3 \eta_1 + \frac{N\eta_2 \eta_3}{\delta_1 \delta_2}}{\delta_1 \delta_2}, \\
\frac{\partial G_3(N,0,0)}{\partial S} &= 0, \\
\frac{\partial G_3(N,0,0)}{\partial E} &= \frac{\eta_3 + \frac{N\eta_2 \eta_3}{\delta_1 \delta_2}}{\delta_1 \delta_2}, \\
\frac{\partial G_3(N,0,0)}{\partial I} &= \frac{1}{\delta_2} \left( \frac{N\eta_2 \eta_3}{\delta_1 \delta_2} + \frac{N^2 \eta_2^2 \eta_3^2}{\delta_1 \delta_2} \right).
\end{align*}
\]
So,
\[
\lambda^2 - \lambda \left( \frac{\delta_1 \delta_2 + N \eta_3}{\delta_1^2 \delta_2} \right) + \left( \frac{\delta_1^2 \delta_2 + \delta_1 N \eta_3 + N^2 \eta_3^2 \delta_1^3}{\delta_1^2 \delta_2^2} \right)
\]

\[
+ \left( \frac{\delta_1^2 \delta_2 + \delta_1 N \eta_3 + N^2 \eta_3^2 \delta_1^3}{\delta_1^2 \delta_2^2} \right) ^2 - \left( \frac{\eta_3 \delta_1 \delta_2 + N \eta_3 \delta_2^2}{\delta_1^2 \delta_2^2} \right) = 0,
\]

where
\[
A = \left( \frac{\delta_1 \delta_2 + N \eta_3}{\delta_1^2 \delta_2} \right) + \left( \frac{\delta_1^2 \delta_2 + \delta_1 N \eta_3 + N^2 \eta_3^2 \delta_1^3}{\delta_1^2 \delta_2^2} \right) = \text{trace } J^*,
\]
\[
B = \left( \frac{\delta_1 \delta_2 + N \eta_3}{\delta_1^2 \delta_2} \right) \left( \frac{\delta_1^2 \delta_2 + \delta_1 N \eta_3 + N^2 \eta_3^2 \delta_1^3}{\delta_1^2 \delta_2^2} \right) - \left( \frac{\eta_3 \delta_1 \delta_2 + N \eta_3 \delta_2^2}{\delta_1^2 \delta_2^2} \right) = \det J^*,
\]
\[
J^* = \begin{bmatrix}
\frac{1}{\delta_1} + \frac{N \eta_3 \delta_1^2}{\delta_1^2 \delta_2} & \frac{N \eta_2 \delta_1}{\delta_1 \delta_2} + \frac{N^2 \eta_3^2 \delta_1^3}{\delta_1^2 \delta_2} \\
\frac{N \eta_2 \delta_1}{\delta_1 \delta_2} + \frac{N^2 \eta_3^2 \delta_1^3}{\delta_1^2 \delta_2} & \frac{1}{\delta_2} + \frac{N \eta_3 \delta_2^2}{\delta_1 \delta_2} + \frac{N^2 \eta_3^2 \delta_1^3}{\delta_1 \delta_2^2}
\end{bmatrix}
\]

To calculate the eigenvalues of $J^*$, the following lemma is proved.

**Lemma 1.** For the quadratic equation, $\lambda^2 - \lambda A + B = 0$, both roots satisfy $|\lambda_i| < 1$, $i = 2, 3$ if and only if the following conditions are satisfied [25]:

\[(1) \quad 1 - A + B > 0,
\]
\[(2) \quad 1 + A + B > 0,
\]
\[(3) \quad B < 1.
\]

Let us define $A = \text{Trace } J^*, B = \det J^*$. Therefore,
\[ A = \left( (\delta_1 + \delta_2)(N\eta_2\eta_3 + \delta_1\delta_2) \right) + N^2\eta_2^2\eta_3^2 > 0, \]

\[ B = \frac{1}{\delta_1\delta_2} + \frac{N\eta_2\eta_3}{\delta_1\delta_2} < 1, \]

\[ f(-1) = 1 + A + B > 0, \]

\[ f(0) = B = \frac{1}{\delta_1\delta_2} + \frac{N\eta_2\eta_3}{\delta_1\delta_2} = \frac{1 + N\eta_2\eta_3}{\delta_1\delta_2} = \frac{1 + N\eta_2\eta_3}{\delta_1\delta_2} < 1 \quad \text{(since } R_0 < 1), \]

\[ \Rightarrow B < 1. \]

Now, for

\[ f(1) = 1 - A + B \]

\[ = \frac{\delta_1^2 + (\delta_1 + \delta_2)(N\eta_2\eta_3 + \delta_1\delta_2) + N^2\eta_2^2\eta_3^2 + N\eta_2\eta_3 + \delta_1\delta_2}{\delta_1\delta_2} \]

\[ > 0. \]  

(23)

As all the conditions of the lemma hold for \( R_0 < 1 \), therefore the absolute value of both eigenvalues of \( J^* \) is less than one, whenever \( R_0 < 1 \). Thus, the numerical scheme in equations (8) and (10) will converge unconditionally to disease-free equilibrium \( (N, 0, 0) \) for any value of time step \( h \) whenever \( R_0 < 1 \) which is also computationally verified in Figure 2(a).

