Global well-posedness for the diffusion equation of population genetics

Ge Yang

Department of Mathematics, Shanghai Maritime University, Shanghai 201306, China

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In this paper, we study the forward diffusion equation of population genetics. We prove the global existence of smooth solutions if the initial value is smooth. We also show that if the initial value is singular on the boundary, in a weighted Sobolev space, the diffusion equation exists a unique weak solution which is a probability density function. Moreover, we investigate the asymptotic behavior of the weak solution by the entropy method.

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1. Introduction

Genetic drift occurs when there is a random variation in the number of offspring contributed by each adult member of a finite population. At one locus in the population, the number of copies of a particular gene randomly varies from generation to generation, and undergoes a kind of random walk. Genetic drift is an evolutionary force that has the tendency to decrease the variation in a population and can influence the effectiveness of mutation and selection. One of the useful mathematical approaches to deal with genetic drift is the diffusion approximation, see [12,20]. Under this approximation, the proportion of individuals of a particular genetic type is treated as a continuous random variable whose distribution obeys a diffusion equation. For example, consider a single genetic locus in a population of $N > 0$ diploid individuals. Let us focus on one allele, denoted as n, at a given locus. The ratio of the total number of copies of allele n in the population, to the total number of all alleles at the locus $2N$, is termed the gene frequency and this can only take the discrete values $1/(2N), 2/(2N), \ldots, 2N/(2N)$. The diffusion approximation approximates the gene frequency as a continuous variable, $x \in [0, 1]$. Let $f(x, t)$ be the probability density of the gene frequency x at time t. Mathematically, the forward diffusion equation reads,

$$\partial_t f(x, t) + \partial_x j(x, t) = 0, \quad x \in (0, 1), \ t > 0, \tag{1.1}$$

E-mail address: geyangmath@gmail.com.

where the quantity $j(x, t)$ is the probability current density – a quantity that characterizes the flow of probability density. The form that $j(x, t)$ takes for a constant population $N > 0$ randomly mating individuals is

$$j(x, t) = M(x)f(x, t) - \frac{1}{4N}\partial_x\big(x(1 - x)f(x, t)\big),$$

where $M(x)$ represents the deterministic part of gene frequency dynamics and is typically taken as a polynomial in x whose coefficients depend on mutation rates, migration rates and selection coefficients.

The initial value

$$f(x, 0) = f_0(x), \quad x \in (0, 1). \tag{1.2}$$

For a thorough introduction to the several aspects of mathematical population genetics, refer to the monographs by [3,10].

The early work, for a class of degenerate parabolic equations in population genetics, has been studied by [11] which clarified the nature of boundaries by using semi-group theory. See [13] for a general discussion of degenerate diffusion equations and the classical monographs [4,9]. Recent works in degenerate equations, for instance, see [16] for the Fokker–Planck equation with solutions in weighted Sobolev spaces, and [2] for the qualitative studies. It seems that most works on the existence for the diffusion equation are restricted to some weighted Sobolev spaces or to lower regularity Sobolev spaces. In this paper, our first interest is

Under what condition, the solution to (1.1) *is of higher regularity?*

We state our first result as follows:

Theorem 1.1. *Suppose that* $\alpha > 0$, $\beta > 0$, *that is* $M(0) < \frac{1}{4N}$, $M(1) > -\frac{1}{4N}$, $s \in \mathbb{N}$, $k \in \mathbb{N}$ *and* $f_0 \in H_0^{2(s+k)}(0, 1)$. *Then* (1.1) *with* (1.2) *admits a unique global weak solution, and moreover, it satisfies*

$$\big\|\partial_t^s\partial_x^k f\big\|_{L^2((0,1)\times(0,T))} \leqslant C_{s,k}\|f_0\|_{H^{2(s+k)}(0,1)} \tag{1.3}$$

for some constant $C_{s,k}$.

Remark 1.1. Theorem 1.1 tells us that if $f_0 \in C^\infty[0, 1]$ is flat at $x = 0$ and $x = 1$, then $f \in C^\infty([0, 1] \times [0, +\infty))$.

In the field of biology, for situations where there is no mutation, the only way for the total probability to be conserved is for probability to accumulate at the boundaries. As a consequence, the approach adopted can lead to solutions to the forward diffusion equation which do not have the property of being smooth and well behaved, see [18]. The authors of [5] studied a class of diffusion equations which are similar to (1.1) with $M(0) = M(1) = 0$, and proved the existence and uniqueness of solutions constructed by a smooth function and two singular measure supported at the endpoints. Recently, the authors studied in [6] replicator-diffusion equations, show that the convective approximation is related to the replicator dynamics and provided some estimate of how accurate is the convective approximation, with respect to the convective-diffusion approximation. But it is not studied for more general cases of $M(x)$ in (1.1).

We give the zero-flux boundary condition,

$$j(0, t) = j(1, t) = 0, \quad t \in (0, T). \tag{1.4}$$

Before stating our results, we fix some notations and give a definition of weak solutions.