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Non-standard numerical method for a mathematical model of RSV epidemiological transmission

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Abstract

Respiratory Syncytial Virus (RSV) has long been recognized as the single most important virus causing acute severe respiratory-tract infections with symptoms ranging from rhinitis to bronchitis in children who may require hospitalization. Outbreaks of RSV occur every year and all children become infected within the first two years of life, and that overloads hospital casualty services. The transmission dynamics of RSV are strongly seasonal. Epidemics occur each winter in temperate climates and often coincide with the seasonal rainfall in tropical climates.

In this paper we develop a non-standard numerical scheme for a SIRS seasonal epidemiological model for RSV transmission. This non-standard numerical scheme preserves the positivity of the continuous model and is applied to approximate the solution using different sizes of step.

Finally this method is compared with some well-known explicit methods and simulations with data from Gambia and Finland are carried out.

Keywords: SIRS; Epidemic model; Non-standard finite differences schemes; Numerical solution

1. Introduction

Respiratory syncytial virus (RSV) has long been recognized as the most important virus causing acute severe respiratory-tract infections, give rise to symptoms ranging from rhinitis to bronchitis in children who require hospitalization. RSV has been also implicated in severe lung diseases in adults, especially in the elderly. Infections with RSV frequently occur in the early years of life and repeated infections are common in all age groups. Outbreaks of RSV occur each year and, because the virus is highly contagious, essentially all children become infected within the first 2 years of life. The transmission dynamics of RSV are strongly seasonal with a pronounced annual component in many countries. Epidemics occur each winter in many temperate climates and are often coincident with seasonal rainfall and religious festivals in tropical countries [1].

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The mathematical models have been revealed as a powerful tool to analyze the epidemiology of the infectious illness, to understand its behavior, to predict its impact and to find out how external factors change the impact. In the case of RSV, the building of a reliable model is a priority in order to predict the medical care requirements for next seasons. Mathematical models for RSV have been developed previously. For instance, in [2], a *SIRS* (susceptible–infectious–recovered–susceptible) and a *MSEIRS* (maternally derived immunity–susceptible–latent–infectious–recovered–susceptible) mathematical models with four possible re-infections are studied and applied with data from Gambia, Singapore, Florida and Finland. In [1] a nested RSV model, stochastic simulations and fitting data from several countries are presented.

In Mathematical epidemiologic and others areas, models are non-linear IVP (initial value problem) systems. But, they do not have solution in closed form (in term of the model parameters only) or it can locally predict the behavior of systems. It is very important to design robust numerical methods to observe the behavior of the solutions numerically for several time steps.

It is well known that the traditional schemes like forward Euler, Runge–Kutta and others to solve nonlinear initial values problems, sometimes fail generating oscillations, bifurcations, chaos and false steady states [3]. Moreover, some methods, despite using adaptative step sizes, still fail (see for instance [4]). One alternative way to prevent all this class of numerical instabilities is the construction of schemes of finite differences using different techniques. The nonstandard finite difference techniques developed by Mickens [5,6] have resulted in the creation of new methods, see [8–15].

The aim of this paper is to present the construction of a nonstandard finite difference scheme for the numerical solution of the *SIRS* model for modeling transmission of respiratory syncytial virus RSV presented by Weber et al. [2], in which we combine a nonstandard difference method and a predictor-corrector. We analyze its behavior for different parameter values of the model. The model is based on the partition of the host population into four subpopulations, this are susceptibles $S(t)$, infectious $I(t)$ and recovered $R(t)$ as in [2]. With this *SIRS* model we are able to discuss how the different epidemiological parameters influence the global behavior in the evolution of the transmission of the RSV.

The organization of this paper is as follows. In Section 2, some mathematical preliminaries and the model of transmission of RSV are proposed. In Section 3 we build the numerical scheme numerical using the nonstandard difference techniques. In Section 4 we analyze the convergence of the scheme. In Section 5 numerical simulations for different parameter values of the model and different step sizes of the numerical scheme are reported and finally, Section 6 ends the paper with discussion and conclusions.

