Titles and abstracts of the talks

Etienne Auclair, Nathalie Peyrard, Régis Sabbadin (Inra de Toulouse)
Labeled Dynamic Bayesian Network learning, with community structure knowledge

Learning interactions between dynamical processes is a widespread but difficult problem in ecological or human sciences. Unlike in other domains (bioinformatics, for example), data is often scarce, but expert knowledge is available. This knowledge can be about the different types of mechanisms driving the processes dynamics or can inform on the interaction network structure.
We propose an original framework, based on Dynamic Bayesian Networks with labeled-edge structure, Stochastic Block Models and 0-1 Linear Programing, that improves network learning when these two types of expert knowledge are available. The approach is illustrated on a problem of ecological interaction network learning.

Prerequisite: The talk will be accessible to anyone with basic knowledge in probability and statistics. Notions on Bayesian network can help.

Simon Boitard, Bertrand Servin (Inra de Toulouse)
Estimating the evolution history of species from genome sequences

DNA sequences of extant individuals from a given species contain rich information about its evolutionary history. Indeed, the genetic diversity patterns observed from these sequences have been shaped by the various evolutionary events that have occured during the evolution of this species: population splits or fusions, migrations between populations, population contractions or expansions ...
One central objective of population genetics is to build statistical procedures to estimate past evolutive events from samples of DNA sequences. Although the stochastic models describing these evolutive processes have been proposed and studied for a long time, developing estimation procedures based on these models is very challenging, because closed form expressions of the likelihood are generally difficult to obtain, and because parameter and data space are

highly dimensional. We review in this talk several strategies that have been developed in this context, focusing more particularly on one specific question: the estimation of population size changes in an isolated population.

Pre-requisites: Basic skills in probability and statistics (concept of statistical estimation, likelihood, usual probability distributions, Markov chains ...). A priori open to a large audience (mathematics / computer science / biology).

Patrick Cattiaux, Fanny Delebecque (Institut de mathématiques de Toulouse)
A few models for the emergence of collective behaviour in population motion– Talk and practical session

The talk aims at introducing a few models for the collective behaviour in the motion of a population of many agents. We will focus on the property of flocking in Cucker-Smale like models. We will then implement some of these models.

Prerequisite: The talk and simulations are meant to be understandable by almost all M1 students, but basic notions on ODEs and probabilities could be helpful.

Pierre Neuvial (Institut de mathématiques de Toulouse)
Introduction to multiple testing in biology and medicine

In this talk, we give an introduction to multiple testing motivated by practical examples in genomics and neuroimaging. We define some of the most commonly used risk measures, as well as methods for controlling these risks.

We also give an overview of some current research directions in the field of multiple testing. In particular, accounting for (i) the exploratory nature of multiple testing problems, and (ii) some intrinsic properties of biomedical data, including their multi-scale nature.

Prerequisite: statistical tests.