Matrix Nonstandard Numerical Schemes for Epidemic Models

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Abstract:- This paper is concerned with the construction and developing of several nonstandard finite difference ($NSFD$) schemes in matrix form in order to obtain numerical solutions of epidemic models. In particular, we deal with a classical SIR epidemic model and a seasonal model associated with the evolution of the transmission of respiratory syncytial virus RSV in the human population. The first model is an autonomous differential equation system, and the second one is a nonautonomous one which generally is more difficult to be solved. The numerical schemes developed here can be used in other general epidemic models based on ordinary differential equations. One advantage of the developed methodology is that can be used easily by the scientific community without special knowledge. In addition, these $NSFD$ schemes which are based on the the nonstandard finite difference methods developed by Mickens solve numerically systems describing epidemics with less computational effort. Finally, with these matrix $NSFD$ schemes it can be exploited more easily matrix operations advantages.

Key–Words: Matrix difference scheme, Nonstandard schemes, Matrix computation, Numerical solution, Epidemic model.

1 Introduction

In engineering and other sciences, many problems are modeled using autonomous and nonautonomous systems of nonlinear differential equations. However, due to highly nonlinearity and the coupling of the differential equations, exact solutions are usually complicated or impossible to determinate. For strong nonlinearity, numerical methods are commonly used. The traditional approach to solve models with strong nonlinearity is to adopt the Euler or Runge-Kutta type numerical schemes. These traditional schemes of finite differences used to solve numerically systems of nonlinear differential equations of initial value raise questions such as what is the truncation error or the region of stability. For instance, forward Euler, Runge-Kutta and others methods to solve nonlinear initial value problems, sometimes fail, generating oscillations, bifurcations, chaos and spurious states [25, 37]. Moreover some methods despite using adaptative step sizes still fail (see [32]).

Using a small time step size in the numerical solution derived by numerical methods can avoid the obtention of incorrect solutions, but at expense of extra computational cost. An efficient numerical method applied over long time intervals, needs, however, the use of time steps which are the maximum possible, consistent with accuracy and stability. This is particularly desirable when used to solve dynamic systems which exhibit smooth long-term behaviour to be

accurately represented on a reasonably coarse mesh [27, 28]. Therefore, it is necessary to construct and develop robust numerical schemes that yield accurate numerical solutions using other techniques, for example, the nonstandard difference method, which was developed by Ronald Mickens [27, 28] and have brought applications in different areas [2, 6, 7, 12, 13, 15, 24, 29] and references therein.

As we mentioned above, classical numerical schemes sometimes fail [5, 25]. One alternative to prevent these classes of numerical instabilities is the construction of schemes using the nonstandard finite-difference method. This technique, developed by Mickens [27, 28] have brought a creation of new numerical schemes preserving the physical properties, especially the stability properties of equilibria of the approximated system [1, 2, 12, 13, 19, 22, 31].

Anguelov and Lubuma [2] have used Mickens' techniques to design nonstandard versions of the explicit and implicit Euler and the second order Runge-Kutta methods. In addition Dimitrov and Kojouharov [14] have designed a variety of such nonstandard finite difference schemes for general two-dimensional systems based on the explicit Euler, the implicit Euler and the second-order Runge-Kutta methods.

In this paper we develop and construct several nonstandard finite difference schemes in matrix form in order to obtain numerical solutions of epidemic models. In particular, we deal with a classical SIR epidemic model and a seasonal model associated with the evolution of the transmission of respiratory syncytial virus RSV in the human population. The first model is an autonomous model and the second is a nonautonomous one which generally is more difficult to be solved. The numerical schemes developed can be used in other general epidemic models which are based on ordinary differential equations. One advantage of the developed methodology is that can be used easily by the scientific community without any special knowledge. In addition these nonstandard numerical schemes which are based on the nonstandard finite difference methods solve numerically the systems describing epidemics with less computational effort. This fact is important since these epidemic models require different unknown parameters and these parameters often needs to be estimated through a computational expensive fitting process to epidemiological data and this process requires that the model be solved several times. One basic property of some of the nonstandard numerical schemes is that they can be used with larger time step sizes, saving computational cost when integrating over long time periods. It is well known that in several cases the Euler method and other well-known methods produce bad approximations simulating the model for large time step sizes.

The first model considers the whooping cough mathematical model presented in [16]. This model is represented by a classical SIR epidemic model. In fact this model was solved in [34] using an unconditionally stable positive $NSFD$ scheme, where the $NSFD$ scheme converge to the steady state for any time step size h. The second epidemic model considers the RSV transmission at population level. This model is based on a nonautonomous system of differential equations which has been studied previously in several works [3, 39]. For this last model also a $NSFD$ scheme of predictor-corrector type has been developed in [7]. However, in this paper the $NSFD$ schemes are developed for both epidemic models using matrix forms in order to improve computational efficiency by means of matrix operations.

