



Bivariate spline solution of time dependent nonlinear PDE for a population density over irregular domains



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ARTICLE INFO

Article history:

Available online 8 September 2015

MSC:

50-030

70-060

70-140

Keywords:

Bivariate splines

Numerical solution

PDE

Allee effect

Ecology

Epidemiology

ABSTRACT

We study a time dependent partial differential equation (PDE) which arises from classic models in ecology involving logistic growth with Allee effect by introducing a discrete weak solution. Existence, uniqueness and stability of the discrete weak solutions are discussed. We use bivariate splines to approximate the discrete weak solution of the nonlinear PDE. A computational algorithm is designed to solve this PDE. A convergence analysis of the algorithm is presented. We present some simulations of population development over some irregular domains. Finally, we discuss applications in epidemiology and other ecological problems.

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1. Introduction

Empirical evidence shows that the structure of environments and spatial scale can systematically influence population development and interactions in a way that can be described by mathematical models [9,11]. The first serious attempt to model population dynamics is credited to Malthus in 1798 [23], who hypothesized that human populations grow geometrically while resources grow arithmetically, thus eventually reaching a point in which the population could not be sustained anymore; this linear growth model is problematic since it allows unbounded population increase. A major refinement was introduced by Verhulst in 1838 [30] by means of a density-dependent logistic term in Malthus' model, predicting population growth if resources were available or population decay if population surpassed resources; this model takes the form $\dot{p} = r_0 p(1 - p/k)$, where p represents population density, r_0 is the rate of growth, and k represents the carrying capacity. Fisher [8] used in 1937 a diffusion operator to study the propagation of advantageous genes in population; the same year, Kolmogorov and his collaborators [14] studied the following reaction–diffusion equations in the

one-dimensional setting:

$$\frac{\partial p}{\partial t} = D \frac{\partial^2 p}{\partial x^2} + kp(1 - p) \text{ and } \frac{\partial p}{\partial t} = D \frac{\partial^2 p}{\partial x^2} + F(p), \quad (1.1)$$

where $F(p)$ satisfies $F(p) \geq 0$, $F(0) = F(1) = 0$, $F'(0) > 0$, $F'(1) < 0$ for $p \in [0, 1]$.

The logistic model has been central to the modern study of population dispersal in spatial domains [3,24]. Skellam's influential paper [27] in 1951 introduced a variation in Kolmogorov's equation for the study of phytoplankton; the resulting model was $p_t = d\Delta p + c_1(x, y)p - c_2(x, y)p^2$. This basic form of population dispersal is applicable in many notable cases ranging from population dispersal to recent models of information diffusion in online social networks [31]. Nevertheless, Skellam's model is too simplistic in most practical cases; it assumes a lack of interactions with other species, and that populations can grow at the same rate at low and high densities. An important refinement to Kolmogorov's model was introduced by Lewis and Kareiva in 1993 [21]. The correlation hypothesis by Allee in 1938 between population size and mean individual fitness [1] was represented in Lewis and Kareiva's model by $p_t = d\Delta p + r_0 p(1 - p/k)(p - \sigma)$, where σ represents the population below the carrying capacity below which the population growth is negative. This is the foundation of the model we study in this paper.

More precisely, we are interested in solution of the following nonlinear time dependent partial differential equation: letting $\Omega \subset \mathbb{R}^2$ be

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a polygonal domain and $\Omega_T = \Omega \times (0, T]$:

$$\begin{cases} \frac{\partial p(\mathbf{x}, t)}{\partial t} = \operatorname{div}(D(p, \mathbf{x})\nabla p(\mathbf{x}, t)) + F(p(\mathbf{x}, t)), \\ p(\mathbf{x}, t) \geq 0, \quad \mathbf{x} \in \Omega, t \in [0, T] \\ p(\mathbf{x}, t) = 0, \quad \mathbf{x} \in \partial\Omega, t \in [0, T] \\ p(\mathbf{x}, 0) = p_0, \quad \mathbf{x} \in \Omega, \end{cases} \quad (1.2)$$

where $D(p, \mathbf{x})$ is a diffusive term, e.g. $D(p, \mathbf{x}) = D > 0$ and $F(p)$ is a growth function, e.g. $F(p) = Ap(1 - p)$ which is a standard logistic growth function with A being a nonnegative weighted function over Ω . In this paper, we shall mainly study $F(p) = Ap(1 - p)(p - \sigma)$, where σ is a positive constant in $[0, 1)$ and $A(x, y)$ are nonnegative functions on $\Omega \times [0, T]$.

Exact solutions to Kolmogorov’s Eq. (1.1) have been found [22]. However, there does not appear to exist an exact solution to the diffusion logistic model with Allee effect; while asymptotics and speed of diffusion waves have been found analytically, the solutions to problem (1.2) over different domains remain mostly numerical. Lewis and Kareiva [21] used finite differences. Roques et al. [26] used a second-order finite elements method. Richter et al. [25] used finite elements in a model that incorporated geographic features and population dispersal.

In this paper, we present in detail a numerical solution to the diffusion logistic problem with Allee effect based on bivariate spline functions over triangulations. Bivariate spline have been studied extensively in different contexts, see [2,10,16,17,19,20]. An advantage of the use of bivariate splines is the ease to generate a smooth density surface over a spatial domain. The differentiability can be useful for some applications which involves the rate of changes of population along different directions at any location inside the domain, as explained in the following section.

