

A MEASURE VALUED DIFFUSION PROCESS DESCRIBING AN n LOCUS MODEL INCORPORATING GENE CONVERSION

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§ 1. Introduction

Probability measure valued diffusion processes have been discussed by many authors, in connection with population genetics. Most papers studying probability measure valued diffusions are mainly concerned with the ones describing single locus models. In this paper, we will discuss a measure valued diffusion describing an n locus model. Random sampling, mutation and gene conversion, a kind of interaction between loci, which was introduced and investigated by T. Ohta in [5], [6], will be taken into consideration.

The first aim of this paper is to give a mathematical justification to the Ohta's results. Let $\mathbf{E}$ be the set $[0, 1]^n$ in R^n . Here, the interval $[0, 1]$ describes the set of alleles, and a point of $\mathbf{E}$, which is an n -ple of alleles, means a chromosome with n loci. The bounded operator B_1 introduced in § 2 describes mutation of the neutral infinitely many allele model in n locus case. A positive constant v is mutation rate. We assume that mutation occurs independently at each locus. The operator B_2 defined in § 2 describes the Ohta's gene conversion. A positive constant λ stands for gene conversion rate. Let $\mathcal{P}(\mathbf{E})$ be the space of probability measures on $\mathbf{E}$. We consider the $\mathcal{P}(\mathbf{E})$ -valued diffusion process with the generator G given in § 2. The known results on the diffusion with the generator G will be stated in Propositions 2.1 and 2.2. For simplicity, it will be omitted to explain the reason why our diffusion process is the stochastic process existing behind the Ohta's arguments. See the paper [8], where the author explained the reason by means of giving a discrete model describing the Ohta's model in 2 locus case with the diffusion approximation. The argument on discrete models and the diffusion approximation in n locus case is essentially the same as in [8].