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Efficient Nonstandard Grünwald-Letnikov Finite Difference Method for Time Fractional SIR Epidemic Model

N. H. Sweilam[1*]; Nourhan Hamdy[2]; Ehab A. El-Sayed[2]; Tarek Emam[3]

[1*] Mathematics Department, Faculty of Science, Cairo University, Giza, Egypt.

[2] Department of Science and Engineering Mathematics, Faculty of Petroleum and Mining Engineering, Suez University, Suez, Egypt

[3] Department of Mathematics, Faculty of Science, Suez University, Suez, Egypt

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ABSTRACT

Nonlinear ordinary differential equations are commonly used for modeling physical, chemical, and biological systems. Understanding the quality and quantity of these systems requires the use of mathematical models and their simulations. Infectious disease mathematical models are widely used by many researchers. In recent years, epidemic models have become a valuable tool for analyzing the dynamics of infectious diseases. Unfortunately, often the analytic solution of such differential equations' models cannot be obtained explicitly. Hence, numerical techniques to study approximately these models are used. One of the simplest numerical techniques is the finite difference methods. This paper aims to present an efficient numerical method to study the fractional time SIR epidemic model. The numerical method that used to study this model is the nonstandard Grünwald-Letnikov finite difference method. Comparative study with the standard methods is done. Various graphs are presented to describe the numerical results. The obtained results indicate that the proposed method has been successful applied to efficiently study the SIR epidemic model.

1. Introduction

It is known that epidemics are one of the most serious issues of health in the world which need to be transacted. Many studies, for a long time, of the dynamics of epidemic diseases have been introduced. Models that include the time derivatives and consist of systems of ordinary differential equations are the most effective approach to study the dynamics of epidemics. In these models, each equation represents the change in the number of bodies in different categories given by continuous variables.

Nonlinear ordinary differential equations (ODEs) are commonly used for modeling physical, chemical, and biological systems. Mathematical models and their simulations are important for understanding the quality and quantity of these systems [1].

Fractional calculus (FC) is a generalization of the integer order calculus [2]. In fractional calculus, researchers try to solve problems with α-order derivatives and integrals, where there are several definitions for derivatives of order α [3][4].

The main goal of this article is to introduce and present nonstandard technique to numerical study the time fractional SIR epidemic model. The constructed method preserves the characteristics of the conservation law. The rest of the paper is structured as follows: In section 2, we introduce the mathematical model for the SIR epidemic model with its equilibrium points. Moreover, the non-standard finite difference method (NSFDM) is introduced in section 3. In section 4, the basic mathematical formulas of the fractional derivatives are introduced. In section 5, the fractional order SIR epidemic model with Grünwald-Letnikov nonstandard finite difference method (GL-NSFDM) discretization is given and the obtained results.

2. Mathematical Model

Here, the mathematical model for the SIR (Susceptible, Infectious, or Recovered) epidemic is introduced , it is related to rubella disease in London, for more details see [5] and tables 1 and 2. This model consists of the following three characteristics, given by the following nonlinear system of differential equation.

* Corresponding author at Cairo University
E-mail addresses: nsweilam@sci.cu.edu.eg (N.H. Sweilam)

$$S'(t) = N\mu - \mu S(t) - N\beta \frac{S(t)I(t)}{1 + aI}, \tag{1}$$

$$I'(t) = N\beta \frac{S(t)I(t)}{1 + aI} - (\mu + \nu)I(t), \tag{2}$$

$$R'(t) = \nu I(t) - \mu R(t). \tag{3}$$

Subjected to the following initial conditions: -

$S(0) = S_0, \quad I(0) = I_0, \quad R(0) = R_0, \quad t > 0, \quad a > 0.$

Also, the list of all parameters and their interpretation are introduced in table 2.

