Thematic semester on

Mathematics Computer science and biology

cimi
Centre International de Mathématiques et d'Informatique
TOULOUSE

Ecology and evolutionary biology, deterministic and stochastic models

Conception graphique : Benoît Colas, Université Toulouse - Jean Jaurès / CPRS - DàR. Illustration : © Golnaz Behrouznia.

CONFERENCE

Invited speakers

- Ingela Alger
- Vincent Bansaye
- Henri Berestycki
- Sylvain Billiard
- Reinhard Bürger
- Nicolas Champagnat
- Jérome Chave
- Troy Day
- Claire De Mazancourt
- Silvia De Monte
- Florence Débarre
- Odo Dieckmann
- Matt Holzer
- Kim-Yeung (Adrian) Lam
- Mark Lewis
- Sébastien Lion
- Ricardo Martinez-Garcia
- François Massol
- Sylvie Méléard
- Todd Parsons
- Benoit Perthame
- Gaël Raoul
- Ophélie Ronce
- Emmanuel Schertzer
- Viet Chi Tran
- Amandine Veber

Organizers

Robin Aguilée, Manon Costa, Grégory Faye, Sylvain Gandon, Sepideh Mirrahimi.

http://www.cimi.univ-toulouse.fr/mib/

From the 9th
to the 13th
of october
2017

Institut
de Mathématiques
de Toulouse,
Amphithéâtre
Laurent Schwartz,
Bâtiment 1R3

	MONDAY 9	TUESDAY 10	WEDNESDAY 11	THIRSDAY 12	FRIDAY 13
9h15-10h	Coffee	R. Martinez-Garcia	V. Bansaye	H. Berestycki	N. Champagnat
10h-10h45	B. Perthame	S. Méléard	O. Ronce	J.Chave	T. Parsons
11h15-12h	S. de Monte	A. Lam	W. Rodriguez	M. Lewis	T. Day
12h-12h45	A. Veber	F. Massol	R. Bürger	C. De Mazancourt	
12h45-14h15	Lunch	Lunch	Lunch	Lunch	Lunch
14h15-15h	S. Lion	I. Alger		M. Holzer	
15h-15h45	O. Diekmann	F. Débarre		S. Billiard	
16h15h-17h	E. Schertzer	G. Raoul		V.C. Tran	

Titles and abstracts

Ingela Alger, Toulouse School of Economics, France
Evolution, maximizing behavior, and pro-sociality

If humans inherit behaviors from their (genetic or cultural) parents and there is a mechanism that determines which parents are more successful than others in producing (genetic or cultural) offspring, in the long run should humans be expected to behave as if they sought to maximize the number of offspring (fitness)? We show that precise answers to this question can be obtained by building on well-known models in evolutionary biology of transmission and selection. In particular, we show that in a large class of evolutionary scenarios, theory delivers precise results on how the degree of pro-sociality of behaviors in strategic interactions depend on processes that govern transmission, such as migration, survival, fecundity, war waging, and loyalty towards parents.
This is a joint work with Laurent Lehmann and Jörgen Weibull

Vincent Bansaye, Centre de Mathématiques Appliquées, Ecole Polytechnique, France
Asymptotic profiles for population dynamics linear models in varying environment

We will present quantitative estimates of the density of populations described by a linear PDE in varying environment. We are focusing on two examples : an age structured population when individuals life length increases in time and a growth diffusion model in non-homogeneous space and varying environment.
The techniques is probabilistic and relies on coupling argument for auxiliary semi groups. This provides Frobenius/ Krein Rutman estimates with explicit speed of convergence in total variation distance. We may then come back to the description of the stochastic branching process corresponding to the individual based model.
This is a joint work with Bertrand Cloez and Pierre Gabriel.

