High-throughput, single-cell RNA sequencing recently emerged as a powerful tool to profile complex and heterogeneous populations as well as individual isolated cells. The talk will address the single-cell sequencing workflow from cell preparation through cell capture, library preparation, sequencing, and data processing and visualization. Strategies will be defined for enhanced cell enrichment, thereby increasing the purity of the isolated cell and decreasing the costs of sequencing. Additionally, BD AbSeq, a novel protein sequencing approach enabled by oligo-conjugated antibodies, for simultaneous detection of mRNA and protein in single cells will be introduced.

A series of standardized experiments that align both flow cytometry and genomic cytometry using a normal mouse model will also be discussed. Comparison of mRNA and protein expression revealed distinct expression profiles for many genes and underscores the importance of multi-omic analysis in single cells. Our study demonstrates the power of combining the BD AbSeq technology with RNA-seq to gain a more comprehensive understanding of cell lineage and function at the single-cell level.

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