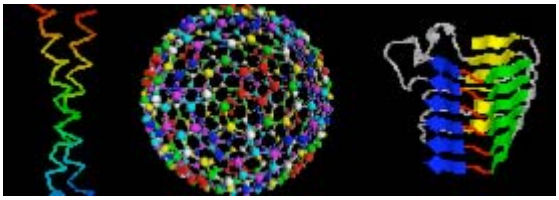
MIT
Department of Mathematics
& The Theory of
Computation Group
At CSAIL



Bioinformatics Seminar

Speaker: Michael Zuker, Department of Mathematical Sciences, Rensselaer Polytechnic Institute
Title: Predicting nucleic acid hybridization and melting profiles.
Date: Monday, 3 April 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:

Many applications in modern biotechnology require an accurate prediction of hybridization, partial hybridization or the competition between folding and hybridization of two single stranded nucleic acid molecules in solution. Current methods often employ simple two-state models to estimate melting temperatures for single stranded nucleic acids or for dimers. Similarly, database searching for likely hybridization sites of a DNA oligonucleotide or putative targets of a ncRNA (non-coding RNA) is often performed using existing tools such as BLAST.

We have undertaken a research program to develop more sophisticated and therefore, we hope, more accurate algorithms and software to predict not just melting temperatures, but entire melting profiles. In parallel, we have also developed a database search method that uses nearest neighbor free energy parameters as the basis for hybridization prediction.

The new UNAFold package implements, in part, the detailed hybridization model. It considers the competition between folding and hybridization, and also allows homo-dimer as well as hetero-dimer formation. Partition function calculations are performed for each single- or double-stranded molecular species and ensemble free energies as well as base pair probabilities are computed as a function of temperature. Ensemble free energies lead directly to heat capacity (Cp) predictions that can be compared directly with measurements from DSC (Differential Scanning Calorimetry) experiments. Similarly, computed probabilities, together with published extinction coefficients, lead to predictions of UV absorbance as a function of temperature.

In contrast, our database search algorithm, named FASTH, considers only the formation of a hetero-dimer between a relatively short oligonucleotide and a very long target, the database. It computes a hash table for the sequence database using a two letter, {puRine, pYrimidene}, alphabet, and quickly identifies regions of potential hybridization ranked by a crude score that is a sum of stacking free energies.

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.

Massachusetts Institute
of Technology
77 Massachusetts Avenue
Cambridge, MA 02139

For General Questions, please contact kvdickey@mit.edu