Wright-Fisher construction of the two-parameter Poisson-Dirichlet diffusion

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The two-parameter Poisson-Dirichlet diffusion, introduced in [3], extends the infinitely-manyneutral-alleles diffusion model, related to Kingman's one-parameter Poisson-Dirichlet distribution and to certain Fleming–Viot processes. The additional parameter has been shown to regulate the clustering structure of the population (see e.g. [4]), but is yet to be fully understood in the way it governs the reproductive process.

This talk will provide a finite-population construction, with finitely many species or alleles, in analogy to what is done in [2] for the infinitely-many-neutral-alleles diffusion model. The approximating model is a K-allele Wright-Fisher model for a population of size N, involving a uniform parent-independent mutation pattern and a specific state-dependent migration mechanism. Suitably scaled, this process converges in distribution to a K-dimensional Wright-Fisher diffusion process as $N \to \infty$. The descending order statistics of the K-dimensional diffusion converge in distribution to the two-parameter Poisson–Dirichlet diffusion as $K \to \infty$.

Convergence of the finite-dimensional diffusion to the two-parameter Poisson-Dirichlet diffusion depends on a delicate balance between reinforcement and redistributive effects in the migration mechanism. Moreover the proof of convergence is nontrivial because the generators do not converge on a core. The strategy for overcoming this difficulty is to prove *a priori* that in the limit there is no "loss of mass", i.e., that, for each limit point of the sequence of finite-dimensional diffusions (after a reordering of components by size), allele frequencies sum to one.

The two-parameter Poisson-Dirichlet diffusion has the two-parameter Poisson-Dirichlet distribution as its unique stationary distribution: In the last part of the talk it will be shown that the two-parameter Poisson-Dirichlet distribution is the weak limit of the stationary distributions of the Wright-Fisher diffusions (modified to account for the rearranging of components in descending order), in analogy to what happens in the one-parameter case, where these stationary distributions are symmetric Dirichlet distributions.

This talk is based on joint work with P. De Blasi, S. N. Ethier, M. Ruggiero and D. Spano ([1]).

References

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