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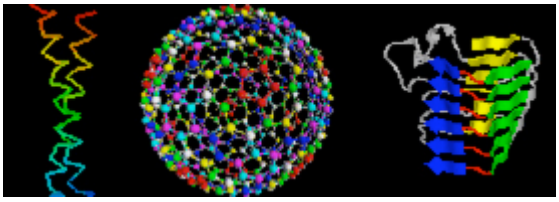

Bioinformatics Seminar

Speaker: Huajun Wang, Molecular Therapeutics Division, Ambergen, Inc.
Title: SED, a Normalization Free Method for DNA Microarray Data Analysis
Date: Monday, 11 April 2005
Time & Location:
Refreshments: 11 am in the Theory of Computation Lab at MIT's Building 32, Stata Center Room G-575
Talk: 11:30 am the Theory of Computation Lab at MIT's Building 32, Stata Center, Room G-575
URL: http://www-math.mit.edu/compbiosem/

Abstract:

Analysis of DNA microarray data usually starts with a normalization step where intensities of different arrays are bought to the same scale so the intensity levels from different arrays can be compared with each other. Both simple total array intensity based and more complex “local intensity level” dependent normalization methods are developed and some widely used. Much less developed are methods for microarray data analysis which bypass the normalization step and therefore give results that are not confounded by possible normalization errors. Instead of working on the raw intensity levels, we proposed a new method for microarray data analysis by mapping each gene’s expression intensity level to a high dimensional space of SEDs (Signs of Expression Difference), the signs of the expression intensity difference between the gene and every other gene on the array. Since SED is unchanged under any monotonic transformation of intensity levels, SED based method is normalization free. When tested on a multi-class tumor classification problem, simple Naive Bayes and Nearest Neighbor method using SED approach gives results comparable with normalized intensity based algorithms. Furthermore, a high percentage of classifiers based on single gene’s SED gives good classification results, suggesting that SED does capture essential information from the intensity levels. SEDs also proved be to more sensitive metrics for identifying biomarker for various cancers types. Testing results on multi-class tumor classification and biomarker discovery problems suggest that SED based, normalization free method of microarray data analysis is feasible and promising.

This is joint work with Hui Huang.

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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