2. Mathematical model

In this section, we presented the continuous mathematical model for the transmission of virus RSV presented by A. Weber in [2], as a first order system of ordinary differential equations *SIRS* (Susceptibles, Infected, Recovered and Susceptibles) and parameters of the form

$$\begin{aligned}
\dot{S}(t) &= \mu - \mu S(t) - \beta(t)S(t)I(t) + \gamma R(t), \qquad S(0) = S_0 > 0\\
\dot{I}(t) &= \beta(t)S(t)I(t) - \nu I(t) - \mu I(t), \qquad I(0) = I_0 > 0\\
\dot{R}(t) &= \nu I(t) - \gamma R(t) - \mu R(t), \qquad R(0) = R_0 > 0,
\end{aligned} \tag{1}$$

under the following hypothesis:

(1) The population is divided in three classes: Susceptibles $S(t)$, who are all individuals that have not the virus, Infected $I(t)$, being all the infected individuals having the virus and able to transmit the illness and Recovered $R(t)$ who are all the individuals not having the virus and with a temporary immunity.

(2) The birth rate and death rate are equals to $\mu > 0$. This means that $\dot{S}(t) + \dot{I}(t) + \dot{R}(t) = 0$ and from (1) one gets $S(t) + I(t) + R(t) = 1$ is invariant. Therefore $S(t) \leq 1$, $I(t) \leq 1$, $R(t) \leq 1$, for all $t \geq 0$.

(3) The meeting coefficient function $\beta(t)$ between clases $S(t)$ and $I(t)$, is a continuous T-periodic function, called the transmission rate, and satisfying $0 < \beta^l := \min_{t\in R} \beta(t) \leq \beta(t) \leq \beta^u := \max_{t\in R} \beta(t)$. Periodicity of the $\beta(t)$ is a way to incorporate the seasonality of the spread in the environment. It is usual to approximate this seasonally-forced by a cosinusoidal function $\beta(t) = b_0(1 + b_1 \cos(2\pi(t + \varphi)))$ where $b_0 \geq 0$ is the baseline transmission

Table 1
The values μ, ν, γ are expressed in rates per year

Country	μ	ν	γ	b_0	b_1	ϕ
Gambia	0.041	36	1.8	60	0.16	0.15
Florida	0.016	36	1.8	62	0.10	0.14
Finland	0.013	36	1.8	44	0.36	0.60
Singapore	0.016	36	1.8	77	0.14	0.28

The phase angle in years is denoted by ϕ [2].

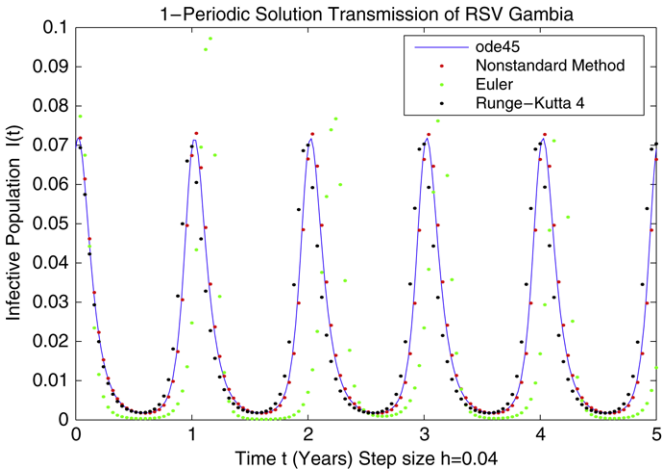

Fig. 1. Numerical approximations of solutions to system (2) in Gambia, using the scheme (8), the explicit Euler, 4th Order Runge–Kutta and the adaptive MatLab solver ode45.

parameter, $0 \leq b_1 \leq 1$ measures the amplitude of the seasonal variation in transmission and $0 \leq \varphi \leq 1$ is the phase angle normalized [2].

(4) The per capita rate of leaving the infected class $I(t)$ is called ν and the per capita rate of recovered class $R(t)$ is γ.

