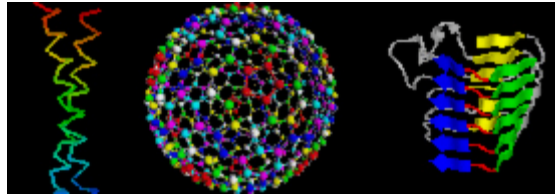**MIT**
Department of Mathematics
& The Theory of
Computation Group
At CSAIL

Bioinformatics Seminar

Speaker: Bonnie Berger, Professor of Applied Mathematics
Head, Computation and Biology Group
Computer Science and Artificial Intelligence Lab
Member of the Affiliated Faculty of Harvard Medical/MIT HST program

Title: Mathematical Challenges in Molecular Biology
Date: Monday, 26 May 2004
Time & Location:
Refreshments: 11:00 am in the Applied Mathematics Common Room at MIT's Building 2, Room 349
Talk: 11:30 am The Applied Mathematics Conference Room Building 2, Room 338
URL: http://www-math.mit.edu/compbiosem/

Abstract:

Recent advances in DNA sequencing technology and high throughput structural genomics initiatives have led to rapid progress in generating large amounts of genomic and proteomic data. Entire human, mouse, drosophila, and yeast genomes have been sequenced, and many are on their way: its been estimated that only a small percentage of the human genome is functional, so one challenge is to identify the functional elements from this sea of noise. The rapid accumulation of data has opened up new possibilities for biologists, while at the same time unprecedented mathematical challenges have emerged due to the mass of data. The question of how to analyze all this new information has only begun to be tackled by researchers. One powerful new approach to this problem is based on the comparison of multiple complete genomes. In particular, we have applied this approach to identifying genes, regulatory regions, non-coding RNA genes, etc. across species in an automated fashion.

As protein coding genes and regulatory motifs are identified, we would like to characterize their functions. Because the biological function of a protein is determined by its 3D structure, an important approach to this problem has been to predict protein structure from sequence. Again a comparative approach, here based on protein structure, has yielded impressive results, both in predicting protein structure from sequence and in functional annotation.

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