

Center for Cardiovascular Bioinformatics & Modeling

Friday, June 3, 2005

9:00-10:00 a.m.

110 Clark Hall

Robust Interpretation of Protein Subcellular Location Patterns in 3D Fluorescence Images

Xiang Chen
Department of Computational Biology
Carnegie Mellon University

Abstract:

Proteomics is the current focus of system biology and location proteomics is an important branch of it, which systematically studies protein subcellular spatial distributions for all proteins expressed in a certain cell type. Traditionally images are analyzed by visual inspection, which suffers from inefficiency and inconsistency. Automated and objective interpretation approaches are in need for location proteomics. We have designed numerical features to describe location patterns in microscope images and developed automated classifiers that distinguish major subcellular patterns with high accuracy (including patterns not distinguishable by visual examination). In addition we have described an automated method that constructs an effective partitioning of the proteins by location based on their location features. An application of these methods in molecular biology study is also covered.