

BIOINFORMATICS SEMINAR

Alignments, Motifs, and Microarrays

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Abstract

High-throughput experimentation technologies such as whole-genome sequencing and gene microarrays are transforming the way we do biology. From the traditional one-organism, few-genes framework we are quickly moving to many-organism, whole-genome studies. These are powered by algorithms, systems, and paradigms from computer science. In this talk we will cover some of the computational techniques we develop towards high-throughput biology. We will talk about methods for whole-genome multiple alignments and application to the human/mouse/rat genomes, gene microarray expression analysis, and regulatory motif-finding based on cross-species conservation and microarray measurements.

Monday March 17, 2003

11:00 a.m. – 1:00 p.m.

(Talk starts at 11:30)

Building NE43, Room 941

Refreshments at 11am in NE43-941

(LCS, 200 Tech Square, Cambridge, MA)



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