



On a cross-diffusion population model deduced from mutation and splitting of a single species[☆]

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ARTICLE INFO

Article history:

Received 8 October 2011

Received in revised form 14 March 2012

Accepted 15 March 2012

Keywords:

Cross-diffusion system

Population dynamics

Existence

Uniqueness

Finite element approximation

Numerical examples

ABSTRACT

We deduce a particular case of the population cross-diffusion model introduced by Shigesada et al. (1979) [1] by using the ideas of mutation and splitting from a single species, as described by Sánchez-Palencia for ODE's systems Sánchez-Palencia (2011) [21]. The resulting equations of the PDE system only differ in the cross-diffusion terms, the corresponding diffusion matrix being self-diffusion dominated, which implies that the well known population segregation patterns of the Shigesada et al. model do not appear in this case. We prove existence and uniqueness of solutions of the PDE system and use a finite element approximation to discuss, numerically, stability properties of solutions with respect to the parameters in comparison with related models.

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1. Introduction

In [1], Shigesada et al. introduced the following time evolution drift-cross diffusion system of partial differential equations to model the interaction between two competitive species:

$$\partial_t u_i - \operatorname{div} J_i = f_i(u_1, u_2) \quad \text{in } Q_T = \Omega \times (0, T), \quad (1)$$

for $i = 1, 2$, in Q_T , where $\Omega \subset \mathbb{R}^N$ is an open and bounded set with Lipschitz boundary, $\partial\Omega$, $T > 0$ is arbitrarily fixed, the unknowns u_i represent population densities, the flow is given by

$$J_i = \nabla(c_i u_i + a_{i1} u_i u_1 + a_{i2} u_i u_2) + d_i u_i \mathbf{q}, \quad (2)$$

f_i are competition Lotka–Volterra type functions,

$$f_i(u_1, u_2) = (\alpha_i - \beta_{i1} u_1 - \beta_{i2} u_2) u_i, \quad \alpha_i, \beta_{ij} \geq 0 \quad i, j = 1, 2, \quad (3)$$

and the field \mathbf{q} is usually given as $\mathbf{q} = \nabla\Phi$, with Φ an environmental potential, modeling areas where the environmental conditions are more or less favorable [1,2]. The above system of equations is completed with non-flux boundary conditions and non-negative initial data:

$$J_i \cdot \nu = 0 \quad \text{on } \partial\Omega \times (0, T), \quad (4)$$

$$u(\cdot, 0) = u_i^0 \geq 0 \quad \text{on } \Omega, \quad (5)$$

for $i = 1, 2$, where ν denotes the exterior unit normal to Ω .

[☆] Supported by the Spanish MEC Project MTM2010-18427.

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This model has received much attention since its introduction due to the interesting spatial pattern formation of its solutions, referred to as *segregation*, and in fact an intense effort has been devoted to the understanding of its mathematical properties, specially to the existence of solutions, see [3–6] for first results under restrictions on the coefficients, mainly condition (6) below, [7,8] for general existence results, [9,10] for the study of the stationary problem, and [11,12] for extensions to several populations and non-homogeneous Lotka–Volterra terms. The numerical approach to the problem has been treated in [13–15], and the search for exact solutions in [16]. Related models have been studied in [17–20] and others. However, it seems that the modeling itself has not been the object of further study, and little more than the somehow ad hoc formulation given by Shigesada et al. in their key work [1] is available. In this article, we propose a derivation of the model in terms of a well known mechanism of population differentiation, see Sánchez-Palencia [21]. Starting with a single species with density u , a solution of certain evolution drift-diffusion PDE, we assume that mutation differentiates this single species into two sub-species with densities u_1 and u_2 , which split in their behaviors such that we still have that $u_1 + u_2 = u$ satisfies the original problem, but u_1 and u_2 solve slightly different PDE's conforming a system which is a special case of the Shigesada et al. model.

As showed by Sánchez-Palencia [21], the strategy of differentiation and splitting in the ODE's model leads to a situation in which there exists a full segment of steady state solutions which includes the cases of coexistence and extinction of one population. The interesting biological feature of the model is that, in general, small perturbations of the Lotka–Volterra terms involving advantages and disadvantages for both populations tend to induce coexistence. Therefore, differentiation–splitting strategies may be understood as mechanisms which promote diversity, rather than optimization of species. However, in general, this does not seem to be the case when cross-diffusion spatial effects of the Shigesada et al. type enter in the modeling, as we numerically demonstrate in Section 4. On the contrary, the effects of population pressure in the context of differentiation–splitting strategies seem to promote only the survival of the best fitted.

With respect to the segregation pattern formation of the Shigesada et al. model, let us mention that they are not expected to arise in our differentiation–splitting model since this mechanism leads to a self-diffusion dominated diffusion matrix. As pointed out by Lou and Ni [9,10] in the context of the stationary problem corresponding to problem (1)–(5), while cross-diffusion helps to create segregation patterns, these patterns do not appear if the intensity of diffusion or self-diffusion is relatively large. Heuristically, we may have an idea of the relative size of diffusion parameters not leading to segregation patterns when considering the diffusion matrix of the system,

$$A(u_1, u_2) = \begin{pmatrix} c_1 + 2a_{11}u_1 + a_{12}u_2 & a_{12}u_1 \\ a_{21}u_2 & c_2 + 2a_{22}u_2 + a_{21}u_1 \end{pmatrix},$$

and observing that under the condition

$$8a_{11} \geq a_{12}, \quad 8a_{22} \geq a_{21}, \tag{6}$$

the diffusion matrix is positive definite

$$\xi^T A(u_1, u_2) \xi \geq \min \{c_1, c_2\} |\xi|^2 \quad \text{for all } \xi \in \mathbb{R}^N,$$

hence yielding a uniform elliptic operator. Therefore, no segregation patterns are expected if condition (6) holds, as is the case for the differentiation–segregation model we shall deduce in Section 2.

The article is organized as follows. In Section 2 we introduce our model and comment on other related models. In Section 3, we state and prove the main analytical results of this article. Finally, in Section 4, we use a finite element approximation to compute several model examples and discuss on the stability of solutions with respect to the parameters of the model.

2. Mathematical model

We start considering the dynamics of one single species population satisfying

$$\begin{cases} \partial_t u - \operatorname{div} J(u) = F(u) & \text{in } \Omega \times (0, T), \\ J(u) \cdot \nu = 0 & \text{on } \partial\Omega \times (0, T), \\ u(\cdot, 0) = u_0 \geq 0 & \text{on } \Omega, \end{cases} \tag{7}$$

where the flow J is given by

$$J(u) = \nabla(cu + au^2) + du\mathbf{q},$$

with $a, c \geq 0$ and $d \in \mathbb{R}$, and where the Lotka–Volterra function is of competitive type

$$F(u) = u(\alpha - \beta u).$$

Here, $\alpha \geq 0$ is the intrinsic growth parameter and $\beta \geq 0$ is related to the carrying capacity of the ecosystem. In the homogeneous space case, i.e., when the PDE of problem (7) reduces to an ODE, the nonlinear term of the Lotka–Volterra function prevents the solution from unbounded increase. From the modeling point of view, observe that the flow J includes terms analogous to those of J_i given in (1). From the analytic point of view, the existence and uniqueness of solutions of

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