

STANFORD UNIVERSITY  
DEPARTMENT OF STATISTICS  
DEPARTMENTAL SEMINAR

4:30 p.m., Tuesday, January 15, 2003  
Sequoia Hall Room 200  
(Cookies at 4:00 in 1st Floor Lounge)

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**Normalization for cDNA Microarray Experiments having many Differentially Expressed Genes**

This talk concerns normalization of cDNA microarray data in which a substantial proportion of genes differ in expression between the two mRNA samples, or there is no symmetry in the expression levels of up/down-regulated genes, and there are no control DNA sequences on the slide. The first step of this approach is to perform global normalization based on dye-swap experiments, and then use a statistical criterion to select a set of (almost) constantly expressed genes. Based on this set, intensity dependent normalization is carried out using local regression method. The usefulness of this method is clearly demonstrated in simulation studies and in the analysis of real data sets. In particular, it is shown in the simulation studies that this method identifies genes with a lower false positive rate and a lower false negative rate than a commonly used method, when a large number of genes are turned up or down.