The importance of solving these epidemic models is due to the fact that mathematical models have been revealed as a important tool in studying the spread and control of infectious diseases [8, 20]. The most recent epidemiological models have involved aspects such as passive immunity, stages of infection, vertical transmission, disease vectors, macroparasitic loads, age structure, social and sexual mixing groups, spatial spread, vaccination, quarantine, and chemotherapy [20]. Several of these models are based upon systems of ordinary differential equations (ODE). In these models commonly the variables represent subpopulations of susceptibles (S), infected (I), recovered (R), latent (E), transmitted diseases vectors, and so forth. Thus, the ODE system describes the dynamics of the different classes of subpopulations in the model [10, 21, 33, 36]. It is important to remark that several numerical methods have been applied to solve epidemic models [7, 9, 24, 26, 35]. In addition, the numerical solution of models with periodic behavior are more difficult to be obtained in general. For instance in [38] the authors find that ADM solutions of Duffing, Van der Pol and Rayleigh equations were not periodic. They proposed an alternative technique where Laplace transformation and Padé approximant were applied to obtain a better periodic solution. However, interesting works investigating the solution of ordinary differential equations systems capable of exhibiting chaotic behavior have been developed successfully in [7, 18]. Therefore, one of the aims of this paper is to investigate numerically the application of nonstandard finite difference schemes in matrix form to seasonal epidemic models represented by systems of nonautonomous nonlinear ordinary differential equations in order to obtain periodic behaviors.

This paper is organized as follows. Section 2 introduces the epidemic mathematical models for the whooping cough SIR and for the transmission of

RSV. These epidemic models are presented in their particular matrix forms. In Section 3 we construct the $NSFD$ schemes using matrix forms of the aforementioned epidemic mathematical models. Numerical simulations using the different $NSFD$ numerical schemes in matrix form for different time step sizes are performed in Section 4. Discussion and conclusions are presented in Section 5.

2 Mathematical models

Many epidemics are modeled by autonomous systems of nonlinear ordinary differential equations which implies the assumption that the parameters of the model are independent of time. However, several diseases present the effect of a seasonally varying contact rate on the behavior of the disease. Thus a nonautonomous system of nonlinear ordinary differential equations is necessary to model the seasonal epidemics. In this way, in order to model these epidemic models it is necessary to rely on both systems of differential equations. These models can be generally described using the following n-dimensional system,

$$\frac{dy}{dt} = f(t,y); \quad y(t_0) = y_0, \tag{1}$$

where $y = [y_1, y_2, ..., y_n]^T : [t_0; T) \longrightarrow \mathbb{R}^n$, the function $f = [f_1, ..., f_n]^T : [0, +\infty) \times \mathbb{R}^n \longrightarrow \mathbb{R}^n$ is differentiable and $y_0 \in \mathbb{R}^n$. The autonomous systems of nonlinear ordinary differential equations can be seen as particular case of system (1), where the system is of the following form:

$$\frac{dy}{dt} = f(y); \quad y(t_0) = y_0, \tag{2}$$

Thus following the ideas proposed by Beretta and Capasso [11, 17] many mathematical epidemic models can be written in the following general matrix form:

$$\frac{dz}{dt} = diag(z)Az + Bz + c, \tag{3}$$

where,

- $z \in \mathbb{R}^n$, being n the number of different classes or subpopulations,
- $c \in \mathbb{R}^n$, is a constant vector associated to the independent terms,
- $A = (a_{ij})$ $i, j = 1, ..., n$, is a real constant matrix associated to the nonlinear terms,
- $B = (b_{ij})$ $i, j = 1, ..., n$, is a real constant matrix associated to the linear terms.

2.1 Mathematical model for the whooping cough (SIR)

In this subsection we present the SIR epidemic model [34], 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 assume immunity in this class. The mathematical model under study is the following:

$$\begin{aligned} \dot{S}(t) &= \mu - \mu S(t) - N\beta S(t)I(t), \\ \dot{I}(t) &= N\beta S(t)I(t) - (\mu + \nu)I(t), \\ \dot{R}(t) &= \nu I(t) - \mu R(t), \end{aligned} \tag{4}$$

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.

In this model since the population is assumed constant and have been normalized to unit one gets that for all time t that

$$S(t) + I(t) + R(t) = 1. \tag{5}$$

It is important to mention that the steady state of (4) is given by the following points: the disease free point $(1, 0, 0)$ and the endemic point $\left(\frac{1}{R_0}, \frac{\mu}{\mu+\nu}(1 - \frac{1}{R_0}), \frac{\nu}{\mu+\nu}(1 - \frac{1}{R_0})\right)$, where $R_0 = \frac{N\beta}{\mu+\nu} > 1$ is the basic reproductive number associated with the model [34].

