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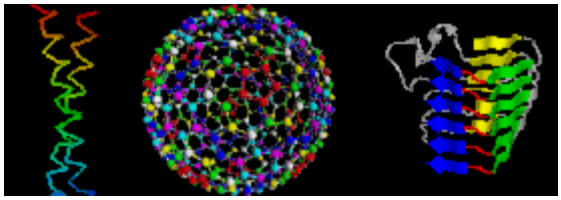

Bioinformatics Seminar
Special Joint Seminar with Applied Math Colloquium

Speaker: Phil Bradley, Postdoctoral Fellow, Department of Biochemistry, University of Washington, Howard Hughes Medical Institute
Title: Folding Algorithms for Protein Structure Prediction
Date: Monday, 23 February 2004
Time & Location:
Refreshments: 3:30 am in the Applied Mathematics Common Room at MIT's Building 2, Room 349
Talk: 4:15pm in Room Building 2, Room 105
URL: http://www-math.mit.edu/compbiosem/

Abstract:

To reach their biologically active state, newly synthesized proteins spontaneously fold from an extended, linear conformation into a compact three-dimensional structure.

This remarkable self-assembly process, *protein folding*, is guided by the amino acid sequence of the protein to a unique final state. Despite several decades of intensive study the process by which sequence determines structure is still not well understood; in particular it is not currently possible to predict a protein's native three-dimensional structure given only its sequence. Recently, however, a class of prediction algorithms based on protein fragment assembly have made considerable headway towards the goal of generating low-resolution structure predictions. In this talk I will introduce the *protein folding* problem, describe these new algorithms, highlight their strengths and weaknesses, and discuss current research directed at improving the reliability and accuracy of their predictions.

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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