Mathematical Models in Ecology and Evolution

21–25 March 2022, Institut Henri Poincaré, Paris

BOOK OF ABSTRACTS

Diala Abu-Awad (U. Paris-Saclay) : Selective sweeps in populations with seedbanks.

We explore how overlapping generations due to seed-dormancy affect the times to and probabilities of fixation of beneficial alleles. We also follow the expected genomic signatures associated with selective sweeps, evaluating our ability to detect them.

Ada Altieri (U. Paris Cité) : Evidence of glassy phases in large randomly interacting ecosystems.

Many complex systems in Nature, from metabolic networks to ecosystems, appear to be poised at the edge of stability, hence displaying enormous responses to external perturbations. This feature, also known in physics as marginal stability, is often the consequence of the complex underlying interaction network, which can induce large-scale collective dynamics, and therefore critical behaviors.

In this talk, I will focus on a benchmark in theoretical ecology, the disordered Lotka-Volterra model, with random interactions and finite demographic noise. Through advanced disordered system techniques, I will unveil a very rich structure in the organization of the equilibria and relate critical features and slow relaxation dynamics to the appearance of disordered glassy-like phases. Finally, I will discuss the generalization of these results to strongly competitive interactions as well as to non-logistic growth functions in the dynamics of the species abundances, which turn out to be of great interest for modeling intra-specific mutualistic effects.

Jean-François Arnoldi (CNRS) : Invasions (and extinctions) in ecological communities : the role of invasion fitness and feedbacks.

Theory in ecology and evolution often relies on the analysis of invasion processes, and general approaches exist to understand the early stages of an invasion. However, predicting the long-term transformations of communities following an invasion remains challenging. I will describe some theoretical work that uses the density dependence of an invading population's growth rate to predict if the invasion will cause large long-term impacts on the invaded community, such as irreversible compositional shifts. We will see that the density dependence of the invasion growth rate is as much a property of the invading population as it is one of the invaded community, which will allow us to clarify the conditions for abrupt community shifts along smooth environmental gradients, triggered by invasions or extinctions. All in all, this theoretical work directs us towards new questions that may enrich the toolset of invasion analysis (for both ecology and evolution), and suggests that indirect interactions and dynamical stability are key determinants of invasion outcomes.

Vincent Bansaye (Ecole Polytechnique) : Epidemics on large random metapopulations and homogenization.

Joint work with Michele Salvi.

We are interested in population dynamics and epidemics for large random metapopulations. The sites of the metapopulation are described by a Poisson point process on the plane and transition rates between the sites depend on their distances. In such a non-homogeneous context, when the number of sites in a given box becomes large, homogenization occurs, leading to a non trivial diffusion of coefficient and spread of epidemics.

Our motivations come from the spread of epidemics on networks (farms, cities, patches. . .). We will introduce an individual-based model including births, deaths and contaminations. We will first justify the existence of such a stochastic process starting from a (spatially) unbounded population distribution, which requires to control what can come from large distances. We will then prove the convergence of the renormalized stochastic process to a reaction diffusion models, with homogenized diffusion coefficients. We may discuss further new and multi-scaling or extensions to more complex large random graphs.

Florence Bansept (Max Planck Institute for Evolutionary Biology) : Selection gradient on life history traits in host-associating microbes.

Joint work with Nancy Obeng, Michael Sieber, Hinrich Schulenburg and Arne Traulsen.

Microbial communities extend the host functional repertoire, thus making the host and its associated microbes a functional unit. We are only beginning to decipher how host and microbe fitnesses are intertwined : while it is now clear that the microbiota has a vast potential to affect the host physiology, less focus has been put to the microbial perspective, *i.e.* to understand what benefit or cost can microbes retrieve from their interaction with their host. In contrast to the common hypotheses of strong and continued coevolution proposed to explain the emergence of such elaborate symbioses, we focus here on the steps that can lead a microbial population to transition from a free-living life-style to an association with a host. In particular, we aim at understanding what selection pressures apply to microbes following a biphasic life cycle, in which they can regularly transit in and outside a host.

We study three simple models of such biphasic life cycles. In the first model, we study a homogeneous microbial population transiting between a host and its environment and perform a sensitivity analysis to show the existence of two different regimes : one where the effect of migration from the environment to the host dominates, and a second where the within-host replication rate matters most. The second model is an SI-inspired compartmental model, which accounts for the habitats' dynamics. We show that microbial propagation across habitats depends on the product of the transmissibilities, which we propose as a new holistic measure of microbial fitness - bearing similitudes with the R0 of epidemiology. In the third model, we combine microbial population and habitats dynamics and derive predictions that are consistent with experimental observations of an increased ability to form biofilms in bacteria evolved in biphasic conditions with *C. elegans*.