The conservation law is clearly satisfied by the successive system of equations, which implies that the population is constant when added together. It is possible to normalize the population to one, since it is assumed to be constant [5]:

$S(t) + I(t) + R(t) = 1.$

The above equation must be valid for any numerical method. The reproduction number of system {(1)-(3)} is given as follows [5]:

$$\mathcal{R}_0 = \frac{N\beta}{\mu + \nu},$$

the system {(1)-(3)} has two equilibrium points as follows [5]:

- $E_0^* = (1, 0, 0)$: $the\ disease - free\ equilibrium;$
- $E^* = (S^*, I^*, R^*)$: $the\ endemic\ equilibrium,$

where

$$E^* = (S^*, I^*, R^*) = \left(\frac{R_0\mu a + NB}{R_0(\mu a + NB)}, \frac{\mu(R_0 - 1)}{\mu a + NB}, \frac{\nu(R_0 - 1)}{\mu a + NB} \right).$$

3. NSFDM

In this section, we introduce several comments that are related to the NSFDM, first proposed by Mickens [6]. The main idea behind the construction of most of the NSFDM 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 because variables representing subpopulations must never have negative values [7]. To be designated as an NSFD, a method must meet at least one of the following criteria [8] [9]:

- In the first-order discrete derivatives, the step-size h in the denominator is not traditional and uses a nonnegative function $\varphi(h)$, such that:

$\varphi(h) = h + O(h^2), as\ h \to 0.$

- A nonlocal approximation is used.

4. Basic fractional preliminaries

We recall several important definitions of the fractional calculus used throughout the remaining sections of this paper.

- Let α be a real nonnegative number. Then the Riemann-Liouville fractional-order integral operator of order α J_a^α defined on $L_1 = [a, b]$ as follows [10] [11]:

$$J_a^\alpha f(x) = \frac{1}{\Gamma(\alpha)} \int_a^x (x - t)^{\alpha - 1} f(t) dt, \quad a < x < b. \tag{4}$$

- Let $\alpha \in \mathbb{R}$ and $m = \lceil \alpha \rceil$. The Riemann-Liouville fractional-order differential operator of order α, D_a^α is defined by [12] for a function f:

$$D_a^\alpha f = D^m J_a^{m-\alpha} f. \tag{5}$$

- Let α be a real nonnegative number. For a positive integer m such that

$m-1 < \alpha \leq m$, the Riemann-Liouville fractional-order differential operator of a function f of order α is defined by [12]:

$$D_a^{\alpha} f(x) = \frac{1}{\Gamma(m-\alpha)} \frac{d^m}{dx^m} \int_a^x (x-t)^{m-\alpha-1} f(t) dt . \quad (6)$$

Where $\Gamma(\cdot)$ is the gamma function.

Now, to apply Mickens scheme, we have chosen this Grünwald−Letnikov fractional derivative approximation as follows, for more details see [13]:

$$D^{\alpha} y(t) = \lim_{h \to 0} h^{-\alpha} \sum_{j=0}^{\frac{t}{h}} \omega_j^{\alpha} \, y(t_{n-j}) = f(t_n, y(t_n)) , \quad n = 1,2,3, \cdots. \quad (7)$$

Where $t_n = nh, \ and \ \omega_j^{\alpha}$, are the Grünwald−Letnikov coefficients define as

$\omega_j^{\alpha} = \left(1 - \frac{1+\alpha}{j}\right) \omega_{j-1}^{\alpha}$ and $\omega_0^{\alpha} = h^{-\alpha}, \ j = 1,2,3, \cdots.$

Proposition 1 , [11] :

Given non negative initial conditions, the solution to (1)-(3) are bounded for all $t \geq 0$. Furthermore, the closed set $C = \{(S,I,R) \in R_+^3 : S + I + R = 1\}$, attracts of (1)-(3) for any initial condition in R_+^3.

Table 1: All variables of system {(1)-(3)} and their definitions.

Variable	Definition
$S(t)$	Susceptible individuals.
$I(t)$	Infective individuals.
$R(t)$	Recovered individuals.
$N(t)$	The total population. $N = S + I + R$

Table 2: All parameters in the system {(1)-(3)} and their interpretation.

Parameter	Interpretation
β	The transmission rate.
μ	The death rate and it is assumed equal to birth rate.
ν	The recovery rate.
a	The inhibitory rate.

