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**Title:** Linear Mixed Model Selection for False Discovery Rate Control in Microarray Data Analysis

**Abstract:**

In a microarray experiment, one experimental design is used to obtain expression measures for all genes. One popular analysis method involves fitting the same linear mixed model for each gene, obtaining gene-specific p-values for tests of interest involving fixed effects, and then choosing a threshold for significance that is intended to control False Discovery Rate (FDR) at a desired level. When some random factors have zero variance components for some genes, the standard practice of fitting the same full linear mixed model for all genes can result in failure to control FDR. We propose a new method which combines results from the fit of full and selected linear mixed models to identify differentially expressed genes and provide FDR control at target levels when the true underlying random effects structure varies across genes.