Nick Barton (Institute of Science and Technology Vienna) : Adaptation in a metapopulation : a stochastic eco-evolutionary model.

Joint work with Himani Sachdeva, Eniko Szep and Oluwafunmilola Olusanya.

The joint distribution of allele frequencies and deme size across a metapopulation can be analysed using the diffusion approximation. Szep et al. (Evolution, 2021) derive an explicit formula for the stationary distribution, and find when a heterogeneous environment can maintain genetic variation. If loci are typically close to fixation, we can make a further approximation, which allows us to follow change through time.

Julien Beresticky (U. Oxford) : The extremal point process of branching Brownian motion in $\mathbb{R}^d$.

Joint work with Yujin H. Kim, Eyal Lubetzky, Bastien Mallein and Ofer Zeitouni.

Consider a branching Brownian motion in $\mathbb{R}^d$ with $d \geq 1$. Where are the particles that have traveled the furthest away from the origin (at a large time t) ? If one conditions by what happened early on in the process, in which direction are we likely to fond the furthest particle ? Can one describe the structure of the extremal point process at large times ? Those questions were already well understood for the case $d = 1$. In this talk I will present some recent results concerning the multidimensional case.

Oana Carja (Carnegie Mellon U.) : TBA

Camille Coron (U. Paris-Saclay) : Ancestors' genetic weights in biparental populations.

Joint work with Yves Le Jan.

Our goal is to study the genetic composition of a population in which each individual has 2 parents, who contribute equally to the genome of their offspring. We use a bi-parental Moran model, which is characterized by its fixed number N of individuals. We fix an individual and consider the proportions of the genomes of all individuals living n time steps later, that come from this individual. When n goes to infinity, these proportions all converge almost surely towards the same random variable. When N then goes to infinity, this random variable multiplied by N (*i.e.* the stationary weight of any ancestor in the whole population) converges in law towards the mixture of a Dirac measure in 0 and an exponential law with parameter 1/2, and the weights of a finite number of ancestors are independent. As a consequence, we obtain that the sequence of increasing weights of all ancestors, when properly rescaled, converges to the function $-2\ln(2(1-u))$ for $u > 1/2$.

Olivier Cotto (INRAE) : The evolution of age-specific choosiness and reproductive isolation in a model with overlapping generations.

The strength of mate choice (choosiness) often varies with age, but theory to understand this variation is scarce. I will approach the evolution of age-specific choosiness from two axes. First, I investigate whether speciation can result in variation of choosiness with age, and whether such variation can in turn affect speciation. I then study how the strength of selection on choosiness changes with age. To approach these questions, I model the genetics of populations with overlapping generations, where females prefer to mate with males matching their phenotype. I will show that speciation can result in the evolution of choosiness changing with age without affecting reproductive isolation between species. I will further present how the strength of selection, affecting both the pace of evolution toward optimal age-specific choosiness and the ability of selection to purge sub-optimal mutations, strongly depends on the life cycle of the organisms under study.

Léonard Dekens (ENS of Lyon) : The best of both worlds : combining population genetics and quantitative genetics models.

Joint work with Sally Otto and Vincent Calvez.

Traits under migration-selection balance are shown to exhibit complex patterns of genetic architecture, with allelic differences of varying magnitude. However, studying the influence of a large number of small allelic effects on the maintenance of spatial polymorphism in a model that also accounts for demographical changes is mathematically challenging, due to the high complexity of the systems that arise.

Here we propose a new methodology that allows us to take into account the combined contributions of a major locus and of a quantitative background resulting from small effect loci, inherited according to the infinitesimal model. In a regime of small variance contributed by the quantitative loci, we found new arguments of convex analysis to justify that traits are concentrated around the major alleles effects according to a normal distribution, which leads to a slow-fast analysis approach. By applying it to a symmetrical two-patch model, we predict an undocumented phenomenon of loss of polymorphism at the major locus despite strong selection for local adaptation under some conditions, where the infinitesimal quantitative background slowly disrupts the fast established symmetrical polymorphism at the major locus, which is confirmed by individual-based simulations. We also provide a comprehensive toolbox designed to describe how to apply our method to more complex population genetic models.

Mete Demircigil (ENS of Lyon) : Aerotactic Waves in Dictyostelium discoideum : When Self-Generated Gradients interact with Expansion by Cell Division.

Joint work with Christophe Anjard, Vincent Calvez, Jean-Paul Rieu et Olivier Cochet-Escartin.

Using a self-generated hypoxic assay, it is shown that *Dictyostelium discoideum* displays a remarkable collective aerotactic behavior : when a cell colony is covered, cells quickly consume the available oxygen and form a dense ring moving outwards at constant speed and density.

