



The University of Chicago
Department of Statistics
Seminars for Second Year PhD Students

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The University of Chicago

“Normalization of Microarray Data”

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110 Eckhart Hall, 5734 S. University Avenue

ABSTRACT

Microarrays have become a popular tool for measuring gene expression levels for thousands of genes simultaneously, and similar technologies are used for other high-throughput biological studies. However, many sources of variation affect the results and make it difficult to compare measurements from different arrays, and even within the same array.

We review several popular preprocessing methods for microarray data which have the general goal of improving within-array and between-array comparisons, concentrating on the two most used technologies: spotted cDNA arrays and Affymetrix high density oligonucleotide arrays.