Henri Berestycki, Centre d'analyse et de mathématique sociales, EHESS, PSL University - Paris
Predators-prey model with competition : emergence of territoriality and packs in animal behavior

I report here on a series of joint works with Alessandro Zilio about systems of predators interacting with a single prey. We consider predators like wolves that can divide into several hostile packs. The questions are to understand the conditions under which predators segregate into packs, whether there is an advantage to have such hostile packs, and to compare the various territory configurations that arise in this context. Mathematically, we focus on the analysis of stationary states, stability issues, and asymptotics of the system when the competition parameter becomes unbounded.

Sylvain Billard, Unité Evolution, Ecologie et Paléontologie, Université de Lille, France
Rejuvenating functional responses with the renewal theory

How fast do interactions occur between individuals is central in ecology. Functional responses are classically used to describe the number of predation, mating, competition, etc. in a given timeframe. Hundreds of different forms of functional responses have been proposed in the ecological and mathematical literature. It is well known that this form can dramatically affect the stability and dynamics of populations. Yet, the forms given to functional responses are generally poorly justified from the individual point of view, most ecologists generally adopting a phenomenological approach, in a purely deterministic framework. Here, we propose a novel and original stochastic approach based on the renewal theory. We show how it is possible to derive classical and novel functional responses from the behaviors of the individuals by modelling the time taken by all activities that must be fulfilled for an interaction to be successful. We show

how a stochastic approximation of the functional responses can be obtained thanks to the renewal theory. We give applications of our theoretical framework and discuss the importance of interactions as a source of stochasticity in ecological models.

Reinhard Bürger,, Universität Wien, Austria
On the theory of two-locus clines on the real line

A population-genetic migration-selection model will be investigated which is continuous in space and time. The model assumes that two diallelic, recombining loci are under spatially varying selection. The habitat is linear and unbounded, and dispersal occurs by diffusion. A classical and important special case occurs if selection is modeled by step functions such that in one region one allele at each locus is advantageous and in the other deleterious. Dominance is admitted. The nonconstant stationary solutions of the resulting system of PDEs are called clines. First, an explicit expression for the single-locus cline with dominance is derived, thus generalizing classical results by Haldane and others. Interestingly, the slope of the cline in the center turns out to be independent of dominance. Second, under the assumption of strong recombination, the first-order approximation of the allele-frequency cline at each of the loci is derived, as is the linkage disequilibrium. This requires a singular perturbation method. In population-genetics terms, the quasi-linkage-equilibrium approximation of the two-locus cline is obtained. The consequences of dominance and linkage for the shape of the two-locus cline are explored for arbitrary recombination rates. Analogous, but more general, models on a bounded habitat and open problems will be discussed briefly.

Nicolas Champagnat, Inria Nancy-Grand Est
A large deviations approach to Hamilton-Jacobi scaling limits of PDE models of adaptive dynamics

This is joint work with Benoît Henry (IECL, Université de Lorraine).
We consider partial differential equations modeling adaptive evolution of a quantitative trait in a population in which mutations are due to a Laplace operator and selection is due to the competition for finitely many resources described by integrals of the population density. A small population and large time scaling of this equations gives rise to a Hamilton-Jacobi limit equation with constraints, first described by Diekmann, Jabin, Mischler, Perthame (2005). We use a probabilistic interpretation of the solution of the PDE as the expectation of a functional of Brownian paths, and large deviations estimates to provide a variational characterization of the limit Hamilton-Jacobi problem. This variational problem can be obtained under more general conditions than those known for the Hamilton-Jacobi limit to hold. In addition, the method can be applied to a large range of mutation operators. We detail the case of finite trait spaces with exponentially small rates of mutations, where uniqueness properties for the limit variational problem can be obtained in some particular cases.

Jérôme Chave, Laboratoire Évolution et Diversité Biologique, Université Toulouse 3, France
Properties of a stochastic model of biodiversity with protracted speciation

Troy Day, Departments of Mathematics & Biology, Queen's University, Canada
When does stochasticity reverse the direction of evolution ?

