Title: Sequencing depth, local sequence and RNA-seq differential analysis

**Speaker:** Guoshuai Cai

**Abstract:** RNA-seq is a common technique for surveying RNA expression. Because sequencing read counts from individuals often show dispersion of measurements significantly larger than that given by Poisson distribution, fine modeling on this so-called overdispersion is required for RNA-seq data analysis. Various methods have been proposed for RNA-seq differential expression detection, each with its own limitations. Here we asked (1) how is the dispersion between technical replicates? (2) is the dispersion specific to each base pair? and (3) how to model mRNA abundance to unlock the integration with numerous established upstream and downstream analyses? To answer these three questions, we studied the properties of RNA-seq read count including its dependency with sequencing depth and local primer sequence. Based on our findings, we propose models for accurate detection of differential expression from RNA-seq data.