



Bioinformatics Seminar

Speaker: David Mathews, MD, PhD, Assistant Professor of Biochemistry & Biophysics, Center for Human Genetics and Molecular Pediatric Disease, Aab Institute of Biomedical Sciences, University of Rochester Medical Center

Title: Predicting Secondary Structures Common to Two RNA Sequences

Date: Monday, 2 May 2005

Time & Location:

Refreshments: 11 am in the Star Conference Room at MIT's Building 32, Stata Center Room D-463

Talk: 11:30 am the Star Conference Room at MIT's Building 32, Stata Center Room D-463

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

Abstract:

Dynalign is a dynamic programming algorithm that finds the lowest free energy secondary structure common to two, unaligned sequences and the sequence alignment that facilitates that structure. Recently, Dynalign has been extended to the prediction of a set of low energy structures. On average, secondary structures predicted by Dynalign are significantly more accurate than secondary structures predicted using a single sequence.

The talk will present the free energy nearest neighbor model for predicting RNA secondary structure stability. The dynamic programming recursions for predicting the set of low energy structures will be discussed. Finally, recently implemented heuristics to speed the calculation will be presented.

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