Bioinformatics Seminar

Speaker: Michael Brudno, University of Toronto
Title: Reconstructing Ancestral Genome Order via Maximum Matching
Date: Monday, 28 November 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

Abstract:
The ancestral order of two genomes can be used, for example, for progressive alignment. The difficulty of applying progressive alignment to whole genomes or other sequences with rearrangements is due to the lack of a general ordering on the alignments - it is possible to order based on either of the two genomes, but not both. We present a novel alignment algorithm that reconstructs a likely ordering of the genome of the ancestor of two organisms. While the genome of this ancestor is not known, one can use the outgroup genomic sequences to establish this order (if reconstructing the ancestor of mouse and rat, then human, dog, and chicken are all outgroups). By making several assumptions we formulate the problem of ordering a set of alignments based on a likely ancestral order as a maximum matching problem.

By using the algorithm above we order these according to their most recent common ancestor, and then align the resulting chain of alignments. This approach has several advantages over previous algorithms: 1) it does not assume a base genome, to which all other genomes are aligned, but creates a symmetric alignment equally valid for all genomes, 2) it penalizes various rearrangement events progressively based on an evolutionary tree, creating a set of alignments that mirrors the evolutionary history of the sequences, and 3) it is able to align short, low similarity syntenic areas based on their adjacency to higher similarity areas even when there has been a rearrangement event between the two areas. I will present the results of some first analyses of whole genome alignment using this algorithm.