There has been considerable interest recently in examining how stochasticity arising from a finite population size can reverse the direction of selection and promote the evolution of traits like altruism and spitefulness that are selected against in very large (deterministic) populations. In this talk I will consider a simple model of spite and of altruistic behaviour and examine how demographic stochasticity affects the evolution of these traits. More broadly I will attempt to

address the question of how one might determine, mathematically, whether stochasticity can reverse the direction of evolution.

Claire De Mazancourt, Station d'écologie théorique et expérimentale du CNRS, Moulis, France
Invariability : measuring and understanding the effect of biodiversity on ecosystem stability

Stability can be defined in many different ways ; different branches of ecology use radically different notions, thus preventing a constructive dialog between them. Theoretical ecology mainly studies asymptotic resilience, while policy applications mainly consider HollingÕs resilience ; however, empirical measures of both resilience notions are problematic and therefore not readily operational. Empirical ecology mainly studies temporal variability, but we lack theoretical grounding for these types of stability measures.
In this talk I will present some new theoretical developments of invariability, the inverse of temporal variability. I will show how invariability relates to other stability measures. I will introduce the Invariability Ð Area Relationship, that spells out how invariability changes with spatial scale. Finally, I will estimate invariability using experimental data to show the mechanisms through which biodiversity stabilize communities.

Silvia De Monte, Eco-evolutionary mathematics team, Institute of Biology of Ecole Normale Supérieur, Paris, France and Max Plank Institute of Evolutionary Biology, Ploen, Germany
Spatio-temporal structure and the evolution of microbial collectives

Microbes are often found within collectives with established functional relevance, be it biofilms, flocks, or sorocarps. How natural selection acts on pluricellular cell aggregates, which are in many cases genetically heterogenous, is not clear. In this talk, I will show that self-organized population structure can create a degree of assortment sufficient to overcome conflicts of interest between cells in aggregation-dispersion life cycles. The evolution of individually costly, collectively functional behaviour is in this case concomitant with the emergence of sizeable groups. I will eventually discuss the effect of spatio-temporal structure on the evolutionary potential of collectives.

Florence Débarre, CNRS, Centre for Interdisciplinary Research in Biology, Collège de France, Paris
Fidelity of parent-offspring transmission and the evolution of social behaviour in structured populations

The theoretical investigation of how spatial structure affects the evolution of social behavior has mostly been done under the assumption that parent-offspring strategy transmission is perfect, i.e., for genetically transmitted traits, that mutation is very weak or absent. In this talk, we investigate the evolution of social behavior in structured populations under arbitrary mutation probabilities. We consider spatially structured populations of fixed size N, in which two types of individuals,A and B, corresponding to two types of social behavior, are competing. Under the assumption of small phenotypic differences (weak selection), we provide a formula for the expected frequency of type A individuals in the population, and deduce conditions for the long-term success of one strategy against another. We then illustrate this result with three common life-cycles (Wright-Fisher,Moran Birth-Death and Moran Death-Birth),and specific population structures. Qualitatively, we find that some life-cycles (Moran Birth-Death,Wright-Fisher, when social interactions affect fecundities) prevent the evolution of altruistic behavior, confirming previous results obtained with perfect strategy transmission. Imperfect strategy transmission also alters the balance between the benefits and costs of staying next to one's kin, leading to surprising results in subdivided populations, in that higher emigration probabilities can be favourable to the evolution of altruistic strategies.

Odo Diekmann, Utrecht University , The Netherlands
Waning and boosting : on the dynamics of immune status

Immune memory continuously wanes, but is occasionally boosted by a new encounter with the pathogen. In an admittedly caricatural description, immune status is captured by a one-dimensional quantity (e.g., antibody titre against pertussis toxin), waning by a differential equation and boosting by a force of infection (assumed to be known) and a map that sends the immune status just before encountering the pathogen to the immune status just after. In [1] this map is derived from a within-host submodel. The dynamics of the distribution of immune status is governed by a linear renewal equation. The solution is obtained by generation expansion, with the generation number corresponding to the number of times the individual became infected. The main result, derived in [2], provides a precise characterization of the stable distribution.
[1] W.F. de Graaf, M.E.E. Kretzschmar, P.M.F. Teunis, O. Diekmann, A two-phase within host model for immune response and its application to seriological profiles of pertussis, Epidemics (2014) 9 : 1-7
[2] O.Diekmann, W.F. de Graaf, M.E.E. Kretzschmar, P.F.M. Teunis, Waning and boosting : on the dynamics of immune status, Submitted to J. Math. Biol.

