

STANFORD UNIVERSITY  
DEPARTMENT OF STATISTICS  
DEPARTMENTAL SEMINAR

4:15 p.m., Tuesday, October 26, 2004  
Sequoia Hall Room 200  
(Cookies at 3:45 in 1st Floor Lounge)

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**Normalization and significant analysis of microarrays using SLIM**

Abstract:

Normalization of microarray data is essential for coping with experimental variations and revealing meaningful biological results. We have developed a normalization procedure based on Semi-Linear In-slide Model (SLIM), which adjusts objectively experimental variations and are applicable to both cDNA microarrays and Affymetrix oligonucleotide arrays. This semiparametric model has a number of interesting features, including the partial consistency phenomenon: the parametric component and the nonparametric component of interest can be consistently estimated, the former possessing parametric rate and the latter having nonparametric rate, while the nuisance parameters can not be consistently estimated. The significant analysis of gene expressions is based on a newly developed weighted t-statistic, which accounts for the heteroscedasticity of the observed log-ratios of expressions, and a balanced sign permutation test. We illustrated the use of the newly developed techniques in a comparison of the expression profiles of neuroblastoma cells that were stimulated with a growth factor, macrophage migration inhibitory factor. The results based on the Affymetrix microarrays with MIF deleted are also presented.