A nonstandard Volterra difference equation for the SIS epidemiological model

Jean M.-S. Lubuma*, Yibeltal A. Terefe

*J. M.-S. Lubuma and Y. A. Terefe
Dept of Mathematics & Applied Mathematics University

Dept of Mathematics & Applied Mathematics, University of Pretoria, Pretoria, South Africa e-mail: jean.lubuma@up.ac.za

Y. A. Terefe

e-mail: yibeltal.terefe@up.ac.za

Abstract By considering the contact rate as a function of infective individuals and by using a general distribution of the infective period, the SIS-model extends to a Volterra integral equation that exhibits complex behaviour such as the backward bifurcation phenomenon. We design a nonstandard finite difference (NSFD) scheme, which is reliable in replicating this complex dynamics. It is shown that the NSFD scheme has no spurious fixed-points compared to the equilibria of the continuous model. Furthermore, there exist two threshold parameters \mathcal{R}_0^c and \mathcal{R}_0^m , $\mathcal{R}_0^c \leq 1 \leq \mathcal{R}_0^m$, such that the disease-free fixed-point is globally asymptotically stable (GAS) for \mathcal{R}_0 , the basic reproduction number, less than \mathcal{R}_0^c and unstable for $\mathcal{R}_0 > 1$, while it is locally asymptotically stable (LAS) and coexists with a LAS endemic fixed-point for $\mathcal{R}_0^c < \mathcal{R}_0 < 1$. A unique GAS endemic fixed-point exists when $\mathcal{R}_0 > \mathcal{R}_0^m$ and $\mathcal{R}_0^m < \infty$. Numerical experiments that support the theory are provided.

Keywords SIS model · Volterra integral equation · Nonstandard finite difference scheme · Dynamics preserving scheme

Mathematics Subject Classification 37N25 · 37N30 · 65C20 · 92B05

1 Introduction

Let S = S(t) and I = I(t) denote the fractions of susceptible and infective individuals at time t, which satisfy the conservation law

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

The classical SIS-model reads as the logistic equation

$$I' = \lambda I(1 - I) - (\mu + \gamma)I, \qquad I(0) = I_0 \ge 0,$$
(2)

where $\lambda > 0$, $\gamma > 0$ and $b = d = \mu > 0$ are the contact, the recovery, the recruitment and the natural death rates, respectively.

Put $I_0(t) = I_0 e^{-(\mu + \gamma)t}$ and $P(t) = e^{-\gamma t}$. Then the SIS-model (2) is equivalent to the following Volterra integral equation (VIE):

$$I(t) = I_0(t) + \int_0^t \lambda I(u)[1 - I(u)]P(t - u)e^{-\mu(t - u)}du.$$
 (3)

In this paper, we assume that λ is a function of the fraction of infective individuals and we make general assumptions on the distribution of the infective period P(t) and on the initial function $I_0(t)$. The fraction I(t) of individuals that are in the infective class at time t > 0 is then given by the SIS–Volterra integral equation (SIS–VIE) ([6]):

$$I(t) = I_0(t) + \int_0^t \lambda(I(u))I(u) [1 - I(u)] P(t - u)e^{-\mu(t - u)} du.$$
 (4)

Unlike the classical SIS-model (2) or (3) where the value $\mathcal{R}_0 = 1$ of the basic reproduction number is a forward bifurcation, the solutions of Eq. (4) have a complex behaviour including the possibility of backward bifurcation phenomenon.

The purpose of this paper is to extend the NSFD approach to the integro-differential equation (4). This is done in the spirit of the exact scheme of the logistic equation (2), which is given in [1,4] and is written for the purpose of this paper in the form of the Volterra difference equation (VDE):

$$I^{k+1} = I_0 + \left[e^{(\lambda - \mu - \gamma)\Delta t} - 1\right] \sum_{i=0}^{k} I^i \left[1 - (\lambda I^{i+1})/(\lambda - \mu - \gamma)\right],\tag{5}$$

where $t_k = k\Delta t$ represents here and after the discrete times, $\Delta t > 0$ being the time step size. Using Mickens' rules on complex denominator functions and nonlocal approximation of nonlinear terms [1,4], we obtain a nonstandard Volterra difference equation (NS-VDE), which is dynamically consistent. To the authors' best knowledge, NSFD schemes have never been developed for Volterra-integral equations, apart from a restrictive situation in [5].

