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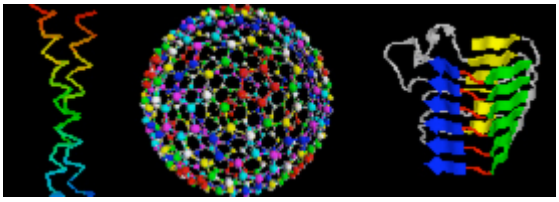

Bioinformatics Seminar

Speakers: J. Waldispuhl, Biology Dept. of Boston College and MIT and P. Clote, Biology Dept. of Boston College
Title: Energy landscape of k-point mutants of an RNA molecule
Date: Monday, 31 October 2005
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:

A k-point mutant of a given RNA sequence s = s_1,...,s_n is an RNA sequence s' = s'_1,...,s'_n obtained by mutating exactly k-positions in s; i.e. Hamming distance between s and s' equals k. To understand the effect of pointwise mutation in RNA, we consider the distribution of energies of all secondary structures of k-point mutants of a given RNA sequence.

Here we describe a novel algorithm to compute the mean and standard deviation of energies of all secondary structures of k-point mutants of a given RNA sequence. We then focus on the tail of the energy distribution, and compute, using the algorithm AMSAG, the k-superoptimal structure; i.e. the secondary structure of a mutant having least free energy over all secondary structures of all k'-point mutants of a given RNA sequence, for k' <= k. Evidence is presented that the k-superoptimal secondary structure is often closer, as measured by base pair distance, and two additional distance measures, to the secondary structure derived by comparative sequence analysis than is the Zuker minimum free energy structure of the original (wild-type or unmutated) RNA.

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