In this way, the epidemic model (4) can be written in the general matrix form (3), where, $z = [S(t); I(t); R(t)]^T$, $c = [\mu; 0; 0]^T$ and the matrix A and B are given by:

$$A = \begin{pmatrix} 0 & -N\beta & 0 \\ N\beta & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \text{ and } B = \begin{pmatrix} -\mu & 0 & 0 \\ 0 & -\mu - \nu & 0 \\ 0 & \nu & -\mu \end{pmatrix}.$$

For details about parameters and hypothesis we refer the readers to [16, 34]. Each one of the parameters values of the model $N\beta$, μ and ν with their numerical values with biological sense are given in Table 1.

2.2 Mathematical seasonal model for the transmission of the respiratory syncytial virus RSV

In this subsection we are concerned with the mathematical seasonal model for the transmission of the

Table 1: Parameters values for the SIR mathematical epidemic model for the whooping cough (4).

$N\beta$	μ	ν
370	0.04	24

respiratory syncytial virus RSV. The mathematical model is based on a system of first order ordinary differential equations and it was proposed in [39]. The model has several parameters that need to be estimated fitting the model to medical data [4]. It is important to mention that the model is fitted to the epidemiological data using some of the developed $NSFD$ schemes with the aim of reducing computational time. In this model without loss of generality, it is assumed that $S(t) + I(t) + R(t) = 1$. The model is the classical $SIRS$ (Susceptibles, Infected, Recovered and Susceptibles), of the following form

$$\begin{aligned} \dot{S}(t) &= \mu - \mu S(t) - \beta(t)S(t)I(t) + \gamma R(t),\ S(0) = S_0 > 0, \\ \dot{I}(t) &= \beta(t)S(t)I(t) - \nu I(t) - \mu I(t),\ I(0) = I_0 > 0, \\ \dot{R}(t) &= \nu I(t) - \gamma R(t) - \mu R(t),\ R(0) = R_0 > 0. \end{aligned} \tag{6}$$

The transmission coefficient function $\beta(t)$ between classes $S(t)$ and $I(t)$ is a continuous T-periodic function, called the transmission rate. This function is generally approximated by a cosinusoidal function $\beta(t) = b_0(1 + b_1\cos(\frac{2\pi}{T}(t + \varphi))$ where $b_0 > 0$ is the baseline transmission parameter, $0 < b_1 \leq 1$ measures the amplitude of the seasonal variation in transmission and $0 \leq \varphi \leq 2\pi$ is the phase angle normalized [39]. In this way, following the ideas proposed by Beretta and Capasso [11, 17] the epidemic model (6) can be written in the following general matrix form,

$$\frac{dz}{dt} = diag(z)Az + Bz + c, \tag{7}$$

where, $z = [S(t); I(t); R(t)]^T$, $c = [\mu; 0; 0]^T$, the matrix A and B are given by:

$$A = \begin{pmatrix} 0 & -\beta(t) & 0 \\ \beta(t) & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \text{ and } B = \begin{pmatrix} -\mu & 0 & \gamma \\ 0 & -\mu-\nu & 0 \\ 0 & \nu & -\mu-\gamma \end{pmatrix}.$$

For details about parameters and hypothesis we refer the reader to [3, 23, 39]. Each one of the parameters values of the model γ, μ, ν, b_0, b_1 and ϕ for particular regions are given in Table 2. Since the parameter values vary for each region, these parameter values are modified in the numerical simulations.

Table 2: Parameters values for the mathematical seasonal model for the transmission of the respiratory syncytial virus RSV (6).

$Region$	b_0	b_1	ϕ	μ	ν	γ
$Valencia(Spain)$	37	0.31	0.9	0.009	36	1.8
$Gambia$	60	0.16	0.15	0.041	36	1.8

3 Construction of the matrix nonstandard numerical schemes

In this section we construct the matrix $NSFD$ schemes for the epidemic mathematical models (4) and (6). The main idea of these nonstandard schemes is to transfer essential properties of the continuous models to the discrete schemes and to obtain accurate and computational inexpensive schemes in order to minimize the fitting process time to obtain the unknown parameters of the models. The approximated solution of the variables representing the subpopulations $S(t), I(t)$ and $R(t)$ need to be positive. Computational inexpensive schemes can be obtained since large time step sizes can be used, saving computational costs when integrating over long time periods.

From herein without loss of generality and for the sake of clarity we obviate the explicit dependence on t. Thus, a one-step numerical scheme with a step size h that approximates the solution $y(tk)$ of model (1) can be written in the following form:

$$D_h(y_k) = F_h(f; y_k), \tag{8}$$

where $D_h(y_k) \approx \frac{dy}{dt}$, $F_h(f; y_k) \approx f(y)$ and $t_k = t_0 + kh$.

