A note on semi-discrete modelling in the life sciences

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Semi-discrete models are a particular class of hybrid dynamical systems that undergo continuous dynamics most of the time but repeatedly experience discrete changes at some given moments. In the life sciences, since the first semi-discrete model was derived to describe population dynamics by Beverton & Holt (Beverton & Holt 1957 In Fisheries investigations, series 2, vol. 19), a large body of literature has been concerned with such modelling approaches. The aim of the present contribution is twofold. On the one hand, it provides a comprehensive introduction to semi-discrete modelling through two illustrative examples: the classical work by Beverton and Holt is recalled and an original example on immigration in a population model affected by a strong Allee effect is worked out. On the other hand, a short overview of the different applications of semi-discrete models in the life sciences is proposed.

Keywords: impulsive differential equations; epidemiology; medicine; population dynamics; Allee effect model; Beverton–Holt model

1. Introduction

The two most classical modelling techniques of biological phenomena are continuous-time and discrete-time models. Continuous-time models in ordinary differential equations, on the one hand, are used to describe the interactions between compartments (cells, animals, etc.) that can, from a macroscopic point of view, be considered as continuous because the processes involved happen randomly in time (prey–predator encounters, cell division, etc.). The Lotka Volterra predator–prey model, the Kermack McKendrick susceptible removed (SIR) epidemic model and Monod’s model of cell (bacteria) growth are typical examples of such systems. On the other hand, some natural phenomena cannot be considered as continuous since they occur at certain moments of

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time only; this is, for instance, the case for animals that reproduce seasonally or animals that are vulnerable to attacks during a certain period of their life cycle only. These characteristics gave rise to discrete-time models (difference equations) that were particularly developed by the consumer–resource modelling community with respect to host–parasitoid interactions (Murdoch et al. 2003). Both modelling approaches have a long history in the biological sciences: to the end of the eighteenth century for continuous-time modelling (Malthus 1798) and to the beginning of the twentieth century for discrete-time modelling (Nicholson & Bailey 1935).

There is, however, a large part of biological systems that does not fit either formalism, more precisely that involves some phenomena that are of a continuous nature and some others that are of a discrete one. The state variables of such systems experience smooth/continuous dynamics most of the time, but at some moments, face abrupt/discrete changes (also termed pulses); at these moments, the variables ‘jump’ from some state value to another. One can think, for instance, to predator–prey or epidemiological systems with seasonal reproduction, emigration processes starting once a density threshold of a population is reached, intermittent drug administration in medical programmes, etc. The modelling of this kind of systems would then naturally involve two different parts, a continuous one in ordinary differential equations and a discrete one in difference equations, yielding what is called a ‘hybrid’ system. The discrete part may occur as the model variables verify some conditions (recall the emigration process described above), this is called an ‘impact model’ (see Maggi & Rinaldi (2006) for an example on forest fires); otherwise, the discrete part occurs at some given instant (e.g. a seasonal process) and is referred to as an ‘impulsive’ or ‘pulsed’ system Bainov & Simeonov (1989). In the contribution, we will concentrate on the latter class of models only, and following Ghosh & Pugliese (2004), Singh & Nisbet (2007), Pachepsky et al. (2008), we will call them ‘semi-discrete models’.

The first semi-discrete approach was probably put forward by Beverton & Holt (1957) in their construction of a discrete-time model analogous to the continuous-time logistic model (Verhulst 1838) on the basis of a semi-discrete model. Since then, a large body of literature has proposed semi-discrete models in almost every field of the life sciences: population dynamics and ecology, plant pathology, epidemiology, medicine, etc. The explicit reference to the use of models that have both continuous and discrete characteristics is usually explicit, but for a non-negligible part, it is not. The semi-discrete modelling may even be difficult to identify since the discrete parts of the models may sometimes be described without equations at all (e.g. Shaw 1994; Jansen & Sabelis 1995; Swinton et al. 1997; Fenton et al. 2001). It actually appears that different bio-modelling communities work on similar mathematical tools with little knowledge of what the others do. The aim of this contribution is twofold: providing an introduction to semi-discrete modelling and giving a short review of the different fields of application in which semi-discrete modelling is used in the life sciences.

This paper is organized as follows. We first present the general mathematical formalism of semi-discrete modelling. We then study two illustrative examples of semi-discrete models, the classical Beverton–Holt model and an invasion model for a population subjected to a strong Allee effect. It is shown, in particular, that taking into account the discrete nature of some phenomena may have an important influence on the behaviour of the system. An overview of the literature
is then proposed. The reviewed results are classified with respect to their fields of application: epidemiology (vaccination strategies and plant diseases), medicine (drug therapy) and population dynamics (harvesting and pest managements programmes, seasonal phenomena and chemostat modelling). When applicable, we highlight the added value of semi-discrete models with respect to their continuous (or discrete) counterpart. Finally, we briefly discuss the advantages and drawbacks of semi-discrete models and some of the actual directions of work in this field.

2. Semi-discrete modelling: a general formalism and two illustrative examples

(a) General formalism

As stated in the introduction, we refer to semi-discrete models as the particular class of hybrid dynamical systems that undergoes continuous dynamics in ordinary differential equations most of the time and that experiences discrete dynamics at some given time instants. A schematic representation of the dynamics followed by a semi-discrete dynamical system is illustrated in figure 1.