In the next section, we give details on the continuous model (4) and state its qualitative behaviour. The construction and dynamic consistency of the NSFD scheme is investigated in Sect. 3. Numerical simulations are provided in Sect. 4, which is followed by concluding remarks in Sect. 5.

2 SIS-Volterra integral equation model

The biological relevance of expressing the contact rate as a function of the infective population has been emphasised in the literature (see [6] and the references therein). This is particularly formalised in [6] in terms of the SIS–VIE (4) under the following assumptions:

$$\lambda(I) > 0$$
 is continuous, and $\lambda(I)I(1-I)$ has continuous derivative, on [0, 1]; (6)

$$P(t) \ge 0$$
 is decreasing, differentiable for $t \ge 0$ and satisfies $P(0^+) = 1$; (7)

$$I_0(t) \ge 0$$
 is decreasing, differentiable and satisfies $\lim_{t \to \infty} I_0(t) = 0$. (8)

For the qualitative analysis, Eq. (4) is written in the equivalent form

$$I(t) = I_0(t) + \mathcal{R}_0 \int_0^t I(u) f(I(u)) \tilde{P}(t-u) du, \tag{9}$$

where: $\mathcal{R}_0 = \lambda(0)\tau$ and $\tau = \int_0^\infty P(u)e^{-\mu u}du$ are the basic reproduction number and the period of infectivity, respectively; $f(I) = \lambda(I)(1-I)/\lambda(0)$; $\tilde{P}(t) = \tau^{-1}P(t)e^{-\mu t}$, $t \geq 0$ so that $\int_0^\infty \tilde{P}(u)du = 1$. With f(I), we associate the quantities:

$$(\mathcal{R}_0^c)^{-1} = \max\{f(I): I = 0 \text{ or } I \in (0,1); f'(I) = 0\},\ (\mathcal{R}_0^m)^{-1} = \min\{f(I): I = 0 \text{ or } I \in (0,1); f'(I) = 0\}.$$

Note finally that $I \in [0, 1]$ is an equilibrium solution of (9) if and only if

$$I = \mathcal{R}_0 I f(I). \tag{10}$$

Theorem 1 [6] Suppose that (6)–(8) hold and $0 \le I_0(t) \le 1$. Then the SIS–VIE (4) has a unique continuously differentiable solution I satisfying $0 \le I(t) \le 1$. Furthermore:

- 1. The DFE is the only equilibrium and it is GAS when $\mathcal{R}_0 < \mathcal{R}_0^c$;
- 2. There exists only one EE, which is GAS when $\mathcal{R}_0 > \mathcal{R}_0^m$ and $\mathcal{R}_0^m < +\infty$, with the DFE being unstable in the larger interval $\mathcal{R}_0 > 1$;
- 3. For $\mathcal{R}_0^c < 1$ and $\mathcal{R}_0^c < \mathcal{R}_0 < 1$, the DFE is LAS and it coexists with at least one LAS equilibrium if $\lambda'(0) \neq \lambda(0)$.

3 Nonstandard finite difference scheme

Let I(t) be the solution of VIE (4). At the discrete time t_{k+1} , we have

$$\begin{split} I(t_{k+1}) &= I_0(t_{k+1}) \\ &+ \sum_{i=0}^k \int_{t_i}^{t_{i+1}} \lambda[I(u)]I(u)[1 - I(u)]P(t_{k+1} - u)e^{-\mu(t_{k+1} - u)}du \\ &= I_0(t_{k+1}) \\ &+ \sum_{i=0}^k \lambda[I(c_i)]I(c_i)[1 - I(c_i)]P(t_{k+1} - c_i) \int_{t_i}^{t_{i+1}} e^{-\mu(t_{k+1} - u)}du, \end{split}$$

where the numbers $c_i \in [t_i, t_{i+1}]$ are obtained by applying the mean-value theorem for integrals. In the spirit of the nonlocal approximation of the nonlinear term in (5), we make the choice $c_i = t_i$ and $c_i = t_{i+1}$ to approximate I(u) and $(1 - I(u))P(t_{k+1} - u)$, respectively. We have approximately