In this way a scheme is called nonstandard if at least one of the following conditions is satisfied [1],

1. $F_h(f; y_k) = g(y_{k+1}; y_k; h)$, where $g(y_{k+1}; y_k; h)$ is a nonlocal approximation of the right-hand side function $f(t, y)$.

2. Discretization of derivative is not traditional, i.e., $D_h(y_k) = \frac{(y_{k+1}-y_k)}{\varphi(h)}$, where $\varphi(h) = h + \mathcal{O}(h^2)$ is a nonnegative real-valued function on $\mathbb{R}$ called denominator function that satisfies the following properties [30]:

   (a) $\varphi(h) = h + \mathcal{O}(h^2)$, and

   (b) $0 \leq \varphi(h) < 1$ for all $h > 0$,.

Through this paper the nontraditional derivative will be computed using $\varphi(h)$ as:

$$\varphi(h) = \frac{1 - e^{-\lambda h}}{\lambda}. \tag{9}$$

On the other hand, the traditional or standard derivative is computed using $\varphi(h) = h$. For the construction of matrix $NSFD$ schemes of models (4) and (6), we rely on the matrix form structure (3). The approximations of temporal derivatives are done by means of a generalized forward scheme of first order. Hence, if $g(t) \in C^1(\mathbb{R})$, let us to define its derivative as

$$\frac{dg(t)}{dt} = \frac{g(t+h) - g(t)}{\varphi(h)} + \mathcal{O}(\varphi(h)) \text{ as } h \longrightarrow 0. \tag{10}$$

Note that the above definition is consistent with the traditional definition of derivative, since

$$\begin{aligned}\frac{dg(t)}{dt} &= \lim_{h\longrightarrow 0}\left\{\frac{g(t+h)-g(t)}{\varphi(h)} + \mathcal{O}(\varphi(h))\right\} \\ &= \lim_{h\longrightarrow 0}\frac{g(t+h)-g(t)}{h}\lim_{h\longrightarrow 0}\frac{h}{\varphi(h)} + \lim_{h\longrightarrow 0}\mathcal{O}(\varphi(h)) \\ &= \dot{g}(t).\end{aligned}$$

3.1 Matrix Euler $NSFD$ scheme

The first numerical scheme is constructed to obtain the solutions $S(t)$, $I(t)$ and $R(t)$ of the models and it is defined in matrix form by

$$\frac{z^{n+1}-z^n}{\varphi(h)} = diag(z^n)Az^n + Bz^n + c, \tag{11}$$

where this particular discretization is made based on the Euler scheme, but with the derivative approximated by a nontraditional form. Thus after rearranging, yields the following explicit form,

$$z^{n+1} = z^n + \varphi(h)\left(diag(z^n)Az^n + Bz^n + c\right). \tag{12}$$

3.2 Matrix $NSFD$ scheme 2

The second numerical scheme is defined in matrix form by

$$\frac{z^{n+1}-z^n}{\varphi(h)} = diag(z^n)Az^n + Bz^{n+1} + c. \tag{13}$$

where this particular discretization is done based on the forward implicit Euler scheme applied only on the terms related to the matrix B and with the derivative approximated by a nontraditional form. In this case one gets the following explicit form,

$$z^{n+1} = \left[I - \varphi(h)B\right]^{-1}\left[z^n + \varphi(h)\left(diag(z^n)Az^n + c\right)\right], \tag{14}$$

if $[I - \varphi(h)B]$ is invertible.

3.3 Matrix $NSFD$ scheme 3

The third numerical scheme is defined in matrix form by

$$\frac{z^{n+1}-z^n}{\varphi(h)} = diag(z^n)Az^{n+1} + Bz^n + c, \tag{15}$$

where this particular discretization is done based on the forward implicit Euler scheme applied only on the nonlinear component. Therefore, after rearranging, it yields the following explicit form,

$$z^{n+1} = \left[I - \varphi(h)diag(z^n)A\right]^{-1}\left[z^n + \varphi(h)\left(Bz^n + c\right)\right], \tag{16}$$

if $[I - \varphi(h)diag(z^n)A]$ is invertible.

3.4 Matrix $NSFD$ scheme 4

The last numerical scheme is defined in matrix form by

$$\frac{z^{n+1}-z^n}{\varphi(h)} = diag(z^n)Az^{n+1} + Bz^{n+1} + c, \tag{17}$$

where this particular discretization is done based on the mixing of the schemes 2 and 3 with the derivative approximated by a nontraditional form. One gets the following explicit form,

$$z^{n+1} = \left[I - \varphi(h)diag(z^n)A - \varphi(h)B\right]^{-1}\left(z^n + \varphi(h)c\right), \tag{18}$$

if $[I - \varphi(h)diag(z^n)A - \varphi(h)B]$ is invertible.