Although most mathematically oriented contributions in semi-discrete (or pulsed, impulsive) systems share the same classical common mathematical formalism (see Agur et al. 1993; Funasaki & Kot 1993; Panetta 1996), some others differ (e.g. Shaw 1994; Ghosh & Pugliese 2004; Singh & Nisbet 2007). It is then important to recall the standard formalism used to describe semi-discrete models. Let $x$ be the vector of state variables at time $t$ and $\tau_k$ be the instants when the discrete changes occur. A semi-discrete model reads

$$\begin{align*}
\frac{dx}{dt} &= f(x, t), \\
x(\tau_k^+) &= F(x(\tau_k), \tau_k),
\end{align*}$$

(2.1)

with $\tau_k^+$ denoting the instant just after $t = \tau_k$. $f(\cdot)$ is the continuous, possibly time-varying, ordinary differential equation followed by the system and $F(\cdot)$ is the discrete component (also termed the pulse or impulse) that may also depend on time. In most of the reviewed literature, $f(\cdot)$ and $F(\cdot)$ are time independent, but this is not necessarily so (e.g. Gubbins & Gilligan 1997b; Choisy et al. 2006; Xiao et al. 2006; Braverman & Mamdani 2008). Moreover, in most of the studied cases, $(\tau_{k+1} - \tau_k)$ is a constant for all $k$, but once again there are examples where it is not (e.g. Lakmeche & Arino 2001; Liu et al. 2005; Nundloll et al. 2008).
There is an important part of semi-discrete models dealing with seasonal processes (such as seasonal reproduction) in which time \( t \) does not refer to the absolute time as in equation (2.1), but rather to the time elapsed between two seasonal processes, i.e. the time within the year. In these approaches, \((\tau_{k+1} - \tau_k)\) is a constant equal to the year’s (or season) length; at each instant \( \tau_k \), time \( t \) is reset to zero (e.g. Gyllenberg et al. 1997; Andreasen & Frommelt 2005; Pachepsky et al. 2008) and the state vector corresponding to the \( k \)th year may be denoted with a subscript \( k \) on \( x \).

A last remark should be given on what models the discrete part of the system. In most approaches, it represents an instantaneous process, e.g. an increase in some drug concentration in blood following a treatment, the death of a proportion of an insect population when a pesticide is applied, the introduction of individuals to increase the size of a population, etc. However, the discrete part of the model may also sum up what happens within a non-empty period of time. Insect populations, for instance, are active and interact with other species during the summer, but are mostly dormant in the winter. A semi-discrete model would then represent what happens during the summer with its continuous part and what happens during the winter (survival of a proportion of a population only, transition from a juvenile to an adult stage, etc.) with its discrete part (Iwasa & Cohen 1989; Ghosh & Pugliese 2004). Hence, strictly speaking, \( \tau_k^+ \) is actually not always the instant just after \( t = \tau_k \).

\[(b) \text{ Illustrative examples}\]

We show, in two simple examples, the consequences of the explicit modelling of discrete phenomena on the predictions of classical continuous-time models. The first example deals with the formulation of the classical discrete-time Beverton–Holt model of population dynamics on the basis of a semi-discrete model. In the second example, the effects of pulsed and continuous immigration strategies on the invasion success of a population undergoing strong Allee effects are compared and contrasted.

(i) Back to basics: the discrete-time Beverton–Holt model

Discrete-time models are appealing to biologists and ecologists as they can produce very complicated dynamical behaviours (cycles, chaos), even with a single variable. However, the principles that underlie the model equations are not always easy to interpret from a biological point of view. Hence, the ‘mechanistic underpinning’ of discrete-time population growth models is of interest (Geritz & Kisdi 2004).

Beverton & Holt (1957) were already concerned with this need for biological interpretation of discrete-time equations. To obtain their population growth models for fish species from mechanistic assumptions, they postulated that the main processes involved in the population’s growth are, on the one hand, seasonal reproduction within a very short period of time and, on the other hand, death processes that occur continuously throughout the season (see also Gyllenberg et al. 1997). We recall here how they derived their simplest and most famous model. Let \( n(t) \) be the population density at time \( t \) and assume that the per capita mortality rate is proportional to its density. We have the semi-discrete model with discrete reproduction at time \( t = kT \) and continuous death between
reproduction instants,
\[
\begin{aligned}
\frac{dn}{dt} &= -\mu n^2, \quad t \neq kT, \\
n(kT^+) &= n(kT) + \alpha n(kT),
\end{aligned}
\]
(2.2)
with \( k \in \mathbb{N}^* \) and where \( \mu \) is the mortality rate, \( \alpha \) the clutch size and \( T \) the season length.

Integrating the continuous part of equation (2.2) for \( t \in (kT,(k+1)T) \) gives
\[
n(t) = \frac{n(kT^+)}{1 + \mu Tn(kT^+)} ,
\]
so that the post-reproduction map of the population density between seasons is
\[
n((k+1)T^+) = \frac{(1 + \alpha)n(kT^+)}{1 + \mu Tn(kT^+)} ,
\]
which is the classical discrete-time ‘Beverton–Holt’ model. This model is a discrete-time model analogous to the continuous-time logistic equation of Verhulst (1838); it has a single globally stable equilibrium, similar transient dynamics and sound biological bases.

