Department of Mathematics,
University of California San Diego

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Center for Computational Mathematics Seminar

Caroline Moosmueller

Johns Hopkins University

Learning Protein Dynamics from Data

Abstract:

Biological data sets, such as gene expressions or protein levels, are often high-dimensional, and thus difficult to interpret. Finding important structural features and identifying clusters in an unbiased fashion is a core issue for understanding biological phenomena. In this talk, we describe the dynamical behavior of the important tumor suppressor gene p53 in a data-driven manner. By using simulations from nonlinear models that describe the experimentally observed oscillatory behavior of p53, we first identify parameters which qualitatively change the behavior of the system. Focusing on these parameters, we then show that the effective dimension of the parameter and state space can be recovered from time-series data, providing a minimal realization of the underlying nonlinear system. To this end, we apply the methods of bifurcation analysis and diffusion maps. This is joint work with M. Kooshkbaghi, D. Sroczynski, Z. Belkhatir, M. Pouryahya, A. Tannenbaum, I. Kevrekid is.

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