As $R(t) + S(t) + I(t) = 1$, using this expression in (1) we have the following equivalent system

$$\begin{aligned} \dot{S}(t) &= k - kS(t) - \beta(t)S(t)I(t) - \gamma I(t), \qquad S(0) = S_0 > 0 \\ \dot{I}(t) &= \beta(t)S(t)I(t) - \omega I(t), \qquad I(0) = I_0 > 0, \\ R(t) &= 1 - S(t) - I(t), \quad \text{for all } t \geq 0, \end{aligned} \tag{2}$$

where $k = \mu + \gamma$ and $\omega = \mu + \nu$. We assume that

$$\gamma < \nu \tag{3}$$

i. e., the per capita rate of recovered is greater than the per capita rate of leaving the infected class.

3. Scheme construction

In this section we develop a numerical scheme that it will be used in the next section to solve the system of ordinary differential equations representing the evolution of the different subpopulations in regard to transmission of virus RSV. The construction of the scheme is based on nonstandard techniques developed by Mickens [5,6].

Let us denote by S^n, I^n, β^n and R^n the approximations of $S(nh)$, $I(nh)$, $R(nh)$ and $\beta(nh)$ respectively for $n = 0, 1, 2\ldots$, and $h > 0$ the step size of the scheme. The discretization of the system (2) and the developing of the numerical method is based on the approximations of the temporal derivatives by a first order forward scheme, using the non-standard difference techniques as we mentioned previously. If $f(t) \in C^1(\mathbb{R})$, we define the derivative

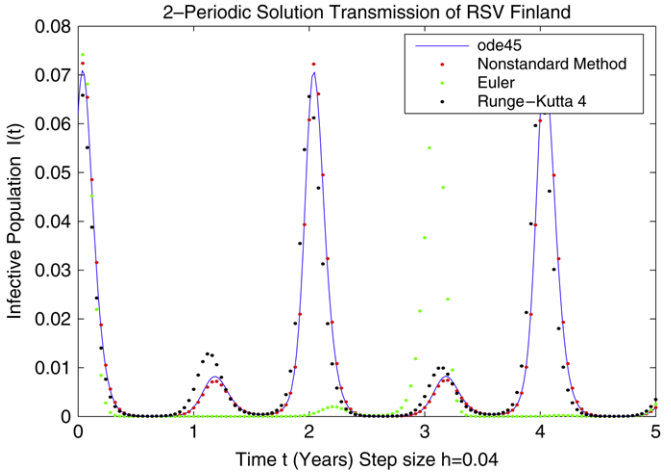

Fig. 2. Numerical approximations of solutions to system (2) in Finland, using the scheme (8), the explicit Euler, 4th Order Runge–Kutta and the adaptive MatLab solver ode45.

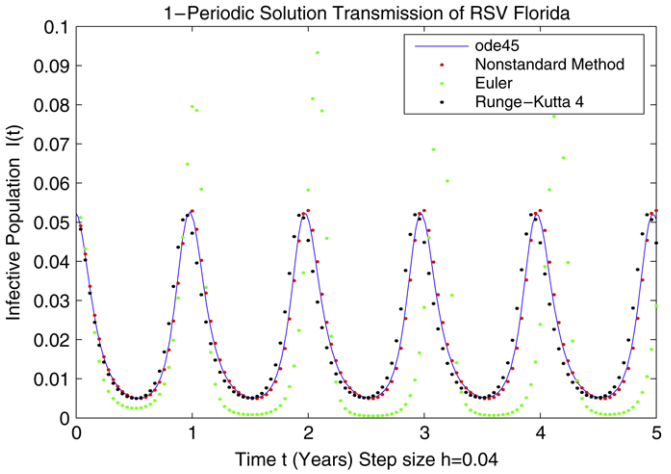

Fig. 3. Numerical approximations of solutions to system (2) in Florida, using the scheme (8), the explicit Euler, 4th Order Runge–Kutta and the adaptive MatLab solver ode45.