5. Fractional order SIR epidemic model

Herein, we consider the SIR model (1-3) using the fractional order derivative. This model consists of three nonlinear differential equations. We generalized the order of the equations to the fractional order α. Also, when $\alpha = 1$ the fractional order system reduces to classical one. The SIR-modified model with GL fractional order derivative represented as follows:

$$D_t^{\alpha} S(t) = \mu - \mu S(t) - N\beta \frac{S(t)I(t)}{1 + aI}, \quad (8)$$

$$D_t^{\alpha} I(t) = N\beta \frac{S(t)I(t)}{1 + aI} - (\mu + \nu)I(t), \quad (9)$$

$$D_t^{\alpha} R(t) = \nu I(t) - \mu R(t), \quad (10)$$

GL-NSFDM

Applying Mickens' scheme by replacing the step size h by a function $\varphi(h)$ and using the Grünwald–Letnikov discretization method [11], yields the following equations:

$$\sum_{j=0}^{n+1} \omega_j^{\alpha} S(t_{n+1-j}) = \mu - \mu S(t_{n+1}) - N\beta \frac{S(t_{n+1})\, I(t_n)}{1 + a\, I(t_n)}, \quad (11)$$

$$\sum_{j=0}^{n+1} \omega_j^{\alpha} I(t_{n+1-j}) = N\beta \frac{S(t_{n+1})\, I(t_n)}{1 + a\, I(t_n)} - (\mu + \nu)\, I(t_{n+1}), \quad (12)$$

$$\sum_{j=0}^{n+1} \omega_j^{\alpha} R(t_{n+1-j}) = \nu\, I(t_{n+1}) - \mu\, R(t_{n+1}), \quad (13)$$

where $\omega_0^{\alpha} = (\varphi(h))^{-\alpha}$, $\varphi(h) = \frac{e^{\mu h} - 1}{\mu}$, then, use the nonlocal approximations for the nonlinear terms and $\varphi(h)$, we obtain:

$$S_{n+1} = \frac{\mu - \sum_{j=1}^{n+1} \omega_j^{\alpha} S_{(n+1-j)}}{(\varphi(h))^{-\alpha} + \mu + N\beta \frac{I_n}{1 + a\, I_n}}, \quad (14)$$

$$I_{n+1} = \frac{N\beta \frac{S_{n+1}\, I_n}{1 + a\, I_n} - \sum_{j=1}^{n+1} \omega_j^{\alpha} I_{(n+1-j)}}{(\varphi(h))^{-\alpha} + (\mu + \nu)}, \quad (15)$$

$$R_{n+1} = \frac{\nu\, I_{(n+1)} - \sum_{j=1}^{n+1} \omega_j^{\alpha} R_{(n+1-j)}}{(\varphi(h))^{-\alpha} + \mu} \quad (16)$$

6. Numerical results

To clarify the results of the method used to solve the presented model, we will study the model at various time steps and show a comparison between the standard finite difference method and the nonstandard finite difference method.

With the initial conditions and the parameters

$S_0 = 0.9, \quad I_0 = 0.05, \quad R_0 = 0.05,$

$\alpha = 0.8, \quad N\beta = 123, \quad \mu = 0.04, \quad \nu = 24, \quad a = 0.01.$

Table 3:

Result obtained by SFDM and NSFDM for $S_0 = 0.9, I_0 = 0.05, R_0 = 0.05, N\beta = 123, \mu = 0.04, \nu = 24, a = 0.01$ with different time step size.

The epidemic model (1)-(3) has a disease-free equilibrium point for $R_0 < 1$ and an endemic equilibrium point for $R_0 > 1$.

we can conclude that NSFDM is unconditionally converge for large h, while the SFDM converge only when h is small.

$\alpha = 0.8$			$\alpha = 1$		
h	NSFDM	SFDM	h	NSFDM	SFDM
0.01	Convergent	Convergent	0.01	Convergent	Convergent
0.1	Convergent	Divergent	0.1	Convergent	Divergent
1	Convergent	Divergent	1	Convergent	Divergent
10	Convergent	Divergent	10	Convergent	Divergent
960	Convergent	Divergent	60	Convergent	Divergent