We propose a simple, yet original PDE model, that enables an analytical qualitative and quantitative study of the phenomenon and reveals that the collective migration gives rise to traveling wave solutions, whose propagation can be explained through the interplay between cell division and the modulation of aerotaxis. The modeling and its conclusions supplement and are confirmed by an experimental investigation of the cell population behavior. This approach also gives rise to an explicit and novel formula of the collective migration speed of cells that encapsulates a surprising combination of expansion by cell division, such as described by the Fisher/KPP equation, and aerotaxis. The conclusions of this model appear to extend to more complex models.

Alison Etheridge (U. Oxford) : The motion of hybrid zones (and how to stop them).

Joint work with Mitch Gooding and Ian Letter.

We consider hybrid zones maintained by selection against heterozygosity at a single bi-allelic locus. In previous work, Etheridge, Freeman and Penington (2017) considered the case in which both homozygotes are equally fit, and the population is distributed across Euclidean space. Here, building on the thesis of the second author, we are interested in the case in which one homozygote is fitter than the other. We are particularly concerned with the interplay between the motion of the hybrid zone and the shape of the habitat, asking, for example, what happens if the population passes through an isthmus, and how this will be affected by the strength of the genetic drift.

Alison Feder (U. Washington) : Modeling the evolution of multi-drug resistance in HIV.

HIV-1 is treated with combination therapies of multiple simultaneous drugs targeting different stages of the viral lifecycle, such that no single mutation confers resistance to all drugs used in a treatment. Complete drug resistance should require the co-occurrence of multiple resistance mutations in a single reverse transcription step - an extremely rare event probabilistically. Nevertheless, HIV does evolve resistance even on combination therapy, suggesting an incomplete understanding of the dynamics at play. In this presentation, I'll describe several key features identified in clinical trial and genetic data that a model of drug resistance evolution must match - namely resistance mutations emerging one at a time in a partially predictable order, even years after therapy onset. I will then describe our efforts to model this process of multi-drug resistance emergence, using temporally- or spatially-varying drug levels within individuals. We find that a model of spatial heterogeneity more straightforwardly matches the patterns found in clinical data, and I close by discussing how we can use these findings to design more evolution-proof combination therapies.

Raphael Forien (INRAE) : How far did your ancestors live ? The decrease of genetic correlation with geographic distance under various forms of long range dispersal.

Joint work with Bastian Wiederhold.

The spatial structure of genetic diversity is mainly shaped by the way individuals disperse their offspring in space. The basic prediction of spatial models in population genetics is that genetic correlation decreases with the geographic distance between two points. When the dispersal of individuals is essentially local (short range dispersal), the shape of these correlations is described by the Wright-Malécot formula, which allows one to infer past dispersal and population density from observed patterns of genetic correlations. This talk will present an extension of the spatial Lambda-Fleming-Viot process introduced by Barton, Etheridge and Véber which allows us to study spatial patterns of genetic diversity under a wide range of long-range dispersal scenarios including grouped dispersal and large scale extinction-recolonisation events at various scales. We shall see that, using a space-time rescaling of this process, one can recover a general description of the genetic correlations under these different scenarios, and that the speed of decrease of these correlations with geographic distance is very sensitive to the choice of the dispersal model.

Coralie Fritsch (INRIA) : Quasi-stationary behavior for the Crump-Young model of chemostat.

Joint work with Bertrand Cloez.

The Crump-Young model consists of two fully coupled stochastic processes modeling the substrate and micro-organisms dynamics in a chemostat. The substrate evolves following an ordinary differential equation, depending on the micro-organisms number. Micro-organims are modeled though a pure jump process whose the jump rates depend on the substrate concentration. It is known that this model extincts almost surely in the sense that micro-organism population vanishes. However, despite its simplicity, the long-time behavior of this process is not well understood. The existence (but not the uniqueness) of quasi-stationary distribution (QSD) as well as some regularity properties of these QSD were proved in the literature. Nevertheless, the long-time behavior of the process before extinction was, until now, unknown.

In this work, we prove that there exists a unique QSD and that, conditionally on the non-extinction, the Crump-Young model converges exponentially fast to this QSD. Convergence of quasi-stationary distribution is usually proved though Hilbert techniques. However, our process is not reversible making these techniques difficult to deal with. To overcome this problem, we use the recent results of Champagnat-Villemonais and Bansaye-Cloez-Gabriel-Marguet, which are a generalization of usual techniques to prove convergence to stationary distribution. The proof is mainly based on hitting time estimates and Lyapunov functions bounds. Due to the deterministic part, the dynamics of the Crump-Young model is highly degenerated. The proof then consists of technical sharp estimates.

Diana Fusco (U. Cambridge) : The inevitable emergence of density-dependent diffusion in expanding phage populations.