as

$$\frac{\mathrm{d}f(t)}{\mathrm{d}t} = \frac{f(t+h) - f(t)}{\varphi(h)} + \mathcal{O}(h) \quad \text{as } h \longrightarrow 0, \tag{4}$$

where $\varphi(h)$ called the denominator functions that satisfy

$$\varphi(h) = 1 - \exp(-h), \quad \text{see for instance [6, p. 19].}$$

Thus, for the first equation of (2), we have

$$\frac{S^{n+1} - S^n}{\varphi(h)} = k - kS^{n+1} - \beta^n S^{n+1} I^n - \gamma I^n, \tag{5}$$

where the second term on the right-side of (5), has the discrete form

$$-S \to -S^{n+1},$$
$$-\beta SI \to -\beta^n S^{n+1} I^n.$$

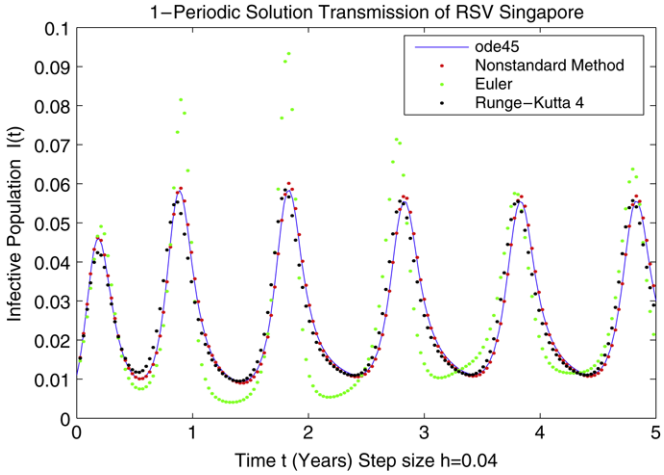

Fig. 4. Numerical approximations of solutions to system (2) in Singapore, using the scheme (8), the explicit Euler, 4th Order Runge–Kutta and the adaptive MatLab solver ode45.

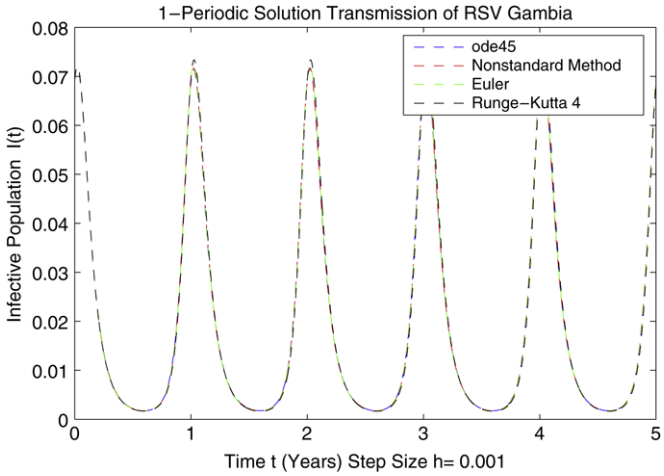

Fig. 5. Numerical solutions to (2) in Gambia with all methods.

One way to determine convergence schemes with an arbitrarily high order of accuracy is *suggested* by converting the original differential equation into an equivalent integral equation [7]. Thus, taking the second equation of (2) as a differential equation of first order in $I(t)$, we have the solution in the interval $[t_0, t]$ for $t > t_0$ given by

$$I(t) = I(t_0) \exp\left(\int_{t_0}^{t} (\beta(u)S(u) - \omega)\, \mathrm{d}u\right),$$

and using the ideas of Mickens in [5, p. 148], we can obtain a scheme by making in the equation above the following substitutions:

$$\begin{cases} t_0 \longrightarrow t_n = \varphi(h)n, \\ t \longrightarrow t_{n+1} = \varphi(h)(n+1), \\ I(t_0) \longrightarrow I^n, \\ I(t) \longrightarrow I^{n+1}, \\ S(t_0) \longrightarrow S^n, \\ S(t) \longrightarrow S^{n+1}. \end{cases}$$

Thus, one gets

$$I^{n+1} = I^n \exp\left(\int_{t_n}^{t_{n+1}} (\beta(u)S(u) - \omega)\,\mathrm{d}u\right),$$

and using the quadrature trapezoidal formula, we concluded that

$$I^{n+1} = I^n \exp\left(\frac{\varphi(h)}{2}(\beta^{n+1}S^{n+1} + \beta^n S^n) - \varphi(h)\omega\right). \tag{6}$$

