

# 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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