



Bayesian analysis for multi-subject time course RNA-seq experiments

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We introduce Bayesian methodology for the analysis of multi-subject time course RNA-seq experiments. Our methodology facilitates the study of gene reactions to certain biological processes through time. Specifically, we develop an empirical Bayes approach to detect differentially expressed genes that reduces the high dimensionality of time course data by empirical orthogonal functions. The proposed model assumes distinct distributions for differentially and non-differentially expressed genes, and borrows strength across genes and subjects to increase detection power. We illustrate the usefulness and flexibility of our methodology with an analysis of an RNA-seq dataset from B cells to study their temporal response pattern to the human influenza vaccine.

Keywords: Bayesian analysis; Gene expression analysis; Markov chain Monte Carlo; Massive datasets; Time series RNA-seq.