(ii) Pulsed immigration in a model with strong Allee effects

In population models, the Allee effect is the reduction of the population growth rate at low density that can, for instance, result from failure in mate searching. The population growth rate may remain positive for small population densities (weak Allee effect) or even drop below zero at some threshold, under which the population will go extinct (strong Allee effect; e.g. Taylor & Hastings 2005). According to Courchamp et al. (1999), one-population growth models with strong Allee effects can be written as
\[
\frac{dx}{dt} = rx \left( \frac{x}{K_a} - 1 \right) \left( 1 - \frac{x}{K} \right) ,
\]
(2.3)
where \( x \) is the population density, \( r \) is the Malthusian parameter, \( K_a \) is the Allee threshold and \( K > K_a \) is the carrying capacity of the environment. Model (2.3) is a very simple example of what is called bi-stability; if at the initial moment the population density is below the Allee threshold, it will decline to extinction, if it is above, it will grow to the carrying capacity of the environment. This bi-stability is typical of a strong Allee effect.

In the following, we investigate the outcome of different immigration strategies, namely continuous and pulsed immigration, for a population subjected to a strong Allee effect. We say that an invasion succeeds if the immigration strategy can drive the population density from \( x = 0 \) to some value above the Allee threshold \( K_a \), and that it fails otherwise. The interaction between strong Allee effects and (continuous) immigration was previously studied by Keitt et al. (2001).

Since we are interested in the invasion process only, i.e. as \( x \) stays beyond the Allee threshold \( K_a \), we assume for mathematical simplicity that the carrying capacity \( K \) is large with respect to \( K_a \), so that model (2.3) can, as long as
\( x \in (0, K_a) \), be approximated by
\[
\frac{dx}{dt} = r x \left( \frac{x}{K_a} - 1 \right).
\]

Actually, the computations we show next may also be worked out with the original Allee effect model (2.3), but they would be unnecessarily complicated and we prefer, for the sake of clarity, to consider this approximation.

In the continuous immigration case, the model reads
\[
\frac{dx}{dt} = r x \left( \frac{x}{K_a} - 1 \right) + \sigma, \quad (2.4)
\]
where \( \sigma \) is the (constant) immigration rate of the population. Let \( T \) be a reference time period (e.g. 1 year), then, according to equation (2.4), \( \sigma T \) individuals migrate into the system during this period.

Consider now the pulsed immigration problem: immigrating individuals are no longer evenly spread over the time period \( T \), but immigrate at one time (or two, etc.). Assume that \( (\sigma T/n) \) individuals immigrate into the system every \( (T/n) \) period of time (with \( n \) some positive integer). Then, for the pulsed immigration problem, we have the semi-discrete model
\[
\begin{align*}
\frac{dx}{dt} &= r x \left( \frac{x}{K_a} - 1 \right), \quad t \neq kT/n, \\
x \left( \frac{kT^+}{n} \right) &= x \left( \frac{kT}{n} \right) + \frac{\sigma T}{n},
\end{align*}
\]
for all \( k \in \mathbb{N}^* \). Note that, during a time period \( T \), \( \sigma T \) individuals migrate into the system modelled by equation (2.5). Hence, the immigration rate (i.e. the number of immigrants per unit time) is the same in the continuous model (2.4) and in the semi-discrete model (2.5); it is simply \( \sigma \). This property is of prime importance because we want to compare the continuous immigration strategy to the pulsed one. As a consequence, as \( n \) approaches \(+\infty\), i.e. as immigration numbers are infinitely small, but immigration occurs at an infinite frequency, model (2.5) reduces to model (2.4). Of course, it is not realistic to imagine an immigration of an ‘infinitely small number of individuals’, the minimum number is one individual. This reveals two things. First, although widely used in, for example, metapopulation models, the continuous immigration metaphor actually lacks biological realism. Second, the pulsed immigration model (2.5), which corrects some of the flaws of the continuous immigration model, is only realistic up to some final \( n \).

In the continuous immigration case (2.4), it is fairly easy to show that the invasion will be successful, i.e. \( x(t, x_0 = 0) \) overshoots \( K_a \) for some \( t > 0 \), if and only if
\[
\sigma > \frac{r K_a}{4}. \quad (2.6)
\]

In the pulsed immigration case (2.5), it is proved in appendix Aa that the invasion succeeds if and only if
\[
\sigma > \frac{n K_a}{T} \tanh \left( \frac{r T}{4n} \right). \quad (2.7)
\]
Again, as \( n \) approaches \(+\infty\), condition (2.7) reduces to equation (2.6) because \( \tanh(z) \) is equivalent to \( z \) at \( z = 0 \).
Let us now compare condition (2.7) with condition (2.6) for some finite $z$. Since $\tanh(z) < z$ for all positive $z$, it is easy to show that invasibility condition (2.6) is more restrictive than condition (2.7). Both strategies will of course succeed if $\sigma$ is large enough, but there are some intermediate values of the immigration rate with which an invasion based on continuous immigration would fail, but its pulsed counterpart would succeed. In other words, given an immigration rate, an invasion may more easily succeed if the immigration strategy is pulsed rather than continuous.