4 Numerical results

In this section, the numerical results for the SIR model and the seasonal mathematical model for the transmission of respiratory syncytial virus RSV using the four matrix proposed $NSFD$ schemes are shown. In order to test the accuracy of the $NSFD$ schemes we perform several numerical simulations varying the time step size. The numerical results are presented in two different subsections: one for the SIR model and other for the seasonal RSV.

Since an exact analytic solution for both epidemic mathematical models are unknown, we take in the numerical comparisons as the true solution the computational expensive 4-th order Runge-Kutta scheme with a very small time step size $h = 0.0001$ after checking its numerical consistency with other numerical schemes. In addition the numerical comparisons are made using the infected population $I(t)$ for two main reasons: the infected population is the most important one and usually this population is the one included in the fitting process to epidemiological data.

4.1 Numerical solution of the whooping cough SIR model

As it was mentioned before this model considers the whooping cough using model presented in [16]. We solve numerically this model using matrix $NSFD$ schemes in order to improve computational efficiency by means of matrix operations. This model has two equilibrium points: the disease free point $(1, 0, 0)$ and the endemic point $\left(\frac{1}{R_0}, \frac{\mu}{\mu+\nu}(1-\frac{1}{R_0}), \frac{\nu}{\mu+\nu}(1-\frac{1}{R_0})\right)$. Thus, numerical solutions need to converge to any of these equilibrium points depending on the parameter values.

In Fig. 1 it can be seen a first numerical simulation using all the numerical schemes with traditional derivative and these results show that they are similar for a time step size $h = 0.0005$ as was expected. In Table 3 it is shown the computation time of of Euler, matrix $NSFD$ and 4-th order Runge-Kutta numerical scheme with time step size $h = 0.0005$. It can be observed that the matrix $NSFD$ schemes and Euler are less expensive in computational time than the 4-th order Runge-Kutta numerical scheme, despite the matrix ordinary differential equation system is small. In an epidemic model where the system to be solved and the simulation time are large, it is expected that the time difference would increase.

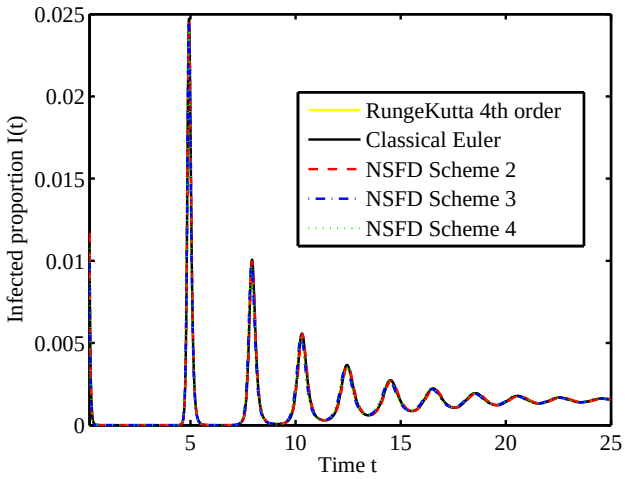

Fig. 1: Numerical comparisons for the SIR model, using Euler and matrix $NSFD$ scheme 4, both with a time step size $h = 0.0005$ for the whooping cough SIR model.

In the next numerical simulations the time step size is increased in order to investigate which numerical scheme can produce the best results with a large time step sizes. In Fig. 2 it can be seen that the Euler classical scheme solution fails to represent the infected $I(t)$ population of the SIR model (4). Notice, that despite the use of the same time step size $h = 0.01$, the $NSFD$ scheme 4 with $\lambda = 1$ converges to the correct endemic equilibrium point. Thus, a first advantage of the $NSFD$ is obtained.

$Time$	Euler	Scheme 2	Scheme 3	Scheme 4	Runge-Kutta
$[0, 25]$	$16.87s$	$16.84s$	$16.12s$	$16.26s$	$54.32s$
$[0, 50]$	$73.9s$	$74.0s$	$77.2s$	$74.7s$	$240.3s$

Table 3: Comparison of the computation time of Euler, matrix $NSFD$ and 4-th order Runge-Kutta numerical schemes with time step size $h = 0.0005$ for the whooping cough SIR model.

In Figs. 3, 4, 5 and 6 it can be observed that despite the use of a large time step size $h = 0.01$, the $NSFD$ schemes converge to the correct equilibrium point. However, the frequency is not captured exactly due to the large time step size. However, it can be seen in 6 that the $NSFD$ scheme 4 produces the best approximation. On the other hand, it can be observed that the graphics of the right hand side obtained using nontraditional derivative do not differ greatly from the ones of the left hand side obtained using the standard derivative, with the exception of 5 where the accuracy of $NSFD$ scheme 3 improves with the nonstandard derivative.

