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Dynamically consistent nonstandard finite difference schemes for epidemiological models

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ABSTRACT

This work is the numerical analysis and computational companion of the paper by Kamgang and Sallet [J.C. Kamgang, G. Sallet, Computation of threshold conditions for epidemiological models and global stability of the disease free equilibrium (DFE), Mathematical Biosciences 213 (2008) 1–12] where threshold conditions for epidemiological models and the global stability of the disease-free equilibrium (DFE) are studied. We establish a discrete counterpart of the main continuous result that guarantees the global asymptotic stability (GAS) of the DFE for general epidemiological models. Then, we design nonstandard finite difference (NSFD) schemes in which the Metzler matrix structure of the continuous model is carefully incorporated and both Mickens' rules (World Scientific, Singapore, 1994) on the denominator of the discrete derivative and the nonlocal approximation of nonlinear terms are used in an innovative way. As a result of these strategies, our NSFD schemes are proved to be dynamically consistent with the continuous model, i.e., they replicate their basic features, including the GAS of the DFE, the linear stability of the endemic equilibrium (EE), the positivity of the solutions, the dissipativity of the system, and its inherent conservation law. The general analysis is made detailed for the MSEIR model for which the NSFD theta method is implemented, with emphasis on the computational aspects such as its convergence, or local truncation error. Numerical simulations that illustrate the theory are provided.

1. Introduction

Dynamical systems are used extensively in the modeling of many natural phenomena; they constitute a central component in applied mathematics and their numerical simulations are of fundamental importance in gaining the correct qualitative and quantitative information on the systems (e.g., [1]). In this work, we study a class of dynamical systems that arise in epidemiology as compartmental models for the spread of various diseases. These models are in the form of initial-value problems for n-dimensional differential systems,

$$\frac{dx}{dt} = A(x)x + f, \qquad x(0) = x_0, \tag{1}$$

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where $x = x(t) : [0, \infty) \to \mathbb{R}^n$ represents the number or density of the populations in the different compartments, $x_0 \in \mathbb{R}^n$ is the vector of initial populations, and f is a given vector function that includes the recruitment or birth rates. Usually, $A(x)$ is a nonlinear real $n \times n$ Metzler matrix. Often, it is possible to distinguish among the components of x two sub-populations: the non-infected individuals (susceptible, recovered, etc.), represented by $y \in \mathbb{R}^{n_1}$, and the infected individuals, either latent or infectious, $z \in \mathbb{R}^{n_2}$ $(n_1 + n_2 = n)$. Under suitable assumptions, classical mathematical theory asserts that for each x_0 the system (1) has a unique, positive, and maximal solution (see, e.g., [2,1]). Furthermore, it is possible to show that the system has equilibrium points, one of which is the Disease Free Equilibrium (DFE) that is the equilibrium state without infected individuals, which is important from the epidemiological point of view. Mathematically, we denote the stability number or the spectral bound of the Jacobian matrix J of the right-hand side of (1), evaluated at the DFE by $\alpha(J)$, i.e.,

$$\alpha(J) \equiv \max\{\mathrm{Re}(\lambda) : \lambda \text{ eigenvalue of } J\}.$$

Then, it can be shown that when

$$\alpha(J) < 0, \tag{2}$$

the DFE is locally asymptotically stable. Condition (2) is in practice equivalent to the Kermack and McKendrick threshold condition [3],

$$\mathcal{R}_0 < 1,$$

where $\mathcal{R}_0$ is the so-called 'basic reproduction number' associated with (1), which essentially is a basic stability number. Moreover, a locally asymptotically stable Endemic Equilibrium (EE) may exist when $\mathcal{R}_0 > 1$. The local behavior of the equilibrium states has been extensively studied in epidemiological models (see, e.g., [4–8]) and in general dynamical systems (see, e.g., [2,1]).

In epidemiological applications, it is important to know whether the DFE is globally asymptotically stable (GAS) under certain threshold conditions. Such information, in case of an epidemic, may be used to design an intervention procedure that would decrease the spread of the disease and eventually eradicate it. However, proving that the DFE is GAS can be very difficult. Various ways were developed to that end and the best known is to construct a Lyapunov function for the system under consideration, [9]. However, to construct such Lyapunov functions is very challenging in most problems of interest. These considerations led Kamgang and Sallet [10] to seek another way to prove that the DFE is GAS. In their paper, they obtained a necessary and sufficient condition for the global asymptotic stability of the DFE under reasonable assumptions.

In this work we follow Kamgang and Sallet [10], and reformulate (1), using the notation $x = (y, z)$, in the following manner,

$$\begin{cases} \dfrac{dy}{dt} = A_1(x)(y - y^*) + A_{12}(x)z, \\ \dfrac{dz}{dt} = A_2(x)z, \end{cases} \tag{3}$$

where $A_1(x)$ and $A_2(x)$ are square matrices of dimensions $n_1 \times n_1$ and $n_2 \times n_2$, respectively, $A_{12}(x)$ is an $n_1 \times n_2$ matrix, and $(y^*, 0) \in \mathbb{R}^{n_1} \times \mathbb{R}^{n_2}$ is the DFE of (3). They proved the following theorem, which can also be found in [11] under some restrictive assumptions:

Theorem 1. *Consider the system (3) on a positively invariant set $\Omega \subset \mathbb{R}^n_+$. Let the following assumptions hold:*

H_1. *The system is dissipative on Ω.*
H_2. *The equilibrium y^* of the sub-system*

$$\frac{dy}{dt} = A_1(x)(y - y^*) \tag{4}$$

is globally asymptotically stable on the canonical projection of Ω on $\mathbb{R}^{n_1}_+$.
H_3. *The matrix $A_2(x)$ is a Metzler matrix and is irreducible for each $x \in \Omega$.*
H_4. *There exists an upper bound matrix $\bar{A}_2$ (in the sense of pointwise order) for the set $\mathcal{M} = \{A_2(x) : x \in \Omega\}$ such that: either $\bar{A}_2 \notin \mathcal{M}$, or $\bar{A}_2 \in \mathcal{M}$ and for each $\bar{x} \in \Omega$ satisfying $\bar{A}_2 = A_2(\bar{x})$ necessarily $\bar{x} \in \mathbb{R}^{n_1}_+ \times \{0\}$.*
H_5. $\alpha\left(\bar{A}_2\right) \leq 0$.

Then, the DFE of (3) is GAS in $\overline{\Omega}$.

Kamgang and Sallet, [10], also presented applications of Theorem 1 to various epidemiological problems, such as models for Tuberculosis and HIV, and we note that it was used in the study of models for vector-borne diseases, [12,13].

Our study is based on Theorem 1 and aims primarily to construct numerical schemes, for systems of type (3), that preserve the global asymptotic stability of the DFE. A key feature of this study is to establish a discrete counterpart of Theorem 1. This guarantees that our numerical schemes are reliable, being dynamically consistent with respect to a wide range of properties of the continuous system (3). These include the dissipativity of the discrete schemes, positivity and boundedness of their solutions, conservation laws, among others. We note that the concept of *topological dynamic consistency* has been introduced