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A probabilistic analysis of a discrete-time evolution in recombination

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ABSTRACT

We study the discrete-time evolution of a recombination transformation in population genetics. The transformation acts on a product probability space, and its evolution can be described by a Markov chain on a set of partitions that converges to the finest partition. We describe the geometric decay rate to this limit and the quasi-stationary behavior of the Markov chain when conditioned on the event that the chain does not hit the limit.

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1. Introduction

Here we study the evolution of the following transformation Ξ acting on the set of probability measures μ on a product measurable space $\prod_{i\in I}\mathcal{A}_i$,

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$$\Xi[\mu] = \sum_{J \subseteq I} \rho_J \, \mu_J \otimes \mu_{J^c}.$$

The vector $\rho = (\rho_J : J \subseteq I)$ is a probability vector, μ_J and μ_{J^c} are the marginals of μ on $\prod_{i \in J} \mathcal{A}_i$ and $\prod_{i \in J^c} \mathcal{A}_i$ respectively, and $\otimes$ means that these marginals are combined in an independent way.

The analysis of Ξ should give an insight in the study of the genetic composition of population under recombination. Genetic information is encoded in terms of sequences of symbols indexed by a finite set of sites. In the process of recombination the children sequences are derived from two parents, a subset of sites (J) is encoded with the maternal symbols and the complementary set (J^c) is encoded with the paternal symbols. The above equation expresses that the pair of sets (J, J^c) constitute a probabilistic object distributed according to ρ. By taking $\rho_J + \rho_{J^c}$ as the weight of the binary partition $\{J, J^c\}$ we can always consider binary partitions instead of sets.

The evolution $(\Xi^n[\mu])$ has been mainly studied in the context of single cross-overs, that is where $I = \{1, .., K\}$ and the pairs of sets (J, J^c) are of the form $J = \{i : i < j\}$, $J^c = \{i : i \geq j\}$. This evolution was introduced by H. Geiringer [11], and firstly solved in the continuous-time case by E. Baake and M. Baake [2], where it is also supplied an important corpus of ideas and techniques to study the discrete-time evolution. More detailed discussions on some of the pioneering works, comments on other significant results, including [6,9,10], as well as the interpretation of the above equation in a broader perspective of recombination in population genetics, can be found in the introductory sections of references [2,4,5] and [15,16].

When studying single cross-over recombination, one the main objectives in [15] and [4] is to express the iterated $\Xi^n[\mu]$ in a simple form which allows its dynamics to be understood. The main tools are Möbius inversion formulae, and commutation relations between Ξ and recombinators, which are idempotent operators that commute, so act as projectors. In my view, some of the main results in this body of works are:

- Theorem 1 in [4] and Proposition 3.3 in [15], that supply a one step recursive decomposition for Ξ^n in terms of the recombinators and give an expression of $\Xi^n[\mu]$ serving to the analysis of the convergence of $\Xi^n[\mu]$ to the distribution $\bigotimes_{J \in \mathcal{D}^*} \mu_J$, where $\mathcal{D}^*$ is the partition whose atoms are the nonempty intersections of the sets J, J^c with $\rho(J) > 0$;
- the construction of a Markov chain by following the ancestry of the genetic material of a selected individual from a population; and Theorem 3 in [4], which states a relation between (Ξ^n) and the Markov chain.

Recently, in [5], the continuous-time evolution was studied in a framework of general partitions other than the binary partitions $\{J, J^c\}$ considered in [2,4] and [15]. It corresponds to study the evolution of the following transformation Ξ acting on the set of probability measures μ on a product measurable space $\prod_{i \in I} \mathcal{A}_i$,

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