This result does not come from the fact that, with a single immigration pulse, the population would overstep the Allee threshold $K_a$ (although it is possible if $\sigma$ is large enough). Indeed, one can show that there always exist immigration rates that would not succeed in a single migration pulse, but do so in several pulses (see appendix A).

Keitt et al. (2001), based on an analysis very similar to the one presented above in the continuous case, show that the interaction between (continuous) migration and strong Allee effects gives rise to what they call ‘invasion pinning’: the spatial front of an invasion may be stopped by the strong Allee effect if the migration rate is too low. The study that was reported above shows that their results still hold true in the case of pulsed immigration, although the upper bound on the migration rate required to exhibit invasion pinning would be smaller than with continuous invasion. This result may have important consequences in the field of biological invasions management. Species can indeed exhibit pulsed migrations through, for instance, accidental transportation by humans; this happens for the gypsy moth, one of the major insect pest in the USA (Sharov & Liebhold 1998). For such organisms, disregarding the fact that the migration is pulsed, rather than continuous, leads to an overestimate in the ‘pinning’ induced by strong Allee effects. As a consequence, it results in the underestimation of the species ability to spread out in the environment (see also Johnson et al. (2006) for a related, but somewhat different, discussion on this issue).

Conversely, in the field of re-introduction biology, repeated pulsed introductions (also termed re-stocking; Armstrong & Seddon (2008)) are worthwhile, as they are likely to enhance re-introduction programme success in comparison to single and continuous ones (see also the discussion on re-stocking by Deredec & Courchamp (2007)).

With this rather simple example that compared pulsed and continuous immigration strategies with the same overall immigration pressure, we have shown one of the important consequences of semi-discrete modelling; although in some cases, semi-discrete models and their purely continuous (or discrete) equivalent give similar results, this is not true, in general. Emergent properties may indeed follow from the explicit consideration of the discrete nature of some phenomena and the continuous nature of some others.

3. Literature overview

Although it is not possible to provide an exhaustive review of the use of semi-discrete (pulsed, impulsive) models in the life sciences, we try to propose a representative overview. The modelling approaches are classified with respect to their application: epidemiology (vaccination strategies and epidemiological
control, plant epidemiology), medicine (mainly drug therapy) and population
dynamics (harvesting and pest management programmes, population and
chemostat models).

(a) Epidemiology

One of the major fields in which semi-discrete models are used is epidemiology,
whether it relates to humans, animals or plants. The most important application
is the comparison between classical (continuous) vaccination and pulsed
vaccination in epidemiological models (Agur et al. 1993). Some other applications
deal with the effect of seasonal demographic processes (birth and death). Another
important field is that of plant epidemiology in which pathogens face seasonal
demographic bottlenecks each winter.

(i) Pulse vaccination strategy

In a seminal paper, Agur et al. (1993) proposed the idea of a ‘pulse vaccination
strategy’ to improve the control of measles epidemics. Instead of a constant
vaccination effort spread throughout the year, they proposed to vaccinate a
proportion of the population within a very short period of time; vaccination was
then a discrete process, while epidemic evolution was assumed continuous. Their
study, based on the numerical analysis of an aged-structured epidemiological
model and on the mathematical analysis of a simple susceptible–infected
(SI) model, yielded the conclusion that pulse vaccination should give better
results than the classical constant vaccination programmes. Pulse vaccination
campaigns performed in 1994 in the UK against measles confirmed the theory
that this strategy has a dramatic impact on the development of the epidemic.

Subsequently, numerous authors compared both vaccination strategies
(continuous versus discrete) for various epidemiological systems. Shulgin
et al. (1998) completed the study by Agur et al. (1993) for the SIR (R for recovered
or removed) model and proved how mixed strategies can affect the level of
infected population. D’Onofrio (2002) considered an SEIR (E for exposed) model
and other more specific ones were examined in D’Onofrio (2005). A complete
mathematical study based on the classical mathematical tools of dynamical
systems was proposed in these papers. Gakkhar & Negi (2008) explored an SIRS
(the second S stands for susceptible too) model with a non-monotonic incidence
rate and proposed a bifurcation analysis, showing that pulse vaccination can lead
to very complex dynamics. Liu et al. (2008b) added a vaccinated class to the
population in the SIR model and a mathematical analysis based on the value
of the threshold $R_0$ was carried out. Meng & Chen (2008) studied, through a
bifurcation analysis, a new SIR model in which the offspring of infected parents
can be infected or susceptible. Again, the complicated dynamics that may arise in
such systems, and not with continuous vaccination, were highlighted. In all these
contributions, pulse vaccination was always shown to be capable of eradicating
the diseases, usually doing better than continuous vaccination.

