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An integro-PDE model for evolution of random dispersal [☆]



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ABSTRACT

We consider an integro-PDE model for a population structured by the spatial variables and a trait variable which is the diffusion rate. Competition for resource is local in spatial variables, but nonlocal in the trait variable. We focus on the asymptotic profile of positive steady state solutions. Our result shows that in the limit of small mutation rate, the solution remains regular in the spatial variables and yet concentrates in the trait variable and forms a Dirac mass supported at the lowest diffusion rate. Hastings [16] and Dockery et al. [14] showed that for two competing species in spatially heterogeneous but temporally constant environment, the slower diffuser always prevails, if all other things are held equal. Our result suggests that their findings may well hold for arbitrarily many or even a continuum of traits.

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1. Introduction

In this paper, we focus on the concentration phenomena in a mutation–selection model for the evolution of random dispersal in a bounded, spatially heterogeneous and temporally constant environment. This model concerns a population structured simultaneously by a spatial variable $x \in D$ and the motility trait $\alpha \in \mathcal{A}$ of the species. Here D is a bounded open domain in \mathbb{R}^N , and $\mathcal{A} = [\underline{\alpha}, \bar{\alpha}]$, with $\bar{\alpha} > \underline{\alpha} > 0$, denotes a bounded set of phenotypic traits. We assume that the spatial diffusion rate is parameterized by the variable α , while mutation is modeled by a diffusion process with constant rate $\epsilon^2 > 0$. Each individual is in competition for resources with all other individuals at the same spatial location. Denoting by $u(t, x, \alpha)$ the population density of the species with trait $\alpha \in \mathcal{A}$ at location $x \in D$ and time $t > 0$, the model is given as

$$\begin{cases} u_t = \alpha \Delta u + [m(x) - \hat{u}(x, t)] u + \epsilon^2 u_{\alpha\alpha}, & x \in D, \alpha \in (\underline{\alpha}, \bar{\alpha}), t > 0, \\ \frac{\partial u}{\partial n} = 0, & x \in \partial D, \alpha \in (\underline{\alpha}, \bar{\alpha}), t > 0, \\ u_\alpha = 0, & x \in D, \alpha \in \{\underline{\alpha}, \bar{\alpha}\}, t > 0, \\ u(0, x, \alpha) = u_0(x, \alpha), & x \in D, \alpha \in (\underline{\alpha}, \bar{\alpha}). \end{cases} \tag{1.1}$$

Here $\Delta = \sum_{i=1}^N \frac{\partial^2}{\partial x_i^2}$ denotes the Laplace operator in the spatial variables,

$$\hat{u}(x, t) := \int_{\underline{\alpha}}^{\bar{\alpha}} u(t, x, \alpha) d\alpha,$$

n denotes the outward unit normal vector on the boundary ∂D of the spatial domain D , and $\frac{\partial}{\partial n} = n \cdot \nabla$. The function $m(x)$ represents the quality of the habitat, which is assumed to be non-constant in x to reflect that the environment is spatially heterogeneous but temporally constant.

The model (1.1) can be viewed as a continuum (in trait) version of the following mutation–selection model considered by Dockery et al. [14], concerning the competition of k species with different dispersal rates but otherwise identical:

$$\begin{cases} \frac{\partial}{\partial t} u_i = \alpha_i \Delta u_i + \left[m(x) - \sum_{j=1}^k u_j \right] u_i + \epsilon^2 \sum_{j=1}^k M_{ij} u_j & \text{in } D \times (0, \infty), \quad i = 1, \dots, k, \\ \frac{\partial}{\partial n} u_i = 0 & \text{on } \partial D \times (0, \infty), \quad i = 1, \dots, k, \\ u_i(x, 0) = u_{i,0}(x) & \text{in } D, \quad i = 1, \dots, k, \end{cases} \tag{1.2}$$

where $0 < \alpha_1 < \alpha_2 < \dots < \alpha_k$ are constants, $m(x) \in C^2(\bar{D})$ is non-constant, M_{ij} is an irreducible real $k \times k$ matrix that models the mutation process so that $M_{ii} < 0$ for all i , and $M_{ij} \geq 0$ for $i \neq j$ and $\epsilon^2 \geq 0$ is the mutation rate.

Model (1.2) was introduced to address the question of evolution of random dispersal. In the case when there is no mutation, i.e. $\epsilon = 0$, this question was considered in [16],

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