



Modeling Gene Expression Kinetics in Cells

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Dupuis Hall, Room 217

The functioning of living cells is fundamentally governed by intracellular biochemical reactions. Since gene expression lies at the core of cellular processes, quantitative modeling of gene expression kinetics offers a powerful lens for understanding cell biology. Because biochemical reactants are often present in low copy numbers, these kinetics are inherently stochastic.

In this talk, I will present how queueing theory can be applied to derive exact steady-state solutions for the joint distribution of nuclear and cytoplasmic mRNA across a broad class of transcription initiation models. I will then discuss how machine learning techniques extend these analytical solutions to systems involving additional molecular species. Building on these solutions, I will show how probability generating functions enable efficient and accurate inference of kinetic rate constants. By incorporating extrinsic noise, this inference framework allows us to precisely quantify bursty expression across thousands of human genes and to link these patterns to biological function. Finally, I will demonstrate how probability generating function-based inference can be integrated into clustering, addressing another fundamental challenge in systems biology.