Rare mutations in evolutionary dynamics

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Abstract

In this paper we study the effect of rare mutations, driven by a marked point process, on the evolutionary behavior of a population. We derive a Kolmogorov equation describing the expected values of the different frequencies and prove some rigorous analytical results about their behavior. Finally, in a simple case of two different quasispecies, we are able to prove that the rarity of mutations increases the survival opportunity of the low fitness species.
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1. Introduction

Evolutionary dynamics describes biological systems in terms of three general principles: replication, selection and mutation. Each biological type – a genome or a phenotype as well as a species – is described by its reproduction rate, or fitness. In force of selection, a population evolves and changes its fitness landscape. Genetic changes can help in reaching some local optimum, or open a path to a new fitness peak, but sometimes they may drift population away from a

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peak, especially if the mutation rate is high. See [13] for an extensive account of the state of the art concerning evolutionary dynamics.

A mixed population of constant size constituted by a fixed number of different types is characterized by the vector collecting the relative abundance of each type: $x = (x_0, x_1, \ldots, x_D)$. By virtue of evolution, this vector draws a path in the simplex

$$S = \left\{ x = (x_0, x_1, \ldots, x_D) \in \mathbb{R}^{D+1} : \sum_{k=0}^{D} x_k = 1, \; x_k \geq 0 \text{ as } k = 0, 1, \ldots, D \right\}.$$

The mechanism of replication/selection is well described by an ordinary differential equation, where the relative fitness measures the balance between death and birth of individuals. Denoting by f_k the absolute fitness of any k-type, by $f = (f_0, f_1, \ldots, f_D)$ the fitness vector, and by $\bar{f} = x \cdot f$ the mean fitness of the population, this equation reads

$$\frac{dx_k}{dt} = \left(f_k - \bar{f} \right) x_k, \quad \text{as } k = 0, 1, \ldots, D. \tag{1.1}$$

Several shapes have been proposed for the absolute fitness. When one is modelling phenotypes, the choice of a constant fitness seems fair, but, starting with the seminal work by Maynard Smith and Price [12], an important amount of research deals with ideas arising from mathematical game theory, see [9] and references therein. In that framework, the individual fitness is taken as a linear function of the population x, i.e. $f(x) = Ax$, where A is the payoff matrix that rules the interplay between different strategies. In this case, equation (1.1) is the celebrated replicator equation introduced by Taylor and Jonker [15].

Concerning mutations, it has to be mentioned the quasispecies equation introduced by Eigen and Schuster [8], where constant fitness were considered. This choice modifies equation (1.1) into

$$\frac{dx_k}{dt} = \sum_{i=0}^{D} f_i \, q_{ik} \, x_i - \bar{f} x_k, \quad \text{as } k = 0, 1, \ldots, D. \tag{1.2}$$

Here the coefficient q_{ik} expresses the proportion of offspring of k-type from a progenitor i, which shows up at any procreation. It is clear that $q_{ik} = \delta_{ik}$ gives back the equation (1.1). When the fitness vector is given by the relation $f(x) = Ax$, as suggested by evolutionary game theory, then equation (1.2) is the well-known replicator–mutator equation, also known as selection–mutation equation, studied in [14].

As a matter of fact, mutations introduce a random ingredient into evolution, that is not enough emphasized in (1.2). Traulsen, Claussen and Hauert [16] pointed out that equation (1.2) can be recovered by assuming that the population follows a generalized Moran process and taking the limit for large population size. Champagnat, Ferrière and Méléard [6] and Jourdain, Méléard and Woyczynski [10] showed that various macroscopic diffusion models can be derived by the same individual stochastic process, by performing different types of rescaling. We also mention [7], where a macroscopic dynamics is deduced by an individual based stochastic description of the mutation process.

Here, we prefer to take a more macroscopic viewpoint, which however takes strongly into account the different regime of mutation processes. We start by modelling the stochastic dynamics