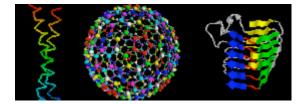**MIT**
Department of Mathematics
& The Theory of
Computation Group
At CSAIL

Bioinformatics Seminar

Speakers: Jacques Cohen, Brandeis University
Title: Towards a comprehensive view of computational approaches in systems biology
Date: Monday, 13 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:

In the past few years the number of available papers describing computational approaches in systems biology has increased significantly. These approaches vary considerably from one another. In this talk we aim to provide a bird's eye view of the various methods that have been proposed to analyze and infer gene regulatory networks. In so doing we are bound to find novel combined approaches that are worth pursuing.

A rough initial classification of the current methods distinguishes between discrete and continuous, macro (genetic networks) and micro (metabolic pathways), analysis (forward) and inference (reverse engineering), stochastic (probabilistic) and non-stochastic. Starting from discrete methods of analysis (e.g., Thomas, Thieffry, de Jong) we proceed to cover existing reverse engineering approaches (e.g., Akutsu, Somogyi) including those based on perturbation (e.g., Karp, Collins). At the micro level we explore recent work done in studying the consistency of biochemical reactions (e.g., Fages, P. Karp).

One of the findings based on this comprehensive view is that it is worth considering model-checkers as filters for networks being tested as possible candidates in the reverse engineering process. We conclude by raising a few questions about research directions in systems biology that are worth exploring.

(Work done jointly with Sam Blasiak)