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  

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.