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Simulations and parameter estimation of a trap-insect model using a finite element approach

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Abstract

Estimating pest population size is of utmost importance in biological control. However field experiments can be difficult and expensive to conduct, with no guarantee that useable results will be produced. In this context, the development of mathematical models and numerical tools is crucial to improve the field experiments by suggesting relevant data which can be used to estimate parameters related to the pest's biology and to the traps (e.g. duration of the experiments, distance of the releases, etc.). Here we develop a trap-insect model (TIM), based on coupled partial differential equations. The model is studied theoretically and a finite element algorithm is developed and implemented. A protocol for parameter estimation is also proposed and tested, with various data. Among other results, we show that entomological knowledge is absolutely necessary for efficient estimation of parameters, in particular population size.

Keywords: Partial differential equations; Chemotaxis; Finite element method; Parameter estimation; Insect trapping

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1. Introduction

In the context of pest control and management, the success of any strategy requires a good understanding of the insect's biology as well as knowledge on its spatial distribution, dispersal capacity, density, etc. Typically the only data available is obtained using traps. Estimating population densities is complicated when little is known on the behaviour of the insects interacting with the traps as well as with the environment. Mark–release–recapture (MRR) experiments are often used to estimate some biological and ecological population parameters, e.g. size, dispersal, survival, etc. Models and estimation methods exist to quantify the size of the population (see [9] for an overview). Programs, like E-SURGE [8], and MARK [40] are also available. They are based on statistical analysis and fitting, and provide estimations of some population parameters using recapture data from particular field experiments (individual tracking). However, with these tools, testing different strategies is costly and time consuming as it requires many field experiments to get results.

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Beyond estimation of population size, optimizing trapping strategies is fundamental in pest control programs (see for instance [2,18]), and trap network is a component of crucial practical importance in terms of capture probabilities [23]. Many studies address this problem by relating the distance to a trap and capture probabilities using statistical distributions such as exponential [11,32] or Cauchy [26] distributions, or empirical logistic equation [4]. More recently, Manoukis et al. [23] used the hyperbolic secant function to model the probability of capture of attracting traps depending on the distance to the trap. In a previous work [14], we addressed the question of trapping networks as we developed a mathematical model for estimating insect population parameters using trap data in various configurations. The dynamics of the insects responding to attractive traps were modelled via an advection–diffusion–reaction equation, where the direction and force of attraction were defined by an analytical function of the space variable. This approach enables the estimation of model parameters and population characteristics using various settings of traps, and comparison of their efficacy via numerical simulations.

In this paper we develop a trap-insect model (TIM), which consists of a chemotaxis model that simulates the spread of a chemical attractant released by traps, coupled with an insect spreading model, in which the insects' response to the attractant is modelled. In [10], the authors developed a mosquito–host model where the spread of the CO_2 released by the hosts is described via an advection–diffusion–reaction, while the response of the mosquitoes is modelled via an individual based random walk process. Here we propose to model simultaneously the spread of the chemical attractant and the dynamics of flying insects, like fruit flies or mosquitoes, using a system of advection–diffusion–reaction equations.

In [14], the solution of the insect model was approximated using a finite difference approach. Here, the solution of the model is approximated using the finite element method [16]. In the finite element method, the domain is subdivided into elementary sub-domains (like triangles in 2D or tetrahedra in 3D) where the approximated solution is piecewise polynomial on the whole domain. Further, this method offers the possibility to refine the mesh around the traps and take into account local dynamics. Numerical approximations of the trap counts are obtained by simulation and used to estimate some parameters of the insects' dynamics.

The paper is structured as follows. We first describe the coupled chemotaxis model. Then, in Sections 3 and 4, we write the problem in variational form and we give some qualitative properties of the solutions. Next, the numerical scheme implementing the finite element method is described in Section 5, followed by some numerical simulations in Section 6. Finally, in Section 7, we consider applications to parameter identification, and specifically the estimation of the size of the insect population. We implement and test a feasible experimental protocol chain, and we discuss the results.

2. The model

It is commonly assumed that insects such as mosquitoes or fruit flies, move according to an isotropic random walk when they are not influenced by any stimulus in a homogeneous wind-free environment. Under such conditions, the movement of the insect population is governed by a simple diffusion equation [37]. Thus, when passive traps are used, insects are neither attracted to nor repulsed from the traps, and move according to a random walk until they “accidentally” get trapped [6]. Yet, the survival of the insect population depends on its ability to locate food and breeding sites, and therefore insects adapt their displacements accordingly [20]. This suggests that insects rather follow a correlated random walk allowing a bias in the insects' movement direction [21,39]. In the deterministic model, the average biased behaviour of the population is modelled via an advection term [30].

To increase the chance of capturing insects, attractive traps are often used. The latter release a chemical attractant (CO_2, pheromone, odour) which spreads. In a 2-dimensional domain, $\Omega \subset \mathbb{R}^2$, the active space of such traps is defined as the area where the concentration of the attractant is above a minimum threshold concentration level which can be detected by the targeted insects [35,29]. In other words, the active space of a trap is the area where its attraction takes place.

Modelling the spread of a chemical attractant in air is a challenge on its own. When it is assumed that the chemical is released at a constant rate, in a homogeneous environment with still air, the active space is a disc centred at the trap [12] and its radius defines the attraction range (i.e. the maximum distance from the trap to which attraction takes place) [35]. However, in the presence of wind, or if the environment is not homogeneous, the spread of the chemical is subjected to turbulences, and in such cases, the active space of the attractant is often described as a ‘plume’ [15]. To circumvent this difficulty, homogeneous spread [30,3] is often assumed when introducing wind in models. In [13],