Matthew Holzer, Department of Mathematical Sciences, George Mason University, USA
Estimating epidemic arrival times using linear spreading theory

We study the dynamics of a spatially structured model of worldwide epidemics and formulate predictions for arrival times of the disease at any city in the network. The model is comprised of a system of ordinary differential equations describing a meta-population SIR compartmental model defined on a network where each node represents a city and edges represent flight paths connecting cities. Making use of the linear determinacy of the system, we consider spreading speeds and arrival times in the system linearized about the unstable disease free state. Two predictions are presented. The first assumes that the dominant transmission pathway between any two cities can be approximated by a one dimensional lattice or homogeneous tree and gives a uniform prediction for arrival times independent of specific network features. The second method considers the full heat kernel solution of the linear system and produces an arrival time estimate that incorporates network features. We test these predictions on a real network describing worldwide airline traffic.

Kim-Yeung (Adrian) Lam, Department of Mathematics, The Ohio State University, USA
Evolution of dispersal : ESS and evolutionary branching

We will survey on some of our recent results concerning evolution of dispersal in the context of reaction-diffusion equations. The concept of evolutionarily stable strategy (ESS) will first be introduced with the pioneering work of Hastings in 1983, where it is proved that the slower diffuser prevails in the class of unconditional dispersal strategies in heterogeneous environments. Then its relation with habitat selection and ideal free distribution will be described. After that, we turn our attention to non-ideal free situations, where the habitat is under the action of a uni-directional drift. We will discuss results concerning both homogeneous and heterogeneous habitats. Finally, we mention related results in a class of mutation-selection models of population structured by space and traits, where ESS appears as a single or multiple stable steady Dirac concentrations. Our methods includes perturbation of eigenvalues of elliptic problems, Hadamard graph transformation, singularity theory, the WKB-ansatz and the method of viscosity solutions. This talk includes joint work with R.S. Cantrell, C. Cosner, M. Golubitsky, W. Hao, Y. Lou and F, Lutscher.

Mark Lewis, University of Alberta, Canada
Generational spreading speeds for integrodifference equations

Some of the most fundamental quantities in population ecology describe the growth and spread of populations. Population dynamics are often characterized by the annual rate of increase, lambda or the generational increase, R0. Analyses involving R0 have deepened our understanding of disease dynamics and life-history complexities beyond that afforded by analysis of annual growth alone. While range expansion is quantified by the annual spreading speed, a spatial analog of lambda, an R0-like expression for the rate of spread is missing. Using integrodifference models, we derive the appropriate generational spreading speed for populations with complex stage-structured life histories. The resulting measure, relevant to locations near the expanding edge of a (re)colonizing population, incorporates both local population growth and explicit spatial dispersal. The calculations for generational spreading speed are often simpler than those for annual spreading speed, and analytic or partial analytic solutions can yield insight into the processes that facilitate or slow a population ?s spatial spread. We analyze the spatial dynamics of teasel as an example to demonstrate the flexibility of our methods and the intuitive insights that they afford. This work is joint with Andrew Bateman, Marty Krkosek and Mike Neubert.

