

PHYSICAL MATHEMATICS SEMINAR

Analytical approaches to characterize complex stochastic systems and interpret single cell fluctuation data

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ABSTRACT:

Biochemical processes are inherently stochastic, creating molecular fluctuations in otherwise identical cells. Such “noise” is widespread but has proven difficult to analyze because nonlinearities make conventional analytical approaches intractable and many systems form large interaction networks that are only partially specified. In this talk I will present recent general results that exactly relate average abundances, lifetimes, step-sizes, and covariances for any pair of components in complex stochastic reaction systems even when the dynamics of other components are left unspecified. Combined with basic mathematical inequalities these relations allow us to rigorously establish what whole classes of systems cannot do, e.g. efficiently assemble complexes without extreme fluctuations in subunit levels, significantly suppress fluctuations without extremely sharp feedback control, or eliminate fluctuations in one component without creating heterogeneity in another. Identifying properties shared by classes of systems also greatly reduces the number of assumptions when testing kinetic models. I will illustrate the power of such an approach by reinterpreting recent mRNA-protein correlation data.

TUESDAY, MARCH 3, 2015
2:30 PM
Building E18, Room 466A

*Reception following in Building E17, Room 401A
(Math Dept. Common Room)*

<http://math.mit.edu/pms/>