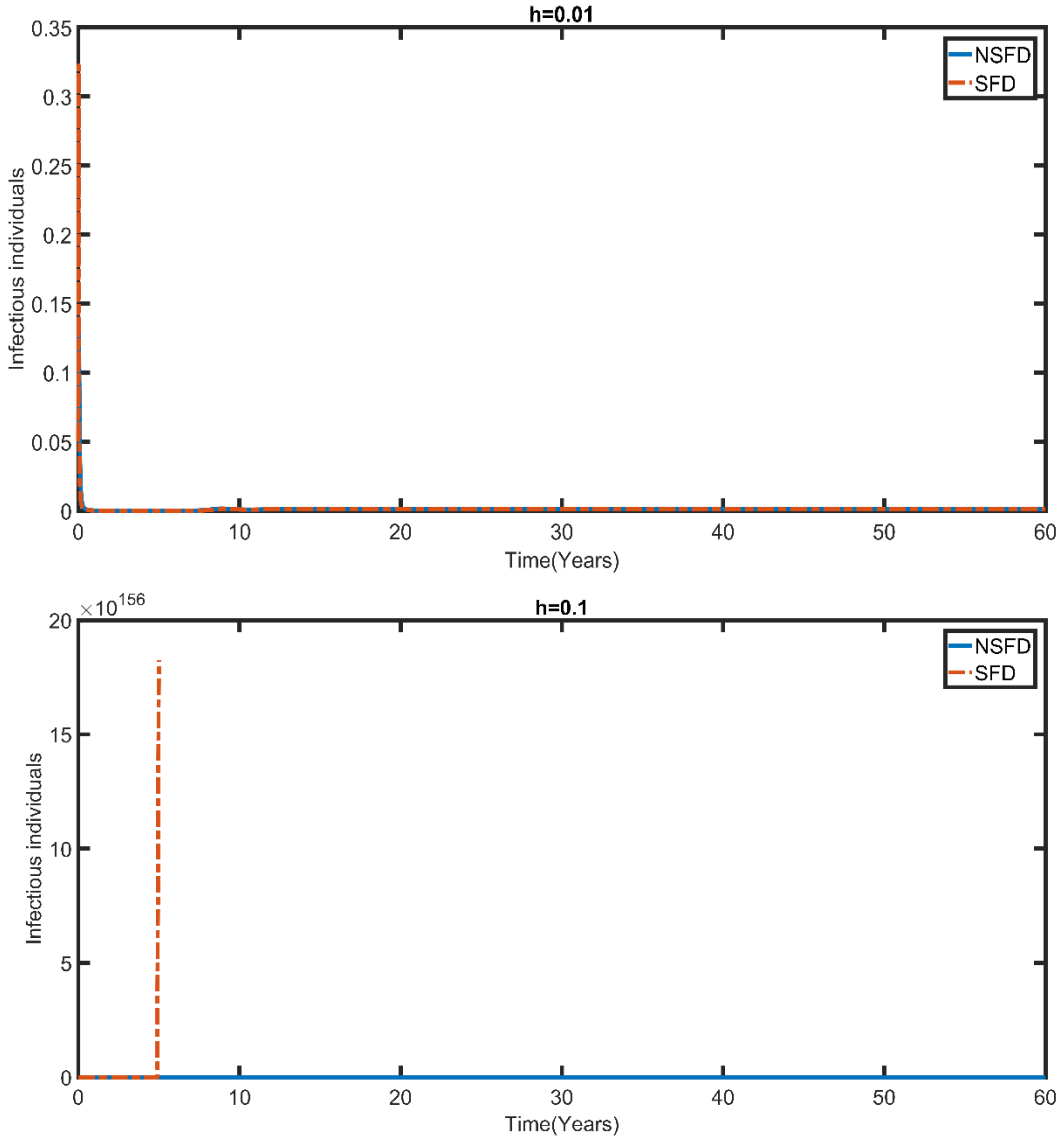

Figure 1. Shows that the NSFD provide good approximations and converge to the endemic equilibrium with different time step size h and $\alpha = 0.8$.

