Postdoctoral Research Project

Genetic Contributions and Site Frequency Spectra in Biparental Moran Models with Finite Selection

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Scientific Context

The aim of this post-doctoral project is to study the genetic structure of a sexually reproducing population, using the simple biparental Moran model framework.

The biparental Moran model is a stochastic discrete time constant size population model, in which at each time step, an individual is replaced by the child of two individuals. In the neutral version of this model, the dying and reproducing individuals are chosen independently and uniformly at random, independently at each time step. Genetic selection can be added by assuming that the choices of these individuals can depend on their genome and more generally on the genetic composition of the population. Recent works (Coron and Le Jan [2022, 2025], Coron and Hénard [2026], Mardomingo Sanz et al. [2026]) have established asymptotic results regarding the proportion of genome transmitted by a given ancestor in several particular cases, assuming that the genome is composed of infinitely many independent loci : the neutral case, the infinite viability selection case, and the finite viability and reproductive selection case assuming a macroscopic initial proportion of advantaged individuals.

Project

A first natural and important next step is to extend these results to the more general and biologically more realistic setting of a unique initial mutant with finite selective advantage, in particular possibly scaling with population size. Mathematical difficulties will arise in this case, due to the possible extinction of advantaged individuals. As in Coron and Hénard [2026] we expect the dynamics of the genetic composition of this initially advantaged individual to be decomposed into a first branching phase involving non-extinction conditioning and random recursive trees, followed by a deterministic transportation. The weak selection regime will be of particular interest.

A second major direction of the project concerns an analysis or a derivation of the Site Frequency Spectrum (SFS) in biparental populations represented by this biparental Moran model. While the classical SFS is well understood in many coalescent-based settings, much less is known in models where inheritance is genuinely biparental and where genealogical contributions are stochastic. Though both questions are linked through the biparental modeling, this second question will be in fact very different since the site frequency spectrum is strongly shaped by time scales, which are not studied in the previously mentioned works (but were studied in Chang [1999] notably). The effect of selection on this biparental SFS will be a particularly interesting question and comparing theoretical SFS with biological data can be a very challenging and ambitious objective of this project.

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Application to landrace and hybrid plants study

The obtained theoretical results will be applied to agricultural systems, within the framework of plants selection and amelioration. Landrace (Galaretto et al. [2026]) through which domestic varieties of a species of plant or animal have developed over time in isolation from other populations of the species, can provide interesting datasets that our model and mathematical study enable to analyze. Indeed, our framework typically enables to predict the genetic introgression of landrace species within hybrid cultures, which is of interest within the context of yield optimization. This application will be done in collaboration with several researchers of the GQE - Le Moulon unit (Diala Abu Awad, who co-authored Mardomingo Sanz et al. [2026] and Stéphane Nicolas and his team who evaluated the genetic contribution of ancestral landraces to modern hybrids (Galaretto et al. [2026], Arca et al. [2023])).

References

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