Sébastien Lion, Centre d'Écologie Fonctionnelle et Évolutive (CEFE) in Montpellier, France
The dynamics of reproductive values

In structured populations, individuals of a given genotype may belong to different classes. Such classes may represent different age groups, developmental stages, sexes, habitats, or spatial locations. Because these classes may have different evolutionary values, a common approach in evolutionary theory, starting with Fisher, has been to weight individuals by class-specific reproductive values. In most models, the reproductive values are calculated as the left eigenvector of a constant projection matrix, either in exponentially growing populations or in populations at demographic equilibrium.
Here, I extend this approach using time-dependent reproductive values. I derive a general version of Price equation for class-structured populations, along with dynamical equations for reproductive values. These equations are valid for general ecological scenarios, including out-of-equilibrium dynamics, density-dependence, environmental feedbacks and genetic polymorphism. Using numerical simulations, I show how these results can be used to analyse selection retrospectively using demographic time series. I also discuss the potential use of these generalised reproductive values for prospective theoretical analyses of selection.

Ricardo Martinez-Garcia, Department of Ecology & Evolutionary Biology, Princeton University, USA
The role of life-history tradeoffs and environmental heterogeneity in D. discoideum diversity

In the social amoebae D. discoideum starvation triggers the aggregation of free-living cells, which culminates in the formation of a multicellular fruiting body made of dead stalk cells and reproductive spores. During this aggregation, amoebae do not completely discriminate against genetic non-relatives, and therefore chimeric fruiting bodies (made of at least two genotypes) have been observed both in the lab and in the wild. Within these chimeras, lab-measured spore contributions indicate a strong skew in the fraction of spores that belong to each genotype. In the traditional perspective on the D. discoideum life cycle, in which fitness is equated to spore production, this skew suggests a strong social antagonism that should result in low genotypic diversity. This, however, is inconsistent with the huge coexistence of strains observed in nature. We (and others) have suggested that this inconsistency arises from the one-dimensional assessment of fitness (spore production), and that the solution lies in a higher dimensional fitness, based on several tradeoffs between multiple life-history traits (spore size versus spore viability, spore production versus staying as non-aggregated cells). In this presentation, I will first show these experimental observations and then introduce a socially-neutral model (i.e.,

no social interactions between genotypes) to theoretically explore multiple life-history traits and tradeoffs in social amoebae. Experimental results regarding apparent social interactions within chimeric mixes can be qualitatively recapitulated under this neutral hypothesis, without needing to invoke social interactions. This allows for simple potential resolutions to the previously paradoxical results, but life-history tradeoffs alone do not resolve strain coexistence. I will conclude by proposing two environmental processes : spore dispersal among different patches and seasonality within a single patch as driving forces of diversity in D. discoideum.

François Massol, CNRS, Unité Evolution, Ecologie et Paléontologie, Université de Lille, France
The evolution of conditional dispersal under different life cycles

Dispersal is an important trait affecting many processes in ecology and evolution, such as the evolution of local adaptation, speciation, extinction risk, invasion success, and species coexistence. Assessing factors affecting the evolution of dispersal is thus of paramount importance to understand these processes at a higher level. While past theoretical studies have modeled the effect of a great variety of processes like kin competition, inbreeding avoidance, spatio-temporal variability and dispersal cost on the evolution of emigration propensity, discrepancies between model predictions have largely been ignored, with little or no attempt at classifying predictions according to their underlying assumptions. Based on a simple, spatially implicit, adaptive dynamics model, this presentation will show some contrasted results on the evolution of condition-dependent emigration in a metapopulation submitted to spatio-temporal variability of habitat quality. Depending on the modeled life cycle and the reliability of cues informing individuals of their home patch quality, emigration can evolve in sometimes opposite ways. In particular, polymorphism of emigration strategies can emerge even in cases of perfect cues and alternative evolutionarily stable strategies can occur when environmental quality is temporally autocorrelated. Life cycles corresponding to hard selection models, in which density regulation occurs at the metapopulation scale, generally produce extreme emigration strategies (total dispersal or total philopatry) whereas local density regulation can lead to more complex strategies. In the latter case, model results highlight the existence of different interpretations for the evolution of emigration, depending on whether emigration helps find a better site to reproduce or a site where density regulation is less harsh. These findings, which emerge from a general and simple model, will be replaced and discussed in the framework of habitat choice.

