Available online at www.sciencedirect.com
ScienceDirect
Journal of Computational and Applied Mathematics 210 (2007) 210–221
JOURNAL OF COMPUTATIONAL AND APPLIED MATHEMATICS
www.elsevier.com/locate/cam

# A discrete time version for models of population dynamics in the presence of an infection

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Received 8 July 2005; received in revised form 3 July 2006

**Abstract**

We present a set of difference equations which represents the discrete counterpart of a large class of continuous model concerning the dynamics of an infection in an organism or in a host population. The limiting behavior of the discrete model is studied and a threshold parameter playing the role of the basic reproduction number is derived.


*MSC:* 39A12; 92D25; 39A10

*Keywords:* Discrete system; Population dynamics; Infection; Qualitative behavior

## 1. Introduction

Most of the continuous problems representing the dynamics of a population in the presence of an infection consists of a set of ordinary differential equations involving typically at least two populations or dependent variables: susceptible individuals ($S(t)$) and infectious ones ($I(t)$). In this paper we choose some continuous-time models representing the spread of an infection in an host population or in an organism [2,7,10,17] and we use them as a starting point for constructing an unifying discretization. It is well known that there are two ways to construct discrete models of population dynamics (and in general of any phenomenon) starting from a continuous one. The first consists of trying to mimic the mechanism underlying the continuous model and deriving a discrete-time system which directly represents the phenomenon; the second instead is inspired by the discretization of the continuous problem. For example difference equations have been classically used for modelling "directly" nonoverlapping populations, because they account for the discrete nature of reproductive events. The "philosophy" of this paper is instead the latter, i.e., we start from a variety of continuous problems and among all the possible discretizations we try to construct a unique one that reproduces the main features of all the continuous problems (see for example [12–15] for a similar approach). We propose the following set of first order difference equations, where $n$ is the discrete-time step (and 1 is its length) which aims to represent the dynamics of a population (for example cells or individuals) in the presence of an infective one

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doi:10.1016/j.cam.2006.10.065

(viruses or infective individuals).

$$
\begin{aligned}
&y(n+1) = \alpha + (1-\beta)y(n) - \psi_I y(n+1)x_I(n+1), \quad n \geqslant 0,\\
&x_1(n+1) = (1-a_1)x_1(n) + \phi_1(y(n))x_L(n), \quad 1 \leqslant I \leqslant L \leqslant m,\\
&x_i(n+1) = (1-a_i)x_i(n) + \phi_i(y(n))x_{i-1}(n), \quad i = 2,\dots,m,\\
&y(0) > 0, \quad x_i(0) > 0, \quad a_i > 0, \ \ i = 1,\dots,m, \ \ \alpha > 0, \ \ \beta > 0, \ \ \psi_I \geqslant 0,\\
&\phi_i : y \in \mathbb{R} \to \phi_i(y) \in \mathbb{R}, \quad i = 1,\dots,m \ \text{ continuous and differentiable.}
\end{aligned} \tag{1.1}
$$

Moreover, we assume that one of the functions $\phi_i(y)$ coincides with $\psi_I y$ depending on the value of $I$ and $L$. More specifically we assume that

$$
\phi_K(y) = \psi_I y, \quad K = \begin{cases} 1 & \text{if } I = L,\\ I+1 & \text{if } I < L. \end{cases} \tag{1.2}
$$

As we shall see in the sequel the assumption (1.2) and the presence of the indexes $I$ and $L$ allows to discretize by (1.1) a very large class of population dynamics models. Generally speaking we can think about $y(n)$, $x_i(n)$, $i = 1,\dots,m$ as the number of individual belonging to different populations which are present in a (biological) system at time $n$. Only the populations $y$ and $x_I$ have a fixed role and they can be envisaged as the susceptible and the infective one, respectively, and they correspond to $S(t)$ and $I(t)$ mentioned at the beginning of the section. The parameters $\beta$, $a_i$ are the relative removal rates (death rates) of populations $y(n)$, $x_i(n)$, respectively, $\alpha$ is the absolute rate at which the population $y(n)$ is provided (birth rate). The functions $\phi_i$ can be interpreted as generic "growth" functions of the populations $x_i(n)$.

The system (1.1) can be viewed as the discretization of the following continuous system:

$$
\begin{cases}
Y'(t) = \alpha - \beta Y(t) - \psi_I Y(t) X_I(t),\\
X_1'(t) = -a_1 X_1(t) + \phi_1(Y(t))X_L(t),\\
X_i'(t) = -a_i X_i(t) + \phi_i(Y(t))X_{i-1}(t), \quad i = 2,\dots,m,
\end{cases} \tag{1.3}
$$

where $\phi_K$ is given by (1.2). We can note that an implicitness is introduced in the treatment of the first equation. In particular the approximation $y(n+1)$ of $Y(n+1)$ is given by a "mixed type" formula, which uses implicit Euler method for the linear part and explicit Euler method for the right-hand side of the first equation, and all the other components of $X_i$ of the solutions of (1.3) are approximated by explicit Euler method.

Compared with continuous models, discrete systems present of course some advantages and some drawbacks. One of the main advantages lies in the easy computability of the solution, but on the other hand, from a mathematical point of view, a discrete system is less "tractable" than its continuous counterpart, because not all the results which are known for differential problem remain valid for difference equations.

The paper is organized as follows. In the next section we report various examples of continuous models which can be discretized by (1.1). In Section 3 we prove some basic properties of the solution of the proposed scheme such as positivity and boundedness which makes it meaningful in the applications. Our main result is proved in Section 4 where the question of the asymptotic behavior of the solution is investigated. We prove a sufficient condition for the vanishing of the sequences $\{x_i(n)\}$ and we derive the expression of the *basic reproduction number*, a threshold parameter which allows to predict whether the infection develops or not. Such a parameter permits to check that, in all the examples quoted in Section 2, the asymptotic behavior of the discrete and continuous problem coincides, therefore our discrete system incorporates the dynamical characteristics (such as positivity and steady states) of the continuous-time models. The analysis of the limiting behavior of the model is completed in Section 5. Finally Section 6 contains some concluding comments.

## 2. Continuous models

In this section we consider different classes of continuous models which are particular cases of (1.3) and therefore can be discretized by means of (1.1). In particular we report the following model representing the spread of HIV-1 infection inside the human organism [7]. Here $S(t)$ represents the number of susceptible cells which are present at time