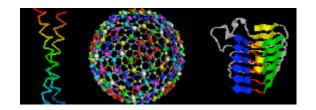**MIT**
Department of Mathematics
& The Theory of
Computation Group
At CSAIL

Bioinformatics Seminar

Speaker: William M Gelbart, Professor, Molecular & Cellular Biology
　　　　　Harvard University
Title:　　　The Comparative Analysis of Insect Genomes
Date:　　　Monday, 6 March 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:

The insects, arguably the most successful group of animals on earth, are emerging as a major focus of attention for genomic analysis. While there were only three insect genome sequences available two years ago, there are now about 20 and several more are in the pipeline.

Insects are of interest to us for basic research and practical reasons. Drosophila melanogaster is a major (the major?) model for many aspects of animal biology. The genus Drosophila has been a major focus of evolutionary studies going back to Dobzhansky's founding of experimental population genetics and evolution. Some insects are important vectors of disease (e.g., the mosquitos), necessary for large scale agriculture as pollinators (e.g., honeybee), producers of commercial materials (e.g., the silkmoth) and are major agricultural pests (e.g, the red flour beetle). Thus, some of the challenges of genomic analysis are how to use such analysis to increase our deep understanding of the very actively studied model, Drosophila melanogaster, to gain insights into how the genes and genomes of closely related species are changing, and to increase the power of typically very small research communities working on insect species of great practical importance.

In this talk, I will focus on some projects we are engaged in relating to the annotation of various dipterans (flies and mosquitos). I'll discuss the basic organization of the dipteran genome from a pre-genomic perspective and what we are learning from the initial comparative sequence analysis of the Drosophila and mosquito genomes that we are examining. In doing so, I'll discuss some of the challenges and pitfalls of analyzing whole genome shotgun draft genome assemblies, and how we can exploit the well-studied species D. melanogaster as well as some of the favorable architectural features of dipteran genomes to recognize and hopefully avoid some of these pitfalls.

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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