Stochastic Models in Biosciences and Climatology

<small>ORGANIZER:</small> Samy Tindel (*University of Nancy, FR)*
Wednesday, July 4, 14:30–16:30, Medium Hall B

<small>TALKS:</small>
Frederi Viens (*Purdue University, USA*), **Long-range dependence in stochastic systems: the case of paleoclimatology**

Nicolas Champagnat (*INRIA Nancy, FR*), **Adaptive dynamics in an individual-based, multi-resources chemostat model**

Samy Tindel (*Université de Lorraine, FR*), **A stochastic model for bacteriophage systems**

Long–range dependence in stochastic systems: the case of paleoclimatology

Frederi Viens
Purdue University, USA

For a number of decades, the theory of continuous stochastic processes has provided a wealth of modeling tools for random systems with complex interactions, by using the building blocks of Brownian motion, martingales, and Markov processes, for instance via differential equations in finite and infinite dimensions. These tools rely heavily on the independence of increments for Brownian motion, which translates into short–range dependence for the resulting differential models. It is becoming increasingly clear to modelers in applications ranging from communications networks, to polymer studies, to financial and geophysical time series, that longer–range interactions are needed in stochastic modeling. When these persistent correlations are in a spatial domain, objects such as stochastic PDEs based on spatial correlated random fields can provide appropriate options, even if under short memory assumptions in time. However, for time-evolution systems, evidence of stochastic long memory means that a change in framework is needed. The basic building block in continuous time then becomes the fractional Brownian motion, which creates technical challenges in the interpretation differential systems. We will present a quick overview of the challenges that exist, particularly in the questions of statistical estimation and calibration, for long–memory models. We will describe some new progress in the context of proxy–based paleo–temperature reconstruction, in which a full Bayesian hierarchical with long-memory Gaussian errors is used. The methodology shows strong evidence of long memory, provides a reconstruction over the past 1000 years which contains a full evaluation of parameter and temperature uncertainty, and exhibits features which are corroborated by some historical evidence.

Adaptive dynamics in an indivi-dual-based, multi-resources chemostat model

Nicolas Champagnat
INRIA Nancy, FR

We consider an evolutionary model of population with competition for resources through a chemostat-type model, where individuals consume several common resources that are constantly supplied. This model describes for example the adaptation of bacteria interacting with their environment composed of resources. Bacteria are characterized by a continuous traits describing their consumption ability for each resource. The population of bacteria is assumed to follow a discrete stochastic dynamics, and the dynamics of resources concentrations is governed by deterministic ODEs. We consider fast resource and birth and death dynamics and a slow mutation rate. We prove that the population behaves on the mutation time scale as a jump process describing successive fast mutant invasions between evolutionary equilibria. In the small mutation steps limit, this process converges to an ODE known as the canonical equation, and we are able to characterize the trait values where evolutionary branching, a form of diversification or speciation, may occur.

A stochastic model for bacteriophage systems

Samy Tindel
Université de Lorraine, FR

Lately Bacteriophage therapies are attracting the attention of several scientific studies. They can be seen as a new and powerful tool to treat bacterial infections or to prevent them in food, animals or even humans. Generally speaking, they consist in inoculating a (benign) virus in order to kill the bacteria known to be responsible for a certain disease. This kind of treatment is known since the beginning of the 20th century, but has been in disuse in the Western world, erased by antibiotic therapies. However, a small activity in this domain has survived in the USSR, and it is now re-emerging (at least at an experimental level), due to the progressive slowdown in antibiotic efficiency (antibiotic resistance). This talk will be devoted to the analysis of a system modeling bacteriophage treatments in a noisy context by a delayed predator/prey type model. In the small noise regime, we show that after a reasonable amount of time the system is close to a bacteria free equilibrium (which is a relevant biologic information) with high probability. Mathematically speaking, our study hinges on concentration techniques for delayed stochastic differential equations.