Ensemble preconditioning schemes for Bayesian inverse problems

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Single-cell and single-molecule experimental techniques expose the randomness of cellular processes and invite a stochastic description. In this talk I will present our efforts to solve inverse problems related to stochastic cellular dynamics. First, we discuss an inference framework that accounts for extrinsic and intrinsic noise contributions present in single-cell measurements. For that, we show that stochastic components of a cellular process (e.g. subnetworks) can be marginalised exactly such that the inference remains tractable. Second, we present single-molecule experimental data to study transcriptional kinetics in live yeast cells. A stochastic models for the system is presented and biophysical parameters such elongation speed, termination rate, etc are inferred from single transcription-site intensities. Moreover, optimal filtering or state estimation is performed to reconstruct the most likely position of single RNAP molecules on the gene. MCMC with tempering is used to estimate parameters and to perform model selection.