



THE UNIVERSITY OF
CHICAGO

Department of Statistics

MASTER'S THESIS PRESENTATION

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Joint Analysis of Differential Gene Expression in Multiple Studies
Using Bayesian Method

THURSDAY, February 15, 2018, at 2:00 PM
Jones 304, 5747 S. Ellis Avenue

ABSTRACT

We introduce a new Empirical Bayes approach for jointly analyzing differential gene expression in multiple studies or under multiple experimental conditions. Our method searches for a small number of latent prior distribution vector to capture the major correlation among multiple studies. Compared with existing methods, the new approach improves both power and effect-size estimation. Model fitting procedures are implemented using expectation maximization (EM) algorithm. For application, we analyzed MTB infection dataset and identified a subset of genes whose regulation was affected specifically by mycobacteria.