

Some Measure-Valued Markov Processes in Population Genetics Theory

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1. Introduction. This paper is concerned with stochastic population models of the following kind. Suppose that a population consists of a large, but finite, number of individuals; and that each individual in the population has a “type” described by an element x of some set S . We are concerned not with the types of particular individuals, but rather with the distributions of types among the whole population. If S is a finite set, with J elements x_1, \dots, x_J , then let p_j denote the frequency of type x_j ($p_j \geq 0$, $p_1 + \dots + p_J = 1$). The vector $p = (p_1, \dots, p_J)$ describes the type distribution; moreover, $p \in \Sigma^J$, where Σ^J is a $(J - 1)$ -dimensional simplex.

In population genetics p ordinarily refers to the frequency distribution of gametes, rather than of individuals, in a population. Thus, for diploid populations, the term “individual” in the present paper should be interpreted as “gamete”. When $J = 2$ the classical Wright-Fisher model describes the changes in frequencies of two possible gametic types (or alleles) at a given gene locus, considering such factors as mutation, random genetic drift, and selective advantages among the various genotypes. By the technique of diffusion approximation, a 1-dimensional diffusion process on the interval $0 \leq p_1 \leq 1$ is obtained [4]. The corresponding diffusion approximation with J types has been discussed in [8], [12], [19] and by other authors. This diffusion process has Σ^J as state space; see §2. Its generator \mathfrak{A}^J has the form (2.1), if an appropriate time scale for the diffusion is chosen. The Wright-Fisher process is a discrete-time Markov chain. Alternatively, one can start with a continuous-time Markov chain of Moran type and obtain a diffusion with the same generator \mathfrak{A}^J . See the Appendix.

The ladder model of Ohta and Kimura [16], [15] considers a countably infinite set of types, which may be interpreted as electrophoretically detectable states at a gene locus. In the ladder model, selective neutrality is assumed; *i.e.*, the type does not affect an individual’s chances in life. We discuss the ladder model in §8.

In this paper, we allow the set S of possible types to be a compact metric space. In particular, S may be a finite interval on the line R^1 , a compact subset