Other authors followed different approaches in order to accurately describe
epidemic dynamics. Wagner & Earn (2008) focused on a particular disease (Polio)
for which the vaccine can sometimes mutate back and actually provoke the
disease. The influence of different vaccination programmes were studied and this
time, pulse vaccination appeared less effective than more classical strategies.
In other papers, seasonality has been added to the epidemiological models to obtain a more precise description of the epidemic (Liu & Jin 2006). Choisy et al. (2006) studied numerically a time-varying SEIR model with pulse vaccinations and warned that such a strategy can actually lead to complex dynamics and an increase of the infected population. Galvani et al. (2007) proposed a model of influenza in which the population was structured in elderly and younger people; seasons were accounted for, as well as a pulse vaccination occurring each autumn. It was shown, through a numerical analysis, that the classical vaccination programme (elderly vaccination) was actually not the best way to control influenza epidemics. The vaccination of younger people instead would give more acceptable results.

(ii) Discrete demographic processes

Other studies were concerned with the influence of discrete demographic processes (seasonal birth or death, discrete culling of a proportion of a population, etc.) on the dynamics of epidemiological systems. For example, Roberts & Kao (1998) considered an SI model with discrete birth processes and applied it to a tuberculosis in possums system. In this particular system, the authors showed that the discrete birth process was well approximated by an easier to study continuous-birth model. Swinton et al. (1997) also studied an SI model with a discrete-birth process. They analysed the influence of fertility control (removal of a proportion of the newborns at each birth) or lethal control (continuous removal of individuals) on the epidemic dynamics and applied it to the problem of bovine tuberculosis transmission by badgers. Their work argued that lethal control of badgers is better than fertility control. Fuhrman et al. (2004) examined an SI model with discrete culling of a proportion of the infected population and concluded that such a strategy made the eradication of a disease possible. Gao et al. (2005) also studied an SI model with birth pulses and seasonal parameters. They performed a bifurcation analysis, showing once more that very complicated dynamics may arise in such systems. Finally, Andreasen & Frommelt (2005) proposed an interesting ‘school-oriented’ epidemic model. The population was structured in age classes corresponding to the student level at school. Each year, the entire cohort of students was instantaneously translated from one school level to the next. A complete mathematical analysis has been carried out, and the model was shown to be able to convincingly mimic recurrent epidemics, such as influenza or measles, but also to produce complex dynamics that were difficult to interpret.

(iii) Plant epidemiology

Another important domain is that of plant epidemiology, which also has a strong link with seasonality. An important proportion of plants are deciduous or cultivated in annual cropping systems so that they mostly disappear from the environment at the end of each year or season. This leads pathogens that are responsible for plant diseases to regularly face demographic bottlenecks at each disappearance of their host population, a situation particularly well described by semi-discrete models. Shaw (1994) first proposed a plant disease model accounting for these demographic bottlenecks. It was numerically shown the very complex dynamics which were induced by these seasonal processes and
it was warned that ‘observed’ chaotic patterns were not necessarily due to some random external forcing. Truscott et al. (1997) examined a fungal root disease model in an annual cropping system. A local mathematical analysis and some simulations allowed to determine parameter values under which the disease was eradicated or persisted. Gubbins & Gilligan (1997a,b) studied the persistence of a continuous-time host plant–parasite system in an environment submitted to discrete perturbations due to cropping. They were particularly interested in the influence of the transmission functions and the type of perturbation on the persistence of the infection. Madden & van den Bosch (2002) presented an SEIR model of a plant pathogen introduced in an annual cropping system with a semi-discrete formalism. They investigated to what extent plant pathogens may be used as biological weapons, and the conditions under which the pathogen may persist from season to season were given.

Zhang & Holt (2001) investigated a plant-two virus model and compared continuous host plant availability (perennial systems) with semi-discrete host plant availability (annual systems). They (numerically) showed that the competitive exclusion principle applies for the continuous system (the virus with the higher reproductive number always outcompeted the other one), while this was not necessarily the case in the semi-discrete model. Conversely, Pietravalle et al. (2006) numerically studied an annual cropping system composed of two cultivars and the evolution of its resistance against a single strain of a pathogen.

The performance of chemical treatments in the control of plant diseases was also studied with semi-discrete models. Vendite & Ghini (1999) modelled the application of fungicide as a discrete process and the evolution of fungicide resistance in the fungal population as a continuous process. They studied the influence of the fungicide dose and showed that small doses are less likely to lead to fungal resistance than large ones. With a similar approach, Hall et al. (2007) studied numerically the influence of the dose and frequency of pesticide use on the evolution of pathogen resistance; they actually recommended the use of frequent and small doses of pesticide, rather than infrequent and large ones.