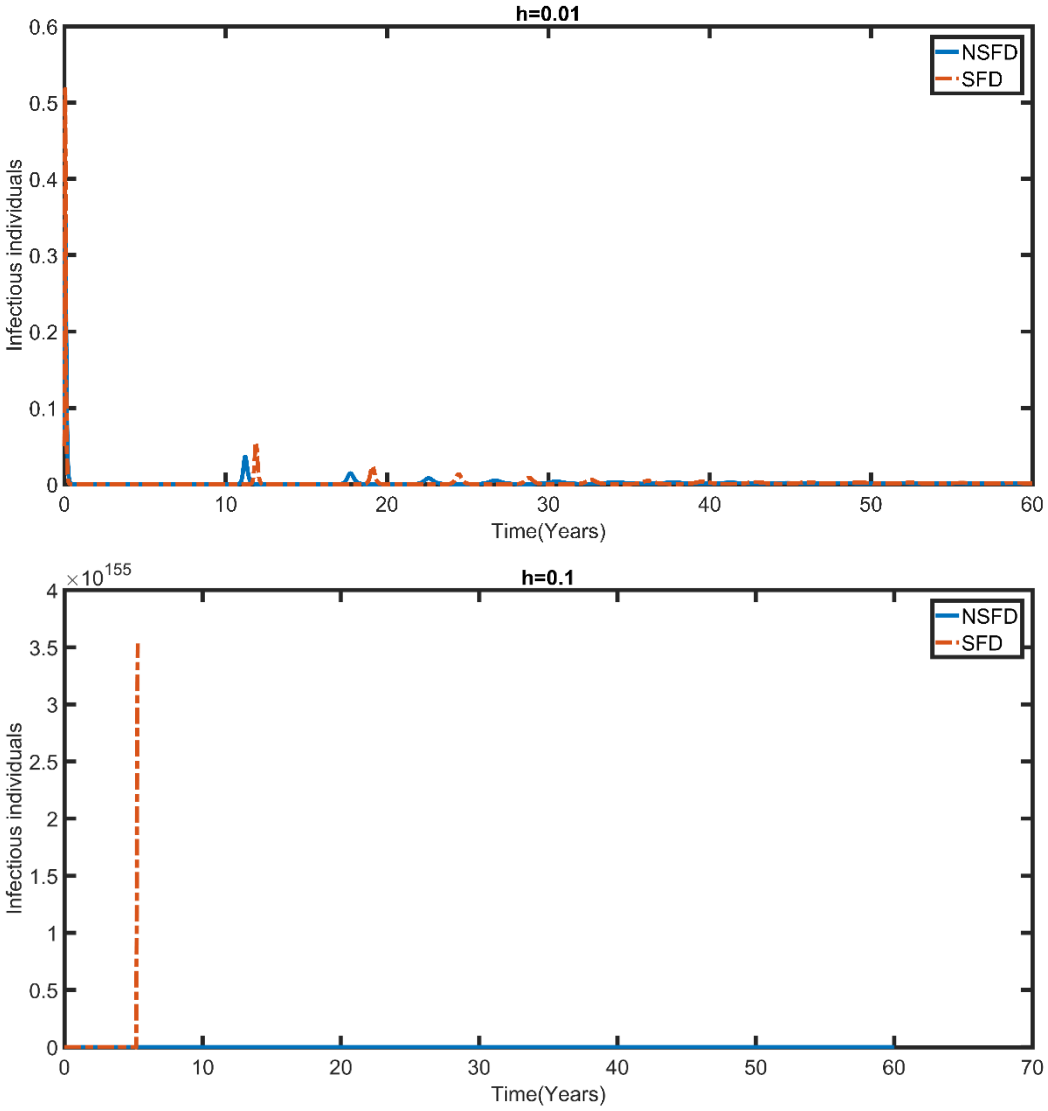

Figure 2. Shows that the NSFD provide good approximations and converge to the endemic equilibrium with different time step size h and $\alpha = 1$.

