On Methods for Normalizing Single-Cell RNA-Seq Data

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Abstract:

High levels of technical variability and artifacts in single-cell RNA-sequencing data (scRNA-seq) present challenges for accurately conducting downstream analyses. In this talk, I will illustrate the motivations for the considerable efforts devoted to overcoming these challenges including methods for normalization. I will introduce SCnorm - a quantile regression framework that enables accurate normalization for scRNA-seq data and establishes a novel evaluation criterion. Finally, I will discuss our ongoing efforts to develop normalization methods that are scalable, robust, and applicable to all scRNA-seq platforms.