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& The Theory of
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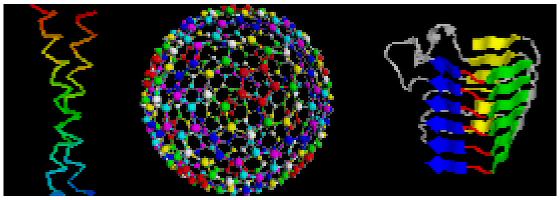

Bioinformatics Seminar

Speaker: Shamil Sunyaev, Ph.D., Brigham and Women's Hospital and Harvard Medical School
Title: " Computational Analysis of the Genome Variation and Divergence”
Date: Monday, 5 April 2004
Time & Location:
Refreshments: 11 am in the Applied Mathematics Common Room at MIT's Building 2, Room 349
Talk: 11:30 am to 1 pm in the Applied Mathematics Conference Room Building 2, Room 338
URL: http://www-math.mit.edu/compbiosem/

Abstract:

New massive data on genomic sequences and DNA polymorphism are now available for large-scale analysis. We analyzed both coding and non-coding regions of the genome and quantified the effect of genetic variation on molecular function and organism fitness. We developed a computational method for predicting the effect of coding single nucleotide polymorphisms (SNPs) on function and structure of proteins. Statistical tests of natural selection suggested that most SNPs in coding regions of functional significance are evolutionarily deleterious. The distribution of fitness effects of substitutions in coding and highly conserved non-coding regions was estimated by comparing sequence divergence in primate and rodent lineages

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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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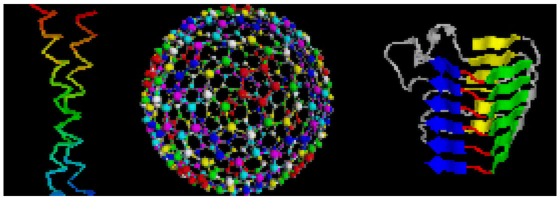
For General Questions, please contact kvdickey@mit.edu



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together with the data on human polymorphism. Applications of this analysis to studies in medical genetics will be discussed.

We also developed a new method for estimating evolutionary distance between genomes based on insertions and deletions rather than substitutions. The method was applied to the human and mouse genomes.

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