5.2. Endemic Equilibrium \( (S_e, E_e, I_e) = (N/R_0, \mu N/\mu + \sigma (1 - 1/R_0), \mu/\beta (R_0 - 1)) \). The value of functions and its derivatives at an endemic point is as

\[ F_1(S_e, E_e, I_e) = \frac{N}{R_0}, \]

\[ F_2(S_e, E_e, I_e) = \frac{\mu N (1 - 1/R_0)}{(\mu + \sigma)}, \]

\[ F_3(S_e, E_e, I_e) = \frac{\mu}{\beta} (R_0 - 1), \]

\[ G_1(S_e, E_e, I_e) = \frac{N}{R_0}, \]

\[ G_2(S_e, E_e, I_e) = \frac{\mu}{\beta} (R_0 - 1), \]

\[ G_3(S_e, E_e, I_e) = \frac{\mu N (1 - 1/R_0)}{(\mu + \sigma)}. \]  

(24)
\( \frac{\partial G_1(S_o, E_o, I_o)}{\partial S} = \frac{1}{1 + \mu \phi(h)R_0} - \frac{N \mu \beta \phi^2(h)(R_0 - 1)}{R_0[1 + e^{-1} + \mu \phi(h)R_0][1 + \phi(h)(\mu + \sigma)][1 + \mu \phi(h)R_0][1 + \phi(h)(\mu + \gamma)]} \)

\( \frac{\partial G_1(S_o, E_o, I_o)}{\partial E} = \frac{-N \mu \beta \phi^2(h)}{R_0[1 + e^{-1} + \mu \phi(h)R_0][1 + \phi(h)(\mu + \sigma)][1 + \mu \phi(h)R_0][1 + \phi(h)(\mu + \gamma)]} \)
\frac{\partial G_1(S, E, I, J)}{\partial I} = \frac{-N\beta \phi (h)}{1 + e^{-1} + \mu \phi (h)R_0} \left[ 1 + \mu \phi (h)R_0 \right] \\
\frac{\partial G_2(S, E, I, J)}{\partial S} = \frac{\mu \beta \phi (h)(R_0 - 1)}{\beta [1 + \phi (h)(\mu + \sigma)] [1 + \mu \phi (h)R_0]}
\frac{\partial G_3(S, E, I, J)}{\partial E} = \frac{1}{[1 + \phi (h)(\mu + \sigma)] [1 + \mu \phi (h)R_0]}
\frac{\partial G_4(S, E, I, J)}{\partial I} = \frac{-N\mu \beta^2 \delta (h)e^{-1}(R_0 - 1)}{\beta [1 + \phi (h)(\mu + \sigma)] [1 + \mu \phi (h)R_0]}
\frac{\partial G_5(S, E, I, J)}{\partial S} = \frac{\mu \beta \phi (h)(R_0 - 1)}{[1 + \phi (h)(\mu + \gamma)] [1 + \mu \phi (h)R_0]}
\frac{\partial G_6(S, E, I, J)}{\partial E} = \frac{1}{[1 + \phi (h)(\mu + \gamma)]}
\frac{\partial G_7(S, E, I, J)}{\partial I} = \frac{-N\mu \beta^2 \delta (h)e^{-1}(R_0 - 1)}{\beta [1 + \phi (h)(\mu + \gamma)] [1 + \mu \phi (h)R_0]}
\frac{\partial G_8(S, E, I, J)}{\partial S} = \frac{\mu \beta \phi (h)(R_0 - 1)}{[1 + \phi (h)(\mu + \gamma)] [1 + \mu \phi (h)R_0]}
Table 1: Comparison of NSFD scheme with Euler and RK-4 schemes.

<table>
<thead>
<tr>
<th>Scheme</th>
<th>0.01</th>
<th>0.1</th>
<th>100</th>
<th>1000</th>
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<tr>
<td>Euler PC</td>
<td>Convergence</td>
<td>Divergence</td>
<td>Divergence</td>
<td>Divergence</td>
</tr>
<tr>
<td>RK-4</td>
<td>Convergence</td>
<td>Divergence</td>
<td>Divergence</td>
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<tr>
<td>NSFDPC</td>
<td>Convergence</td>
<td>Convergence</td>
<td>Convergence</td>
<td>Convergence</td>
</tr>
</tbody>
</table>

(a) Disease-free equilibrium

(b) Disease-free equilibrium

(c) Endemic equilibrium

(d) Susceptible fraction

Figure 3: Continued.
Infected fraction
Exposed fraction
\(0\)
\(1\)
\(2\)
\(3\)
\(4\)
\(5\)
\(6\)
\(7\)
\(8\)
\(0\)
\(0.5\)
\(1\)
\(1.5\)
\(2\)
\(2.5\)
\(3\)
\(3.5\)
\(4\)
\(4.5\)
\(5\)
\(\times 10^5\)
\(\times 10^5\)
NSFD-PC
100 200 300 400 500 600
cobian of EE remains less than one, if the largest eigenvalue against each step size, and Figure 2(b) shows that, for all step sizes, the spectral radius of the Jacobian of EE remains less than one, if \(R_0 > 1\), which implies that the numerical scheme in equations (8) and (10) is unconditionally convergent if \(R_0 > 1\), for all step sizes.

