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*Cell Type Identification in Single-cell Genomics and its  
Applications*

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**Abstract:** Advances in techniques for measuring genomics in cell-level resolution provide great opportunities to reveal the cell heterogeneity. When dealing with single-cell genomics sequencing data, the most fundamental and critical step is to accurately identify cell types (celltyping). Once cell types are identified, the understanding of cell signatures, cellular composition and cell dynamics can broaden the knowledge of biological processes and potentially cure diseases. Traditional approaches of celltyping in single-cell genomics data are based on unsupervised clustering, expert's knowledge, and manual curation, which are labor intensive. With continuous accumulation of high-quality single-cell genomics data, supervised celltyping becomes more and more popular due to its accuracy, robustness, and efficiency. In this seminar, the speaker will first introduce a benchmark study in supervised celltyping in single-cell RNA-sequencing data. Based on the experience gained from the benchmark study, the speaker will then introduce the supervised celltyping methods specifically developed for single-cell chromatin accessibility (scATAC-seq) data. Finally, with the accurately identified cell types, the speaker will introduce a method developed to identify cellular activity in bulk differential expression study with the usage of cell-type-specific marker information.

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