Statistics Seminar

Department of Mathematics and Statistics

DATE:	Thursday, March 5, 2026
TIME:	1:30pm – 2:30pm
LOCATION:	WH 100E
SPEAKER:	Aliu Adebiyi, Binghamton University
TITLE:	Bayesian hierarchical pathway-structured model for RNA-seq differential expression

Abstract

High-throughput RNA-seq experiments routinely measure thousands of genes across experimental conditions, but many standard differential expression (DE) tools, such as DESeq2 and limma–voom, treat genes as exchangeable units and ignore known biological pathway structure. In this project I develop and evaluate a Bayesian hierarchical pathway-structured model for bulk RNA-seq DE analysis in a two-group setting, using the airway dataset as a real-data case study. The model operates on voom-transformed log-expression values and introduces pathway-specific random effects on gene-level log fold changes, allowing genes within the same pathway to borrow strength primarily from each other while retaining gene-specific variability. I compare posterior gene-level and pathway-level summaries to DESeq2 and limma-voom on the airway data, and conduct a simulation study mimicking the airway design to assess power, false discovery rate, and effect-size estimation accuracy under known pathway-structured truth. The results suggest that the proposed Bayesian model achieve gene-level effect estimates that agree closely with DESeq2 and limma-voom, provide interpretable pathway-level posterior summaries, and offer competitively improved operating characteristics in simulations, particularly in terms of error control and shrinkage-informed estimation.

NOTE: It is an ongoing research that still needs room for advanced improvement for publication.