(b) Medicine

Semi-discrete models have also been used in the medical sciences, mainly in the modelling of drug administration. To our knowledge, one of the first authors who investigated this theme was Panetta (1996, 1998). In these contributions, two semi-discrete models of chemotherapeutic cancer treatment were proposed, in which the evolution of the tumours was described continuously, while the chemotherapeutic treatments were modelled as discrete processes. These models were quite simple so that a complete mathematical analysis was performed, investigating different therapeutic strategies. Lakmeche & Arino (2000, 2001) extended these results by considering more general models. In Lakmeche & Arino (2000), in particular, an important bifurcation theorem for two-dimensional systems was proved; under some conditions, it guaranteed the existence of a stable non-trivial periodic solution emerging from a ‘trivial’ one. This contribution was major in the field of semi-discrete modelling and used in almost all references that perform bifurcation analyses. Optimal protocols of drug administration in cancer immunotherapy were investigated through a numerical optimization algorithm in Cappuccio et al. (2007).
With respect to medical problems other than cancer, Smith & Schwartz (2008) analysed the influence of frequency and intensity of vaccine administration, approximated as a discrete process, in a continuous-time within-host human immunodeficiency virus (HIV) model. They theoretically showed that sufficiently large or frequent vaccine administration would keep the infection arbitrarily low. A final medical domain concerned with semi-discrete models is endocrinology. Kroll (2000) studied the effects of continuous and pulse hormone (parathyroid hormone) releases in a continuous model of bone formation. It appeared that pulse hormone administration was better than continuous administration, which, according to the author, explained some of the osteoporosis mechanisms. More recently in chronobiology, Vidal et al. (2009) modelled luteinizing hormone (LH) secretion and evolution using a time-variable semi-discrete model that accounted for variations in the photoperiod. The dynamical patterns produced by the model were very close to observations made on ewes. A similar approach was proposed by Shurilov et al. (2009) to model the regulation of non-basal testosterone secretion in males through pulses of gonadotropin-releasing hormone (GnRH).

(c) Population dynamics

With epidemiology, population dynamics modelling is the major (and historical) field in which semi-discrete models have been used. The approaches are even more diverse than for epidemic problems. We report here different studies related to the modelling of populations, some work considering harvest and pest management problems and finally the application of the technique to chemostat modelling.

(i) Population models

The mathematical modelling of population dynamics is an important field of application of dynamical systems. We highlight, in this section, different applications of semi-discrete modelling to population biology issues.

Some studies on population dynamics with impulsive birth were developed in Ballinger & Liu (1997). The permanence of population growth was studied using classical mathematical tools. Other interacting population models with birth pulses have been studied, showing that complex dynamics may arise (e.g. Tang & Chen 2004). Recently, Wang et al. (2008) also considered the influence of birth pulses and other impulsive perturbations on evolutionary game dynamics.

In line with the important work by Beverton & Holt (1957) recalled in §2b(i), the first set of contributions is concerned with the rationale that underlies discrete-time models of population dynamics. de Roos et al. (1992) proposed a semi-discrete modelling technique dedicated to structured populations that extends the classical discrete-time Leslie matrix models. Such techniques were mode recently used to model structured populations in an evolutionary context (Persson & de Roos 2003; van de Wolfshaar 2008). Nedorezov & Nedorezova (1995) provided mechanistic arguments to the formulations of some discrete-time models on the basis of semi-discrete ones (continuous death and discrete reproduction at some fixed moments). A complete mathematical analysis was proposed for one-dimensional population models. Gyllenberg et al. (1997) used the same kind of models to compare different reproduction strategies. The ‘mechanistic underpinning’ discrete-time model was further developed by

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Geritz & Kisdi (2004) with a stage-structured consumer–resource semi-discrete model (continuous consumer–resource interaction, discrete consumer death and reproduction). A time-scale separation in the continuous part was assumed to simplify the model, so that a complete mathematical analysis was possible. A similar approach was developed by Eskola & Parvinen (2007) to derive discrete-time Allee effect models. Eskola & Geritz (2007) proposed mechanistic arguments to the derivation of other discrete-time population models. Following the same modelling techniques, Rueffler et al. (2006, 2007) studied the evolutionary dynamics of resource specialization. Kisdi & Utz (2005) put the model by Geritz & Kisdi (2004) in the spatially explicit context of a patchy environment and studied the formation of patterns along a chain of patches. Utz et al. (2007) prolonged this work, adding a more detailed structure of the consumer population to the model and proposed an explanation to the emergence of an Allee effect.

The dynamics of population interactions with seasonal reproduction was first evoked in Hochberg et al. (1990), who studied the possible exclusion or not of a mutant population in a host–parasitoid–pathogen system using numerical tools. Later, Briggs & Godfray (1996) developed a season-dependent model describing insect–pathogen interactions. A local stability and bifurcation analysis showed the emergence of complex dynamics. Seasonal population dynamics of ticks (ticks are active during summer and dormant during winter) were described by Ghosh & Pugliese (2004), and their influence on disease transmission of tick-borne diseases was investigated mathematically. On the basis of a similar model of tick dynamics, Ding (2007) proposed a numerical method to find the optimal protocol of pesticide application to control tick population.

More recently, Singh & Nisbet (2007) derived a semi-discrete host–parasitoid model with stage structure of the host population depending on their status (parasitized or not). The influence of the functional response on the durability of the host–parasitoid interaction was studied, and their conclusion contradicted classical results obtained from discrete-time models. Pachepsky et al. (2008) analysed a consumer–resource model with continuous reproduction of the resource and discrete-time reproduction of the consumer. The model was shown to produce dynamics representative of classical consumer–resource models, but also showed a richer dynamical behaviour than these. Following the same modelling idea, Akhmetzhanov et al. (in preparation) studied a semi-discrete seasonal consumer–resource system. The consumers were assumed to be optimal foragers so that the within-season dynamics (continuous part) was formulated as an optimal control problem and analytically solved. A numerical bifurcation analysis of the long-term dynamics of such a system was also proposed and compared with the case of consumers that were non-optimal foragers. This work was actually also a reminiscence of previous works by Schaffer (1983) and Iwasa & Cohen (1989) on the optimal allocation of resources by plants for growth in seasonal systems.

