Abstract

Fine-scale models, such as stochastic master equations, can provide a very accurate description of the real genetic regulatory system, but inadequate time series data and technological limitations on cell specific measurements in biological experiments prevent the accurate inference of the parameters of such a fine-scale model. Furthermore, the use of fine-scale stochastic models is restricted by the inherent computational complexity involved in its simulation.

In this talk, the effect on the predictive performance and control outcome of coarse-scale Markov chain modeling, as compared to fine scale stochastic master equation models will be analyzed. A reduction mapping that maintains the collapsed steady state probability distribution of stochastic master equation models will be presented and bounds on the control performance analyzed.

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