1. 10X Genomics Single Cell Multiome ATAC + Gene Expression

Video: https://www.youtube.com/watch?v=rjke1BWcyBA

Info page: https://www.10xgenomics.com/products/single-cell-multiome-atac-plus-gene-expression

2. CITE-seq

Video: https://www.youtube.com/watch?v=2f8ptGrAGak

Info page: https://cite-seq.com/

OG publication: https://www.nature.com/articles/nmeth.4380

the three types of datasets are all processed to a pretty large degree:

1. scATAC-seq (chromatin accessibility) is TF-IDF normalized

Background:
https://en.wikipedia.org/wiki/Tf%E2%80%93idf#External_links_and_suggested_reading

Code:
https://muon.readthedocs.io/en/latest/api/generated/muon.atac.pp.tfidf.html?highlight=tfidf

2. scRNA-seq (gene expression) is library-size normalized or log1p normalized
Background/discussion from Seurat: https://github.com/satijalab/seurat/issues/3630

Code: https://scanpy.readthedocs.io/en/stable/generated/scanpy.pp.normalize_per_cell.html

3. CITE-seq (surface protein Levels) is denoised and scaled by background

Background: https://cran.r-project.org/web/packages/dsb/readme/README.html

Code: https://muon.readthedocs.io/en/latest/omics/citeseq.html#dsb