



Stochastic Models in Ecology, Evolution and Genetics

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Program Booklet

fixation/coexistence transitions and discuss the non-equilibrium properties of the two regimes.

A population model with non-neutral mutations using branching processes with immigration

Jean-François Delmas
(École des Ponts ParisTech)

We consider a stationary continuous model of random size population with non-neutral mutations using a continuous state branching process with non-homogeneous immigration. We assume the type (or mutation) of the immigrants is random given by a constant mutation rate measure. We determine some genealogical properties of this process such as: distribution of the time to the most recent common ancestor (MRCA), bottleneck effect at the time to the MRCA (which might be drastic for some mutation rate measures), favorable type for the MRCA, asymptotics of the number of ancestors. This is a joint work with H. Bi.

On impulse fire events in a tree-grass interactions model in savanna ecosystem

Yves Dumont
(CIRAD)

Savanna is a grassland ecosystem characterized by various trees density. Since decades, this ecosystem has been extensively studied to understand its longterm and spatial evolution under several environmental factors, like climate changes, rainfall, browsers... and big fire events. To this end various theoretical models have been developed and discussed the last forty years. In this talk, we mainly focus on the modelling of fire events. Until now, in most of the models, fire events have been taken into account continuously. This is not really realistic. We propose to consider fire as discrete events that lead to a system of impulse differential equations. The model is mathematically well posed and a qualitative analysis shows that it derives richer longterm dynamics than the

related continuous fires model. In addition, we will introduce some randomness in the fire events. Finally, using appropriate numerical methods, we will illustrate the talk with various numerical simulations.

Modelling DNA sequence evolution with interacting particle systems

Mikael Falconnet
(Université d'Évry)

To study the changes in DNA sequences, one usually deals with the finite product of i.i.d. continuous-time Markov chains modelling single site nucleotide substitutions. A consequence of the independence is that in a long DNA sequence at equilibrium the frequency of a dinucleotide xy should be the product of the x and y frequencies. But this is actually not the case in some biological contexts. Indeed, it is well known that the dinucleotide CpG is less frequently present in many mammals DNA than it would be expected from base composition. This phenomenon is related to DNA methylation: the substitution rate of cytosine by thymine is higher in methylated CpG's than in other dinucleotides. Therefore, more realistic substitution models incorporating such neighboring effects have been introduced. But substitutions are not the only way to alter DNA sequences. For example, one may add several extra nucleotides to a DNA sequence by insertions, or remove them by deletions. We consider Markov processes defined on the integer lattice, that allow for substitution according to a Markovian kernel depending of the neighborhood and also for a single "cut-and-paste" mechanism, and we provide sufficient conditions for the process to be ergodic. Joint work with N. Gantert and E. Saada

Linearization methods in the control of PDMP associated to gene networks

Dan Goreac
(Université Paris-Est Marne-la-Vallée)

The aim of this talk is to present some applications of linear programming methods in the control of piecewise deterministic Markov processes associated