

# INTERPRETING MICROARRAY EXPERIMENTS USING FUNCTIONAL GENOMICS

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**Abstract :** The advent of microarray and other “omics” technologies has enabled us to study relative gene expression profiles across a series of conditions, many thousands of genes at a time. However, accurately interpreting the results from microarray experiments has proven to be a nontrivial exercise. Much of the research effort thus far has focused on obtaining gene-specific scores of one kind or another, and in addressing the multiple comparisons issues that arise when studying thousands of genes simultaneously. They have also tended to treat genes individually, essentially ignoring the relationships among the genes. These relationships carry highly relevant information for understanding the biological mechanisms underlying the observed gene expression changes in the genes. With the evolution of gene annotation databases, it has now become feasible to incorporate biological information about genes into the analysis of gene expression data. In this talk, we present a structured approach to incorporating gene function and gene pathway information into the analysis of gene expression data. We create gene function scores based on this information and use these scores to identify important gene categories for a given experiment. We illustrate our approach with a case study from the toxicogenomics area. Our results show that the approaches based on gene function scores yield functionally more interpretable results than methods that rely solely on gene-specific scores.