

BIOF 048: Singe Cell RNA Seq Analysis

Bulk transcriptomes have provided considerable insights and fostered the discovery and characterization of GRN (Gene Regulatory Network)s. However, bulk transcriptomes provide population-based averaged measurements which blur cell heterogeneity and developmental dynamics of asynchronous cell populations. Single-cell transcriptome technologies (scRNA-seq) capture cell heterogeneity and thus are useful for the discovery of cell populations, identification of cell mutants, and quantification of subpopulations. Leveraging on the ability of generating thousands of individual measurements from scRNA-seq, lots of methods have been developed to capture spatial or temporal information from cell populations. This workshop will introduce basic steps of the scRNA-seq processing, starting from fastq coming off 10x sequencer to spatial and temporal analysis using popular R packages. Then, we will discuss case studies that can be addressed using scRNA-seq.

Class Type: Workshop

Program: Bioinformatics and Data Science