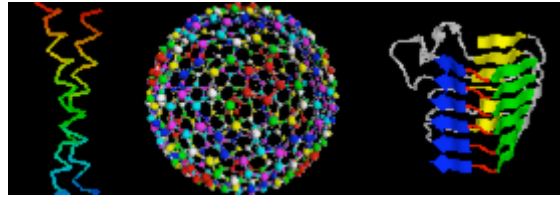**MIT**
Department of Mathematics
& The Theory of
Computation Group
At CSAIL

Bioinformatics Seminar

Speakers: Paul de Bakker, Massachusetts General Hospital
Department of Molecular Biology
Title: Human Genome Variation and Risk to Common Disease
Date: Monday, 27 February 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:

With the recent completion of the International HapMap Project and the
availability of high-throughput genotyping technologies, it has now become
possible to comprehensively test common genetic variation for a etiological role
in complex traits and common disease. The HapMap provides insight into the
fine-scale patterns of linkage disequilibrium, haplotype block structure, and
hotspots of recombination. I will describe computational strategies to association
testing through linkage disequilibrium on a genome-wide scale.   Given that
HapMap is based only 270 individuals from four populations, it is essential that
we evaluate how well the observed LD structure in HapMap will transfer across
different population samples. I will present empirical data that support the
efficacy of HapMap in genome-wide association studies.

Massachusetts Institute
of Technology
77 Massachusetts Avenue
Cambridge, MA 02139

For General Questions, please contact kvdickey@mit.edu