(ii) Impulsive harvesting

Impulsive harvesting, the instantaneous removal of a proportion of a continuously growing population, has recently been considered in several research articles. Some harvesting problems linked to annual cropping systems have
already been reported in the plant epidemiology of §3a(iii) and will not be repeated here; some problems related to harvests are also reported in the pest management of §3c(iii).

Ives et al. (2000) studied the effects of recurrent periodic mortality events induced by harvests on the dynamics of a predator–prey system, modelling an aphid parasitoid interaction in an alfalfa field. Alfalfa was harvested several times a year, which induced some periodic mortality events on both predator and prey populations. The authors showed, through a numerical analysis, that such a system exhibited complicated dynamical patterns that were not possible without accounting for the harvest events. Following this idea, some papers studied the complex dynamics produced by population models experiencing impulsive harvesting (e.g. Liu & Chen 2008). Using a somewhat different approach, Drury & Lodge (2008) identified a kind of ‘semi-discrete hysteresis’ due to impulsive harvesting in an intraguild predation model. This phenomenon is probably common to a large part of semi-discrete models whose continuous part is bistable.

An important direction of research is the optimal management of renewable resources (Clark 1990). Some authors were interested in this question by considering impulsive harvesting rather than continuous harvesting. Zhang et al. (2003) studied the impulsive harvesting policy that maximized the per unit time sustainable yield for a single population with logistic growth. Independently, Xiao et al. (2006) later proposed a similar analysis for a population following logistic growth with periodic carrying capacity and a Malthusian parameter, accounting for seasonal variations in the ecosystem. Dong et al. (2007) studied this issue for a population with (periodic time varying) Gompertz growth and not logistic growth. These contributions showed that optimal continuous harvesting was superior to optimal impulsive harvesting, but argued that the differences were small and that impulsive harvesting would be easier to apply to real-life situations. Braverman & Mamdani (2008) also considered the same issue, but assumed that harvesting has some harmful effects on the population. They showed that, in this situation, (optimal) impulsive harvesting gave better results than (optimal) continuous harvesting.

(iii) Pest management

The control of insect pests in cropping systems is mainly based on the application of chemical pesticides and/or the release of natural enemies of the pests. Since these two processes are, by their very nature, discrete phenomena (instantaneous death after pesticide application, instantaneous increase in the natural enemy density after a release), pest management modelling has made a significant use of semi-discrete models. Jansen & Sabelis (1995) analysed first the consequences of recurrent death processes induced by pesticide on a tri-trophic chain (plant–pest–natural enemy). Although there was no mathematical analysis, the evolutionary consequences of pesticide use and its consequences for the design of pest management programmes were discussed.

Lu et al. (2003) analysed a predator–prey (pest–natural enemy) model with an impulsive use of a pest-specific pesticide. They showed that pesticide use may lead to both population extinction, to the natural enemy extinction.
only and to the persistence of both species. Most modern pest management programmes are so-called ‘integrated’ pest managements: chemical pesticides are coupled with biological control, i.e. the release of natural enemies of the pests. Liu et al. (2005) studied a predator–prey model with both pulses of pesticide and release of biological control agents. A mathematical analysis of the conditions under which the pest was eradicated and a numerical bifurcation analysis showing various routes to very complicated dynamics were proposed. Similar studies were performed with various forms of predator–prey models (e.g. Li et al. 2006), more complicated food chains (Georgescu & Morosanu 2008; Xiang et al. 2008) and stage-structured populations (Shi & Chen 2008), to cite a few.

Some other contributions related to pest management focused on the effect of dose and release frequency of biological control agents on the efficiency of biological control. Mailleret & Grognard (2006, 2009) showed that frequent small releases should be preferred to large and infrequent ones, a recommendation that is even more important when biological control agents interfere with each other (Nundloll et al. in press, submitted). In a similar context, Nundloll et al. (2008) analysed the effects of pulse harvesting on a biological control model with discrete natural enemy releases. It is shown, in particular, that in a biological control context, biological control agents should not be released more frequently than the pulse harvesting operates.

(iv) Chemostat models

The idea of studying the effects of nutrient pulsing in the chemostat is due to Ebenhoh (1988), who proposed an algae competition model that was mainly studied numerically. It was shown that multiple species can coexist in a chemostat with pulsed nutrient input. Funasaki & Kot (1993) followed the same modelling and studied a mass–action tri-trophic chain (nutrient–phytoplankton–zooplankton) in a chemostat with nutrient pulses. Through a mathematical analysis and simulations, they showed the emergence of very rich dynamics. Conversely, Song & Zhao (2006) considered a two nutrient–one micro-organism system in a chemostat with synchronized pulses of the two nutrients. The extinction and permanence of the population were studied. Wang et al. (2007) followed the same idea with a Monod-type tri-trophic food chain and pulse input and removal. A numerical bifurcation analysis enlightened the route to complicated dynamics. The same authors also studied, in a similar way, food chains with other functional responses (Beddington and Tessiet type). More recently, Toth (2008) explored resonance and chaos in a single species chemostat model with nutrient pulses. Stage-structured population was used to describe the micro-organism population, and bifurcation and simulation analyses illustrated the complex dynamics produced.

