Workshop of the ERC project MUSEUM : MUlti- Scale Eco-Evolutionary population dynaMics

Rapport sur les contributions

https://indico.math.cnrs.fr/e/14899

ID de Contribution: **1** Type: **Non spécifié**

Genetic and demographic constraints on adaptation: insights from Integro-projection models and research challenges

mercredi 7 janvier 2026 14:00 (45 minutes)

The concept of evolutionary potential is central to many questions in evolutionary biology and key in particular to our understanding of adaptation prospects to ongoing global changes. I will illustrate how understanding limits to adaptation necessitates to integrate together genetic and demographic constraints. I will deal with structured heterogeneous populations, where different individuals make different contributions to the demography and evolution of the population, because they belong to different stages in the life cycle, have a different age and size, affecting their growth, fecundity and survival. We use 30 years of demographic surveys in the endangered highly endemic plant Centaurea corymbosa to predict under which conditions boosting the genetic diversity through assisted gene flow could rescue the small declining populations from short-term extinction in an already too warm climate. Through this example, I will introduce Integro-Projection Models, which have become extremely popular in population dynamics studies in recent years, but are the subject of controversies about how evolution is integrated. These Integro-Projection models, which emerged from empirical research, have been explored exclusively numerically and are potentially an area of research where greater mathematical insight could lead to some breakthrough in their validation and use.

Orateur: RONCE, Ophélie (Institut des sciences de l'évolution-Montpellier)

ID de Contribution: **2**

Type: **Non spécifié**

Exposé

mercredi 7 janvier 2026 14:45 (45 minutes)

Orateur: GUERAND, Jessica (Institut Montpelliérain Alexander Grothendieck)

ID de Contribution: **3** Type: **Non spécifié**

Pause café

ID de Contribution: **4** Type: **Non spécifié**

Niche construction as an emerging phenomenon between fast ecological and slow evolutionary timescales in individual-based models

mercredi 7 janvier 2026 16:00 (45 minutes)

The concept of evolutionary potential is central to many questions in evolutionary biology and key in particular to our understanding of adaptation prospects to ongoing global changes. I will illustrate how understanding limits to adaptation necessitates to integrate together genetic and demographic constraints. I will deal with structured heterogeneous populations, where different individuals make different contributions to the demography and evolution of the population, because they belong to different stages in the life cycle, have a different age and size, affecting their growth, fecundity and survival. We use 30 years of demographic surveys in the endangered highly endemic plant Centaurea corymbosa to predict under which conditions boosting the genetic diversity through assisted gene flow could rescue the small declining populations from short-term extinction in an already too warm climate. Through this example, I will introduce Integro-Projection Models, which have become extremely popular in population dynamics studies in recent years, but are the subject of controversies about how evolution is integrated. These Integro-Projection models, which emerged from empirical research, have been explored exclusively numerically and are potentially an area of research where greater mathematical insight could lead to some breakthrough in their validation and use.

Orateur: CHAMPAGNAT, Nicolas (Inria Nancy)

ID de Contribution: **5** Type: **Non spécifié**

Old and new results on time-inhomogeneous branching Brownian motion

mercredi 7 janvier 2026 16:45 (45 minutes)

Time-inhomogeneous Branching Brownian motion (BBM and its discrete counterpart, time-inhomogeneous branching random walks (BRW) may be considered as models for populations undergoing reproduction and dispersion, in an environment that changes slowly over a large time scale T. They have also been studied intensely by physicists and mathematicians as toy models for so-called spin glasses. In this talk, I will first recall classic results (limiting free energy, asymptotics of maximum) which exhibit an interesting explicit dependence on the environment. I will then present recent results. In particular, I will present a study with Alexandre Legrand on a variant of the model with a finite number N of particles, for which we are able to obtain the second-order correction term for its propagation speed. In particular, this correction term exhibits an interesting phase transition when N = exp(T^{1/3}). Based on http://arxiv.org/abs/2402.04917 .

