Splicing analysis in single-cell RNA-seq

Guido Sanguinetti*[1]

[1]University of Edinburgh – University of Edinburgh, University of Edinburgh – France

Abstract

Single-cell omics technologies have revolutionised our understading of stochasticity and heterogeneity in gene expression. So far, these technology have not been prominently used to assay variability at the transcript, rather than gene, level; this is because technical difficulties in RNA capture lead to a high level of missing data, so that identify and quantify the different splicing isoforms within a cell is challenging. Here, we take a Bayesian approach and attack the isoform quantification problem by also learning a regression prior which informs splicing quantification based on sequence content. We introduce BRIE, Bayesian Regression for Isoform Estimation, and show that it leads to robust and reproducible splicing estimate quantifications on both simulated and real single cell RNA-seq data sets.

*Speaker