



Bioinformatics Seminar

Speaker: Karen Sachs MIT Biological Engineering
(Lauffenburger Group)

Title: Bayesian network models of biological signaling pathways

Date: Monday, 20 March 2006

Time & Location:

Refreshments: 11 am in the Theory of Computation Lab at MIT's
Building 32, Stata Center Room G-575

Talk: 11:30 am the Theory of Computation Lab at MIT's Building 32,
Stata Center, Room G-575

URL: <http://www-math.mit.edu/compbiosem/>

Abstract:

Cells respond to their environment via protein signaling pathways, in which signaling molecules become chemically, physically or locationally modified, gain new functional capabilities, and affect subsequent molecules in the cascade, culminating in a phenotypic cellular response. This cellular response often includes an element of transcriptional regulation, a process which has been the object of much recent work in biological modeling, due to the availability of data in this domain (i.e. from microarrays). A comprehensive model would include both the upstream signaling pathway and downstream transcriptional pathway; however, efforts to model signaling pathways are often limited by the small amount of available data, due to the difficulty in measuring the molecules involved.

We recently introduced an approach to model signaling pathways using Bayesian network structure learning applied to single cell data. The data is acquired from a flow cytometer, a machine capable of detecting quantities of the active states of signaling molecules in individual cells (up to ~12 molecules at a time), at a rate of thousands of cells per minute. Using the single cell approach, we were able to reconstruct a model of T-cell signaling in primary human cells, completely de novo and with reasonably high accuracy. I will discuss extensions we are pursuing, including an approach to expand model size beyond the measurement capability of the flow cytometer, as well as an effort to map differences in signaling among different cell types, disease states or stimulus conditions.

The seminar is co-hosted by Professor Peter Clote of Boston College's Biology and Computer Science Departments and MIT Professor of Applied Math Bonnie Berger. Professor Berger is also affiliated with CSAIL & HST.

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