Orateur: MAILLARD, Pascal (Institut de mathématiques de Toulouse)

ID de Contribution: **6** Type: **Non spécifié**

Pathogen evolution in finite populations

jeudi 8 janvier 2026 09:15 (45 minutes)

The theory of life-history evolution provides a powerful framework to understand the evolutionary dynamics of pathogens. It assumes, however, that host populations are large and that one can neglect the effects of demographic stochasticity. Here, we expand the theory to account for the effects of finite population size on the evolution of pathogen virulence. We show that demographic stochasticity introduces additional evolutionary forces that can qualitatively affect the dynamics and the evolutionary outcome. We will discuss the importance of the shape of the pathogen fitness landscape on the balance between mutation, selection and genetic drift. This analysis reconciles Adaptive Dynamics with population genetics in finite populations. We will also discuss how to expand this theoretical framework to study the effect of demographic stochasticity on multilocus evolution of pathogens.

Orateur: GANDON, Sylvain (Centre d'écologie fonctionnelle et évolutive-Montpellier)

ID de Contribution: **7** Type: **Non spécifié**

Exposé

jeudi 8 janvier 2026 10:30 (45 minutes)

Orateur: TRAN, Viet Chi (Inria Lille)

ID de Contribution: **8**

Type: **Non spécifié**

Pause café

ID de Contribution: **9** Type: **Non spécifié**

Concentration in selection-mutation models: error estimates and asymptotic expansions

jeudi 8 janvier 2026 11:15 (45 minutes)

n this presentation we study an integro-differential equation which describes the evolutionary dynamics of a population structured by a phenotypic trait. This population undergoes asexual reproduction, competition, selection, and mutation. We provide an asymptotic analysis of the model, assuming that the mutations have small effects. A standard approach for the analysis of the qualitative properties of the solutions of such an equation is to apply a logarithmic transformation, which yields a Hamilton–Jacobi equation with constraint. When the reproduction term is a concave function of the trait, it has been established that the solution is classical. We rigorously derive a first-order asymptotic expansion of the solution. This expansion allows us to approximate the moments of the phenotypic density. This result establishes a connection between the approximations of the phenotypic density obtained via the Hamilton-Jacobi approach and relevant biological quantities, which are more suitable from a modeling perspective. This is a joint work with my PhD advisors, Sepideh Mirrahimi and Jean-Michel Roquejoffre.

Orateur: GUINET, Caroline (Institut de mathématiques de Toulouse)

ID de Contribution: **10** Type: **Non spécifié**

Exposé

ID de Contribution: **11** Type: **Non spécifié**

Evolution of the (co)variances of quantitative traits in stage-structured populations.

jeudi 8 janvier 2026 14:45 (45 minutes)

The speed of evolution of a phenotypic trait increases with the proportion of its variation that is transmitted to the next generation. The genetic variance for the trait is thus considered a good measure of evolutionary potential. The former can be computed from the joint distribution of the different gene copies that determine the trait value in the population. Evolutionary forces such as genetic drift, selection, recombination, mutation, and migration shape these distributions and thus the evolution of genetic variance. Many theoretical models for the evolution of quantitative traits, however, assume that genetic variance is constant through time and identical among different sub-groups of individuals in the population. Yet many populations are structured, with groups of individuals differing in sex, age, size, or developmental stage, which may differ in the amount of genetic variance they harbour for different traits. For instance, previous theory has shown that genetic variance for a trait subject to multiple selection episodes through the course of life decreases with age. Conversely, genetic variance for a trait expressed for the first time late in life is predicted to be higher than that for a trait first expressed when individuals are still young. However, we lack theoretical expectations for other types of structured populations, where individuals vary in the time they spend in different stages.

Here, we develop a set of general recursions to predict the change across time and stages of both the mean and the variance of a Gaussian-distributed trait affecting transitions between discrete stages in a structured population. We track the variation in the phenotypic trait value, the component of the trait that is transmitted to the next generation (the breeding value), and their covariation. We illustrate our predictions by parameterizing the model using demographic data on stage transitions for various plant species and exploring different scenarios of selection on the phenotypic trait. In particular, we show how genetic variance accumulates in some stages and is depleted in others, and how this affects the probability of escaping extinction while adapting to a new environment.