$$I(t_{k+1}) \simeq I_0(t_{k+1}) + \sum_{i=0}^k \lambda [I(t_i)] I(t_i) [1 - I(t_{i+1})]$$

$$\times P(t_{k+1} - t_{i+1}) [e^{-\mu(t_{k+1} - t_{i+1})} - e^{-\mu(t_{k+1} - t_i)}] / \mu$$

$$= I_0(t_{k+1}) + \phi \sum_{i=0}^k \lambda [I(t_i)] I(t_i) [1 - I(t_{i+1})] P[(k-i) \Delta t] e^{-\mu(k-i) \Delta t},$$

where the complex denominator function that appeared naturally is $\phi = \phi(\Delta t) = (1 - t)$ $e^{-\mu \Delta t})/\mu$. Denoting by I^i an approximation of $I(t_i)$, we finally obtain the NS-VDE

$$I^{k+1} = I_0(t_{k+1}) + \phi(\Delta t) \sum_{i=0}^{k} \lambda(I^i) I^i [1 - I^{i+1}] P[(k-i)\Delta t] e^{-\mu(k-i)\Delta t}.$$
 (11)

The terminology NS-VDE is motivated by the fact that Eq. (11) can be written as an approximation of the Volterra integro-differential equation obtained by formally differentiating Eq. (4) with respect to time. In that equivalent formulation, we have a NSFD scheme in the sense of [1,4].

Our NSFD scheme is convergent due to the property $\phi(\Delta t) = \Delta t + O[(\Delta t)^2]$. We want to show that the NSFD scheme is dynamically consistent with the properties in Theorem 1. If Eq. (11) is solved for I^{k+1} , the conservation law $S^k + I^k = 1$ [see Eq. (1)] and mathematical induction on k yield the next theorem.

Theorem 2 For the NS VDE (11): $0 \le I_0(t) \le 1$ implies $0 \le I^k \le 1 \ \forall k$.

Theorem 3 The NS-VDE (11) preserves the equilibria as follows:

- 1. The disease-free equilibrium point is the disease-free fixed point,
- 2. There is no endemic fixed point for $\mathcal{R}_0 < \mathcal{R}_0^c$,
- 3. There exists at least one endemic fixed point for $\mathcal{R}_0 > \mathcal{R}_0^c$, 4. There exists exactly one endemic fixed point for $\mathcal{R}_0 > \mathcal{R}_0^m$, $\mathcal{R}_0^m < \infty$.

Proof It can be shown that I^* is a fixed-point of the NS-VDE (11) if and only if I^* satisfies (10), the characterising equation of equilibria of the continuous model in Theorem 1.

Below, we refine the denominator function used so far so that, as in (5), it involves the key parameters of the continuous model:

$$\phi(\Delta t) = (1 - e^{-q\Delta t})/q \text{ where } q \ge \max\left\{\mu, \max_{I \in [0,1]} \lambda(I), 2 \max_{I \in [0,1]} \lambda^2(I)\right\}. \tag{12}$$

Theorem 4 With (12) in the NS-VDE (11), we have the following:

- 1. The disease-free fixed point is LAS for $\mathcal{R}_0 < 1$ and unstable for $\mathcal{R}_0 > 1$;
- 2. At least one endemic fixed point I_e given in Theorem 3 (3) is LAS under the specific condition: $\lambda'(I_e) < \min\{-1 - \lambda(I_e), -\lambda(I_e)/I_e\}.$
- 3. For $\mathcal{R}_0^c < \mathcal{R}_0 < 1$ and $\lambda'(0) \neq \lambda(0)$, the LAS disease-free fixed point coexists with at least one LAS endemic fixed point;
- 4. For $\mathcal{R}_0 < \mathcal{R}_0^c$, the disease-free fixed point is GAS and for $\mathcal{R}_0 > \mathcal{R}_0^m$ with $\mathcal{R}_0^m < \infty$, the endemic fixed point is GAS.

Proof The LAS is obtained by linearization of the VDE (11) about the fixed-point and by using some variants of the Jury conditions in [2,3], which motivates the requirement in item (2) of the theorem. The GAS follows from Bolzano-Weierstrass theorem that permits to show that the limit set of the bounded sequence (I^k) is reduced to one LAS fixed-point.

