International Conference on Optimization, Simulation and Control

Extending Nonstandard Finite Difference Scheme for the SIR Epidemic Model

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Abstract

This paper aims to develop the new scheme of computing an ordinary differential equations system according to the rules for extending a non-standard finite difference scheme (NSFD). In existing non-standard finite difference methods, denominator functions for the discrete derivatives are the same. But in new method these functions are different for each equations. Using this method, we computed the SIR model. Numerical comparisons confirm that the accuracy of new method is better than that of other standard methods such as the second-order Runge-Kutta method, the Euler method and some ready-made MATLAB codes.

Keywords

Nonstandard finite difference scheme; SIR model; Conservation law.

Introduction

Standard Finite Scheme: $X'(t) \approx \frac{X(t+h)-X(t)}{h}$

Nonstandard Finite Scheme[1]: $X'(t) \approx \frac{X(t+h)-X(t)}{\psi(h)}, \psi(h) = h + O(h^2)$

For example, $\psi(h) = \frac{\exp(\mu h)-1}{\mu}$.

We address systems ODEs where we separate a linear and a nonlinear part[2]:

$$X' = AX(t) + B\big(X(t)\big) \tag{1}$$

The analytical solution: $X(t+h) = e^{hA}X(t) + \int_t^{t+h} e^{(t+h-s)A}B\big(X(s)\big)ds$

We will therefore prefer the more general form

$$X_{k+1} = e^{hA}X_k + (e^{hA} - I)A^{-1}B(X_k, X_{k+1}) \tag{2}$$

Here, we define the renormalization matrix $\Phi(h) = \big(e^{hA} - I\big)A^{-1}$, and we can replace the e^{hA} by $I + \Phi(h)A$ in (2) to obtain

$$\Phi^{-1}(h)(X_{k+1} - X_k) = AX_k + B(X_k, X_{k+1}) \tag{3}$$

Where the renormalization matrix verifies the property

$$\Phi(h) = hI + O(h^2) \text{ as } h \to 0.$$

Rule2': *The first order derivatives in a non standard scheme for a system of ordinary differential equations should be approximated as*

$$X' \simeq \Phi(h)^{-1}(X_{k+1} - \Psi(h)X_k)$$

where

$$\Phi(h) = hI + O(h^2) \text{ as } h \longrightarrow 0$$

and

$$\Psi(h) = I + O(h^2) \text{ as } h \longrightarrow 0.$$

The SIR model with Demography

Here, matrix formulation of the SIR epidemic model introduced in [3] is presented:

$$\begin{aligned} S' &= \Lambda - \beta SI - \mu S \\ I' &= \beta SI - \alpha I - \mu I \\ R' &= \alpha I - \mu R \end{aligned} \tag{4}$$

where

- *S(t)* – Susceptible individuals;
- *I(t)* – Infective individuals;
- *R(t)* – Recovered individuals;
- Λ – the birth rate;
- β – the transmission rate;
- α – the recovery rate;
- μ – the death rate.

Construction of New Scheme

$$\frac{S^{n+1} - S^n}{\phi_1} = \Lambda - \mu S^n - \beta S^{n+1} I^n$$

$$\frac{I^{n+1} - I^n}{\boldsymbol{\phi_2}} = -(\alpha + \mu)I^n + \beta S^{n+1} I^n \tag{5}$$

$$\frac{R^{n+1} - R^n}{\phi_1} = -\mu R^n + \alpha I^n + \frac{\boldsymbol{\phi_1 - \phi_2}}{\boldsymbol{\phi_1 \phi_2}}\big(\boldsymbol{I^{n+1} - I^n}\big)$$

$$\Phi^{-1}(h) = \begin{pmatrix} \phi_1^{-1} & 0 & 0 \\ 0 & \phi_2^{-1} & 0 \\ 0 & \frac{\phi_2 - \phi_1}{\phi_2 \phi_1} & \phi_1^{-1} \end{pmatrix} \tag{6}$$

$$\phi_1(h) = \frac{1 - e^{-h\mu}}{\mu}, \quad \phi_2(h) = \frac{1 - e^{-h(\alpha+\mu)}}{\alpha + \mu} \tag{7}$$

Conservation Law

The model of the total population is $N'(t) = \Lambda - \mu N$, where $N = S + I + R$. The population size is not constant, but it is asymptotically constant, since $N(t) \to \frac{\Lambda}{\mu}$ as $t \to \infty$. This limit must be valid for any numerical method.

Theorem 1. $\lim_{t\to\infty}[S(t) + I(t) + R(t)] = \frac{\Lambda}{\mu}$.

Theorem 2. $\lim_{n\to\infty}[S^n + I^n + R^n] = \frac{\Lambda}{\mu}$.

