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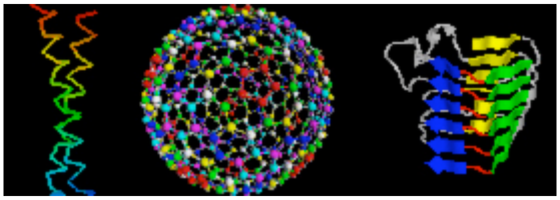

# Bioinformatics Seminar

Speaker: Michael I. Jordan, Department of Electrical Engineering and Computer Science, Department of Statistics, University of California, Berkeley
Title: Bayesian Bioinformatics
Date: Monday, 14 February 2005
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/

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Abstract:
One of the advantages of Bayesian statistics is its ability to integrate multiple sources of information---to "share statistical strength" among components of a hierarchical probabilistic model. This virtue has particular relevance in bioinformatics, where many core inferential problems---e.g., phylogenetic analysis, linkage analysis, haplotype phasing---are already naturally expressed in probabilistic terms. I will discuss our recent work on Bayesian inferential methodology in three areas in bioinformatics: (1) The prediction of molecular function based on homology, where Bayesian inference in a reconciled phylogeny is used to predict function of unannotated proteins from sparse functional annotations. We present results for 100 Pfam families. (2) Haplotype clustering and phasing, using a novel approach based on Dirichlet process priors. I present a hierarchical version of the Dirichlet process which allows us to infer relationships among haplotypes in multiple sub-populations. (3) Comparative genomics, where phylogenetic inference combines with Markovian inference to provide sensitive detection of conserved structure.

[Joint work with Steven Brenner, Barbara Engelhardt, Jon McAuliffe, Lior Pachter, Yee Whye Teh, and Eric Xing].

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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*