MPIDS Seminar



From single-cell experiments to statistical inference of gene expression models: A physicist's perspective

Dr. Yen Ting Lin

T-6 and T-CNLS, Los Alamos National Laboratory, USA

What happens when a mathematical physicist studying random processes collaborates with biologists studying stochastic gene expression in single cells? In this talk, I will first introduce an experimental technique - single-molecule RNA fluorescent in situ hybridization (sm RNA FISH) which measures transcribed mRNA and the discrete state of activation in a single cell, and provides a "snapshot" of the stochastic process of gene expression. Then, I will discuss how we use a class of coarse-grained stochastic models, formulated as continuous-time and individual-based chemical reactions in a well-mixed environment, to infer kinetic properties of stochastic gene expression from the experimental data. I will present an accurate sampling procedure (up to 1000-fold speed-up compared to conventional algorithms) to efficiently solve the problem numerically. The increased efficiency permits us to go beyond standard fitting procedures and enter to the realm of statistical inference. In the final part of the talk, I will present a high-level description of how we carry out the full-scale Bayesian analysis on our continuous-time probabilistic models using data from discretetime observations. The outcome of the analysis, the uncertainty quantification of the parameters and model structures, will be presented.

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Max Planck Institute for Dynamics and Self-Organization Department of Living Matter Physics Prof. Dr. Ramin Golestanian Email: ramin.golestanian@ds.mpg.de, Phone: +49-(0)551/5176-100 Am Faßberg 17, 37077 Göttingen, Germany