4 Numerical experiments

It is known that standard finite difference methods do not preserve the dynamics of the (classical SIS-) logistic equation (2) (see [1]). Thus, it is not necessary to generate here simulations for classical numerical methods. The theoretical analysis in the previous section

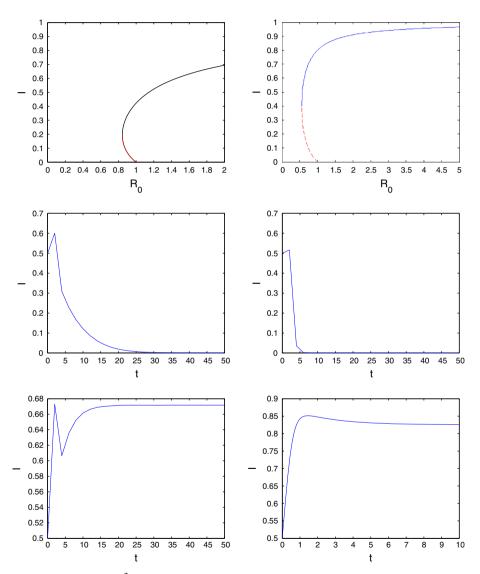


Fig. 1 Left for $λ(I) = -I^2 + I + 1/3$: backward bifurcation when $\mathcal{R}_0 ≥ \mathcal{R}_0^c$ (top), GAS of DFE (middle) with μ = 0.4, $I_0(t) = \frac{1}{2}e^{-0.5t}$ and $P(t) = e^{-0.1t}$ and GAS of EE (bottom) for $1 < \mathcal{R}_0 = \frac{5}{3}$ with μ = 0.1, $I_0(t) = \frac{1}{2}e^{-0.2t}$ and $P(t) = e^{-0.1t}$; Right for λ(I) = 1 + 5I: backward bifurcation if $\mathcal{R}_0 > \mathcal{R}_0^c$ (top), GAS of DFE (middle) if $\mathcal{R}_0 = 0.54 < \frac{5}{9}$, $I_0(t) = \frac{1}{2}e^{-t}$, $P(t) = e^{-t}$ and μ = 0.85 and GAS of EE, $I_e = 0.83$, for $\mathcal{R}_0 = \frac{10}{9}$ with μ = 0.4, $I_0(t) = \frac{1}{2}e^{-\frac{1}{2}t}$ and $P(t) = e^{-\frac{1}{2}t}$

is illustrated by taking $\lambda(I)=-I^2+I+\frac{1}{3}$, which satisfies the needed conditions, with $\mathcal{R}_0^c=0.83$ and $\mathcal{R}_0^m=1$. On the left of Fig. 1, the following properties of the NS-VDE with q=2 in (12) are displayed in accordance with Theorem 4: backward bifurcation (top), GAS of disease-free fixed-point (middle) and GAS of endemic fixed-points (bottom). We also take $\lambda(I)=1+5I$. Then $\mathcal{R}_0^c=\frac{5}{9}$ and $\mathcal{R}_0^m=1$. On the right of Fig. 1, the properties listed above are preserved in the same order by the NS-VDE with q=102. The fact that this $\lambda(I)$ satisfies rather the realistic condition $\lambda'(I^*)<(\lambda(I^*))/(1-I^*)$ that holds for a LAS endemic equilibrium I^* of the continuous model than the stronger condition in part (2) of Theorem 4, suggests that this theorem is valid under this realistic condition. In all figures $\Delta t=2$, a large value that is not acceptable for classical numerical methods.

5 Conclusion

We designed for the first time a NSFD scheme for the SIS-Volterra integral equation. The scheme replicates the positivity and boundedness of the solution as well as the complex stability properties of equilibria, including the backward bifurcation phenomenon. This was achieved by using Mickens's rules [4].

Fitting contact rates that depend on infective individuals with real data is our interest for future research. We are also extending this study to more general distribution functions P(t) of infective individuals and focusing on NSFD schemes for such cases, including delay differential equations in epidemiology.

Acknowledgments The authors acknowledge the financial support of the DST/NRF SARChI Chair in Mathematical Models and Methods in Bioengineering and Biosciences.

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