

## Increasing Experimental Power by Integrating Heterogeneous Biological Datasets

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### Abstract

The identification of gene expression changes (differences in gene activity levels) between biological conditions is an essential step in the search for candidate disease genes, drug targets, and discriminative biomarkers. Unfortunately, a widely used experimental technique for this task—the DNA microarray—is notorious for generating noisy data. One strategy for mitigating the effects of noise is to repeat the experiment many times and average the results, although this is often costly and sometimes impossible given limited resources.

In this talk, I will describe two novel computational methods for more accurately identifying gene expression changes at no additional cost. The first—SVD Augmented Gene expression Analysis Tool (SAGAT)—integrates the vast number of publicly available microarray datasets using matrix decomposition to identify modules of genes with similar expression. The second—Noisy-Or Optimization for Differential Expression analysis (NOODLE)—uses a Bayesian network-based approach to integrate microarray datasets from two important classes of biomolecules (messenger RNAs and microRNAs). I will show how use of these methods can increase experimental power by as much as a factor of three. In addition, my results will demonstrate the improved biological insight gained by integrating heterogeneous datasets.

### About the Speaker

Dr. Bernie J. Daigle, Jr. is an Assistant Professor in the Department of Biological Sciences at the University of Memphis. He received his B.S. in Biology from Cornell University with a concentration in Genetics and Development. His Ph.D. research at Stanford University focused on developing and applying bioinformatics tools that integrate biological knowledge with transcriptomics data. In his postdoctoral work, conducted at the University of California, Santa Barbara, Dr. Daigle continued his bioinformatics research while also beginning projects focused on modeling and analysis of stochastic biochemical systems. At the University of Memphis, Dr. Daigle conducts research in both areas. Current projects in his lab involve the integration of genome-scale datasets to identify biomarkers for human disease and the application of computational methods for characterizing promoter architecture from single-cell gene expression data. In addition to his primary appointment, Dr. Daigle has a secondary appointment in the Department of Computer Science at UofM and is a faculty affiliate with the Bioinformatics Program.

*Lunch in Dunn Hall 336 - 1:30pm*