Reaction-diffusion waves have long been used to describe the growth and spread of populations undergoing a spatial range expansion. Such waves are generally classed as either pulled, where the dynamics are driven by the very tip of the front and stochastic fluctuations are high, or pushed, where cooperation in growth or dispersal results in a bulk-driven wave in which fluctuations are suppressed. These concepts have been well studied experimentally in populations where the cooperation leads to a density-dependent growth rate. By contrast, relatively little is known about experimental populations that exhibit a density-dependent dispersal rate.

Using bacteriophage T7 as a test organism, we present novel experimental measurements that demonstrate that the diffusion of phage T7, in a lawn of host *E. coli*, is hindered by steric interactions with host bacteria cells. The coupling between host density, phage dispersal and cell lysis caused by viral infection results in an effective density-dependent diffusion rate akin to cooperative behavior. Using a system of reaction-diffusion equations, we show that this effect can result in a transition from a pulled to pushed expansion. Moreover, we find that a second, independent density-dependent effect on phage dispersal spontaneously emerges as a result of the viral incubation period, during which phage is trapped inside the host unable to disperse. Our results indicate both that bacteriophage can be used as a controllable laboratory population to investigate the impact of density-dependent dispersal on evolution, and that the genetic diversity and adaptability of expanding viral populations could be much greater than is currently assumed.

Léo Girardin (CNRS) : Demographic feedbacks can hamper the spatial spread of a gene drive.

Joint work with Florence Débarre, Lena Klay and Vincent Calvez.

The topic of this two-part talk will be reaction–diffusion models for the fixation and invasion of a gene drive (an allele biasing inheritance, increasing its own transmission to offspring) in a spatially structured population. The originality of the models that will be presented is that the gene drive is susceptible of decreasing the total carrying capacity of the population locally in space. This tends to generate an opposing demographic advection that the gene drive has to overcome in order to invade. Due to these opposing forces, the prediction of the sign of the traveling wave speed is difficult.

The first part will report on a joint work with F. Debarre on the simplest case where heterozygous individuals are nonexistent or negligible. Despite the simplifying assumptions, we only achieved partial analytical results. These will be presented, commented and completed by numerical simulations.

In the second part I will present recent new findings due to Lena Klay, in collaboration with V. Calvez, F. Debarre and myself, on asymptotic regimes and on more complex cases where the heterozygous population is non-negligible.

Quentin Griette (U. Bordeaux) : Sharp discontinuous traveling waves in a hyperbolic cell-cell repulsion equation.

This talk concerns a hyperbolic model of cell-cell repulsion with a dynamics in the population of cells. More precisely, we consider a population of cells producing a field (the “pressure”) which induces a motion of the cells following the opposite of the gradient. The field indicates the local density of population and we assume that cells try to avoid crowded areas and prefer locally empty spaces which are far away from the carrying capacity. We analyze the well-posedness property of the associated Cauchy problem on the real line. We start from bounded initial conditions and we consider some invariant properties of the initial conditions such as the continuity, smoothness and monotonicity. We also describe in detail the behavior of the level sets near the propagating boundary of the solution and we find that an asymptotic jump is formed on the solution for a natural class of initial conditions. Finally, we prove the existence of sharp traveling waves for this model, which are particular solutions traveling at a constant speed, and argue that sharp traveling waves are necessarily discontinuous. This analysis is confirmed by numerical simulations of the PDE problem.

Chris Henderson (U. Arizona) : Pushmi-pullyu fronts and population dynamics.

Invasions in population dynamics are often characterized as either ‘pushed’ or ‘pulled.’ Biologically this is related to the Allee affect, while mathematically, this distinction is whether the front is driven by nonlinear dynamics at the front (pushed) versus linear dynamics beyond the front (pulled). In this talk, I will present a family of models in which an intermediate ‘pushmi-pullyu’ behavior occurs. The analysis of these models is delicate as both the nonlinear dynamics at the front and linear dynamics beyond the front play nontrivial roles. The goal of the talk is to connect disparate models (taxis, combustion, probabilistic) in this context as well as to display a few of the mathematical tools used in their study such as a new weighted Nash inequality.

Benoît Henry (IMT Lille Douai) : Time-reversal of the spine of branching processes near stationarity.

Joint work with Vincent Calvez, Sylvie Méléard and Viet Chi Tran.

It is usual to approximate PDE in biology using branching processes as microscopic models. The behavior of such processes, when linear, can then be investigated using tools such as many-to-one formulas and the associated spine processes. This process is typically a time-inhomogeneous Markov process. In this talk, we will discuss some homogenization phenomenon arising when approximating a PDE at stationarity for the time-reversed spine process.

Adrian Lam (Ohio State U.) : On the problem of Dockery et al. and the evolution of dispersal.

Joint work with Stephen Cantrell, Yuan Lou and Benoît Perthame.