Sylvie Méléard, Centre de Mathématiques Appliquées, Ecole Polytechnique, France
The effect of competition and horizontal inheritance on invasion, fixation and evolution

In a large range of species, horizontal transfer of information, such as genetic mobile elements, plasmids, endosymbionts or cultural traits, affects the adaptation of populations and the evolution of species. Understanding how they are affected is a huge challenge, in particular for microorganisms since it plays a main role in the virulence evolution or in bacterial antibiotics resistances. We propose a general eco-evolutionary stochastic model of population dynamics with clonal reproduction and mutations, including competition for resources and exchange of genes, as in the conjugation for plasmids in bacteria cells. We study different asymptotics of this general birth and death process depending on the respective demographic, ecological and transfer time scales and on the population size. We show how the gene transfer can drastically affect the evolutionary outcomes.

Todd Parsons, Laboratoire de Probabilités et Modèles Aléatoires, Université Pierre et Marie Curie, France

Benoit Perthame, Laboratoire Jacques-Louis Lions, UPMC, UPD, CNRS and INRIA-Mamba,

France
Adaptive evolution : a population point of view

We analyze a mathematical formalism describing a population characterized by a continuous adaptive trait. With appropriate scaling, we show that, asymptotically, specific traits are selected, the fittest in an environment which is constantly modified by the population evolution. The case of a non-proliferative advantage requires to extend the formalism and opens new mathematical questions.

Gaël Raoul, CNRS, Centre de Mathématiques Appliquées, Ecole Polytechnique, France
Macroscopic limit from a structured population model to the Kirkpatrick-Barton model

We are interested in PDE models that are used in evolutionary ecology to investigate the effect of climate change on species' range. More precisely, we will consider the Spatial Infinitesimal Model, a Kinetic model, and the Kirkpatrick-Barton model, a macroscopic model. Our goal will be to provide a rigorous macroscopic limit between those two models. We will also detail a biological study of the effect of pollen dispersion, where the macroscopic limit mentioned has been useful.
To describe the macroscopic limit from the Spatial Infinitesimal Model to the Kirkpatrick-Barton model, we take advantage of a Tanaka inequality satisfied by the reproduction operator, combined to parabolic estimates to control the spatial dynamics of the solution. As a by-product of this argument, we obtain estimates on a higher moment of solutions of the kinetic model, provided the reproduction rate is large enough.

Willy Rodriguez, Institut de Mathématiques de Toulouse
Challenges when applying stochastic models to reconstruct the demographic history populations

One of the main goals in population genetics is to build statistical procedures allowing to reconstruct major events in the evolution of species. Many stochastic process have been proposed to describe the way genetic diversity changes over time. Nowadays, the rapid development of DNA sequencing technologies is expanding the horizons of population genetic studies. It is expected that genomic data will increase our ability to reconstruct the history of populations. However, it also poses big challenges. This talk will be focus on the Coalescence, a stochastic process widely used in population genetics. I will discuss how the coalescence times between genes can be related with past demographic events and I will mention some popular methods allowing to infer coalescence times based on genetic data. I will emphasize the notion that the time until coalescence can be considered a "lifetime" random variable. This notion allows to see a clear link between population size changes and changes in the "coalescence rate". Finally I will comment some potentially confusing results that arise when some hypothesis of the models are violated.

