

Abstract: In this talk, we will consider stochastic models and computational algorithms to study the evolution of interacting populations over time. We will focus on methods used to study gene regulation, cell signalling, stem-cell development, but also epidemics of infectious diseases. We will consider two examples: a circadian (i.e. 24-hour) endogenous clock and a signalling system controlling the immune response to inflammation. I will first introduce the Markov processes used in this setting and then focus on a model described by Stochastic Differential Equations (SDEs) called phase-corrected Linear Noise Approximation (pcLNA). pcLNA takes advantage of the transversal stability of systems that macroscopically present attractive limit cycles to perform long-time accurate yet fast stochastic simulation. We will discuss how to compute the likelihood of time-series data and how to perform sensitivity analysis. We will then explore Bayesian inference to estimate model parameters using a parallel-tempering Markov Chain Monte Carlo method.