BIOINFORMATICS SEMINAR

Making predictions from function, phenotype and protein network data

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ABSTRACT:

I will cover four topics with the unifying theme of making predictions from functional genomics data:

1) Machine learning methods can exploit patterns in gene function annotation databases to make new function predictions in yeast and fly;
2) A similar approach can be used to make phenotype predictions;
3) Analysis of network topology can stratify error-prone protein interaction data by confidence;
4) A probabilistic network of protein-protein interactions is useful in ranking candidate members of protein complexes.

Monday February 24, 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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