

*Application of Bayesian Decomposition to Gene Expression Analysis of Deletion Mutation Data*

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Many methods have been proposed for the analysis of microarray data. In general, these methods are borrowed from data mining and ignore the underlying biology which gives rise to the data. Of particular concern is the failure of the methods in use to allow expression levels for a single gene to be explained as arising from multiple, different stimuli. Bayesian Decomposition, originally developed for mixture analysis, overcomes this problem by permitting the discovered patterns within the expression data to overlap, permitting genes to belong to multiple groups. We present results of the application of Bayesian Decomposition to the deletion mutation data, demonstrating its ability to assign genes which are regulated by multiple pathways to multiple coexpression groups.