To investigate the evolution of dispersal in spatially heterogeneous environments, Dockery et al. in 1998 formulated a diffusion-competition system of N species which are identical except for their diffusion rates, and conjectured that the slowest diffusing species always competitively exclude all its counterparts. A continuum version of the problem was formulated by Perthame and Souganidis in 2016. In this selection-mutation model, the population is structured by both space and the diffusion rate, and where mutation acts on the latter phenotypic variable. The rare mutation limit of the time-dependent solution is believed to be well described by certain Hamilton-Jacobi equation with a constraint, but rigorous results are limited to the case without spatial structure. In this talk, we will describe some recent progress on both problems by introducing the concept of principal Floquet bundle for parabolic equations.

Sébastien Lion (CNRS) : Multi-morph eco-evolutionary dynamics : time scales and population structure

Our understanding of the evolution of quantitative traits in nature is still limited by the challenge of including realistic trait distributions in the context of frequency-dependent selection and ecological feedbacks. In this talk, I will discuss a recently introduced "oligomorphic approximation" which bridges the gap between adaptive dynamics and quantitative genetics approaches and allows for the joint description of the dynamics of ecological variables and of the moments of multimodal trait distributions. My talk will focus on two main points : (1) time scales, that is how this approach can be used to predict both the long-term evolutionary endpoints and the short-term transient dynamics of the eco-evolutionary process, and (2) population structure, that is how the concept of reproductive value can be used to obtain a lower-dimensional approximation of the dynamics of class-structured populations.

Apolline Louvet (Ecole Polytechnique et U. Paris Cité) : A family of stochastic measure-valued population genetics processes for expanding populations.

Joint work with Amandine Véber.

Population expansions in dimension 2 or higher are characterized by the emergence of sectors at the front edge, in which all individuals have the same genetic type. This phenomenon is a consequence of stochasticity in reproduction at the front, where population densities are lower and genetic drift more pronounced. Yet little is known of the properties of these sectors, partly due to a lack of population genetics processes adapted to an expansion setting.

In this talk, I will present a family of stochastic population genetics processes allowing to study expanding populations, based on the spatial Lambda-Fleming Viot process. Their key feature is the use of "ghost individuals" to model empty areas, adapting a concept from interacting particle systems theory and first introduced in population genetics in Hallatschek & Nelson (2008) and Durrett & Fan (2016). These ghost individuals can reproduce as well, modeling local extinctions due to stochasticity in reproduction, but with a strong selective disadvantage against "real individuals".

Then, I will focus on the limiting process obtained by letting the selective advantage of real individuals become infinitely strong, that is, assuming local extinctions are no longer possible. This limiting process is reminiscent of the Eden growth model, but continuous in space, and associated to tools allowing to study genetic diversity. I will explain to what extent its growth properties are similar to the ones of the Eden model.

Frithjof Lutscher (U. Ottawa) : Movement at and of patch boundaries.

As organisms move across a landscape, they encounter habitats of different quality (patches). At patch boundaries, they have various movement options, such as stay in the current patch or leave it. In the first part of my talk, I will present a population-level model for this boundary behaviour in the form of a reaction-diffusion equation, derived from a stochastic movement model at the individual level. With this model, I will study the evolution of dispersal and habitat preference and formulate an "optimal" movement strategy. Some organisms, known as ecosystem engineers, are able to modify their physical environment in their favour. Their engineering activity can move the boundary of a patch and expand their suitable habitat in space. In the second part of my talk, I will expand the model from the first part and include an additional equation to represent the movement of the boundary. I will analyze traveling wave solutions of the resulting free boundary problem and give results in terms of the speed of range expansion of the species.

Ailene MacPherson (Simon Fraser U.) : The Eco-Evolutionary Maintenance of Genetic Variation.

A longstanding aim of evolutionary biology is to identify and characterize the processes that maintain genetic diversity counteracting its loss from directional selection and genetic drift. In 1949 JBS Haldane suggested that antagonistic coevolution should maintain variation due to its negative-frequency-dependent-like reciprocal natural selection. Here I will present some recent and ongoing work on testing the robustness of this component of the Red Queen Hypothesis. Specifically, I will examine if and how interactions between three ecological processes (species interactions, habitat structure, and population dynamics) impact the evolution of genetic diversity. In doing so I will highlight important overarching principles and practices of eco-evolutionary modelling.

Ignacio Madrid Canales (Ecole Polytechnique) : Probabilistic inference of the steady-state distribution of an age-size structured population from single-cell data.

We aim to study the steady-state cell size distribution of a population of E. coli cells, integrating information collected at the individual scale. To that extent, we propose a stochastic individual-based dynamic model which can be calibrated using temporal single-cell lineage data acquired via microfluidic techniques. In particular, this data also grants access to the age structure, which then can be used to to provide a more precise non-Markovian characterisation of the growing population. Using probabilistic techniques, we prove the exponential convergence of the expected value of our stochastic process towards the unique stationary distribution, which can also be observed in real time in the data. A brief heuristic idea of the sufficient criteria for convergence which were used are discussed. We finally compare the predicted distributions to empirical distributions issued from macroscopic observations to validate the proposed micro-to-macro links for healthy and perturbed bacterial populations under different growing conditions.

