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PhD project

Title : Probabilistic models in quantitative genetics

Quantitative genetics is a field of evolutionary biology studying the evolution through time of the distribution of a quantitative phenotype or trait as a result of the major evolutionary forces (drift, mutation, selection, recombination). It assumes that the value of a phenotypic trait has an environmental component and a heritable component driven mostly by additive effects of many loci, effectively neglecting interactions between many genes and assuming no one gene has too great of an influence on phenotype.

Quantitative genetics have been applied to model experimental evolution, adaptation in fluctuating environments, phenotypic evolution from fossils, or the mutation-selection equilibrium. More recently, quantitative genetics have spurred new interest in the context of Genome-Wide Association Studies studies obtained from massive sequencing data.

Though the field was founded, as is generally considered, by Fisher and Wright around 1918, its mathematical foundations are still not fully understood. For instance, it was only in 2017 that the infinitesimal model was derived as a scaling limit of a discrete

model as the number of loci tends to infinity. In this PhD project, we aim at consolidating these foundations by starting from first principles in discrete probabilistic models in order to derive rigorous theoretical predictions. Specifically, we aim at going from macroscopic descriptions (a stochastic population evolving under selection) to the microscopic underlying structures.

From a mathematical standpoint, this project will make use of advanced probabilistic technics : stochastic processes, diffusions, branching processes, martingales and interacting particle systems. At the end of his/her PhD, the candidate will acquire an expertise in both theoretical biology (population genetics, quantitative genetics) and Probability Theory. The perquisite is a solid background in Probability (including measure theory and some knowledge in stochastic processes – e.g., Brownian motion, stochastic differential equations). Some knowledge in population genetics is not mandatory and but will be a plus.