Our numerical solution of this PDE is slightly different from the classic approach in a few ways. Instead of defining a weak solution in terms of test functions defined on domain $\Omega_T = \Omega \times (0, T]$, we define a discrete weak solution of the PDE using test functions defined on Ω together with the first order divided difference in time. See Definition 4.1. Another difference from the classic approach is that we use an optimization approach to establish the existence, uniqueness, stability and other properties of this discrete weak solution. We shall use bivariate splines to approximate the discrete weak solution using the discrete weak solution in the finite dimensional spline space. We are able to show that spline discrete weak solution converges to the discrete weak solution in $H^1(\Omega)$ as the size of underlying triangulation goes to zero.

It is clear that there are three nonlinearities in (1.2): the nonlinear diffusive term $D(p, \mathbf{x})$, the nonlinear growth function $F(p)$ and non-linearity condition $0 \leq p(\mathbf{x}, t) \leq 1$ for all x, t which is essential to the theory presented. We have to design a convergent computational algorithm to find bivariate spline solutions and establish how well our bivariate spline solutions are close to the exact discrete weak solution. We implement our computational algorithm in MATLAB. With the numerical solution, we are able to simulate how a population disperses over the area Ω of interest. In particular, we are able to see how the Allee constant σ plays a significant role in the population development.

2. Biological motivation: vector-borne disease

The dispersal patterns of a species in a given environment depends on the spatial scale considered, the temporal scale studied, the physical size of the model organism, and the life history the species. In most vector-borne disease dynamics, the dispersal of hosts and vectors has to be considered independently. In the case of mosquito-borne disease (e.g. malaria), human movement is a problem of a fundamentally different nature as compared to vector movement [4,28].

We focus in this paper on the dispersal of mosquitoes, which can be characterized by the diffusion–reaction framework presented in (1.2). Note that we propose Allee dynamics. The study of Allee effect in insects is common in the context of biological invasions [12,15]; however, the question of invasibility is not necessary to study the density dependence of a dispersal process. There is evidence that supports the assumption of Allee dynamics in this context; it has been shown that human-dependent mosquito populations (e.g. mosquito species that transmit malaria) can rapidly collapse when the population is reduced below realistic non-zero thresholds [13].

Vector control is often the tool of choice to manage mosquito-borne disease. When mosquitoes are removed from an area, or the population is brought to a level that drives local extinction, it can be repopulated by dispersal from neighboring areas. But landscapes are not even; instead, there are transitions in the patterns of vegetation cover which determine diffusivity and the suitability of local environments for the establishment and dispersal of mosquitoes. The effect of this spatial heterogeneity on population dispersal can be accounted for by (1.2), where $D(p, \mathbf{x})$ allows individual consideration of diffusivity in each segment of the spatial domain. The bivariate spline solution results in a smooth density surface over the entire spatial domain, which is very convenient to determine gradients of dispersal in all directions at all times.

Fig. 1 offers an example of the type of problem that could be solved with the approach presented in this paper. It depicts a map of vegetation cover for Colombia, in the Northwest corner of South America. The region on the right side of the map shows the location where resistance to the insecticide DDT was recorded for the first time in *Anopheles darlingi* in 1990 [29]. There are two fundamental questions in public health that could be addressed using the methods presented in this paper: (i) what is the likely pattern of dispersal of advantageous genes conferring *Anopheles* mosquito’s resistance to insecticides and/or repellents, and (ii) what is the likely dispersal and re-population by mosquito of areas subject to vector control. In order to answer these questions with actionable recommendations, we would need to consider multiple scales, the interaction between vectors and hosts, and epidemiological data for calibration of models. The scope of this paper is limited to the numerical solution of (1.2) via bivariate splines to solve one piece of this puzzle: vector dispersal.

We present in Section 7.2 numerical simulations using the geometry of the City of Bandiagara, Mali, as a proof of concept. In this example we did not consider a space-dependent diffusivity due to local variations in the landscape. We plan to undertake the calibration of this model with actual malaria data in a posterior study using the same locality, since Bandiagara has been the subject of many modeling exercises [5,6].

3. Preliminaries

For the sake of completeness, we list a number of lemmas used in this paper, which are special cases of well-known results.

Lemma 3.1. For $a, b \geq 0$ and any $\alpha > 0$ we have

$$ab \leq \frac{\alpha}{2}a^2 + \frac{1}{2\alpha}b^2$$

Lemma 3.2 (Ladyzhenskaya’s inequality). For any $p \in H_0^1(\Omega)$ for $\Omega \subset \mathbb{R}^2$ we have the following inequality.

$$\|p\|_{L^4} \leq C\|p\|_{L^2}^{1/2}\|\nabla p\|_{L^2}^{1/2}$$

Theorem 3.1 (Rellich–Kondrachov). Suppose that Ω is bounded with Lipschitz boundary. Then we have the following compact injection:

$$H^1(\Omega) \subset L^2(\Omega)$$

That is, any bounded sequence in $H^1(\Omega)$ has a subsequence which converges to an $L^2(\Omega)$ function in L^2 norm.

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