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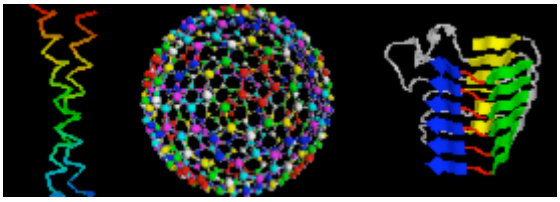

Bioinformatics Seminar

Speaker: Manolis Kellis, MIT CompBio group, CSAIL, Broad Institute
Title: Whole-genome comparative genomics in the fly.
Date: Monday, 24 April 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:

Comparative genomics has emerged as a powerful method for discovering biological DNA signals in any genome, by virtue of their conservation across related species. To that end, dozens of complete mammalian, fly, and fungal species have been recently sequenced, enabling powerful new methods for signal discovery. In this talk, I will discuss our recent work comparing 12 *Drosophila* genomes, for gene identification, regulatory motif discovery, and genome evolution.

For gene identification, modeling mutation patterns in coding and non-coding regions allows us to pinpoint genes and exons with very high accuracy. This has allowed us to revisit the gene content of the fly genome with surprising results: hundreds of previously defined gene models appear spurious, reducing the overall gene count; at the other end of the conservation spectrum, we find thousands of new exons, representing novel multi-exon genes, novel alternatively spliced gene forms, and many isolated exons.

In the area of gene regulation, searching for repeated, conserved sequence patterns has resulted in a dictionary of candidate regulatory motifs in the fly. These overlap strongly with known bindings sites of developmentally important regulators, show enrichment in genes with tissue-specific expression, and correlate strongly with known and novel microRNA genes. Moreover, with 12 aligned fly genomes, we can pinpoint individual motif instances with high confidence, enabling us to piece together complete networks of gene regulation.

Finally, we have studied the evolution of gene families, where probabilistic models of gene and genome evolution enable us to identify orthologous genes with much higher confidence than traditional methods, distinguish gene gain and loss events, and understand the evolutionary dynamic of large gene families.

The fly model provides the unique opportunity to understand the biology of a complete animal genome to unprecedented detail. It benefits from a combination of classical genetics, systematic experimentation, embryo visualization, and powerful genomics, bringing us closer than ever to understanding the many mysteries of genome biology.

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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