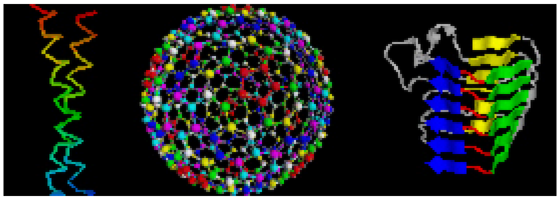
MIT
Department of Mathematics
& The Theory of
Computation Group
At CSAIL



Bioinformatics Seminar

Speaker: John Aarch, Harvard Medical School, Department of Genetics and Lipper Center for Computational Genetics
Title: Multicellular genetic network modeling: directions and issues
Date: Monday, 9 February 2004
Time & Location:
Refreshments: 11 am in the Applied Mathematics Common Room at MIT's Building 2, Room 349
Talk: 11:30 am to 1 pm in the Applied Mathematics Conference Room Building 2, Room 338
URL: http://www-math.mit.edu/compbiosem/

Abstract:

A key goal of recent systems biology is to generate mathematical models of genetic networks capable of explaining the increasing amounts of molecular data that are becoming available on cellular processes. Many models of genetic networks have now been constructed, but most of them focus only on intracellular behavior; meanwhile, most biology involves mutually interacting cells whose behavior is governed by multicellular networks. This presentation reviews key directions and issues in multicellular genetic network modeling, including systems that have been extensively modeled, mathematical modeling techniques in use, options for representing cell populations, passive and active genetic networking, and the prospects of multicellular metabolic network modeling.

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.

Massachusetts Institute
of Technology
77 Massachusetts Avenue
Cambridge, MA 02139

For General Questions, please contact kvdickey@mit.edu