

**Scalable Bioinformatics Methods for Single-cell RNA-seq Analysis**

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Single-cell RNA sequencing (scRNA-seq) enables gene expression profiling of hundreds of thousands of individual cells. This has opened up new opportunities in all areas of biological and biomedical research. Yet, there are a number of analytical challenges associated with analysing scRNA-seq data. In this talk, we will discuss two major challenges - scalability and dropouts - and some bioinformatics methods developed by our laboratory to deal with these challenges.