

# Résumés

**Diala ABU AWAD**

**The effect of the timing of selection on the mutation load, inbreeding depression and population size.** If and how the genetic load affects population size has been long debated as on one hand it has been suggested that high genetic loads lead to extinction, and on the other hand, density-dependent factors are expected reduce its demographic impact. This implies that the timing of selection during the life cycle could be an important factor. In addition, population genetics models calculating the expected genetic loads and levels of inbreeding depression ignore the potential effects of demography on these variables. Here we propose a deterministic model in continuous time where deleterious mutations affect individual fitness in one of three ways: by decreasing mating success, fecundity or survival. The genetic load, inbreeding depression and population size are variables that emerge from the model. Our results are compared to the expectations from the fundamental model of natural selection. We find that these three variables are affected by the timing of selection and can diverge from results obtained from the fundamental model; notably, contrary to expectations, when selection is on survival, the genetic load decreases when recurrent deleterious mutations are very deleterious. Our results emphasize the importance of integrating both population demography and genetics in order to study the demographic impact and, more generally, the fate of deleterious mutations.

**Airam BLANCAS BENÍTEZ**

**On branching process with rare neutral mutations.** In this talk we study the genealogical structure of a Galton-Watson process with neutral mutations, where the initial population is large and mutation rate is small. Namely, we extend in two directions the results obtained in 2010 by Bertoin.

Assuming that the reproduction law is critical and has finite variance, we ensure that conditionally to non-extinction there exists a measure under which the process of the sizes of allelic sub-populations converges towards a continuous state branching processes with immigration in discrete time. In addition, we establish this convergence in the situation where the reproduction law is in the domain of attraction of an alpha-stable distribution.

**Manon COSTA**

**Modélisation stochastique de l'évolution dans un réseau de proies et de prédateurs.** Dans cet exposé je présenterai un modèle individu centré pour l'évolution d'une communauté de proies et prédateurs. Nous nous intéresserons au comportement dans une échelle de grande population de ce processus. Nous verrons qu'alors le processus stochastique peut être approché par un processus déterministe dont nous étudierons le comportement en temps long. Dans un deuxième temps, nous supposons l'existence de mutations. En se plaçant dans l'échelle des mutations, nous considérerons la convergence vers un processus de saut représentant l'action de la sélection naturelle sur le réseau.

**Miraine DAVILA**

**A time reversal duality for branching processes and applications.** We consider a random forest  $\mathcal{F}$ , defined as a sequence of i.i.d. splitting trees, each started at time 0 from a single

ancestor (with a specific distribution, different from that of the descendants), stopped at the first tree having survived up to a fixed time  $T$ . We denote by  $(\xi_t, 0 \leq t \leq T)$  the population size process associated to this forest, and we prove that if the splitting trees are supercritical, then the time-reversed process  $(\xi_{T-t}, 0 \leq t \leq T)$ , has the same distribution as  $(\xi_t^{\natural}, 0 \leq t \leq T)$ , the corresponding width process of an equally defined forest  $\mathcal{F}^{\natural}$ , but where the underlying splitting trees are subcritical, or equivalently, obtained by conditioning on ultimate extinction. The results are based on an identity between the contour of these random forests truncated up to  $T$  and the duality property of Lévy processes. This identity allows us to also derive other useful properties such as the distribution of the population size process conditional on the coalescent of individuals at  $T$ , which has applications in epidemiology.

**Hélène LEMAN**

**Influence d'une structure spatiale sur le comportement en temps long d'une population.** De nombreux modèles mathématiques ont été développés afin d'étudier finement l'évolution phénotypique d'une population. Ici, on se concentrera plus particulièrement sur l'influence d'une structure spatiale sur l'évolution de ces populations. On présentera un modèle individus-centré qui suit l'évolution de chaque individu, lors des naissances, morts et déplacements spatiaux de ceux-ci. La population sera ainsi décrite par des processus markoviens. On étudiera ensuite le comportement moyen de la population, c'est-à-dire le comportement en grande population, qui s'écrit sous forme d'un système non-local de type Lotka-Volterra. Nous chercherons à comprendre son comportement en temps long pour répondre à ces problématiques: quels paramètres interviennent dans l'extinction des populations? ou dans l'apparition d'une nouvelle espèce?

**Elma NASSAR**

**Phenotypic Adaptation in the Moving Optimum Model: A Poissonian Stochastic Equation.** In a recent work of Kopp and Hermisson (2009), the authors treat adaptation of a population to a linear degradation of its fitness and compute the distribution of the adaptative substitutions via a complicated recurrence formula. Nevertheless, they could not predict survival or extinction. The starting point of this work is to introduce a Poissonian Stochastic Equation that describes the evolution of the phenotype of a population, and study whether the solution is recurrent or transient. This is quite easy to check for the solution of a Brownian Stochastic Equation. Our work can be considered as a sort of generalization of this case.

**Mathieu RICHARD**

**Descente de l'infini des processus de naissance et mort:** Dans ce travail, on considère un processus de naissance et mort markovien  $X$  et on s'intéresse à des propriétés de type *descente de l'infini* de ce processus. Celles-ci permettent de bien comprendre comment  $X$  se comporte au voisinage de  $+\infty$ .

Après avoir énoncé un critère simple sur les taux de naissance et mort pour que  $X$  descende de l'infini, on expliquera pourquoi cela permet de définir  $\mathbb{P}_{\infty}$ , la loi de  $X$  partant d'une taille initiale infinie. Sous cette probabilité  $\mathbb{P}_{\infty}$ , on s'intéressera ensuite au comportement de  $X(t)$  quand  $t \rightarrow 0$  (loi des grands nombres, théorème central limite). On montrera en particulier que  $X$  est équivalent à une fonction vitesse déterministe  $v$ .

On appliquera ensuite ce résultat à l'étude de processus de naissance et mort en environnements fluctuants dans lesquels l'environnement influe sur l'intensité de la compétition entre individus. On donnera des conditions nécessaires pour obtenir une extinction p.s. de la population.

**Charline SMADI-LASSERRE**

**An Eco-Evolutionary approach of Adaptation and Recombination in a large population of varying size.** We identify the genetic signature left by a selective sweep in the vicinity of an allele fixed by positive selection. We consider a sexually reproducing haploid population

with non constant population size described by a birth and death process with density dependent competition between individuals. Parameter  $K$  scales the population size, and we study the limit behaviour for large  $K$ . We focus on two linked loci: one under selection and a neutral one. We distinguish soft selective sweep occurring after an environmental change, from hard selective sweep occurring after a new mutation. In the first case, we express the variations of neutral allele proportions as a function of the ecological parameters, recombination probability and solutions of a deterministic two-dimensional Lotka-Volterra system with competition. In the case of strong selective sweep, we find two recombination regimes. In the strong one, the recombination probability per reproductive event is large with respect to  $1/\log K$  and the selective sweep does not modify the neutral proportions. In the weak regime, the recombination probability per reproductive event is of order  $1/\log K$ , and the natural selection on the mutant drives an increase in frequency of the neutral allele carried by the first mutant. We express this increase as an explicit function of the ecological parameters, recombination probability and  $K$ .