Convergence to travelling waves in Fisher’s population genetics model with a non-Lipschitzian reaction term

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Abstract

We begin by a brief presentation of a well-known mathematical model for population genetics due to R. A. Fisher (1937) where a population is divided into three classes of genotypes, aa, AA, and aA. The mathematical model is represented by a reaction-diffusion equation for the unknown relative density \( u(x,t) \) of the population of allele A at the point \( x \in \mathbb{R} \) of the habitat at time \( t \in \mathbb{R^+} \). An important question from Population Biology is if genetic diversity is preserved at certain location and at certain time. We will show that this is a “dynamic problem” that requires a dynamical system approach by convergence to a travelling wave.

Our first mathematical result will be on travelling waves with a degenerate or singular diffusion (like the \( p \)-Laplacian) and possibly nonsmooth (e.g., non-Lipschitzian), bi-stable reaction term. We will show that, in spite of nonuniqueness for the one-dimensional ordinary differential equation, the travelling wave \( u(x,t) = v(x-ct) \) and its speed \( c \) are unique (up to a spatial shift in the argument). In order to answer our genetic diversity problem, we have to know if the two extreme values 0 and 1 of the solution (i.e., the profile of travelling wave) \( v(x) \) are reached within a bounded spatial interval \([z_0,z_1]\subset \mathbb{R}\). Namely, the genetic diversity is lost in \((-\infty,z_0]\) thanks to \( v = 0 \), and in \([z_1,\infty)\) thanks to \( v = 1 \).

Our second result establishes the long-time convergence to a travelling wave for the classical Brownian diffusion (i.e., the linear Laplace operator) combined with a non-Lipschitzian reaction term. We will briefly explain the “mechanism” that yields the desired convergence.

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