# Simple location models for microarray data

## John Kloke and Patrick Kimes

Department of Mathematics, Pomona College

*E-Mail:* TBP

*Abstract:*   Analysis of microarray experiments has become an important component of biological research. Even though much work has gone into normalization of microarray data, the expression values for many of the genes do not follow a normal distribution. For the genes with heavier tailed distributions, using Wilcoxon or sign scores results in more efficient use of the microarrays. Using simple data-based simulation techniques applied to a null microarray dataset we explore efficiency and power for the one and two sample location problems.