

MEETING ABSTRACT

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# Empirical Bayesian selection of hypothesis testing procedures for analysis of digital gene expression data

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## Background

Differential expression analysis of digital gene expression data involves performing a large number of hypothesis tests that compare the expression count data of each gene or transcript across two or more biological conditions. The assumptions of any specific hypothesis-testing method will probably not be valid for each of a very large number of genes. Thus, computational evaluation of assumptions should be incorporated into the analysis to select an appropriate hypothesis-testing method for each gene.

## Materials and methods

Here, we generalize earlier work to introduce two novel procedures that use estimates of the empirical Bayesian probability (EBP) of overdispersion to select or combine results of a standard Poisson likelihood ratio test and a quasi-likelihood test for each gene. These EBP-based procedures simultaneously evaluate the Poisson-distribution assumption and account for multiple testing. With adequate power to detect overdispersion, the new procedures select the standard likelihood test for each gene with Poisson-distributed counts and the quasi-likelihood test for each gene with overdispersed counts.

## Results

The new procedures outperformed previously published methods in many simulation studies. We also present a real-data analysis example and discuss how the framework used to develop the new procedures may be generalized to further enhance performance.

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