Numerical Results

Numerical solution provided by the new and standard schemes with parameter values and initial conditions: $S_0 = 0.9,\ I_0 = 0.05,\ R_0 = 0.05, \Lambda = 10, \mu = 0.1, \alpha = 3, \beta = 0.05$. Epidemic Equilibrium: $S^* = 62,\ I^* = 1.23, R^* = 36.77$.

Figure 1. New Scheme. **(h=1)**

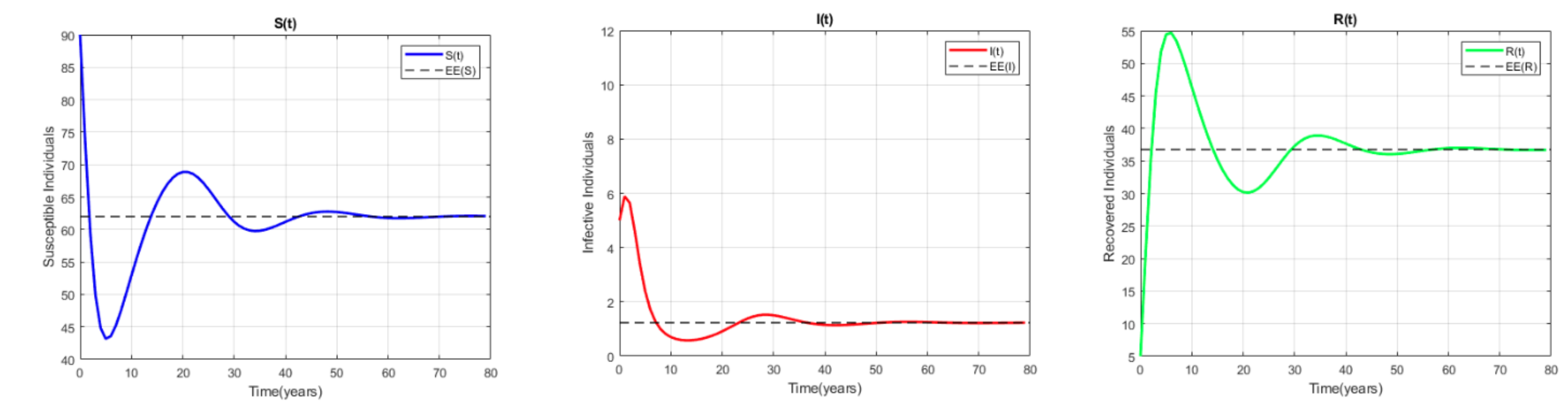


Figure 2. Standard Scheme. **(h=1)**

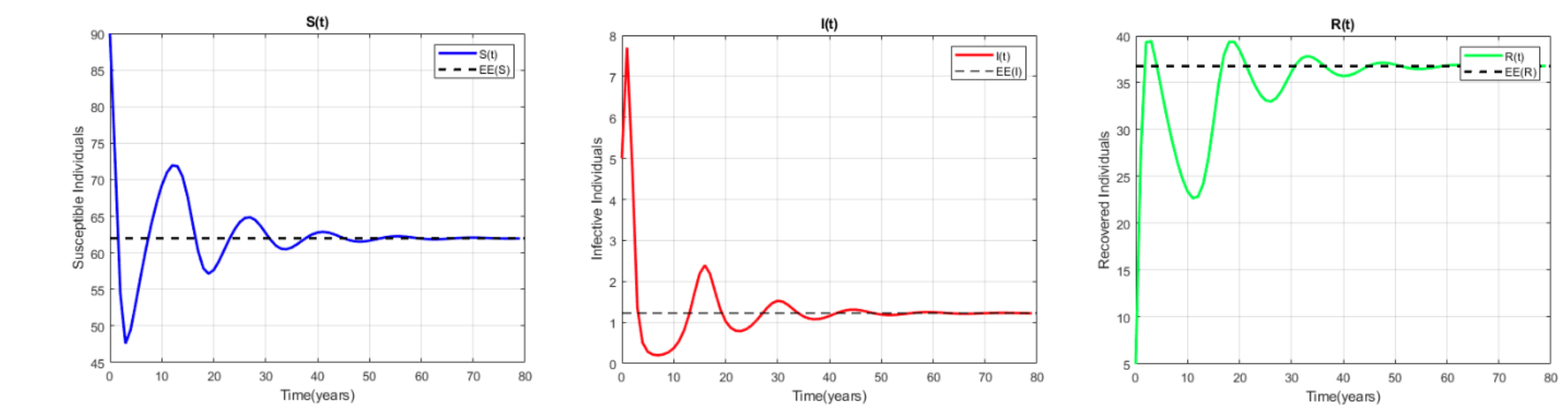


Figure 3. New Scheme. **(h=2)**

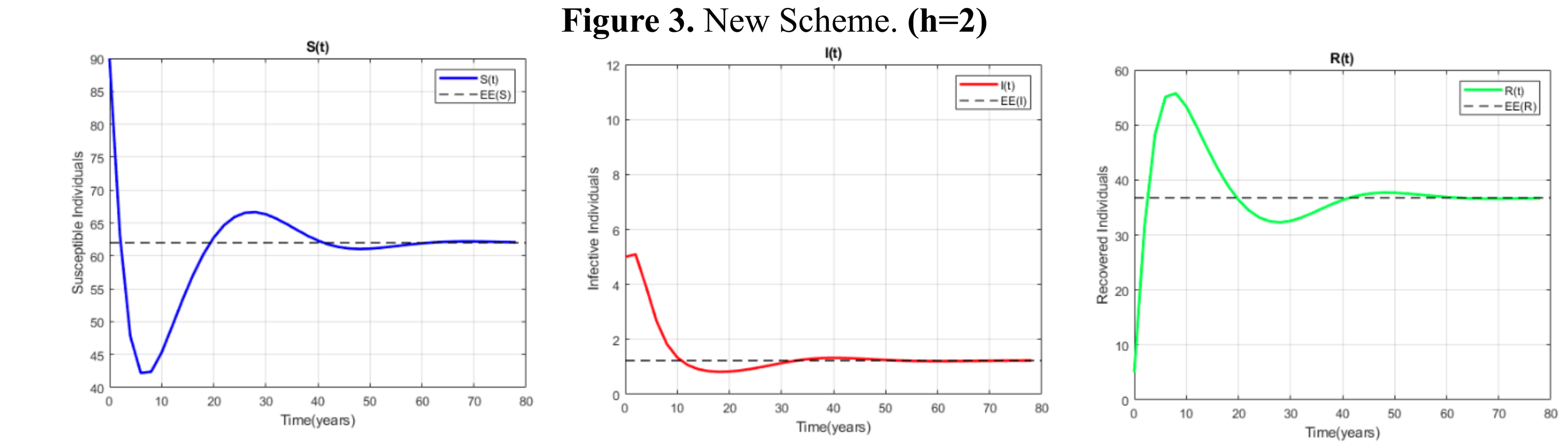
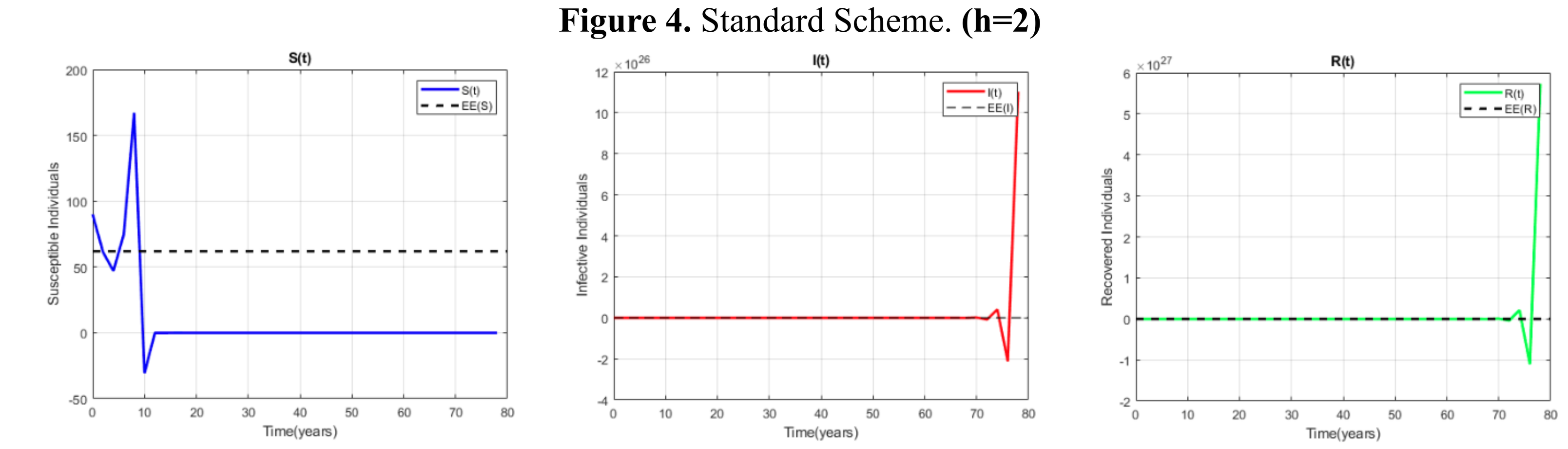


Figure 4. Standard Scheme. **(h=2)**



Conclusions

By comparing the numerical results obtained from the new scheme and standard scheme, it was shown that the extending method is made unconditionally stable by preserving conservation law for each step-size (*h*=1, *h*=2). It is also confirmed that standard scheme do not converge to the epidemic equilibrium point for *h*=2. Therefore, it can be concluded that the new scheme preserve features of the SIR epidemic model.

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