David McLeod (U. Montpellier) : Effects of epistasis and recombination between vaccine-escape and virulence alleles on the dynamics of pathogen adaptation.

Pathogen adaptation to public health interventions, such as vaccination, may take tortuous routes and involve multiple mutations at different locations in the pathogen genome, acting on distinct phenotypic traits. Yet how these multilocus adaptations jointly evolve is poorly understood. Here we consider the joint evolution of two adaptations : pathogen escape from the vaccine-induced immune response, and adjustments to pathogen virulence affecting transmission or clearance. We elucidate the role played by epistasis and recombination, with an emphasis on the different protective effects of vaccination. We show that vaccines blocking infection, reducing transmission and/or increasing clearance generate positive epistasis between the vaccine-escape and virulence alleles, favouring strains that carry both mutations, whereas vaccines reducing virulence mortality generate negative epistasis, favouring strains that carry either mutation, but not both. High rates of recombination can affect these predictions. If epistasis is positive, frequent recombination can prevent the transient build-up of more virulent escape strains. If epistasis is negative, frequent recombination between loci can create an evolutionary bistability, favouring whichever adaptation is more accessible.

Philipp Messer (Cornell U.) : Modeling gene drive dynamics in continuous-space populations.

Rapid evolutionary processes can produce drastically different outcomes when studied in well-mixed populations as compared to spatially explicit models. Such differences could be particularly relevant for so-called “gene drives”, which can be engineered to spread genetic modifications through a population in just a few generations to induce population collapse. While laboratory experiments in mosquitoes and modeling in panmictic populations have shown that a gene drive can rapidly eliminate a population, it remains unclear if these results translate to natural environments where individuals inhabit a larger continuous landscape. In this talk, I will present our recent work on modeling the dynamics of gene drives in spatially continuous populations. I will show that the release of a suppression drive should often result in what we term “chasing” dynamics, in which wild-type individuals recolonize areas where the drive has locally eliminated the population. Despite the drive subsequently reconquering these areas, complete population suppression often fails to occur or is substantially delayed. This increases the likelihood that the drive is lost or that resistance evolves. Our results demonstrate that the population dynamics of suppression gene drives are determined by a complex interplay of genetic and ecological factors, highlighting the need for realistic spatial modeling to predict the outcome of drive releases in natural populations.

Cheryl Mentuda (U. Picardie Jules Verne) : Optimal Control of a Dengue-Dengvaxia Model : Comparison Between Vaccination and Vector Control.

Dengue is the most common mosquito-borne viral infection transmitted disease. It is due to the four types of viruses (DENV-1, DENV-2, DENV-3, DENV-4), which transmit through the bite of infected *Aedes aegypti* and *Aedes albopictus* female mosquitoes during the daytime. The first globally commercialized vaccine is Dengvaxia, also known as the CYD-TDV vaccine, manufactured by Sanofi Pasteur. This paper presents a Ross-type epidemic model to describe the vaccine interaction between humans and mosquitoes using an entomological mosquito growth population and constant human population. After establishing the basic reproduction number $\mathcal{R}_0$, we present three control strategies : vaccination, vector control, and the combination of vaccination and vector control. We use Pontryagin's minimum principle to characterize optimal control and apply numerical simulations to determine which strategies best suit each compartment. Results show that vector control requires shorter time applications in minimizing mosquito populations. Whereas vaccinating the primary susceptible human population requires a shorter time compared to the secondary susceptible human.

Sepideh Mirrahimi (CNRS) : Filling the gap between individual-based evolutionary models and Hamilton-Jacobi equations.

Joint work with Nicolas Champagnat, Sylvie Méléard and Chi Tran.

An approach based on Hamilton-Jacobi equations has been developed during the last two decades to study quantitative genetics models, leading to an analytical description of the phenotypic density. Such Hamilton-Jacobi equations are derived, in the regime of small mutational variance, from integro-differential models, which are themselves derived from stochastic individual based models in the limit of large populations. These equations are hence derived in two steps, each of them being an asymptotic derivation, considering first large populations and next small mutational effects.

In this work, we derive such a Hamilton-Jacobi equation, directly from a stochastic individual based model. This derivation allows a better understanding of the results obtained by the Hamilton-Jacobi approach and would lead to a rectification of the approach taking into account possible extinctions of sub-populations.

Florian Patout (INRAE) : Ancestral lineages in mutation selection equilibria with moving optimum.

