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CHICAGO

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DISSERTATION PRESENTATION AND DEFENSE

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Generalized Adaptive Shrinkage Methods and Applications in Genomic Studies

MONDAY, August 20, 2018, at 2:00 PM
Jones 304, 5747 S. Ellis Avenue

ABSTRACT

Shrinkage procedures have played an important role in helping improve estimation accuracy for a variety of applications. In genomics studies, the gene-specific sample statistics are usually noisy, especially when sample size is limited. Hence some shrinkage methods (e.g. “limma”) have been proposed to increase statistical power in identifying differentially expressed genes. Motivated by the success of shrinkage methods, Stephens (2016) proposed a novel approach, Adaptive Shrinkage (ASH) for large-scale hypothesis testing including false discovery rate and effect size estimation, based on the fundamental “unimodal assumption” (UA) that the distribution of the actual unobserved effects has a single mode.

Even though ASH primarily dealt with normal or student-t distributed observations, the idea of UA can be widely applied to other types of data. In this dissertation, we propose a general flexible Bayesian shrinkage framework based on UA, which is easily applicable to a wide range of settings. This framework allows us to deal with data involving other noise distributions (gamma, F, Poisson, binomial, etc.). We illustrate its flexibility in a variety of genomics applications including: differential gene expression analysis on RNA-seq data; comparison between bulk RNA-seq and single cell RNA-seq data; gene expression distribution deconvolution for single cell RNA-seq data, etc.