MIT
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& The Theory of
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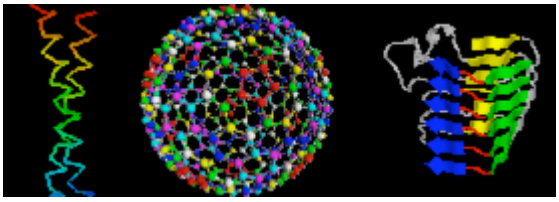

Bioinformatics Seminar

Speaker: Ken Dill, Professor of Biophysics, UCSF
Title: Protein folding: Is it still a problem?
Date: Monday, 6 November 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:

Two interesting challenges have each been called the protein folding "problem": (1) to devise a computer algorithm to predict the native structure of a protein, and (2) to understand how a protein can fold up physically in times as short as microseconds, despite searching a large complex energy landscape. We have been interested in the physics problem and in applying such insights to protein structure prediction. We believe proteins break their large global optimization problem into smaller local optimization problems. After all, proteins don't have the time, the inclination, or the smarts to do much more. I will describe some tests of this approach in CASP, the community-wide protein structure prediction event.

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