Ophélie Ronce, CNRS, l'Institut des Sciences de l'Évolution de Montpellier (ISEM), France
Maladaptive shifts in life history in a changing environment

Populations confronted to a changing environment, as occurs under climate change, must adapt fast enough to persist. Several theoretical models have formalized such demographic and evolutionary challenges and predicted the critical speed of environmental change, or the critical amount of genetic variance, above or below which, respectively, the population is doomed. Many species confronted to climate change have complex life cycles, with individuals in different stages differing in their ecology, their sensitivity to a changing climate and their contribution to population growth. Building on theoretical tools from evolutionary demography, we used a quantitative genetics model to predict the dynamics of adaptation in a stage-structured population confronted to a steadily changing environment. Our model assumes that the same

phenotypic trait affects different transitions in the life cycle, with different optimal phenotypic values maximizing different fitness components, which generates de facto a trade-off between life history traits. In a constant environment, the population evolves towards an equilibrium trait value, which represents the best compromise given the trade-off between life history traits. In a changing environment however, the mean phenotype in the population will lag behind this optimal compromise. We show that this adaptive lag may result in a shift along the trade-off between life history traits, with negative consequences for some fitness components, but, less intuitively, improvements in some others. These shifts in life history could easily be wrongly interpreted as adaptations to the new environment, while they only reflect the inability of the population to adapt fast enough and are associated with lower fitness. More generally, we show how the critical speed of environmental change depends on its specific effects on different components of the life cycle.

Emmanuel Schertzer, Centre for Interdisciplinary Research in Biology, Collège de France
Relating coalescence and extinction in the Moran model

Consider a simple (neutral) Moran model in which each individual reproduces at rate 1 and whose offspring replaces one individual in the population chosen uniformly at random. At a given time, the genealogy of the present population is described in terms of the celebrated n-Kingman coalescent. Using the Look-Down representation of Donnelly and Kurtz, I will show that there exists a strong relation between the coalescent process and the extinction of types in the Moran model. As a by product of this approach, I will present a method that allows to reconstruct the history of the present types from the the observation of the genetic diversity in the population.This is joint work with Amaury Lambert and Guillaume Achaz.

Viet Chi Tran, Laboratoire Paul Painlevé, Université des Sciences et Technologies de Lille, France
Phylogenies in a population with competition

We consider a population structured by a neutral marker and an adaptive trait, that are supposed to be completely linked (hence neglecting recombination). The population evolves through births and deaths, and individuals compete together, in a logistic way and depending on their adaptive traits. The marker is neutral with respect to competition and selection.
In a large population with rare mutations, we show that the stochastic individual-based model can be approximated by the following process. Restricting to the trait distribution, we recover the Trait Substitution Sequence process (Metz et al. 96, Champagnat 06) or the Polymorphic Evolution Sequence (Champagnat and Méléard 11), depending on whether the invasion of an advantageous mutant implies or not its fixation. During the invasion, the neutral marker associated with the original mutant hitchhikes, thus creating a bottleneck. Then, genetic diversity is rebuilt following a Fleming-Viot or Wright-Fisher (in bi-allelic cases) process.
From these results, we can show that the phylogenies in this limit are Kingman coalescent processes whose characteristics depend on all the traits present in the population, and with bottlenecks. The effective population sizes appear to be the stationary solutions of the dynamical system associated with the traits present in the population.
The first part is a work with S. Billiard, R. Ferrière and S. Méléard. The second part is a work in progress with F. Austerlitz, R. Chaix, C. Lepers, S. Méléard and M. Porte.

Amandine Veber, CNRS, Centre de Mathématiques Appliquées, Ecole Polytechnique, France
The infinitesimal model of phenotypic evolution - a microscopic approach

In the infinitesimal model, one or several quantitative traits are described as the sum of a genetic and a non-genetic component, the first being distributed within families as a normal random variable centred at the average of the parental genetic components, and with a variance independent of the parental traits. The idea behind the normal distribution of the genetic component

is that the genetic part of the trait of interest is the sum of the 'infinitesimal? contributions of the allelic states at a very large number of loci. This model has been widely used in quantitative genetics, but less so in evolutionary biology and the precise conditions under which it holds has remained rather vague. In this talk, we shall provide a mathematical justification of the model as the limit as the number M of loci tends to infinity of a model with Mendelian inheritance, which includes different evolutionary processes (genetic drift, recombination, selection, mutation, population structure,?). This is a joint work with Nick Barton (IST Austria) and Alison Etheridge (Oxford University).