

RUTGERS UNIVERSITY
DEPARTMENT OF STATISTICS AND BIOSTATISTICS
HILL CENTER #501, BUSCH CAMPUS, PISCATAWAY

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Seminar

Speaker: Edo Airoldi, Princeton University

Title: Statistical analysis of complex biological systems

Date: Wednesday September 24, 2008

Time: 3:20 PM

Place: 552 Hill Center

Abstract

Modern technology has transformed the concept of data in the biological, social and computational sciences. Data collections about a number of biological systems, for instance, have grown large and heterogeneous, in terms of both the units of analysis and the measurements on such units. This increase in the complexity of data, however, has hardly translated into a richer understanding of fundamental mechanisms and principles. This problem is paramount in modern biology, where complex experimental probes about genes, proteins and enzymes promise key insights about the function and organization of small molecules in the cell, and about the development of disease. In this talk, I aim at demonstrating the advantages of a mechanistic approach to systems biology with two case studies. In the first case study, a model of how proteins interact grounds the data analysis in the context of accepted theories and empirical observations, and posterior (variational) inference reveals proteins' multifaceted functional role. This model predicts cellular events that we can measure---the goal is to drive experimentation in large event spaces. In the second case study, a model of cellular growth exposes growth-specific programs of gene expression and suggests the notion of “effective growth rate” of a cellular culture. This model opens a window on cellular events that we cannot measure by quantifying effective growth at a temporal resolution that is not accessible with technology (minutes rather than hours)---this result contributes to a system-level understanding of the connections among growth rate, metabolism, environmental stress response, and the cell division cycle.