"Integrated analysis of multimodal single-cell data"

Abstract: Massively parallel, multi-modal technologies represent an exciting opportunity to move beyond the transcriptome, and explore how multiple aspects of cellular identity define behavior and function. We introduce a new computational framework 'weighted-nearest neighbor' analysis, that learns the relative information content of each modality in each cell, and constructs a joint neighbor graph that integrates the complementary data types together. When applied to a CITE-seq dataset simultaneously profiling cellular transcriptomes and hundreds of surface proteins, our work characterizes the extensive multimodal heterogeneity in human blood, and demonstrates the necessity of defining cellular states from multiple perspectives.

Rahul Satija, PhD, is a Core Member and Assistant Investigator at the New York Genome Center, with a joint appointment as Assistant Professor at Center for Genomics and Systems Biology at NYU. Dr. Satija's group focuses on developing computational and experimental methods to sequence and interpret the molecular contents of a single cell. His group applies single cell genomics to understand the causes and consequences of cell-to-cell variation, with a particular focus on immune regulation and early development. His group has developed and maintained the R package Seurat for the analysis, exploration, and integration of single-cell data. Dr. Satija holds a BS in Biology and Music from Duke University, and obtained his PhD in Statistics from Oxford University as a Rhodes Scholar. Prior to joining NYGC, he was a postdoctoral researcher at the Broad Institute of Harvard and MIT, where he developed new methods for single cell analysis.