Topic: Probability theory with applications to population genetics.

Advisor: Emmanuel Schertzer.

Description: Coalescent theory has become one of the central mathematical frameworks in modern population genetics. Since Kingman's foundational work in the 1980s, coalescent processes have provided a powerful probabilistic description of genealogies in large populations, with deep connections to stochastic processes, statistical inference, and evolutionary biology. They form the backbone of many models used today to interpret genomic data.

While classical coalescents are now well understood, nested coalescents—gene genealogies evolving within higher-level structures remain mathematically unexplored. These models arise naturally in many contexts: genes evolving within diverging species, viral gene trees embedded in transmission trees during epidemics, and more generally, genealogies interacting across multiple biological scales.

The goal of this PhD thesis is to develop the mathematical foundations of nested coalescent processes. This includes: analysing their structure through connections with branching processes, especially continuous-state branching processes (CSBP); exploring links with Le Gall's stochastic snakes and related genealogical constructions; characterising the resulting mutational patterns, such as the site frequency spectrum (SFS), generated by nested genealogies.

Applications: Understanding how nested coalescents shape genetic data will help improve methods for inferring species trees and transmission histories from genomic information. The project combines probability theory, stochastic processes, and population genetics, offering opportunities for both theoretical developments and applications.

Candidate Profile: The successful candidate should have a strong background in probability theory and stochastic processes, together with a strong motivation to apply these mathematical tools to biological questions.