

STANFORD UNIVERSITY  
DEPARTMENT OF STATISTICS  
JOINT STATISTICS/BIOSTATISTICS SEMINAR

2:00 p.m., Monday, April 5, 2004  
MSOB x303

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**Some recent progress in microarray analysis**

Abstract:

In this talk I will present two recent results from our group on the analysis of microarray data. The first concerns the computation of gene expression indexes based on probe-level data from Affymetrix oligonucleotide arrays. The method generalizes the probe-level models used by software such as dChip and RMA, to explicitly model the effects of cross-hybridization of non-target RNAs. We show that by modeling such cross-hybridization effects we can improve the accuracy of the expression index estimates substantially. The second result is a clustering algorithm designed to detect smaller sets of tightly regulated genes from a collection of microarray profiles. In contrast to standard clustering methods, this "tight cluster" method does not attempt to assign every gene to the cluster, and therefore the quality of the resulting clusters will not be contaminated by the inclusion of genes with loosely similar patterns.

Information about Workshop in Biostatistics can be found at: <http://www.stanford.edu/dept/HRP/Workshoplist.htm>