

On the Diffusion Approximation of Wright–Fisher Models with Several Alleles and Loci and its Geometry

Dissertation

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2014

Abstract

The present thesis is located within the context of the diffusion approximation of Wright–Fisher models and the Kolmogorov equations describing their evolution.

First, a systematic approach to the diffusion approximation of recombinational two- or more loci Wright–Fisher models is presented. As a point of departure a specific Kolmogorov backward equation of a recombinational two-loci model is chosen, to which – with the help of some information geometrical methods – the underlying Wright–Fisher model is identified. Furthermore, the two most common underlying models (RUZ and RUG) are compared and the evolution is contrasted with Brownian motion. Subsequently, the model is extended by an integration of the concepts of natural fitness and mutation as well as by allowing an arbitrary number of alleles and of loci respectively (the latter requiring recombination masks) and finally coarse-graining by schemata. Simultaneously, the corresponding Kolmogorov backward equations are stated. Eventually, a geometric analysis of multi-loci linkage equilibrium states is carried out.

Subsequently, a discussion of analytical solution schemes for the Kolmogorov equations for the diffusion approximation of Wright–Fisher models is presented: Starting from the simplest setting of a 1-dimensional Wright–Fisher model, a unique extended solution which also accounts for the dynamics of the model on lower-dimensional strata of the domain is constructed, utilising the concept of (boundary) flux of a solution; an analysis of the moments of the distribution confirms the findings. A similar treatment is then carried out for the corresponding Kolmogorov backward equation, yielding analogous results of existence and uniqueness for an extended solution, for which the configuration on the boundary turns out to be crucial. Additionally, the long-term behaviour of solutions is analysed, and a comparison between such solutions of the forward and the backward equation is made.

Next, the preceding results are transported to the n -dimensional Wright–Fisher model (1 locus, n alleles): With solution schemes for the interior of the domain existing in

the literature, an extension scheme for a successive determination of the solution on lower-dimensional boundary strata is developed by the concept of (boundary) flux. It is demonstrated that this extended solution fulfils a corresponding moments condition for the entire domain, whose connection to the underlying Wright–Fisher model is illustrated. Thereupon, existence and uniqueness of an extended solution on the entire domain are shown. Furthermore, the corresponding Kolmogorov backward equation is examined, for which similarly a (backward) extension scheme is presented, which allows extending a solution in a boundary stratum to all adjacent higher-dimensional entities of the domain along a certain path. In total, the existence of a solution of the Kolmogorov backward equation in the entire domain is shown for arbitrary boundary data.

Eventually, the hitherto missing uniqueness assertion for the previously constructed stationary backward extensions is established through a successive blow-up of the domain which resolves the critical incompatibilities of solutions. Lastly, several other aspects of this scheme are discussed, particularly, in what way the required additional regularity of solutions relates to reasonable properties of the underlying Wright–Fisher model.