

Systèmes de branchement, équations de réaction-diffusion
et modèles de population
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Branching systems, reaction-diffusion equations and population models
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Interplay between scales for eco-evolutionary mathematical models

Understanding how mutant cells emerge or how our cells become resistant to antibiotics are major challenges in biology. Our aim is to develop mathematical models that can keep track of small subpopulations in approximations of large populations.

After presenting some eco-evolution problems, we will introduce the basic individual-based stochastic model for the dynamics of a trait-structured population, with density-dependent competition. Traits are vertically inherited unless a mutation occurs. We will make the link with a nonlinear integro-differential equation by its approximation in large population. We will show how this process is coupled with the historical process describing the lineages of individuals. We will deduce a method to obtain the ancestral trajectory of an individual randomly sampled in a large population, in direct time and in reverse time.

We will next consider the case where traits can also be horizontally transferred by unilateral conjugation with frequency-dependent rate. Our goal is to analyse the trade-off between natural evolution to higher birth rates on one side, and transfer which drives the population towards lower birth rates on the other side. We will focus on a trait taking finitely many values and a parameter scaling where individual mutations are rare and not small, but the global mutation rate tends to infinity. This implies that negligible subpopulations may have a strong contribution to evolution. We will quantify the asymptotic dynamics of subpopulation sizes on a logarithmic scale.

In the last lecture, we will focus on a parameter scaling where individual mutations are small but not rare, and where the grid mesh for the trait values becomes smaller and smaller. When considering the evolution of the population in long time scales, the contribution of small subpopulations is important. Here again, we will quantify the asymptotic dynamics of subpopulation sizes on a logarithmic scale. We will establish that under our rescaling, the stochastic discrete process converges to the viscosity solution of a Hamilton-Jacobi equation.