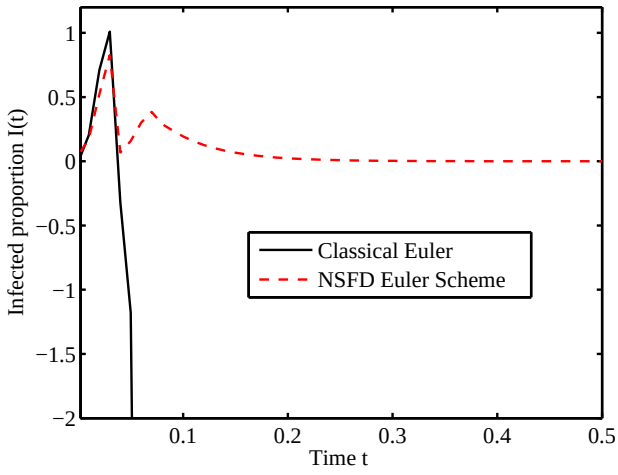

Fig. 2: Numerical comparisons for the SIR model, using Euler and $NSFD$ scheme 4 with $\lambda = 1$, both with a time step size $h = 0.01$.

4.2 Numerical solution of the seasonal RSV model

As in previous subsection we take the 4-th order Runge-Kutta scheme with a very small time step size $h = 0.0001$ as the exact solution of the seasonal RSV model for numerical comparisons purposes. As the

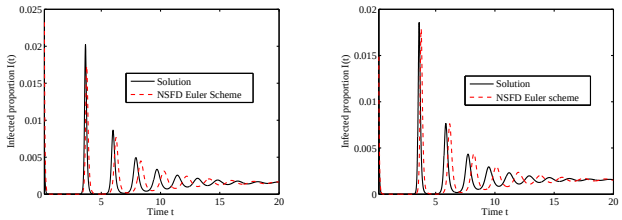

Fig. 3: Numerical comparisons for the SIR model, using $NSFD$ Euler scheme with a time step size $h = 0.01$. On the right hand side with the nonstandard derivative using $\lambda = 1$ (see expression 9).

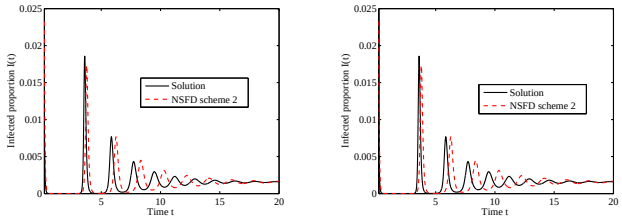

Fig. 4: Numerical comparisons for the SIR model, using $NSFD$ scheme 2 with a time step size $h = 0.005$. On the right hand side with the nonstandard derivative using $\lambda = 1$ (see expression 9).

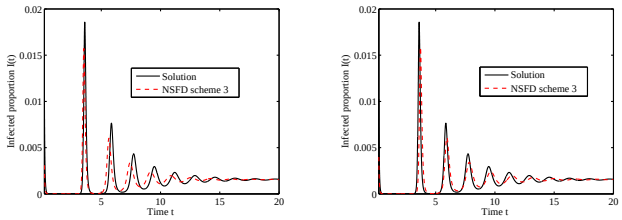

Fig. 5: Numerical comparisons for the SIR model, using $NSFD$ scheme 3 with a time step size $h = 0.005$. On the right hand side with the nonstandard derivative using $\lambda = 10$ (see expression 9).

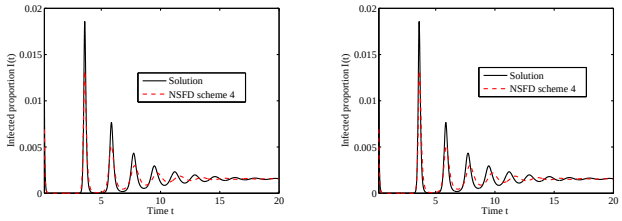

Fig. 6: Numerical comparisons for the SIR model, using $NSFD$ scheme 4 with a time step size $h = 0.005$. On the right hand side is with the nonstandard derivative using $\lambda = 1$ (see expression 9).

contact rate parameter β is very important from the epidemic dynamic point of view, different values were taken in the numerical simulations for the seasonal RSV model. In order to show clearly the numerical results, two different types of $NSFD$ schemes are presented; schemes with standard derivative and with nontraditional derivative. These numerical results are presented in different subsections. In this way it is easy to observe the effects of nonlocal approximations and nontraditional derivatives.

