

# **5<sup>th</sup> Annual Joint Bioinformatics Workshop**

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by

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## ***Making Sense of Large-Scale Microarray Data***

### ***ABSTRACT***

It is now possible to address molecular biological questions simultaneously in the context of entire pathways, gene families, chromosomal location, inferred evolutionary history, or a large array of experimental or field conditions, if those data are integrated properly. Such integration, however, requires increasingly sophisticated data management and analysis tools. Data interpretation requires the effort of the entire research community, drawing on experts for each gene, gene family and pathway. To increase our understanding of function of specific genes and expand our holistic understanding of metabolism, we need software that enables the analysis of disparate data types (microarray, metabolomics and proteomics) in the context of metabolic and developmental networks to propose new insights about gene function. This talk will describe our Plant Expression database for data access and MetNet, an integrated platform for visualization and interpretation of metabolic network data.