BIOINFORMATICS SEMINAR

A motif-based profile scanning approach for genome-wide prediction of signaling pathways

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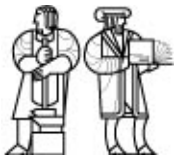
ABSTRACT:

The rapid increase in genomic information requires new techniques to infer protein function and predict protein-protein interactions. Bioinformatics identifies modular signaling domains within protein sequences with a high degree of accuracy. In contrast, little success has been achieved in predicting short linear sequence motifs within proteins targeted by these domains to form complex signaling networks. Here we describe a peptide library-based searching algorithm, accessible over the World Wide Web, that identifies sequence motifs likely to bind to specific protein domains such as 14-3-3, SH2, and SH3 domains, or likely to be phosphorylated by specific protein kinases such as Src and AKT. Predictions from database searches for proteins containing motifs matching two different domains in a common signaling pathway provides a much higher success rate. This technology facilitates prediction of cell signaling networks within proteomes, and could aid in the identification of drug targets for the treatment of human diseases.

Monday April 7, 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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