In Fig. 7 it can be seen a first numerical simulation for the seasonal RSV model using all the numerical schemes with traditional derivative and these results show that they are similar for a time step size $h = 0.0001$ as was expected. In Table 4 it is shown the computation time of of Euler, matrix $NSFD$ and 4-th order Runge-Kutta numerical scheme with time step size $h = 0.0001$. It can be observed that the matrix $NSFD$ schemes and Euler are less expensive in computational time than the 4-th order Runge-Kutta numerical scheme, despite the matrix ordinary differential equation system is small. Notice that in this case the time step size need to be smaller due to the more complex periodic behavior of the system.

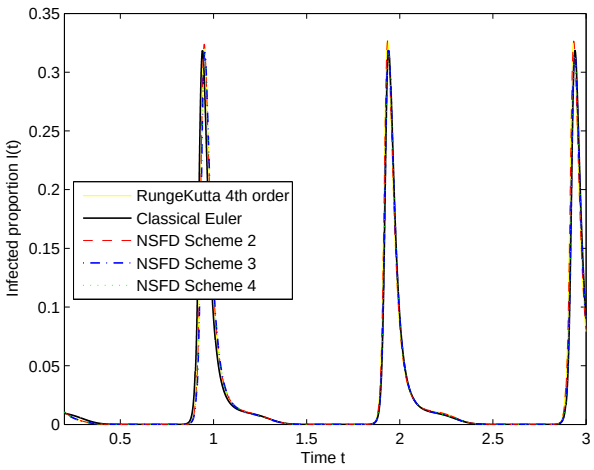

Fig. 7: Numerical comparisons for the SIR model, using Euler and $NSFD$ scheme 4, both with a time step size $h = 0.0001$ for the seasonal RSV model.

$Time$	Euler	Scheme 2	Scheme 3	Scheme 4	Runge-Kutta
$[0, 3]$	$37.9s$	$36.0s$	$40.5s$	$34.6s$	$93.9s$
$[0, 25]$	$83.2s$	$100.4s$	$88.8s$	$88.9s$	$256.9s$

Table 4: Comparison of the computation time of Euler, matrix $NSFD$ and 4-th order Runge-Kutta numerical schemes with time step size $h = 0.0001$ for the seasonal RSV model.

4.2.1 Matrix $NSFD$ schemes with nonlocal approximations and traditional derivative

Here it is shown several numerical results using the matrix $NSFD$ when traditional derivative is used. In Fig. 8 it can be seen the solutions representing the infected $I(t)$ population of the respiratory syncytial virus RSV model (6). It is clear from Fig. 8 that an excellent agreement exists between the solution, the Euler scheme and the $NSFD$ scheme 2, both with a time step size $h = 0.001$. However, in Fig. 9 it can be observed that these schemes fails when the time step size is increased to $h = 0.002$ for the Euler scheme and $h = 0.01$ for $NSFD$ scheme 2. It is important to remark that $NSFD$ scheme 2 achieves better results for larger time step sizes than Euler scheme as it was expected. For the matrix $NSFD$ numerical schemes 2 and 3, the scenario is similar but these schemes fail with smaller time step sizes as it can be seen in Fig. 10. Next subsection will be devoted to introduce the nontraditional derivative to observe its effect on the accuracy of the solutions.

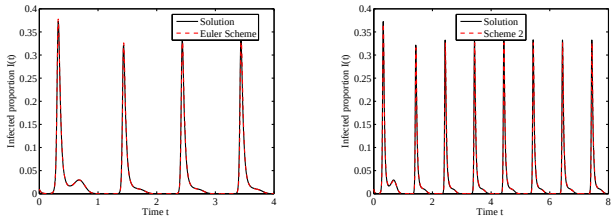

Fig. 8: Numerical comparisons between the solution of RSV model, Euler scheme and the $NSFD$ scheme 2, both with a time step size $h = 0.001$

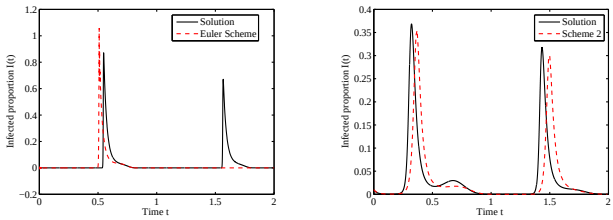

Fig. 9: Numerical comparisons between the solution of RSV model, Euler scheme and the $NSFD$ scheme 2 with time step sizes $h = 0.002$ and $h = 0.01$ respectively.