Finally, on the same way, we have

$$\begin{aligned} S(t) = {} & \exp\left(-\int_{t_0}^{t} (k + \beta(u)I(u)\mathrm{d}u)\right) S_0 \\ & + \exp\left(-\int_{t_0}^{t} (k + \beta(u)I(u)\mathrm{d}u)\right) \int_{t_0}^{t} (k - \gamma I(\tau)) \exp\left(-\int_{t_0}^{\tau} (k + \beta(u)I(u)\mathrm{d}u)\right) \mathrm{d}\tau \end{aligned}$$

and we present the following scheme as a corrector of (5)

$$\begin{aligned} S^{n+1} = {} & S^n \exp\left(-\frac{\varphi(h)}{2}(2k + \beta^{n+1}I^{n+1} + \beta^n I^n)\right) + \frac{\varphi(h)}{2}(k - \gamma I^{n+1}) \\ & + \frac{\varphi(h)}{2}(k - \gamma I^n) \exp\left(-\frac{\varphi(h)}{2}(\beta^{n+1}I^{n+1} - \beta^n I^n)\right). \end{aligned} \tag{7}$$

After rearranging the explicit formulations, we obtain the following discrete system:

$$S_p^{n+1} = \frac{\varphi(h)(k - \gamma I^n) + S^n}{1 + \varphi(h)k + \varphi(h)\beta^n I^n}, \tag{8a}$$

$$I^{n+1} = I^n \exp\left(\frac{\varphi(h)}{2}(\beta^{n+1}S_p^{n+1} - \beta^n S^n) - \varphi(h)\omega\right), \tag{8b}$$

$$\begin{aligned} S_c^{n+1} = {} & S^n \exp\left(-\frac{\varphi(h)}{2}(2k + \beta^{n+1}I^{n+1} + \beta^n I^n)\right) + \frac{\varphi(h)}{2}(k - \gamma I^{n+1}) \\ & + \frac{\varphi(h)}{2}(k - \gamma I^n) \exp\left(-\frac{\varphi(h)}{2}(\beta^{n+1}I^{n+1} - \beta^n I^n)\right), \end{aligned} \tag{8c}$$

and

$$R^{n+1} = 1 - S_c^{n+1} - I^{n+1}. \tag{8d}$$

From the systems (8), we can see that the positivity requirement is satisfaced if $S(t) \leq \omega/\beta^l$ for all $t \geq 0$ ($\beta^l = \min_{t\in[0,T]} \beta(t)$) and $0 < h < h_c$, where h_c is a critical value, that for this case we obtain $h_c \leq 0.1$, see [14]. To calculate, using this scheme, we proceed as follows:

(i) Select values S^0, I^0, R^0, such that $S^0 + I^0 + R^0 = 1$.
(ii) Calculate S^1 from (8a).
(iii) Using this value of S^1 and I^0, calculate I^1 from (8b).
(iv) Correct the value S_c^1, using S^0, I^1 and the Eq. (8c).
(v) Calculate R^1 from (8d).
(vi) Repeat all of the above steps, for $n = 1, 2, 3 \ldots$.

Thus, we get the numerical solution of system (2).

4. Numerical simulations

To illustrate the behavior of the numerical solution of scheme (8), we perform several simulations. In a sequence of executions runs, we change the parameters of the model using the set of biologically feasible parameter values given in Table 1.