Many populations can somehow adapt to rapid environmental changes. To understand this fast evolution, we investigate the genealogy of individuals inside those populations. More precisely, we use a deterministic model to describe the phenotypic density of a population under selection when the fitness optimum moves at constant speed. We study the inside dynamics of this population using the neutral fractions approach. We then define a Markov process characterizing the distribution of ancestral phenotypic lineages inside the equilibrium. This construction yields qualitative as well as quantitative properties on the phenotype of typical ancestors. In particular, we show that in asexual populations typical ancestors of present individuals carried traits much closer to the fitness optimum than most individuals alive at the same time. We also investigate more deeply the asymptotic regime of small mutation effects. In this regime, we obtain an explicit formula for the typical ancestral lineage using the description of the solutions of Hamilton Jacobi equation as a minimizer of an optimization problem. In addition, we compare our deterministic results on lineages with the lineages of stochastic models.

Stephan Peischl (U. Bern) : When does gene flow facilitate evolutionary rescue ?

A major (if subtle) shift in thinking about ecology and evolution over the past generation has been the growing appreciation of how intertwined adaptation and population dynamics are, and how often they proceed on similar time-scales. This new perspective has been recently thrown into high relief by the need to understand how species may respond to environmental change caused by human activity. It seems certain that a substantial fraction of our planet's current biodiversity will be lost to extinction as species' habitats change at an accelerating rate. Some species, however, may be able to escape that fate by adapting, shifting their geographical ranges, or both. This leads to the questions of when, where and how might adaptation allow species to survive, leading to 'evolutionary rescue'. Some basic answers to those questions come from theory. In this talk I will present recent work on understanding how gene flow, spatial structure and habitat fragmentation affect the probability for evolutionary rescue. I start with a simple analytically tractable model for evolutionary rescue in a two-deme model with gene flow. This model can be analyzed in detail and our main result is a simple condition for when migration facilitates evolutionary rescue, as opposed as no migration. We further investigated the roles of asymmetries in gene flow and/or carrying capacities, and the effects of density regulation and local growth rates on evolutionary rescue. I will also present simulation results of multi-deme models. We find that in many cases spatially structured models can be translated into a simpler island model using an appropriately scaled effective migration rate. Finally, I will discuss continuous space models and highlight analogies to models of evolutionary rescue via modification of the distribution of fitness effects in non-recombining organisms, such as many viral populations.

Gael Raoul (CNRS) : Range dynamics for a spatially structured asexual population.

Natural populations live in a heterogeneous environment and tend to adapt their phenotypes to their local environment. To understand the range dynamics of a population, we thus need to consider the spatial propagation of the population, but also its evolutionary dynamics. Starting from simple 1D linear environments, we will discuss how we can try to consider more complex situations : populations living in the 2D plane, and populations living in an environment that has a general heterogeneity at large scales. We will discuss how we can take advantage of stochastic phenomena to derive a simple macroscopic description of a population range.

Lionel Roques (INRAE) : Adaptation in a heterogeneous environment. A host in the middle.

We analyze a system of nonlocal reaction-diffusion equations describing the dynamics of adaptation of K phenotypically structured populations, under the effects of mutation, selection and migration in a K-patches environment, each patch being associated with a different phenotypic optimum in R^n. We give a characterization of the large-time behavior of the solution (persistence or extinction) based on the sign of a principal eigenvalue. We show that migration between environments decreases the chances of persistence. We mainly focus on the comparison between the case $K = 2$ (2 hosts) *vs.* the case $K = 3$ (3 hosts). We show that the "fitness gain" obtained when a third host is added to the system can be positive or negative, depending on the position of the third host in the phenotypic space. Thus, the presence of a third host can cause a "springboard" effect, a common pattern in zoonotic diseases, or on the contrary impede adaptation.

Denis Roze (CNRS) : Quantifying the evolutionary advantage of recombination in finite populations.

One of the most widely cited hypotheses to explain the evolutionary maintenance of sex and recombination states that recombination increases the efficiency of natural selection by reducing interference among selected loci. Until recently, this possible benefit of recombination was quantified analytically only in the case of haploid, randomly mating organisms, with selection acting at a few loci only. In this talk, I will present recent analytical and simulation results quantifying the strength of selection for recombination along continuous chromosomes in finite, diploid populations. Interestingly, selection for recombination caused by recurrent deleterious mutations can often be approximated by a simple function of the effective population size and the chromosomal mutation rate and genetic map length (average number of crossovers at meiosis). The results will then be extended to the case of partially inbred populations (by considering partially self-fertilizing hermaphroditic organisms), and to the effect of transposable elements, representing an important source of mutation in the genomes of eukaryotes.

Himani Sachdeva (U. Vienna) : Polygenic local adaptation in sub-divided populations : effects of linkage disequilibria and genetic drift.

