Cellular deconvolution with single-cell DNA methylation and RNA sequencing references



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Bulk tissue omics such as transcriptomics and epigenomics usually have larger sample sizes than single-cell data, but they reflect the average values across diverse cell types and are highly influenced by cellular fractions. It is thus critical to estimate cellular fractions to both deconfound differential analyses and infer cell type-specific (CTS) omics from bulk data. In this talk, Dr. Wang will introduce two new methods that integrate single-cell and tissue-level omics data: 1) HiDecon (Hierarchical Deconvolution), a coordinate-wise descent algorithm that uses single-cell RNA-seq references and a hierarchical cell type tree to estimate rare cellular fractions in bulk data; 2) scMD (single cell Methylation Deconvolution) that reliably estimates cellular fractions from tissue-level DNA methylation data with ultrahigh dimensional and ultra-sparse single-cell DNA methylation references. If time allows, he will demonstrate that the estimated cellular fractions enable CTS downstream analyses that gain population-level CTS insights.

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