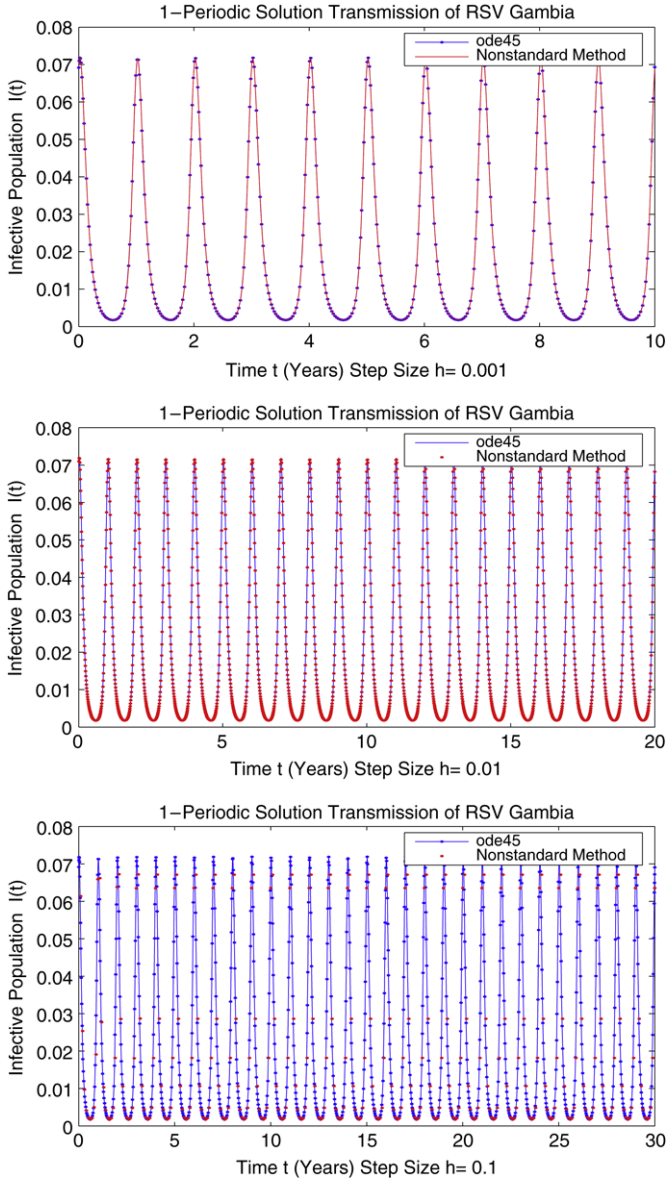

Fig. 6. Numerical approximations of solutions to system (2) in Gambia, using the scheme (8) with with larger values of the time as $t = 10, 20, 30$ years.

Parameters μ, ν, γ correspond to birth rate, rate of recovered, rate of immunity lost respectively and b_0, b_1, ϕ are average of transmission parameter, amplitude of the seasonal fluctuation and phase angle normalized in the transmission rate $\beta(t)$ for the transmission of virus RSV.

4.1. Numerical results and comparison with other schemes

In order to test convergence and stability properties of the schemes, we perform several numerical simulations with different values for the parameters of the model according to the Table 1 with different step sizes. We compare the performance of the method (8), the explicit Euler method, the explicit 4th Order Runge–Kutta using $h = 0.04$ and they were compared with the solution computed by the adaptive MatLab solver ode45. Solutions of the Euler and 4th Order Runge–Kutta methods are not correct and Figs. 1–4, show this fact. Now, for a relatively small step size $h = 0.001$ all three methods achieve the correct solution, (see Fig. 5).

