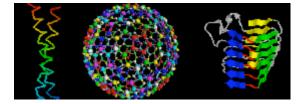
MIT Department of Mathematics & The Theory of Computation Group At CSAIL



Bioinformatics Seminar

Speaker: Qicheng Ma, Novartis Title: Clustering protein sequences with a novel metric transformed from sequence similarity scores and sequence alignments with neural networks Date: Monday, 11 May 2004 Time & Location Refreshments: 11 am in the Applied Mathematics Common Room at MIT's Building 2, Room 349 Talk: 11:30 am to 1 pm in the Applied Mathematics Conference Room Building 2, Room 338 URL: http://www-math.mit.edu/compbiosem/

Abstract:

Clustering of protein sequences from different organisms has been used to identify orthologous and paralogous protein sequences, to find protein sequences unique to an organism, and to derive the phylogenetic profile for a cluster of protein sequences. These are some of the essential components of a comparative genomics study of protein sequences across several genomes.

Algorithms used to cluster protein sequences can be either domain-based or family-based. All the clustering methods start with an all-against-all pairwise protein sequence similarity searches. The domain-based clustering methods organize the protein sequence universe into domain clusters where domains are the structural units of proteins, e.g., COG. Family-based clustering methods group protein sequences into families, which contain a group of evolutionarily related proteins that share similar domain architecture, e.g., PROTONET.

We propose a novel family-based clustering method to address two problems: how to detect whether two aligned sequences have similar domain structures; and how o quantify transitive homologies through intermediate sequences to detect remote homologies at the superfamily level. These two problems are simultaneously solved by a new metric for clustering of protein sequences.

The seminar is co-hosted by Professor Peter Clote of Boston College's Biology and Computer Science Departments and MIT Professor of Applied Math Bonnie Berger. Professor Berger is also affiliated with CSAIL & HST.

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For General Questions, please contact kvdickey@mit.edu