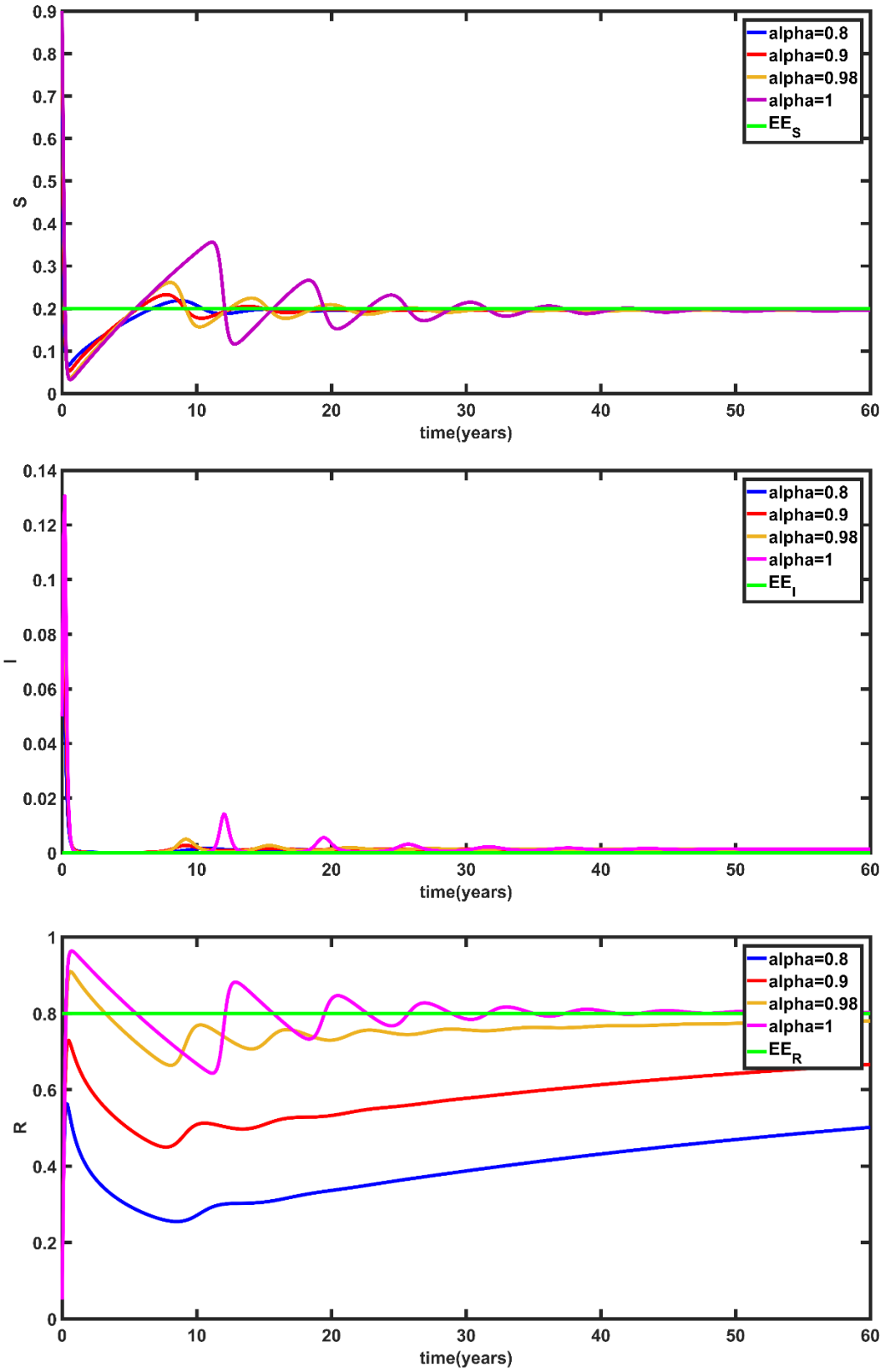

Figure 3. Numerical simulation of the all variables of the SIR model at different α.

Shows that the method provides good approximations and converge to the endemic equilibrium.

Conclusion

In this work, we used non-standard finite difference methods (NSFD) to study numerically the time fractional SIR pandemic model. From the numerical results presented in this paper, it can be concluded that the fractional order model for SIR is a broadening and more appropriate than the integer order model. Furthermore, the NSFD scheme being discussed here is more effective in solving the fractional order model for the SIR model than the SFD scheme. The positivity of the solution is preserved, and the stability regions are larger than the SFD method. Thus, it is possible to conclude that the NSFD method retains the characteristics of the SIR epidemic model.

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