Orateur: OFFRESSON, Julien (Institut des sciences de l'évolution-Montpellier)

ID de Contribution: **12**

Type: **Non spécifié**

Pause café

ID de Contribution: **13** Type: **Non spécifié**

Analysis of the infinitesimal model by an hilbertian approach

jeudi 8 janvier 2026 16:00 (45 minutes)

In this talk I am considering a model for the dynamics of a population—distributed according to a phenotypic trait—that reproduces sexually and is subject to selection and competition. Sexual reproduction is modeled via a nonlinear integral term, known as Fisher's "infinitesimal model", which prescribes that the phenotypic trait of the offspring follows a Gaussian distribution around the mean of the parents' traits. Under the assumption that the reproduction variance is small compared to the selection variance, I am focusing on an explicit description of the dynamics obtained by writing the solution on a well-chosen polynomial basis. This description allows us to study the existence of stationary distributions and their stability.

The talk is based on a collaboration with Sepideh Mirrahimi.

Orateur: HILLAIRET, Matthieu (Institut Montpelliérain Alexander Grothendieck)

ID de Contribution: **14** Type: **Non spécifié**

On the approximation of the use of Hermite functions for quantum and statistical physics

jeudi 8 janvier 2026 16:45 (45 minutes)

We propose a new approach to discretize the von Neumann equation, which is efficient in the semi-classical limit. This method is first based on the so called Weyl's variables to address the stiffness associated with the equation. Then, by applying a truncated Hermite expansion of the density operator, we successfully handle this stiffness. Additionally, we develop a finite volume approximation for practical implementation and conduct numerical simulations to illustrate the efficiency of our approach. This asymptotic preserving numerical approximation, combined with the use of Hermite polynomials, provides an efficient tool for solving the von Neumann equation in all regimes, near classical or not.

Orateur: FILBET, Francis (Institut de mathématiques de Toulouse)

ID de Contribution: **15**

Type: **Non spécifié**

Buffet

ID de Contribution: **16** Type: **Non spécifié**

Evolutionary ecology of structured populations

vendredi 9 janvier 2026 09:15 (45 minutes)

In natural populations, individuals may have different vital rates depending on their age, size, location, infection status, or immunity. This demographic heterogeneity has important ecological and evolutionary consequences. In evolutionary epidemiology, two important sources of heterogeneity are imperfect vaccination and infection age structure. As a result of this heterogeneity, hosts do not have the same quality for the pathogen depending on their immune or age class. In this talk I will discuss theoretical results that show how this variation in host quality can affect the evolution of pathogen life history traits (e.g. transmission, virulence…).

Orateur: LION, Sébastien (Centre d'écologie fonctionnelle et évolutive-Montpellier)

ID de Contribution: **17**

Type: **Non spécifié**

Pause café

ID de Contribution: **18** Type: **Non spécifié**

Recovering an initial distribution of telomere lengths from measurements of senescence times

vendredi 9 janvier 2026 10:30 (45 minutes)

Telomeres are repetitive sequences situated at both ends of the chromosomes of eukaryotic cells. At each cell division, they are eroded until they reach a critical length that triggers a state in which the cell stops to divide: the senescent state. In this work, we are interested in the link between the initial distribution of telomere lengths and the distribution of senescence times. We propose a method to retrieve the initial distribution of telomere lengths, using only measurements of senescence times. Our approach relies on approximating our models with transport equations, which provide natural estimators for the initial telomere lengths distribution. We investigate this method from a theoretical point of view by providing bounds on the errors of our estimators, pointwise and in all Lebesgue spaces. We also
illustrate it with estimations on simulations, and discuss its limitations related to the curse of dimensionality.

Orateur: OLAYÉ, Jules (Institut de mathématiques de Toulouse)

ID de Contribution: **19** Type: **Non spécifié**

Sustainable spatial management strategies of agricultural areas

vendredi 9 janvier 2026 11:15 (45 minutes)

In this talk I will present a joint and ongoing work with Madeleine Kubasch and Nicolas Loeuille. We are interested in the question of how does spatial heterogeneity of an agricultural landscape impact conservation and yield goal. We developed a model for the ecological dynamics of a metacommunity in an agricultural landscape and study both theoretically and numerically which strategies allow reconciling conservation and yield goals.

Orateur: COSTA, Manon (Institut de mathématiques de Toulouse)