4. Conclusion

In this article, the different kinds of applications of semi-discrete modelling in life sciences have been briefly reviewed. Although it was not possible to be exhaustive, it is hoped that no major contribution has been forgotten. The main
advantages of semi-discrete modelling compared with its continuous or discrete counterpart are

(i) it allows an accurate description of some phenomena that cannot be accounted for using ‘classical’ modelling techniques,
(ii) semi-discrete models can exhibit emergent properties (e.g. the immigration model in §2b(ii)),
(iii) as a special case of emergent properties (mostly a consequence of their discrete component), semi-discrete models can produce very complicated dynamics (coexistence of multiple complicated attractors, chaos, etc.), even in low dimensions. As such, they can provide explanations, neglected with other modelling approaches, to the real-life observation of complex dynamics, and
(iv) semi-discrete models are extremely versatile and can be used to describe a large variety of systems.

There remains, however, shortcomings, not restricted to semi-discrete modelling but yet important, that can restrain its wider adoption

(i) as a combination of a discrete and a continuous component, such systems are intrinsically complex and their mathematical analysis is more difficult than purely continuous or discrete models; a consequence is that numerical computing is sometimes the only way to study such systems and
(ii) since semi-discrete models easily produce complex dynamics, there is an important risk that these dynamics are mathematical artefacts and do not correspond to real phenomena. This issue is, however, common to most modelling techniques (Sherratt et al. 1997).

Notwithstanding these drawbacks, semi-discrete models are mathematical tools that cannot be ignored when modelling biological phenomena. The formalism that we proposed in §2a is even a little narrow in comparison to what can actually be put in a semi-discrete context. Liu et al. (2008a) recently proposed an HIV infection model with a structured population described by a continuous parameter (age since infection), rather than with different variables, and pulsed drug administration. In this contribution, the continuous part of the model is then a system of partial differential equations, not of ordinary differential equations. Akhmet et al. (2006) also studied a predator–prey semi-discrete partial differential equation model, but related to diffusion of the populations in space. Other recent work was also concerned with the effects of time delay in the continuous part of their models (e.g. Gao et al. 2006, 2007; Li & Fan 2007), or those of stochasticity (Wagner & Earn 2008).

To finish with, one should notice that most of the actual work seems dedicated to modify the continuous part of the semi-discrete models, while the discrete part remains classical. A future direction of work may be to consider biological systems that require the discrete part to be altered as well.

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Appendix A

(a) Computation of the invasibility condition (2.7)

From the form of the RHS of the continuous part of equation (2.5), it is possible to obtain an analytical expression for the population density, as long as it stays below the Allee threshold $K_a$. Indeed, through a classical separation of variables technique, we get, for a population initiated at $x_0 < K_a$ at time $t_0 > 0$,

$$x(t) = \frac{x_0 K_a e^{-r(t-t_0)}}{K_a - x_0 (1 - e^{-r(t-t_0)})},$$

as long as $x(t)$ remains below $K_a$. From this equation, it is possible to deduce the one-dimensional map of post-immigration population densities,

$$x\left(\frac{(k+1)T}{n}\right) = \frac{\sigma T}{n} + \frac{x(kT/n)K_a e^{-rT/n}}{K_a - x(kT/n)(1 - e^{-rT/n})}, \quad (A1)$$

as long as $x(kT/n)$ does not overshoot $K_a$. Then, a necessary and sufficient condition for the invasion to succeed is that there exists a positive integer $k_s$ such that

$$x\left(\frac{(k_s+1)T}{n}\right) \geq K_a.$$ 

Since the RHS of equation (A1) is increasing in $x(kT/n)$ and positive at zero, a simple argument based on a cobweb plot drawing shows that the invasion succeeds if

$$\omega = \frac{\sigma T}{n} + \frac{\omega K_a e^{-rT/n}}{K_a - \omega (1 - e^{-rT/n})} \quad (A2)$$

does not have a solution $\omega^* \in (0, K_a)$. Some algebra shows that a sufficient condition for this to hold is

$$1 - \frac{\sigma T}{nK_a} < \left(1 + \frac{\sigma T}{nK_a}\right) e^{-rT/2n},$$

which after some manipulations is shown to be the same as equation (2.7).

Now suppose that equation (2.7) does not hold. Then, some calculations show that equation (A2) has at least one solution. Moreover, this solution is positive and smaller than $K_a$, therefore preventing the invasion from success; this shows that the sufficient invasibility condition (2.7) is necessary for the success of the invasion.

(b) Invasion after multiple pulses, not after a single one in equation (2.5)

From model (2.5), in one pulse, $(\sigma T/n)$ individuals migrate into the system. Since the initial population density is zero, a necessary condition for the invasion to succeed after one single pulse is

$$\frac{\sigma T}{n} \geq K_a.$$
Since \(\tanh(\cdot)\) is smaller than one, it is then easily seen from condition (2.7) that there always exist immigration rates that allow invasions to succeed after multiple pulses, though it would fail after a single one.

References


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