Environmental adaptation often involves spatially heterogeneous selection at many genetic loci. Thus, the evolutionary consequences of hybridisation between populations adapted to different environments depend on the coupled dynamics of multiple loci under selection, migration and genetic drift, making them challenging to predict. In this talk, I will introduce theoretical approximations that accurately capture the effect of such coupling on allele frequencies at individual loci, while also accounting for the stochastic effects of genetic drift. These approximations will then be used to analyse hybridisation in a subdivided population with multiple habitats under divergent selection. I will discuss when polygenic local adaptation can be maintained in a sub-divided population despite migration and how this affects neutral gene flow between habitats.

Sebastian Schreiber (UC Davis) : Coevolution of habitat choice in a stochastic world.

Joint work with Alex Hening and Dang Nguyen.

Species live and interact in patchy landscapes where environmental conditions vary both in time and space. In the face of this spatial-temporal heterogeneity, species may coevolve how they select habitat patches. Under equilibrium conditions, coevolution of patch-selection is predicted to give rise to ideal-free distributions of all species : their per-capita growth rates are zero in occupied patches and negative in unoccupied patches. While ideal-free distributions explain observed empirical patterns including enemy-free space and the ghost of competition past, they do not explain why some species occupy sink patches, why competitors have overlapping spatial ranges, or why predators avoid highly productive patches. To understand these patterns, we analyze stochastic Lotka-Volterra models accounting for spatial heterogeneity, environmental stochasticity, and any number of interacting species. We derive an analytically tractable characterization of coevolutionarily stable strategies (coESS) for patch-selection and introduce a numerical algorithm for solving for a coESS. The analytic characterization shows whenever there is selection for a species to occupy multiple patches, their local stochastic growth rates will be negative in the occupied patches i.e. all populations are sink populations. Applying our methods to models of antagonistic interactions reveals that environmental stochasticity can partially exorcise the ghost of competition past, select for new forms of enemy-free and victimless space, and generate hydra effects over evolutionary time scales. To provide additional perspective on our results, we discuss how they relate to the Modern Portfolio Theory of economics. Our results highlight how environmental stochasticity can reverse or amplify evolutionary outcomes due to species interactions or spatial heterogeneity.

Michael Scott (U. East Anglia) : Equilibrium allele frequencies in terms of invasion and fixation conditions.

Joint work with Matthew Osmond.

Genetic variation can be maintained by balancing selection. This requires that an allele ‘invades’ (increases in frequency when rare) but does not ‘fix’ (declines near 100% frequency). Balancing selection pushes these alleles towards an intermediate ‘equilibrium’ frequency. Here, we use a general formulation to show that the equilibrium frequency can often be written as a simple ratio of the conditions for invasion and fixation. This relationship requires that marginal fitness increases linearly with allele frequency, a common assumption in population genetic models. We therefore connect many models in the same framework and provide a concise and interpretable expression for equilibrium frequency.

Corina Tarnita (Princeton U.) : The evolution of eusociality.

Elisa Thébault (CNRS) : Interaction between competition and predation shapes the emergence of species niche clustering patterns.

Joint work with Matilda Haraldsson.

Understanding the mechanisms underlying species coexistence and the maintenance of highly diverse communities has been a central issue in ecology for decades. Historically much emphasis has been made on the importance of limiting similarity, showing that species should differ in their ecological niche – *e.g.* in their resource utilization – to allow stable coexistence. However, recent theoretical studies have also revealed that species can also coexist over ecological scales by being sufficiently similar, leading to distinctive clustering patterns of species distribution along the niche axis with groups of similar species separated by gaps in between.

While various mechanisms have been shown to promote the emergence of niche clustering and its stability over time, all the mechanisms studied so far still rely on competition among species. Despite the potential generality of niche clustering patterns recently outlined in several theoretical and empirical studies, we still know nothing of how these clusters translates into more complex communities including trophic interactions. Here, by studying a classical predator-prey Lotka-Volterra model, we investigate how competition and predation interact to shape the distribution of prey and predators along their niche axes and lead to the emergence of clusters on these axes.

Nicolas Vauchelet (U. Sorbonne Paris Nord) : Mathematical modeling of a replacement strategy to control vector-borne diseases.

In order to control epidemics of mosquito-borne diseases for which there is no vaccine, such as dengue fever, several strategies aim to act directly on the mosquito population. One of these strategies consists of introducing a bacterium, called Wolbachia, which blocks the transmission of the pathogen. Since this bacterium is maternally transmitted, the idea is to release Wolbachia-infected mosquitoes to replace the wild population. In this presentation, we will present a mathematical modeling of such a strategy and will propose a study of the resulting system of equations to optimize the strategy.

Jennifer Williams (U. British Columbia) : Eco-evolutionary dynamics of range expansions.