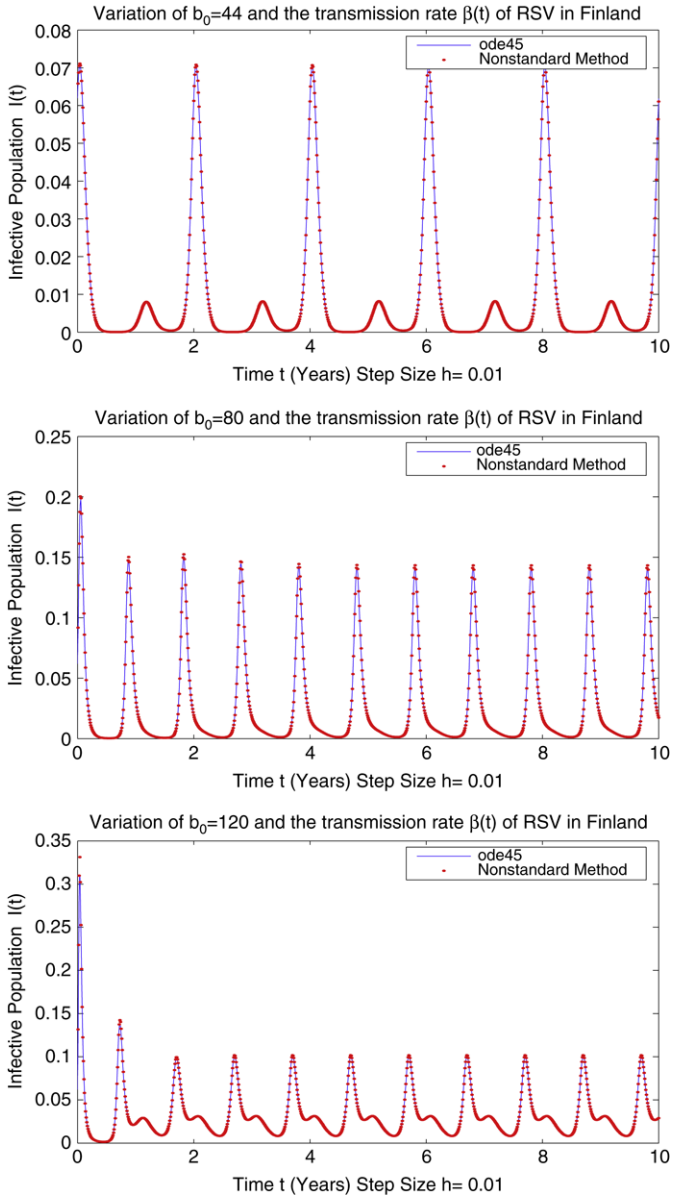

Fig. 7. Numerical approximations of solutions to system (2), using the scheme (8) with the variation of b_0 for Finland.

4.2. *Numerical results for very large time*

We present further simulations of the method with larger values of the time as $t = 10, 20, 30$ years and h such as: $h = 0.001, 0.01, 0.1$ respectively, and it shows that preserve positivity periodic solutions. The profiles of infective populations for $h = 0.001, 0.01, 0.1$ portrayed in the graphics of Fig. 6 for Gambia, confirm that the scheme (8) is stable for step sizes less than $h = 0.1$. This simulation verify the behavior positive T-periodic of the solution and is globally asymptotically stable [16]. Furthermore, in the rate of transmission $\beta(t)$, the parameter $b_0 \geq 0$ is changed considerably and we make simulation with $b_0 = 44, 80, 120$ and the value parameters corresponding to Finland. In Fig. 7 we can see that the scheme preserve the positivity of the solutions, although the periodicity of solutions change.

5. Conclusions

In this paper, we propose a numerical scheme to solve a *SIRS* model for the transmission of virus RSV which is a first-order ODE system and we analyze its behavior.

We applied the theory of nonstandard numerical methods to construct a nonstandard scheme. We combined nonlocal approximations to transform the original system of differential Eq. (2) into an equivalent system of integral equation, for solving the *SIRS* model for the transmission of virus RSV. This numerical scheme is analyzed and tested in several numerical simulations and we can see that the scheme preserves essential positivity properties of exact solutions of the *SIRS* model.

The classical explicit Euler and explicit fourth order Runge–Kutta schemes are compared with the scheme proposed in (8). The forward Euler and fourth order Runge–Kutta schemes diverge for small step-sizes, in general for $h > 0.01$. On the other hand, the scheme proposed in (8), shows convergence in all the numerical simulations performed for step size less than $h_c = 0.1$ and any initial condition.

We can see from the numerical simulations, that this *SIRS* model predicts the endemic effect of the transmission of virus RSV for realistic parameter values taken from [2], for Gambia, Finland, Florida and Singapore and are illustrated in Figs. 1–7 where the numerical simulation were done for large time and different step size. This epidemic model of temporary immunity is interesting to understand the evolution of virus RSV as well as other diseases with similar characteristics.

One future work is the introduction of vaccination programs in the *SIRS* model to see how this would affect the evolution of the transmission of virus RSV and make numerical simulations to analyze the optimal parameter values for the vaccination programs.

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