

## **Using Non-parametric Methods in the Context of Multiple Testing to Determine Differentially Expressed Genes.**

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CAMDA00 Dataset 2: Leukemia

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Our focus is on the Golub et al. ALL/AML oligo-nucleotide array data set with regard to the question of detecting differentially expressed genes between pairs of sample types. We use this data set to analyze methods of predicting differential expression between ALL T-cells versus ALL B-cells. To this end, we employ recently developed non-parametric methods for attaching statistical measures of confidence to such predictions, in the context of multiple testing. In particular, we apply the method of using t-statistics, with p-values calculated through permutations, and with the Westfall and Young step-down approach to correct for multiple testing, developed by Dudoit et al. We also use PaGE, developed at CBIL, for assigning confidence to predictions by calculating false-positive rates directly from empirical "gene-independent" distributions. We compare the performance of these methods on the Golub et al. data, as well as analyze the effect of the number of replicates on a variety of issues relating to the prediction of differential expression. In addition, we investigate the shape of the scatter plots and conclude that shifted intensities are more reasonable for data such as the Golub et al. data set, when an approach based on ratios is used. We also investigate the usage of "absent calls" in oligo-nucleotide array data.

### **Keywords**

Gene expression, differential expression, microarray, westfall and young, PaGE

### **Tools**

Tools are available at:

<http://www.cbil.upenn.edu/PaGE/> <http://www.cbil.upenn.edu/tpWY/>

### **website**

<http://www.cbil.upenn.edu>