



Bioinformatics Seminar

Speaker: Julien Gagneur, EMBL/HTFG Center

Title: Molecular Networks Decomposition and the Computation of Elementary Modes

Date: Monday, 27 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:

Molecular networks provide the structure of dynamic systems driving cell biology. Systematic application of current technologies and genome annotation have enabled the construction of large networks of protein interactions and metabolic networks for several model organisms. These resulting molecular networks are large and complex and their large-scale analysis poses several computational challenges.

In this talk, I will first focus on decomposition techniques that facilitate the analysis of molecular networks by dividing them into subnetworks. I will show a method that decomposes metabolic networks into independent parts and its application to E.coli metabolism. Another method, named modular decomposition, applies to protein interaction networks and derives the logical rules that proteins follow to assemble and form particular protein complexes. Modular decomposition is applied to the human TNF-alpha signaling pathway.

The second part of the talk focuses on the computation of elementary modes, which are minimal functional units in a metabolic network. This question is equivalent to the classical vertex enumeration problem from combinatorial geometry. However, state-of-the-art methods are limited in practice when dealing with large networks. I will show practical improvements of the algorithm and address the issue of distributed computation.

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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