

BIOINFORMATICS SEMINAR

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Computational and Experimental Studies of Transcription Factor Binding

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ABSTRACT:

In this era of whole genome sequences, one of the major challenges is determining the regulatory networks of cells. This requires knowing the complete set of regulatory genes and all of their targets, as well as knowing whether the interactions are positive or negative (and ideally quantitative information about their effects) and under what conditions they are active. A more modest, intermediate goal is the determination of all of the DNA-binding transcription factors (TFs) and their regulatory binding sites within the genome. This talk will describe our work on several related problems:

1. For a known TF, determining its specificity so that the genes it regulates can be predicted from the genome sequence
2. For sets of co-regulated genes, discovering the common DNA patterns likely to represent TF binding sites
3. Identifying sets of TF binding sites likely to act in concert (perhaps cooperatively) to control expression
4. Utilizing phylogenetic information to aid in the pattern discovery process
5. If time permits, a bit about regulatory motifs in RNA sequences involved in post-transcriptional regulation.

Monday April 28, 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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