BIOINFORMATICS SEMINAR

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A protocol for evaluating local structure alphabets

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ABSTRACT:

An important problem in computational biology is predicting the structure of the large number of putative proteins discovered by genome sequencing projects. Fold-recognition methods attempt to solve the problem by relating the target proteins to known structures, searching for template proteins homologous to the target. Remote homologs which may have significant structural similarity are often not detectable by sequence similarities alone.

To address this, we incorporated predicted local structure, a generalization of secondary structure, into two-track profile HMMs. We did not rely on a simple helix-strand-coil definition of secondary structure, but experimented with a variety of local structure descriptions, following a principled protocol to establish which descriptions are most useful for improving fold recognition and alignment quality.

The protocol evaluates the conservation, predictability, usefulness in fold recognition, and usefulness in alignment for a local structure alphabet.

Monday April 14, 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)

Dr. Karplus' invitation is possible because of the generous support of Genome Therapeutics Corporation, with special thanks to Dr. Kim Fechtel.

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