6. Numerical Results and Discussion

All the methods showed the convergence for small step sizes in Table 1. However, for large values of step sizes, only the normalized NSFDPC converge to the correct disease-free point for \(\beta = 0.1 \times 10^{-5}\) as well as the correct endemic point for \(\beta = 0.3 \times 10^{-5}\). This means that, for the value of the basic reproductive number (threshold parameter), \(R_0 < 1\); then, DFE is stable, i.e., solution to the system \((S, E, I, R)\) are converging to it. This can be seen from Figures 3(a)–3(c) for \(h = 0.01\). Also, for the value of the basic reproductive number (threshold parameter) \(R_0 > 1\), then EE is stable, i.e., solution to the system \((S, E, I, R)\) is converging to it. This can be seen from Figures 3(d)–3(f) for \(h = 0.01\).

Figures 4(a)–4(c) show how the NSFDPC method of DFE converges to the equilibrium point for different step sizes. Figures 4(d)–4(f) show how the NSFDPC method of EE converges to the equilibrium point for different step sizes.

For comparison with the well-known RK-4 method to system (1), using the parameter values given in Table 2, it is found that, in Figures 5(a)–5(f), the numerical solution converges for \(h = 0.01\) for both equilibrium points, and...
Figure 4: Time plots of susceptible and infected population using the NSFDPC method with different step sizes: (a) $h = 0.1$, (b) $h = 10$, and (c) $h = 1000$. 
Table 2: Parameters value of the measles model.

<table>
<thead>
<tr>
<th>Parameters</th>
<th>$N$</th>
<th>$\mu$</th>
<th>$\sigma$</th>
<th>$\gamma$</th>
</tr>
</thead>
<tbody>
<tr>
<td>DFE</td>
<td>$5 \times 10^7$ year$^{-1}$</td>
<td>0.02</td>
<td>45.6 year$^{-1}$</td>
<td>73 year$^{-1}$</td>
</tr>
<tr>
<td>EE</td>
<td>$(S_0, E_0, I_0) = (N, 0, 0), \beta = 0.1 \times 10^{-5}$</td>
<td>$(S_e, E_e, I_e) = (2.435 \times 10^7, 1.125 \times 10^4, 7022.671), \beta = 0.3 \times 10^{-5}$</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Disease-free equilibrium

(a) Susceptible fraction

(b) Exposed fraction

(c) Infected fraction

(d) Endemic equilibrium

Figure 5: Continued.
Figure 6 shows overflow for a critical value of step size, i.e., \( h = 0.1 \) of DFE and EE, respectively.

Another popular numerical method is the Euler predictor-corrector (E-PC) technique, which employs the explicit Euler method as a predictor and the trapezoidal rule as the corrector. This combination is second-order accurate but has similar stability properties in PECE mode to the explicit Euler method alone. Figures 7(a)–7(f) show convergence results for \( h = 0.01 \) in both cases that are DFE and EE. The value of \( h = 0.1 \) which produces overflow when solving the system with the parameter values of Table 2 for the PECE combination can be seen in Figure 8.

Thus, the presented numerical results demonstrated that NSFDPC has better convergence property following the Euler PC and RK-4, as shown in Figure 9. It is proved that the approximations made by other standard numerical methods experience difficulties in preserving either the stability or the positivity of the solutions or both but NSFDPC is unconditionally convergent.
Figure 7: Time plots of population using the Euler-PC method with $h = 0.01$. 
7. Conclusions

In this paper, a normalized NSFDPC for the SEIR model concerning the transmission dynamics of measles is constructed and analysed. This proposed numerical scheme is very competitive. It is qualitatively stable, that is, it double refines the solution and gives realistic results even for large step sizes. It is dynamically consistent with a continuous system and unconditionally convergent and satisfies the positivity of the state variables involved in the system. Simulations are carried out and its usefulness is compared with a well-known numerical method of standard difference schemes such as RK4 and Euler predictor-corrector method. The standard finite difference schemes are highly dependent on step sizes and initial value problems, but NSFDPC is independent of these two features which make it more practical. Also, this method saves computation time and memory.

Figure 8: Divergence graphs of the population using the Euler-PC method with step size $h = 0.1$.

Figure 9: Comparative convergence graphs of the NSFDPC method.
Data Availability

The data used to support the findings of this study are available from the corresponding author upon request.

Conflicts of Interest

The authors declare no conflicts of interest.

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