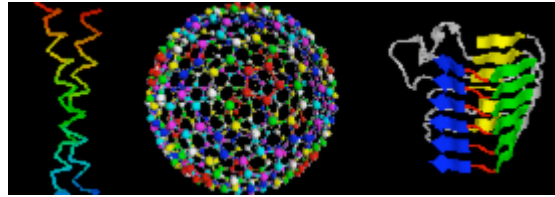


MIT
Department of Mathematics
& The Theory of
Computation Group
At CSAIL



Bioinformatics Seminar

Speaker: Norbert Perrimon, Howard Hughes Medical Institute, Department of Genetics, Harvard Medical School

Title: Functional genomic and network analysis in *Drosophila*

Date: Monday, 28 March 2005

Time & Location: **** PLEASE NOTE LOCATION****

Refreshments: 11 am in the STAR conference room at MIT's Building 32, Stata Center Room D-463

Talk: 11:30 am in the STAR conference room at MIT's Building 32, Stata Center Room D-463

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

Abstract:

The incredible properties of siRNAs have provided novel tools to create efficient gene knock out, and in combination with the availability of full genome sequences opened up the road to large scale functional genomic projects. I will discuss our ongoing functional genomic screens using RNAi interference in *Drosophila* cells. In addition, I will discuss data mining approaches of RNAi screens and our plans at using the RNAi-derived functional information to determine the structure of signaling networks.

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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For General Questions, please contact kvdickey@mit.edu