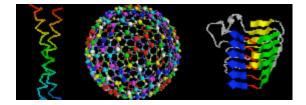
MIT Department of Mathematics & The Theory of Computation Group At CSAIL



## **Bioinformatics Seminar**

Speaker: Simon Kasif, BU Title: Advances in Functional and Comparative Genomics: Towards Computer Assisted Biology? Date: Monday, 4 October 2004 Time & Location: \*\*\*PLEASE NOTE TIME & PLACE 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: <u>http://www-math.mit.edu/compbiosem/</u>

Abstract:

There are two complementary research directions in computational biology: one is aiming to build physical and in some cases physically realizable models of biological systems (systems biology), the other is focusing on building knowledge tools (databases, inference algorithms, active learning & experiment design frameworks and laboratory process automation) deployed in mapping genotypes into phenotypes. We use the term of Intelligent Computer Assisted Biology to describe this research paradigm. A simplistic view of the second direction is as an attempt to model a biologist rather than biological systems.

In the spirit of modeling a Boston area biotechnologist who is typically involved in ten or more projects we will touch on a few topics. First explore some of the parallels between problems in AI and solutions for problems in comparative genomics. We describe several advances in comparative genomics and their application to analysis of Human, Mouse and Rat genomes using computational and evolutionary analysis techniques.

We then describe progress in functional annotation of genomes focusing on functional annotation and protein variability. We hypothesize a three tier organization of living organisms based on conserved, partially variable and highly variable elements and describe the application of this approach to organization of microbial organisms.

Finally we describe a few technological advances using novel computational paradigms that enable us to reduce the cost of certain genotyping procedures. If time permits.....

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For General Questions, please contact kvdickey@mit.edu

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.