4.2.2 $NSFD$ schemes with nonlocal approximations and nonstandard derivative

In this subsection numerical results are computed using the nontraditional derivative. In Fig. 11 it can be seen that the nonstandard Euler scheme (12) improves

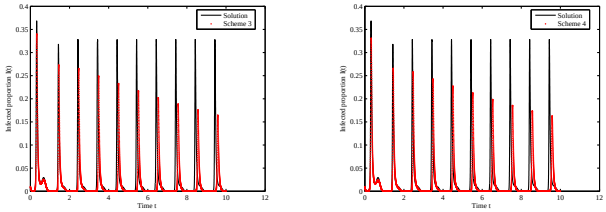

Fig. 10: Numerical comparisons between the solution of RSV model, $NSFD$ schemes 3 and 4, both with a time step size $h = 0.001$

the accuracy of the traditional Euler scheme. This fact is important since it means that the process fitting can be done with the nonstandard Euler scheme without the use of a smaller time step size, that will require more computation time. When b_1 is increased to 1000 in order to increase the stiffness of the seasonal model, the $NSFD$ scheme 2 with traditional derivative fails to give a solution for a time step size $h = 0.01$ and this same $NSFD$ scheme with nontraditional derivative at least gives an approximate solution as it can be seen in Fig. 12. Finally in Fig. 13 it can be observed the solutions when b_0 is increased to 700.

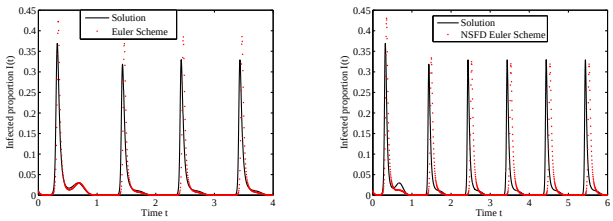

Fig. 11: Numerical comparisons between the solution of RSV model, Euler scheme and the $NSFD$ Euler scheme with $\lambda = 100$ when a time step size $h = 0.005$ is used in both schemes.

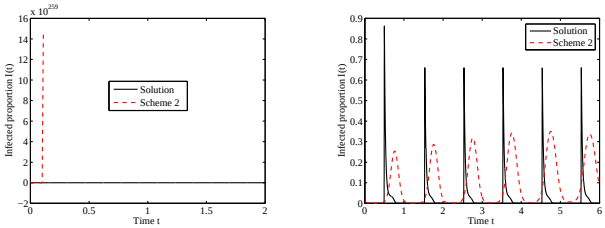

Fig. 12: Numerical comparisons between the solution of RSV model, $NSFD$ scheme 2 with and without the traditional derivative. We use $\lambda = 4500$ and a time step size $h = 0.01$ for both schemes. In addition b_1 is increased to 1000 in order to increase the stiffness of the model.

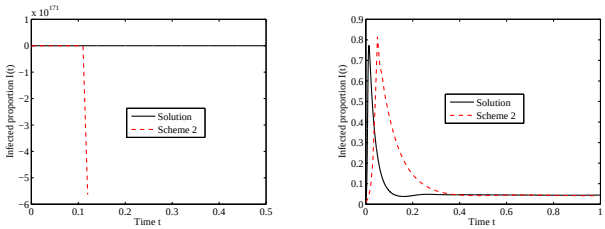

Fig. 13: Numerical comparisons between the solution of RSV model, $NSFD$ scheme 2 with and without the traditional derivative. We use $\lambda = 250$ and a time step size $h = 0.01$ for both schemes. In addition b_0 is increased to 700 in order to increase the stiffness of the model and $b_1 = 100$.

5 Discussion and conclusions

One of the aims of this paper was to investigate numerically the application of matrix $NSFD$ schemes to epidemic models represented by systems of autonomous and nonautonomous nonlinear ordinary differential equations. In addition, it was constructed in a easy way these matrix $NSFD$ such they can be used easily by the scientific community without any special knowledge. Moreover, with these matrix $NSFD$ schemes it can be exploited matrix operations advantages.

Thus, we have concerned with a classical SIR epidemic model and a seasonal model associated with the evolution of the transmission of respiratory syncytial virus RSV in the human population. The first model was an autonomous model, and the second one was a nonautonomous one which generally is more difficult to be solved.

Numerical results for the SIR epidemic model and the seasonal RSV model show that matrix $NSFD$ schemes converge to the correct equilibrium point with large time step sizes. However, the frequency of the true solution is not reproduced exactly when large time step sizes are used with some matrix $NSFD$ schemes. Further research is necessary in order to create in a more straightforward way these schemes where the accuracy could be improved for large time step sizes. We conclude that the developed nonstandard schemes are competitive and preserve essential properties of the continuous epidemic models and large time step sizes can be used, thus making it more economical to use when integrating over long time periods.

Finally, it should be mentioned that the developed numerical schemes can be used in other general epidemic models which are based on first order nonlinear ordinary differential equations and the fitting process to epidemiological data can reduce the computational effort to obtain different unknown parameters of the epidemic models.

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