



RNA Innovation Seminar
Monday, October 1st at 3:00pm
ABC Seminar rooms, Biomedical Research
Science Building (BSRB), 109 Zina Pitcher

Shiquan Sun, PhD is a postdoctoral research fellow from Xiang Zhou's group in Department of Biostatistics. He is interested in developing novel analytical approaches to model or analyze differential expression in bisulfite sequencing, bulk RNA sequencing or single-cell RNA sequencing data.

“Heritability estimation and differential analysis of count data with generalized linear mixed models in genomic sequencing studies”

Abstract:

Large-scale genomic sequencing studies provide great opportunities to accurately model molecular trait-related heritability estimation and differential expression (DE) analysis, including RNA sequencing and bisulfite sequencing studies etc. Heritability estimation and differential analysis in sequencing studies require the development of statistical methods that can properly account for the count nature of the sequencing data and that is computationally efficient for large datasets. Here, we develop a method, PQLseq (Penalized Quasi-Likelihood for sequencing count data), to enable effective and efficient heritability estimation and differential analysis within the generalized linear mixed model framework. With extensive simulations and real data applications, we show that PQLseq is the only method currently available that can produce unbiased heritability estimates for sequencing count data, and is well suited for differential analysis in large sequencing studies, providing calibrated type I error control and more power DE detection. Our method is implemented in the PQLseq R package, freely available at www.xzlab.org/software.html and CRNA.